

Supplementary Table S2-1 LC-MS/MS identification of plasma membrane proteins in *Arabidopsis* suspension cultured cells (T87 line) at lag phase (8-day-old)

AGI	Accession	Protein description	Functional categories	Cys	Calc. grav y	TMHMM	Aramemnon	Calc.M W	TargetP	Curated Loc.	TAIR Loc.	GFP/YFP loc.	PI	Calc.PI	protein score
At2g21130	gi 2443757	cyclophilin	cell growth/division	4	-0.249	0		18.46					6.11	8.32	43
At1g54690	gi 15221875	GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	cell growth/division	0	-0.251	0		14.78	C				9.93	10.34	34
At2g30620	gi 15224536	histone H1.2	cell growth/division	0	-0.606	0		28.49				15496452(nucleus - SUBA); 15496452(unclear - SUBA);	10.83	10.34	105
At4g27230	gi 21617982	histone H2A-like protein	cell growth/division	0	-0.264	0		13.83	M				5.83	10.05	51
At1g07790	gi 21617908	histone H2B	cell growth/division	0	-0.810	0		16.40		nucleus		16195344(nucleus - SUBA);	6.13	10.34	71
At5g22880	gi 1617013	histone H2B like protein	cell growth/division	0	-0.678	0		15.73		nucleus		16463096(nucleus - SUBA); 11251092(nucleus - SUBA);	10.34	10.05	24
At2g37470	gi 15224292	histone H2B, putative	cell growth/division	0	-0.654	0		15.08		nucleus			6.13	10.34	71
At5g65350	gi 15238430	histone H3	cell growth/division	1	-0.537	0		15.59	C	nucleus			7.71	10.34	44
At2g05210	gi 4755192	hypothetical protein	cell growth/division	17	-0.207	0		53.92					9.01	6.54	319
At5g57970	gi 15242914	methyladenine glycosylase family protein	cell growth/division	4	-0.468	0		38.65	C				6.32	5.26	23
At3g57150	gi 15230232	NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase	cell growth/division	6	-0.716	0		63.03					5.01	7.14	35
At3g13210	gi 10172609	probable cell cycle control protein; crooked neck-like protein	cell growth/division	11	-0.751	0		78.10					5.83	6.82	51
At4g29090	gi 2583130	putative non-LTR retroelement reverse transcriptase	cell growth/division	12	-0.390	0		66.71	S				5.64	9.33	27
At5g62410	gi 12382276	SMC2-1	cell growth/division	12	-0.589	0		132.60					10.09	7.14	32
At1g31970	gi 15222526	STRS1 (STRESS RESPONSE SUPPRESSOR 1); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid	cell growth/division	6	-0.468	0		59.60					10.34	7.14	24
At5g03340	gi 11265361	transitional endoplasmic reticulum ATPase - Arabidopsis thaliana	cell growth/division	14	-0.384	0		89.96					10.6	5.08	374
At5g37140	gi 15240114	tRNA-splicing endonuclease positive effector-related	cell growth/division	14	-0.228	0		77.29					8.39	7.14	15
At3g46520	gi 15231447	ACT12 (ACTIN-12); structural constituent of cytoskeleton	cell structure	4	-0.222	0		41.80			mitochondrion & cytoskeleton		5.01	6.44	35
At1g68560	gi 4163997	alpha-xylosidase precursor	cell structure	11	-0.213	0		102.40	S		cell wall (sensu Magnoliophyta)		6.32	7.05	69
At5g15500	gi 15242318	ankyrin repeat family protein	cell structure	3	0.003	4	4	39.69	S				9.33	6.44	55
At5g65020	gi 15238320	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding	cell structure	2	-0.526	0		36.27					5.67	6.44	22
At1g35720	gi 1429207	annexin	cell structure	2	-0.603	0		36.20		plastid	cytosol & membrane		7.7	5.21	110
At5g16970	gi 15237888	AT-AER (alkenal reductase); 2-alkenal reductase	cell structure	5	-0.096	0		38.13			cytosol & nucleus	16299173(cytosol - SUBA); 16299173(nucleus - SUBA);	6.06	5.26	28
At5g42100	gi 15238298	ATBG_PAP; glucan endo-1,3-beta-D-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	cell structure	6	0.065	1		45.36	S		cell wall (sensu Magnoliophyta) & anchored to	17270015(endoplasmic reticulum - SUBA); 17270015(plasma membrane -SUBA);	7.03	8.93	54
At1g75680	gi 15222328	AtGH9B7 (Arabidopsis thaliana glycosyl hydrolase 9B7); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	cell structure	5	-0.329	1	1	57.87	S				6.77	7.14	1867
At1g53840	gi 15220958	ATPME1; pectinesterase	cell structure	8	-0.211	1	1	64.15					8.53	9.01	1043

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At3g14300	gi 15231826	ATPMEPCRC; pectinesterase	cell structure	16	-0.187	1	1	105.63					9.49	9.01	19
At1g01980	gi 15217586	ATSEC1A; FAD binding / catalytic/ electron carrier/ oxidoreductase	cell structure	8	-0.219	0		60.10	S				4.85	9.01	429
At1g66250	gi 12323569	beta-1,3-glucanase precursor, putative; 34016-35272	cell structure	6	0.042	0		54.21	S		anchored to		6.32	5.46	23
At3g13560	gi 9280308	beta-1,3-glucanase-like protein	cell structure	7	0.053	1		54.42	S	plasma membrane	anchored to		10.07	5.9	85
At5g20230	gi 16203	blue copper-binding protein	cell structure	3	0.197	0	1	20.05	S		anchored to	16143720(plasma membrane -SUBA);	10.03	4.68	1085
At1g32860	gi 6910583	CDS	cell structure	1	0.006	1		45.42	S	plasma membrane	anchored to		10.09	7.75	95
At3g20130	gi 15231052	CYP705A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen	cell structure	7	-0.091	1	3	58.71	S				6.32	9.1	23
At4g37410	gi 15235541	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen	cell structure	6	-0.140	1		57.17	S				4.97	9.1	29
At5g42080	gi 2267213	dynammin-like GTP binding protein	cell structure	6	-0.276	0		68.17			thylakoid membrane (sensu Viridiplant ae) & microtubul e & cell	14750520(cytoskelet on -SUBA); 12671086(plasma membrane -SUBA); 9463364(plastid - SUBA);	10.12	8.47	443
At1g70710	gi 2440033	endo-1,4-beta-glucanase	cell structure	6	-0.192	1		54.61	S				10.53	9.33	405
At1g74790	gi 5882745	F25A4.24	cell structure	28	-0.310	2	1	75.23	S	plasma membrane	anchored to		5.09	6.44	2561
At4g20830	gi 30685222	FAD-binding domain-containing protein	cell structure	4	-0.151	1		63.56	S		cell wall (sensu Magnoliop hyta)		9.61	9.01	4343
At4g12730	gi 13377778	fasciclin-like arabinogalactan-protein 2	cell structure	3	-0.076	0		43.45	S	plasma membrane	anchored to		9.78	6.14	149
At5g55730	gi 15240570	FLA1 (FASCICLIN-LIKE ARAB INO GALACTAN 1)	cell structure	4	-0.039	0		44.85	S	plasma membrane	anchored to		6.26	8.93	4367
At5g44130	gi 15241423	FLA13 (FASCICLIN-LIKE ARABINO GALACTAN PROTEIN 13 PRECURSOR)	cell structure	1	0.016	0		26.21	S	plasma membrane	cell wall (sensu Magnoliop hyta) & anchored to		8.32	8.93	102
At2g04780	gi 18395849	FLA7 (FASCICLIN-LIKE ARABINO GALACTAN 7)	cell structure	1	0.161	0		26.85	S	plasma membrane	anchored to		6.06	8.93	1712
At2g45470	gi 18406799	FLA8 (FASCICLIN-LIKE ARABINO GALACTAN PROTEIN 8)	cell structure	2	0.130	0	1	43.08	S	plasma membrane	anchored to		5.43	8.93	1768
At1g03870	gi 18379157	FLA9 (FASCICLIN-LIKE ARABINO GALACTAN 9)	cell structure	1	0.000	0		26.12	S		anchored to		8.93	8.93	534
At4g31140	gi 15235840	glycosyl hydrolase family 17 protein	cell structure	7	0.061	1		52.72	S	plasma membrane	anchored to		7.92	8.93	825
At5g18220	gi 15238768	glycosyl hydrolase family 17 protein	cell structure	7	-0.127	1		53.87	S		anchored to		7.92	8.93	825
At5g56590	gi 15241268	glycosyl hydrolase family 17 protein	cell structure	10	-0.158	0		55.60	S		anchored to		7.92	8.93	825
At5g58480	gi 30697080	glycosyl hydrolase family 17 protein	cell structure	6	-0.087	1		52.37	M		anchored to		7.92	8.93	825
At2g01630	gi 18379267	glycosyl hydrolase family 17 protein / beta- 1,3-glucanase, putative	cell structure	7	0.099	0		53.99	S	plasma membrane	anchored to		5.78	8.93	923
At3g47040	gi 15232711	glycosyl hydrolase family 3 protein	cell structure	10	-0.101	0		69.65					6.13	7.14	4754
At5g04885	gi 30680681	glycosyl hydrolase family 3 protein	cell structure	12	-0.022	0		72.30	S		anchored to		6.13	7.14	4754
At5g20940	gi 22326918	glycosyl hydrolase family 3 protein	cell structure	9	-0.038	0		67.65	S				6.13	7.14	4754

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At2g30870	gi 15224582	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione	cell structure	0	-0.075	0	1	24.23	S	not plastid			6.32	10.34	23
At4g34830	gi 11074037	hypothetical protein	cell structure	22	-0.252	1	1	119.77	C	plastid			5.23	8.06	82
At5g10890	gi 15238287	myosin heavy chain-related	cell structure	4	-0.827	0		34.28	_				9.66	6.44	26
At4g13010	gi 15235549	oxidoreductase, zinc-binding dehydrogenase family protein	cell structure	4	0.035	0		34.44	_	envelope- inner- peripheral- stromal-side	thylakoid membrane (sensu Viridiplant ae)	12368288(plastid - SUBA);	6.11	5.26	17
At5g61130	gi 30697478	PDCB1 (PLASMODESMATA CALLOSE-BINDING PROTEIN 1); callose binding / polysaccharide binding	cell structure	10	-0.122	0		20.37	S		cell wall (sensu Magnoliop hyta) & anchored to		6.06	8.93	28
At5g48450	gi 8777375	pectinesterase-like protein	cell structure	4	-0.193	0		61.10	S				8.66	5.26	231
At3g49120	gi 405611	peroxidase	cell structure	9	-0.077	0		38.83	S		cell wall (sensu Magnoliop hyta)	16284776(extracellu lar -SUBA);	9.57	7.57	322
At5g17820	gi 15238030	peroxidase 57 (PER57) (P57) (PRXR10)	cell structure	8	-0.105	1		34.10	S		cell wall (sensu Magnoliop hyta)		10.1	9.08	507
At5g64100	gi 15237613	peroxidase, putative	cell structure	8	-0.073	1		35.68	S				9.47	9.08	308
At4g31840	gi 15236544	plastocyanin-like domain-containing protein	cell structure	3	0.076	2	1	18.96	S		anchored to		8.99	5.26	1746
At5g15350	gi 15242279	plastocyanin-like domain-containing protein	cell structure	2	0.008	2	1	19.44	S		anchored to		8.99	5.26	1746
At5g25090	gi 15238698	plastocyanin-like domain-containing protein	cell structure	3	0.099	1		19.77	S	plasma membrane	anchored to		8.99	5.26	1746
At5g53870	gi 15238868	plastocyanin-like domain-containing protein	cell structure	3	-0.492	1		38.40	S		anchored to		8.99	5.26	1746
At1g42550	gi 24025422 0	PMI1 (PLASTID MOVEMENT IMPAIRED1)	cell structure	5	-0.626	0		78.95	S	plasma membrane			8.84	6.44	47
At4g25240	gi 4454012	Pollen-specific protein precursor like	cell structure	5	-0.168	1		65.88	S	plasma membrane	anchored to plasma membrane & anchored to		6.56	5.26	1248
At1g62790	gi 15221585	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	cell structure	8	0.308	2		15.71	S		anchored to		6.52	9.01	520
At2g13820	gi 15225509	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	cell structure	8	0.620	0	1	16.82	S				6.52	9.01	520
At2g03430	gi 4335756	putative ankyrin	cell structure	3	-0.191	0		25.92	_				6.32	6.44	23
At2g33240	gi 20196856	putative myosin heavy chain	cell structure	34	-0.496	0		200.64	S				10.7	5.56	1510
At2g34730	gi 3132472	putative myosin heavy chain	cell structure	9	-0.711	0		94.61	_		mitochond rion		4.97	6.44	29
At3g06830	gi 39104585	putative pectin methylesterase	cell structure	11	-0.190	1	1	61.89	S				6.13	8.87	71
At3g58100	gi 6735322	putative protein	cell structure	7	-0.074	2		19.17	S		anchored to		5.32	8.93	4660
At4g03340	gi 7529254	putative protein	cell structure	5	-0.283	1	1	51.67	M				5.76	8.59	242
At4g03230	gi 4262151	putative receptor kinase	cell structure	24	-0.254	0	1	96.20	S				10.11	8.27	39
At3g08900	gi 6403494	putative reversibly glycosylatable polypeptide	cell structure	9	-0.213	0		41.28	_			15879561(golgi - SUBA); 15879561(unclear - SUBA);	8.76	9.08	16
At2g25060	gi 4559346	similar to early nodulins	cell structure	4	0.165	0		19.48	S	plasma membrane	anchored to		10.7	6.82	516

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At1g64760	gi 5042412	Similar to glucan endo-1,3-beta-glucosidase precursor	cell structure	7	0.029	2	1	52.28	S	plasma membrane	anchored to		4.94	8.93	589
At4g00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19	cell structure	11	-0.305	0		45.20	S	plasma membrane			12.24	6	198
At5g51480	gi 15242108	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase	cell structure	3	-0.205	1		66.41	S	plasma membrane	anchored to		5.87	5.26	1265
At2g19130	gi 15224721	S-locus lectin protein kinase family protein	cell structure	21	-0.247	1	1	92.34	S				7.03	8.27	54
At3g46550	gi 15231453	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding	cell structure	3	0.367	1	2	44.24	S	plasma membrane	external side of plasma membrane & anchored to		5.57	8.93	383
At5g19770	gi 15241168	TUA3; structural constituent of cytoskeleton	cell structure	11	-0.154	0		49.66					4.95	6.44	723
At4g20890	gi 15233429	TUB9; GTP binding / GTPase/ structural molecule	cell structure	12	-0.332	0		49.66				10737809(nucleus - SUBA);	4.69	6.44	360
At4g27520	gi 21592865	unknown	cell structure	2	-0.313	1		35.06	S		anchored to		9.26	5.26	2334
At1g78830	gi 17644159	unknown protein	cell structure	12	-0.313	1		50.34	S		cell wall (sensu Magnoliophyta)		4.86	8.27	1983
At5g64080	gi 10176956	unnamed protein product	cell structure	8	0.643	2	2	17.97	S		anchored to		8.61	9.01	469
At1g11330	gi 5734724	Very similar to receptor-like protein kinase	cell structure	24	-0.247	1	1	94.15	S	plasma membrane			10.04	8.27	1067
At4g01700	gi 15234281	chitinase, putative	disease/defence	8	-0.396	0		31.47	S				9.04	6.26	1063
At1g20440	gi 388259	cor47	disease/defence	0	-1.249	0		29.90				10737809(cytosol - SUBA); 10737809(nucleus - SUBA);	6.9	10.34	61
At1g32090	gi 15222569	early-responsive to dehydration protein-related / ERD protein-related	disease/defence	6	0.031	7	8	93.13	S	plasma membrane			9.11	9.1	627
At1g30360	gi 18397470	ERD4 (early-responsive to dehydration 4)	disease/defence	7	0.298	10	10	81.94	S				9.28	9.1	2326
At1g12280	gi 8778651	F5O11.3	disease/defence	26	-0.133	0		102.64	S				10.12	6.04	341
At2g43610	gi 15224319	glycoside hydrolase family 19 protein	disease/defence	16	-0.171	1		30.00	S				4.68	6.26	97
At3g09440	gi 15232682	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	disease/defence	8	-0.394	0		71.15			cytosol		4.97	9.01	256
At4g23670	gi 15236566	major latex protein-related / MLP-related	disease/defence	2	-0.742	0		17.52					5.95	10.34	40
At5g22060	gi 535588	putative	disease/defence	11	-0.773	0		46.44				10737809(peroxisome -SUBA);	9.66	9.01	26
At3g11010	gi 6016693	putative disease resistance protein	disease/defence	10	-0.135	1	1	99.02					10.49	6.12	135
At4g23260	gi 3021278	putative protein	disease/defence	16	-0.059	1	1	72.77	S				6.6	5.76	38
At5g43470	gi 32364507	resistance protein Hod3	disease/defence	17	-0.276	0		104.68					5.52	6.26	25
At5g47910	gi 3242789	respiratory burst oxidase protein D	disease/defence	10	-0.241	4	5	103.91					10.58	9.27	1087
At1g12210	gi 15221250	RFL1 (RPS5-like 1); ATP binding / protein binding	disease/defence	29	-0.166	0		101.45					8.39	6.26	15
At1g20780	gi 42562204	SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein	disease/defence	14	-0.016	0		88.38					6.59	6.26	21
At4g02450	gi 3193303	T14P8.5	disease/defence	1	-0.532	0		25.47					8.32		53
At3g53990	gi 30693971	universal stress protein (USP) family protein	disease/defence	2	-0.168	0		17.79					8.84	6.44	47
AtCg00120	gi 7525018	ATP synthase CF1 alpha subunit	energy	1	-0.048	0		55.33		thylakoid-peripheral-stromal-side	thylakoid membrane (sensu Viridiplantae) & chloroplast ATP synthase complex	10737809(nucleus - SUBA);	5.19	8.93	587

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AtCg00480	gi 7525040	ATP synthase CF1 beta subunit	energy	1	-0.090	0		53.94	_	thylakoid-peripheral-stromal-side	thylakoid membrane (sensu Viridiplantae) & proton-transporting ATP synthase, catalytic core		5.38	8.93	663
At3g04120	gi 166706	cystolic glyceraldehyde-3-phosphate dehydrogenase	energy	2	-0.129	0		36.92	_	not plastid	cytosol & mitochondrion	10737809(cytosol - SUBA);	11.04	6.62	523
At3g55440	gi 414550	cytosolic triose phosphate isomerase	energy	4	0.076	0		27.17	_	not plastid	mitochondrion		5.24	5.26	316
At1g02180	gi 30678256	ferredoxin-related	energy	11	0.117	0		24.79	S				7.05	7.05	560
At1g65930	gi 15218869	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	energy	6	-0.321	0		45.75	_				6.13	7.14	71
At4g32840	gi 15233959	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase	energy	7	-0.170	0		50.79	_				9.26	9.1	18
At1g79550	gi 15219412	PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase	energy	1	0.134	0		42.13	_				5.49	8.93	94
At5g09600	gi 2864622	putative protein	energy	1	-0.032	1	1	23.45	M		mitochondrion		5.32	8.93	4660
AtCg00490	gi 1944432	ribulosebiphosphate carboxylase	energy	9	-0.272	0		52.96	_	plastid stroma	thylakoid membrane (sensu Viridiplantae) & chloroplast		6.32	9.08	23
At3g56190	gi 15228848	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein	intracellular traffic	8	-0.517	0		32.76	_				5.21		1224
At1g17620	gi 11762174	At1g17620	intracellular traffic	8	-0.017	1	1	28.29	_	plasma membrane			9.95		103
At5g03540	gi 22326587	ATEXO70A1 (exocyst subunit EXO70 family protein A1); protein binding	intracellular traffic	3	-0.395	0		72.30	_				6.06	4.74	28
At5g08680	gi 22326673	ATP synthase beta chain, mitochondrial, putative	intracellular traffic	3	-0.143	0		59.86	M	mitochondria	mitochondrion		6.06	4.19	399
At5g64370	gi 9759413	beta-ureidopropionase	intracellular traffic	8	-0.298	0		45.55	_	cytosol			5.97	9.01	161
At3g08530	gi 12321552	clathrin heavy chain, putative	intracellular traffic	22	-0.171	0		193.27	_				10.92	5.25	42
At1g71820	gi 7239509	EST gb AA712174 comes from this gene	intracellular traffic	13	-0.324	0		85.68	_				6.96		36
At2g33120	gi 600710	formerly called HAT24; synaptobrevin-related protein	intracellular traffic	6	-0.122	1	1	24.93	S	plasma membrane	endosome & plasma membrane	15342965(plasma membrane -SUBA); 15610358(unclear - SUBA);	10.92	9.07	128
At3g17440	gi 18401508	NPSN13 (NOVEL PLANT SNARE 13)	intracellular traffic	3	-0.548	1	1	30.41	_	plasma membrane		15342965(plasma membrane -SUBA);	5.52	4.74	25
At4g21450	gi 3080389	putative membrane associated protein	intracellular traffic	1	-0.882	0		32.96	_	plasma membrane			9.93	9.39	73
At5g12370	gi 14586367	putative protein	intracellular traffic	10	-0.166	0		89.70	_				5.32		4660
At2g32670	gi 2914706	putative synaptobrevin	intracellular traffic	7	-0.038	2	1	32.69	S		endosome & plasma membrane	15342965(plasma membrane -SUBA);	9.06	4.74	481
At4g15780	gi 27805752	RecName: Full=Vesicle-associated membrane protein 724; Short=AtVAMP724; AltName: Full=SYBL1-like protein	intracellular traffic	3	-0.439	0		22.15	_		plasma membrane	15342965(plasma membrane -SUBA);	11.57	9.31	181
At3g10380	gi 18398855	SEC8 (SUBUNIT OF EXOCYST	intracellular traffic	10	-0.266	0		116.61	_				8.76	4.74	16

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At3g52400	gi 5701797	syntaxin protein	intracellular traffic	4	-0.544	1	1	37.84	_	plasma membrane	plasma membrane	15342965(plasma membrane -SUBA);	9.95	8.57	333
At3g11820	gi 15229865	SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor	intracellular traffic	3	-0.573	1	1	37.96	_	plasma membrane	plasma membrane	1510001862300000 44(plasma membrane -SUBA); 16570657(plasma membrane -SUBA); 15703292(plasma membrane -SUBA); 15342965(plasma membrane -SUBA);	9.06	4.74	862
At5g08080	gi 18415701	SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor	intracellular traffic	2	-0.556	1	1	34.23	_	plasma membrane		18088326(plasma membrane -SUBA); 15342965(plasma membrane -SUBA);	6.09	4.74	1771
At3g09740	gi 18398623	SYP71 (SYNTAXIN OF PLANTS 71); protein transporter	intracellular traffic	3	-0.515	1	1	29.98	_	plasma membrane	integral to membrane	15342965(endoplas mic reticulum -	5.09	4.74	1179
At1g45688	gi 18401556	unknown protein	intracellular traffic	4	-0.352	1	1	37.20	C	plasma membrane			4.86		1983
At1g76850	gi 12322227	unknown protein	intracellular traffic	15	-0.462	0		121.90	_	plasma membrane			10.78		100
At3g08600	gi 18398173	unknown protein	intracellular traffic	4	-0.092	1	1	34.73	M				4.86		1983
At3g17350	gi 15229029	unknown protein	intracellular traffic	18	-0.210	0		31.22	S				4.86		1983
At4g28100	gi 18417127	unknown protein	intracellular traffic	16	0.044	2	1	33.10	S		anchored to		4.86		1983
At4g31130	gi 15235839	unknown protein	intracellular traffic	4	0.433	4	3	20.75	S				4.86		1983
At5g11890	gi 15239804	unknown protein	intracellular traffic	8	-0.236	1	1	31.44	C				4.86		1983
At5g19230	gi 15239685	unknown protein	intracellular traffic	6	0.244	1	2	20.51	S		anchored to		4.86		1983
At5g62630	gi 14423506	Unknown protein	intracellular traffic	28	-0.370	0		75.62	S		anchored to		8.34		33
At1g21380	gi 18394983	VHS domain-containing protein / GAT domain-containing protein	intracellular traffic	5	-0.647	0		55.79	_				4.85	4.74	429
At5g58060	gi 15242933	YKT61	intracellular traffic	4	-0.413	0		22.54	S			15342965(unclear - SUBA);	6.96	4.74	119
At5g36880	gi 14532364 5	acetyl-CoA synthetase, putative / acetate- CoA ligase, putative	metabolism	16	-0.172	0		76.73	C	plastid stroma			10.09	5.93	95
At5g11520	gi 15239078	ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-	metabolism	4	-0.103	0		48.96	C	peroxisome	plastid		5.01	5.26	35
At5g58090	gi 16604491	AT5g58090/k21119_70	metabolism	8	-0.043	0		52.21	M	plasma membrane	anchored to		6.16		817
At4g35790	gi 18419668	ATPLDELTA; phospholipase D	metabolism	13	-0.403	0		98.92	_		microtubul e cytoskelet on &		6.4	7.05	448
At4g29360	gi 7269834	beta-1, 3-glucanase-like protein	metabolism	9	-0.027	1		57.66	S		anchored to		7.52		143
At5g17920	gi 55670112	Chain A, A. Thaliana Cobalamine Independent Methionine Synthase	metabolism	6	-0.141	0		84.36	_	not plastid	cytosol	15024005(cytosol - SUBA);	7.52	6.09	143
At2g43750	gi 572517	cysteine synthase	metabolism	5	0.018	0		41.66	C	plastid stroma	mitochond rion & plastid		9.52	8.14	485
At3g25860	gi 9279589	dihydrolipoamide S-acetyltransferase	metabolism	1	0.045	0		50.08	C	plastid	chloroplast stroma		6.92	8.34	49
At1g43710	gi 15218445	emb1075 (embryo defective 1075); carboxy- lyase/ catalytic/ pyridoxal phosphate binding	metabolism	12	-0.261	0		54.08	_				8.39	9.33	15
At1g34430	gi 8778253	F12K21.24	metabolism	1	0.131	0		48.31	C	envelope- inner- peripheral-			8.8	8.93	369

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At5g54500	gi 15239652	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as	metabolism	0	-0.108	0		21.80	_				4.97	10.34	29
At2g36850	gi 240254594	GSL8 (GLUCAN SYNTHASE-LIKE 8); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	metabolism	17	0.041	10	15	191.64	_				8.02	6.54	368
At3g25610	gi 15230859	haloacid dehalogenase-like hydrolase family protein	metabolism	16	-0.077	8	9	136.28	M	plasma membrane			6.17		345
At4g00490	gi 3912919	hypothetical protein	metabolism	10	-0.357	0	1	61.40	C	plastid stroma			5.95	8.85	40
At4g16155	gi 7159284	lipoamide dehydrogenase	metabolism	8	0.026	0		60.15	C	plastid		11575725(plastid - SUBA);	9.5	7.29	52
At4g23850	gi 15236634	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase	metabolism	13	-0.144	0		74.51	_				6.92	6.55	49
At4g11850	gi 15234335	PLDGAMMA1; phospholipase D	metabolism	10	-0.345	0		95.59	_				8.32	7.05	53
At4g11830	gi 42566498	PLDGAMMA2; phospholipase D	metabolism	11	-0.367	0		92.40	_				5.26	7.05	48
At2g18730	gi 4185139	putative diacylglycerol kinase	metabolism	11	-0.246	0		53.88	_				6.36	7.58	1885
At3g03780	gi 14532772	putative methionine synthase	metabolism	6	-0.152	0		84.59	_		cytosol	15024005(cytosol - SUBA);	6.09	7.14	348
At4g26690	gi 4455192	putative protein	metabolism	8	0.051	0		82.56	M	plasma membrane	anchored to		9.5	5.32	52
At4g13940	gi 32967699	S-adenosyl-L-homocystein hydrolase	metabolism	11	-0.127	0		53.38	_				5.66	7.05	80
At5g55480	gi 15240520	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	metabolism	7	-0.045	1		84.17	S	plasma membrane	anchored to membrane		5.45	9.01	6500
At1g66970	gi 30697435	SVL2 (SHV3-LIKE 2); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	metabolism	8	-0.018	1		83.79	S		anchored to		5	9.01	350
At5g58070	gi 15242942	TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter	metabolism	0	-0.678	0		21.43	_			17151019(vacuole - SUBA);	7.48	10.34	86
At3g07020	gi 2462931	UDP-glucose:sterol glucosyltransferase	metabolism	6	-0.241	0		69.32	C	plasma membrane			5.64	7.14	27
At3g54200	gi 15232445	unknown protein	metabolism	5	0.107	1	1	25.79	_	plasma membrane			4.86		1983
At5g35930	gi 8885525	unnamed protein product	metabolism	44	-0.047	0		115.60	S				8.61	5.93	469
At3g05530	gi 5669047	19S proteasome regulatory complex subunit S6A	protein destination and storage	5	-0.442	0		47.48	_	cytosol	proteasome regulatory particle, base subcomplex (sensu Eukaryota) & nucleus	15610358(cytosol - SUBA); 15610358(nucleus - SUBA);	7.14	4.91	368
At1g45000	gi 15219503	26S proteasome regulatory complex subunit p42D, putative	protein destination and storage	3	-0.384	0		44.76	_	cytosol		15496452(nucleus - SUBA);	6.11	4.19	43
At2g32730	gi 15225733	26S proteasome regulatory subunit, putative	protein destination and storage	8	-0.065	1		108.98	_	not plastid	proteasome regulatory particle, base subcomplex (sensu Eukaryota)		5.83	4.19	51
At5g23540	gi 14533454	26S proteasome regulatory subunit, putative	protein destination and storage	1	-0.243	0		34.35	_	not plastid	nucleus		5.83	4.19	51
At1g04730	gi 15219798	AAA-type ATPase family protein	protein destination and storage	18	-0.478	0		108.01	_				6.92	6.56	49
At3g56450	gi 15228924	ALPHA-SNAP1; binding / soluble NSF attachment protein	protein destination and storage	13	-0.398	0		43.88	M				7.88	8.93	734
At2g02800	gi 15227042	APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	protein destination and storage	3	-0.381	0		46.29	C		nucleus & cytoplasm	15610358(cytosol - SUBA); 15610358(nucleus - SUBA);	9.67	9.01	116

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At1g11910	gi 1354272	aspartic proteinase	protein destination and	13	0.042	1		54.61	S	vacuole			5.01	5.37	35
At1g62290	gi 22330379	aspartyl protease family protein	protein destination and	12	-0.067	1		55.75	S				5.7	5.75	455
At3g02740	gi 15232960	aspartyl protease family protein	protein destination and storage	13	-0.024	0	1	52.81	S		anchored to		5.7	5.75	455
At3g09830	gi 22242392 7	AT3G09830	protein destination and storage	5	-0.433	0		46.79	C	plasma membrane			10.11	9.01	39
At3g52500	gi 16209647	AT3g52500/F22O6_120	protein destination and storage	14	-0.148	0		51.01	S		cell wall (sensu Magnoliop hyta)		5.26	8.53	48
At3g63260	gi 15229398	ATMRK1; kinase/ protein serine/threonine/tyrosine kinase	protein destination and storage	12	-0.296	0		42.58	_				6.23	5.79	147
At3g04810	gi 15229361	ATNEK2 (NIMA-RELATED KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	protein destination and storage	9	-0.555	0		68.04	_				10.34	5.79	24
At1g63500	gi 24025431 1	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein	protein destination and storage	10	-0.237	0		47.65	S				5.96	5.79	1026
At1g69840	gi 15222481	band 7 family protein	protein destination and storage	5	-0.217	0		31.41	_			17151019(vacuole - SUBA);	5.3	4.74	1514
At3g01290	gi 18395770	band 7 family protein	protein destination and storage	4	-0.069	0		31.32	_			15060130(plasma membrane -SUBA);	5.3	4.74	1514
At5g62740	gi 15241939	band 7 family protein	protein destination and storage	5	-0.101	0		31.43	_			15319477(plasma membrane -SUBA);	5.3	4.74	1514
At1g65240	gi 4646203	Belongs to PF 00026 Eukaryotic aspartyl protease family	protein destination and storage	13	0.023	1		51.83	S	plasma membrane	anchored to		5.64	5.33	27
At2g39660	gi 15225520	BIK1 (BOTRYTIS-INDUCED KINASE1); kinase	protein destination and storage	4	-0.336	0		44.10	C		nucleolus & plasma membrane & nucleus & cytoplasm	15610358(unclear - SUBA);	10.11	9.01	39
At4g35230	gi 18418600	BSK1 (BR-SIGNALING KINASE 1); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	protein destination and storage	12	-0.477	0		56.82	_	plasma membrane			5.51	9.01	637
At5g46570	gi 15237465	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	protein destination and storage	9	-0.397	0		54.97	_				8.32	9.01	53
At4g00710	gi 22328189	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	protein destination and storage	14	-0.374	0		54.91	_				5.87	9.01	766
At1g05690	gi 42561724	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator	protein destination and storage	19	-0.313	0		41.53	C				9.26	9.13	18
At4g01610	gi 18411686	cathepsin B-like cysteine protease, putative	protein destination and storage	15	-0.235	0		39.42	S				9.93	5.75	34
At5g47850	gi 15238823	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase	protein destination and storage	27	-0.093	2	1	83.78	S				6.11	9.01	17
At3g26940	gi 15231654	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	protein destination and storage	8	-0.414	0		48.51	C				9.66	9.01	26
At3g13470	gi 15231255	chaperonin, putative	protein destination and storage	7	-0.056	0		63.34	C	plastid stroma	mitochond rion		9.66	9.1	26
At3g18190	gi 15229595	chaperonin, putative	protein destination and	8	0.085	0		57.78	C				9.66	9.1	26
At1g05840	gi 6850312	Contains similarity to nucellin from Hordeum vulgare gb U87148. ESTs gb T22068, gb F14251, gb F14237,	protein destination and storage	15	0.005	0	1	53.30	S		anchored to membrane		6.54	5.75	294
At1g53430	gi 8671883	Contains similarity to receptor-like serine/threonine kinase from Arabidopsis thaliana gb AF024648 and contains multiple leucine rich PF 00560 repeats and protein kinase PF 00069 domain. ESTs gb T04455, gb N38129 come from this gene	protein destination and storage	16	-0.204	1	1	113.98	S				9.66	5.79	26



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At1g55490	gi 15222729	CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding	protein destination and storage	7	-0.112	0		63.81	C	plastid stroma			9.66	9.1	26
At1g12470	gi 8778633	F5O11.22	protein destination and storage	19	-0.271	0		113.08	_				6.59	6.44	21
At3g58880	gi 15231588	F-box family protein	protein destination and storage	15	0.205	0		50.76	_				5.52	5.75	25
At3g60040	gi 15232242	F-box family protein	protein destination and storage	22	0.067	0	2	94.20	_				5.52	5.75	25
At5g25860	gi 15239511	F-box family protein	protein destination and storage	17	-0.198	0		51.94	_				5.52	5.75	25
At4g23940	gi 18416240	FtsH protease, putative	protein destination and storage	4	-0.214	3	3	105.54	C				9.49	4.74	19
At5g02500	gi 397482	heat shock protein 70 cognate	protein destination and storage	7	-0.436	0		71.36	_	cytosol	cytosol		7.88	5.03	734
At4g37910	gi 4467097	heat shock protein 70 like protein	protein destination and storage	5	-0.295	0		73.08	M	mitochondria	mitochondrion & mitochondrial matrix		5.31	9.1	98
At2g17760	gi 25347778	hypothetical protein At2g17760 [imported] - Arabidopsis thaliana	protein destination and storage	14	-0.113	1		56.03	S		anchored to		6.73	5.07	202
At1g79560	gi 4835753	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from	protein destination and storage	5	-0.341	2	2	115.11	C		chloroplast		6.59	4.74	21
At1g04210	gi 15219675	leucine-rich repeat family protein / protein kinase family protein	protein destination and storage	32	-0.390	0		125.16	_				6.27	5.79	698
At3g23750	gi 15229508	leucine-rich repeat family protein / protein kinase family protein	protein destination and storage	10	-0.095	2	1	99.97	S	plasma membrane			6.27	5.79	698
At5g42020	gi 1303695	luminal binding protein (BiP)	protein destination and storage	5	-0.467	1		73.56	S		endoplasmic reticulum & endoplasmic	11226186(endoplasmic reticulum - SUBA);	8.57	5.11	238
At5g09590	gi 15242459	MTHSC70-2 (MITOCHONDRIAL HSP70 2); ATP binding	protein destination and storage	4	-0.306	0		72.99	M	mitochondria	mitochondrion & mitochondrial matrix		9.93	9.1	73
At1g69960	gi 15222511	PP2A (SERINE/THREONINE PROTEIN PHOSPHATASE 2A); protein serine/threonine phosphatase	protein destination and storage	11	-0.301	0		35.04	_				9.26	5.79	18
At5g10080	gi 110741881	predicted GPI-anchored protein	protein destination and storage	16	-0.233	0		57.96	S		anchored to		5.7	5.75	455
At5g02290	gi 166809	protein kinase	protein destination and storage	4	-0.356	0		43.53	C				10.11	9.01	39
At4g35600	gi 3367578	protein kinase - like protein	protein destination and storage	3	-0.368	0		46.34	C	plasma membrane			9.66	9.01	26
At1g07870	gi 15223024	protein kinase family protein	protein destination and storage	8	-0.500	0		46.76	_				8.75	9.01	763
At1g25390	gi 15222572	protein kinase family protein	protein destination and storage	17	-0.371	2	1	70.86	S				8.75	9.01	763
At1g54610	gi 15221868	protein kinase family protein	protein destination and storage	8	-0.620	0		63.29	_				8.75	9.01	763
At1g70520	gi 15223169	protein kinase family protein	protein destination and storage	18	-0.233	2	1	72.00	S				8.75	9.01	763
At1g70530	gi 15223170	protein kinase family protein	protein destination and storage	15	-0.125	1	1	71.61	S				8.75	9.01	763
At2g23200	gi 15227790	protein kinase family protein	protein destination and storage	7	-0.277	2	1	93.38	S				8.75	9.01	763
At2g28590	gi 15226901	protein kinase family protein	protein destination and storage	10	-0.401	0		47.28	_				8.75	9.01	763
At2g28940	gi 30684071	protein kinase family protein	protein destination and storage	4	-0.263	0		39.12	S				8.75	9.01	763
At2g39360	gi 15225078	protein kinase family protein	protein destination and storage	11	-0.131	1	1	91.32	S				8.75	9.01	763
At3g06620	gi 15230753	protein kinase family protein	protein destination and storage	10	-0.518	0		86.06	_				8.75	9.01	763
At3g54030	gi 15232406	protein kinase family protein	protein destination and storage	13	-0.316	0		54.79	S	plasma membrane			8.75	9.01	763
At4g02010	gi 30679031	protein kinase family protein	protein destination and storage	10	-0.163	2	2	79.05	_	plasma membrane			8.75	9.01	763
At4g02630	gi 15235432	protein kinase family protein	protein destination and storage	3	-0.393	1	1	54.74	M				8.75	9.01	763
At4g11470	gi 15233389	protein kinase family protein	protein destination and storage	20	-0.200	2	1	74.68	S				8.75	9.01	763
At4g23200	gi 15236421	protein kinase family protein	protein destination and storage	22	-0.091	0		72.63	S				8.75	9.01	763
At4g38830	gi 15234824	protein kinase family protein	protein destination and storage	15	-0.146	1	1	74.36	S				8.75	9.01	763
At5g01020	gi 30679085	protein kinase family protein	protein destination and storage	9	-0.347	0		45.62	C				8.75	9.01	763
At5g24010	gi 15237872	protein kinase family protein	protein destination and storage	11	-0.123	1	1	91.82	S	plasma membrane			8.75	9.01	763

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At5g39020	gi 15241610	protein kinase family protein	protein destination and	10	-0.050	2	1	90.45	S				8.75	9.01	763
At5g41260	gi 15237604	protein kinase family protein	protein destination and	11	-0.409	0		54.63					8.75	9.01	763
At5g51770	gi 15242183	protein kinase family protein	protein destination and	10	-0.530	0	1	73.33	C				8.75	9.01	763
At5g57610	gi 15242791	protein kinase family protein	protein destination and	11	-0.665	0		117.45					8.75	9.01	763
At1g76370	gi 15223033	protein kinase, putative	protein destination and	8	-0.284	0		42.32					5.91	9.01	321
At2g17220	gi 18398350	protein kinase, putative	protein destination and	4	-0.420	0		45.55	C	not plastid			5.91	9.01	321
At2g41970	gi 15227478	protein kinase, putative	protein destination and	6	-0.301	0		39.38					5.91	9.01	321
At3g46290	gi 15231393	protein kinase, putative	protein destination and storage	10	-0.183	1	1	91.47	S	plasma membrane			5.91	9.01	321
At5g03320	gi 15242720	protein kinase, putative	protein destination and	5	-0.509	0		47.01	C				5.91	9.01	321
At5g56460	gi 15241220	protein kinase, putative	protein destination and storage	7	-0.344	0		45.87		plasma membrane			5.91	9.01	321
At5g59700	gi 15238498	protein kinase, putative	protein destination and	9	-0.194	2	1	91.97	S				5.91	9.01	321
At3g24540	gi 9294048	protein kinase-like protein	protein destination and	6	-0.293	1	1	55.70					8.51	9.01	2665
At4g28400	gi 18417190	protein phosphatase 2C, putative / PP2C, putative	protein destination and storage	3	-0.323	0		31.02					6.67	4.19	433
At4g04910	gi 7267250	putative component of vesicle-mediated transport	protein destination and storage	9	-0.120	0		81.49					5.9	6.56	223
At3g48820	gi 7576220	putative protein	protein destination and	10	-0.333	1		49.48	S				5.32	8.85	4660
At1g06700	gi 7523708	Putative protein kinase	protein destination and storage	6	-0.325	0		39.82		plasma membrane			5.87	7.14	1174
At2g07180	gi 19423982	putative protein kinase	protein destination and	7	-0.504	0		49.21					5.87	9.01	1174
At2g39110	gi 3928095	putative protein kinase	protein destination and	4	-0.371	0		48.88					6.58	9.55	83
At1g69790	gi 12325185	putative protein kinase; 3853-2084	protein destination and	5	-0.339	0		42.70	C				6.54	9.72	780
At2g29000	gi 3461842	putative receptor-like protein kinase	protein destination and	14	-0.241	2	1	98.09	S				6.08	6.37	132
At2g28000	gi 21554572	putative rubisco subunit binding-protein alpha subunit	protein destination and storage	3	0.002	0		62.07	C	plastid stroma	mitochond rion & chloroplas		5.05	9.1	96
At1g56140	gi 12321749	receptor protein kinase, putative	protein destination and	16	-0.117	2	1	113.60	M				6.27	5.79	698
At4g08850	gi 7267528	receptor protein kinase-like protein	protein destination and storage	14	-0.193	2	3	115.42		plasma membrane			5.72	5.79	3135
At5g60900	gi 166846	receptor-like protein kinase	protein destination and	19	-0.408	0		84.52	S				7.71	4.94	44
At3g14840	gi 11994595	receptor-like serine/threonine kinase	protein destination and storage	5	0.390	2	1	12.49	S	plasma membrane			5.95	5.79	1584
At5g38810	gi 75262707	RecName: Full=Putative F-box protein	protein destination and	7	-0.405	0		30.26					6.32	9.03	69
At2g16600	gi 15227259	ROC3; peptidyl-prolyl cis-trans isomerase	protein destination and	4	-0.323	0		18.49		not plastid			8.65	9.1	521
At5g58290	gi 15237159	RPT3 (REGULATORY PARTICLE TRIPLE-A ATPASE 3); ATPase	protein destination and storage	3	-0.343	0		45.75		cytosol	proteasom e regulatory particle, base subcomple x (sensu Eukaryota)		5.42	4.19	89
At4g23270	gi 3021279	serine/threonine kinase	protein destination and	15	-0.103	2	1	71.62	S				7.44	9.01	166
At2g47060	gi 79324935	serine/threonine protein kinase, putative	protein destination and	6	-0.338	0		39.93					8.97	7.14	293
At3g17410	gi 22331138	serine/threonine protein kinase, putative	protein destination and	6	-0.302	0		39.56					8.97	7.14	293
At5g35580	gi 62319981	serine/threonine protein kinase-like	protein destination and	6	-0.613	0		56.17					5.21	9.25	1224
At1g09070	gi 3426060	src2-like protein	protein destination and storage	2	-0.704	0		34.19			endoplasm ic reticulum & protein storage	16723734(vacuole - SUBA);	10.09	6.44	95
At1g70490	gi 4056469	Strong similarity to gb M95166 ADP- ribosylation factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb AA712956, gb T46403, gb T46050, gb AT100391 and gb Z25043	protein destination and storage	1	-0.191	0		20.59	M				6.97	8.93	964
At2g05920	gi 18396193	subtilase family protein	protein destination and	10	-0.090	1		80.02	S				9.45	8.85	358
At1g26970	gi 8778850	T7N9.2	protein destination and	6	-0.333	0		45.53	C				9.49	9.79	19

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At1g16670	gi 9989053	Unknown protein	protein destination and	8	-0.318	0		43.29					4.86	9.01	1983
At5g43260	gi 10177388	unnamed protein product	protein destination and	8	-0.064	1		10.07	C				8.61	9.1	469
At5g51540	gi 9758196	unnamed protein product	protein destination and storage	12	-0.388	0	2	79.93	M		thylakoid membrane (sensu Viridiplant ae)		8.61	4.74	469
At5g56380	gi 10177837	unnamed protein product	protein destination and	14	-0.092	0		49.91					8.61	5.75	469
At2g14720	gi 1737220	vacuolar sorting receptor homolog	protein destination and storage	35	-0.401	1	1	69.81	S		Golgi trans face	ISI:0002263170000 12(golgi -SUBA); 16980567(vacuole - SUBA);	5.52	6.44	25
At2g42360	gi 15227929	zinc finger (C3HC4-type RING finger) family protein	protein destination and storage	8	-0.332	1	1	26.44					5.67	9.01	22
At5g01520	gi 15241003	zinc finger (C3HC4-type RING finger) family protein	protein destination and storage	10	-0.364	0		28.05					5.67	9.01	22
At2g36160	gi 15227588	40S ribosomal protein S14 (RPS14A)	protein synthesis	1	-0.468	0		16.26		cytosol			10.6	8.93	374
At1g04270	gi 1107485	40S ribosomal protein S15	protein synthesis	0	-0.354	0		17.13		cytosol	cytosolic ribosome (sensu Eukaryota)		7.08	10.34	1226
At5g09510	gi 15242436	40S ribosomal protein S15 (RPS15D)	protein synthesis	0	-0.319	0		17.07		cytosol; cytosol		15496452(nuclear - SUBA);	10.34	10.34	24
At2g04390	gi 15228141	40S ribosomal protein S17 (RPS17A)	protein synthesis	0	-0.582	0		16.05	M	cytosol		15496452(nucleus - SUBA);	10.04	10.34	1067
At3g02080	gi 15232844	40S ribosomal protein S19 (RPS19A)	protein synthesis	1	-0.508	0		15.83		cytosol	cytosolic ribosome (sensu Eukaryota)		10.09	8.93	95
At5g61170	gi 15240154	40S ribosomal protein S19 (RPS19C)	protein synthesis	1	-0.396	0		15.70		cytosol	cytosolic ribosome (sensu Eukaryota)		7.7	8.93	110
At2g41840	gi 15227443	40S ribosomal protein S2 (RPS2C)	protein synthesis	4	-0.411	0		30.88		cytosol	cytosolic ribosome (sensu Eukaryota)		6.32	5.26	23
At5g28060	gi 15241125	40S ribosomal protein S24 (RPS24B)	protein synthesis	1	-0.874	0		15.42	M	cytosol	cytosolic ribosome (sensu Eukaryota)		10.53	8.93	405
At2g21580	gi 15226590	40S ribosomal protein S25 (RPS25B)	protein synthesis	0	-0.805	0		12.07					10.7	10.34	516
At4g39200	gi 15234970	40S ribosomal protein S25 (RPS25E)	protein synthesis	0	-0.756	0		12.05		cytosol	cytosolic ribosome (sensu Eukaryota)		10.7	10.34	1510
At3g56340	gi 15228895	40S ribosomal protein S26 (RPS26C)	protein synthesis	6	-0.881	0		14.63			cytosolic ribosome (sensu Eukaryota)		6.13	7.14	71
At3g43980	gi 15229840	40S ribosomal protein S29 (RPS29A)	protein synthesis	5	-0.720	0		6.43	M				10.07	4.74	85
At5g35530	gi 15238533	40S ribosomal protein S3 (RPS3C)	protein synthesis	3	-0.121	0		27.46		cytosol	cytosolic ribosome (sensu Eukaryota)	15496452(nucleus - SUBA);	9.57	4.19	322
At4g29390	gi 15233565	40S ribosomal protein S30 (RPS30B)	protein synthesis	0	-1.281	0		6.89	M				12.24	10.34	198
At3g04840	gi 15229364	40S ribosomal protein S3A (RPS3aA)	protein synthesis	4	-0.522	0		29.85		cytosol	cytosolic ribosome (sensu Eukaryota)		5.76	5.26	242

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At3g02560	gi 15232926	40S ribosomal protein S7 (RPS7B)	protein synthesis	0	-0.520	0		22.20	_	cytosol	cytosolic ribosome (sensu Eukaryota)		9.78	10.34	149
At5g62300	gi 7671404	40S ribosomal protein	protein synthesis	2	-0.394	0		13.88	_	cytosol			10.18	9.73	60
At2g37190	gi 15228098	60S ribosomal protein L12 (RPL12A)	protein synthesis	2	-0.330	0		17.94	_	cytosol	cytosolic ribosome (sensu Eukaryota)		5.23	6.44	82
At4g27090	gi 15236981	60S ribosomal protein L14 (RPL14B)	protein synthesis	0	-0.353	0		15.51	_	cytosol	cytosolic ribosome (sensu Eukaryota)		10.03	10.34	1085
At1g27400	gi 15223501	60S ribosomal protein L17 (RPL17A)	protein synthesis	3	-0.799	0		19.90	_	cytosol			10.12	4.19	443
At1g67430	gi 15220431	60S ribosomal protein L17 (RPL17B)	protein synthesis	3	-0.801	0		19.85	_	cytosol	cytosolic ribosome (sensu Eukaryota)		10.12	4.19	341
At2g34480	gi 15226755	60S ribosomal protein L18A (RPL18aB)	protein synthesis	2	-0.733	0		21.31	M	cytosol	cytosolic ribosome (sensu Eukaryota)		10.49	6.44	135
At3g49910	gi 15229631	60S ribosomal protein L26 (RPL26A)	protein synthesis	0	-0.949	0		16.95	M	cytosol	cytosolic ribosome (sensu Eukaryota)	15496452(nucleus - SUBA);	6.6	10.34	38
At2g19730	gi 15224835	60S ribosomal protein L28 (RPL28A)	protein synthesis	1	-0.622	0		15.90	_	cytosol	cytosolic ribosome (sensu Eukaryota)		10.58	8.93	1087
At4g29410	gi 15233567	60S ribosomal protein L28 (RPL28C)	protein synthesis	1	-0.599	0		15.91	_	cytosol			11.04	8.93	523
At5g56710	gi 15241902	60S ribosomal protein L31 (RPL31C)	protein synthesis	1	-0.882	0		13.80	_		cytosolic ribosome (sensu Eukaryota)		9.95	8.93	103
At5g46430	gi 15237436	60S ribosomal protein L32 (RPL32B)	protein synthesis	1	-0.723	0		15.48	M				10.78	8.93	100
At3g09500	gi 15232693	60S ribosomal protein L35 (RPL35A)	protein synthesis	0	-0.762	0		14.29	_				10.92	10.34	128
At2g39390	gi 15225083	60S ribosomal protein L35 (RPL35B)	protein synthesis	0	-0.659	0		14.23	_	cytosol	cytosolic ribosome (sensu Eukaryota)		10.92	10.34	42
At2g43460	gi 15224284	60S ribosomal protein L38 (RPL38A)	protein synthesis	2	-0.554	0		8.12	_	cytosol	cytosolic ribosome (sensu Eukaryota)		9.95	6.44	333
At3g09630	gi 15232723	60S ribosomal protein L4/L1 (RPL4A)	protein synthesis	2	-0.379	0		44.70	_	cytosol	cytosolic ribosome (sensu Eukaryota)		11.57	6.44	181
At2g01250	gi 15226212	60S ribosomal protein L7 (RPL7B)	protein synthesis	1	-0.574	0		28.17	_	cytosol			9.93	8.93	73
At2g47610	gi 15226635	60S ribosomal protein L7A (RPL7aA)	protein synthesis	4	-0.564	0		29.13	_	cytosol		15496452(nucleus - SUBA);	8.34	5.26	33
At1g33120	gi 18398753	60S ribosomal protein L9 (RPL90B)	protein synthesis	2	-0.351	0		22.02	_	cytosol	cytosolic ribosome (sensu Eukaryota)	15496452(nucleus - SUBA);	6.36	6.44	1885
At4g10450	gi 15235114	60S ribosomal protein L9 (RPL90D)	protein synthesis	2	-0.294	0		21.97	_	cytosol			9.52	6.44	485

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At1g43170	gi 15218306	ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	protein synthesis	5	-0.581	0		44.56	_	cytosol	cytosolic large ribosomal subunit (sensu Eukaryota) & cytosolic ribosome (sensu Eukaryota)	15496452(nucleus - SUBA);	10.18	4.74	60
At5g58420	gi 17979233	AT5g58420/mqj2_10	protein synthesis	2	-0.497	0		29.82	M	cytosol	cytosolic ribosome (sensu Eukaryota)		9.78	6.44	170
At5g60390	gi 227202852	AT5G60390	protein synthesis	6	-0.325	0		49.50	_		mitochondrion & nucleus & cytoplasmic ribosome & cytosolic ribosome (sensu Eukaryota)	15610358(cytosol - SUBA); 15610358(nucleus - SUBA);	4.53	4.85	31
At3g49010	gi 15229064	ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	protein synthesis	0	-0.924	0		23.77	_	cytosol	cytosolic ribosome (sensu Eukaryota)	15496452(nucleus - SUBA);	11.02	10.34	259
At2g37270	gi 15228111	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	protein synthesis	2	-0.177	0		22.99	_	cytosol	cytosolic ribosome (sensu Eukaryota)		9.69	6.44	1110
At1g56070	gi 6056373	elongation factor EF-2	protein synthesis	16	-0.228	0		93.89	_	not plastid			5.89	4.85	1169
At1g20620	gi 8778617	F5M15.5	protein synthesis	7	-0.482	0		56.70	_	peroxisome	mitochondrion & peroxisome	10737809(nucleus - SUBA);	9.66	9.1	26
At5g66470	gi 10177528	GTP-binding protein-like	protein synthesis	4	-0.421	0		48.93	C	plastid			5.01	6.59	35
At4g02930	gi 1149571	mitochondrial elongation factor Tu	protein synthesis	4	-0.117	0		49.41	C	not plastid	mitochondrion		5.19	4.85	114
At3g52880	gi 15231702	monodehydroascorbate reductase, putative	protein synthesis	3	-0.064	0		46.49	_	peroxisome	peroxisomal matrix		5.95	4.19	40
At1g22780	gi 15219950	PFL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome	protein synthesis	1	-0.680	0		17.55	_	cytosol			10.54	8.93	1672
At3g60240	gi 7576200	protein synthesis initiation factor-like	protein synthesis	14	-0.746			187.55	M				7.06	6.31	556
At3g09680	gi 6682246	putative 40S ribosomal protein S23	protein synthesis	3	-0.551	0		15.77	M	cytosol			10.2	4.19	716
At2g39460	gi 2654122	ribosomal protein L23a	protein synthesis	0	-0.763	0		17.44	_		cytosolic ribosome (sensu Eukaryota) & large ribosomal subunit		9.33	10.2	55
At5g20180	gi 15241288	ribosomal protein L36 family protein	protein synthesis	3	-0.261	0		11.43	_				6.32	4.19	23
At3g48930	gi 166867	ribosomal protein S11 (probable start codon at bp 67)	protein synthesis	4	-0.512	0		17.96	_		cytosolic ribosome (sensu Eukaryota)	10737809(nucleus - SUBA);	9.67	10.56	116
At3g61110	gi 6850878	ribosomal protein S27	protein synthesis	6	-0.301	0		9.60	_	cytosol			5.82	7.14	109
At5g10360	gi 2224751	ribosomal protein S6	protein synthesis	4	-0.813	0		28.16	_	cytosol			10.91	5.26	362
At2g36620	gi 18404176	RPL24A (ribosomal protein L24); structural constituent of ribosome	protein synthesis	3	-1.016	0		18.85	M	cytosol			10.7	4.19	1190

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At1g23290	gi 15220698	RPL27AB; structural constituent of ribosome	protein synthesis	1	-0.539	0		16.29	_		cytosolic ribosome (sensu Eukaryota) & large ribosomal subunit	15496452(nucleus - SUBA);	10.5	8.93	62
At4g00100	gi 3193323	similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first	protein synthesis	1	-0.499	0		17.09	M	cytosol			9.66	10.39	26
At2g33370	gi 2341028	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene	protein synthesis	3	-0.184	0		15.03	M	cytosol			6.96	4.19	36
At1g70600	gi 15223190	structural constituent of ribosome	protein synthesis	1	-0.605	0		16.46	_	cytosol			10.59	8.93	229
At2g36170	gi 18404062	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A)	protein synthesis	4	-0.638	0		14.73	_				9.94	5.26	482
At3g26360	gi 9294294	unnamed protein product	protein synthesis	8	-0.290	0	1	20.55	M				5.67	9.96	22
At1g74000	gi 1754987	strictosidine synthase	secondary metabolism	3	0.024	0		34.67	S		cell wall (sensu Magnoliophyta)		6.96	4.19	36
At1g74010	gi 15221105	strictosidine synthase family protein	secondary metabolism	3	0.155	0		34.18	S		cell wall (sensu Magnoliophyta)		6.11	4.19	17
At1g74020	gi 1754983	strictosidine synthase	secondary metabolism	5	0.070	0		35.29	S				6.96	4.19	36
At4g34050	gi 21595512	caffeoyl-CoA O-methyltransferase-like	secondary metabolism	2	-0.335	0		29.16	_		cytosol		4.97	6.44	29
At4g34460	gi 42573173	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding	signal transduction	14	-0.225	0		41.01	_			17158913(cytosol - SUBA); 17158913(golgi - SUBA); 17492287(nucleus - SUBA); 17492287(plasma membrane -SUBA); 17158913(plasma membrane -SUBA); 16679415(plasma	5.64	7.14	27
At1g35160	gi 14532442	At1g35160/T32G9_30	signal transduction	2	-0.531	0		30.19	_		nuclear envelope & plasma membrane & cytoplasm	15659648(cytoskeleton -SUBA); 15659648(cytosol - SUBA); 15659648(nucleus - SUBA);	4.97	6.44	29
At1g68400	gi 14190425	At1g68400/T2E12_5	signal transduction	12	-0.232	1	1	73.52	S				7.59	6.55	30
At3g07390	gi 18426884	AT3g07390/F21O3_10	signal transduction	4	0.137	0	2	27.93	C	plasma membrane	extracellular region & anchored		9.3	5.26	4395
At5g01600	gi 15241018	ATFER1; ferric iron binding / iron ion	signal transduction	0	-0.253	0		28.18	C	plastid stroma			5.73	8.93	1634
At3g56090	gi 15228818	ATFER3 (ferritin 3); binding / ferric iron binding / oxidoreductase/ transition metal	signal transduction	1	-0.294	0		28.84	C	plastid stroma			5.54	8.93	708
At2g40300	gi 15225679	ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal	signal transduction	1	-0.269	0		29.03	C	plastid stroma			6.16	8.93	655
At4g38580	gi 15233937	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding	signal transduction	4	-0.418	0		17.02	_				9.26	8.93	158
At4g35860	gi 15233367	ATGB2 (GTP-BINDING 2); GTP binding	signal transduction	4	-0.254	0		23.18	_				6.06	7.14	28

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At2g17820	gi 18398532	ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase	signal transduction	16	-0.229	2	3	135.45	_				6.32	4.85	23
At1g11300	gi 145335397	ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine	signal transduction	41	-0.181	2	3	184.36	S				10.11	8.44	39
At5g49780	gi 240256419	ATP binding / kinase/ protein serine/threonine kinase	signal transduction	20	-0.200	1	2	114.57	S				6.06	6.55	28
At3g08510	gi 15231929	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	signal transduction	7	-0.474	0		66.12	M	plasma membrane			6.08	9.1	642
At5g03520	gi 15242773	ATRAB8C; GTP binding	signal transduction	3	-0.302	0		24.04	_			15972698(cytosol - SUBA); 15972698(golgi - SUBA);	7.63	7.14	46
At5g47520	gi 15238115	AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding	signal transduction	2	-0.322	0		24.45	_				5.98	7.14	115
At5g20020	gi 1668706	atran2	signal transduction	6	-0.419	0		25.06	_		nucleus & cytoplasm	15610358(unclear - SUBA);	6.65	7.14	77
At3g49750	gi 15229606	AtRLP44 (Receptor Like Protein 44); protein binding	signal transduction	6	0.015	1	1	29.99	S				8.2		812
At4g18760	gi 15234009	AtRLP51 (Receptor Like Protein 51); protein binding	signal transduction	7	0.024	1	1	46.07	C	plasma membrane			8.75		2584
At3g25290	gi 18404500	auxin-responsive family protein	signal transduction	3	0.204	6	5	42.56	S				5.74	5.26	403
At5g35735	gi 18421491	auxin-responsive family protein	signal transduction	3	0.022	5	5	43.87	S				5.74	5.26	403
At4g12980	gi 15235545	auxin-responsive protein, putative	signal transduction	4	0.238	5	5	42.23	S				9.73	5.26	245
At4g39400	gi 15235059	BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	signal transduction	23	-0.086	2	1	130.55	S		endosome & plasma membrane	ISI:00022578070005(plasma membrane -SUBA); 16473966(plasma membrane -SUBA); 16461582(plasma membrane -SUBA); 16236160(plasma membrane -SUBA); 12150928(plasma membrane -SUBA); 10938344(plasma	6.11	8.27	17
At1g55610	gi 15222751	BRL1 (BRI 1 LIKE); kinase	signal transduction	25	-0.056	2	1	127.43	S	plasma membrane			6.11	6.54	17
At3g13380	gi 15231225	BRL3 (BRI1-LIKE 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	signal transduction	24	-0.062	1	1	126.66	S				6.11	8.27	17
At4g29900	gi 4914414	Ca <sup>2+</sup> -transporting ATPase-like protein	signal transduction	12	0.038	8	9	116.86	_	plasma membrane			7.85	6.31	3489
At3g61050	gi 1769895	CaLB protein	signal transduction	2	0.023	1		55.10	M				9.49	6.31	19
At5g24430	gi 22136058	calcium dependent protein kinase-like protein	signal transduction	7	-0.369	0		66.52	_	plasma membrane			7.15	6.31	197
At1g05150	gi 15220436	calcium-binding EF hand family protein	signal transduction	14	-0.419	0		90.17	_	plasma membrane			6.31	6.31	982
At2g32450	gi 15225686	calcium-binding EF hand family protein	signal transduction	13	-0.412	0		90.23	_	plasma membrane			6.31	6.31	982
At1g18210	gi 15221030	calcium-binding protein, putative	signal transduction	3	-0.449	0		18.35	_				10.92	6.31	42
At3g51850	gi 1314711	calcium-dependent protein kinase	signal transduction	10	-0.403	0	1	59.38	_				5.7	6.25	455
At3g57530	gi 6706424	calcium-dependent protein kinase	signal transduction	8	-0.507	0	1	60.94	_	plasma membrane	nucleus		5.7	5.99	455
At2g41410	gi 16213	calmodulin like protein	signal transduction	5	-0.359	0		23.44	C				6.96	6.31	36
At4g23650	gi 15236560	CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/	signal transduction	4	-0.534	0		59.34	C			12913141(cytosol - SUBA); 12913141(nucleus - SUBA);	5.95	6.31	632

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At1g52540	gi 5903051	Contains PF 00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from	signal transduction	6	-0.398	0		39.87	-	plasma membrane			6.77		1867
At1g71830	gi 7239510	Contains similarity to the somatic embryogenesis receptor-like kinase from <i>Daucus carota</i> gb AC007454; It contains 3 leucine rich repeat domains PF 00560 and a eukaryotic protein kinase domain PF 00069	signal transduction	8	-0.111	2	1	69.02	S		plasma membrane	16621602(endoplasmic reticulum - SUBA); 17693538(plasma membrane -SUBA); 16621602(plasma membrane -SUBA); 16473966(plasma membrane -SUBA); 16231101(plasma membrane -SUBA); 15592873(plasma membrane -SUBA); 12101128(plasma membrane -SUBA):	5.62	9.01	45
At4g23160	gi 10176701	copina-like retrotransposable element	signal transduction	32	-0.143	2	3	141.39	-				6.16	6.78	655
At5g07300	gi 7576168	copine-like protein	signal transduction	5	-0.125	0	2	64.03	-				5.13		211
At4g21940	gi 15234656	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein	signal transduction	7	-0.454	0	1	62.58	C				5.83	6.31	51
At3g20410	gi 15231140	CPK9 (calmodulin-domain protein kinase 9); calmodulin-dependent protein kinase/ kinase	signal transduction	7	-0.457	0	1	60.36	-	plasma membrane		17999643(plasma membrane -SUBA); 17337534(plasma membrane -SUBA); 12913141(plasma membrane -SUBA):	5.83	6.31	745
At3g10620	gi 8567796	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative	signal transduction	4	-0.540	0		24.62	C	plastid			5.53	5.26	145
At2g03150	gi 42568895	emb1579 (embryo defective 1579); binding / calcium ion binding	signal transduction	6	-1.126	0		150.91	M				5.64	7.14	27
At1g53420	gi 7769864	F12M16.30	signal transduction	12	-0.191	2	2	107.49	S				5.96	6.46	1026
At1g49100	gi 7770331	F27J15.13	signal transduction	14	-0.201	2	1	98.87	S				7.03	7.55	54
At1g43890	gi 8778652	F9C16.3	signal transduction	6	-0.276	0		23.53	S				4.97	5.69	29
At3g51550	gi 15230520	FER (FERONIA); kinase/ protein kinase	signal transduction	13	-0.257	2	1	98.15	S	plasma membrane			5.82	9.1	1659
At5g23980	gi 9758223	FRO2 homolog	signal transduction	8	0.183	9	10	80.25	S				9.37	9.01	58
At4g09000	gi 1255987	GF14chi isoform	signal transduction	2	-0.440	0		29.93	-		nucleus		5.7	4.68	455
At4g17530	gi 2245111	GTP-binding RAB1C like protein	signal transduction	4	-0.273	0		22.32	S				5.89	7.14	600
At4g28490	gi 15235312	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine	signal transduction	23	-0.016	1	1	109.10	S				7.03	6.56	54
At3g51740	gi 15231029	IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	signal transduction	15	-0.095	2	1	90.26	S	plasma membrane	cell wall (sensu Magnoliophyta)		7.62	8.27	1454
At2g19230	gi 24025447	kinase	signal transduction	12	-0.239	2	1	99.01	S				5.76	9.1	242
At1g34300	gi 15218576	lectin protein kinase family protein	signal transduction	22	-0.166	3	2	91.29	S				8.33	8.44	407
At5g60270	gi 15239260	lectin protein kinase family protein	signal transduction	7	-0.079	2	1	73.96	S				8.33	8.44	407
At1g51800	gi 15218033	leucine-rich repeat protein kinase, putative	signal transduction	14	-0.181	1	1	99.64	S				5.93	9.1	1816
At2g01820	gi 15226361	leucine-rich repeat protein kinase, putative	signal transduction	13	-0.180	1	1	101.96	S	plasma membrane	cell wall (sensu Magnoliophyta)		5.93	9.1	1816
At2g14510	gi 15225949	leucine-rich repeat protein kinase, putative	signal transduction	13	-0.172	1	1	97.64	S				5.93	9.1	1816
At2g28970	gi 15227015	leucine-rich repeat protein kinase, putative	signal transduction	14	-0.153	1	1	87.29	S				5.93	9.1	1816
At5g59670	gi 22327979	leucine-rich repeat protein kinase, putative	signal transduction	14	-0.215	1	1	97.03	S				5.93	9.1	1816
At1g06840	gi 15222211	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	13	-0.180	1	1	103.92	-	plasma membrane			8.6	6.55	6712



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At1g25320	gi 18395641	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	15	-0.073	1	2	76.43	S	plasma membrane			8.6	6.55	6712
At1g27190	gi 15223445	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	17	-0.013	1	1	65.43	S				8.6	6.55	6712
At2g26730	gi 15225780	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	7	-0.190	1	1	71.75	S	plasma membrane			8.6	6.55	6712
At2g31880	gi 15225153	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	8	-0.158	2	1	71.11	S				8.6	6.55	6712
At3g02880	gi 15233013	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	8	-0.091	2	1	67.75	S	plasma membrane	cell wall (sensu Magnoliophyta)		8.6	6.55	6712
At3g08680	gi 15231955	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	10	-0.136	2	1	69.41	S	plasma membrane	cell wall (sensu Magnoliophyta)		8.6	6.55	6712
At3g28450	gi 15233004	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	16	-0.102	2	1	66.95	S	plasma membrane			8.6	6.55	6712
At3g53590	gi 15231843	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	11	-0.232	0	1	87.50	M				8.6	6.55	6712
At5g10020	gi 15238044	leucine-rich repeat transmembrane protein kinase, putative	signal transduction	11	-0.169	1	1	114.72	S	plasma membrane			8.6	6.55	6712
At1g55020	gi 9857526	lipoxygenase - partial coding sequence	signal transduction	2	-0.438	0		98.05	-				5.65	6.44	131
At5g16590	gi 15237379	LRR1; ATP binding / kinase/ protein serine/threonine kinase	signal transduction	10	-0.027	2	1	67.46	S	plasma membrane	cell wall (sensu Magnoliophyta)		8.76	6.55	1718
At1g21880	gi 18395044	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR)	signal transduction	15	0.328	1	1	33.40	S		anchored to		4.85		761
At2g17120	gi 18398317	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR)	signal transduction	20	0.040	1		37.74	S	plasma membrane	anchored to		5.93		558
At5g06320	gi 15239999	NHL3	signal transduction	9	-0.089	1	1	25.95	-	plasma membrane	plasma membrane	14666423(unclear - SUBA);	9.35		1629
At1g27460	gi 18396347	NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding	signal transduction	12	-0.149	0		76.87	-	plasma membrane			8.76	6.31	16
At1g73080	gi 15219370	PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein	signal transduction	18	-0.042	2	1	122.90	S				6.58	6.56	83
At1g77630	gi 30699276	peptidoglycan-binding LysM domain-containing protein	signal transduction	18	0.243	0	1	44.15	S	plasma membrane	anchored to		4.98		2007
At4g38530	gi 557880	phosphoinositide-specific phospholipase C	signal transduction	9	-0.513	0		64.95	-				6.06	8.8	28
At1g49740	gi 18402763	phospholipase C/ phosphoric diester	signal transduction	14	-0.186	0		39.83	S				9.26	6.31	18
At5g58670	gi 18424132	PLC1 (PHOSPHOLIPASE C 1);	signal transduction	11	-0.492	0		64.32	-				6.4	9.1	448
At1g08700	gi 15223879	presenilin family protein	signal transduction	5	0.529	7	8	49.31	S				9.26	4.74	18
At2g33580	gi 15226133	protein kinase family protein / peptidoglycan-binding LysM domain-	signal transduction	13	-0.117	1	1	72.57	S				5.68	6.55	504
At3g24550	gi 13877617	protein kinase-like protein	signal transduction	6	-0.563	1	1	69.27	C	plasma membrane; plasma membrane			8.51	7.14	2665
At5g10290	gi 8953410	protein serine/threonine kinase-like protein	signal transduction	10	-0.202	1	1	68.66	S				9.3	5.85	4395
At2g02220	gi 15227264	PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase	signal transduction	23	-0.164	1	1	112.36	S				5.18	6.54	20
At2g16250	gi 4544402	putative LRR receptor protein kinase	signal transduction	14	-0.128	2	1	99.71	S	plasma membrane	cell wall (sensu Magnoliophyta)		4.95	8.26	723
At3g46280	gi 7799016	putative protein	signal transduction	3	-0.162	1	1	50.50	S				6.32	4.97	23
At5g01950	gi 7329668	putative protein	signal transduction	14	-0.191	1	3	106.23	S				5.32	6.55	4660
At1g51820	gi 9802784	Putative protein kinase	signal transduction	13	-0.140	1	1	98.10	S				6.06	6.47	28
At1g51850	gi 9802795	Putative protein kinase	signal transduction	14	-0.222	1	1	96.12	S				5.52	5.83	25

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At1g51910	gi 9802791	Putative protein kinase	signal transduction	9	-0.228	1	1	98.68	S				5.73	5.48	1634
At1g67890	gi 16604649	putative protein kinase	signal transduction	11	-0.621	0		85.22					5.54	7.6	708
At2g28960	gi 3461838	putative receptor-like protein kinase	signal transduction	13	-0.278	2	1	98.97	S				5.76	9.1	242
At2g37050	gi 4371296	putative receptor-like protein kinase	signal transduction	15	-0.202	1	1	103.49	S	plasma membrane			5.76	5.75	242
At1g29730	gi 9972371	Putative receptor-like serine/threonine	signal transduction	23	-0.154	1		107.68	S				9.16	7.25	370
At1g29740	gi 9972372	Putative receptor-like serine/threonine kinase - partial protein	signal transduction	24	-0.122	3	1	116.53	S				9.78	6.64	170
At4g34440	gi 3641836	putative serine/threonine protein kinase	signal transduction	8	-0.626	1	1	70.90	C				6.06	6.07	28
At4g17170	gi 15235981	RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase	signal transduction	4	-0.230	0		23.17	_				6.96	7.14	36
At5g24390	gi 15238518	RabGAP/TBC domain-containing protein	signal transduction	12	-0.582	0		60.63	C				6.59	7.14	21
At5g59840	gi 15238542	Ras-related GTP-binding family protein	signal transduction	3	-0.298	0		23.83	_				8.35	7.14	261
At1g15530	gi 15218220	receptor lectin kinase, putative	signal transduction	7	-0.131	2	1	73.15	M				11.57	9.1	181
At1g51790	gi 12321675	receptor protein kinase, putative	signal transduction	15	-0.174	1	1	97.78	S				6.68	5.75	629
At5g49760	gi 8978273	receptor protein kinase-like	signal transduction	13	-0.129	2	1	104.71	S				6.11	5.87	17
At5g16900	gi 9755691	receptor protein kinase-like protein	signal transduction	14	-0.148	1	1	97.25	S				5.72	9.1	3135
At4g18250	gi 4375833	receptor serine/threonine kinase-like protein	signal transduction	36	-0.221	1	1	95.27	C				10.34	6.63	24
At1g11350	gi 4008010	receptor-like protein kinase	signal transduction	21	-0.174	1	1	93.24	S				10.11	7.43	39
At4g23250	gi 4008012	receptor-like protein kinase	signal transduction	30	-0.182	3	2	111.65	S				4.97	6.56	778
At5g65240	gi 16648949	receptor-like protein kinase	signal transduction	10	-0.197	1	1	68.77	S				10.11	5.36	39
At3g46330	gi 6522612	receptor-like protein kinase homolog	signal transduction	14	-0.211	2	1	98.68	S				5.76	9.1	242
At4g23190	gi 4127461	receptor-like protein kinase, RLK3	signal transduction	16	-0.292	2	1	74.14	S				7.59	7.78	30
At1g29750	gi 2465923	receptor-like serine/threonine kinase	signal transduction	27	-0.147	1	3	111.56	S				6.6	7.4	38
At3g56100	gi 26996940 9	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-LIKE KINASE; Flags:	signal transduction	11	-0.013	2	3	77.33	_				7.59	5.75	30
At1g51810	gi 75334565	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51810; Flags: Precursor	signal transduction	13	-0.161	1	1	82.82	_				11.02	5.62	259
At2g48010	gi 15227189	RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase	signal transduction	16	-0.051	1	1	67.22	S	plasma membrane			7.03	4.85	54
At1g48480	gi 18402209	RKL1; ATP binding / kinase/ protein serine/threonine kinase	signal transduction	7	-0.190	2	1	71.13	S	plasma membrane			8.3	5.75	1259
At3g17840	gi 18401662	RLK902; ATP binding / kinase/ protein serine/threonine kinase	signal transduction	7	-0.066	1	1	70.41	S	plasma membrane			6.15	5.75	2327
At1g61380	gi 18407151	SD1-29 (S-DOMAIN-1 29); carbohydrate binding / kinase/ protein kinase	signal transduction	22	-0.133	2	2	89.90	S				10.11	8.44	39
At4g23180	gi 3021270	serine/threonine kinase-like protein	signal transduction	15	-0.170	2	1	74.28	_				10.6	6.56	374
At4g23300	gi 3021282	serine/threonine kinase-like protein	signal transduction	17	-0.180	2	1	73.85	S				9.26	7.43	158
At1g56145	gi 6056375	Similar to serine/threonine kinases	signal transduction	15	-0.103	2	1	111.79	S				6.06	8.43	28
At4g12420	gi 15234551	SKU5; copper ion binding / oxidoreductase	signal transduction	3	-0.236	0		65.64	S		cell wall (sensu Magnoliop hyta) & plasma membrane & anchored to	12119380(extracellu lar -SUBA); 12119380(plasma membrane -SUBA);	9.16		6686
At1g61390	gi 15219917	S-locus protein kinase, putative	signal transduction	20	-0.236	2	3	93.05	M				10.11	8.44	39
At1g61490	gi 15219935	S-locus protein kinase, putative	signal transduction	19	-0.151	2	2	89.94	S				10.11	8.44	39
At1g61550	gi 15220528	S-locus protein kinase, putative	signal transduction	19	-0.128	1	2	89.40	S				10.11	8.44	39
At4g32300	gi 2864613	S-receptor kinase -like protein	signal transduction	19	-0.154	1	1	89.74	S				8.35	8.44	268

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At1g53730	gi 15220928	SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	signal transduction	6	-0.201	2	1	78.09	S				10.18	7.14	60
At3g14350	gi 30683104	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	signal transduction	7	-0.231	1	1	77.64	S	plasma membrane			10.09	7.14	32
At1g70250	gi 2194117	Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698)	signal transduction	30	-0.100	0	1	87.51	S				6.23	6.1	147
At3g45600	gi 15231187	TET3 (TETRASPANIN3)	signal transduction	11	0.246	4	4	31.89	S				8.93		442
At5g54380	gi 15239630	THE1 (THESEUS1); kinase/ protein kinase	signal transduction	14	-0.037	1	1	93.30	S	plasma membrane			8.42	9.1	271
At1g66150	gi 15218941	TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	signal transduction	10	-0.131	1	1	102.39	S				9.93	8.85	34
At3g24660	gi 15230141	TMKL1 (transmembrane kinase-like 1); ATP binding / kinase/ protein	signal transduction	13	-0.081	1	1	73.35	S				8.18	5.75	41
At5g46700	gi 15237490	TRN2 (TORNADO 2)	signal transduction	14	0.562	4	4	30.29	S				8.36		650
At2g44790	gi 15224960	UCC2 (UCLACYANIN 2); copper ion binding / electron carrier	signal transduction	3	0.017	2		20.35	S		anchored to		5.83		979
At1g35710	gi 14596041	Unknown protein	signal transduction	12	-0.127	2	1	124.11	S				8.05	6.02	971
At2g23810	gi 13272397	unknown protein	signal transduction	16	0.230	4	1	30.66	S	plasma membrane			6.06		28
At4g17280	gi 24025597	unknown protein	signal transduction	3	0.137	2	1	31.56	S				4.86	5.26	1983
At1g66880	gi 10177797	unnamed protein product	signal transduction	53	-0.301	1	1	144.43	S				5.67	5.78	22
At5g43980	gi 9758557	unnamed protein product	signal transduction	13	-0.188	1	1	32.61	S		cell wall (sensu Magnoliophyta)		8.61	9.1	469
At1g56120	gi 6056372	Very similar to receptor-like serine/threonine kinase	signal transduction	20	-0.088	1	1	114.58	M				4.53	6.02	31
At5g01310	gi 15240948	basic helix-loop-helix (bHLH) family	transcription	16	-0.535	0		101.39	C				9.66	4.85	26
At2g34160	gi 52696237	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At2g34160	transcription	0	-0.475	0		14.62	_				4.53	5.34	31
At1g20220	gi 8778978	Contains similarity to pigpen protein from Mus musculus gb AF224264 and contains protein of unknown function DUF78 PF 01918 domain. ESTs gb N38077, gb BE037702, gb AV442191, gb AV441368, gb Z17998, gb AV527266, gb AV520794	transcription	1	-1.095	0		33.76	_		cell wall (sensu Magnoliophyta)		9.65	5.34	205
At3g61260	gi 15233068	DNA-binding family protein / remorin family protein	transcription	2	-0.765	0		23.14	_				5.55	5.34	90
At2g45820	gi 601843	DNA-binding protein	transcription	2	-0.814	0		20.97	_	plasma membrane			6.06	8.63	399
At5g52470	gi 6003681	fibrillarlin homolog	transcription	3	-0.392	0		32.83	M		nucleolus	15827145(nucleus - SUBA); 10829025(nucleus - SUBA); 10806224(nucleus - SLIBA);	10.09	6.44	32
At5g41315	gi 22327493	GL3 (GLABROUS 3); protein binding / transcription factor	transcription	14	-0.433	0		70.54	_		nucleus	15590742(nucleus - SUBA); 14561633(nucleus - SUBA);	6.32	4.85	23
At5g64610	gi 15237745	HAM1 (HISTONE ACETYLTRANSFERASE OF THE MYST FAMILY 1); H3/H4 histone acetyltransferase/ histone acetyltransferase/	transcription	12	-0.586	0		51.44	_				8.76	9.33	16
At5g22650	gi 30688577	HD2B (HISTONE DEACETYLASE 2B); histone deacetylase	transcription	1	-1.120	0		32.35	_			15144374(nucleus - SUBA);	4.68	8.93	97

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At3g18100	gi 18401769	MYB4R1 (myb domain protein 4R1); transcription factor	transcription	20	-0.940	0		96.09	_				5.67	6.02	22
At1g76010	gi 18410994	nucleic acid binding	transcription	1	-1.210	0		37.38	_				5.01	5.34	35
At1g65330	gi 15218644	PHE1 (PHERES1); DNA binding / transcription factor	transcription	6	-0.557	0		31.95	_				5.64	7.14	27
At1g77800	gi 12323292	putative phorbol ester / diacylglycerol binding protein; 61157-67783	transcription	52	-0.644	0		156.70	_				6.59	5.34	21
At3g53460	gi 681902	RNA-binding protein cp29	transcription	2	-0.488	0		36.01	C	plastid stroma	chloroplast	16633814(plastid - SUBA);	5.18	6.44	20
At5g64200	gi 9843653	splicing factor SC35	transcription	0	-1.584	0		35.17	_		nuclear speck	15133128(nucleus - SUBA);	11.54	10.34	81
At1g27750	gi 6693023	T22C5.20	transcription	22	-0.362	0		117.45	_				9.66	5.34	26
At1g02080	gi 42561615	transcriptional regulator-related	transcription	37	-0.082	0		263.90	_				8.76	5.34	16
At3g15030	gi 8777486	unnamed protein product	transcription	2	-0.818	0		45.96	_				8.61	6.44	469
At5g24450	gi 9758533	unnamed protein product	transcription	10	-0.705	0		63.64	_				8.61	5.34	469
At4g20380	gi 30685085	zinc finger protein (LSD1)	transcription	14	-0.139	0		19.56	M			16957775(cytosol - SUBA); 16957775(nucleus - SUBA);	5.64	6.31	27
At2g39350	gi 15225076	ABC transporter family protein	transporters	5	0.087	6	6	82.33	_				9.5	4.85	52
At5g06530	gi 18415230	ABC transporter family protein	transporters	6	0.051	5	6	82.93	_				9.5	4.85	52
At3g30842	gi 9294504	ABC transporter-like protein	transporters	13	-0.067	11	11	160.13	_				7.52	4.85	143
At3g47780	gi 4741195	ABC transporter-like protein	transporters	18	-0.059	7	6	105.05	_				7.52	4.85	143
At2g47000	gi 15226477	ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	transporters	8	0.107	9	11	139.03	_	plasma membrane	membrane		6.16	4.85	817
At4g30190	gi 15234666	AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	transporters	7	0.097	8	10	104.40	_	plasma membrane	plasma membrane	16851869(plasma membrane -SUBA); 15923333(plasma membrane -SUBA); 15722471(plasma membrane -SUBA); 11226186(plasma membrane -SUBA);	6.54	9.01	780
At5g57350	gi 15242103	AHA3; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	transporters	9	0.052	8	10	104.45	_	plasma membrane	plasma membrane		6.73	9.01	202
At3g47950	gi 30692952	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	transporters	6	0.128	8	10	105.72	_	plasma membrane			6.08	7.14	132
At2g07560	gi 15225747	AHA6 (Arabidopsis H(+)-ATPase 6);	transporters	10	0.028	9	10	105.01	_				6.58	7.14	83
At1g80660	gi 6730723	aha9, 5' partial; 1-2403	transporters	8	0.005	8	10	105.21	_				4.68	9.01	98
At5g04930	gi 18414733	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative	transporters	18	0.018	10	10	130.33	_				5.26		48
At1g44100	gi 608673	amino acid permease	transporters	10	0.485	10	11	52.54	_				8.57	8.85	238
At2g38290	gi 7140936	ammonium transporter	transporters	3	0.536	11	11	50.77	_	plasma membrane	plasma membrane	16699542(plasma membrane -SUBA); 16649109(plasma membrane -SUBA); 12481062(plasma membrane -SUBA); 17026539(plasma membrane -SUBA);	7.71	4.19	44
At4g13510	gi 15236300	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	transporters	9	0.360	9	10	53.58	S	plasma membrane	plasma membrane	16917981(plasma membrane -SUBA);	7.08	4.19	1226
At4g38510	gi 15010616	AT4g38510/F20M13_70	transporters	2	-0.273	0		54.31	_				6.11	6.44	17
At5g26340	gi 15010580	AT5g26340/F9D12_17	transporters	7	0.520	12	12	57.42	_	plasma membrane			9.16	9.1	370
At3g47730	gi 22331647	ATATH1; ATPase, coupled to transmembrane movement of substances /	transporters	15	0.083	6	6	108.69	M				8.05	4.85	971

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At5g61730	gi 15240334	ATATH11; ATPase, coupled to transmembrane movement of substances /	transporters	13	0.113	6	6	104.50	M				4.95	4.85	723
At3g45060	gi 15230589	ATNRT2.6; nitrate transmembrane	transporters	8	0.385	11	11	58.64	_				6.6	8.85	38
At1g08090	gi 15223123	ATNRT2:1 (NITRATE TRANSPORTER 2:1); nitrate transmembrane transporter	transporters	10	0.312	11	11	57.71	_			17573350(endoplasmic reticulum - SUBA); 17583518(plasma membrane -SUBA); 17573350(plasma	5.67	8.85	22
At2g38940	gi 15224985	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	transporters	6	0.323	11	12	58.60	_	plasma membrane			8.35	9.33	2091
At1g57990	gi 15217805	ATPUP18; purine transmembrane transporter	transporters	6	0.435	10	10	44.18	_	plasma membrane	membrane		6.9	7.14	61
At5g57110	gi 8843813	Ca <sup>2+</sup> -transporting ATPase-like protein	transporters	11	0.028	6	9	116.18	_	plasma membrane	plasma membrane	16267044(plasma membrane -SUBA); 16230331(plasma membrane -SUBA);	7.85	7.05	3489
At3g54700	gi 186511064	carbohydrate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	transporters	6	0.319	7	9	58.33	_				8.35	9.33	268
At1g11260	gi 16520	glucose transporter	transporters	7	0.484	12	12	57.61	_	plasma membrane			9.1	9.1	754
At1g69480	gi 12597793	hypothetical protein	transporters	12	-0.179	8	8	90.60	_				9.01	9.33	319
At5g40780	gi 30693666	LHT1; amino acid transmembrane	transporters	6	0.484	11	11	49.81	_				5.64	8.85	27
At5g58270	gi 9187883	mitochondrial half-ABC transporter	transporters	4	-0.018	5	6	80.42	M	mitochondria	mitochondrion	17517886(mitochondrion -SUBA); 11158531(mitochondrion -SUBA);	6.06	4.85	28
At1g72150	gi 15218382	PATL1 (PATELLIN 1); transporter	transporters	2	-0.535	0		64.05	_				4.82	8.93	614
At1g22530	gi 15219901	PATL2 (PATELLIN 2); transporter	transporters	1	-0.533	0		76.01	_				4.92	8.93	221
At3g16340	gi 18401096	PDR1; ATPase, coupled to transmembrane movement of substances	transporters	14	0.063	13	13	160.30	C				8.53	4.85	750
At2g26910	gi 15225814	PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	transporters	13	0.078	13	12	161.27	_				7.52	4.85	143
At2g37280	gi 15228112	PDR5 (PLEIOTROPIC DRUG RESISTANCE 5); ATPase, coupled to transmembrane movement of substances	transporters	19	0.065	13	13	160.25	_				8.32	4.85	53
At1g59870	gi 15218936	PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane	transporters	15	0.047	13	13	165.08	C		plasma membrane	16473969(plasma membrane -SUBA);	8.08	4.85	3150
At5g49990	gi 9758398	permease	transporters	6	0.498	11	12	57.32	_				9.8	8.93	68
At3g55320	gi 15233244	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances	transporters	16	0.092	13	11	155.16	_				10.34	4.85	24
At3g62150	gi 15228695	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances	transporters	7	0.095	9	11	139.76	_	plasma membrane			6.43	4.85	588
At4g32390	gi 15236781	phosphate translocator-related	transporters	5	0.592	9	10	39.02	S				6.32	4.74	23
At5g43350	gi 15239848	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen	transporters	6	0.351	11	12	57.62	S				9.11	9.33	2525

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At4g35100	gi 1688296	plasma membrane intrinsic protein PIP3	transporters	4	0.451	6	6	29.74	_	plasma membrane	plasma membrane	16236160(plasma membrane -SUBA); 10737809(plasma membrane -SUBA);	10.18	5.26	60
At2g18960	gi 166746	plasma membrane proton pump H+ ATPase	transporters	8	0.077	10	10	104.23	_	plasma membrane			6.25	9.01	389
At3g55740	gi 15228183	PROT2 (PROLINE TRANSPORTER 2); L-proline transmembrane transporter/ amino acid transmembrane transporter	transporters	3	0.653	11	11	48.09	_		plasma membrane	15618414(plasma membrane -SUBA);	6.59	8.85	21
At2g29940	gi 3420057	putative ABC transporter	transporters	13	0.053	11	12	159.87	_				7.52	4.85	143
At2g36380	gi 4581139	putative ABC transporter	transporters	16	0.051	12	12	164.21	M				5.19	7.52	587
At2g27810	gi 3860251	putative membrane transporter	transporters	7	0.196	11	12	76.68	C	plasma membrane		16982705(plasma membrane -SUBA);	6.4	9.47	448
At1g69870	gi 12325237	putative peptide transporter; 37139-33250	transporters	9	0.246	10	11	68.42	_	plasma membrane			5.23	9.08	82
At5g43360	gi 2149973	putative proton/phosphate cotransporter	transporters	6	0.388	11	12	57.26	_				5.38	9.11	663
At2g37180	gi 15228096	RD28 (RESPONSIVE TO DESICCATION 28); water channel	transporters	4	0.501	6	6	30.43	_				5.95	5.26	40
At1g30410	gi 75333513	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABCC.12; Short=AtABCC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName: Full=Multidrug resis	transporters	16	0.126	12	13	164.21	_				5.52	4.85	25
At2g24520	gi 12230479	RecName: Full=ATPase 5, plasma membrane-type; AltName: Full=Proton	transporters	11	0.073	10	10	102.66	_				6.11	7.14	43
At3g51670	gi 15230555	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	transporters	3	-0.450	0		46.51	_				7.59	8.93	30
At1g32050	gi 15222550	secretory carrier membrane protein (SCAMP) family protein	transporters	5	0.233	4	4	30.06	_		mitochond rion		10.92	8.93	42
At1g66950	gi 5103820	Similar to gb Z70524 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF 00005 ABC transporter family. ESTs gb N97039 and gb T43169	transporters	14	0.025	12	14	165.20	C				8.05	4.85	1936
At2g25600	gi 30682817	SPIK (Shaker Pollen Inward K+ channel); cyclic nucleotide binding / inward rectifier potassium channel/ potassium channel	transporters	9	-0.121	5	4	99.20	_				8.39	9.08	15
At3g19930	gi 15230987	STP4 (SUGAR TRANSPORTER 4); carbohydrate transmembrane transporter/ monosaccharide transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen	transporters	7	0.559	11	12	57.10	_	plasma membrane			8.36	9.1	1046
At1g71880	gi 15217601	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	transporters	7	0.472	12	12	54.86	_			18359840(plasma membrane -SUBA); 16581873(plasma membrane -SUBA);	9.04	9.1	92
At1g30690	gi 14334978	unknown protein	transporters	1	-0.586	0		61.19	_				6.08	4.9	642
At4g16370	gi 15451020	Unknown protein	transporters	13	0.295	10	10	71.29	_				4.86	9.08	1983
At5g61740	gi 10176867	unnamed protein product	transporters	12	-0.029	4	4	93.92	_	plasma membrane			8.61	4.85	469
At1g13210	gi 15222212	ACA.I (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding	unknown	17	-0.080	9	10	136.59	M				6.54	6.54	294
At1g31810	gi 18647910	actin binding	unknown	18	-0.502	0		135.52	_				9.49	6.51	19
At5g09610	gi 15242461	APUM21 (Arabidopsis Pumilio 21); RNA binding / binding	unknown	5	-0.575	0		58.78	_				9.66	8.11	26
At1g52320	gi 15450411	At1g52320/F19K6_7	unknown	3	-0.831	0		46.66	_				6.06	7.81	28
At1g51640	gi 15217995	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding	unknown	15	-0.379	0		76.20	_				5.52	8.02	25

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At1g78880	gi 15219232	balbiani ring 1-related / BR1-related	unknown	7	-0.163	2	2	50.11	_	plasma membrane			9.66	9.54	26
At3g49670	gi 15229189	BAM2 (BARELY ANY MERISTEM 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	unknown	16	0.036	1	1	109.25	S				5.95	5.95	40
At4g23630	gi 15236556	BTI1 (VIRB2-INTERACTING PROTEIN 1)	unknown	2	-0.068	3	4	30.53	_			15494553(cytosol - SUBA);	8.32	8.32	102
At4g11220	gi 15237093	BTI2 (VIRB2-INTERACTING PROTEIN 2)	unknown	2	-0.144	3	4	30.28	_			15494553(cytosol - SUBA);	8.32	8.61	102
At1g51570	gi 15217968	C2 domain-containing protein	unknown	10	-0.235	3	3	89.16	_				5.64	9.13	27
At4g20260	gi 15235363	DREPP plasma membrane polypeptide family protein	unknown	0	-0.706	0		24.58	_	plasma membrane		15060130(plasma membrane -SUBA);	4.99	4.99	660
At4g00310	gi 18411286	EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8)	unknown	4	-0.848	0		33.19	_				8.39	5.74	15
At1g61900	gi 3367523	ESTs gb AA728658 and gb N95943 come from this gene	unknown	23	0.067	0		47.03	S		anchored to		6.25	6.26	210
At1g03230	gi 18379072	extracellular dermal glycoprotein, putative / EDGP, putative	unknown	12	0.232	0		46.15	S				9.33	9.33	243
At3g24255	gi 8778279	F14D16.18	unknown	9	-0.363	0		84.88	_				8.39	6.94	15
At1g28340	gi 6560758	F3M18.23	unknown	9	-0.139	1	2	68.42	S				9.66	8.57	26
At3g66652	gi 15230765	fip1 motif-containing protein	unknown	18	-1.273	0		113.34	_				9.49	5.68	19
At1g27090	gi 15223426	glycine-rich protein	unknown	4	-0.825	0		46.02	_			15141064(cytosol - SUBA); 15141064(unclear - SUBA);	5.26	5.26	1203
At4g02030	gi 30428194	glycosyltransferase family 14 protein	unknown	5	-0.336	0		88.52	_				6.65	5.9	77
At1g26130	gi 15222647	haloacid dehalogenase-like hydrolase family protein	unknown	22	-0.004	10	10	133.80	M				6.17	5.91	345
At3g52470	gi 15231227	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	unknown	4	0.182	1	1	23.10	S				6.11	9.8	17
At1g65010	gi 5042434	Hypothetical protein	unknown	9	-0.890	0		149.73	C				8.35	4.92	2091
At2g30480	gi 11074141	hypothetical protein	unknown	11	-1.138	0		71.09	_				7.63	5.21	46
At5g17460	gi 9755770	hypothetical protein	unknown	1	-1.174	0		35.92	M				9.01	7.62	319
At2g18210	gi 67848448	hypothetical protein At2g18200	unknown	0	-0.748	0		14.43	M				6.9	10.49	61
At1g72270	gi 12323666	hypothetical protein; 75067-63678	unknown	60	-0.008	0	4	312.05	_		mitochond rion		5.64	5.57	27
At5g04420	gi 15237715	kelch repeat-containing protein	unknown	5	-0.407	0		56.66	_				9.49	5.65	19
At3g15410	gi 2760084	leucine-rich repeat protein	unknown	10	-0.111	0		64.11	M				4.97	6.01	29
At1g25570	gi 42562316	leucine-rich repeat protein-related	unknown	11	-0.022	1	1	68.97	S				5.08	5.23	134
At4g36945	gi 4006878	MAP3K-like protein kinase	unknown	16	-0.268			43.70	S				8.2	4.99	812
AtMg0052	gi 13449330	maturase	unknown	9	-0.246	0		75.45	_				6.06	10.06	28
At3g03530	gi 18396577	NPC4 (NONSPECIFIC PHOSPHOLIPASE C4); hydrolase, acting on ester bonds / phospholipase C	unknown	8	-0.587	0		60.72	_		plasma membrane		5.82	5.82	109
At4g20740	gi 15233383	pentatricopeptide (PPR) repeat-containing protein	unknown	17	-0.169	0		82.43	C				8.57	8.26	174
At5g61800	gi 15240355	pentatricopeptide (PPR) repeat-containing protein	unknown	13	-0.001	0		56.05	M				8.57	8.66	174
At1g09520	gi 18391032	protein binding / zinc ion binding	unknown	13	-0.475	0		28.03	C				9.66	8.77	26
At1g59820	gi 5080816	Putative ATPase	unknown	26	-0.045	8	7	137.75	M				8.53	7.84	1043
At5g50200	gi 13624657	putative component of high affinity nitrate transporter	unknown	4	-0.130	1	1	23.40	S				5.01	9.28	35
At2g01050	gi 7267525	putative protein	unknown	6	-0.376	0		56.34	_				5.32	8.36	4660
At3g44150	gi 7635460	putative protein	unknown	8	0.027	0		27.09	S				5.98	9.23	115
At3g57430	gi 6706414	putative protein	unknown	22	-0.029	0		99.28	C	plastid			5.32	6.94	4660
At3g60920	gi 8388608	putative protein	unknown	30	-0.225	0	4	211.75	_				5.32	5.77	4660
At4g32285	gi 2864615	putative protein	unknown	5	-0.537	0		70.56	_				5.32	5.77	4660
At4g33700	gi 3549672	putative protein	unknown	6	0.183	3	5	47.11	S	plasma membrane			5.32	5.73	4660
At5g01730	gi 7327832	putative protein	unknown	19	-0.678	0		128.62	_				8.75	4.56	2584
At5g30520	gi 7413621	putative protein	unknown	2	0.310	0		13.24	M				5.32	4.98	4660

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At5g27650	gi 30690738	PWWP domain-containing protein	unknown	6	-0.693	0		118.10					5.67	6.34	22
At5g22140	gi 22326972	pyridine nucleotide-disulphide oxidoreductase family protein	unknown	2	-0.165	0		39.71					8.32	9.23	53
At5g14770	gi 223635763	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial; Flags: Precursor	unknown	19	-0.007	0		105.32	M			15269332(mitochondrion -SUBA);	9.69	8.37	1110
At4g18060	gi 16974680	SH3 domain-containing protein 3	unknown	3	-0.572	0		39.53	M				6.58	6.4	837
At1g78740	gi 3834329	Similar to gi 2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig	unknown	6	0.179	0		32.83	M				6.92	8.14	49
At1g11820	gi 3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene	unknown	1	0.048	1		42.35	S				5.26	5.66	48
At5g16020	gi 15237248	stress protein-related	unknown	9	-0.257	2	1	73.34	S				5.64	5.34	27
At1g17820	gi 9665060	Strong similarity to a hypothetical protein T18K17.13 gi 6598861 from Arabidopsis thaliana BAC T18K17 gb AC010556 and contains a PH PF00169 domain	unknown	9	-0.518	1		90.11	S				6.59	9.08	21
At2g20990	gi 18399541	SYTA (SYNAPTOTAGMIN A)	unknown	4	-0.256	1	1	61.75	S				7.18	7.18	88
At3g01185	gi 5091549	T10024.18	unknown	6	-0.089	0		16.81	S				5.52	7.56	25
At2g19580	gi 15224802	TET2 (TETRASPANIN2)	unknown	14	0.363	4	3	30.13	S				9.93	8.81	34
At4g28050	gi 15234374	TET7 (TETRASPANIN7)	unknown	17	0.201	4	4	29.93	S				9.78	8.86	149
At4g30430	gi 15234743	TET9 (TETRASPANIN9)	unknown	15	0.225	4	3	31.06	S				8.84	8.84	70
At2g31290	gi 15224649	ubiquitin thiolesterase	unknown	6	-0.526	0		48.70	M				5.18	9.2	20
At1g17147	gi 11683010	unknown	unknown	1	-0.515			10.90					9.26	4.89	2334
At3g45460	gi 11683126	unknown	unknown	24	-0.229	0		44.78					9.26	8.34	2334
At5g46680	gi 21618238	unknown	unknown	14	-0.058	0		52.51					9.26	8.89	2334
At1g22250	gi 30687784	unknown protein	unknown	8	-0.661	0		22.77					4.86	8.73	1983
At1g64050	gi 15222608	unknown protein	unknown	16	-0.752	0		72.90					4.86	9.54	1983
At2g03350	gi 18395537	unknown protein	unknown	2	-0.274	0		20.17					4.86	9.57	1983
At2g21990	gi 15227126	unknown protein	unknown	2	-0.421	0		27.64	C				4.86	9.3	1983
At2g25800	gi 3643603	unknown protein	unknown	12	-0.308	0		109.97	C				4.86	8.38	1983
At2g26570	gi 15225334	unknown protein	unknown	2	-0.803	0		89.30					4.86	5.01	1983
At2g27260	gi 18401372	unknown protein	unknown	3	-0.363	1	1	27.58					4.86	9.59	1983
At2g28310	gi 30683843	unknown protein	unknown	5	-0.469	1	1	43.18	M				4.86	8.76	1983
At2g30600	gi 1946359	unknown protein	unknown	21	-0.190	0		92.18					4.86	5.71	1983
At2g31410	gi 18402657	unknown protein	unknown	2	-1.245	0		22.70					4.86	10.11	1983
At2g40980	gi 15226796	unknown protein	unknown	11	-0.331	0		69.11	C				4.86	5.32	1983
At2g41800	gi 15227437	unknown protein	unknown	5	0.023	0		40.37	S		cell wall (sensu Magnoliophyta)		4.86	9.22	1983
At2g44260	gi 18406495	unknown protein	unknown	6	-0.425	0	1	60.95					4.86	5.74	1983
At2g46150	gi 15225931	unknown protein	unknown	4	0.017	1	1	24.10	C				4.86	9.78	1983
At4g08760	gi 15236604	unknown protein	unknown	11	-0.507	0		58.89					4.86	9.49	1983
At4g27595	gi 24025609	unknown protein	unknown	8	-0.888	0		138.01	C				4.86	5.04	1983
At4g33390	gi 15234171	unknown protein	unknown	3	-0.750	0		87.11					4.86	5.06	1983
At4g35730	gi 79497106	unknown protein	unknown	5	-0.741	0		52.20	C		mitochondrion		4.86	8.13	1983
At4g40020	gi 15236102	unknown protein	unknown	4	-1.080	0		70.03					4.86	5.19	1983
At5g06970	gi 22326641	unknown protein	unknown	16	-0.287	0		124.53					4.86	5.88	1983
At5g19240	gi 15239686	unknown protein	unknown	4	0.084	0		21.34	S				4.86	6.57	1983
At5g28237	gi 26452400	unknown protein	unknown	11	-0.169	0		50.65	M				4.86	6.58	1983
At5g41280	gi 15237619	unknown protein	unknown	13	-0.087	0		31.88	S		anchored to		4.86	5.56	1983
At5g42370	gi 13430796	unknown protein	unknown	8	-0.201	1	1	50.34	S				4.86	9.07	1983
At5g56170	gi 15241141	unknown protein	unknown	8	0.117	0		18.46	S		anchored to		4.86	6.26	1983
At1g69290	gi 12325092	unknown protein; 45065-49536	unknown	9	-0.133	0		73.89	C				6.92	7.57	305
At1g60995	gi 12323328	unknown protein; 69131-60853	unknown	6	-0.095			71.73					9.49	6.11	19



AGI	Accession	Protein description	Functional categories	Cys	Calc.gravy	TMHMM	Aramemnon	Calc.MW	TargetP	Curated Loc.	TAIR Loc.	GFP/YFP loc.	PI	Calc.PI	protein score
At2g15025	gi 9294045	unnamed protein product	unknown	5	0.288			20.71					8.61	4.73	469
At5g39970	gi 10176989	unnamed protein product	unknown	28	-0.199	0		75.62	S		anchored to		4.85	5.12	429
At5g58160	gi 8777317	unnamed protein product	unknown	16	-0.379	0	1	146.32	S				8.61	6.62	469

Accession no., AGI, Arabidopsis gene index. MapManBin, gene function 'bin' used by MapMan. Cys, cysteine residue content in a protein. Calc. gravity, grand average of hydropathicity index indicates the solubility of the proteins. TMHMM, prediction of transmembrane proteins (<http://www.cbs.dtu.dk/services/TMHMM/>). Aramemnon, consensus prediction of transmembrane proteins (<http://aramemnon.botanik.uni-koeln.de>). Calc. MW, the calculated molecular weight (kDA). TargetP, the location predicted by TargetP in combination with LumenP and TMHMM (L:lumen; S: Stroma; M: Membrane; A: ambiguous). Curated Loc., subcellular localization curated by van Wijk lab. Tair Loc., subcellular localization suggested by TAIR (with PubMed reference). PI, PI value. Calc PI, the calculated pI value. GFP/YFP loc., Localization data based on GFP/YFP experiments. (obtained from SUBA and other databases).

Supplementary Table S2-2 Cold- and ABA-responsive proteins in *Arabidopsis* suspension cultured cells (T87 line) at lag growth phase (8-day-old)

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g13210	probable cell cycle control protein; crooked neck-like protein [Arabidopsis thaliana]	cell growth/division		0.31		0.33
At5g03340	transitional endoplasmic reticulum ATPase - Arabidopsis thaliana	cell growth/division	2.15		2.87	
At2g21130	cyclophilin [Arabidopsis thaliana]	cell growth/division	2.75		2.55	
At1g31970	STRS1 (STRESS RESPONSE SUPPRESSOR 1); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis	cell growth/division	2.32			
At4g29090	putative non-LTR retroelement reverse transcriptase [Arabidopsis	cell growth/division		0.26		
At5g57970	methyladenine glycosylase family protein [Arabidopsis thaliana]	cell growth/division		0.32		
At5g37140	tRNA-splicing endonuclease positive effector-related [Arabidopsis	cell growth/division		0.41		
At5g65020	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis thaliana]	cell structure		0.38		0.36
At5g20940	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	cell structure		0.34		0.40
At4g03230	putative receptor kinase [Arabidopsis thaliana]	cell structure		0.22		0.15
At4g03340	glycosyltransferase family 14 protein [Arabidopsis thaliana]	cell structure		0.21		
At1g53840	ATPME1; pectinesterase [Arabidopsis thaliana]	cell structure	2.95		2.59	
At3g14300	ATPMEPCRC; pectinesterase [Arabidopsis thaliana]	cell structure	2.86		2.23	
At1g66250	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis	cell structure	4.53		4.44	
At3g13560	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	cell structure	3.22		3.30	
At4g37410	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	cell structure	9.75		53.10	
At1g74790	F25A4.24 [Arabidopsis thaliana]	cell structure	3.90		3.72	
At4g20830	FAD-binding domain-containing protein [Arabidopsis thaliana]	cell structure	3.31		3.19	
At4g12730	fasciclin-like arabinogalactan-protein 2 [Arabidopsis thaliana]	cell structure	4.68		4.07	
At5g55730	FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1) [Arabidopsis thaliana]	cell structure	4.36		3.44	
At5g44130	FLA13 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 13 PRECURSOR) [Arabidopsis thaliana]	cell structure	6.00		7.43	
At2g04780	FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) [Arabidopsis thaliana]	cell structure	4.58		2.50	
At2g45470	FLA8 (FASCICLIN-LIKE ARABINOOGALACTAN PROTEIN 8) [Arabidopsis thaliana]	cell structure	4.90		4.86	
At1g03870	FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) [Arabidopsis thaliana]	cell structure	5.12		3.36	
At2g01630	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana]	cell structure	2.89		3.18	
At4g31140	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure	2.39		3.28	
At5g56590	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure	2.79		2.53	
At5g04885	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	cell structure	3.90		3.37	
At2g30870	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase	cell structure	2.00		3.31	
At5g48450	pectinesterase-like protein [Arabidopsis thaliana]	cell structure	2.59		3.13	
At5g17820	peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana]	cell structure	4.46		5.57	
At1g42550	PMI1 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	cell structure	3.83		2.52	
At4g25240	Pollen-specific protein precursor like [Arabidopsis thaliana]	cell structure	3.27		2.47	
At2g13820	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	cell structure	6.29		2.38	
At3g58100	putative protein [Arabidopsis thaliana]	cell structure	2.66		3.22	

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At5g51480	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase [Arabidopsis thaliana]	cell structure	4.87		2.47	
At3g46550	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding [Arabidopsis thaliana]	cell structure	3.73		2.09	
At4g27520	unknown [Arabidopsis thaliana]	cell structure	4.44		12.30	
At1g78830	unknown protein [Arabidopsis thaliana]	cell structure	2.53		10.18	
At1g75680	AtGH9B7 (Arabidopsis thaliana glycosyl hydrolase 9B7); catalytic/hydrolase, hydrolyzing O-glycosyl compounds	cell structure	3.13			
At1g01980	ATSEC1A; FAD binding / catalytic/ electron carrier/ oxidoreductase [Arabidopsis thaliana]	cell structure	3.49			
At5g20230	blue copper-binding protein [Arabidopsis thaliana]	cell structure	4.99			
At1g32860	CDS [Arabidopsis thaliana]	cell structure	4.37			
At5g18220	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure	5.35			
At5g61130	PDCB1 (PLASMODESMATA CALLOSE-BINDING PROTEIN 1); callose binding / polysaccharide binding [Arabidopsis thaliana]	cell structure	2.75			
At5g25090	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	cell structure	4.65			
At4g31840	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	cell structure	9.08			
At1g62790	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	cell structure	5.81			
At2g33240	putative myosin heavy chain [Arabidopsis thaliana]	cell structure	2.38			
At2g34730	putative myosin heavy chain [Arabidopsis thaliana]	cell structure	3.44			
At2g25060	similar to early nodulins [Arabidopsis thaliana]	cell structure	7.25			
At5g64080	unnamed protein product [Arabidopsis thaliana]	cell structure	6.26			
At1g68560	alpha-xylosidase precursor [Arabidopsis thaliana]	cell structure			3.36	
At5g15500	ankyrin repeat family protein [Arabidopsis thaliana]	cell structure			193.46	
At5g42100	ATBG_PAP; glucan endo-1,3-beta-D-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	cell structure			4.05	
At1g70710	endo-1,4-beta-glucanase [Arabidopsis thaliana]	cell structure			2.45	
At5g58480	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure			2.23	
At3g49120	peroxidase [Arabidopsis thaliana]	cell structure			29.08	
At4g20890	TUB9; GTP binding / GTPase/ structural molecule [Arabidopsis thaliana]	cell structure			3.64	
At5g43470	resistance protein Hod3 [Arabidopsis thaliana]	disease/defence		0.32		
At4g23260	putative protein [Arabidopsis thaliana]	disease/defence		0.47		
At4g01700	chitinase, putative [Arabidopsis thaliana]	disease/defence	2.51		4.89	
At1g20440	cor47 [Arabidopsis thaliana]	disease/defence	3.81		8.24	
At1g30360	ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	disease/defence	2.35		2.04	
At2g43610	glycoside hydrolase family 19 protein [Arabidopsis thaliana]	disease/defence	2.57		5.88	
At3g53990	universal stress protein (USP) family protein [Arabidopsis thaliana]	disease/defence	4.18		5.71	
At4g02450	T14P8.5 [Arabidopsis thaliana]	disease/defence	2.07			
At3g09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) [Arabidopsis thaliana]	disease/defence	3.49			
At5g47910	respiratory burst oxidase protein D [Arabidopsis thaliana]	disease/defence	4.05			
At3g11010	putative disease resistance protein [Arabidopsis thaliana]	disease/defence	8.68			
At4g23670	major latex protein-related / MLP-related [Arabidopsis thaliana]	disease/defence			57.46	
At5g22060	putative [Arabidopsis thaliana]	disease/defence			3.87	
At1g20780	SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase [Arabidopsis thaliana]	disease/defence			3.15	
At4g32840	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase [Arabidopsis thaliana]	energy		0.28		0.29
AtCg00490	ribulosebiphosphate carboxylase [Arabidopsis thaliana]	energy		0.22		
At5g09600	putative protein [Arabidopsis thaliana]	energy		0.40		

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g55440	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	energy	3.37		4.39	
AtCg00480	ATP synthase CF1 beta subunit [Arabidopsis thaliana]	energy	2.41		2.27	
At1g79550	PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase [Arabidopsis thaliana]	energy	2.02			
AtCg00120	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	energy	6.81			
At1g76850	unknown protein [Arabidopsis thaliana]	intracellular traffic		0.44		
At5g08680	ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana]	intracellular traffic	4.80		2.45	
At1g71820	EST gb AA712174 comes from this gene [Arabidopsis thaliana]	intracellular traffic	2.90		2.38	
At3g10380	SEC8 (SUBUNIT OF EXOCYST COMPLEX 8) [Arabidopsis thaliana]	intracellular traffic	2.17		2.42	
At4g28100	unknown protein [Arabidopsis thaliana]	intracellular traffic	5.03		3.15	
At3g08600	unknown protein [Arabidopsis thaliana]	intracellular traffic	2.74		2.17	
At3g56190	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein [Arabidopsis thaliana]	intracellular traffic	2.69			
At1g17620	At1g17620 [Arabidopsis thaliana]	intracellular traffic	3.18			
At2g33120	formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	intracellular traffic	2.24			
At3g52400	syntaxin protein [Arabidopsis thaliana]	intracellular traffic	2.53			
At3g11820	SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor [Arabidopsis thaliana]	intracellular traffic	2.49			
At5g08080	SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor [Arabidopsis thaliana]	intracellular traffic	2.74			
At3g09740	SYP71 (SYNTAXIN OF PLANTS 71); protein transporter [Arabidopsis thaliana]	intracellular traffic	2.47			
At1g45688	unknown protein [Arabidopsis thaliana]	intracellular traffic	2.00			
At5g19230	unknown protein [Arabidopsis thaliana]	intracellular traffic	2.83			
At5g62630	Unknown protein [Arabidopsis thaliana]	intracellular traffic	2.84			
At5g11890	unknown protein [Arabidopsis thaliana]	intracellular traffic	3.11			
At5g64370	beta-ureidopropionase [Arabidopsis thaliana]	intracellular traffic			2.58	
At3g17350	unknown protein [Arabidopsis thaliana]	intracellular traffic			4.32	
At1g21380	VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana]	intracellular traffic			5.27	
At5g58060	YKT61 [Arabidopsis thaliana]	intracellular traffic			2.74	
At5g17920	Chain A, A. Thaliana Cobalamine Independent Methionine Synthase	metabolism		0.28		0.49
At5g36880	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative [Arabidopsis thaliana]	metabolism		0.12		
At5g11520	ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana]	metabolism		0.23		
At4g11850	PLDGAMMA1; phospholipase D [Arabidopsis thaliana]	metabolism		0.48		
At4g35790	ATPLDDELTA; phospholipase D [Arabidopsis thaliana]	metabolism	2.02		4.99	
At1g43710	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	metabolism	3.75		6.70	
At1g34430	F12K21.24 [Arabidopsis thaliana]	metabolism	3.18		2.91	
At2g18730	putative diacylglycerol kinase [Arabidopsis thaliana]	metabolism	3.42		3.77	
At3g03780	putative methionine synthase [Arabidopsis thaliana]	metabolism	3.33		2.11	
At4g26690	putative protein [Arabidopsis thaliana]	metabolism	4.58		4.57	
At5g55480	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	metabolism	4.19		4.03	
At5g58090	AT5g58090/k21119_70 [Arabidopsis thaliana]	metabolism	2.65			
At4g29360	beta-1, 3-glucanase-like protein [Arabidopsis thaliana]	metabolism	4.63			
At3g25860	dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana]	metabolism	2.27			

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At5g54500	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor [Arabidopsis thaliana]	metabolism	2.47			
At4g16155	lipoamide dehydrogenase [Arabidopsis thaliana]	metabolism	2.45			
At4g23850	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase [Arabidopsis thaliana]	metabolism	2.24			
At1g66970	SVL2 (SHV3-LIKE 2); glycerophosphodiester phosphodiesterase/kinase [Arabidopsis thaliana]	metabolism	3.77			
At5g58070	TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter [Arabidopsis thaliana]	metabolism	2.91			
At3g54200	unknown protein [Arabidopsis thaliana]	metabolism	2.86			
At1g35710	Unknown protein [Arabidopsis thaliana]	metabolism			3.32	
At5g10080	aspartyl protease family protein [Arabidopsis thaliana]	protein destination and storage		0.27		0.49
At3g26940	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	protein destination and storage		0.26		0.31
At1g12470	F5O11.22 [Arabidopsis thaliana]	protein destination and storage		0.41		0.34
At3g58880	F-box family protein [Arabidopsis thaliana]	protein destination and storage		0.42		0.35
At5g51770	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.29		0.44
At2g23200	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.46		0.22
At5g56460	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage		0.16		0.27
At5g03320	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage		0.35		0.47
At4g28400	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	protein destination and storage		0.44		0.12
At2g39110	putative protein kinase [Arabidopsis thaliana]	protein destination and storage		0.41		0.34
At2g39110	serine/threonine protein kinase, putative [Arabidopsis thaliana]	protein destination and storage		0.35		0.34
At5g56380	unnamed protein product [Arabidopsis thaliana]	protein destination and storage		0.31		0.40
At1g45000	26S proteasome regulatory complex subunit p42D, putative [Arabidopsis thaliana]	protein destination and storage		0.28		
At1g04730	AAA-type ATPase family protein [Arabidopsis thaliana]	protein destination and storage		0.45		
At1g62290	aspartyl protease family protein [Arabidopsis thaliana]	protein destination and storage		0.41		
At3g18190	chaperonin, putative [Arabidopsis thaliana]	protein destination and storage		0.42		
At3g60040	F-box family protein [Arabidopsis thaliana]	protein destination and storage		0.21		
At5g01020	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.25		
At5g41260	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.30		
At5g57610	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.38		
At2g28940	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage		0.42		
At2g17220	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage		0.30		
At2g29000	putative receptor-like protein kinase [Arabidopsis thaliana]	protein destination and storage		0.16		
At1g56140	receptor protein kinase, putative [Arabidopsis thaliana]	protein destination and storage		0.36		
At1g16670	Unknown protein [Arabidopsis thaliana]	protein destination and storage		0.45		
At5g01520	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	protein destination and storage		0.31		
At5g42020	luminal binding protein (BiP) [Arabidopsis thaliana]	protein destination and storage				0.07
At3g02740	aspartyl protease family protein [Arabidopsis thaliana]	protein destination and storage	2.49		2.79	
At3g52500	AT3g52500/F22O6_120 [Arabidopsis thaliana]	protein destination and storage	2.72		4.29	
At1g63500	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	2.29		2.27	
At1g69840	band 7 family protein [Arabidopsis thaliana]	protein destination and storage	2.18		2.41	
At1g65240	Belongs to PF00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	protein destination and storage	2.58		3.86	
At5g46570	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	2.67		3.48	

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At1g05690	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	protein destination and storage	2.71		2.80	
At5g47850	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase [Arabidopsis thaliana]	protein destination and storage	4.12		5.35	
At2g17760	hypothetical protein At2g17760 [imported] - Arabidopsis thaliana	protein destination and storage	3.68		7.24	
At1g79560	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this gene [Arabidopsis thaliana]	protein destination and storage	2.65		7.57	
At2g39360	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	3.95		6.98	
At4g23200	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	3.34		4.09	
At4g02630	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	3.19		2.83	
At5g24010	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	2.39		2.19	
At1g70520	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	2.98		2.10	
At3g46290	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	3.18		2.28	
At2g16600	ROC3; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	protein destination and storage	2.33		2.81	
At4g23270	serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	4.67		2.38	
At3g56450	ALPHA-SNAP1; binding / soluble NSF attachment protein [Arabidopsis thaliana]	protein destination and storage	3.42			
At2g02800	APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	2.03			
At3g09830	AT3G09830 [Arabidopsis thaliana]	protein destination and storage	2.58			
At4g00710	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	2.51			
At1g53430	Contains similarity to receptor-like serine/threonine kinase from Arabidopsis thaliana gb AF024648 and contains multiple leucine rich PF00560 repeats and protein kinase PF00069 domain. ESTs gb T04455, gb N38129 come from this gene	protein destination and storage	3.04			
At5g25860	F-box family protein [Arabidopsis thaliana]	protein destination and storage	2.82			
At4g23940	FtsH protease, putative [Arabidopsis thaliana]	protein destination and storage	3.09			
At4g37910	heat shock protein 70 like protein [Arabidopsis thaliana]	protein destination and storage	3.68			
At3g23750	leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	2.15			
At1g69960	PP2A (SERINE/THREONINE PROTEIN PHOSPHATASE 2A); protein serine/threonine phosphatase [Arabidopsis thaliana]	protein destination and storage	2.43			
At1g54610	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	2.41			
At3g54030	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	2.43			
At4g04910	putative component of vesicle-mediated transport [Arabidopsis	protein destination and storage	2.37			
At3g48820	putative protein [Arabidopsis thaliana]	protein destination and storage	2.61			
At1g06700	Putative protein kinase [Arabidopsis thaliana]	protein destination and storage	2.09			
At4g08850	receptor protein kinase-like protein [Arabidopsis thaliana]	protein destination and storage	2.64			
At3g14840	receptor-like serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	2.50			
At1g70490	Strong similarity to gb M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb AA712956, gb T46403, gb T46050, gb AI100391 and gb Z25043 come from this gene	protein destination and storage	2.61			
At2g42360	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis	protein destination and storage	20.03			
At1g11910	aspartic proteinase [Arabidopsis thaliana]	protein destination and storage			5.24	
At1g05840	Contains similarity to nucellin from Hordeum vulgare gb U87148. ESTs gb T22068, gb F14251, gb F14237, gb F14242 come from this gene [Arabidopsis thaliana]	protein destination and storage			9.03	
At1g07870	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage			2.48	

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At2g07180	putative protein kinase [Arabidopsis thaliana]	protein destination and storage			2.17	
At3g17410	serine/threonine protein kinase, putative [Arabidopsis thaliana]	protein destination and storage			3.14	
At2g47610	60S ribosomal protein L7A (RPL7aA) [Arabidopsis thaliana]	protein synthesis		0.24		0.11
At1g04270	40S ribosomal protein S15 [Arabidopsis thaliana]	protein synthesis		0.44		0.42
At4g02930	mitochondrial elongation factor Tu [Arabidopsis thaliana]	protein synthesis		0.42		
At2g04390	40S ribosomal protein S17 (RPS17A) [Arabidopsis thaliana]	protein synthesis	5.64		2.15	
At3g02080	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	protein synthesis	2.62		3.15	
At5g61170	40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana]	protein synthesis	9.87		7.15	
At5g35530	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	protein synthesis	2.27		2.11	
At4g29390	40S ribosomal protein S30 (RPS30B) [Arabidopsis thaliana]	protein synthesis	45.98		44.25	
At3g04840	40S ribosomal protein S3A (RPS3aA) [Arabidopsis thaliana]	protein synthesis	2.73		2.33	
At5g46430	60S ribosomal protein L32 (RPL32B) [Arabidopsis thaliana]	protein synthesis	3.42		2.92	
At1g33120	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	protein synthesis	3.46		2.92	
At2g37270	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana]	protein synthesis	4.88		3.11	
At5g60390	elongation factor 1-alpha [Arabidopsis thaliana]	protein synthesis	3.61		3.62	
At1g56070	elongation factor EF-2 [Arabidopsis thaliana]	protein synthesis	2.13		2.78	
At2g33370	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene [Arabidopsis thaliana]	protein synthesis	4.37		2.54	
At2g36160	40S ribosomal protein S14 (RPS14A) [Arabidopsis thaliana]	protein synthesis	3.86			
At2g21580	40S ribosomal protein S25 (RPS25B) [Arabidopsis thaliana]	protein synthesis	5.86			
At4g39200	40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana]	protein synthesis	4.26			
At3g43980	40S ribosomal protein S29 (RPS29A) [Arabidopsis thaliana]	protein synthesis	4.85			
At5g62300	40S ribosomal protein [Arabidopsis thaliana]	protein synthesis	6.17			
At2g37190	60S ribosomal protein L12 (RPL12A) [Arabidopsis thaliana]	protein synthesis	2.35			
At1g27400	60S ribosomal protein L17 (RPL17A) [Arabidopsis thaliana]	protein synthesis	6.63			
At1g67430	60S ribosomal protein L17 (RPL17B) [Arabidopsis thaliana]	protein synthesis	10.64			
At2g19730	60S ribosomal protein L28 (RPL28A) [Arabidopsis thaliana]	protein synthesis	6.11			
At4g29410	60S ribosomal protein L28 (RPL28C) [Arabidopsis thaliana]	protein synthesis	3.26			
At5g56710	60S ribosomal protein L31 (RPL31C) [Arabidopsis thaliana]	protein synthesis	2.51			
At2g39390	60S ribosomal protein L35 (RPL35B) [Arabidopsis thaliana]	protein synthesis	2.11			
At2g43460	60S ribosomal protein L38 (RPL38A) [Arabidopsis thaliana]	protein synthesis	6.72			
At4g10450	60S ribosomal protein L9 (RPL90D) [Arabidopsis thaliana]	protein synthesis	2.49			
At1g43170	ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome [Arabidopsis thaliana]	protein synthesis	2.51			
At1g22780	PFL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana]	protein synthesis	6.49			
At5g20180	ribosomal protein L36 family protein [Arabidopsis thaliana]	protein synthesis	2.17			
At1g20620	F5M15.5 [Arabidopsis thaliana]	protein synthesis			7.69	
At2g36170	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana]	protein synthesis			2.26	
At1g74020	strictosidine synthase [Arabidopsis thaliana]	secondary metabolism	5.34		28.87	
At1g74010	strictosidine synthase family protein [Arabidopsis thaliana]	secondary metabolism	4.16			
At4g34050	caffeoyl-CoA O-methyltransferase-like protein [Arabidopsis thaliana]	secondary metabolism			11.81	
At2g14510	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction		0.13		0.19
At4g34440	putative serine/threonine protein kinase [Arabidopsis thaliana]	signal transduction		0.13		0.13
At4g28490	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction		0.17		0.16
At2g19230	kinase [Arabidopsis thaliana]	signal transduction		0.18		0.38
At4g23180	serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction		0.29		0.29

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g10620	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative [Arabidopsis thaliana]	signal transduction		0.36		0.48
At1g11300	ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	signal transduction		0.39		0.39
At5g59840	Ras-related GTP-binding family protein [Arabidopsis thaliana]	signal transduction		0.39		0.38
At1g35160	At1g35160/T32G9_30 [Arabidopsis thaliana]	signal transduction		0.04		
At2g17820	ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase [Arabidopsis thaliana]	signal transduction		0.32		
At5g49780	ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction		0.29		
At1g55610	BRL1 (BRI 1 LIKE); kinase [Arabidopsis thaliana]	signal transduction		0.11		
At3g61050	CaLB protein [Arabidopsis thaliana]	signal transduction		0.22		
At3g57530	calcium-dependent protein kinase [Arabidopsis thaliana]	signal transduction		0.40		
At2g03150	emb1579 (embryo defective 1579); binding / calcium ion binding [Arabidopsis thaliana]	signal transduction		0.28		
At2g28970	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction		0.29		
At1g67890	putative protein kinase [Arabidopsis thaliana]	signal transduction		0.12		
At1g29740	Putative receptor-like serine/threonine kinase - partial protein [Arabidopsis thaliana]	signal transduction		0.32		
At4g18250	receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction		0.44		
At3g46330	receptor-like protein kinase homolog [Arabidopsis thaliana]	signal transduction		0.38		
At1g61380	SD1-29 (S-DOMAIN-1 29); carbohydrate binding / kinase/ protein kinase [Arabidopsis thaliana]	signal transduction		0.29		
At1g70250	Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698) [Arabidopsis thaliana]	signal transduction		0.29		
At1g66880	unnamed protein product [Arabidopsis thaliana]	signal transduction		0.43		
At3g53590	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction				0.25
At1g73080	PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction				0.45
At1g51790	receptor protein kinase, putative [Arabidopsis thaliana]	signal transduction				0.49
At4g34460	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding [Arabidopsis thaliana]	signal transduction	3.80		7.06	
At3g07390	AT3g07390/F21O3_10 [Arabidopsis thaliana]	signal transduction	3.77		3.01	
At5g01600	ATFER1; ferric iron binding / iron ion binding [Arabidopsis thaliana]	signal transduction	6.67		14.32	
At3g08510	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	signal transduction	2.50		3.69	
At4g18760	AtRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	signal transduction	3.57		2.69	
At4g39400	BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2.13		4.58	
At5g24430	calcium dependent protein kinase-like protein [Arabidopsis thaliana]	signal transduction	2.12		2.59	
At2g32450	calcium-binding EF hand family protein [Arabidopsis thaliana]	signal transduction	2.28		2.46	
At1g05150	calcium-binding EF hand family protein [Arabidopsis thaliana]	signal transduction	2.92		3.09	
At1g52540	Contains PF 00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene	signal transduction	2.71		4.00	
At4g21940	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2.32		2.23	
At1g43890	F9C16.3 [Arabidopsis thaliana]	signal transduction	2.80		2.19	



AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g51740	IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	3.08		2.41	
At1g51800	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	2.64		3.80	
At3g02880	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3.27		2.26	
At1g06840	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3.52		2.91	
At3g08680	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	2.38		3.90	
At2g26730	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	2.93		4.44	
At2g31880	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	4.39		5.01	
At5g16590	LRR1; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2.78		2.27	
At1g21880	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) [Arabidopsis thaliana]	signal transduction	3.73		2.30	
At2g17120	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) [Arabidopsis thaliana]	signal transduction	2.78		2.85	
At5g06320	NHL3 [Arabidopsis thaliana]	signal transduction	3.51		3.10	
At1g77630	peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	signal transduction	5.97		4.86	
At5g58670	PLC1 (PHOSPHOLIPASE C 1); phospholipase C [Arabidopsis thaliana]	signal transduction	3.22		14.06	
At2g16250	putative LRR receptor protein kinase [Arabidopsis thaliana]	signal transduction	3.97		4.18	
At5g24390	RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	signal transduction	6.58		7.40	
At1g15530	receptor lectin kinase, putative [Arabidopsis thaliana]	signal transduction	2.60		3.39	
At4g23190	receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	signal transduction	3.24		4.45	
At3g56100	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-LIKE KINASE; Flags: Precursor	signal transduction	4.79		5.76	
At4g12420	SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana]	signal transduction	3.34		3.15	
At3g45600	TET3 (TETRASPANIN3) [Arabidopsis thaliana]	signal transduction	2.48		4.10	
At2g23810	unknown protein [Arabidopsis thaliana]	signal transduction	2.70		3.69	
At2g40300	ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding [Arabidopsis thaliana]	signal transduction	5.34			
At4g38580	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding [Arabidopsis thaliana]	signal transduction	2.18			
At4g35860	ATGB2 (GTP-BINDING 2); GTP binding [Arabidopsis thaliana]	signal transduction	3.64			
At5g03520	ATRAB8C; GTP binding [Arabidopsis thaliana]	signal transduction	3.40			
At5g47520	AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding [Arabidopsis thaliana]	signal transduction	2.85			
At5g20020	atran2 [Arabidopsis thaliana]	signal transduction	2.45			
At3g49750	AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana]	signal transduction	3.23			
At3g25290	auxin-responsive family protein [Arabidopsis thaliana]	signal transduction	3.56			
At4g12980	auxin-responsive protein, putative [Arabidopsis thaliana]	signal transduction	3.37			
At2g41410	calmodulin like protein [Arabidopsis thaliana]	signal transduction	3.04			
At3g51550	FER (FERONIA); kinase/ protein kinase [Arabidopsis thaliana]	signal transduction	2.84			
At4g17530	GTP-binding RAB1C like protein [Arabidopsis thaliana]	signal transduction	3.75			
At5g60270	lectin protein kinase family protein [Arabidopsis thaliana]	signal transduction	2.36			
At2g01820	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	2.70			

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g28450	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	2.61			
At3g24550	protein kinase-like protein [Arabidopsis thaliana]	signal transduction	2.64			
At3g46280	putative protein [Arabidopsis thaliana]	signal transduction	4.91			
At1g51850	Putative protein kinase [Arabidopsis thaliana]	signal transduction	2.66			
At4g17170	RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase [Arabidopsis thaliana]	signal transduction	2.19			
At5g16900	receptor protein kinase-like protein [Arabidopsis thaliana]	signal transduction	2.11			
At3g17840	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2.62			
At1g61390	S-locus protein kinase, putative [Arabidopsis thaliana]	signal transduction	11.13			
At4g32300	S-receptor kinase -like protein [Arabidopsis thaliana]	signal transduction	2.64			
At3g14350	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	signal transduction	2.41			
At1g66150	TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2.61			
At5g43980	unnamed protein product [Arabidopsis thaliana]	signal transduction	2.30			
At5g35735	auxin-responsive family protein [Arabidopsis thaliana]	signal transduction			6.05	
At4g29900	Ca <sup>2+</sup> -transporting ATPase-like protein [Arabidopsis thaliana]	signal transduction			3.41	
At4g09000	GF14chi isoform [Arabidopsis thaliana]	signal transduction			5.10	
At2g33580	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	signal transduction			6.96	
At1g51810	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51810; Flags: Precursor	signal transduction			3.65	
At1g53730	SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	signal transduction			2.70	
At4g17280	unknown protein [Arabidopsis thaliana]	signal transduction			13.94	
At1g27750	T22C5.20 [Arabidopsis thaliana]	transcription		0.17		0.13
At2g34160	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At2g34160	transcription		0.43		0.37
At3g15030	unnamed protein product [Arabidopsis thaliana]	transcription		0.46		0.18
At5g01310	basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana]	transcription	2.50			
At3g61260	DNA-binding family protein / remorin family protein [Arabidopsis thaliana]	transcription	2.54			
At2g45820	DNA-binding protein [Arabidopsis thaliana]	transcription	2.66			
At5g52470	fibrillarlin homolog [Arabidopsis thaliana]	transcription		0.21		
At5g24450	unnamed protein product [Arabidopsis thaliana]	transcription		0.32		
At1g02080	Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]	transcription		0.33		
At3g53460	RNA-binding protein cp29 [Arabidopsis thaliana]	transcription		0.41		
At1g02080	transcriptional regulator-related [Arabidopsis thaliana]	transcription			4.34	
At1g80660	aha9, 5' partial; 1-2403 [Arabidopsis thaliana]	transporters		0.15		0.15
At2g26910	PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters		0.29		0.31
At4g32390	phosphate translocator-related [Arabidopsis thaliana]	transporters		0.31		0.36
At1g30410	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABCC.12; Short=AtABCC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName:	transporters		0.22		0.26

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At3g51670	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	transporters		0.29		0.30
At3g62150	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters		0.04		
At2g25600	SPIK (Shaker Pollen Inward K <sup>+</sup> channel); cyclic nucleotide binding / inward rectifier potassium channel/ potassium channel [Arabidopsis thaliana]	transporters		0.20		
At3g47780	ABC transporter-like protein [Arabidopsis thaliana]	transporters		0.41		
At4g38510	AT4g38510/F20M13_70 [Arabidopsis thaliana]	transporters		0.50		
At1g08090	ATNRT2:1 (NITRATE TRANSPORTER 2:1); nitrate transmembrane transporter [Arabidopsis thaliana]	transporters				0.41
At3g47950	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	transporters	2.27		10.31	
At5g04930	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	transporters	2.73		2.69	
At4g13510	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana]	transporters	2.42		2.63	
At3g47730	ATATH1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	transporters	2.75		3.01	
At2g38940	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	transporters	2.81		3.40	
At5g57110	Ca <sup>2+</sup> -transporting ATPase-like protein [Arabidopsis thaliana]	transporters	2.67		2.59	
At1g69480	hypothetical protein [Arabidopsis thaliana]	transporters	3.91		7.41	
At3g16340	PDR1; ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	3.04		4.24	
At3g55320	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	3.33		2.35	
At5g43350	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen	transporters	2.81		3.03	
At4g35100	plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]	transporters	2.35		6.18	
At2g27810	putative membrane transporter [Arabidopsis thaliana]	transporters	3.14		2.11	
At1g69870	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	transporters	3.97		10.43	
At3g30842	ABC transporter-like protein [Arabidopsis thaliana]	transporters	2.32			
At2g38290	ammonium transporter [Arabidopsis thaliana]	transporters	2.24			
At5g26340	AT5g26340/F9D12_17 [Arabidopsis thaliana]	transporters	3.36			
At5g61730	ATATH11; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	transporters	3.20			
At1g11260	glucose transporter [Arabidopsis thaliana]	transporters	2.64			
At5g58270	mitochondrial half-ABC transporter [Arabidopsis thaliana]	transporters	2.26			
At1g59870	PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	transporters	2.65			
At2g24520	RecName: Full=ATPase 5, plasma membrane-type; AltName: Full=Proton pump 5	transporters	43.03			
At3g19930	STP4 (SUGAR TRANSPORTER 4); carbohydrate transmembrane transporter/ monosaccharide transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	transporters	2.43			
At1g71880	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	transporters	3.25			

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At2g39350	ABC transporter family protein [Arabidopsis thaliana]	transporters			3.50	
At5g57350	AHA3; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	transporters			4.12	
At1g44100	amino acid permease [Arabidopsis thaliana]	transporters			5.31	
At1g57990	ATPUP18; purine transmembrane transporter [Arabidopsis thaliana]	transporters			5.94	
At1g72150	PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana]	transporters			6.56	
At2g37280	PDR5 (PLEIOTROPIC DRUG RESISTANCE 5); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters			11.52	
At5g49990	permease [Arabidopsis thaliana]	transporters			14.00	
At2g29940	putative ABC transporter [Arabidopsis thaliana]	transporters			14.75	
At2g37180	RD28 (RESPONSIVE TO DESICCATION 28); water channel [Arabidopsis thaliana]	transporters			16.38	
At1g71880	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	transporters	3.25			0.07
At1g31810	actin binding [Arabidopsis thaliana]	unknown		0.38		0.36
At1g51640	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding [Arabidopsis thaliana]	unknown		0.42		0.40
At4g23630	BTI1 (VIRB2-INTERACTING PROTEIN 1) [Arabidopsis thaliana]	unknown		0.32		0.24
At4g00310	EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana]	unknown		0.29		0.44
At3g15410	leucine-rich repeat protein [Arabidopsis thaliana]	unknown		0.32		0.38
At4g06544	putative protein [Arabidopsis thaliana]	unknown		0.22		0.46
At5g30520	putative protein [Arabidopsis thaliana]	unknown		0.23		0.24
At5g14770	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial; Flags: Precursor	unknown		0.23		0.33
At2g31290	ubiquitin thiolesterase [Arabidopsis thaliana]	unknown		0.40		0.41
At1g17147	unknown [Arabidopsis thaliana]	unknown		0.30		0.14
At2g26570	unknown protein [Arabidopsis thaliana]	unknown		0.23		0.37
At4g08760	unknown protein [Arabidopsis thaliana]	unknown		0.33		0.20
At5g58160	unnamed protein product [Arabidopsis thaliana]	unknown		0.23		0.30
At1g22250	unknown protein [Arabidopsis thaliana]	unknown		0.09		
At4g32285	putative protein [Arabidopsis thaliana]	unknown		0.25		
At4g11220	BTI2 (VIRB2-INTERACTING PROTEIN 2) [Arabidopsis thaliana]	unknown		0.26		
At3g57430	putative protein [Arabidopsis thaliana]	unknown		0.30		
At5g28237	unknown protein [Arabidopsis thaliana]	unknown		0.31		
At2g15025	unnamed protein product [Arabidopsis thaliana]	unknown		0.33		
At3g24255	F14D16.18 [Arabidopsis thaliana]	unknown		0.36		
AtMg00520	maturase [Arabidopsis thaliana]	unknown		0.41		
At1g09520	protein binding / zinc ion binding [Arabidopsis thaliana]	unknown		0.41		
At4g27595	unknown protein [Arabidopsis thaliana]	unknown		0.41		
At1g26130	haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	unknown		0.43		
At5g61800	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	unknown		0.47		
At4g35730	unknown protein [Arabidopsis thaliana]	unknown				0.40
At1g13210	ACA.1 (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding [Arabidopsis thaliana]	unknown	4.06		4.24	
At1g52320	At1g52320/F19K6_7 [Arabidopsis thaliana]	unknown	10.72		14.22	
At4g20260	DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana]	unknown	2.99		10.00	
At1g03230	extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana]	unknown	2.70		5.16	

AGI	Protein description	Functional categories	Responsive plasma membrane proteins			
			CA		ABA	
			Increased	Decreased	Increased	Decreased
At5g17460	hypothetical protein [Arabidopsis thaliana]	unknown	20.65		9.43	
At2g30480	hypothetical protein [Arabidopsis thaliana]	unknown	3.57		3.98	
At4g36945	MAP3K-like protein kinase [Arabidopsis thaliana]	unknown	4.30		2.92	
At3g45460	unknown [Arabidopsis thaliana]	unknown	11.19		6.69	
At2g25800	unknown protein [Arabidopsis thaliana]	unknown	2.71		3.63	
At2g28310	unknown protein [Arabidopsis thaliana]	unknown	2.97		3.13	
At2g27260	unknown protein [Arabidopsis thaliana]	unknown	5.77		2.81	
At2g21990	unknown protein [Arabidopsis thaliana]	unknown	10.19		2.34	
At5g19240	unknown protein [Arabidopsis thaliana]	unknown	2.37		2.20	
At1g78880	balbiani ring 1-related / BR1-related [Arabidopsis thaliana]	unknown	2.09			
At1g61900	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	unknown	4.74			
At1g28340	F3M18.23 [Arabidopsis thaliana]	unknown	2.21			
At1g27090	glycine-rich protein [Arabidopsis thaliana]	unknown	2.32			
At5g04420	kelch repeat-containing protein [Arabidopsis thaliana]	unknown	2.04			
At1g25570	leucine-rich repeat protein-related [Arabidopsis thaliana]	unknown	2.60			
At3g44150	putative protein [Arabidopsis thaliana]	unknown	2.32			
At3g60920	putative protein [Arabidopsis thaliana]	unknown	3.71			
At1g11820	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene [Arabidopsis thaliana]	unknown	2.06			
At1g17820	Strong similarity to a hypothetical protein T18K17.13 gi 6598861 from Arabidopsis thaliana BAC T18K17 gb AC010556 and contains a PH PF 00169 domain	unknown	2.45			
At4g28050	TET7 (TETRASPANIN7) [Arabidopsis thaliana]	unknown	2.17			
At5g46680	unknown [Arabidopsis thaliana]	unknown	6.67			
At2g46150	unknown protein [Arabidopsis thaliana]	unknown	2.13			
At4g40020	unknown protein [Arabidopsis thaliana]	unknown	3.95			
At5g42370	unknown protein [Arabidopsis thaliana]	unknown	6.19			
At5g39970	unnamed protein product [Arabidopsis thaliana]	unknown	2.84			
At1g51570	C2 domain-containing protein [Arabidopsis thaliana]	unknown			20.30	
At2g40980	unknown protein [Arabidopsis thaliana]	unknown			8.89	
At2g41800	unknown protein [Arabidopsis thaliana]	unknown			7.11	
At4g33700	putative protein [Arabidopsis thaliana]	unknown			3.51	
At5g56170	unknown protein [Arabidopsis thaliana]	unknown			3.31	
At2g19580	TET2 (TETRASPANIN2) [Arabidopsis thaliana]	unknown			2.58	

Cold acclimation was conducted at 2°C for 2 days and ABA treatment (25µM) was conducted at 23°C for 1 day. The protein was reported to increased or decreased protein in their abundance when its abundance was higer (fold change >2) or lower (<0.5) after cold accliamtion or ABA treatment than control cells.

Supplementary Table 3-1 LC-MS/MS identification of differential expressed proteins of plasma membrane in Arabidopsis T87 suspension-cultured cells.

Accession no., AGI, Arabidopsis gene index. MapManBin, gene function 'bin' used by MapMan. Cys, cysteine residue content in a protein. Calc. gravity, grand average of hydropathicity index indicates the solubility of the proteins. TMHMM, prediction of transmembrane proteins (<http://www.cbs.dtu.dk/services/TMHMM/>). Aramemnon, consensus prediction of transmembrane proteins (<http://aramemnon.botanik.uni-koeln.de>). Calc. MW, the calculated molecular weight (kDa). TargetP, the location predicted by TargetP in combination with LumenP and TMHMM (L: lumen; S: Stroma; M: Membrane; A: ambiguous). Curated Loc., subcellular localization curated by van Wijk lab. Tair Loc., subcellular localization suggested by TAIR (with PubMed reference). PI, PI value. Calc PI, the calculated pi value. GFP/YFP loc., Localization data based on GFP/YFP experiments. (obtained from SUBA and other databases).

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep_MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravity	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep_BinName
AT1G49240	gi1669389	actin 8 [Arabidopsis thaliana]	Cell growth/division	actin 8	actin 8 (ACT8)	not plastid		31.1 cell.organisation	31.1		0	-		Actin(1)	4	-0.181	41.86	5.37	15028209(Total chloroplast); 15539469(vacuole); 16358359(cell suspension (Gamborg)); 16526091(Cu-binding root); 15815986(seedling); 15815986(Leaf); 15276459(trichomes); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17317660(Plasma Membrane proteome); 17407188(cotyledon); 17916636(root (NaCl stress)); 18814325(cotyledon);		0.83	0.825	2	cell.organisation
AT3G46520	gi15231447	actin-12 [Arabidopsis thaliana]	Cell growth/division	actin-12	actin 12 (ACT12)		mitochondrion & cytoskeleton	31.1 cell.organisation	31.1		0	-		Actin(1)	4	-0.222	41.8	5.37	MitroDB(Mitochondrial proteome); 16242667(mature Pollen); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 18599647(seed proteome); 18814325(cotyledons); 19546170(mature pollen grains); 18796151(cell wall (hypocotyl));		0.263	0.236	21	cell.organisation
AT1G35720	gi1429207	annexin [Arabidopsis thaliana]	Cell growth/division	annexin 1	Annexin - AnnAt1, involved in Golgi-mediated secretion	cytosol	cytosol & membrane	31.1 cell.organisation	31.1		0	-		Annexin(4)	2	-0.603	36.2	5.21	15028209(Total chloroplast); 11826309(thylakoid peripheral&lumen); 16207701(chloroplast stroma); 16287169(Cell Wall proteome); 15539469(vacuole); 16242667(mature Pollen); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension- Cd-up); 16502469(cell suspension-CD-down); 16526091(Cu-binding root);		0.795	0.797	6	cell.organisation
AT2G34040	gi18403429	Apoptosis inhibitory protein 5 (API5) [Arabidopsis thaliana]	Cell growth/division	Apoptosis inhibitory protein 5 (API5)	apoptosis inhibitory 5 (API5) family protein			33.99 development.unspecified	33.99		0	-		API5(1) DUF965(1)	6	-0.456	61.65	8.05	19200160(flower-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.231	0.244	27	development.unspecified

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT1G52540	gi5903051	Contains PF00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene [Arabidopsis thaliana]	Cell growth/division	Protein kinase superfamily protein	protein kinase, putative	plasma membrane		33.99 development.unspecified	33.99		0	-		Pkinase(1) Pkinase_Tyr(1) RIO1(1)	6	-0.398	39.87	5.71	15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	development.unspecified
AT2G21130	gi2443757	cyclophilin [Arabidopsis thaliana]	Cell growth/division	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase			31.3.1 cell.cycle.peptidylprolyl isomerase	31.3.1		0	-		Pro_isomerase(1)	4	-0.249	18.46	8.32	16242667(mature Pollen); 16247729(mature Pollen); 16400686(floem_sap B. napa); 17644812(plasma membrane - suspension cells); 18814325(cotyledons); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 18716313(secreted proteins (cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(leaves); 18445580(leaves);		0.546	0.828	7	cell.cycle.peptidylprolyl isomerase
AT2G21130	gi2443757	cyclophilin [Arabidopsis thaliana]	cell growth/division	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase			31.3.1 cell.cycle.peptidylprolyl isomerase	31.3.1		0	-		Pro_isomerase(1)	4	-0.249	18.46	8.32	16242667(mature Pollen); 16247729(mature Pollen); 16400686(floem_sap B. napa); 17644812(plasma membrane - suspension cells); 18814325(cotyledons); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 18716313(secreted proteins (cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(leaves); 18445580(leaves);		0.546	0.828	7	cell.cycle.peptidylprolyl isomerase
AT1G29030	gi10764848	FIK23.1 [Arabidopsis thaliana]	Cell growth/division	Apoptosis inhibitory protein 5 (API5)				33.99 development.unspecified	33.99		0	-		API5(1) GRP(1)	6	-0.516	62.28	8.91			0	0	0	development.unspecified
AT1G74790	gi5882745	F25A4.24 [Arabidopsis thaliana]	Cell growth/division	catalytics	unknown protein	plasma membrane	anchored to membrane	31.1 cell.organisation	31.1	1	2	S			28	-0.31	75.23	5.28	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(PlasmaMembrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 18998720(SA-induced secreted proteome (cell culture)); 19525416(leaf		0.036	0.04	410	cell.organisation
AT1G06760	gi116314	histone H1-1 [Arabidopsis thaliana]	Cell growth/division	winged-helix DNA-binding transcription factor family protein				28.1.3 DNA.synthesis/chromatin structure.histone	28.1.3		0	-		Linker_histone(1)	0	-0.57	28.95	10.77			0	0	0	DNA.synthesis/chromatin structure.histone

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT5G59870	gi15238549	histone H2A 6 [Arabidopsis thaliana]	Cell growth/division	histone H2A 6	histone H2A, putative	nucleus		28.1.3 DNA.synthesis/c hromatin structure.histone	28.1.3		0	-		CBFD_NFYB_HMF(1) Histone(1)	0	-0.345	15.97	10.55	15496452(nucleolus); 17660356(tonoplast (Brassica oleracea buds)); 19995728(propylastid (Brassica napus)); 18814325(cotyledons); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19376835(leaf phosphoproteins); 19423572(leaf (wt and clpr2-1)); 20061580(chloroplast envelope)		0.5	0.644	31	DNA.synthesis/c hromatin structure.histone
AT1G52740	gi15219078	histone H2A protein 9 [Arabidopsis thaliana]	Cell growth/division	histone H2A protein 9	histone H2A, putative	nucleus		28.1.3 DNA.synthesis/c hromatin structure.histone	28.1.3		0	-		CBFD_NFYB_HMF(1) Histone(1)	0	-0.341	14.27	10.28	15539469(vacuole); 18814325(cotyledons); 19525416(leaf (wt and clpr4-1 mutant)); 19714877(interactomes 14-3-3 complexes (cell culture)); 20706207(contaminants cell cycle interactome (cell culture)); 20061580(chloroplast envelope)		0.41	0.571	33	DNA.synthesis/c hromatin structure.histone
AT5G59910	gi15238563	histone H2B [Arabidopsis thaliana]	Cell growth/division	Histone superfamily protein	histone H2B	nucleus		28.1.3 DNA.synthesis/c hromatin structure.histone	28.1.3		0	-		CBFD_NFYB_HMF(1) Histone(1)	0	-0.76	16.45	10	15496452(nucleolus); 19200160(flowers-stage 12); 17216043(leaf); 19114538(guard cells Arabidopsis leaf);		0.267	0.274	44	DNA.synthesis/c hromatin structure.histone
AT5G22880	gi1617013	histone H2B like protein [Arabidopsis thaliana]	Cell growth/division	histone B2	histone H2B,	nucleus		28.1.3 DNA.synthesis/c hromatin structure.histone	28.1.3		0	-		CBFD_NFYB_HMF(1) Histone(1)	0	-0.678	15.73	10.05	15496452(nucleolus); 19546170(mature pollen grains); 20166762(guard cells (Arabidopsis));	16463096(nucleus -SUBA); 11251092(nucleus -SUBA);	0.324	0.328	17	DNA.synthesis/c hromatin structure.histone
AT1G18680	gi15221835	HNH endonuclease domain-containing protein [Arabidopsis thaliana]	Cell growth/division	HNH endonuclease domain-containing				28.1 DNA.synthesis/c hromatin structure	28.1		0	C		HNH(1)	10	-0.574	20.29	8.67			0	0	0	DNA.synthesis/c hromatin structure
AT3G54870	gi15541717	kinesin-like protein [Arabidopsis thaliana]	Cell growth/division	Armadillo/beta-catenin repeat family protein / kinesin motor family protein				31.1 cell.organisation	31.1		0	C		Arm(3) Fib_alpha(1) Kinesin(1) Myosin_tail_1(1) Synaptobrevin(1)	7	-0.654	105.2	7.03			0.01	0.01	12	cell.organisation
AT2G35980	gi15227542	late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	Cell growth/division	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family			chloroplast	33.99 development.unsigned	33.99	1	1	-		Hin1(1)	5	-0.07	25.66	9.95		14666423(plastid -SUBA);	0	0	0	development.unsigned
AT5G57970	gi15242914	methyladenine glycosylase family protein [Arabidopsis thaliana]	cell growth/division	DNA glycosylase superfamily protein				28.2 DNA.repair	28.2		0	C		Adenine_glyco(1)	4	-0.468	38.65	9.71			0	0	0	DNA.repair
AT3G13210	gi10172609	probable cell cycle control protein; crooked neck-like protein [Arabidopsis thaliana]	cell growth/division	crooked neck protein, putative / cell cycle protein, putative	crooked neck protein, putative / cell cycle protein, putative			31.3 cell.cycle	31.3		0	-		DUF733(1) HAT(5) Mad3_BUB1_(1) Suf(1)	11	-0.751	78.1	6.82			0.021	0.022	33	cell.cycle
AT3G51690	gi4895169	putative helicase [Arabidopsis thaliana]	Cell growth/division	PIF1 helicase				28.99 DNA.unsigned	28.99		0	-		DUF889(1)	4	-0.301	37.42	6.41			0	0	0	DNA.unsigned
AT4G29090	gi2583130	putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	Cell growth/division	Ribonuclease H-like superfamily protein				28.99 DNA.unsigned	28.99		0	S		RnaseH(1)	12	-0.39	66.71	9.26			0	0	0	DNA.unsigned
AT3G49670	gi15229189	receptor-like kinase BAM2 [Arabidopsis thaliana]	Cell growth/division	Leucine-rich receptor-like protein kinase family protein				33.99 development.unsigned	33.99	1	1	S		LRR_1(4) LRRNT_2(1) Pkinase(1)	16	0.036	109.25	5.95	17317660(Plasma Membrane proteome); 19334764(plasma membrane (cell culture));		0	0	0	development.unsigned
AT1G31970	gi15222526	STRS1 (STRESS RESPONSE SUPPRESSOR 1); ATP binding / ATP-dependent helicase/ nucleic acid binding [Arabidopsis thaliana]	cell growth/division	DEA(D/H)-box RNA helicase family protein	STRS1 (STRESS RESPONSE SUPPRESSOR 1); ATP-dependent			28.1 DNA.synthesis/c hromatin structure	28.1		0	-		DEAD(1) DUF1253(1) Helicase_C(1) Rifin_STEVOR(1)	6	-0.468	59.6	8.69	18463617(suspension cells-phosphorylated proteins); 19376835(leaf phosphoproteins)		0.043	0.045	240	DNA.synthesis/c hromatin structure
AT1G08130	gi8778834	T6D22.23 [Arabidopsis thaliana]	Cell growth/division	DNA ligase 1	DNA ligase 1 (AtLIG1) mitochondrial and nucleus-translation init. starts	cytosol; mitochondria		28.1.5* DNA.synthesis/c hromatin structure.synthesis; 28.2 DNA.repair	28.1.5*; 28.2	1	0	C		DNA_ligase_A_C(1) DNA_ligase_A_M(1) DNA_ligase_A_N(1)	13	-0.341	87.74	8.2	16790030(mitochondrion -SUBA); 15270689(mitochondrion -SUBA); 16790030(nucleus -SUBA);	0.033	0.036	381	DNA.synthesis/c hromatin structure.synthesis; DNA.repair	



AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT3G45600	gi 15231187	TET3 (TETRASPANIN3) [Arabidopsis thaliana]	Cell growth/division	tetraspanin3	TET3 (TETRASPANIN3)			33.99 development.unspecified	33.99	4	4	S		Gemini_mov(1) Tetraspanin(1)	11	0.246	31.89	8.93	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 17660356(tonoplast (Brassica oleracea buds)); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane		0.105	0.119	109	development.unspecified
AT4G28050	gi 15234374	TET7 (TETRASPANIN7) [Arabidopsis thaliana]	Cell growth/division	tetraspanin7				33.99 development.unspecified	33.99	4	4	S		Tetraspanin(1)	17	0.201	29.93	8.86	19546170(mature pollen grains);		0	0	0	development.unspecified
AT5G46700	gi 15237490	Tetraspanin family protein [Arabidopsis thaliana]	Cell growth/division	Tetraspanin family protein	TET1/TRN2 (TETRASPANIN2)			33.99 development.unspecified	33.99	4	4	S		Oxidored_q3(1) Tetraspanin(1)	14	0.562	30.29	8.36	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf wt and clpr4-1		0.03	0.03	217	development.unspecified
AT4G30430	gi 15234743	tetraspanin9 [Arabidopsis thaliana]	Cell growth/division	tetraspanin9				33.99 development.unspecified	33.99	3	4	S		Tetraspanin(1)	15	0.225	31.06	8.84	17317660(Plasma Membrane proteome);		0	0	0	development.unspecified
AT5G03340	gi 11265361	transitional endoplasmic reticulum ATPase - Arabidopsis thaliana	cell growth/division	ATPase, AAA-type, CDC48 protein	cell division cycle protein 48, putative (CDC48)	not plastid		31.2 cell.division	31.2		0	-		AAA(2) AAA_2(1) AAA_3(1) AAA_5(1) Arch_ATPase(1) CDC48_2(1) CDC48_N(1) Mg_chelat	14	-0.384	89.96	5.08	16287169(Cell Wall proteome); 16358359(cell suspension (Gamborg)); 16055689(Glutathionylated suspension cell); 16400686(floem_sap B. napa); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 18599647(seed proteome); 18463617(suspension cells-phosphorylated proteins); 19452453(14-3-3-interacting proteins); 19546170(mature pollen grains); 19525416(leaf wt and clpr4-1		0.426	0.432	15	cell.division
AT5G37140	gi 15240114	tRNA-splicing endonuclease positive effector-related [Arabidopsis thaliana]	cell growth/division	P-loop containing nucleoside triphosphate hydrolases superfamily				28.1 DNA.synthesis/chromatin structure	28.1		0	-		AAA(1) DEAD(1) ResIII(1) UvrD-helicase(1)	14	-0.228	77.29	8.8			0	0	0	DNA.synthesis/chromatin structure
AT4G20890	gi 15233429	TUB9; GTP binding / GTPase/ structural molecule [Arabidopsis thaliana]	Cell growth/division	tubulin beta-9 chain	tubulin beta-9 chain (TUB9)	nucleus		31.1 cell.organisation	31.1		0	-		Tubulin(1) Tubulin_C(1)	12	-0.332	49.66	4.69	16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-CD-up); 16502469(cell suspension-CD-down); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 18431481(chloroplast); 18814325(cotyledons); 19546170(mature pollen grains);	10737809(nucleus -SUBA);	0.559	0.592	47	cell.organisation

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AT1G04820	gi15220329	tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana]	Cell growth/division	tubulin alpha-4 chain	tubulin alpha-2/alpha-4 chain (TUA4)	not plastid		31.1 cell.organisation	31.1		0	-		Tubulin(1) Tubulin_C(1)	12	-0.195	49.54	4.92	15060130(Plasma Membrane proteome); 16287169(Cell Wall proteome); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-Cd-up); 16247729(mature Pollen); 15276459(trichomes); 11402211,12068 122,15047896,1 6679420,170281 49(seed-all-Jobpapers); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cells); 16287169(Cell Wall proteome); 16358359(cell suspension (Gamborg)); 11402211,12068 122,15047896,1 6679420,170281 49(seed-all-Jobpapers); 17317660(Plasma Membrane proteome); 17407188(cotyledon); 17644812(plasma membrane - suspension cells); 18599647(seed proteome); 18633119(young leaf); 18463617(suspension cells-phosphorylated proteins); 15061425(leaf total membranes); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf		0.651	0.695	41	cell.organisation
AT5G19770	gi15241168	tubulin alpha-3/alpha-5 chain [Arabidopsis thaliana]	Cell growth/division	tubulin alpha-3	tubulin alpha-3/alpha-5 chain (TUA3)	not plastid		31.1 cell.organisation	31.1		0	-		Tubulin(1) Tubulin_C(1)	11	-0.154	49.66	4.95	15060130(Plasma Membrane proteome); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf		0.713	0.825	65	cell.organisation
AT2G23810	gi13272397	unknown protein [Arabidopsis thaliana]	Cell growth/division	tetraspanin8	TET8 (TETRASPANIN8)	plasma membrane		33.99 development.unspecified	33.99	1	4	S		Tetraspanin(1)	16	0.23	30.66	8.86	15060130(Plasma Membrane proteome); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf		0.077	0.078	115	development.unspecified
AT3G19130	gi26451217	unknown protein [Arabidopsis thaliana]	Cell growth/division	RNA-binding protein 47B				28.99 DNA.unspecified	28.99		0	-		GRP(1) MPPN(1) RRM_1(3) RRM_3(1) X_fast-SP_rel(1)	3	-0.787	48.12	6.08	18463617(suspension cells-phosphorylated proteins); 19672695(oligo(dT) mRNA-binding proteins (cell culture));		0.062	0.07	144	DNA.unspecified
AT5G39970	gi10176989	unnamed protein product [Arabidopsis thaliana]	Cell growth/division	catalytics			anchored to membrane	35.1 not assigned.no ontology	35.1		0	S		DUF26(1)	28	-0.199	75.62	5.12			0	0	0	not assigned.no ontology
AT5G64940	gi8843758	ABC transporter-like [Arabidopsis thaliana]	Cell structure	ABC2 homolog 13	ABC1 kinase 5 (ABC1K5) also OSA1	envelope-inner-integral		26.56* misc.ABC1k family	26.56*	2	1	C		ABC1(1) APH(1)	2	-0.32	86.02	9.27	12938931(Total chloroplast envelope); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(80S polysomal fraction);		0.293	0.304	113	misc.ABC1k family

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AT5G09810	gi15242516	actin 7 [Arabidopsis thaliana]	Cell structure	actin 7	actin 7 (ACT7) / actin 2	not plastid	mitochondrion	31.1 cell.organisation	31.1		0	-		Actin(1) Phosphodiester(1)	4	-0.179	41.74	5.31	15815986(Seedling); 15815986(Leaf); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15908592(Carboxylated seed protein); 16618929(UNK NOWN-LOPIT-callus); 15734904(S-	15496452(unclear-SUBA);	0.844	0.84	2	cell.organisation
AT1G68560	gi14163997	alpha-xylosidase precursor [Arabidopsis thaliana]	Cell structure	alpha-xylosidase 1	alpha-xylosidase (XYL1)	cell wall	cell wall (sensu Magnoliophyta)	26.3 misc.gluco-galacto- and mannosidases	26.3		0	S		Glyco_hydro_31(1)	11	-0.213	102.4	6.31	15728209(tonoplast); 15593128(Cell Wall proteome); 15815986(Leaf); 17526915(glyco proteome cell wall (stems)); 17660356(tonoplast (Brassica oleracea buds)); 18324730(apoplast leaf); 19200160(flower-stage 12); 18796151(cell wall (hypocotyl)); 18716313(secreted proteins (cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture));		0.513	0.524	37	misc.gluco-galacto- and mannosidases
AT5G15500	gi15242318	ankyrin repeat family protein [Arabidopsis thaliana]	Cell structure	Ankyrin repeat family protein				31.1 cell.organisation	31.1	4	4	S		Ank(1)	3	0.003	39.69	9.66			0	0	0	cell.organisation
AT5G65020	gi15238320	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis thaliana]	Cell structure	annexin 2	Annexin - AnnAt2 - involved in Golgi-mediated secretion	cytosol		31.1 cell.organisation	31.1		0	-		Annexin(4)	2	-0.526	36.27	5.77	11826309(mycoid peripheral&lumen); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16400686(floem_sap B. napa); 15815986(Siliquae); 15815986(Leaf); 18814325(cotyledons); 19200160(flower-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 10508356(mature		0.388	0.356	6	cell.organisation

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AT5G62690	gi13605867	AT5g62700/MRG21_12 [Arabidopsis thaliana]	Cell structure	tubulin beta chain 2	tubulin beta-2/beta-3 chain (TUB2)	not plastid		31.1 cell.organisation	31.1		0	-		Tubulin(1) Tubulin_C(1)	12	-0.421	50.74	4.7	15496452(nucleus -SUBA); 15496452(unclear -SUBA);	0.707	0.694	3	cell.organisation	
AT5G42100	gi15238298	ATBG_PAP: glucan endo-1,3-beta-D-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	Cell structure	beta-1,3-glucanase_putative	glucan endo-1,3-beta-D-glucosidase/ hydrolase (ATBG_PAP/ATBG_PPAP)		cell wall (sensu Magnoliophyta) & anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		1	S		Glyco_hydro_17(1)	6	0.065	45.36	7.03	17270015(endoplasmic reticulum -SUBA); 17270015(plasma membrane -SUBA);	0.292	0.315	43	misc.beta 1,3 glucan hydrolases	
AT1G75680	gi15222328	AtGH9B7 (Arabidopsis thaliana glycosyl hydrolase 9B7); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Cell structure	glycosyl hydrolase 9B7	glycosyl hydrolase family 9 protein, endo-beta-1,4-glucanase			10.6.1 cell wall.degradation, cellulases and beta-1,4-glucanases	10.6.1	1	1	S		Glyco_hydro_9(1)	5	-0.329	57.87	6.77	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis	0.152	0.162	64	cell wall.degradation, cellulases and beta-1,4-glucanases	
AT1G53840	gi15220958	ATPME1: pectinesterase [Arabidopsis thaliana]	Cell structure	pectin methylesterase 1	ATPME1 (pectin methylesterase 1); pectinesterase			10.8.1 cell wall.pectin*esterases.PME	10.8.1	1	1	-		Chordopox_A13 L(1) Mod_r(1) Pectinesterase(1) PME1(1)	8	-0.211	64.15	8.53	16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds));	0.084	0.091	111	cell wall.pectin*esterases.PME	
AT3G14300	gi15231826	ATPMEPCRC: pectinesterase [Arabidopsis thaliana]	Cell structure	pectinesterase family protein				10.8.1 cell wall.pectin*esterases.PME	10.8.1	1	1	-		Pectinesterase(1) PME1(3)	16	-0.187	105.63	8.38		0	0	0	cell wall.pectin*esterases.PME	

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AT1G01980	gi15217586	ATSEC1A; FAD binding / catalytic/ electron carrier/ oxidoreductase [Arabidopsis thaliana]	Cell structure	FAD-binding Berberine family protein	FAD-binding domain-containing protein			26.8 misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	26.8		0	S		BBE(1) FAD_binding_4(81)		-0.219	60.1	9.01	19546170(mature pollen grains); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant));		0.02	0.022	406	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
AT1G66250	gi12323569	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein		anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		0	S		Glyco_hydro_17(1) X8(1)	6	0.042	54.21	5.46	12805588(GBI-anchored-callus); 17317660(Plasma Membrane proteome); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1		0.139	0.143	63	misc.beta 1,3 glucan hydrolases
AT1G66250	gi12323569	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein		anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		0	S		Glyco_hydro_17(1) X8(1)	6	0.042	54.21	5.46	12805588(GBI-anchored-callus); 17317660(Plasma Membrane proteome); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1		0.139	0.143	63	misc.beta 1,3 glucan hydrolases
AT3G13560	gi9280308	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		1	S		Glyco_hydro_17(1) X8(1)	7	0.053	54.42	5.9	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0.093	0.107	90	misc.beta 1,3 glucan hydrolases
AT3G13560	gi9280308	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		1	S		Glyco_hydro_17(1) X8(1)	7	0.053	54.42	5.9	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0.093	0.107	90	misc.beta 1,3 glucan hydrolases
AT3G47000	gi15232707	beta-glucosidase [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase family protein	glycosyl hydrolase family 3 protein			10.6.1 cell wall.degradation, cellulases and beta -1,4-	10.6.1		0	-		Glyco_hydro_3(1) Glyco_hydro_3_C(1)	9	-0.082	66.31	5.2	19525416(leaf (wt and clpr4-1 mutant));		0.084	0.086	132	cell wall.degradation, cellulases and beta -1,4-
AT3G47050	gi15232713	beta-glucosidase [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase family protein	glycosyl hydrolase family 3 protein			10.6.1 cell wall.degradation, cellulases and beta -1,4-	10.6.1		0	-		Glyco_hydro_3(1) Glyco_hydro_3_C(1)	9	-0.139	67.25	5.28	15539469(vacuole);		0.041	0.042	28	cell wall.degradation, cellulases and beta -1,4-

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AT3G22600	gi 18403453	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	Cell structure	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			anchored to membrane	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	26.21		0	S		Tryp_alpha_amy1(1)	8	0.041	17.31	5.04	18436743(specific to roots);		0	0	0	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT5G20230	gi 16203	blue copper-binding protein [Arabidopsis thaliana]	Cell structure	blue-copper-binding protein	plastocyanin-like domain-containing protein		anchored to membrane	26.19 misc.plastocyanin-like	26.19	1	0	S		Cu_bind_like(1) MGC-24(1)	3	0.197	20.05	4.68	15539469(vacuole); 16247729(mature Pollen); 12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 18998720(SA-induced secreted proteome (cell culture)); 19546170(mature pollen grains); 19525416(leaf	16143720(plasma membrane - SUBA);	0.148	0.164	53	misc.plastocyanin-like
AT5G20230	gi 16203	blue copper-binding protein [Arabidopsis thaliana]	Cell structure	blue-copper-binding protein	plastocyanin-like domain-containing protein		anchored to membrane	26.19 misc.plastocyanin-like	26.19	1	0	S		Cu_bind_like(1) MGC-24(1)	3	0.197	20.05	4.68	15539469(vacuole); 16247729(mature Pollen); 12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 18998720(SA-induced secreted proteome (cell culture)); 19546170(mature pollen grains); 19525416(leaf	16143720(plasma membrane - SUBA);	0.148	0.164	53	misc.plastocyanin-like
AT2G03505	gi 22325443	carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	Cell structure	Carbohydrate-binding X8 domain superfamily				26.3 misc.glucosyl, galacto- and mannosidases	26.3		0	S		Keratin_B2(1) X8(1)	8	0.099	17.55	5.44			0	0	0	misc.glucosyl, galacto- and mannosidases
AT1G32860	gi 6910583	CDS [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase superfamily protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		1	S		Glyco_hydro_17(1)	1	0.006	45.42	7.75	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma		0	0	0	misc.beta 1,3 glucan hydrolases
AT1G32860	gi 6910583	CDS [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase superfamily protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		1	S		Glyco_hydro_17(1)	1	0.006	45.42	7.75	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma		0	0	0	misc.beta 1,3 glucan hydrolases
AT3G20130	gi 15231052	CYP705A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	Cell structure	cytochrome P450, family 705, subfamily A, polypeptide				26.10 misc.cytochrome P450	26.1	3	1	S		p450(1)	7	-0.091	58.71	8.93	19334764(plasma membrane (cell culture));		0	0	0	misc.cytochrome P450
AT4G37410	gi 15235541	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	Cell structure	cytochrome P450, family 81, subfamily F, polypeptide 4				26.10 misc.cytochrome P450	26.1		1	S		p450(1)	6	-0.14	57.17	8.77	16618929(ER-LOPIT-callus); 18436743(specific to roots); 19292762(Ubiquitin-affinity seedling (10 d));		0	0	0	misc.cytochrome P450

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AT5G53870	gi15238868	early nodulin-like protein 1 [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 1	plastocyanin-like domain-containing protein		anchored to membrane	26.19 misc.plastocyanin-like	26.19		1	S		Cu_bind_like(1) PT(1)	3	-0.492	38.4	9.2	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	misc.plastocyanin-like
AT1G70710	gi2440033	endo-1,4-beta-glucanase [Arabidopsis thaliana]	Cell structure	glycosyl hydrolase 9B1	CEL1 (cellulase 1); hydrolyzing O-glycosyl compounds			10.6.1 cell wall.degradation.cellulases and beta -1,4-glucanases	10.6.1		1	S		Glyco_hydro_9(1)	6	-0.192	54.61	9.33	18431481(chloroplast); 19200160(flowers-stage 12); 1925416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture));		0.126	0.143	167	cell wall.degradation.cellulases and beta -1,4-glucanases
AT1G30740	gi15221497	FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	Cell structure	FAD-binding Berberine family protein				26.8 misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	26.8		0	S		BBE(1) FAD_binding_4(1)	4	-0.193	59.87	8.71			0	0	0	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
AT4G20830	gi30685222	FAD-binding domain-containing protein [Arabidopsis thaliana]	Cell structure	FAD-binding Berberine family protein	FAD-binding domain-containing protein		cell wall (sensu Magnoliophyta)	26.8 misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	26.8		1	S		BBE(1) FAD_binding_4(1)	4	-0.151	63.56	9.61	15215502(vacuolar proteome); 15276431(Mitochondrial proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome); 18538804(apoplast); 17644812(plasma membrane -		0.274	0.287	49	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
AT4G12730	gi13377778	fasciclin-like arabinogalactan-protein 2 [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan 2	FLA2	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(2) Kp4(1)	3	-0.076	43.45	6.14	14317539(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19200160(flowers-stage 12); 19036721(sterol		0.199	0.225	139	cell wall.cell wall proteins.AGPs

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AT4G12730	gi11337778	fasciclin-like arabinogalactan-protein 2 [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan 2	FLA2	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(2) Kp4(1)	3	-0.076	43.45	6.14	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19200160(flowers-stage 12); 19336721(leaf Wall proteome); 12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 18998720(SA-14506206(plasma membrane (phosphorylated)); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall proteins.AGPs)		0.199	0.225	139	cell wall.cell wall proteins.AGPs
AT5G55730	gi115240570	FLA1 (FASCICLIN-LIKE ARABINOGALACTAN 1) [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan 1	fasciclin-like arabinogalactan-protein (FLA1)	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(2)	4	-0.039	44.85	6.26	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 18998720(SA-14506206(plasma membrane (phosphorylated)); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall proteins.AGPs)		0.316	0.358	58	cell wall.cell wall proteins.AGPs
AT5G44130	gi115241423	FLA13 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 13 PRECURSOR) [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan protein 13 precursor	fasciclin-like arabinogalactan-protein, putative	plasma membrane	cell wall (sensu Magnoliophyta) & anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(1)	1	0.016	26.21	5.53	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall proteins.AGPs)		0.227	0.276	44	cell wall.cell wall proteins.AGPs



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AT2G04780	gi18395849	FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan 7	fasciclin-like arabinogalactan-protein (FLA7)	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(1)	1	0.161	26.85	6.06			0.106	0.115	158	cell wall.cell wall proteins.AGPs
AT2G45470	gi18406799	FLA8 (FASCICLIN-LIKE ARABINOOGALACTAN PROTEIN 8) [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan protein 8	fasciclin-like arabinogalactan-protein (FLA8)	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1	1	0	S		Fasciclin(1) Leader_Thr(1)	2	0.13	43.08	5.43			0.362	0.395	58	cell wall.cell wall proteins.AGPs
AT1G03870	gi18379157	FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) [Arabidopsis thaliana]	Cell structure	FASCICLIN-like arabinogalactan 9	FLA9	plasma membrane	anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1		0	S		Fasciclin(1)	1	0	26.12	8.93			0.194	0.273	106	cell wall.cell wall proteins.AGPs
AT1G29660	gi15220512	GDSL esterase/lipase [Arabidopsis thaliana]	Cell structure	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-motif lipase/hydrolase family protein	not plastid		26.28 misc.GDSL-motif lipase	26.28		0	S		DUF1027(1) Lipase_GDSL(1)	9	-0.224	40.14	5.19			0.505	0.594	55	misc.GDSL-motif lipase

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AT2G01630	gi18379267	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	plasma membrane	anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		0	S		Glyco_hydro_17(1) X8(1)	7	0.099	53.99	5.78	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(PlasmaMembrane-LOPIT-callus); 17317660(Plasm		0.048	0.052	134	misc.beta 1,3 glucan hydrolases
AT5G18220	gi15238768	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Cell structure	O-Glycosyl hydrolases family 17 protein			anchored to membrane	35.1 not assigned.no ontology	35.1		1	S		Glyco_hydro_17(1) X8(1)	7	-0.127	53.87	5.7			0	0	0	not assigned.no ontology
AT5G04885	gi30680681	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase family 3 protein	glycosyl hydrolase family 3 protein		anchored to membrane	26.3 misc.glucosyl, galacto- and mannosidases	26.3		0	S		Glyco_hydro_3(1) Glyco_hydro_3_C(1)	12	-0.022	72.3	6.12	16618929(PlasmaMembrane-LOPIT-callus); 17317660(PlasmaMembrane proteome); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf);		0.044	0.046	152	misc.glucosyl, galacto- and mannosidases
AT5G20940	gi22326918	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	Cell structure	Glycosyl hydrolase family 3 protein	Glycosyl hydrolase protein			26.3 misc.glucosyl, galacto- and mannosidases	26.3		0	S		Glyco_hydro_3(1) Glyco_hydro_3	9	-0.038	67.65	9.21	18436743(specif ic to seeds);		0	0	0	misc.glucosyl, galacto- and mannosidases
AT4G03340	gi304281941	glycosyltransferase family 14 protein [Arabidopsis thaliana]	Cell structure	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein				26.2 misc.UDP glucosyl and glucuronyl transferases	26.2	1	1	M		Branch(1)	5	-0.283	51.67	8.59			0	0	0	misc.UDP glucosyl and glucuronyl transferases
AT2G30870	gi15224582	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase [Arabidopsis thaliana]	Cell structure	glutathione S-transferase PHI 10	glutathione transferase -Phi class (ATGSTF10) - very abundant	cytosol		26.9 misc. glutathione S transferases	26.9	1	0	S		Glutaredoxin(1) GST_C(1) GST_N(1)	0	-0.075	24.23	5.49	16287169(Cell Wall proteome); 15539469(vacuole); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-Cd-up); 16526091(Cu-binding root); 16055689(Glutathionylated suspension cell); 15815986(Silique); 15815986(seedling); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15150623(GST		0.665	0.654	2	misc.glutathione S transferases
AT4G28365	gi17485901	hypothetical protein F2009.30 - Arabidopsis thaliana	Cell structure	early nodulin-like protein 3			anchored to membrane	26.19 misc.plastocyanin-like	26.19		1	S		Cu_bind_like(1)	2	-0.199	21.6	6.78			0	0	0	misc.plastocyanin-like
AT3G16460	gi15228218	jacalin-like lectin domain-containing protein [Arabidopsis thaliana]	Cell structure	Mannose-binding lectin superfamily protein	jacalin lectin family protein	peroxisome		26.16 misc.myrosinase s-lectin-jacalin	26.16		0	-		Jacalin(4)	0	-0.375	72.47	5.31	14017000(vacuolar proteome); 16526091(Cu-binding root); 15815986(seedling); 15815986(Leaf); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 16618929(UNK NOWN-LOPIT-callus); 17407188(cotyledon); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total membranes); 18599647(seed proteome); 18324730(apoplast leaf); 18014235(leaf	10737809(peroxisome -SUBA);	0.572	0.565	14	misc.myrosinase s-lectin-jacalin



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AT3G49120	gi 405611	peroxidase [Arabidopsis thaliana]	Cell structure	peroxidase CB	peroxidase, Atpx34	cell wall	cell wall (sensu Magnoliophyta)	26.12 misc.peroxidases	26.12		0	S		peroxidase(1)	9	-0.077	38.83	7.57	14595688(Cell Wall proteome); 15539469(vacuole); 18538804(apoplast); 17293592(total seedlings 7# light and dark grown); 17151019(vacuole - suspension cell); 17526915(glycocalyx cell wall (stems)); 18998720(SA-induced secreted proteome (cell culture)); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19816138(rossetta)	16284776(extracellular -SUBA);	0.411	0.446	50	misc.peroxidases
AT5G17820	gi 15238030	peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana]	Cell structure	Peroxidase superfamily protein			cell wall (sensu Magnoliophyta)	26.12 misc.peroxidases	26.12		1	S		peroxidase(1)	8	-0.105	34.1	10.1	14595688(Cell Wall proteome); 17432890(leaf total membranes); 18436743(specific to roots); 18796151(cell wall (hypocotyl)); 19334764(plasma membrane (cell		0.521	0.55	26	misc.peroxidases
AT5G64100	gi 15237613	peroxidase 69 [Arabidopsis thaliana]	Cell structure	Peroxidase superfamily protein				26.12 misc.peroxidases	26.12		1	S		peroxidase(1)	8	-0.073	35.68	9.47	14595688(Cell Wall proteome); 16618929(UNK NOWN-LOPIT-callus); 17293592(total seedlings 7# light and dark grown); 18436743(specific to roots); 18796151(cell wall (hypocotyl)); 19334764(plasma membrane (cell		0.269	0.325	125	misc.peroxidases
AT4G31840	gi 15236544	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 15	plastocyanin-like domain-containing protein		anchored to membrane	26.19 misc.plastocyanin-like	26.19	1	2	S		Cu_bind_like(1)	3	0.076	18.96	8.99	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma		0.13	0.149	38	misc.plastocyanin-like
AT5G25090	gi 15238698	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 13	plastocyanin-like domain-containing protein	plasma membrane	anchored to membrane	26.19 misc.plastocyanin-like	26.19		1	S		Cu_bind_like(1)	3	0.099	19.77	9.03	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma		0.059	0.07	103	misc.plastocyanin-like

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AT1G42550	gi240254220	PM11 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	Cell structure	plastid movement impaired1	PM11 (PLASTID MOVEMENT IMPAIRED1)	plasma membrane		31.1 cell.organisation	31.1		0	-		CDC27(1)	5	-0.649	93.88	5.24	14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19854466(leaf); 12805386(GPI anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.237	0.237	48	cell.organisation
AT4G25240	gi4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	Cell structure	SKU5 similar 1	SKS1 (SKU5 SIMILAR 1); copper ion binding	plasma membrane	anchored to plasma membrane & anchored to membrane	26.7 misc.oxidases - copper, flavone etc.	26.7		1	S		Cu-oxidase(1) Cu-oxidase_2(1) Cu-oxidase_3(1)	5	-0.168	65.88	6.89	17216043(leaf); 19376835(leaf phosphoproteins);		0.049	0.056	136	misc.oxidases - copper, flavone etc.
AT4G28300	gi7269684	predicted proline-rich protein [Arabidopsis thaliana]	Cell structure	Protein of unknown function				10.5.4 cell wall.cell wall proteins.HRGP	10.5.4		0	-		DUF1421(1) DUF827(1) Extensin_2(1)	2	-0.945	54.11	5.83			0	0	0	cell wall.cell wall proteins.HRGP
AT1G62790	gi15221585	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Cell structure	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			anchored to membrane	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	26.21		2	S		Toxin_5(1) Tryp_alpha_amy1(1)	8	0.308	15.71	8.11			0	0	0	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT2G13820	gi15225509	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Cell structure	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein				26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	26.21	1	0	S		Tryp_alpha_amy1(1)	8	0.62	16.82	6.52	14517339(GPI anchored suspension cells); 17317660(Plasma Membrane proteome); 18436743(specific to roots); 19334764(plasma membrane (cell		0	0	0	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT2G16430	gi15227205	purple acid phosphatase 10 [Arabidopsis thaliana]	Cell structure	purple acid phosphatase 10			cell wall (sensu Magnoliophyta)	26.13 misc.acid and other phosphatases	26.13		0	M		Metallophos(1)	2	-0.609	40.91	6.05	16287169(Cell Wall proteome); 17526915(glyco proteome cell wall (stems)); 19546170(mature pollen grains); 18716313(secreted proteins (cell culture)); 19888209(80S polysomal fraction);		0.034	0.015	13	misc.acid and other phosphatases

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AT4G21450	gi3080389	putative membrane associated protein [Arabidopsis thaliana]	Cell structure	PapD-like superfamily protein	vesicle-associated membrane family protein / VAMP family protein	plasma membrane		31.4 cell.vesicle transport	31.4		0	-		Motile_Sperm(1)	1	-0.882	32.96	9.39	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins		0	0	0	cell.vesicle transport
AT2G33240	gi20196856	putative myosin heavy chain [Arabidopsis thaliana]	Cell structure	myosin XI D				31.1 cell.organisation	31.1		0	S		bZIP_2(1) cw18(1) DIL(1) IQ(5) MAP7(1) Myosin_head(1) Myosin_N(1) Myosin_tail_1	34	-0.496	200.64	5.56			0	0	0	cell.organisation
AT2G34730	gi3132472	putative myosin heavy chain [Arabidopsis thaliana]	Cell structure	myosin heavy chain-related		mitochondrion		31.1 cell.organisation	31.1		0	-		BRE1(1) DHC_N1(1) DUF1351(1) DUF73(1) DUF827(1) Myosin_tail_1(1) Prefoldin_2(1)	9	-0.711	94.61	5.18	MitoDB(Mitochondrial proteome);		0.008	0.009	380	cell.organisation
AT2G33240	gi20196856	putative myosin heavy chain [Arabidopsis thaliana]	Cell structure	myosin XI D				31.1 cell.organisation	31.1		0	S		bZIP_2(1) cw18(1) DIL(1) IQ(5) MAP7(1) Myosin_head(1) Myosin_N(1) Myosin_tail_1	34	-0.496	200.64	5.56			0	0	0	cell.organisation
AT1G11580	gi2895512	putative pectin methylesterase [Arabidopsis thaliana]	Cell structure	methylesterase PCR A	ATPMEPCRA; pectinesterase			10.8.1 cell wall.pectin*esterases.PME	10.8.1	1	1	S		Pectinesterase(1) PMEI(1)	8	-0.197	61.69	8.94	14595688(Cell Wall proteome); 16618929(UNK NOWN-LOPIT-callus); 17151019(vacuole - suspension cell); 18998720(SA-induced secreted proteome (cell culture)); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 18796151(cell wall (hypocotyl)); 19334764(plasma membrane (cell culture)); 19714877(interactomes 14-3-3 complexes (cell culture))		0.311	0.336	243	cell wall.pectin*esterases.PME
AT3G58100	gi6735322	putative protein [Arabidopsis thaliana]	Cell structure	plasmodesmata callose-binding protein 5			anchored to membrane	26.4 misc.beta 1,3 glucan hydrolases	26.4		2	S		X8(1)	7	-0.074	19.17	4.97	16602701(GPI-anchored Plasma membrane suspension cells); 17293592(total seedlings 7# light and dark grown); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	misc.beta 1,3 glucan hydrolases
AT4G34830	gi5123699	putative protein [Arabidopsis thaliana]	Cell structure	Pentatricopeptide repeat (PPR) superfamily protein	MRL1 (PPR protein) - rbcL MRNA stabilization	plastid		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	26.54*	1	1	C		PPR(10)	22	-0.252	119.77	8.06	18431481(chloroplast);		0.134	0.144	257	misc.pentatricopeptide (PPR) repeat-containing protein

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AT4G03230	gi4262151	putative receptor kinase [Arabidopsis thaliana]	Cell structure	S-locus lectin protein kinase family protein				29.4 protein_postranslational modification	29.4	1	0	S		APH(1) B_lectin(1) EGF_2(1) PAN_1(1) PAN_2(1) Pkinase_Tyr(1) S_locus_glycop(1)	36	-0.283	113.56	5.82			0	0	0	protein_postranslational modification
AT2G21280	gi18399648	Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	Cell structure	NAD(P)-binding Rossmann-fold superfamily protein	GCI (Giant Chloroplast 1) - plastid division	envelope-inner-peripheral-stromal-side	plastid	31.2.5 cell.division.plastid	31.2.5		0	C		3Beta_HSD(1) DapB_N(1) DUF1731(1) Epimerase(1) NAD_binding_4(1) RmlD_sub_bind(1)	5	0.023	37.75	9.31	15028209(Total chloroplast); 12938931(Total chloroplast envelope); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 20061580(chloroplast envelope (inner+outer)); 12805388(GPI-anchored-callus); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19200160(flowe r-stage 12); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));	15208387(plastid -SUBA);	0.305	0.342	43	cell.division.plastid
AT2G25060	gi4559346	similar to early nodulins [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 14	plastocyanin-like domain-containing protein	plasma membrane	anchored to membrane	26.19 misc.plastocyanin-like	26.19		0	S		Cu_bind_like(1)	4	0.165	19.48	6.82	12805388(GPI-anchored-callus); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19200160(flowe r-stage 12); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.264	0.308	42	misc.plastocyanin-like
AT2G25060	gi4559346	similar to early nodulins [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 14	plastocyanin-like domain-containing protein	plasma membrane	anchored to membrane	26.19 misc.plastocyanin-like	26.19		0	S		Cu_bind_like(1)	4	0.165	19.48	6.82	12805388(GPI-anchored-callus); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19200160(flowe r-stage 12); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.264	0.308	42	misc.plastocyanin-like
AT4G00340	gi6049881	Similar to receptor-like protein kinase precursor; F5110.19 [Arabidopsis thaliana]	Cell structure	receptor-like protein kinase 4	RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); sugar binding	plasma membrane		26.16 misc.myrosinase s-lectin-jacalin	26.16		1	S		APH(1) B_lectin(1) PAN_1(1) PAN_2(1) Pkinase(1) S_locus_glycop(1)	20	-0.225	90.83	8.24	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome);		0.032	0.038	244	misc.myrosinase s-lectin-jacalin

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AT5G51480	gi15242108	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	SKU5 similar 2	SKS2 (SKU5 SIMILAR 2); copper ion binding	plasma membrane	anchored to membrane	26.7 misc.oxidases - copper, flavone etc.	26.7		1	S		Cu-oxidase(1) Cu-oxidase_2(1) Cu-oxidase_3(1)	3	-0.205	66.41	5.87		0	0	0	misc.oxidases - copper, flavone etc.		
AT4G12420	gi15234551	SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	Cupredoxin superfamily protein	multi-copper oxidase (SKU5)-dual localized in plasma membrane & cell wall	cell wall; plasma membrane	cell wall (sensu Magnoliophyta) & plasma membrane & anchored to membrane	35.1 not assigned.no ontology	35.1		0	S		Cu-oxidase(1) Cu-oxidase_2(1) Cu-oxidase_3(1)	3	-0.236	65.64	9.16		12119380(extrac ellular -SUBA); 12119380(plasm a membrane - SUBA);	0.361	0.41	71	not assigned.no ontology	
AT3G46550	gi15231453	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding [Arabidopsis thaliana]	Cell structure	Fasciclin-like arabinogalactan family protein	SOS5 (SALT OVERLY SENSITIVE 5)	plasma membrane	external side of plasma membrane & anchored to membrane	10.5.1 cell wall.cell wall proteins.AGPs	10.5.1	2	1	S		Fasciclin(2)	3	0.367	44.24	5.57		14517339(GPI anchored suspension cells); 17317660(Plasm a Membrane proteome); 17644812(plasm a membrane -	0	0	0	cell wall.cell wall proteins.AGPs	
AT3G52400	gi15701797	syntaxin protein [Arabidopsis thaliana]	Cell structure	syntaxin of plants 122	SYN122 (syntaxin 122); SNAP receptor	plasma membrane	plasma membrane	31.4 cell.vesicle transport	31.4	1	1	-		DUF827(1) MSG(1) SNARE(1) Syntaxin(1)	4	-0.544	37.84	8.57		14506206(Plasm a Membrane proteome); 14506206(plasm a membrane (phosphorylated ); 15308754(plasm a membrane (phosphorylated ); 17317660(Plasm a Membrane proteome); 17644812(plasm a membrane - suspension cells); 18463617(suspe nsion cells- phosphorylated proteins); 19334764(plasm a membrane (cell	15342965(plasm a membrane - SUBA);	0	0	0	cell.vesicle transport
AT2G25730	gi118400918	uncharacterized protein [Arabidopsis thaliana]	Cell structure	unknown protein; Has 157 Blast hits to 144 proteins in 62 species: Archae - 0; Bacteria - 0; Metazoa - 101; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 21 (source: NCBI)	tetratricopeptide repeat (TPR)-containing protein			26.33* misc.tetratricopeptide repeat (TPR) unknown function	26.33*	2	0	-		TPR_2(1)	47	-0.269	274.78	5.65		15276459(tricho mes); 19546170(matur e pollen grains); 19888209(80S polysomal fraction); 20706207(cell cycle interactome (cell culture));	0.007	0	35	misc.tetratricopeptide repeat (TPR) unknown function	



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AT4G27520	gi 21592865	unknown [Arabidopsis thaliana]	Cell structure	early nodulin-like protein 2	plastocyanin-like domain-containing protein	not plastid	anchored to membrane	26.19 misc.plastocyanin-like	26.19		1	S		Cu_bind_like(1) PT(1)	2	-0.313	35.06	9.35	15028209(Total chloroplast); 15539469(vacuole); 12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16618929(PlasmaMembrane-LOPT-callus); 18538804(apoplast); 18538804(total leaf); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture));		0.281	0.306	30	misc.plastocyanin-like
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	Curculin-like (mannose-binding) lectin family protein	curculin-like (mannose-binding) lectin family protein, similar to S glycoprotein	not plastid	cell wall (sensu Magnoliophyta)	26.16 misc.myrosinase s-lectin-jacalin	26.16		1	S		B_lectin(1) PAN_1(1) PAN_2(1)	12	-0.313	50.34	8.74	15593128(Cell Wall proteome); 15815986(Leaf); 17317660(Plasma Membrane proteome); 18538804(apoplast); 17828791(total leaf); 18324730(apoplast leaf); 18796151(cell wall (hypocotyl)); 18716313(secreted proteins (cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19888209(leaves		0.442	0.462	32	misc.myrosinase s-lectin-jacalin
AT3G03790	gi 6006862	unknown protein [Arabidopsis thaliana]	Cell structure	ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein				31.2 cell.division	31.2		0	C		Ank(2) RCC1(4) Spb1_C(1)	9	-0.458	118.29	9.17			0.013	0.013	726	cell.division
AT5G64080	gi 10176956	unnamed protein product [Arabidopsis thaliana]	Cell structure	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			anchored to membrane	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	26.21	2	2	S		Tryp_alpha_ami(1)	8	0.643	17.97	6.47	14517339(GPI anchored suspension cells);		0.06	0.068	80	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT1G11330	gi 5734724	Very similar to receptor-like protein kinase [Arabidopsis thaliana]	Cell structure	S-locus lectin protein kinase family protein	S-locus lectin protein kinase family protein	plasma membrane		26.16 misc.myrosinase s-lectin-jacalin	26.16	1	1	S		APH(1) B_lectin(1) PAN_1(1) PAN_2(1) Pkinase(1) Pkinase_Tyr(1) RIO1(1) S_locus_g	24	-0.247	94.15	8.27	16618929(PlasmaMembrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18686298(tonoplast - phosphoproteom		0	0	0	misc.myrosinase s-lectin-jacalin
AT2G27130	gi 18401329	xyloglen-like protein 11 [Arabidopsis thaliana]	Cell structure	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			anchored to membrane	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	26.21	1	1	S		Tryp_alpha_ami(1)	10	0.252	18.09	4.71	14517339(GPI anchored suspension cells);		0	0	0	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT3G49750	gi 15229606	AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana]	Disease/defence	receptor like protein 44				20.1 stress.biotic	20.1	1	1	S		LRR_1(2) LRRNT_2(1)	6	0.015	29.99	8.2	17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica		0	0	0	stress.biotic
AT4G01700	gi 15234281	chitinase, putative [Arabidopsis thaliana]	Disease/defence	Chitinase family protein				20.1 stress.biotic	20.1		0	S		Glyco_hydro_19(1)	8	-0.396	31.47	9.04	14595688(Cell Wall proteome); 19334764(plasma membrane (cell culture));		0.139	0.084	63	stress.biotic

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AT1G20440	gi 388259	cor47 [Arabidopsis thaliana]	Disease/defence	cold-regulated 47	dehydrin (COR47), cold-induced - cytosol & nucleus	cytosol; nucleus		20.2.99 stress.abiotic.unspecified	20.2.99		0	-		Dehydrin(1)	0	-1.249	29.9	4.75	15276459(trichomes); 18814325(cotyledons); 18931141(peroxisomes-high&low purity (cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19253305(phosphoproteins (etiolated seedling)); 19376835(leaf	10737809(cytosol -SUBA); 10737809(nucleus -SUBA);	0.574	0.569	7	stress.abiotic.unspecified
AT2G02130	gi 15226878	defensin-like protein 1 [Arabidopsis thaliana]	Disease/defence	low-molecular-weight cysteine-rich 68				20.1 stress.biotic	20.1		1	S		Gamma-thionin(1) SLR1-BP(1)	8	0.004	8.54	9.63			0.312	0	40	stress.biotic
AT1G32090	gi 15222569	early-responsive to dehydration protein-related/ERD protein-related [Arabidopsis thaliana]	Disease/defence	early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration protein-related/ERD protein-related	plasma membrane		20.2.3 stress.abiotic.drought/salt	20.2.3	8	7	S		DUF221(1)	6	0.031	93.13	9.11	14206206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(sterol biosynthesis		0	0	0	stress.abiotic.drought/salt
AT1G30360	gi 18397470	ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Disease/defence	Early-responsive to dehydration stress protein (ERD4)	ERD4 protein	not plastid		20.2.3 stress.abiotic.drought/salt	20.2.3	10	10	S		DUF221(1)	7	0.298	81.94	9.28	16028209(Total chloroplast); 12938931(Total chloroplast envelope); 15539469(vacuole); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19200160(flowe		0.372	0.362	31	stress.abiotic.drought/salt
AT2G43610	gi 15224319	glycoside hydrolase family 19 protein [Arabidopsis thaliana]	Disease/defence	Chitinase family protein	glycoside hydrolase family 19 protein			20.1 stress.biotic	20.1		1	S		Chitin_bind_1(1) Glyco_hydro_19(1)	16	-0.171	30	9.54	16618929(Plasma Membrane-LOPIT-callus); 19334764(plasma membrane (cell culture)); 19714877(intera ctomes 14-3-3 complexes (cell culture));		0.331	0.388	86	stress.biotic

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AT3G09440	gi15232682	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) [Arabidopsis thaliana]	Disease/defence	Heat shock protein 70 (Hsp70) family protein	HSP70 (HSC70-3) (not plastid)	not plastid	cytosol	20.2.1 stress.abiotic.heat	20.2.1		0	-		HSP70(1) MreB_Mbl(1)	8	-0.394	71.15	4.97	14707099(vacuolar proteome); 16287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 16358359(cell suspension (Gamborg)); 16502469(cell suspension-Cd-up); 16247729(mature Pollen); 15815986(seedling); 15815986(Leaf); 11402211.12068122.15047896.16679420.17028149(seed-all-Jobpapers); 15908592(Carboxylated seed protein); 17317660(Plasma Membrane proteome); 16526091(Cu-binding root); 15815986(Silique); 15815986(seedling); 15815986(Leaf); 11402211.12068122.15047896.16679420.17028149(seed-all-Jobpapers); 17293592(total seedlings 7# light and dark grown); 17916636(root (NaCl stress)); 17028151(leaf defense proteome); 17075075(Cd2+-response proteins root); 18814325(cotyledons); 19304200(Plasma Membrane proteome); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 19376835(leaf		0.818	0.808	5	stress.abiotic.heat
AT4G23670	gi15236566	major latex protein-related / MLP-related [Arabidopsis thaliana]	Disease/defence	Polyketide cyclase/dehydrase and lipid transport superfamily protein	Pathogenesis-related protein Bet v 1 family	not plastid		20.2.99 stress.abiotic.unspecified	20.2.99		0	-		Bet_v_1(1)	2	-0.742	17.52	5.91	15060130(Plasma Membrane proteome); 16526091(Cu-binding root); 15815986(Silique); 15815986(seedling); 15815986(Leaf); 11402211.12068122.15047896.16679420.17028149(seed-all-Jobpapers); 17293592(total seedlings 7# light and dark grown); 17916636(root (NaCl stress)); 17028151(leaf defense proteome); 17075075(Cd2+-response proteins root); 18814325(cotyledons); 19304200(Plasma Membrane proteome); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 19376835(leaf		0.636	0.701	26	stress.abiotic.unspecified
AT4G02600	gi15235429	MLO-like protein 1 [Arabidopsis thaliana]	Disease/defence	Seven transmembrane MLO family protein	ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); calmodulin binding	plasma membrane		20.1.3 stress.biotic.signalling	20.1.3	7	7	-		Mlo(1)	8	0.192	59.13	8.71	15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 19376835(leaf		0	0	0	stress.biotic.signalling
AT5G22060	gi1535588	putative [Arabidopsis thaliana]	Disease/defence	DNAJ homologue 2	DnaJ heat shock protein, putative (J3), identical to AtJ3	peroxisome		20.2.1 stress.abiotic.heat	20.2.1		0	-		DnaJ(1) DnaJ_C(1) DnaJ_CXXCXGXG(1)	11	-0.773	46.44	6.69	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma	10737809(peroxisome -SUBA);	0.086	0.068	15	stress.abiotic.heat
AT3G11010	gi6016693	putative disease resistance protein [Arabidopsis thaliana]	Disease/defence	receptor like protein 34				20.1.7 stress.biotic.PR-proteins	20.1.7	1	1	-		LRR_1(11) LRRNT_2(1)	10	-0.135	99.02	6.12			0	0	0	stress.biotic.PR-proteins
AT4G23260	gi3021278	putative protein [Arabidopsis thaliana]	Disease/defence	cysteine-rich RLK (RECEPTOR-)				20 stress; 30.2.17 signalling,recept	20; 30.2.17	1	1	S		DUF26(2) Kdo(1) Pkinase(1)	16	-0.059	72.77	5.76			0	0	0	stress; signalling.receptor kinases.DUF
AT4G23260	gi3021278	putative protein [Arabidopsis thaliana]	Disease/defence	cysteine-rich RLK (RECEPTOR-)				20 stress; 30.2.17 signalling,recept	20; 30.2.17	1	1	S		DUF26(2) Kdo(1) Pkinase(1)	16	-0.059	72.77	5.76			0	0	0	stress; signalling.receptor kinases.DUF
AT2G32680	gi15225727	receptor like protein 23 [Arabidopsis thaliana]	Disease/defence	receptor like protein 23				20.1.7 stress.biotic.PR-proteins	20.1.7	1	2	S		LRR_1(9)	14	-0.062	98.48	6.28			0	0	0	stress.biotic.PR-proteins

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AT5G43470	gi 32364507	resistance protein Hod3 [Arabidopsis thaliana]	Disease/defence	Disease resistance protein (CC-NBS-LRR class) family				20.1 stress.biotic	20.1		0	-		NACHT(1) NB-ARC(1) PLU-1(1)	17	-0.276	104.68	6.27	17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins)		0	0	0	stress.biotic
AT5G47910	gi 3242789	respiratory burst oxidase protein D [Arabidopsis thaliana]	Disease/defence	respiratory burst oxidase homologue D				20.1.1 stress.biotic.respiratory burst	20.1.1	5	4	-		efhand(1) FAD_binding_6(1) FAD_binding_8(1) Ferric_reduct(1) NAD_binding_6(1) NA	10	-0.241	103.91	9.27	16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19334764(plasma membrane (cell culture)); 19376835(leaf		0	0	0	stress.biotic.respiratory burst
AT1G20780	gi 42562204	SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase [Arabidopsis thaliana]	Disease/defence	senescence-associated E3 ubiquitin ligase 1				20.1 stress.biotic	20.1		0	-		Adaptin_N(1) Arm(3) Granulin(1) HEAT(1) PUL(1) Skp1_POZ(1) U-	14	-0.016	88.38	5.76	17644812(plasma membrane - suspension cells);		0	0	0	stress.biotic
AT4G02450	gi 3193303	T14P8.5 [Arabidopsis thaliana]	Disease/defence	HSP20-like chaperones superfamily protein	glycine-rich protein - lots of repeats	not plastid		35.1.40 not assigned.no ontology.glycine rich proteins	35.1.40		0	-		Collagen(1) CS(1) Fork_head_N(1)	1	-0.532	25.47	4.44	13813980(seedling); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17644812(plasma membrane - suspension cells); 18599647(seed proteome); 19200160(flower-stage 12); 19546170(mature pollen grains); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(80S polysomal fraction); 19888209(leaves); 19376835(leaf phosphoproteins)		0.274	0.269	16	not assigned.no ontology.glycine rich proteins
AT4G19530	gi 15235064	TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	Disease/defence	disease resistance protein (TIR-NBS-LRR class) family				20.1.7 stress.biotic.PR-proteins	20.1.7		0	-		LRR_3(1) MobB(1) NACHT(1) NB-ARC(1) TIR(1)	31	-0.369	132.51	7.48	17272265(ubiquitinated proteins (suspension cells)); 20706207(contaminants cell cycle interactome (cell		0	0	0	stress.biotic.PR-proteins
AT3G53990	gi 30693971	universal stress protein (USP) family protein [Arabidopsis thaliana]	Disease/defence	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress protein (USP)	not plastid		20.2.2 stress.abiotic.cold	20.2.2		0	-		Usp(1)	2	-0.168	17.79	5.66	16400686(floem_sap B. napa); 15815986(Leaf); 17407188(cotyledon); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(leaves); 19423572(leaf (wt and clpr2-1)); 20516081(tagged-26S		0.706	0.712	6	stress.abiotic.cold

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ATCG00120	gi 7525018	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	Energy	ATP synthase subunit alpha	CF1a - atpA	thylakoid-peripheral-stromal-side	thylakoid membrane (sensu Viridiplantae) & chloroplast ATP synthase complex	1.1.4	1.1.4		0	-		3HCDH_N(1) ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1)	1	-0.048	55.33	5.19	10737809(nucleus -SUBA);	0.945	0.946	2	PS.lightreaction. ATP synthase	
ATCG00480	gi 7525040	ATP synthase CF1 beta subunit [Arabidopsis thaliana]	Energy	ATP synthase subunit beta	CF1b - atpB	thylakoid-peripheral-stromal-side	thylakoid membrane (sensu Viridiplantae) & proton-transporting ATP synthase, catalytic core (sensu Eukaryota)	1.1.4	1.1.4		0	-		ABC_tran(1) ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1)	1	-0.09	53.94	5.38		0.96	0.961	2	PS.lightreaction. ATP synthase	
AT2G36530	gi 15227987	bifunctional enolase 2/transcriptional activator [Arabidopsis thaliana]	Energy	Enolase	Enolase (ENO2), also LOS2 (Low expression of osmotically responsive genes 1)	cytosol; nucleus	nucleus & cytoplasm	4.12	4.12	1	0	-		Enolase_C(1) Enolase_N(1)	5	-0.19	47.72	5.54		0.779	0.8	17	glycolysis.enolase	

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AT3G04120	gi1166706	cytosolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]	Energy	glyceraldehyde-3-phosphate dehydrogenase C subunit 1	glyceraldehyde-3-phosphate dehydrogenase C-1 (GapC-1)	cytosol	cytosol & mitochondrion	4.9 glycolysis.glyceraldehyde 3-phosphate dehydrogenase	4.9		0	-		DapB_N(1) Gp_dh_C(1) Gp_dh_N(1) Semiialdhyde_dh(1)	2	-0.129	36.92	6.62	10737809(cytosol -SUBA);	0.822	0.844	6	glycolysis.glyceraldehyde 3-phosphate dehydrogenase
AT3G55440	gi1414550	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	Energy	triosephosphate isomerase	triosephosphate isomerase-2 (TPI-2)	not plastid	mitochondrion	4.8 glycolysis.TPI	4.8		0	-		TIM(1)	4	0.076	27.17	5.39		0.886	0.931	4	glycolysis.TPI
AT1G02180	gi30678256	ferredoxin-like protein [Arabidopsis thaliana]	Energy	ferredoxin-related				1.1.5.2 PS.lightreaction.other electron carrier (ox/red).ferredoxin	1.1.5.2		0	S			11	0.117	24.79	7.05		0	0	0	PS.lightreaction.other electron carrier (ox/red).ferredoxin
AT3G52930	gi15231715	fructose-bisphosphate aldolase, class I [Arabidopsis thaliana]	Energy	Aldolase superfamily protein	Aldolase	cytosol		4.7 glycolysis.aldolase	4.7		0	-		Glycolytic(1)	6	-0.231	38.54	6.05		0.791	0.795	8	glycolysis.aldolase

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AT5G03690	gi17064980	fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]	Energy	Aldolase superfamily protein	fructose-bisphosphate aldolase (FBPA)			4.7 glycolysis.aldolase	4.7		0	M		Glycolytic(1)	5	-0.206	42.91	9.02	16247729(mature Pollen); 17293592(total seedlings 77 light and dark grown); 18463617(suspension cells-phosphorylated proteins); 18814325(cotyledons); 19525416(leaf (wt and clpr4-1 mutant)); 20706207(contaminants cell cycle interactome (cell culture)); 19423572(leaf		0.137	0.154	59	glycolysis.aldolase
AT1G04410	gi15219721	malate dehydrogenase [Arabidopsis thaliana]	Energy	Lactate/malate dehydrogenase family protein	malate dehydrogenase, cytosolic,	cytosol		8.2.9 TCA / org.transformation.other organic acid transformaitons.cyt MDH	8.2.9		0	-		Ldh_1_C(1) Ldh_1_N(1)	6	0.013	35.57	6.11	14617066(Nuclear proteome); 16207701(chloroplast stroma); 15539469(vacuole); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-Cd-up); 16247729(mature Pollen); 16400686(floem_sap B. napa); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 15052571(soluble leaf); 15908592(Carbo		0.726	0.711	4	TCA / org.transformation.other organic acid transformaitons.cyt MDH
AT4G32840	gi15233959	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase [Arabidopsis thaliana]	Energy	phosphofructokinase 6				4.4 glycolysis.PPFK	4.4		0	-		DUF356(1) PFK(1)	7	-0.17	50.79	6.61	14617066(Nuclear proteome); 16242667(mature Pollen); 16358359(cell suspension (M&Skoog)); 16400686(floem_sap B. napa); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 15052571(soluble leaf); 15276459(trichomes); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15734904(S-nitrosylated suspension cells or leaf); 17217660(Plasma		0	0	0	glycolysis.PPFK
AT1G79550	gi15219412	PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase [Arabidopsis thaliana]	Energy	phosphoglycerate kinase	phosphoglycerate kinase	not plastid		4.10 glycolysis.phosphoglycerate kinase	4.1		0	-		PGK(1) WI12(1)	1	0.134	42.13	5.49	14617066(Nuclear proteome); 16242667(mature Pollen); 16358359(cell suspension (M&Skoog)); 16400686(floem_sap B. napa); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 15052571(soluble leaf); 15276459(trichomes); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15734904(S-nitrosylated suspension cells or leaf); 17217660(Plasma		0.808	0.9	24	glycolysis.phosphoglycerate kinase
AT5G35790	gi3021305	plastidic glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]	Energy	glucose-6-phosphate dehydrogenase 1	glucose-6-phosphate 1-dehydrogenase	plastid stroma		7.1.1 OPP.oxidative PP.G6PD	7.1.1		0	C		G6PD_C(1) G6PD_N(1)	7	-0.386	65.43	7.61	18431481(chloroplast); 19452453(14-3-3-interacting proteins); 19525416(leaf (wt and clpr4-1 mutant)); 20423899(chloroplast); 19114538(guard cells Arabidopsis leaf); 19423572(leaf (wt and clpr2-1)); 20061580(chloroplast envelope		0.542	0.593	87	OPP.oxidative PP.G6PD
AT5G09600	gi2864622	putative protein [Arabidopsis thaliana]	Energy	succinate dehydrogenase 3-1			mitochondrion	8.1.7 TCA / org.transformation.TCA.succinate dehydrogenase	8.1.7	1	1	M		Sdh_cyt(1)	1	-0.032	23.45	9.96			0	0	0	TCA / org.transformation.TCA.succinate dehydrogenase

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ATCG00490	gi 1944432	ribulosebiphosphate carboxylase [Arabidopsis thaliana]	Energy	ribulose-biphosphate carboxylases	Rubisco large subunit (RBCL)	plastid stroma	thylakoid membrane (sensu Viridiplantae) & chloroplast	1.3.1 PS.calvin cycle.rubisco large subunit	1.3.1		0	-		RuBisCO_large(1) RuBisCO_large_N(1)	9	-0.272	52.96	5.88	12760290(rota chloroplast envelope); 11826309(thylakoid peripheral&lumen); 15322131(Thylakoid-stripped); 16207701(chloroplast stroma); 16287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 16923014(cold-stress responsive chloroplast); 11402211.12068122.15047896.16679420.17028149(seed-all-Jobpapers); 15908592(Carboxylated seed protein); 15734004(s		0.935	0.951	9	PS.calvin cycle.rubisco large subunit
AT3G56190	gi 15228848	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein [Arabidopsis thaliana]	Intracellular traffic	alpha-soluble NSF attachment protein 2	alpha-soluble NSF attachment protein 2 / alpha-SNAP2 / ASNAP2	not plastid		35.1 not assigned.no ontology	35.1		0	-		NSF(2) TPR_2(1)	8	-0.517	32.76	5.2	15215502(Vacuolar proteome); 15539469(vacuole); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane)		0.325	0.333	29	not assigned.no ontology
AT5G08680	gi 22326673	ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana]	Intracellular traffic	ATP synthase alpha/beta family protein	H+-transporting ATP synthase beta chain	mitochondria	mitochondrion	9.9 mitochondrial electron transport / ATP synthesis.F1-ATPase	9.9		0	M		ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1)	3	-0.143	59.86	6.06	16055689(Glutathionylated suspension cell); 15815986(Siliqua); 15815986(seedling); 15815986(Leaf); 15908592(Carboxylated seed protein); 17407188(leaf)		0.682	0.773	89	mitochondrial electron transport / ATP synthase.F1-ATPase
AT5G64370	gi 9759413	beta-ureidopropionase [Arabidopsis thaliana]	Intracellular traffic	beta-ureidopropionase	beta-ureidopropionase (BETA-UP), also PYD3	cytosol		23.2 nucleotide metabolism.degradation	23.2		0	-		CN_hydrolase(1)	8	-0.298	45.55	5.92	16055689(Glutathionylated suspension cell); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis leaf);		0.118	0.126	51	nucleotide metabolism.degradation
AT4G29610	gi 3818575	cytidine deaminase 6 [Arabidopsis thaliana]	Intracellular traffic	Cytidine/deoxycytidylate deaminase family protein	cytidine deaminase, putative / cytidine aminohydrolase			23.2 nucleotide metabolism.degradation	23.2		0	-		dCMP_cyt_deam_1(1) dCMP_cyt_deam_2(1)	9	-0.105	32.04	5.58	19525416(leaf (wt and clpr4-1 mutant));		0.222	0.199	3	nucleotide metabolism.degradation



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AT2G33120	gi 600710	formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	Intracellular traffic	synaptobrevin-related protein 1	synaptobrevin family protein	plasma membrane	endosome & plasma membrane	31.4 cell.vesicle transport	31.4	1	1	S		Synaptobrevin(1)	6	-0.122	24.93	9.07	15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 17151019(vacuole - suspension cell); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowers-stage 12); 19525416(leaf 12); 19722399(leaf chloroplast); MitoDB(Mitochondrial proteome); 15276431(Mitochondrial proteome); 16358359(cell suspension (Gamborg)); 16247729(mature Pollen); 16055689(Glutathionylated suspension cell); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15908592(Carbohydrazide)	15342965(plasma membrane - SUBA); 15610358(unclear -SUBA);	0.167	0.078	14	cell.vesicle transport
AT5G08670	gi 17939849	mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana]	Intracellular traffic	ATP synthase alpha/beta family protein	H+-transporting ATP synthase beta chain	mitochondria	mitochondrion	9.9 mitochondrial electron transport / ATP synthesis.F1-ATPase	9.9		0	M		ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1)	3	-0.152	59.63	6.13	15539469(vacuole); 16358359(cell suspension (Gamborg)); 16502469(cell suspension-Cd-up); 16400686(floem_sap B. napo); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 15276459(trichomes); 16618929(UNK NOWN-LOPIT-callus); 18538804(apoplast); 18538804(total leaf); 17407188(cotyledon); 17151019(vacuole - suspension cell); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane)		0.685	0.765	86	mitochondrial electron transport / ATP synthase.F1-ATPase
AT4G09320	gi 16396	nucleoside diphosphate kinase [Arabidopsis thaliana]	Intracellular traffic	Nucleoside diphosphate kinase family protein	NDPK1 - very abundant & multiple localizations	cytosol; nucleus; peroxisome		23.4.10 nucleotide metabolism.phosphotransfer and pyrophosphatase.nucleoside diphosphate kinase	23.4.10		0	-		NDK(1)	3	0.006	18.81	8.43	15539469(vacuole); 16358359(cell suspension (Gamborg)); 16502469(cell suspension-Cd-up); 16400686(floem_sap B. napo); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 15276459(trichomes); 16618929(UNK NOWN-LOPIT-callus); 18538804(apoplast); 18538804(total leaf); 17407188(cotyledon); 17151019(vacuole - suspension cell); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane)		0.704	0.763	21	nucleotide metabolism.phosphotransfer and pyrophosphatase.nucleoside diphosphate kinase
AT3G11130	gi 6016683	putative clathrin heavy chain [Arabidopsis thaliana]	Intracellular traffic	Clathrin, heavy chain	clathrin heavy chain	not plastid		31.4 cell.vesicle transport	31.4		0	S		Clathrin(7) Clathrin-link(1) Clathrin_propel(7)	23	-0.156	193.25	5.26	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane)		0.603	0.596	2	cell.vesicle transport

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AT2G32670	gi 2914706	putative synaptobrevin [Arabidopsis thaliana]	Intracellular traffic	vesicle-associated membrane protein 725	ATVAMP725 (vesicle-associated membrane protein 725)		endosome & plasma membrane	31.4 cell.vesicle transport	31.4	1	2	S		Synaptobrevin(1)	7	-0.038	32.69	9.53	19546170(mature pollen grains); 20166762(guard cells (Arabidopsis));	15342965(plasma membrane - SUBA);	0	0	0	cell.vesicle transport
AT3G17810	gi 15229529	pyrimidine 1 [Arabidopsis thaliana]	Intracellular traffic	pyrimidine 1	dihydropyrimidine dehydrogenase (DHODH) also PYD1; homologue of C reinhardtii Tba1; translation D1 proteins	plastid		23.2 nucleotide metabolism.degradation	23.2		0	C		DHO_dh(1)	7	-0.276	46.85	6.37	18431481(chloroplast); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19816138(rossette leaves); 20423899(chloroplast); 19888209(leaves); 19114538(guard cells Arabidopsis);		0.359	0.399	61	nucleotide metabolism.degradation
AT2G07698	gi 14916970	RecName: Full=ATP synthase subunit alpha, mitochondrial	Intracellular traffic	ATPase, F1 complex, alpha subunit protein	ATP synthase alpha chain, mitochondrial	not plastid	mitochondrion	9.9 mitochondrial electron transport / ATP synthesis.F1-ATPase	9.9	3	3	S		ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1) MAP7(1)	6	-0.066	85.93	5.44	12938931(chloroplast envelope); 15215502(vacuolar proteome); 15276431(Mitochondrial proteome); 15539469(vacuole); 15496452(nucleolus); 16242667(mature Pollen); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15276431(mitochondrial membranes-suspension cells); 17293592(total seedlings 7 light and dark grown);		0.422	0.428	256	mitochondrial electron transport / ATP synthesis.F1-ATPase
AT2G20990	gi 18399541	synaptotagmin A [Arabidopsis thaliana]	Intracellular traffic	synaptotagmin A	ATSYTA/NTM C2T1.1/NTMC2 TYPE1.1/SYTA			35.1.19 not assigned.no ontology.C2 domain-containing protein	35.1.19	1	1	S		C2(2)	4	-0.256	61.75	7.18	15359409(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7 light and dark grown); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane		0.29	0.3	55	not assigned.no ontology.C2 domain-containing protein
AT3G11820	gi 15229865	SNAP receptor/ protein anchor [Arabidopsis thaliana]	Intracellular traffic	SNAP receptor	SYP121 (syntaxin 121); SNAP receptor	plasma membrane	plasma membrane	31.4 cell.vesicle transport	31.4	1	1	-		DUF837(1) Geminin(1) GRP(1) SNARE(1) Syntaxin(1)	3	-0.573	37.96	9.06	15060130(Plasma Membrane proteome); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19376835(leaf	ISI-000186230600044(plasma membrane - SUBA); 16570657(plasma membrane - SUBA); 15703292(plasma membrane - SUBA); 15342965(plasma membrane - SUBA);	0.107	0.113	21	cell.vesicle transport

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AT5G08080	gi18415701	SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor [Arabidopsis thaliana]	Intracellular traffic	syntaxin of plants 132	SYP132 (syntaxin 132); SNAP receptor	plasma membrane		31.4 cell.vesicle transport	31.4	1	1	-		SNARE(1) Syntaxin(1)	2	-0.556	34.23	6.09	153092007(plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane proteome)	18088326(plasma membrane - SUBA); 15342965(plasma membrane - SUBA);	0.069	0.072	170	cell.vesicle transport
AT3G09740	gi18398623	SYP71 (SYNTAXIN OF PLANTS 71); protein transporter [Arabidopsis thaliana]	Intracellular traffic	syntaxin of plants 71	syntaxin 71 (SYP71)	plasma membrane	integral to membrane	31.4 cell.vesicle transport	31.4	1	1	-		SNARE(1)	3	-0.515	29.98	5.09	153092007(plasma Membrane proteome); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane proteome)	15342965(endoplasmic reticulum -SUBA);	0.32	0.321	2	cell.vesicle transport
AT1G01050	gi6715648	T2SK16.5 [Arabidopsis thaliana]	Intracellular traffic	pyrophosphatase 1	norganic diphosphatase/pyrophosphatase (AtPPA1)		nucleus & cytoplasm	23.4.99 nucleotide metabolism.phosphotransfer and pyrophosphatase.misc	23.4.99		0	M		Pyrophosphatase (1)	3	-0.448	24.48	5.73	19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(80S polysomal fraction); 19888209(leaves); 19508356(mature pollen grains)	15610358(unclear -SUBA);	0.368	0.371	30	nucleotide metabolism.phosphotransfer and pyrophosphatase.misc
AT5G39510	gi6690274	v-SNARE AtVT11a [Arabidopsis thaliana]	Intracellular traffic	Vesicle transport v-SNARE family protein	vesicle transport v-SNARE 11 (VT11) / vesicle soluble NSF attachment protein receptor VT11a (VT11A) - multiple locations	ER; golgi; vacuole	late endosome & trans-Golgi network vesicle & Golgi trans face	31.4 cell.vesicle transport	31.4	1	1	-		Sec20(1) V-SNARE(1)	2	-0.436	24.95	9.47	15539469(vacuole); 15815986(Leaf); 16618929(vacuole); 11226186(endoplasmic reticulum -LOPIT-callus); 17151019(vacuole - suspension cell); 16947054(golgi -SUBA); 11226186(golgi -SUBA); 19546170(mature pollen grains); 11226186(vacuole -SUBA); 19525416(leaf (wt and clpr4-1 mutant)); 15797025(vacuole -SUBA); 19334764(plasma membrane (cell	16947054(endoplasmic reticulum -SUBA); 11226186(endoplasmic reticulum -SUBA); 16947054(golgi -SUBA); 11226186(golgi -SUBA); 11226186(vacuole -SUBA); 15797025(vacuole -SUBA); 15342965(vacuole -SUBA);	0.154	0.166	43	cell.vesicle transport

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AT1G17620	gi11762174	At1g17620 [Arabidopsis thaliana]	Intracellular traffic	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	unknown protein	plasma membrane		35.2 not assigned.unknown	35.2	1	1	-		Hin1(1)	8	-0.017	28.29	10.05	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasma membrane detergent resistant microdomains (DRM));		0	0	0	not assigned.unknown
AT2G33120	gi1600710	formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	Intracellular traffic	synaptobrevin-related protein 1	synaptobrevin family protein	plasma membrane	endosome & plasma membrane	31.4 cell.vesicle transport	31.4	1	1	S		Synaptobrevin(1)	6	-0.122	24.93	9.07	15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 17151019(vacuole - suspension cell); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowers-stage 12); 19525416(leaf	15342965(plasma membrane - SUBA); 15610358(unclear -SUBA);	0.167	0.078	14	cell.vesicle transport
AT5G12370	gi14586367	putative protein [Arabidopsis thaliana]	Intracellular traffic	exocyst complex component sec10	SEC10 (EXOCYST COMPLEX COMPONENT SEC10)			35.1 not assigned.no ontology	35.1		0	-		CHASE3(1) COG4(1) Laminin_I(1) Ldh_L_C(1) MCPsignal(1) PE(1) Sec10(1)	10	-0.166	89.7	5.23	17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell		0.103	0.113	75	not assigned.no ontology
AT3G10380	gi18398855	SEC8 (SUBUNIT OF EXOCYST COMPLEX 8) [Arabidopsis thaliana]	Intracellular traffic	subunit of exocyst complex 8	SEC8 (secretion 8)			31.4 cell.vesicle transport	31.4		0	-		DUF783(1) Erp_C(1) Sec8_exocyst(1)	10	-0.266	116.61	5.61	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19376835(leaf phosphoproteins); 19114538(guard		0.063	0.064	174	cell.vesicle transport
AT3G52400	gi15701797	syntaxin protein [Arabidopsis thaliana]	Intracellular traffic	syntaxin of plants 122	SYP122 (syntaxin 122); SNAP receptor	plasma membrane	plasma membrane	31.4 cell.vesicle transport	31.4	1	1	-		DUF827(1) MSG(1) SNARE(1) Syntaxin(1)	4	-0.544	37.84	8.57	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19334764(plasma membrane (cell	15342965(plasma membrane - SUBA);	0	0	0	cell.vesicle transport

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AT1G45688	gi18401556	unknown protein [Arabidopsis thaliana]	Intracellular traffic	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown	unknown protein	plasma membrane		35.2 not assigned.unknown	35.2	1	1	C		Hin1(1)	4	-0.352	37.2	9.9	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19376835(leaf phosphoproteins)		0	0	0	not assigned.unknown
AT5G11890	gi15239804	unknown protein [Arabidopsis thaliana]	Intracellular traffic	FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA)				35.2 not assigned.unknown	35.2	1	1	C		Hin1(1)	8	-0.236	31.44	9.76	17317660(Plasma Membrane proteome);		0	0	0	not assigned.unknown
AT1G76850	gi12322227	unknown protein [Arabidopsis thaliana]	Intracellular traffic	exocyst complex component sec5	SEC5A (EXOCYST COMPLEX COMPONENT SEC5)	plasma membrane		35.2 not assigned.unknown	35.2		0	-		Dor1(1) DUF584(1) PRMT5(1) TPD52(1)	15	-0.462	121.9	5.58	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19245862(nuclear phosphoproteins (seedlings & cell culture));		0.024	0.025	95	not assigned.unknown
AT5G62630	gi14423506	Unknown protein [Arabidopsis thaliana]	Intracellular traffic	hipl2 protein precursor	HIPL2 (HIPL2 PROTEIN PRECURSOR); catalytic		anchored to membrane	35.2 not assigned.unknown	35.2		0	S		Metallothio_5(1)	28	-0.37	75.62	4.86	12805588(GBI-anchored-callus); 17317660(Plasma Membrane proteome);		0.029	0.033	437	not assigned.unknown
AT1G21380	gi18394983	VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana]	Intracellular traffic	Target of Myb protein 1	VHS domain-containing protein / GAT domain-containing protein			31.4 cell.vesicle transport	31.4		0	-		GAT(1) HEAT(1) VHS(1)	5	-0.647	55.79	4.85	19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19376835(leaf phosphoproteins)		0.121	0.122	57	cell.vesicle transport
AT5G58060	gi15242933	YKT61 [Arabidopsis thaliana]	Intracellular traffic	SNARE-like superfamily protein	YKT61 (similar to yeast SNARE YKT61)	not plastid		31.4 cell.vesicle transport	31.4		0	S		Synaptobrevin(1)	4	-0.413	22.54	6.96	17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture));	15342965(unclear -SUBA);	0.362	0.373	3	cell.vesicle transport

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AT5G17920	gi15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Arabidopsis thaliana]	Metabolism	Cobalamin-independent synthase family protein	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (ATCIMS) - abundant	cytosol	cytosol	13.1.3.4 amino acid metabolism.synthesis.aspartate family.methionine	13.1.3.4		0	-		Meth_synt_1(1) Meth_synt_2(1)	6	-0.141	84.36	6.09	16247729(mature Pollen); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-Cd-up); 16502469(cell suspension-CD-down); 16247729(mature Pollen); 16526091(Cu-binding root); 16055689(Glutathionylated suspension cell); 16400686(floem_sap B. napa); 15815986(Silique); 15815986(seedling); 15815986(leaf)	15024005(cytosol -SUBA);	0.804	0.815	19		amino acid metabolism.synthesis.aspartate family.methionine
AT5G36880	gi145323645	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative [Arabidopsis thaliana]	Metabolism	acetyl-CoA synthetase	acetyl-CoA synthetase (acetate-CoA ligase)	plastid stroma		11.1.8 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	11.1.8		0	C		AMP-binding(1)	16	-0.172	76.73	5.41	15028209(Total chloroplast); 16207701(chloroplast stroma); 18463617(suspension cells-phosphorylated proteins); 18431481(chloroplast); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 20423899(chloroplast); 19376835(leaf phosphoproteins); 20166762(guard cells (Arabidopsis)); 19114538(guard cells)		0.478	0.49	27		lipid metabolism.FA synthesis and FA elongation.acyl coa ligase
AT2G38280	gi18404701	AMP deaminase [Arabidopsis thaliana]	Metabolism	AMP deaminase, putative / myoadenylate deaminase, putative	FAC1 (EMBRYONIC FACTOR1); AMP deaminase		microsome	23.2 nucleotide metabolism.degradation	23.2		1	S		A_deaminase(1)	10	-0.41	95.13	5.88	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19253305(phosphoproteins (etiolated seedling)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 19114538(guard cells)		0.031	0.032	233		nucleotide metabolism.degradation
AT5G11520	gi15239078	ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana]	Metabolism	aspartate aminotransferase 3	aspartate aminotransferase (ASP3) (YLS4)	plastid	plastid	13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	13.1.1.2.1		0	C		Aminotran_1_2(1)	4	-0.103	48.96	9.34	12134131(Peroxisomal proteome); 12154131(Peroxisomal proteome); 16247729(mature Pollen); 17432890(leaf total membranes); 17951448(peroxisome (leaves)); 18931141(peroxisomes-high&low purity (cell culture)); 18931141(peroxisomes-high purity (cell culture)); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.367	0.429	76		amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase



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AT3G25860	gi 9279589	dihydroipoamide S-acetyltransferase [Arabidopsis thaliana]	Metabolism	2-oxoacid dehydrogenases acyltransferase family protein	E2 - dihydroipoamide acetyltransferase, plastid - subunit of pyruvate dehydrogenase complex	plastid	chloroplast stroma	11.1.31	11.1.31		0	C		2-oxoacid_dh(1) Biotin_lipoyl(1) E3_binding(1)	1	0.045	50.08	8.34	15022277(Total chloroplast); 12938931(Total chloroplast envelope); 15821981(crude & pure 80S ribosome); 15052571(soluble leaf); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15908592(Carboxylated seed protein); 14764908(mitochondria-suspension cells); 17293592(total seedlings 7# light and dark grown); 17432890(leaf total		0.508	0.564	57	lipid metabolism.FA synthesis and FA elongation.pyruvate DH
AT1G43710	gi 15218445	emb1075 (embryo defective 1075); carboxylase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	Metabolism	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein				13.2.7 amino acid metabolism.degradation.histidine	13.2.7		0	-		Aminotran_5(1) Pyridoxal_deC(1)	12	-0.261	54.08	5.8	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 13028209(Total chloroplast); 12938931(Total chloroplast envelope); 15821981(crude & pure 80S ribosome); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 18431481(chloroplast); 19200160(flowers-stage 12); 19546170(mature pollen grains); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane - suspension		0	0	0	amino acid metabolism.degradation.histidine
AT1G34430	gi 8778253	F12K21.24 [Arabidopsis thaliana]	Metabolism	2-oxoacid dehydrogenases acyltransferase family protein	Plastidial Dihydroipoamide Acetyltransferase, pyruvate DH complex	envelope-inner-peripheral-stromal-side		11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	11.1.31		0	C		2-oxoacid_dh(1) ACP_syn_III_C(1) AIRC(1) Biotin_lipoyl(1) E3_binding(1)	1	0.131	48.31	8.8	15022277(Total chloroplast); 12938931(Total chloroplast envelope); 15821981(crude & pure 80S ribosome); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 18431481(chloroplast); 19200160(flowers-stage 12); 19546170(mature pollen grains); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane - suspension		0.501	0.54	41	lipid metabolism.FA synthesis and FA elongation.pyruvate DH
AT5G54500	gi 15239652	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor [Arabidopsis thaliana]	Metabolism	flavodoxin-like quinone reductase 1	flavodoxin-like quinone reductase (FQR1). putative, similar to 1,4-benzoquinone reductase	not plastid		11.8 lipid metabolism.exotics (steroids, squalene etc)	11.8		0	-		Flavodoxin_1(1) FMN_red(1)	0	-0.108	21.8	5.96	147007096(vacuolar proteome); 15060130(Plasma Membrane proteome); 16358359(cell suspension (M&Skoog)); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 17317660(Plasma Membrane proteome); 17828791(total leaf); 17293592(total seedlings 7# light and dark grown); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension		0.598	0.6	5	lipid metabolism.exotics (steroids, squalene etc)



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AT4G31140	gi15235840	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	35.1 not assigned.no ontology	35.1		1	S		Glyco_hydro_17(1) Glyco_hydro_18(1) Glyco_hydro_53(1) X8(1)	7	0.061	52.72	5.8	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall (stems)); 19036721(sterol dependent		0.196	0.217	58	not assigned.no ontology
AT5G56590	gi15241268	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein		anchored to membrane	35.1 not assigned.no ontology	35.1		0	S		Glyco_hydro_17(1) X8(1)	10	-0.158	55.6	7.91	14517339(GPI anchored suspension cells); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall (stems)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.073	0.088	237	not assigned.no ontology
AT5G58480	gi30697080	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	O-Glycosyl hydrolases family 17 protein			anchored to membrane	35.1 not assigned.no ontology	35.1		1	M		Glyco_hydro_17(1) X8(1)	6	-0.087	52.37	7.67	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	not assigned.no ontology
AT4G16155	gi7159284	lipamide dehydrogenase [Arabidopsis thaliana]	Metabolism	dihydropyridyl dehydrogenases	E3 - dihydrolipamide dehydrogenase 2 (ptlpd2), plastid- subunit of pyruvate dehydrogenase complex	plastid		11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	11.1.31		0	-		DAO(1) FAD_binding_2(1) GIDA(1) H10933_like(1) Pyr_redox_1(1) Pyr_redox_2(1) Pyr_r	9	0.065	67.09	7.66	13028209(Total chloroplast); 12938931(Total chloroplast envelope); 18431481(chloroplast); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 20423899(chloroplast); 19888209(80S polysomal fraction); 19888209(leaves); 19114538(guard cells Arabidopsis thaliana)	11575725(plastid -SUBA);	0.487	0.553	82	lipid metabolism.FA synthesis and FA elongation.pyruvate DH

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AT4G23850	gi15236634	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase [Arabidopsis thaliana]	Metabolism	AMP-dependent synthetase and ligase family protein	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase	not plastid		11.1.9 lipid metabolism.FA synthesis and FA elongation.long chain fatty acid CoA ligase	11.1.9		0	-		AMP-binding(1)	13	-0.144	74.51	5.64		0.308	0.305	6	lipid metabolism.FA synthesis and FA elongation.long chain fatty acid CoA ligase		
AT5G20980	gi30688090	methionine synthase 3 [Arabidopsis thaliana]	Metabolism	methionine synthase 3	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase (MS3)	plastid stroma	chloroplast	13.1.3.4.3 amino acid metabolism.synthesis.aspartate family.methionine.methionine synthase	13.1.3.4.3		0	C		Meth_synt_1(1) Meth_synt_2(1) Occludin_ELL(1)	8	-0.177	90.6	8.17		15024005(plastid-SUBA);	0.144	0.15	67	amino acid metabolism.synthesis.aspartate family.methionine.methionine synthase	
AT1G21640	gi18395013	NAD kinase 2 [Arabidopsis thaliana]	Metabolism	NAD kinase 2	NADK2 - NADPH synthesis	plastid stroma		18.21* Co-factor and vitamine metabolism.NAD/NADP	18.21*		0	C		NAD_kinase(1)	19	-0.351	109.19	7.5		18431481(chloroplast); 20423899(chloroplast);	16244906(plastid-SUBA);	0.177	0.188	147	Co-factor and vitamine metabolism.NAD/NADP
AT4G11850	gi15234335	PLDGAMMA1; phospholipase D [Arabidopsis thaliana]	Metabolism	phospholipase D gamma 1	phospholipase D gamma 1 (PLD[gamma]1)			11.9.3.1 lipid metabolism.lipid degradation.lyso phospholipases.phospholipase D	11.9.3.1		0	-		C2(1) Peptidase_C32(1) PLDc(2)	10	-0.345	95.59	8.32		16618929(Plasma Membrane-LOPIT-callus); 19452453(14-3-3-interacting proteins); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0	0	0	lipid metabolism.lipid degradation.lyso phospholipases.phospholipase D
AT2G18730	gi4185139	putative diacylglycerol kinase [Arabidopsis thaliana]	Metabolism	diacylglycerol kinase 3				11.3.5 lipid metabolism.Phospholipid synthesis.diacylglycerol kinase	11.3.5		0	-		DAGK_acc(1) DAGK_cat(1)	11	-0.246	53.88	7.58		17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasm		0	0	0	lipid metabolism.Phospholipid synthesis.diacylglycerol kinase

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AT3G03780	gi 14532772	putative methionine synthase [Arabidopsis thaliana]	Metabolism	methionine synthase 2	methionine synthase (AtMS2)	cytosol	cytosol	13.1.3.4.3 amino acid metabolism.synthetase.aspartate family.methionine synthase	13.1.3.4.3		0	-		Meth_synth_1(1) Meth_synth_2(1) Occludin_ELL(1)	6	-0.152	84.59	6.08	15024005(cytosol -SUBA); 15815986(Leaf); 18538804(apoplast); 18538804(total leaf); 17293592(total seedlings 7# light and dark grown); 17916636(root (NaCl stress)); 17644812(plasma membrane - suspension cells); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (DRM) proteins (Cell cultures));		0.641	0.649	19	amino acid metabolism.synthetase.aspartate family.methionine synthase
AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	Metabolism	PLC-like phosphodiesterase family protein	MRH5/SHV3 (morphogenesis of root hair 5); glycerophosphodiester phosphodiesterase/kinase	plasma membrane	anchored to membrane	11.9.3.3 lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase	11.9.3.3		0	M		GDPD(1)	8	0.051	82.56	5.32	12603388(CGT-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17526915(glyco proteome cell wall (stems)); 18716313(secreted proteins (cell culture)); 19026721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (DRM) proteins (Cell cultures));		0.332	0.309	34	lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase
AT4G27270	gi 3269288	putative protein [Arabidopsis thaliana]	Metabolism	Quinone reductase family protein	quinone reductase family protein	plasma membrane		11.8 lipid metabolism.exotics (steroids, squalene etc)	11.8		0	-		Flavodoxin_1(1) FMN_red(1)	0	-0.034	21.79	6.08	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 17828791(total leaf); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (DRM) proteins (Cell cultures));		0.244	0.199	5	lipid metabolism.exotics (steroids, squalene etc)

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AT4G26690	gi4455192	putative protein [Arabidopsis thaliana]	Metabolism	PLC-like phosphodiesterase family protein	MRH5/SHV3 (morphogenesis of root hair 5); glycerophosphodiester phosphodiesterase/kinase	plasma membrane	anchored to membrane	11.9.3.3 lipid metabolism.lyso phospholipases.glycerophosphodiester phosphodiesterase	11.9.3.3		0	M		GDPD(1)	8	0.051	82.56	5.32		0.332	0.309	34	lipid metabolism.lyso phospholipases.glycerophosphodiester phosphodiesterase	
AT4G36750	gi15234512	Quinone reductase family protein [Arabidopsis thaliana]	Metabolism	Quinone reductase family protein	quinone reductase family protein	plasma membrane		11.8 lipid metabolism.exotics (steroids, squalene etc)	11.8		0	-		Flavodoxin_1(1) FMN_red(1)	2	-0.21	28.76	5.17		0.143	0.188	110	lipid metabolism.exotics (steroids, squalene etc)	
AT4G13940	gi132967699	S-adenosyl-L-homocystein hydrolase [Arabidopsis thaliana]	Metabolism	S-adenosyl-L-homocysteine hydrolase	S-adenosyl-L-homocysteine hydrolase (HOG11);	not plastid		13.2.3.4 amino acid metabolism.degradation.aspartate family.methionine	13.2.3.4		0	-		2-Hacid_dh_C(1) AdoHcyase(1) AdoHcyase_NAD(1) AlaDh_PNT_C(1) IlvN(1) Malic_M(1)	11	-0.127	53.38	5.66		0.757	0.754	16	amino acid metabolism.degradation.aspartate family.methionine	
AT1G32440	gi18920620	Strong similarity to a pyruvate kinase isozyme G, chloroplast precursor from Nicotiana tabacum gb/Z28374. It contains a pyruvate kinase domain PF00224. EST gb/A1996399 comes from this gene [Arabidopsis thaliana]	Metabolism	plastidial pyruvate kinase 3	pyruvate kinase (typically homotetramer)			11.1.30 lipid metabolism.FA synthesis and FA elongation.pyruvate kinase	11.1.30		0	C		HpcH_Hpal(1) PK(1) PK_C(1)	6	-0.111	62.62	7.68		0.291	0.322	68	lipid metabolism.FA synthesis and FA elongation.pyruvate kinase	
AT1G73370	gi15219457	sucrose synthase 6 [Arabidopsis thaliana]	Metabolism	sucrose synthase 6	Sucrose synthase 6 (SUS6)			2.2.1.5 major CHO metabolism.degradation.sucrose.Susy	2.2.1.5		0	-		Glycos_transf_1(1) Sucrose_synth(1)	13	-0.391	106.88	8.13		0.117	0.121	105	major CHO metabolism.degradation.sucrose.Susy	

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AT5G55480	gi15240520	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	Metabolism	SHV3-like 1	glycerophosphoryl diester phosphodiesterase family protein	plasma membrane	anchored to membrane	11.9.3.3 lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase	11.9.3.3		1	S		GDPD(1)	7	-0.045	84.17	5.45	16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells);		0.265	0.277	40	lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase
AT1G66970	gi30697435	SVL2 (SHV3-LIKE 2); glycerophosphodiester phosphodiesterase/ kinase [Arabidopsis thaliana]	Metabolism	SHV3-like 2	glycerophosphoryl diester phosphodiesterase family protein,	plasma membrane	anchored to membrane	11.9.3.3 lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase	11.9.3.3		1	S		GDPD(1)	8	-0.018	83.79	4.99	16602701(GPI-anchored Plasma membrane suspension cells); 18538804(apoplast); 18538804(total leaf); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19816138(rose tle leaves); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19888209(leaves); 20166762(whole plant); 19276951(mitochondrial proteome); 15539469(vacuole); 15815986(Silique); 15815986(seedling); 15815986(Leaf); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 16618929(ER-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cells);		0.439	0.456	42	lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester phosphodiesterase
AT5G58070	gi15242942	TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter [Arabidopsis thaliana]	Metabolism	temperature-induced lipocalin	lipocalin, putative	vacuole		11 lipid metabolism	11		0	-		Lipocalin(1) Lipocalin_2(1)	0	-0.678	21.43	5.98	17151019(vacuole -SUBA); 17151019(vacuole - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.511	0.525	22	lipid metabolism
AT1G66980	gi9755449	Unknown protein [Arabidopsis thaliana]	Metabolism	suppressor of npr1-1 constitutive 4				11.9.3.3 lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester	11.9.3.3	3	1	M		GDPD(1) Pkinase(1) Pkinase_Tyr(1)	16	-0.058	123.83	6.25	19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0	0	0	lipid metabolism.lipid degradation.lyso phospholipases.glycerophosphodiester

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AT3G54200	gi15232445	unknown protein [Arabidopsis thaliana]	Metabolism	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	unknown protein	plasma membrane		35.1 not assigned.no ontology	35.1	1	1	-		Hin1(1)	5	0.107	25.79	9.82		0.111	0.16	94	not assigned.no ontology		
AT1G35710	gi14596041	Unknown protein [Arabidopsis thaliana]	Metabolism	Protein kinase family protein with leucine-rich repeat domain	leucine-rich repeat transmembrane protein kinase, putative			30.2.12 signalling.recept or kinases.leucine rich repeat XII	30.2.12	1	2	S		Baculo_PEP_C(1) Kdo(1) LRR_1(15) LRRNT_2(1) Pkinase(1)	12	-0.127	124.11	6.02		0.007	0.008	895	signalling.recept or kinases.leucine rich repeat XII		
AT1G45000	gi15219503	26S proteasome regulatory complex subunit p42D, putative [Arabidopsis thaliana]	Protein destination and storage	AAA-type ATPase family protein	26S proteasome regulatory complex subunit (RPT4b)	cytosol		29.5.11.20 protein.degradati on.ubiquitin.proteasom	29.5.11.20		0	-		AAA(1) AAA_2(1) AAA_3(1) AAA_5(1) eIF-1a(1) Sigma54_activat (1)	3	-0.384	44.76	8.25		15496452(nucleus -SUBA);	0.446	0.49	55	protein.degradati on.ubiquitin.proteasom	
AT1G04730	gi15219798	AAA-type ATPase family protein [Arabidopsis thaliana]	Protein destination and storage	P-loop containing nucleoside triphosphate hydrolases superfamily				29.5.9 protein.degradati on.AAA type	29.5.9		0	-		AAA(1) AAA_5(1) Rad17(1) SRP54(1)	14	-0.518	107.02	6.88		0	0	0	protein.degradati on.AAA type		
AT3G56450	gi15228924	ALPHA-SNAP1; binding / soluble NSF attachment protein [Arabidopsis thaliana]	Protein destination and storage	alpha-soluble NSF attachment protein 1	alpha-soluble NSF attachment protein 1 (ASNAP1)			29.3.4.99 protein.targeting.secretory pathway.unspecif ied	29.3.4.99		0	M			13	-0.398	43.88	7.87			0.1	0.123	117	protein.targeting.secretory pathway.unspecif ied	
AT2G02800	gi15227042	APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Protein destination and storage	protein kinase 2B			nucleus & cytoplasm	29.4.1.57 protein.postransl ational modification.kin ase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	C		Pkinase(1)	3	-0.381	46.29	9.67		17317660(Plasm a Membrane proteome); 17644812(plasm a membrane - suspension cells);	15610358(cytosol -SUBA); 15610358(nucleus -SUBA);	0	0	0	protein.postransl ational modification.kin ase.receptor like cytoplasmatic kinase VII

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AT1G11910	gi1354272	aspartic proteinase [Arabidopsis thaliana]	Protein destination and storage	aspartic proteinase A1	aspartyl protease family protein	vacuole		29.5.4	29.5.4		1	S		Alpha-amylase_C(1) Asp(1) SapB_1(1) SapB_2(1)	13	0.042	54.61	5.37	15215502(Vacuolar proteome); 15539469(vacuole); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17828791(total leaf); 17293592(total seedlings 7# light and dark grown); 17916636(root (NaCl stress)); 18931141(peroxisomes-high&low purity (cell culture)); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with		0.48	0.501	76	protein.degradation.aspartate protease
AT1G62290	gi22330379	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination and storage	Sapoin-like aspartyl protease family protein	aspartyl protease family protein			29.5.4	29.5.4		1	S		Asp(1) SapB_1(1) SapB_2(1)	12	-0.067	55.75	5.97	15215502(Vacuolar proteome); 15539469(vacuole); 17293592(total seedlings 7# light and dark grown); 18599647(seed		0.078	0.088	237	protein.degradation.aspartate protease
AT3G02740	gi15232960	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein			anchored to membrane	29.5.4	29.5.4	1	0	S		Asp(1)	13	-0.024	52.81	5.7	17317660(Plasma Membrane proteome); 18796151(cell wall (hypocotyl)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	protein.degradation.aspartate protease
AT5G10080	gi15238055	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein			anchored to membrane	29.5.4	29.5.4		0	S		Asp(1)	16	-0.233	57.96	6.17	14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 19260003(detergent resistant plasma		0.021	0.024	215	protein.degradation.aspartate protease
AT3G09830	gi222423927	AT3G09830 [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	protein kinase, putative	plasma membrane		29.4.1.57	29.4.1.57		0	C		Pkinase_Tyr(1)	5	-0.433	46.79	9.53	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma		0	0	0	protein.posttranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT3G52500	gi16209647	AT3g52500/F2206_120 [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein	aspartyl protease family protein	not plastid	cell wall (sensu Magnoliophyta)	29.5	29.5		0	S		Asp(1)	14	-0.148	51.01	8.53	14595688(Cell Wall proteome); 17407188(cotyledon); 17526915(glyco proteome cell wall (stems)); 17432890(leaf total membranes); 19200160(flowers-stage 12); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasm		0.343	0.355	122	protein.degradation

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AT3G52500	gi16209647	AT3g52500/F22O6_120 [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein	aspartyl protease family protein	not plastid	cell wall (sensu Magnoliophyta)	29.5 protein.degradation	29.5		0	S		Asp(1)	14	-0.148	51.01	8.53	14595688(Cell Wall proteome); 17407188(cotyledon); 17526915(glyco proteome cell wall (stems)); 17432890(leaf total membranes); 19200160(flowers-stage 12); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis thaliana); 15028209(tobacco chloroplast); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660270(GFP-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0.343	0.355	122	protein.degradation
AT1G63500	gi240254311	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase protein with tetratricopeptide repeat domain				29.4 protein_postranslational modification	29.4		0	-		Pkinase(1) Pkinase_Tyr(1) TPR_2(1)	13	-0.432	54.8	5.96	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis thaliana); 15028209(tobacco chloroplast); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660270(GFP-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	protein_postranslational modification
AT1G69840	gi15222481	band 7 family protein [Arabidopsis thaliana]	Protein destination and storage	SPFH/Band 7/PHB domain-containing membrane-associated protein family	SPSH domain protein /band 7 protein	vacuole		29.5 protein.degradation	29.5		0	-		Band_7(1)	5	-0.217	31.41	5.3	15028209(tobacco chloroplast); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660270(GFP-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant	17151019(vacuole -SUBA);	0.311	0.324	62	protein.degradation
AT1G65240	gi14646203	Belongs to PF00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein	aspartyl protease family protein	plasma membrane	anchored to membrane	29.5.4 protein.degradation.aspartate protease	29.5.4		1	S		Asp(1)	13	0.023	51.83	5.33	14595688(Cell Wall proteome); 17407188(cotyledon); 17526915(glyco proteome cell wall (stems)); 17432890(leaf total membranes); 19200160(flowers-stage 12); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis thaliana); 15028209(tobacco chloroplast); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17660270(GFP-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	protein.degradation.aspartate protease



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AT1G65240	gi 4646203	Belongs to PF00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein	aspartyl protease family protein	plasma membrane	anchored to membrane	29.5.4 protein.degradation.on.aspartate protease	29.5.4		1	S		Asp(1)	13	0.023	51.83	5.33	16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	protein.degradation.on.aspartate protease
AT5G46570	gi 15237465	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Protein destination and storage	BR-signaling kinase 2	protein kinase family protein			29.4 protein.postranslational modification	29.4		0	-		Pkinase(1) Pkinase_Tyr(1)	9	-0.397	54.97	5.47	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis		0.043	0.045	226	protein.postranslational modification
AT4G00710	gi 22328189	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Protein destination and storage	BR-signaling kinase 3				29.4 protein.postranslational modification	29.4		0	-		Pkinase(1) Pkinase_Tyr(1)	14	-0.374	54.91	5.87	17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma		0	0	0	protein.postranslational modification
AT1G05690	gi 42561724	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	Protein destination and storage	BTB and TAZ domain protein 3				29.5.11.4.5.2 protein.degradation.on.ubiquitin.E3.BTB/POZ Cullin3.BTB/PO	29.5.11.4.5.2		0	C		BTB(1) TIL(1) zf-TAZ(1)	19	-0.313	41.53	9.13			0	0	0	protein.degradation.on.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ
AT5G47850	gi 15238823	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase [Arabidopsis thaliana]	Protein destination and storage	CRINKLY4 related 4				30.2.26 signalling.receptor kinases.crinkly	30.2.26	1	2	S		APH(1) Pkinase_Tyr(1) RIO1(1)	27	-0.093	83.78	7.05			0	0	0	signalling.receptor kinases.crinkly like
AT3G26940	gi 15231654	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	C		Pkinase(1)	8	-0.414	48.51	9.18			0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT5G58870	gi 18424166	cell division protease ftsH-9 [Arabidopsis thaliana]	Protein destination and storage	FTSH protease 9	FtsH9	plastid	chloroplast	29.5.7 protein.degradation.on.metalloprotease	29.5.7	2	0	C		AAA(1) AAA_2(1) AAA_3(1) AAA_5(1) Arch_ATPase(1) FtsH_ext(1) Miro(1) MMR_HSR1(1)	4	-0.253	87.84	7.66	18431481(chloroplast); 19114538(guard cells Arabidopsis leaf); 20061580(chloroplast envelope (inner+outer));		0.057	0.062	364	protein.degradation.on.metalloprotease
AT3G18190	gi 15229595	chaperonin, putative [Arabidopsis thaliana]	Protein destination and storage	TCP-1/cpn60 chaperonin family protein	TCP-1/cpn60 chaperonin family	not plastid		29.6 protein.folding	29.6		0	C		Cpn60_TCP1(1)	8	0.085	57.78	7.58	10222007(mature Pollen); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension - Cd-up); 17407188(cotyledon); 17293592(total seedlings 7# light and dark grown); 19200160(flowers-stage 12); 19546170(mature pollen grains); 20118269(developing seeds); 19525416(leaf wt and clpr4-1 mutant); 19888209(80S polysomal fraction); 19888209(leaves);		0.537	0.551	56	protein.folding

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AT1G05840	gi6850312	Contains similarity to nucellin from <i>Hordeum vulgare</i> gb/U87148. ESTs gb/T22068, gb/F14251, gb/F14237, gb/F14242 come from this gene [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein			anchored to membrane	29.5.4 protein.degradati on.aspartate protease	29.5.4	1	0	S		Asp(1)	15	0.005	53.3	5.75			0	0	0	protein.degradati on.aspartate protease
AT1G05840	gi6850312	Contains similarity to nucellin from <i>Hordeum vulgare</i> gb/U87148. ESTs gb/T22068, gb/F14251, gb/F14237, gb/F14242 come from this gene [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein			anchored to membrane	29.5.4 protein.degradati on.aspartate protease	29.5.4	1	0	S		Asp(1)	15	0.005	53.3	5.75			0	0	0	protein.degradati on.aspartate protease
AT1G53430	gi8671883	Contains similarity to receptor-like serine/threonine kinase from <i>Arabidopsis thaliana</i> gb/AF024648 and contains multiple leucine rich PF00567 repeats and protein kinase PF00069 domain. ESTs gb/T04455, gb/N38129 come from this gene	Protein destination and storage	Leucine-rich repeat transmembrane protein kinase	leucine-rich repeat protein / protein kinase family protein			30.2.8.2 signalling.recept or kinases.leucine rich repeat VIII-2	30.2.8.2	1	1	S		LRR_1(2) Pkinase_Tyr(1)	16	-0.204	113.98	5.51	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19525416(leaf (wt and clpr4-1 mutant)); 19253305(phosphoproteins (etiolated seedling)); 19334764(plasma membrane (cell culture));		0.017	0.019	959	signalling.recept or kinases.leucine rich repeat VIII-2
AT4G12570	gi15235410	E3 ubiquitin-protein ligase UPL5 [Arabidopsis thaliana]	Protein destination and storage	ubiquitin protein ligase 5				29.5.11.4.1 protein.degradati on.ubiquitin.E3. HECT	29.5.11.4.1		0	-		HECT(1) ubiquitin(1)	15	-0.305	100.37	6.26			0	0	0	protein.degradati on.ubiquitin.E3. HECT
AT1G03230	gi18379072	extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana]	Protein destination and storage	Eukaryotic aspartyl protease family protein	extracellular dermal glycoprotein, putative / EDGP	not plastid		35.1 not assigned.no ontology	35.1		0	S			12	0.232	46.15	9.33	15593128(Cell Wall proteome); 17916636(root (NaCl stress)); 17526915(glyco proteome cell wall (stems)); 18796151(cell wall (hypocotyl)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19714877(intera ctomes 14-3-3 complexes (cell culture)); 19423572(leaf		0.495	0.499	31	not assigned.no ontology
AT1G09070	gi10764861	FK23.21 [Arabidopsis thaliana]	Protein destination and storage	soybean gene regulated by cold-2			endoplasmic reticulum & protein storage vacuole	29.3.4.3 protein.targeting. secretory pathway.vacuole	29.3.4.3		0	-		C2(1)	2	-0.704	34.19	6.44	19546170(mature pollen grains); 16723734(vacuole -SUBA);		0	0	0	protein.targeting. secretory pathway.vacuole
AT1G12470	gi8778633	F5011.22 [Arabidopsis thaliana]	Protein destination and storage	zinc ion binding	Pep3/Vps18/deep orange family protein			29.3.4.3 protein.targeting. secretory pathway.vacuole	29.3.4.3		0	-		Clathrin(1) Pep3_Vps18(1) UVR(1) Vps39_2(1) zf-C3HC4(1)	18	-0.276	112.32	5.19	19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis leaf);		0.049	0.051	157	protein.targeting. secretory pathway.vacuole
AT3G58880	gi15231588	F-box family protein [Arabidopsis thaliana]	Protein destination and storage	F-box/RNI-like superfamily protein				29.5.11.4.3.2 protein.degradati on.ubiquitin.E3. SCF.FBOX	29.5.11.4.3.2		0	-		F-box(1) LRR_2(1)	15	0.205	50.76	7.5			0	0	0	protein.degradati on.ubiquitin.E3. SCF.FBOX
AT3G60040	gi15232242	F-box family protein [Arabidopsis thaliana]	Protein destination and storage	F-box family protein				29.5.11.4.3.2 protein.degradati on.ubiquitin.E3. SCF.FBOX	29.5.11.4.3.2	2	0	-		F-box(1) LRR_2(1) PPR(4) RnaseH(1)	22	0.067	94.2	8.45	17151019(vacuole - suspension cell); 17216043(leaf);		0	0	0	protein.degradati on.ubiquitin.E3. SCF.FBOX
AT5G25860	gi15239511	F-box family protein [Arabidopsis thaliana]	Protein destination and storage	F-box/RNI-like superfamily protein				29.5.11.4.3.2 protein.degradati on.ubiquitin.E3. SCF.FBOX	29.5.11.4.3.2		0	-		F-box(1) LRR_2(1)	17	-0.198	51.94	8.55	14760709(Vacuolar proteome);		0	0	0	protein.degradati on.ubiquitin.E3. SCF.FBOX
AT4G23940	gi18416240	FtsH protease, putative [Arabidopsis thaliana]	Protein destination and storage	FtsH extracellular protease family	FtsH1, inactive FtsH	plastid		29.5.7 protein.degradati on.metalloprotease	29.5.7	3	3	C		AAA(1) AAA_2(1) AAA_3(1) AAA_5(1) FtsH_ext(1) Mg_chelatase(1) NACHT(1) Peptidase	4	-0.214	105.54	7.64	16618929(MITOPLASTID-LOPT-callus); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20061580(chloroplast envelope (inner+outer));		0.081	0.086	235	protein.degradati on.metalloprotease

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AT5G02490	gi15241847	heat shock protein 70 [Arabidopsis thaliana]	Protein destination and storage	Heat shock protein 70 (Hsp 70) family protein	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)		cytosol	29.6 protein.folding	29.6		0	-		HSP70(1) Hydantoinase_A (1) MreB_Mbl(1)	7	-0.42	71.39	5.03		0.478	0.434	5	protein.folding	
AT4G37910	gi14467097	heat shock protein 70 like protein [Arabidopsis thaliana]	Protein destination and storage	mitochondrial heat shock protein 70-1	mtHsc70-1	mitochondria	mitochondrion & mitochondrial matrix	29.6 protein.folding	29.6		0	M		FtsA(1) HSP70(1) MreB_Mbl(1)	5	-0.295	73.08	5.51		0.444	0.45	1	protein.folding	
AT5G02500	gi1166765	heat shock protein HSP70-1 [Arabidopsis thaliana]	Protein destination and storage	heat shock cognate protein 70-1	HSP70-1 (HSC70-1) (not plastid) - very abundant	cytosol; nucleus	cytosol	29.6 protein.folding	29.6		0	-		HSP70(1) Hydantoinase_A (1) MreB_Mbl(1)	7	-0.436	71.36	5.03		0.848	0.842	5	protein.folding	

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AT1G56410	gi15223533	heat shock protein-70 cognate protein [Arabidopsis thaliana]	Protein destination and storage	heat shock protein 70 (Hsp70) family protein	HSP70t-1 (not plastid)			29.6 protein.folding	29.6		0	-		HSP70(1) Hydantoinase_A(1) MreB_Mbl(1)	6	-0.367	68.36	5.22	15028209(Total chloroplast); 12938931(Total chloroplast envelope); 16358359(cell suspension (M&Skoog)); 16502469(cell suspension-Cd-up); 17407188(cotyledon); 18814325(cotyledons); 20118269(developing seeds); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 20706207(costa		0.297	0.224	5	protein.folding
AT1G22870	gi2462837	hypothetical protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase family protein with ARM repeat domain				29.4 protein.postranslational modification	29.4		0	-		DUF1421(1) HEAT(1) Kinase_Tyr(1)	9	-0.266	100.06	7.24	19546170(mature pollen grains);		0	0	0	protein.postranslational modification
AT2G17760	gi25347778	hypothetical protein At2g17760 [imported] - Arabidopsis thaliana	Protein destination and storage	Eukaryotic aspartyl protease family protein	aspartyl protease family protein		anchored to membrane	29.5.4 protein.degradation.aspartate protease	29.5.4		1	S		Asp(1) DUF1888(1)	14	-0.113	56.03	5.07	18716313(secreted proteins (cell culture)); 19260003(detergent resistant plasma membrane (DRM) proteins		0	0	0	protein.degradation.aspartate protease
AT1G79560	gi4835753	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb A1100347 come from this gene [Arabidopsis thaliana]	Protein destination and storage	FTSH protease 12	FtsH12	plastid	chloroplast	29.5.7 protein.degradation.metalloprotease	29.5.7	2	2	C		AAA(1) AAA_2(1) AAA_3(1) AAA_5(1) DUF1697(1) Mg_chelata(1) NACHT(1) Peptidase_	5	-0.341	115.11	6.49	16618929(MITOPLASTID-LOPIT-callus); 18431481(chloroplast); 19995728(propylastid (Brassica napus)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20061580(chloroplast envelope (inner+outer));		0.181	0.19	91	protein.degradation.metalloprotease
AT5G35340	gi15238774	P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	Protein destination and storage	P-loop containing nucleoside triphosphate hydrolases superfamily protein	MSP1 protein, putative / intramitochondrial sorting protein, putative	not plastid		29.5.11.20 protein.degradation.ubiquitin.proteasom	29.5.11.20	1	1	S		AAA(1) AAA_3(1) AAA_5(1) ABC_tran(1) Bac_DnaA(1) DUF1871(1) NACHT(1) ResIII(1) S	4	-0.254	44.85	5.72	19995728(propylastid (Brassica napus)); 19525416(leaf (wt and clpr4-1 mutant)); 19376835(leaf phosphoproteins)		0.074	0.079	124	protein.degradation.ubiquitin.proteasom
AT1G69960	gi15222511	PP2A (SERINE/THREONINE PHOSPHATASE 2A); protein serine/threonine phosphatase [Arabidopsis thaliana]	Protein destination and storage	serine/threonine protein phosphatase 2A				29.4 protein.postranslational modification	29.4		0	-		Metallophos(1)	11	-0.301	35.04	4.86	19546170(mature pollen grains);		0	0	0	protein.postranslational modification
AT5G38650	gi15240969	Proteasome maturation factor UMP1 [Arabidopsis thaliana]	Protein destination and storage	Proteasome maturation factor UMP1	proteasome maturation factor UMP1 family protein			29.5.11.20 protein.degradation.ubiquitin.proteasom	29.5.11.20		0	-		UMP1(1)	0	-0.575	15.81	6.59			0.099	0.123	53	protein.degradation.ubiquitin.proteasom
AT5G49470	gi10177613	protein kinase [Arabidopsis thaliana]	Protein destination and storage	PAS domain-containing protein tyrosine kinase family				29.4 protein.postranslational modification	29.4	2	0	-		Kdo(1) Pkinase_Tyr(1)	7	-0.611	54.55	6.06			0	0	0	protein.postranslational modification
AT1G07870	gi15223024	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	-		APH(1) Pkinase(1) Pkinase_Tyr(1)	8	-0.5	46.76	8.45	17644812(plasma membrane - suspension cells);		0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT1G54610	gi15221868	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein.postranslational modification; 29.4.1 protein.postranslational modification.kin	29.4; 29.4.1		0	-		Pkinase(1) Pkinase_Tyr(1)	8	-0.62	63.29	9.49	17317660(Plasma Membrane proteome); 19376835(leaf phosphoproteins); 19114538(guard cells Arabidopsis		0	0	0	protein.postranslational modification; protein.postranslational modification.kinase
AT2G23200	gi15227790	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				30.2.16 signalling.receptor kinases.Catharanthus roseus-like	30.2.16	1	2	S		PduL(1) Pkinase(1) Pkinase_Tyr(1) RIO1(1)	7	-0.277	93.38	5.97	18686298(tonoplast - phosphoproteome (leaves));		0	0	0	signalling.receptor kinases.Catharanthus roseus-like RLK1
AT2G28940	gi30684071	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	S		APH(1) Pkinase(1) Pkinase_Tyr(1)	4	-0.263	39.12	8.84	15815986(Leaf);		0.026	0.028	123	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII

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AT2G39360	gi 15225078	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				30.2.16 signalling.recept or kinases.Catharan thus roseus-like RLK1	30.2.16	1	1	S		APH(1) Pkinase(1) Pkinase_Tyr(1)	11	-0.131	91.32	6.13	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension		0	0	0	signalling.recept or Kinases.Catharan thus roseus-like RLK1
AT3G06630	gi 15230754	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	protein kinase family protein				29.4 protein.postransl ational modification	29.4		0	-		Kdo(1) PAS(1) PAS_3(1) PAS_4(1) Pkinase_Tyr(1)	10	-0.529	75.18	7.94			0	0	0	protein.postransl ational modification
AT3G22750	gi 18403507	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein.postransl ational modification	29.4		0	-		Pkinase_Tyr(1)	11	-0.467	42.72	7.93	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19376835(leaf phosphoproteins)		0	0	0	protein.postransl ational modification
AT3G54030	gi 15232406	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase protein with tetratricopeptide repeat domain	protein kinase family protein	plasma membrane		29.4 protein.postransl ational modification	29.4		0	S		Pkinase(1)	13	-0.316	54.79	6.11	14506206(plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19376835(leaf phosphoproteins)		0	0	0	protein.postransl ational modification
AT3G63260	gi 15229398	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein.postransl ational modification	29.4		0	-		Pkinase(1)	12	-0.296	42.58	6.23	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins)		0	0	0	protein.postransl ational modification
AT4G02630	gi 15235432	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	Tak kinase			29.4.1 protein.postransl ational modification.kin ase	29.4.1	1	1	M		Pkinase(1)	3	-0.393	54.74	7.28	17317660(Plasma Membrane proteome); 17216043(leaf); 19376835(leaf phosphoproteins)		0	0	0	protein.postransl ational modification.kin ase
AT4G14780	gi 15233574	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein.postransl ational modification	29.4		0	-		Pkinase_Tyr(1)	11	-0.438	40.73	8.19	19546170(mature pollen grains); 19334764(plasma membrane (cell culture));		0	0	0	protein.postransl ational modification
AT4G31170	gi 15235845	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein.postransl ational	29.4		0	-		Pkinase(1)	7	-0.246	46.08	5.97			0	0	0	protein.postransl ational modification
AT5G01020	gi 30679085	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postransl ational modification.kin ase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	C		Pkinase(1) Pkinase_Tyr(1)	9	-0.347	45.62	9.21	17317660(Plasma Membrane proteome); 19376835(leaf phosphoproteins);		0	0	0	protein.postransl ational modification.kin ase.receptor like cytoplasmatic kinase VII

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AT5G24010	gi 15237872	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	protein kinase family protein	plasma membrane		30.2.16 signalling.receptor or kinases.Catharan thus roseus-like RLK1	30.2.16	1	1	S		APH(1) Pkinase(1)	11	-0.123	91.82	7.6	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant		0	0	0	0	0	signalling.receptor or Kinases.Catharan thus roseus-like RLK1
AT5G41260	gi 15237604	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase protein with tetratricopeptide repeat domain				29.4 protein.postranslational modification	29.4		0	-		Pkinase(1) Pkinase_Tyr(1)	11	-0.409	54.63	5.92	17317660(Plasma Membrane proteome); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0	0	0	0	0	protein.postranslational modification
AT5G51770	gi 15242183	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.61 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase X	29.4.1.61	1	0	C		Pkinase_Tyr(1)	10	-0.53	73.33	9.39			0	0	0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase X
AT5G57610	gi 15242791	protein kinase family protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain				29.4 protein.postranslational modification	29.4		0	-		PB1(1) Pkinase_Tyr(1)	11	-0.665	117.45	5.6	19376835(leaf phosphoproteins);		0	0	0	0	0	protein.postranslational modification
AT3G59410	gi 7801691	protein kinase like [Arabidopsis thaliana]	Protein destination and storage	protein kinase family protein				29.4 protein.postranslational modification	29.4		0	-		APH(1) HGTP_anticon(1) Pkinase(1) Pkinase_Tyr(1) RWD(1)	19	-0.397	140.32	5.42	19546170(mature pollen grains);		0	0	0	0	0	protein.postranslational modification
AT2G17220	gi 18398350	protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	protein kinase	not plastid		29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	C		Pkinase(1)	4	-0.42	45.55	9.44			0	0	0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT3G46290	gi 15231393	protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	hercules receptor kinase I	protein kinase, putative	plasma membrane		30.2.16 signalling.receptor or kinases.Catharan thus roseus-like RLK1	30.2.16	1	1	S		APH(1) Pkinase_Tyr(1)	10	-0.183	91.47	5.91	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(UNK NOWN-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol dependent detergent		0	0	0	0	0	signalling.receptor or Kinases.Catharan thus roseus-like RLK1
AT5G03320	gi 15242720	protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	Protein kinase (plastid? - interesting)			29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	C		Pkinase(1)	5	-0.509	47.01	9.34	19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom e (leaves));		0.021	0.024	54	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII

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AT5G56460	gi15241220	protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	protein kinase, putative	plasma membrane		29.4.1.57 protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	-		Pkinase(1)	7	-0.344	45.87	7.14	15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT3G06640	gi12321912	protein kinase, putative; 42705-46677 [Arabidopsis thaliana]	Protein destination and storage	PAS domain-containing protein tyrosine kinase family protein				29.4 protein_postranslational modification	29.4		0	-		Fmp27_SW(1) Kdo(1) PAS(1) PAS_3(1) PAS_4(1) Pkinase(1)	11	-0.407	82.14	8.63			0	0	0	protein_postranslational modification
AT3G62220	gi15228711	protein kinase-domain containing protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.58 protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		Pkinase(1)	5	-0.292	39	8.47			0	0	0	protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII
AT2G30730	gi15224556	protein kinase-like protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.58 protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		APH(1) Pkinase(1) Pkinase_Tyr(1)	4	-0.188	37.55	5.71			0	0	0	protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII
AT3G46140	gi15231346	protein kinase-related protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4 protein_postranslational	29.4		0	-		Pkinase_Tyr(1)	8	-0.274	42.45	8.64			0	0	0	protein_postranslational modification
AT4G28400	gi18417190	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	Protein destination and storage	Protein phosphatase 2C family protein	protein phosphatase 2C (PP2C), putative			29.4.5 protein_postranslational modification.phosphatase	29.4.5		0	-		PP2C(1)	3	-0.323	31.02	7.79	17216043(leaf); 19376835(leaf phosphoproteins); 20706207(contaminants cell cycle		0.138	0.167	82	protein_postranslational modification.phosphatase
AT5G14670	gi2462736	putative ADP-ribosylation factor [Arabidopsis thaliana]	Protein destination and storage	ADP-ribosylation factor A1B	ADP-ribosylation factor (ATARFA1B)	not plastid		29.3.4.99 protein.targeting.secretory pathway.unspecified	29.3.4.99		0	M		Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	1	-0.206	21.54	6.43	18463617(suspension cells-phosphorylated proteins); 19525416(leaf (wt and clpr4-1 mutant)); 19423572(leaf (wt and clpr2-		0.574	0.61	20	protein.targeting.secretory pathway.unspecified
AT4G04910	gi7267250	putative component of vesicle-mediated transport [Arabidopsis thaliana]	Protein destination and storage	AAA-type ATPase family protein	NSF (N-ETHYLMALEIMIDE SENSITIVE FACTOR): ATP binding / binding / nucleoside-triphosphate/ nucleotide binding	not plastid		29.5.9 protein.degradation.AAA type	29.5.9		0	-		AAA(2) AAA_2(1) AAA_5(1) Arch_ATPase(1) CDC48_2(1) CDC48_N(1) NACHT(1) Pox_C4_C1	9	-0.12	81.49	5.74	15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 19452453(14-3-3-interacting proteins); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis		0.271	0.291	66	protein.degradation.AAA type
AT2G03530	gi4335747	putative integral membrane protein [Arabidopsis thaliana]	Protein destination and storage	urecide permease 2				29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX	29.5.11.4.3.2	9	9	S		7tm_4(1) BPD_transp_2(1) DUF1632(1) DUF6(1) FAE_3-kCoA_syn1(1) MFS_1(1)	7	0.43	43.54	9.13	17317660(Plasma Membrane proteome);		0	0	0	protein.degradation.ubiquitin.E3.SCF.FBOX
AT3G48820	gi7576220	putative protein [Arabidopsis thaliana]	Protein destination and storage	Glycosyltransferase family 29 (sialyltransferase) family protein				29.7 protein.glycosylation	29.7		1	S		Glyco_transf_29(1)	10	-0.333	49.48	9.24	16618929(Golgi);		0	0	0	protein.glycosylation
AT3G53780	gi7629998	putative protein [Arabidopsis thaliana]	Protein destination and storage	RHOMBOID-like protein 4	rhomboid protease 4 (AtRBL4)			29.5.5 protein.degradation.serine	29.5.5	7	6	-		BioY(1) Rhomboid(1)	9	0.554	29.45	9.26	17317660(Plasma Membrane proteome);		0	0	0	protein.degradation.serine protease

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AT4G13190	gi 4753653	putative protein [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	-		APH(1) Pkinase(1)	6	-0.303	43.22	6.04			0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT4G35230	gi 3080427	putative protein [Arabidopsis thaliana]	Protein destination and storage	BR-signaling kinase I	protein kinase family protein	plasma membrane		29.4.1.52 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase II	29.4.1.52		0	-		Pkinase_Tyr(1)	12	-0.477	56.82	5.52	15308754(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(PlasmaMembrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.141	0.137	68	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase II
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	serine/threonine protein kinase, putative	plasma membrane		29.4.1.58 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		APH(1) Pkinase_Tyr(1)	6	-0.325	39.82	7.14	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant));		0.139	0.142	216	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII
AT1G56720	gi 9954741	Putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.55 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase V	29.4.1.55	1	1	-		APH(1) Pkinase(1)	4	-0.366	54.94	9.08	18463617(suspension cells-phosphorylated proteins);		0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase V
AT2G07180	gi 19423982	putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein	protein kinase, putative			29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	-		Pkinase(1) Pkinase_Tyr(1)	7	-0.504	49.21	8.45	15276459(epidermis); 19546170(mature pollen grains); 19245862(nuclear phosphoproteins (seedlings & cell		0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT4G33080	gi 4455322	putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family				29.4 protein.postranslational modification	29.4		0	-		Pkinase(1) Pkinase_C(1) Pkinase_Tyr(1)	8	-0.615	60.43	5.52			0	0	0	protein.postranslational modification
AT2G39110	gi 3928095	putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	29.4.1.57		0	-		Pkinase(1)	4	-0.371	48.88	9.55			0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII
AT1G34750	gi 15218759	putative protein phosphatase 2C 10 [Arabidopsis thaliana]	Protein destination and storage	Protein phosphatase 2C family protein				29.4 protein.postranslational modification	29.4		0	-		PP2C(1)	3	-0.398	30.98	7.13	17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma		0	0	0	protein.postranslational modification



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AT2G20630	gi18399423	putative protein phosphatase 2C 20 [Arabidopsis thaliana]	Protein destination and storage	PP2C induced by AVRRPM1	protein phosphatase 2C (PP2C), putative			29.4.5 protein_postranslational modification.phosphatase	29.4.5		0	-		PP2C(1) SpoIE(1)	2	-0.293	30.5	5.74	15815986(seedling); 18538804(total leaf); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(leaves); 19114538(guard cell); 14306206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteome)		0.28	0.287	78		protein_postranslational modification.phosphatase
AT1G22280	gi18395099	putative protein phosphatase 2C 9 [Arabidopsis thaliana]	Protein destination and storage	phytochrome-associated protein phosphatase type 2C	protein phosphatase 2C, putative / PP2C, putative	plasma membrane		29.4 protein_postranslational modification	29.4		0	-		PP2C(1) SpoIE(1)	3	-0.41	30.72	6.67	15815986(seedling); 18538804(total leaf); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(leaves); 19114538(guard cell); 14306206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteome)		0.046	0.048	177		protein_postranslational modification
AT2G42960	gi15228043	putative receptor-like protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.55 protein_postranslational modification.kinase.receptor like cytoplasmatic kinase V	29.4.1.55	1	1	-		APH(1) Pkinase(1)	6	-0.34	55.19	8.82	18463617(suspension cells-phosphorylated proteins);		0	0	0		protein_postranslational modification.kinase_receptor like cytoplasmatic kinase V
AT2G29000	gi3461842	putative receptor-like protein kinase [Arabidopsis thaliana]	Protein destination and storage	Leucine-rich repeat protein kinase family protein				29.4 protein_postranslational modification	29.4	1	2	S		LRR_1(1) LRRNT_2(1) Pkinase_Tyr(1) SH3_4(1)	14	-0.241	98.09	6.37	19334764(plasma membrane (cell culture));		0	0	0		protein_postranslational modification
AT2G28000	gi21554572	putative rubisco subunit binding-protein alpha subunit [Arabidopsis thaliana]	Protein destination and storage	chaperonin-60alpha	Cpn60-alpha-1	plastid stroma	mitochondrion & chloroplast	29.6 protein.folding	29.6		0	C		Cpn60_TCP1(1) NAD_binding_3(1) zf-ZPR1(1)	3	0.002	62.07	5.09	13028209(Total chloroplast); 12938931(Total chloroplast envelope); MitoDB(Mitochondrial proteome); 11826309(thylakoid peripheral&lumen); 16207701(chloroplast stroma); 15821981(crude & pure 80S ribosome); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16055689(Glutathionylated suspension cell); 15815986(Siliques)		0.846	0.917	50		protein.folding
AT5G56340	gi15241188	RING/U-box domain-containing protein [Arabidopsis thaliana]	Protein destination and storage	RING/U-box superfamily protein	zinc finger (C3HC4-type RING finger) family protein			29.5.11.4.2 protein.degradation.ubiquitin.E3.RING	29.5.11.4.2		0	-		PHD(1)	10	-0.863	44.36	5.37			0.033	0.033	150		protein.degradation.ubiquitin.E3.RING

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AT2G16600	gi15227259	ROC3; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	Protein destination and storage	rotamase CYP 3	peptidyl-prolyl cis-trans isomerase, cytosolic / cyclophilin / rotamase (ROC3; Cyp3)	not plastid		29.6 protein.folding	29.6		0	-		Pro_isomerase(1)	4	-0.323	18.49	8.66	16247729(Gamborg); 16400686(floem_sap B. napa); 15815986(Siliquae); 15815986(seedling); 18538804(total leaf); 17407188(cotyledon); 17293592(total seedlings 77 light and dark grown); 17644812(plasma membrane - suspension cells); 18431481(chloroplast); 18814325(cotyledons); 19200160(flowe		0.711	0.728	7	protein.folding
AT1G55490	gi15222729	RuBisCO large subunit-binding protein subunit beta [Arabidopsis thaliana]	Protein destination and storage	chaperonin 60 beta	Cpn60-beta-2	plastid stroma		29.6 protein.folding	29.6		0	C		Cpn60_TCP1(1) GTP_EFTU_D2(1)	7	-0.112	63.81	6.21	15028209(Total chloroplast); 12938931(Total chloroplast envelope); 12766230(Total chloroplast envelope); 16207701(chloroplast stroma); 15821981(crude & pure 80S ribosome); 16923014(cold-stress responsive chloroplast); 15815986(seedling); 15815986(Leaf); 15276459(trichomes); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17317660(Plasma Membrane		0.828	0.909	55	protein.folding
AT2G05920	gi62321128	serine protease like protein [Arabidopsis thaliana]	Protein destination and storage	Subtilase family protein	subtilase family protein			29.5.1 protein.degradation.subtilases	29.5.1		1	S		PA(1) Peptidase_S8(1) Subtilisin_N(1)	10	-0.09	80.02	8.58	14595688(Cell Wall proteome); 15593128(Cell Wall proteome); 17526915(glyco proteome cell wall (stems)); 18716313(secreted proteins (cell culture)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant));		0.359	0.361	204	protein.degradation.subtilases
AT1G48210	gi15221111	serine/threonine protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.58 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		APH(1) Pkinase(1)	5	-0.316	39.59	8.93	17317660(Plasma Membrane proteome); 19334764(plasma membrane (cell culture));		0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII
AT2G47060	gi79324935	serine/threonine protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.58 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		Pkinase(1)	6	-0.338	39.93	6.94	19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell		0	0	0	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VIII

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AT3G17410	gi 22331138	serine/threonine protein kinase, putative [Arabidopsis thaliana]	Protein destination and storage	Protein kinase superfamily protein				29.4.1.58 protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII	29.4.1.58		0	-		APH(1) Pkinase_Tyr(1)	6	-0.302	39.56	8.97	17644812(plasma membrane - suspension cells); 19200160(flowe r-stage 12); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasm		0	0	0	protein_postranslational modification.kinase.receptor like cytoplasmatic kinase VIII
AT5G28290	gi 15241745	serine/threonine-protein kinase Nek3 [Arabidopsis thaliana]	Protein destination and storage	NIMA-related kinase 3				29.4 protein_postranslational	29.4		0	-		Pkinase_Tyr(1)	9	-0.473	63.76	9.53	20706207(cell cycle interactome (cell		0	0	0	protein_postranslational modification
AT3G44200	gi 145339108	serine/threonine-protein kinase Nek5 [Arabidopsis thaliana]	Protein destination and storage	NIMA (never in mitosis, gene A)-related 6				29.4 protein_postranslational	29.4		0	-		Kdo(1) Pkinase(1)	15	-0.707	106.39	6.75			0	0	0	protein_postranslational modification
AT1G09100	gi 2342675	Similar to probable Mg-dependent ATPase (pirS56671). ESTs gbT46782.gbAA04798 come from this gene [Arabidopsis thaliana]	Protein destination and storage	26S proteasome AAA-ATPase subunit RPT5B	26S protease regulatory subunit (RPT5b)	cytosol		29.5.11.20 protein.degradation.ubiquitin.proteasom	29.5.11.20		0	-		AAA(1) AAA_2(1) AAA_3(1) AAA_5(1)	4	-0.385	47.04	4.9	11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 20118269(developing seeds); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20706207(cell cycle interactome (cell		0.206	0.207	140	protein.degradation.ubiquitin.proteasom
AT1G61360	gi 15219912	S-like receptor protein kinase [Arabidopsis thaliana]	Protein destination and storage	S-locus lectin protein kinase family protein				29.4 protein_postranslational modification	29.4	1	1	S		B_lectin(1) PAN_2(1) Pkinase_Tyr(1) S_locus_glycop	22	-0.223	90.94	6.03			0	0	0	protein_postranslational modification
AT4G32300	gi 2864613	S-receptor kinase -like protein [Arabidopsis thaliana]	Protein destination and storage	S-domain-2 5				29.4 protein_postranslational modification	29.4	1	1	S		APH(1) B_lectin(1) CcmD(1) Metallothio_2(1) PAN_3(1) Pkinase(1) Pkinase_Tyr(1)	19	-0.154	89.74	6.08	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells);		0	0	0	protein_postranslational modification
AT1G70490	gi 4056469	Strong similarity to gbM95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gbZ25826, gbR90191, gbN65697, gbAA713150, gbT46332, gbAA040967, gbAA712956, gbT46403, gbT46050, gbA1100391 and gbZ25043 come from this gene	Protein destination and storage	Ras-related small GTP-binding family protein	ADP-ribosylation factor (ATARFA1D)	not plastid		29.3.4.99 protein.targeting.secretory pathway.unspecified	29.3.4.99		0	M		Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	1	-0.191	20.59	6.43	15339469(vacuole); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19200160(flowe r-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis leaf); 19423572(leaf		0.597	0.635	20	protein.targeting.secretory pathway.unspecified
AT1G61370	gi 3056593	T1F9.14 [Arabidopsis thaliana]	Protein destination and storage	S-locus lectin protein kinase family protein				29.4 protein_postranslational modification	29.4	1	2	S		B_lectin(1) PAN_1(1) PAN_2(1) Pkinase(1) RIO1(1) S_locus_glycop	20	-0.163	90.86	5.26			0	0	0	protein_postranslational modification

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AT1G27750	gi 6693023	T22C5.20 [Arabidopsis thaliana]	Protein destination and storage	nucleic acid binding				29.5.11 protein.degradati on.ubiquitin	29.5.11		0	-		Extensin_2(1) Picorna_P3A(1) RRM_1(1) SPOC(1)	22	-0.362	117.45	6.4	18463617(suspension cells-phosphorylated proteins);		0	0	0	protein.degradati on.ubiquitin
AT1G01740	gi 15223469	tetratricopeptide repeat domain-containing protein kinase [Arabidopsis thaliana]	Protein destination and storage	Protein kinase protein with tetratricopeptide repeat domain				29.4 protein_postransl ational modification	29.4		0	-		Kdo(1) Pkinase(1) Pkinase_Tyr(1)	11	-0.281	54.04	5.45	17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasm		0	0	0	protein.postransl ational modification
AT5G23720	gi 10176839	unnamed protein product [Arabidopsis thaliana]	Protein destination and storage	dual specificity protein phosphatase family protein				29.4 protein_postransl ational modification	29.4		0	-		Act-Frag_cataly(1) DSPc(1)	16	-0.591	104.24	5.97	17407188(cotyledon);		0.014	0.015	612	protein.postransl ational modification
AT5G56380	gi 10177837	unnamed protein product [Arabidopsis thaliana]	Protein destination and storage	F-box/RN1-like/FBD-like domains-containing				29.5.11.4.3.2 protein.degradati on.ubiquitin.E3. SCF.FBOX	29.5.11.4.3.2		0	-		F-box(1) FBD(1) LRR_2(1)	14	-0.092	49.91	8.89			0	0	0	protein.degradati on.ubiquitin.E3. SCF.FBOX
AT5G57950	gi 9758364	unnamed protein product [Arabidopsis thaliana]	Protein destination and storage	26S proteasome regulatory subunit, putative	26S proteasome regulatory subunit	cytosol		29.5.11.20 protein.degradati on.ubiquitin.proteasom	29.5.11.20		0	-		PDZ(1)	2	-0.22	24.26	5.07	19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19888209(80S polysomal		0.035	0.036	205	protein.degradati on.ubiquitin.proteasom
AT4G00330	gi 6049872	weak similarity to receptor protein kinase [Arabidopsis thaliana]	Protein destination and storage	calmodulin-binding receptor-like cytoplasmic kinase 2	CRCK2 (calmodulin-binding receptor-like cytoplasmic kinase 2); kinase			29.4.1.54 protein_postransl ational modification.kin ase.receptor like cytoplasmic kinase IV	29.4.1.54		0	M		APH(1) Pkinase(1) Pkinase_Tyr(1)	4	-0.527	46.18	9.26			0	0	0	protein.postransl ational modification.kin ase.receptor like cytoplasmic kinase IV
AT2G42360	gi 15227929	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Protein destination and storage	RING/U-box superfamily protein				29.5.11.4.2 protein.degradati on.ubiquitin.E3. RING	29.5.11.4.2	1	1	-		Cl_4(1) zf-C3HC4(1)	8	-0.332	26.44	8.87			0	0	0	protein.degradati on.ubiquitin.E3. RING
AT5G01520	gi 15241003	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Protein destination and storage	RING/U-box superfamily protein				29.5.11.4.2 protein.degradati on.ubiquitin.E3. RING	29.5.11.4.2		0	-		DNA_ligase_ZBD(1) DnaJ_CXXCXG XG(1) zf-	10	-0.364	28.05	8.45			0	0	0	protein.degradati on.ubiquitin.E3. RING
AT2G36160	gi 15227588	40S ribosomal protein S14 (RPS14A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S11 family protein	40S ribosomal protein S14 (RPS14A)	cytosol		29.2.1.2.1.14 protein.synthesis.ribosomal protein.eukaryoti c.40S subunit.S14	29.2.1.2.1.14		0	-		Ribosomal_S11(1)	1	-0.468	16.26	10.6	13028209(total chloroplast); 15734919(80S cytosolic ribosomes); 16247729(mature Pollen); 16618929(UNK NOWN-LOPPT-callus); 17317660(Plasma Membrane proteome); 18538804(total leaf); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18814325(cotyledons); 19546170(mature pollen grains); 19470840(leaf		0.6	0.618	11	protein.synthesis.ribosomal protein.eukaryoti c.40S subunit.S14

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AT3G11510	gi 15229775	40S ribosomal protein S14-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S11 family protein	40S ribosomal protein S14 (RPS14B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.14 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S14	29.2.1.2.1.14		0	-		Ribosomal_S11(1)	1	-0.501	16.27	10.6	15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 15815986(Silique); 18538804(total leaf); 17934214(cytosolic ribosome); 18633119(young leaf); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf wt and clpr4-1 mutant); 19376835(leaf phosphoproteins)		0.6	0.618	11	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S14
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	Protein synthesis	cytosolic ribosomal protein S15	40S ribosomal protein S15 (RPS15A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.15 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15	29.2.1.2.1.15		0	-		Ribosomal_S19(1)	0	-0.354	17.13	10.34	15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 18814325(cotyledons); 18931141(peroxisomes-high&low purity (cell culture)); 19200160(flowers-stage 12); 20118269(developing seeds); 19036721(detergent resistant plasma membrane)		0.493	0.69	26	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	Protein synthesis	cytosolic ribosomal protein S15	40S ribosomal protein S15 (RPS15A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.15 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15	29.2.1.2.1.15		0	-		Ribosomal_S19(1)	0	-0.354	17.13	10.34	15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 18814325(cotyledons); 18931141(peroxisomes-high&low purity (cell culture)); 19200160(flowers-stage 12); 20118269(developing seeds); 19036721(detergent resistant plasma membrane)		0.493	0.69	26	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15
AT5G09500	gi 15242434	40S ribosomal protein S15-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S19 family protein	40S ribosomal protein S15 (RPS15C)	cytosol		29.2.1.2.1.15 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15	29.2.1.2.1.15		0	-		Ribosomal_S19(1)	0	-0.2	16.75	10.52	17934214(cytosolic ribosome); 18814325(cotyledons); 19546170(mature pollen grains); 19888209(80S polysomal fraction);		0.113	0	24	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15

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ATSG09510	gi 15242436	40S ribosomal protein S15-4 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S19 family protein	40S ribosomal protein S15 (RPS15D)	cytosol; cytosol		29.2.1.2.1.15	29.2.1.2.1.15		0	-		Ribosomal_S19(1)	0	-0.319	17.07	10.34	15496452(nucleolus); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 18814325(cotyledons); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19329564(peroxisomes (leaf)); 16287169(Chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16247729(mature Pollen); 15815986(Silique); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18931141(peroxisomes-high&low purity (cell culture)); 19546170(mature chloroplast); 16287169(Chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNKNOWN-LOPIT-calls); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total membranes); 18431481(chloroplast); 19546170(mature pollen grains); 19429840(ubiquitinated or	15496452(unclear -SUBA);	0.414	0.597	26	protein.synthesis, ribosomal protein.eukaryotic.40S subunit.S15
AT1G07770	gi 15223001	40S ribosomal protein S15a-1 [Arabidopsis thaliana]	Protein synthesis	ribosomal protein S15A	ribosomal protein S15A (RPS15A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.515	29.2.1.2.1.515		0	-		Ribosomal_S8(1)	1	-0.162	14.81	9.89	16287169(Chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16247729(mature Pollen); 15815986(Silique); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18931141(peroxisomes-high&low purity (cell culture)); 19546170(mature chloroplast); 16287169(Chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNKNOWN-LOPIT-calls); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total membranes); 18431481(chloroplast); 19546170(mature pollen grains); 19429840(ubiquitinated or		0.569	0.534	2	protein.synthesis, ribosomal protein.eukaryotic.40S subunit.S15A
AT2G09990	gi 15226676	40S ribosomal protein S16-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S5 domain 2-like superfamily protein	40S ribosomal protein S16 (RPS16A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.16	29.2.1.2.1.16		0	-		Ribosomal_S9(1)	4	-0.43	16.63	10.21	16287169(Chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNKNOWN-LOPIT-calls); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total membranes); 18431481(chloroplast); 19546170(mature pollen grains); 19429840(ubiquitinated or		0.349	0.378	34	protein.synthesis, ribosomal protein.eukaryotic.40S subunit.S16
AT3G04230	gi 15229252	40S ribosomal protein S16-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S5 domain 2-like superfamily protein	40S ribosomal protein S16 (RPS16B)	cytosol		29.2.1.2.1.16	29.2.1.2.1.16		0	-		Ribosomal_S9(1)	3	-0.489	16.59	10.19	16287169(Chloroplast); 15496452(nucleolus); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19329564(peroxisomes (leaf)); 15496452(nucleolus); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19329564(peroxisomes (leaf));		0.192	0.207	49	protein.synthesis, ribosomal protein.eukaryotic.40S subunit.S16

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AT2G04390	gi15228141	40S ribosomal protein S17 (RPS17A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal S17 family protein	40S ribosomal protein S17 (RPS17A)	cytosol		29.2.1.2.1.17 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S17	29.2.1.2.1.17		0	M		Ribosomal_S17e(1)	0	-0.582	16.05	10.04	15496452(nucleolus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 18814325(cotyledons); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 10287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 15815986(Silique); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19888209(leaves)	15496452(nucleolus -SUBA);	0.56	0.581	33	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S17
AT3G02080	gi15232844	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S19e family protein	40S ribosomal protein S19 (RPS19A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.19 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19	29.2.1.2.1.19		0	-		Ribosomal_S19e(1)	1	-0.508	15.83	10.09	10287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 15815986(Silique); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19888209(leaves)		0.476	0.464	26	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19
AT5G61170	gi15240154	40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S19e family protein	40S ribosomal protein S19 (RPS19C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.19 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19	29.2.1.2.1.19		0	-		Ribosomal_S19e(1)	1	-0.396	15.7	10.22	15539469(vacuole); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19423572(leaf (wt and clpr2-		0.385	0.31	26	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19
AT5G15520	gi15242322	40S ribosomal protein S19-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S19e family protein	40S ribosomal protein S19 (RPS19B)	cytosol		29.2.1.2.1.19 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19	29.2.1.2.1.19		0	-		Ribosomal_S19e(1)	1	-0.471	15.82	10.14	15496452(nucleolus); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 18931141(peroxisomes-high&low purity (cell culture)); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis		0.245	0.12	29	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S19

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AT2G41840	gi15227443	40S ribosomal protein S2-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S5 family protein	40S ribosomal protein S2 (RPS2C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.2 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S2	29.2.1.2.1.2		0	-		Ribosomal_S5(1) Ribosomal_S5_C(1)	4	-0.411	30.88	10.3	15499432(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16247729(mature Pollen); 15815986(Siliquae); 17934214(cytosolic ribosome); 17828791(total leaf); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins); 18814325(cotyledons); 18931141(peroxisomes- 15499432(nucleolus); 15734919(80S cytosolic ribosomes); 18538804(total leaf); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 20423899(chloroplast); 19114538(guard cells Arabidopsis leaf); 15496452(nucleus -SUBA); 15496452(unclear -SUBA);		0.414	0.536	71	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S2
AT5G02960	gi15242574	40S ribosomal protein S23-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S12/S23 family protein	40S ribosomal protein S23 (RPS23B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.23 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S23	29.2.1.2.1.23		0	M		Ribosomal_S12(1)	2	-0.539	15.74	10.37	15499432(nucleolus); 15734919(80S cytosolic ribosomes); 18538804(total leaf); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 20423899(chloroplast); 19114538(guard cells Arabidopsis leaf); 15496452(nucleus -SUBA); 15496452(unclear -SUBA);		0.275	0.542	79	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S23
AT3G04920	gi15229845	40S ribosomal protein S24-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S24e family protein	40S ribosomal protein S24 (RPS24A)	cytosol		29.2.1.2.1.24 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S24	29.2.1.2.1.24		0	M		Ribosomal_S24e(1)	0	-0.814	15.37	10.7	15499432(nucleolus); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 18538804(total leaf); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18431481(chloroplast); 19200160(flowers-stage 12); 19546170(mature pollen grains); 16026731(leaf); 15496452(nucleus -SUBA); 15496452(unclear -SUBA);		0.308	0.331	22	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S24



AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT5G28060	gi 15241125	40S ribosomal protein S24-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S24e family protein	40S ribosomal protein S24 (RPS24B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.24 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S24	29.2.1.2.1.24		0	M		Ribosomal_S24e(1)	1	-0.874	15.42	10.53	15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPIT-callus); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total membranes); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 1988209(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 19200160(flowe r-stage 12); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 1988209(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture))		0.316	0.339	22	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S24
AT2G21580	gi 15226590	40S ribosomal protein S25 (RPS25B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S25 family protein	40S ribosomal protein S25 (RPS25B)	cytosol		29.2.1.2.1.25 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S25	29.2.1.2.1.25		0	-		Ribosomal_S25(1)	0	-0.805	12.07	10.7	15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 1988209(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 19200160(flowe r-stage 12); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture))		0.287	0.333	37	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S25
AT4G39200	gi 15234970	40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S25 family protein	40S ribosomal protein S25 (RPS25E)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.25 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S25	29.2.1.2.1.25		0	-		Ribosomal_S25(1)	0	-0.756	12.05	10.7	15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture))		0.426	0.495	35	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S25
AT4G34555	gi 18418472	40S ribosomal protein S25-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S25 family protein	40S ribosomal protein S25, putative	cytosol		29.2.1.2.1.25 protein.synthesis.ribosomal.protein.eukaryotic.40S	29.2.1.2.1.25		0	-		Ribosomal_S25(1)	0	-0.804	12.02	10.7	17934214(cytosolic ribosome); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture))		0.241	0.28	35	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S25
AT2G40510	gi 15226694	40S ribosomal protein S26-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S26e family protein	40S ribosomal protein S26 (RPS26A)	cytosol		29.2.1.2.1.26 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S26	29.2.1.2.1.26		0	-		Ribosomal_S26e(1)	6	-0.816	14.84	11.09	15028209(Total chloroplast); 17934214(cytosolic ribosome); 18814325(cotyledons); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 1988209(80S polysomal fraction); 20061580(chloroplast envelope		0.511	0.613	43	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S26

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AT5G47930	gi 15238845	40S ribosomal protein S27-3 [Arabidopsis thaliana]	Protein synthesis	Zinc-binding ribosomal protein family protein	40S ribosomal protein S27 (RPS27D)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.27 protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S27	29.2.1.2.1.27		0	-		Ribosomal_S27e(1)	6	-0.336	9.49	9.24	15821981(crude & pure 80S ribosome); 17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19525416(leaf wt and clpr4-1 mutant); 19888209(80S polysomal fraction); 19376835(leaf phosphoproteins); 19114538(guard cells Arabidopsis thaliana); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17272265(ubiquitinated proteins (suspension cells)); 18998720(SA-induced secreted proteome (cell culture)); 18931141(peroxisomes-high&low purity (cell culture)); 18931141(peroxisomes-high purity (cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0.369	0	2	protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S27
AT1G23410	gi 15220742	40S ribosomal protein S27a-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S27a/Ubiquitin family protein	ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA)	cytosol		29.2.1.2.1.27 protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S27	29.2.1.2.1.27		0	-		Ribosomal_S27(1) ubiquitin(1)	4	-0.709	17.67	9.77	17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17272265(ubiquitinated proteins (suspension cells)); 18998720(SA-induced secreted proteome (cell culture)); 18931141(peroxisomes-high&low purity (cell culture)); 18931141(peroxisomes-high purity (cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0.391	0.408	12	protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S27
AT3G43980	gi 15229840	40S ribosomal protein S29 (RPS29A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S14p/S29e family protein				29.2.1.2.1.29 protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S29	29.2.1.2.1.29		0	M		Ribosomal_S14(1)	5	-0.72	6.43	10.07	17934214(cytosolic ribosome); 18463617(suspension cells-phosphorylated proteins); 19200160(flowers-stage 12); 19546170(mature pollen grains); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 18538804(total leaf); 17934214(cytosolic ribosome); 17916636(root (NaCl stress)); 17432890(leaf total membranes); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S29
AT5G35530	gi 15238533	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S3 family protein	40S ribosomal protein S3 (RPS3C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.3 protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S3	29.2.1.2.1.3		0	-		KH_1(1) KH_2(1) Ribosomal_S3_C(1)	3	-0.121	27.46	9.57	15496452(nucleolus); 15821981(crude & pure 80S ribosome); 18538804(total leaf); 17934214(cytosolic ribosome); 17916636(root (NaCl stress)); 17432890(leaf total membranes); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant	15496452(nucleus -SUBA);	0.411	0.419	10	protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S3
AT4G29390	gi 15233565	40S ribosomal protein S30 (RPS30B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S30 family protein	40S ribosomal protein S30 (RPS30B)	cytosol		29.2.1.2.1.30 protein.synthesis.ribosomal.protein.eukaryoti.c.40S	29.2.1.2.1.30		0	M		Ribosomal_S30(1)	0	-1.281	6.89	12.24	15496452(nucleolus); 17934214(cytosolic ribosome);		0.194	0.5	43	protein.synthesis.ribosomal.protein.eukaryoti.c.40S subunit.S30

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AT2G31610	gi15225107	40S ribosomal protein S3-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S3 family protein	40S ribosomal protein S3 (RPS3A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.3 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3	29.2.1.2.1.3		0	-		KH_2(1) Ribosomal_S3_C(1)	3	-0.083	27.52	9.57	15025299(total chloroplast); 15539469(vacuole); 15821981(crude & pure 80S ribosome); 16400686(floem_sap B. napa); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17916636(root (NaCl stress)); 17432890(leaf total membranes); 18431481(chloroplast); 18814325(cotyledons); 18931141(peroxisomes-high&low purity (cell culture)); 18021141(whole plant)		0.592	0.609	10	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3
AT3G04840	gi15229364	40S ribosomal protein S3A (RPS3aA) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S3Ae	40S ribosomal protein S3A (RPS3aA)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.53 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3A	29.2.1.2.1.53		0	-		Ribosomal_S3Ae(1)	4	-0.522	29.85	9.78	15025299(total chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 7d light and dark grown); 18463617(suspension cells-phosphorylated proteins); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell culture))		0.401	0.518	65	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3A
AT4G34670	gi15236171	40S ribosomal protein S3a-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S3Ae	40S ribosomal protein S3A (RPS3aB)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.53 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3A	29.2.1.2.1.53		0	-		Ribosomal_S3Ae(1)	3	-0.564	29.8	9.75	15025299(total chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell culture))		0.37	0.477	65	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S3A

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AT5G07090	gi 9759565	40S ribosomal protein S4 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4 (RPS4B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.4 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S4	29.2.1.2.1.4		0	M		KOW(1) Ribosomal_S4e(1) RS4NT(1) S4(1)	2	-0.517	29.87	10.18		0.607	0.668	23	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S4	
AT4G31700	gi 15236042	40S ribosomal protein S6-1 [Arabidopsis thaliana]	Protein synthesis	ribosomal protein S6	40S ribosomal protein S6 (RPS6A)	cytosol		29.2.1.2.1.6 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S6	29.2.1.2.1.6		0	-		Ribosomal_S6e(1)	4	-0.898	28.37	10.61		0.292	0.28	15	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S6	
AT5G20290	gi 15241316	40S ribosomal protein S8-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S8e family protein	40S ribosomal protein S8 (RPS8A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.8 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S8	29.2.1.2.1.8		0	-		Ribosomal_S8e(1)	2	-0.923	24.99	10.32	15496452(nucleus -SUBA);	0.495	0.64	58	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S8	

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AT5G15200	gi15242241	40S ribosomal protein S9-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S4	40S ribosomal protein S9 (RPS9B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.9 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S9	29.2.1.2.1.9		0	-		Ribosomal_S4(1)_S4(1)	1	-0.778	23.04	10.17	15020277(total chloroplast); 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18633119(young leaf); 17660356(tonoplast (Brassica napus leaf))		0.49	0.539	32	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S9
AT5G39850	gi15242498	40S ribosomal protein S9-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S4	40S ribosomal protein S9 (RPS9C)	cytosol		29.2.1.2.1.9 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S9	29.2.1.2.1.9		0	-		Ribosomal_S4(1)_S4(1)	1	-0.801	23.16	10.34	18538804(total leaf); 17934214(cytosolic ribosome); 17407188(cotyledon); 17432890(leaf total membranes); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell wall))		0.269	0.296	71	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S9
AT5G62300	gi7671404	40S ribosomal protein [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S10p/S20e family protein	40S ribosomal protein S20 (RPS20C).	cytosol		29.2.1.2.1.20 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S20	29.2.1.2.1.20		0	-		Ribosomal_S10(1)_S10(1)	2	-0.394	13.88	9.73	16287169(Cell Wall proteome); 18538804(total leaf); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19429840(ubiquitinated or associated with ubiquitinated proteins)		0.29	0.26	2	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S20
AT5G62300	gi7671404	40S ribosomal protein [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S10p/S20e family protein	40S ribosomal protein S20 (RPS20C).	cytosol		29.2.1.2.1.20 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S20	29.2.1.2.1.20		0	-		Ribosomal_S10(1)_S10(1)	2	-0.394	13.88	9.73	16287169(Cell Wall proteome); 18538804(total leaf); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19429840(ubiquitinated or associated with ubiquitinated proteins)		0.29	0.26	2	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S20
AT2G37190	gi15228098	60S ribosomal protein L12 (RPL12A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L11 family protein	60S ribosomal protein L12 (RPL12A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.12 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L12	29.2.1.2.2.12		0	-		Ribosomal_L11(1)_Ribosomal_L11_N(1)	2	-0.33	17.94	9.06	14617066(nuclear proteome); 15539469(vacuole); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 16358359(cell suspension (Gamborg)); 16247729(mature Pollen); 16400686(floem sap B. napo); 15815986(Siliqua); 18538804(total leaf); 17934214(cytosolic ribosome); 18431481(chloroplast); 18814325(cotyledons); 19546170(mature pollen grains)		0.596	0.574	5	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L12

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub. 15028209(total chloroplast); 15215502(Vacu olar proteome); 15496452(nucle olus); 15821981(crude &pure 80S ribosome); 15734919(80S cytolic ribosomes); 16618929(ER- LOPT-callus); 17934214(cytos olic ribosome); 17151019(vacuo le - suspension cell); 19200160(flowe r-stage 12); 19546170(matur e pollen grains); 19036721(deterg ent resistant plasma membrane proteome); 17317660(Plasm a Membrane proteome); 17934214(cytos olic ribosome); 17151019(vacuo le - suspension cell); 18931141(perox isomes- high&low purity (cell culture)); 18931141(perox isomes-high purity (cell culture)); 19200160(flowe r-stage 12); 19546170(matur e pollen grains); 19036721(deterg ent resistant plasma membrane proteome); 15215502(Vacu olar proteome); 15496452(nucle olus); 15821981(crude &pure 80S ribosome); 15734919(80S cytolic ribosomes); 18538804(total leaf); 17934214(cytos olic ribosome); 17432890(leaf total membranes); 19546170(matur e pollen grains); 19525416(leaf wt and clpr4-1 15028209(total chloroplast); 15215502(Vacu olar proteome); 17317660(Plasm a Membrane proteome); 18538804(total leaf); 17934214(cytos olic ribosome); 17828791(total leaf); 17151019(vacuo le - suspension cell); 18431481(chlor oplast); 18931141(perox isomes- high&low purity (cell culture)); 19200160(flowe r-stage 12); 19546170(matur e pollen grains); 19036721(deterg ent resistant	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT4G27090	gi 15236981	60S ribosomal protein L14-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L14	60S ribosomal protein L14 (RPL14B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.14 protein.synthesis. ribosomal protein.eukaryoti c.60S subunit.L14	29.2.1.2.2.14		0	-		KOW(1) Ribosomal_L14e (1)	0	-0.353	15.51	10.03		0.455	0.483	12	protein.synthesis, ribosomal protein.eukaryoti c.60S subunit.L14	
AT1G27400	gi 15223501	60S ribosomal protein L17 (RPL17A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17 (RPL17A)	cytosol		29.2.1.2.2.17 protein.synthesis. ribosomal protein.eukaryoti c.60S subunit.L17	29.2.1.2.2.17		0	-		Ribosomal_L22 (1)	3	-0.799	19.9	10.12		0.375	0.505	46	protein.synthesis, ribosomal protein.eukaryoti c.60S subunit.L17	
AT1G67430	gi 15220431	60S ribosomal protein L17 (RPL17B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17 (RPL17B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.17 protein.synthesis. ribosomal protein.eukaryoti c.60S subunit.L17	29.2.1.2.2.17		0	-		Ribosomal_L22 (1)	3	-0.801	19.85	10.12		0.377	0.509	46	protein.synthesis, ribosomal protein.eukaryoti c.60S subunit.L17	
AT3G05590	gi 15230011	60S ribosomal protein L18-2 [Arabidopsis thaliana]	Protein synthesis	ribosomal protein L18	60S ribosomal protein L18 (RPL18B)	cytosol	large ribosomal subunit	29.2.1.2.2.18 protein.synthesis. ribosomal protein.eukaryoti c.60S subunit.L18	29.2.1.2.2.18		0	-		L15(1) Ribosomal_L18e (1)	1	-0.427	20.93	10.97		0.422	0.475	2	protein.synthesis, ribosomal protein.eukaryoti c.60S subunit.L18	

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AT5G27850	gi15241061	60S ribosomal protein L18-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L18 (RPL18C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.18 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L18	29.2.1.2.2.18		0	-		L15(1) Ribosomal_L18e(1)	1	-0.418	20.97	10.96	15215502(Vacuolar proteome); 15821981(crude & pure 80S ribosome); 16618929(UNK NOWN-LOPIT-callus); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20166762(guard cells (Arabidopsis)); 19423572(leaf		0.508	0.568	2	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L18
AT1G29970	gi12324168	60S ribosomal protein L18A, putative; 23187-20334 [Arabidopsis thaliana]	Protein synthesis	60S ribosomal protein L18A-1				29.2.1.2.2.518 protein.synthesis.ribosomal.protein.eukaryotic.60S	29.2.1.2.2.518	2	2	-				0.15	17.47	5.29			0	0	0	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L18A
AT1G09590	gi18391042	60S ribosomal protein L21-1 [Arabidopsis thaliana]	Protein synthesis	Translation protein SH3-like family protein	60S ribosomal protein L21 (RPL21A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.21 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L21	29.2.1.2.2.21		0	M		Ribosomal_L21e(1)	1	-0.686	18.65	10.46	13028209(tonoplast chloroplast); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 18633119(young leaf); 18814325(cotyledons); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19423572(leaf	15496452(nucleus -SUBA);	0.39	0.41	13	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L21
AT1G57660	gi18406015	60S ribosomal protein L21-2 [Arabidopsis thaliana]	Protein synthesis	Translation protein SH3-like family protein	60S ribosomal protein L21 (RPL21E)	cytosol		29.2.1.2.2.21 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L21	29.2.1.2.2.21		0	M		Ribosomal_L21e(1)	1	-0.675	18.71	10.52	17934214(cytosolic ribosome); 18633119(young leaf); 18814325(cotyledons); 19200160(flowe r-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis leaf); 19423572(leaf		0.463	0.487	13	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L21
AT3G05560	gi15230008	60S ribosomal protein L22-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal L22e protein family	60S ribosomal protein L22-2 (RPL22B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.22 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L22	29.2.1.2.2.22		0	-		Ribosomal_L22e(1)	1	-0.648	14.02	9.57	15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17660356(tonoplast (Brassica oleracea buds)); 18814325(cotyledons); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19036721(detergent resistant		0.508	0.543	15	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L22

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AT5G27770	gi15241051	60S ribosomal protein L22-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal L22c protein family	60S ribosomal protein L22 (RPL22C)	cytosol		29.2.1.2.2.22 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L22	29.2.1.2.2.22		0	-		Ribosomal_L22c(1)	1	-0.676	14.05	9.57		0.508	0.538	15	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L22	
AT3G53020	gi15231730	60S ribosomal protein L24-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L24c family protein	60S Ribosomal_L24c(1) - STV1 (SHORT VALVE1)	cytosol		29.2.1.2.2.24 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L24	29.2.1.2.2.24		0	M		Ribosomal_L24c(1)	2	-0.956	18.63	10.78		0.202	0	26	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L24	
AT3G49910	gi15229631	60S ribosomal protein L26-1 [Arabidopsis thaliana]	Protein synthesis	Translation protein SH3-like family protein	60S ribosomal protein L26 (RPL26A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.26 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L26	29.2.1.2.2.26		0	M		KOW(1)	0	-0.949	16.95	10.79	15496452(nucleus-SUBA);	0.322	0.341	27	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L26	



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AT1G23290	gi 15220698	60S ribosomal protein L27a-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L18e/L15 superfamily protein	RPL27A (RIBOSOMAL PROTEIN L27A); regulated by TCP20.	cytosol	cytosolic ribosome (sensu Eukaryota) & large ribosomal subunit	29.2.1.2.2.527 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L27A	29.2.1.2.2.527		0	-		L15(1)	1	-0.539	16.29	10.5	15496452(nucleus-SUBA);		0.432	0.597	43	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L27A
AT1G70600	gi 15223190	60S ribosomal protein L27a-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L27A (RPL27aC)	cytosol		29.2.1.2.2.527 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L27A	29.2.1.2.2.527		0	-		L15(1)	1	-0.605	16.46	10.59			0.432	0.597	43	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L27A
AT2G19730	gi 15224835	60S ribosomal protein L28 (RPL28A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal L28e protein family	60S ribosomal protein L28 (RPL28A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.28 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L28	29.2.1.2.2.28		0	-		Ribosomal_L28e(1)	1	-0.622	15.9	10.58			0.259	0.268	55	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L28
AT4G29410	gi 15233567	60S ribosomal protein L28 (RPL28C) [Arabidopsis thaliana]	Protein synthesis	Ribosomal L28e protein family	60S ribosomal protein L28 (RPL28C)	cytosol		29.2.1.2.2.28 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L28	29.2.1.2.2.28		0	-		Ribosomal_L28e(1)	1	-0.599	15.91	11.04			0.203	0.21	36	protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L28

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AT5G56710	gi 15241902	60S ribosomal protein L31 (RPL31C) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L31c family protein	60S ribosomal protein L31 (RPL31C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.31 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L31	29.2.1.2.2.31		0	-		Ribosomal_L31c(1)	1	-0.882	13.8	9.95	16287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 19200160(flowe r-stage 12);		0.311	0.902	83	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L31
AT5G46430	gi 15237436	60S ribosomal protein L32 (RPL32B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L32e	60S ribosomal protein L32 (RPL32B)	cytosol		29.2.1.2.2.32 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L32	29.2.1.2.2.32		0	M		Ribosomal_L32e(1)	1	-0.723	15.48	10.78	17934214(cytosolic ribosome); 19546170(mature pollen grains); 17216043(leaf); 19334764(plasma membrane (cell culture));		0.293	0.439	49	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L32
AT4G18100	gi 15236757	60S ribosomal protein L32-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L32e	60S ribosomal protein L32 (RPL32A)	cytosol		29.2.1.2.2.32 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L32	29.2.1.2.2.32		0	M		Ribosomal_L32e(1)	1	-0.715	15.5	10.89	15496452(nucleolus); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPIT-callus); 18538804(total leaf); 17934214(cytosolic ribosome); 17660356(tonop last (Brassica oleracea buds)); 18814325(cotyledons); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 10525416(leaf		0.323	0.488	49	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L32
AT2G39390	gi 15225083	60S ribosomal protein L35 (RPL35B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal L29 family protein	60S ribosomal protein L35 (RPL35B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.35 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35	29.2.1.2.2.35		0	-		Ribosomal_L29(1)	0	-0.659	14.23	10.92	15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction); 19888209(leaves		0.301	0.321	26	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35
AT3G09500	gi 15232693	60S ribosomal protein L35-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal L29 family protein	60S ribosomal protein L35 (RPL35A)	cytosol		29.2.1.2.2.35 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35	29.2.1.2.2.35		0	-		Ribosomal_L29(1)	0	-0.762	14.29	10.92	15496452(nucleolus); 17934214(cytosolic ribosome); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19888209(leaves); 19376835(leaf phosphoproteins)		0.325	0.333	23	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35
AT3G55170	gi 15233198	60S ribosomal protein L35-3 [Arabidopsis thaliana]	Protein synthesis	Ribosomal L29 family protein	60S ribosomal protein L35 (RPL35C)	cytosol		29.2.1.2.2.35 protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35	29.2.1.2.2.35		0	-		Ribosomal_L29(1)	0	-0.754	14.18	10.92	17934214(cytosolic ribosome); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins)		0.171	0.206	53	protein.synthesis.ribosomal.protein.eukaryoti.c.60S.subunit.L35

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AT5G02610	gi 15241881	60S ribosomal protein L35-4 [Arabidopsis thaliana]	Protein synthesis	Ribosomal L29 family protein	60S ribosomal protein L35 (RPL35D)	cytosol		29.2.1.2.2.35	29.2.1.2.2.35		0	-		Ribosomal_L29(1)	0	-0.728	14.33	10.92	15060130(Plasma Membrane proteome); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell		0.244	0.189	26	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L35
AT2G43460	gi 15224284	60S ribosomal protein L38 (RPL38A) [Arabidopsis thaliana]	Protein synthesis	Ribosomal L38e protein family	60S ribosomal protein L38 (RPL38A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.38	29.2.1.2.2.38		0	-		Ribosomal_L38e(1)	2	-0.554	8.12	9.95	15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19888209(80S polysomal fraction); 19022297(total chloroplast); 15215502(vacuolar proteome); 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNKNOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total		0.565	0.5	2	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L38
AT3G09630	gi 15232723	60S ribosomal protein L4-1 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L4/L1 family	60S ribosomal protein L4/L1 (RPL4A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.141	29.2.1.2.2.141		0	-		Ribosomal_L4(1)	2	-0.379	44.7	10.34	15060130(Plasma Membrane proteome); 15215502(vacuolar proteome); 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNKNOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17432890(leaf total		0.446	0.448	8	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L4/L1
AT5G39740	gi 15242467	60S ribosomal protein L5-2 [Arabidopsis thaliana]	Protein synthesis	ribosomal protein L5 B	60S ribosomal protein L5 (RPL5B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.5	29.2.1.2.2.5		0	M		Ribosomal_L18p(1)	1	-0.783	34.44	9.18	15060130(Plasma Membrane proteome); 15215502(vacuolar proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 20166762(guard cells (Arabidopsis));		0.495	0.567	55	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L5

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AT2G01250	gi15226212	60S ribosomal protein L7-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L30/L7 family protein	60S ribosomal protein L7 (RPL7B)	cytosol		29.2.1.2.2.7	29.2.1.2.2.7		0	-		Ribosomal_L30(N1)	1	-0.574	28.17	9.94		15028209(Total chloroplast); 15215502(Vacuolar proteome); 16287169(Cell Wall proteome); 15734919(80S cytolic ribosomes); 15815986(Siliqu); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 7# light and dark grown); 17151019(vacuole - suspension cell); 17432890(leaf total		0.545	0.55	6	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L7
AT3G13580	gi15231288	60S ribosomal protein L7-4 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L30/L7 family protein	60S ribosomal protein L7 (RPL7D)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.7	29.2.1.2.2.7		0	-		Ribosomal_L30(N1)	1	-0.648	28.43	9.95		15028209(Total chloroplast); 15821981(crude & pure 80S ribosome); 15734919(80S cytolic ribosomes); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19888209(80S polysomal		0.377	0.382	73	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L7
AT2G47610	gi15226635	60S ribosomal protein L7A (RPL7aA) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L7A (RPL7aA)	cytosol		29.2.1.2.2.57	29.2.1.2.2.57		0	-		Ribosomal_L7Ae(1)	4	-0.564	29.13	10.14		15028209(Total chloroplast); 15496452(nucleolus); 15734919(80S cytolic ribosomes); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma	15496452(nucleus -SUBA);	0.35	0.361	19	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L7A
AT1G33120	gi18398753	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L6 family	60S ribosomal protein L9 (RPL90B)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.9	29.2.1.2.2.9		0	-		Ribosomal_L6(2)	2	-0.351	22.02	9.48		15028209(Total chloroplast); 15215502(Vacuolar proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 16400686(floem sap B. napa); 15815986(Siliqu); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17828791(total leaf); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18814325(cotyle	15496452(nucleus -SUBA);	0.665	0.581	1	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L9

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AT4G10450	gi15235114	60S ribosomal protein L9 (RPL90D) [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L6 family	60S ribosomal protein L9 (RPL90D)	cytosol		29.2.1.2.2.9	29.2.1.2.2.9		0	-		Ribosomal_L6(2)	2	-0.294	21.97	9.52	15734919(80S cytosolic ribosomes); 15815986(Siliquae); 17934214(cytosolic ribosome); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19423572(leaf)		0.546	0.524	3	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L9
AT1G43170	gi15218306	ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	ribosomal protein 1	60S ribosomal protein L3 (RPL3A)	cytosol	cytosolic large ribosomal subunit (sensu Eukaryota) & cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.3	29.2.1.2.2.3		0	-		Ribosomal_L3(1)	5	-0.581	44.56	10.18	15215502(vacuolar proteome); 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 19200160(flowers-stage 12)	15496452(nucleus -SUBA);	0.378	0.384	11	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L3
AT1G69410	gi13937159	At1g69410/F10D13.8 [Arabidopsis thaliana]	Protein synthesis	eukaryotic elongation factor 5A-3	eukaryotic translation initiation factor 5A, putative / eIF-5A, putative			29.2.3	29.2.3		0	-		EFP_N(1) eIF-5a(1) KOW(1)	4	-0.449	17.21	5.56	16400686(floem_sap B. napa); 18814325(cotyledons); 19525416(leaf (wt and clpr4-1 mutant)); 17028209(total chloroplast); 15215502(Vacuolar proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 15276459(trichomes); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17151019(vacuole - suspension cell)		0.222	0.304	69	protein.synthesis, initiation
AT5G02870	gi13605831	AT5g02870/F9G14_180 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L4/L1 family	60S ribosomal protein L4/L1 (RPL4D)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.141	29.2.1.2.2.141		0	-		Ribosomal_L4(1)	2	-0.375	44.72	10.31	15215502(Vacuolar proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17151019(vacuole - suspension cell)	15496452(nucleus -SUBA);	0.346	0.348	128	protein.synthesis, ribosomal protein.eukaryotic.60S subunit.L4/L1

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AT5G58420	gi17979233	AT5g58420/mqj2_10 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4 (RPS4D)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.4 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S4	29.2.1.2.1.4		0	M		KOW(1) Ribosomal_S4e(1) RS4NT(1) S4(1)	2	-0.497	29.82	10.22	15496452(nucleolus); 15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 18633119(young leaf); 18463617(suspension cells-phosphorylated proteins); 19525416(leaf (wt and clpr4-1 mutant)); 20423899(chloroplast); 20166762(guard cells (Arabidopsis)); 19114538(guard cells Arabidopsis thaliana)		0.504	0.587	40	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S4
AT2G37270	gi15228111	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	ribosomal protein 5B	40S ribosomal protein S5 (RPS5A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.5 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S5	29.2.1.2.1.5		0	-		Ribosomal_S7(1)	2	-0.177	22.99	9.69	15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 15815986(Silique); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 17293592(total seedlings 77 light and dark grown); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18431481(chloroplast); 18814325(cotyledon)		0.464	0.647	48	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S5
AT5G60390	gi295789	elongation factor 1-alpha [Arabidopsis thaliana]	Protein synthesis	GTP binding Elongation factor Tu family protein	elongation factor 1-alpha / EF-1-alpha	cytosol; nucleus	mitochondrion & nucleus & cytoplasm	29.2.4 protein.synthesis.elongation	29.2.4		0	-		GTP_EFTU(1) GTP_EFTU_D2(1) GTP_EFTU_D3(1) MMR_HSR1(1)	6	-0.325	49.5	9.19	14506206(Mitochondrial proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15539469(vacuole); 16247729(mature Pollen); 16400686(floem sap B. napa); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17407188(cotyledon); 18599647(seed proteome); 18633119(young leaf); 18814325(cotyledon)	15610358(cytosol -SUBA); 15610358(nucleus -SUBA);	0.519	0.517	6	protein.synthesis.elongation

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AT1G56070	gi 6056373	elongation factor EF-2 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S5/Elongation factor G/III/V family protein	elongation factor 2, EF-2	not plastid		29.2.4 protein.synthesis.elongation	29.2.4		0	-		ATP_bind_1(1) EFG_C(1) EFG_IV(1) GTP_EFTU(1) GTP_EFTU_D2(1) MMR_HSR1(1)	16	-0.228	93.89	5.9	15908592(Carbo nylated seed protein); 16618929(UNK NOWN-LOPIT-callus); 17407188(cotyle don); 17293592(total seedlings 77 light and dark grown); 17151019(vacuo le - suspension		0.735	0.741	2	protein.synthesis, elongation
AT1G20620	gi 8778617	F5M15.5 [Arabidopsis thaliana]	Protein synthesis	catalase 3	catalase 3 (CAT3)	peroxisome	mitochondrion & peroxisome	21.6 redox.dismutases and catalases	21.6		0	-		Catalase(1)	7	-0.482	56.7	7.31	15928209(Total chloroplast); 12938931(Total chloroplast envelope); MitoDB(Mitoch ondrional proteome); 12154131(Perox isomal proteome); 16287169(Cell Wall proteome); 15539469(vacuo le); 12154131(Perox isomal proteome); 15821981(crude & pure 80S ribosome); 16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16502469(leaf	10737809(uncle ar -SUBA);	0.746	0.743	6	redox.dismutases and catalases
AT5G08180	gi 15241537	H/ACA ribonucleoprotein complex subunit 2-like protein [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	nucleus		29.2.1.1.3.99 protein.synthesis.ribosomal.prokaryotic.unknown organellar.unknown	29.2.1.1.3.99		0	-		Ribosomal_L7Ae(1)	5	-0.201	16.95	9.46	15496452(nucle olus); 19525416(leaf wt and clpr4-1 mutant); 19376835(leaf phosphoproteins)	15496452(nucle ar -SUBA);	0.179	0.115	18	protein.synthesis, ribosomal protein.prokaryotic.unknown organellar.unknown
AT4G02930	gi 1149571	mitochondrial elongation factor Tu [Arabidopsis thaliana]	Protein synthesis	GTP binding Elongation factor Tu family protein	elongation factor Tu (EF-Tu)	not plastid	mitochondrion	29.2.4 protein.synthesis.elongation	29.2.4		0	C		ATP_bind_1(1) CbiA(1) GTP_EFTU(1) GTP_EFTU_D2(1) GTP_EFTU_D3(1) MMR_HSR1(1)	4	-0.117	49.41	6.25	MitoDB(mitoch ondrional proteome); 16287169(Cell Wall proteome); 16242667(matur e Pollen); 16358359(cell suspension (M&Skoog)); 16247729(matur e Pollen); 11402211,12068 122,15047896,1 6679420,170281 49(seed-all- Jobpapers); 16618929(UNK NOWN-LOPIT-callus); 17137349(ATP-binding-mitochondria cell suspension); 18599647(seed proteome); 18814325(cotyle don);		0.5	0.606	1	protein.synthesis, elongation

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AT1G22780	gi15219950	PFL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S13/S18 family	40S ribosomal protein S18 (RPS18A)	cytosol		29.2.1.2.1.18 protein.synthesis. ribosomal protein.eukaryoti c.40S subunit.S18	29.2.1.2.1.18		0	-		Ribosomal_S13(1)	1	-0.68	17.55	10.54		0.395	0.412	15	protein.synthesis, ribosomal protein.eukaryoti c.40S subunit.S18	
AT3G60240	gi17576200	protein synthesis initiation factor-like [Arabidopsis thaliana]	Protein synthesis	eukaryotic translation initiation factor 4G	eukaryotic translation initiation factor (EIF4G)			29.2.3 protein.synthesis. initiation	29.2.3			M		Dehydrin(1) Extensin_2(1) HPC2(1) MA3(1) MIF4G(1) Neuromodulin(1)	14	-0.746	187.55	7.5		0.059	0.06	213	protein.synthesis, initiation	
AT1G57720	gi14334818	putative elongation factor 1B gamma [Arabidopsis thaliana]	Protein synthesis	Translation elongation factor EF1B, gamma chain	elongation factor 1B-gamma, putative / eEF-1B gamma	not plastid		29.2.4 protein.synthesis. elongation	29.2.4		0	-		EF1G(1) GST_C(1) GST_N(1)	4	-0.35	46.4	5.54		0.61	0.611	2	protein.synthesis, elongation	
AT2G16360	gi115502824	RecName: Full=40S ribosomal protein S25-1	Protein synthesis	Ribosomal protein S25 family protein	40S ribosomal protein S25 (RPS25A)	cytosol		29.2.1.2.1.25 protein.synthesis. ribosomal protein.eukaryoti c.40S subunit.S25	29.2.1.2.1.25		0	M		Ribosomal_S25(1)	2	-0.591	14.31	10.98		0.208	0.299	51	protein.synthesis, ribosomal protein.eukaryoti c.40S subunit.S25	
AT2G47570	gi109893093	RecName: Full=Putative 60S ribosomal protein L18-1	Protein synthesis	Ribosomal protein L18e/L15 superfamily protein				29.2.1.2.2.18 protein.synthesis. ribosomal protein.eukaryoti c.60S	29.2.1.2.2.18		0	-		L15(1) Ribosomal_L18e(1)	2	-0.403	14.9	10.46		0	0	0	protein.synthesis, ribosomal protein.eukaryoti c.60S subunit.L18	



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AT1G58983	gi 6566279	RF12 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S5 family protein	40S ribosomal protein S2, putative	cytosol		29.2.1.2.1.2 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S2	29.2.1.2.1.2		0	-		Ribosomal_S5(1) Ribosomal_S5_C(1)	4	-0.434	30.77	10.26	16287169(Cell Wall proteome); 17934214(cytosolic ribosome); 19525416(leaf (wt and clpr4-1 mutant));		0.359	0.429	71	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S2
AT5G20180	gi 15241288	ribosomal protein L36 family protein [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L36				29.2.1.1.3.2.36 protein.synthesis.ribosomal.protein.prokaryotic.unknown.organelle.50S subunit.L36	29.2.1.1.3.2.36		0	-		Ribosomal_L36(1)	3	-0.261	11.43	10.45			0	0	0	protein.synthesis.ribosomal.protein.prokaryotic.unknown.organelle.50S subunit.L36
AT3G48930	gi 166867	ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]	Protein synthesis	Nucleic acid-binding, OB-fold-like protein	40S structural constituent of ribosome (EMB1080) (RPS11A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.11 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S11	29.2.1.2.1.11		0	-		Ribosomal_S17(1)	4	-0.512	17.96	10.56	16287169(Cell Wall proteome); 15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 19200160(flowers-stage 12); 19546170(mature pollen grains); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction);	10737809(nucleus -SUBA);	0.313	0.35	38	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S11
AT3G60770	gi 7329687	ribosomal protein S13-like [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S13/S15	40S ribosomal protein S13 (RPS13A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.1.13 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S13	29.2.1.2.1.13		0	M		Ribosomal_S13_N(1) Ribosomal_S15(1)	1	-0.505	17.1	10.39	13028209(Total chloroplast); 16287169(Cell Wall proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 17934214(cytosolic ribosome); 17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture));	15496452(nucleus -SUBA); 15496452(nucleus -SUBA);	0.477	0.496	10	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S13
AT3G61110	gi 6850878	ribosomal protein S27 [Arabidopsis thaliana]	Protein synthesis	ribosomal protein S27	40S ribosomal protein S27 (ARS27A)	cytosol		29.2.1.2.1.27 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S27	29.2.1.2.1.27		0	-		Ribosomal_S27e(1)	6	-0.301	9.6	9.06	16287169(Cell Wall proteome); 15734919(80S cytosolic ribosomes); 17934214(cytosolic ribosome); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant));		0.384	0	2	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S27
AT5G10360	gi 2224751	ribosomal protein S6 [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein S6e	40S ribosomal protein S6 (RPS6B) - EMB3010	cytosol		29.2.1.2.1.6 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S6	29.2.1.2.1.6		0	-		Ribosomal_S6e(1)	4	-0.813	28.16	10.83	13734919(80S cytosolic ribosomes); 15276459(trichomes); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf);		0.293	0.282	15	protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.S6

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AT1G07960	gi1532175	similar to protein disulfide isomerase [Arabidopsis thaliana]	Protein synthesis	PDI-like 5-1				21.1 redox.thioredoxin	21.1		0	S		Thioredoxin(1)	5	-0.122	16.57	4.98			0.068	0.082	61	redox.thioredoxin
AT4G00100	gi13193323	similar to ribosomal protein S13 (Pfam: S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]	Protein synthesis		ribosomal protein S13A	40S ribosomal protein S13 (RPS13A)	cytosol	29.2.1.2.1.13 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S13	29.2.1.2.1.13		0	M		Ribosomal_S13_N(1) Ribosomal_S15(1)	1	-0.499	17.09	10.39	15496452(nucleolus); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 18814325(cotyledons); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis		0.397	0.41	10	protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S13
AT2G33370	gi12341028	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene [Arabidopsis thaliana]	Protein synthesis		Ribosomal protein L14p/L23e family protein	60S ribosomal protein L23 (RPL23B)	cytosol	29.2.1.2.2.23 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L23	29.2.1.2.2.23		0	M		Ribosomal_L14(1)	3	-0.184	15.03	10.48	15496452(nucleolus); 17934214(cytosolic ribosome); 19525416(leaf (wt and clpr4-1 mutant)); 19888209(80S polysomal fraction);		0.579	0.538	16	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L23
AT4G02230	gi13377797	T2H3.3 [Arabidopsis thaliana]	Protein synthesis		Ribosomal protein L19e family protein	60S ribosomal protein L19 (RPL19C)	cytosol	29.2.1.2.2.19 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L19	29.2.1.2.2.19		0	M		Ribosomal_L19e(1)	1	-1.098	24.2	11.39	15734919(80S cytosolic ribosomes); 17317660(Plasma Membrane proteome); 17934214(cytosolic ribosome); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19888209(80S polysomal fraction);		0.188	0.156	22	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L19
AT5G42980	gi15239136	thioredoxin H3 [Arabidopsis thaliana]	Protein synthesis	thioredoxin 3	thioredoxin h3 (Trx H3)	cytosol	cytosol	21.1 redox.thioredoxin	21.1		0	-		AhpC-TSA(1) Redoxin(1) Thioredoxin(1)	3	0.163	13.11	5.06	13276431(mitochondrial proteome); 16207701(chloroplast stroma); 15539469(vacuole); 15593128(Cell Wall proteome); 16358359(cell suspension (Gamborg)); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 16618929(UNK NOWN-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome);		0.568	0.691	44	redox.thioredoxin

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AT4G11420	gi15233360	translation initiation factor eIF-3 subunit 10 [Arabidopsis thaliana]	Protein synthesis	eukaryotic translation initiation factor 3A	EIF3A (eukaryotic translation initiation factor 3A)	not plastid		29.2.3 protein.synthesis.initiation	29.2.3		0	-		DREPP(1) DUF1682(1) HDV_ag(1) PCI(1) Vicilin_N(1)	6	-0.794	114.3	9.21		0.338	0.343	24	protein.synthesis.initiation		
AT1G77840	gi15218142	translation initiation factor eIF-5 [Arabidopsis thaliana]	Protein synthesis	Translation initiation factor IF2/IF5	eukaryotic translation initiation factor 5, putative / eIF-5, putative		nucleus & cytoplasm	29.2.3 protein.synthesis.initiation	29.2.3		0	-		DUF572(1) EcoEL_RC(1) eIF-5_eIF-2B(1) TFIIB_Zn_Ribbon(1) W2(1)	6	-0.743	48.64	5.49		15610358 (cytosol -SUBA); 15610358 (nucleus -SUBA);	0	0	0	protein.synthesis.initiation	
AT2G36170	gi18404062	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana]	Protein synthesis	Ubiquitin supergroup; Ribosomal protein L40e	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A)	cytosol		29.2.1.2.2.40 protein.synthesis.ribosomal.protein.eukaryotic.c.60S subunit.L40	29.2.1.2.2.40		0	-		Ribosomal_L40e(1) ubiquitin(1)	4	-0.638	14.73	9.94		15496452 (nucleolus); 17934214 (cytosolic ribosome); 19546170 (mature pollen grains);	0.414	0.439	12	protein.synthesis.ribosomal.protein.eukaryotic.c.60S subunit.L40	
AT2G44120	gi127311547	Unknown protein [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L30/L7 family protein	60S ribosomal protein L7 (RPL7C)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.7 protein.synthesis.ribosomal.protein.eukaryotic.c.60S subunit.L7	29.2.1.2.2.7		0	-		Ribosomal_L30(1) Ribosomal_L30_N(1)	1	-0.459	27.94	9.94		15028209 (total chloroplast); 15215502 (vacuolar proteome); 15496452 (nucleolus); 15821981 (crude & pure 80S ribosome); 15734919 (80S cytosolic ribosomes); 18538804 (total leaf); 17934214 (cytosolic ribosome); 17432890 (leaf total membranes); 18431481 (chloroplast); 18931141 (peroxisomes-high&low purity (cell culture)); 19200160 (flower-stage 12); 19200160 (flower-stage 12); 19200160 (flower-stage 12);	15496452 (nucleolus -SUBA); 15496452 (nucleolus -SUBA);	0.388	0.378	6	protein.synthesis.ribosomal.protein.eukaryotic.c.60S subunit.L7
AT5G52650	gi18953720	unnamed protein product [Arabidopsis thaliana]	Protein synthesis	RNA binding Plectin/S10 domain-containing protein	40S ribosomal protein S10 (RPS10C)	cytosol		29.2.1.2.1.10 protein.synthesis.ribosomal.protein.eukaryotic.c.40S subunit.S10	29.2.1.2.1.10		0	-		S10_pectin(1)	2	-0.633	19.55	9.63		16287169 (Cell Wall proteome); 15734919 (80S cytosolic ribosomes); 17934214 (cytosolic ribosome); 17407188 (cotyledon); 17432890 (leaf total membranes); 19546170 (mature pollen grains); 19525416 (leaf (wt and clpr4-1 mutant));		0.235	0.24	32	protein.synthesis.ribosomal.protein.eukaryotic.c.40S subunit.S10

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AT1G14320	gi17682	Wilm's tumor suppressor homologue [Arabidopsis thaliana]	Protein synthesis	Ribosomal protein L16p/L10e family protein	60S ribosomal protein L10 (RPL10A)	cytosol	cytosolic ribosome (sensu Eukaryota)	29.2.1.2.2.10 protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L10	29.2.1.2.2.10		0	M		Ribosomal_L10e(1) Ribosomal_L16(1)	8	-0.454	24.92	10.5	15215502(vacuolar proteome); 15496452(nucleolus); 15821981(crude & pure 80S ribosome); 15734919(80S cytosolic ribosomes); 16618929(UNK NOWN-LOPT-callus); 17934214(cytosolic ribosome); 17151019(vacuole - suspension cell); 18633119(young leaf); 19200160(flowers-stage 12); 19429840(ubiquitinated or associated with ubiquitinated		0.273	0.306	41	protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L10
AT4G34050	gi21595512	caffeoyl-CoA O-methyltransferase-like protein [Arabidopsis thaliana]	Secondary metabolism	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	caffeoyl-CoA 3-O-methyltransferase, putative	not plastid	cytosol	16.2.1.6 secondary metabolism.phenylpropanoids.lignin biosynthesis.CCoAOMT	16.2.1.6		0	-		Methyltransf_3(1)	2	-0.335	29.16	5.13	16358359(cell suspension (M&Skoog)); 16502469(cell suspension-CD-down); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 18538804(total leaf); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19423572(leaf		0.456	0.506	34	secondary metabolism.phenylpropanoids.lignin biosynthesis.CCoAOMT
AT3G57030	gi6911873	putative protein [Arabidopsis thaliana]	Secondary metabolism	Calcium-dependent phosphotriesterase superfamily protein	strictosidine synthase family protein		cell wall (sensu Magnoliophyta)	16.4.1 secondary metabolism.N misc.alkaloid-like	16.4.1		1	S		SGL(1) Str_synth(1)	3	0.009	41	7.71	16618929(ER-LOPT-callus); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis		0.067	0.076	291	secondary metabolism.N misc.alkaloid-like
AT1G74020	gi1754983	strictosidine synthase [Arabidopsis thaliana]	Secondary metabolism	strictosidine synthase 2	SS2 (STRICTOSIDINE SYNTHASE 2); strictosidine synthase			16.4.1 secondary metabolism.N misc.alkaloid-like	16.4.1		0	S		Arylesterase(1) SGL(1) Str_synth(1)	5	0.07	35.29	5.6	15539469(vacuole); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19714877(intera		0.352	0.386	37	secondary metabolism.N misc.alkaloid-like
AT1G74010	gi15221105	strictosidine synthase family protein [Arabidopsis thaliana]	Secondary metabolism	Calcium-dependent phosphotriesterase superfamily protein			cell wall (sensu Magnoliophyta)	16.4.1 secondary metabolism.N misc.alkaloid-like	16.4.1		0	S		SGL(1) Str_synth(1)	3	0.155	34.18	8.27	16247729(mature Pollen); 19546170(mature pollen grains); 18716313(secreted proteins (cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane		0	0	0	secondary metabolism.N misc.alkaloid-like

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AT2G42590	gi18406007	14-3-3-like protein GF14 mu [Arabidopsis thaliana]	Signal transduction	general regulatory factor 9	14-3-3 protein GF14 mu (grf9) - plastid localization suggested	not plastid	nucleus & chloroplast stroma & cytoplasm	30.7 signalling.14-3-3 proteins	30.7		0	-		14-3-3(1)	2	-0.499	29.52	4.86	15610358(cytosol -SUBA); 15610358(nucleus -SUBA);	0.669	0.653	6	signalling.14-3-3 proteins	
AT4G34460	gi42573173	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding [Arabidopsis thaliana]	Signal transduction	GTP binding protein beta 1	AGB1 (GTP BINDING PROTEIN BETA 1); nucleotide binding			30.5 signalling.G-proteins	30.5		0	-		WD40(7)	14	-0.225	41.01	6.85	17158913(cytosol -SUBA); 17158913(golgi -SUBA); 17492287(nucleus -SUBA); 17492287(plasma membrane -SUBA); 17158913(plasma membrane -SUBA); 16679415(plasma membrane -SUBA);	0.029	0.029	89	signalling.G-proteins	
AT1G35160	gi14532442	At1g35160/T32G9_30 [Arabidopsis thaliana]	Signal transduction	GF14 protein phi chain	14-3-3 protein GF14 phi (grf4) - cytosol&nucleus	cytosol; nucleus	nuclear envelope & plasma membrane & cytoplasm	30.7 signalling.14-3-3 proteins	30.7		0	-		14-3-3(1)	2	-0.531	30.19	4.79	16358359(cell suspension (Gamborg)); 16358359(cell suspension (M&Skoog)); 16619310(14-3-3 proteins); 17317660(Plasma Membrane proteome); 18538804(total leaf); 17407188(cotyledon); 18463617(suspension cells-phosphorylated proteins); 19452453(14-3-3-interacting proteins); 18814325(cotyledons); 18931141(peroxisomes-high&low purity (cell culture));	15659648(cytoskeleton -SUBA); 15659648(cytosol -SUBA); 15659648(nucleus -SUBA);	0.637	0.654	12	signalling.14-3-3 proteins
AT1G71830	gi15081616	At1g71830/F14O23_24 [Arabidopsis thaliana]	Signal transduction	somatic embryogenesis receptor-like kinase 1			plasma membrane	30.2.2 signalling.receptor kinases.leucine rich repeat II	30.2.2	1	2	S		APH(1) LRR_1(4) LRRNT_2(1) Pkinase_Tyr(1)	8	-0.111	69.02	5.32	17317660(Plasma Membrane proteome); 17644812(plasma membrane -suspension cells); 16473966(plasma membrane -SUBA); 16231101(plasma membrane -suspension cells); 15592873(plasma membrane -SUBA); 12101128(plasma membrane -SUBA); 15592873(unclear -SUBA);	0	0	0	signalling.receptor kinases.leucine rich repeat II	

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AT3G07390	gi18426884	AT3g07390/F21O3_10 [Arabidopsis thaliana]	Signal transduction	auxin-responsive family protein	auxin-responsive protein / auxin-induced protein (AIR12)	plasma membrane	extracellular region & anchored to membrane	17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	17.2.3	2	0	C		DUF568(1)	4	0.137	27.93	8.37	16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 18998720(SA-induced secreted proteome (cell culture));		0.132	0.159	112	hormone metabolism.auxin.induced-regulated-responsive-activated
AT3G56090	gi13358191	AT3g56090 [Arabidopsis thaliana]	Signal transduction	ferritin 3	Ferritin-3	plastid stroma		15.2 metal handling.binding.chelation and storage	15.2		0	C		Ferritin(1)	1	-0.294	28.84	5.54	12938931(Total chloroplast envelope); 17934214(cytosolic ribosome); 17432890(leaf total membranes); 18431481(chloroplast); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20423899(chloroplast); 19888209(80S polysomal		0.429	0.526	52	metal handling.binding.chelation and storage
AT5G10260	gi158331779	At5g10260 [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog H1E	AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding			30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.246	23.13	7.67	19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.179	0.145	12	signalling.G-proteins
AT5G01600	gi15241018	ATFER1; ferric iron binding / iron ion binding [Arabidopsis thaliana]	Signal transduction	ferretin 1	Ferritin-1	plastid stroma		15.2 metal handling.binding.chelation and storage	15.2		0	C		Ferritin(1) Pox_D5(1)	0	-0.253	28.18	5.73	14729914(mitochondrial-peripheral&lumen); 14729914(thylakoid stripped); 16242667(mature Pollen); 15815986(Silique); 15815986(Leaf); 11402211.12068122.15047896.16679420.17028149(seed-all-Jobpapers); 17407188(cotyledon); 17432890(leaf total membranes); 18633119(stroma); 18431481(chloroplast); 19200160(flowers-stage 12); 19546170(mature		0.42	0.514	72	metal handling.binding.chelation and storage
AT2G40300	gi15225679	ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding [Arabidopsis thaliana]	Signal transduction	ferritin 4	Ferritin-4 - dually targeted plastid & mito	mitochondria; plastid		15.2 metal handling.binding.chelation and storage	15.2		0	C		Ferritin(1)	1	-0.269	29.03	6.16	12938931(Total chloroplast envelope); 18633119(stroma); 18431481(chloroplast); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 20423899(chloroplast);		0.355	0.444	56	metal handling.binding.chelation and storage

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AT4G38580	gi15233937	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding [Arabidopsis thaliana]	Signal transduction	farnesylated protein 6	HMA protein	plasma membrane		15.2 metal handling.binding.chelation and storage	15.2		0	-		HMA(1)	4	-0.418	17.02	9.26	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	metal handling.binding.chelation and storage
AT4G3860	gi15233367	ATGB2 (GTP-BINDING 2); GTP binding [Arabidopsis thaliana]	Signal transduction	GTP-binding 2	Ras-related GTP-binding protein			30.5 signalling.G-proteins	30.5		0	-		Arf(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	4	-0.254	23.18	6.52	17407188(cotyledon); 18431481(chloroplast); 19525416(leaf (wt and clpr4-1 mutant)); 19423572(leaf (wt and clpr2-1)); 20061580(chloroplast envelope		0.664	0.645	9	signalling.G-proteins
AT4G39990	gi1184985	ATGB3 [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A4B	RAS GTP binding protein (ATGB3/ATRA B11G/ATRABA 4B)			30.5 signalling.G-proteins	30.5		0	-		Arf(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.326	24.41	5.82	16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture));		0.268	0.275	20	signalling.G-proteins
AT2G17820	gi18398532	ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase [Arabidopsis thaliana]	Signal transduction	histidine kinase 1				17.4.2 hormone metabolism.cytokin.signal transduction	17.4.2	3	2	-		Cache_1(1) HATPase_c(1) HisKA(1) Response_reg(1)	16	-0.229	135.45	6.32			0.034	0.034	1145	hormone metabolism.cytokin.signal transduction
AT1G11300	gi145335397	ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Signal transduction	protein serine/threonine kinases;protein kinases;ATP binding;sugar binding;kinases;carbohydrate				30.2.24 signalling,receptor or kinases.S-locus glycoprotein like	30.2.24	3	2	S		B_lectin(2) DUF348(1) PAN_1(1) PAN_2(2) Pkinase(1) Pkinase_Tyr(1) RIO1(1) S_locu	41	-0.181	184.36	8.44			0	0	0	signalling.receptor kinases.S-locus glycoprotein like
AT5G49780	gi240256419	ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.8.1 signalling,receptor or kinases.leucine	30.2.8.1	2	1	-		APH(1) CDC50(1) LRR_1(2) Pkinase(1)	10	-0.28	95.04	6.06			0	0	0	signalling.receptor kinases.leucine rich repeat VIII-
AT3G08510	gi15231929	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	Signal transduction	phospholipase C 2	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	plasma membrane		30.4.4 signalling.phosphoinositides.phosphoinositide phospholipase C	30.4.4		0	M		C2(1) ehand_like(1) PI-PLC-X(1) PI-PLC-Y(1)	7	-0.474	66.12	6.08	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 18814325(cotyledons); 19260003(detergent resistant		0.112	0.116	87	signalling.phosphoinositides.phosphoinositide phospholipase C
AT5G03520	gi15242773	ATRAB8C; GTP binding [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog 8C	AtRAB1d/AtRab8C; GTP binding -multiple locations	cytosol; golgi; plasma membrane		30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.302	24.04	7.62	19525416(leaf (wt and clpr4-1 mutant)); 15972698(golgi -SUBA);	15972698(cytosol -SUBA); 15972698(golgi -SUBA);	0.315	0.322	18	signalling.G-proteins
AT5G47520	gi15238115	AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A5A				30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.322	24.45	5.98	15060130(Plasma Membrane proteome); 17151019(vacuole - suspension cell);		0	0	0	signalling.G-proteins

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AT5G20020	gi1668706	atran2 [Arabidopsis thaliana]	Signal transduction	RAS-related GTP-binding nuclear protein 2	GTP-binding nuclear protein (RAN-2)paralogue to A15g55190	not plastid	nucleus & cytoplasm	30.5 signalling G-proteins	30.5		0			Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	6	-0.419	25.06	6.38	15610358(unclear -SUBA);	0.398	0.416	16	signalling.G-proteins	
AT4G18760	gi15234009	ATRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	Signal transduction	receptor like protein 51	leucine-rich repeat family protein	plasma membrane		35.1 not assigned.no ontology	35.1	1	1	C		LRR_1(4)	7	0.024	46.07	8.75	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19200160(flowers-stage 12); 19036721(detergent resistant	0	0	0	not assigned.no ontology	
AT3G25290	gi18404500	auxin-responsive family protein [Arabidopsis thaliana]	Signal transduction	Auxin-responsive family protein				17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	17.2.3	5	6	S		Cytochrom_B561(1) DUF568(1)	3	0.204	42.56	9.67	16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins	0	0	0	hormone metabolism.auxin.induced-regulated-responsive-activated	
AT5G35735	gi18421491	auxin-responsive family protein [Arabidopsis thaliana]	Signal transduction	Auxin-responsive family protein				17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	17.2.3	5	5	S		Cytochrom_B561(1) DUF568(1)	3	0.022	43.87	9.58	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins	0	0	0	hormone metabolism.auxin.induced-regulated-responsive-activated	
AT4G12980	gi15235545	auxin-responsive protein, putative [Arabidopsis thaliana]	Signal transduction	Auxin-responsive family protein				17.2.3 hormone metabolism.auxin.induced-regulated-responsive-activated	17.2.3	5	5	S		Cytochrom_B561(1) DUF568(1) PHO4(1)	4	0.238	42.23	9.73	19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19114538(guard	0.038	0.041	162	hormone metabolism.auxin.induced-regulated-responsive-activated	





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AT3G61050	gi1769895	CaLB protein [Arabidopsis thaliana]	Signal transduction	Calcium-dependent lipid-binding (CaLB domain) family protein	NTMC2T4/NTMC2TYPE4; lipid binding			30.3 signalling.calciuum	30.3		1	M		C2(1)	2	0.023	55.1	8.22	16618929(UNK NOWN-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane detergent resistant microdomains (DRM)); 19334764(plasma membrane (cell culture));		0.267	0.275	146	signalling.calciuum
AT5G24430	gi22136058	calcium dependent protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Calcium-dependent protein kinase (CDPK) family protein	calcium-dependent protein kinase, putative / CDPK, putative	plasma membrane		30.3 signalling.calciuum	30.3		0	-		APH(1) Kdo(1) Pkinase_Tyr(1)	7	-0.369	66.52	8.46	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant		0	0	0	signalling.calciuum
AT1G05150	gi15220436	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	Calcium-binding tetratricopeptide family protein	calcium-binding EF hand family protein	plasma membrane		30.3 signalling.calciuum	30.3		0	-		BTAD(1) ehand(1) TPR_1(3) TPR_2(2) TPR_4(1) ZZ(1)	14	-0.419	90.17	6.31	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0	0	0	signalling.calciuum

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AT2G32450	gi 15225686	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	Calcium-binding tetratricopeptide family protein	calcium-binding EF hand family protein	plasma membrane		30.3 signalling.calci m	30.3		0	-		BTAD(1) efhand(1) TPR_1(4) TPR_2(2) TPR_4(1) ZZ(1)	13	-0.412	90.23	6.32	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.035	0.035	44	signalling.calci m
AT3G57530	gi 6706424	calcium-dependent protein kinase [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 32	calmodulin-dependent protein kinase/kinase 32 (CPK32)	plasma membrane	nucleus	30.3 signalling.calci m	30.3	1	0	-		efhand(4) Pkinase_Tyr(1)	8	-0.507	60.94	5.99	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0	0	0	signalling.calci m
AT5G19450	gi 15239742	calcium-dependent protein kinase 19 [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 19	calmodulin-dependent protein kinase/kinase 19 (CDPK19)	plasma membrane		30.3 signalling.calci m	30.3	1	0	-		efhand(4) Pkinase(1) Pkinase_Tyr(1)	7	-0.418	59.94	5.96	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures));	12913141(plasma membrane - SUBA);	0	0	0	signalling.calci m
AT4G04720	gi 15234435	calcium-dependent protein kinase 21 [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 21				30.3 signalling.calci m	30.3	1	0	-		efhand(4) Pkinase(1) Pkinase_Tyr(1)	6	-0.465	59.9	6.21	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures));	12913141(plasma membrane - SUBA);	0	0	0	signalling.calci m

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AT4G23650	gi15236560	calcium-dependent protein kinase 6 [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 6	calcium-dependent protein kinase, putative (CDPK) - cytosol & nucleus	cytosol; nucleus		30.3 signalling.calcium	30.3		0	C		efhand(4) Kdo(1) Pkinase(1) Pkinase_Tyr(1) Sigma70_ECF(1)	4	-0.534	59.34	5.95	15539469(vacuole); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 19200160(flowers-stage 12); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 17216043(leaf); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 19114538(guard	12913141(cytosol -SUBA); 12913141(nucleus -SUBA);	0.112	0.13	238	signalling.calcium
AT2G41410	gi16213	calmodulin like protein [Arabidopsis thaliana]	Signal transduction	Calcium-binding EF-hand family protein				30.3 signalling.calcium	30.3		0	C		Dockerin_1(1) efhand(3) efhand_like(1)	5	-0.359	23.44	4.74	17317660(Plasma Membrane proteome); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0	0	0	signalling.calcium
AT4G29050	gi15235547	concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	Signal transduction	Concanavalin A-like lectin protein kinase family protein	lectin protein kinase family protein			30.2.19 signalling.receptor kinases.legume-	30.2.19	1	1	S		Kdo(1) Lectin_legB(1) Pkinase(1)	8	-0.102	74.74	6.79			0	0	0	signalling.receptor kinases.legume-lectin
AT1G52540	gi5903051	Contains PF00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein	protein kinase, putative	plasma membrane		33.99 development.unsigned	33.99		0	-		Pkinase(1) Pkinase_Tyr(1) RIO1(1)	6	-0.398	39.87	5.71	15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant		0	0	0	development.unsigned
AT4G04700	gi5706728	contains similarity to eukaryotic protein kinase domain (Pfam: PF00069, score=272.9, E=4.1e-78, N=1) [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 27				30.3 signalling.calcium	30.3		0	-		APH(1) efhand(4) efhand_like(1) Pkinase(1) Trehalase_Ca-	8	-0.481	54.9	5.05			0	0	0	signalling.calcium
AT4G21940	gi15234656	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 15				30.3 signalling.calcium	30.3	1	0	C		efhand(4) GAD(1) GnsAB(1) Pkinase(1) Pkinase_Tyr(1) SRP_SPB(1)	7	-0.454	62.58	5.83			0	0	0	signalling.calcium
AT4G23230	gi22328878	cysteine-rich receptor-like protein kinase 15 [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein)				30.2.17 signalling.receptor kinases.DUF26	30.2.17	1	1	-		DUF26(1) Kdo(1) Pkinase(1) Pkinase_Tyr(1)	9	-0.113	56.46	8.42			0	0	0	signalling.receptor kinases.DUF26
AT1G70530	gi15223170	cysteine-rich receptor-like protein kinase 3 [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-				30.2.17 signalling.receptor kinases.DUF26	30.2.17	1	1	S		DUF26(2) Pkinase_Tyr(1)	15	-0.125	71.61	8.71	17317660(Plasma Membrane proteome);		0	0	0	signalling.receptor kinases.DUF26
AT3G10620	gi8567796	diadenosine 5',5"-P1,P4-tetraphosphate hydrolase, putative [Arabidopsis thaliana]	Signal transduction	nudix hydrolase homolog 26	diadenosine 5',5"-P1,P4-tetraphosphate hydrolase (AtNUDX26)	plastid		30.4.3 signalling.phosphoinositides.bis(5-nucleosyl)-tetraphosphatase	30.4.3		0	C		NUDIX(1)	4	-0.54	24.62	8.3	19546170(mature pollen grains);		0.051	0.067	206	signalling.phosphoinositides.bis(5-nucleosyl)-tetraphosphatase
AT2G03150	gi42568895	emb1579 (embryo defective 1579); binding / calcium ion binding [Arabidopsis thaliana]	Signal transduction	ATP/GTP-binding protein family				30.5 signalling.G-proteins	30.5		0	M		DiD_M(1) DUF1777(1) efhand(1) MAP7(1) Merzoite_SPA M(1) PPP4R2(1) S-antigen(1)	6	-1.126	150.91	6.15	18463617(suspension cells-phosphorylated proteins); 19376835(leaf phosphoproteins);		0	0	0	signalling.G-proteins
AT1G07410	gi8778562	F22G5.24 [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A2B	Ras-related GTP-binding protein, putative			30.5 signalling.G-proteins	30.5		0	-		AIG1(1) Arf(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.282	23.69	6.44	17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 20061580(chloroplast envelope		0.21	0.153	15	signalling.G-proteins

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AT1G43890	gi 8778652	F9C16.3 [Arabidopsis thaliana]	Signal transduction	RAB GTPASE HOMOLOG B18	Ras-related GTP-binding protein (ATRAB18)			30.5 signalling.G-proteins	30.5		0	S		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	6	-0.276	23.53	5.69	16618929(UNK NOWN-LOPT-callus); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19525416(leaf wt and clpr4-1		0.476	0.5	16	signalling.G-proteins
AT1G43890	gi 8778652	F9C16.3 [Arabidopsis thaliana]	Signal transduction	RAB GTPASE HOMOLOG B18	Ras-related GTP-binding protein (ATRAB18)			30.5 signalling.G-proteins	30.5		0	S		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	6	-0.276	23.53	5.69	16618929(UNK NOWN-LOPT-callus); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19525416(leaf wt and clpr4-1		0.476	0.5	16	signalling.G-proteins
AT3G51550	gi 15230520	FER (FERONIA); kinase/ protein kinase [Arabidopsis thaliana]	Signal transduction	Malectin/receptor-like protein kinase family protein	FER (FERONIA); kinase/ protein kinase	plasma membrane		30.2.16 signalling.receptor kinases.Cathartus roseus-like RLK1	30.2.16	1	2	S		Pkinase_Tyr(1)	13	-0.257	98.15	5.82	14506206(plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated		0.041	0.045	229	signalling.receptor kinases.Cathartus roseus-like RLK1
AT5G38480	gi 166717	GF14 psi chain [Arabidopsis thaliana]	Signal transduction	general regulatory factor 3	14-3-3 protein GF14 psi (grf3/RC11) - cytosol and plasma membrane	cytosol; plasma membrane		30.7 signalling.14-3-3 proteins	30.7		0	-		14-3-3(1)	2	-0.399	28.61	4.75	1628716(Center Wall proteome); 15539469(vacuole); 16358359(cell suspension (M&Skoog)); 16619310(14-3-3 proteins); 11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 17317660(Plasma Membrane proteome); 18538804(total leaf); 17293592(total seedlings 77 light and dark grown); 17137349(ATP-binding-mitochondria cell suspension); 17644812(plasma membrane		0.702	0.722	13	signalling.14-3-3 proteins

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AT4G09000	gi1255987	GF14chi isoform [Arabidopsis thaliana]	Signal transduction	general regulatory factor 1	14-3-3 protein GF14 chi (grf1)	not plastid	nucleus	30.7	30.7		0	-		14-3-3(1)	2	-0.44	29.93	4.68	15020277(total chloroplast); 14617066(Nuclear proteome); 15539469(vacuole); 16358359(cell suspension (Gamborg)); 16502469(cell suspension-CD-down); 16619310(14-3-3 proteins); 15276459(epidermis); 17317660(Plasma Membrane proteome); 18538804(apoplast); 18538804(total leaf); 17407188(cotyledon); 17293592(total seedlings 7# light)		0.876	0.878	2	signalling.14-3-3 proteins
AT4G17530	gi12245111	GTP-binding RAB1C like protein [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog 1C	Ras-related GTP-binding protein, putative, very strong similarity to RAB1C	nucleus		30.5	30.5		0	S		Arf(1) ATP_bind_1(1) Glutaredoxin(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	4	-0.273	22.32	5.27	1500130(Plasma Membrane proteome); 15539469(vacuole); 16247729(mature Pollen); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19546170(mature pollen grains); 20118269(developing seeds); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 17317660(Plasma Membrane proteome); 15276431(Mitochondrial proteome); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total		0.644	0.623	1	signalling.G-proteins
AT4G28490	gi15235312	HAE (HAESA): ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich receptor-like protein kinase family protein				30.2.11	30.2.11	1	1	S		APH(1) Baculo_PEP_C(1) LRR_1(12) LRRNT_2(1) Pkinaset(1)	23	-0.016	109.1	6.39			0	0	0	signalling.receptor kinases.leucine rich repeat XI
AT3G01290	gi18395770	Hypersensitive-induced response protein 3 [Arabidopsis thaliana]	Signal transduction	SPFH/Band 7/PHB domain-containing membrane-associated protein family	band 7 family protein	plasma membrane		35.1	35.1		0	-		Band_7(1)	4	-0.069	31.32	5.67	15060130(Plasma Membrane proteome); 15276431(Mitochondrial proteome); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total	15060130(plasma membrane - SUBA);	0.533	0.545	27	not assigned.no ontology



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AT2G14510	gi15225949	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.1 signalling.recept or kinases.leucine	30.2.1	1	1	S		LRR_1(1) Pkinase(1) Pkinase_Tyr(1)	13	-0.172	97.64	7.19			0	0	0	signalling.recept or kinases.leucine rich repeat I
AT2G28970	gi15227015	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S		APH(1) LRR_1(2) Pkinase(1) Pkinase_Tyr(1)	14	-0.153	87.29	6.08			0	0	0	signalling.recept or kinases.misc
AT1G06840	gi15222211	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane		30.2.8.1 signalling.recept or kinases.leucine rich repeat VIII-1	30.2.8.1	1	2	S		APH(1) LRR_1(2) LRRNT_2(1) Pkinase(1) SKG6(1) SNARE_assoc(1)	15	-0.15	105.63	6.4	16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19114538(guard cells Arabidopsis thaliana)		0	0	0	signalling.recept or kinases.leucine rich repeat VIII-1
AT2G26730	gi15225780	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane		30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	1	S		LRR_1(3) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	7	-0.19	71.75	7.22	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell wall proteome));		0.078	0.08	73	signalling.recept or kinases.leucine rich repeat III
AT2G31880	gi15225153	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.11 signalling.recept or kinases.leucine rich repeat XI	30.2.11	1	2	S		LRR_1(2) LRRNT_2(1) Pkinase_Tyr(1)	8	-0.158	71.11	9.2	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane		0.012	0.014	136	signalling.recept or kinases.leucine rich repeat XI
AT3G02880	gi15233013	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	2	S		DUF1191(1) Glycophorin_A(1) LRR_1(1) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	8	-0.091	67.75	8.61	15308754(plasma membrane (phosphorylated)); 16287169(Cell Wall proteome); 14506206(plasma membrane (phosphorylated)); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes);		0.311	0.323	99	signalling.recept or kinases.leucine rich repeat III
AT3G08680	gi15231955	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	2	S		LRR_1(2) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	10	-0.136	69.41	7.62	15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19376835(leaf phosphoproteins); 19114538(guard		0	0	0	signalling.recept or kinases.leucine rich repeat III



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AT3G28450	gi15233004	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane		30.2.10 signalling.recept or kinases.leucine rich repeat X	30.2.10	1	2	S		LRR_1(2) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	16	-0.102	66.95	6.36	12085724(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins); 18431481(chloroplast); 19036721(detergent resistant plasma membrane (DRM) proteins)		0.061	0.071	191	signalling.recept or kinases.leucine rich repeat X
AT3G53590	gi15231843	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.8.1 signalling.recept or kinases.leucine	30.2.8.1	1	0	M		APH(1) LRR_1(5) Pkinase_Tyr(1)	11	-0.232	87.5	7.62			0	0	0	signalling.recept or kinases.leucine rich repeat VIII
AT2G01210	gi15226197	leucine-rich repeat transmembrane protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	0	S		LRR_1(3) LRRNT_2(1) Pkinase_Tyr(1)	18	-0.118	78.31	5.75	13060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18633119(stroma); 18431481(chloroplast); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins)		0.022	0.023	66	signalling.recept or kinases.leucine rich repeat III
AT5G16590	gi15237379	LRR1; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	2	S		Glycophorin_A(1) LRR_1(1) LRRNT_2(1) OAD_gamma(1) Pkinase(1) Pkinase_Tyr(1)	10	-0.027	67.46	8.76	14506206(plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins)		0.12	0.133	140	signalling.recept or kinases.leucine rich repeat III

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AT1G21880	gi18395044	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	lysm domain GPI-anchored protein 1 precursor	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR)	plasma membrane	anchored to membrane	35.1 not assigned.no ontology	35.1	1	1	S		LysM(2)	15	0.328	33.4	4.79	12805588(GBI-anchored-callus); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf 12-200588(GPI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18796151(cell wall (hypocotyl)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 16618929(plasma membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane detergent resistant microdomains (DRM))		0.184	0.199	54	not assigned.no ontology
AT2G17120	gi18398317	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	lysm domain GPI-anchored protein 2 precursor	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR)	plasma membrane	anchored to membrane	35.1 not assigned.no ontology	35.1		1	S		LysM(2)	20	0.04	37.74	5.93	12805588(GBI-anchored-callus); 14517339(GPI anchored suspension cells); 16602701(GPI-anchored Plasma membrane suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18796151(cell wall (hypocotyl)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 16618929(plasma membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane detergent resistant microdomains (DRM))		0.117	0.136	54	not assigned.no ontology
AT5G06320	gi15239999	NHL3 [Arabidopsis thaliana]	Signal transduction	NDR1/HIN1-like 3	NHL3 (NDR1/HIN1-like 3)	plasma membrane	plasma membrane	35.1 not assigned.no ontology	35.1	1	1	-		Hin1(1)	9	-0.089	25.95	9.35	14666423(unclear -SUBA);		0.216	0.237	84	not assigned.no ontology
AT1G27460	gi18396347	NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding [Arabidopsis thaliana]	Signal transduction	no pollen germination related 1	NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding	plasma membrane		30.3 signalling.calcium	30.3		0	-		TPR_1(1) TPR_2(1)	12	-0.149	76.87	5.7	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-		0	0	0	signalling.calcium

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AT1G73080	gi15219370	PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	PEP1 receptor 1	protein serine/threonine kinase - PEPR1 (PEP1 RECEPTOR 1);			30.2.11 signalling.recept or kinases.leucine rich repeat XI	30.2.11	1	2	S		DUF912(1) LRR_1(8) LRRNT_2(1) Pkinase_Tyr(1)	18	-0.042	122.9	6.58	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.006	0	3	signalling.recept or kinases.leucine rich repeat XI
AT1G77630	gi30699276	peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	Signal transduction	Peptidoglycan-binding LysM domain-containing protein	peptidoglycan-binding LysM domain-containing protein	plasma membrane	anchored to membrane	35.1 not assigned.no ontology	35.1	1	0	S		LysM(2) Phage_tail_X(1)	18	0.243	44.15	4.98	14517339(GPI anchored suspension cells); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19260003(detergent resistant plasma		0	0	0	not assigned.no ontology
AT3G08660	gi15231953	phototropic-responsive NPH3-like protein [Arabidopsis thaliana]	Signal transduction	Phototropic-responsive NPH3 family				30.11 signalling.light	30.11	1	0	C		BTB(1) Exomuc_X-T(1) NPH3(1)	13	-0.272	65.73	5.59			0	0	0	signalling.light
AT5G58670	gi18424132	PLC1 (PHOSPHOLIPASE C 1); phospholipase C [Arabidopsis thaliana]	Signal transduction	phospholipase C1	phospholipase C1			30.4.4 signalling.phosphoinositides.phosphoinositide phospholipase C	30.4.4		0	-		C2(1) ehand_like(1) PI-PLC-X(1) PI-PLC-Y(1)	11	-0.492	64.32	6.4	18686298(tonoplast - phosphoproteome (leaves));		0	0	0	signalling.phosphoinositide phospholipase C
AT2G33580	gi15226133	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.21 signalling.recept or kinases.lysine motif	30.2.21	1	1	S		LysM(1) Pkinase(1) Pkinase_Tyr(1)	13	-0.117	72.57	5.68	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell		0	0	0	signalling.recept or kinases.lysine motif
AT1G70520	gi15223169	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein kinase) 2				30.2.17 signalling.recept or kinases.DUF 26	30.2.17	1	2	S		DUF26(2) Pkinase_Tyr(1) RIO1(1)	18	-0.233	72	8.75	17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19260003(detergent resistant plasma membrane (DRM) proteins		0	0	0	signalling.recept or kinases.DUF 26
AT4G23200	gi15236421	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein				30.2.17 signalling.recept or kinases.DUF 26	30.2.17		0	S		APH(1) DUF26(2) Pkinase(1) Pkinase_Tyr(1)	22	-0.091	72.63	6.3	15539469(vacuole);		0	0	0	signalling.recept or kinases.DUF 26
AT5G38260	gi15240865	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.20 signalling.recept or kinases.wheat LRK10 like	30.2.20	1	1	S		ABC1(1) Pkinase(1) Pkinase_Tyr(1)	24	-0.191	71.41	5.94			0	0	0	signalling.recept or kinases.wheat LRK10 like
AT3G24550	gi13877617	protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	proline extensin-like receptor kinase 1	ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1)	plasma membrane; plasma membrane		30.2.22 signalling.recept or kinases.proline extensin like	30.2.22	1	1	C		Extensin_2(1) Pkinase_Tyr(1) TMEM9(1) TPP_enzyme_C(1)	6	-0.563	69.27	8.51	16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 17216043(leaf); 19334764(plasm		0.037	0.042	266	signalling.recept or kinases.proline extensin like
AT3G53840	gi7630004	protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.25 signalling.recept or kinases.wall associated kinase	30.2.25	1	2	S		Pkinase(1) TFIIB_Zn_Ribbon(1)	28	-0.137	70.69	8.32			0	0	0	signalling.recept or kinases.wall associated kinase
AT5G10290	gi8953410	protein serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	leucine-rich repeat transmembrane protein kinase family protein				30.2.2 signalling.recept or kinases.leucine rich repeat II	30.2.2	1	1	S		Adeno_E3_CR2(1) APH(1) LRR_1(3) LRRNT_2(1) Pkinase_Tyr(1)	10	-0.202	68.66	5.85	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.leucine rich repeat II
AT2G02220	gi15227264	PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	phytosulfokin receptor 1				30.2.10 signalling.recept or kinases.leucine	30.2.10	1	1	S		FNIP(1) LRR_1(5) LRRNT_2(1) Pkinase_Tyr(1)	23	-0.164	112.36	6.58	18463617(suspension cells-phosphorylated proteins);		0	0	0	signalling.recept or kinases.leucine rich repeat X

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AT4G23310	gi15236453	putative cysteine-rich receptor-like protein kinase 23 [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein	receptor-like protein kinase, putative			30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	S		APH(1) DUF26(3) Kdo(1) Pkinase(1)	23	-0.067	92.32	8.21	19525416(leaf (wt and clpr4-1 mutant));		0.013	0.014	461	signalling.recept or kinases.DUF26
AT2G33870	gi1707014	putative GTP-binding protein [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A1H	Ras-related GTP-binding protein, putative			30.5 signalling.G-proteins	30.5		0	-		Arf(1) GTP_EFTU(1) MMR(1) MMR_HSR1(1) Ras(1)	2	-0.347	24.34	5.31	19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.155	0.193	44	signalling.G-proteins
AT3G24660	gi15230141	putative kinase-like protein TMKL1 [Arabidopsis thaliana]	Signal transduction	transmembrane kinase-like 1				30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	1	S		LRR_1(2) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	13	-0.081	73.35	5.87	16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 19245862(nuclear phosphoproteins (seedlings & cell		0	0	0	signalling.recept or kinases.leucine rich repeat III
AT2G16250	gi4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.14 signalling.recept or kinases.leucine rich repeat XIV	30.2.14	1	2	S		LRR_1(4) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	14	-0.128	99.71	8.26	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma		0.008	0.008	38	signalling.recept or kinases.leucine rich repeat XIV
AT2G16250	gi4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat transmembrane protein kinase, putative	plasma membrane	cell wall (sensu Magnoliophyta)	30.2.14 signalling.recept or kinases.leucine rich repeat XIV	30.2.14	1	2	S		LRR_1(4) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	14	-0.128	99.71	8.26	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma		0.008	0.008	38	signalling.recept or kinases.leucine rich repeat XIV
AT3G46280	gi7799016	putative protein [Arabidopsis thaliana]	Signal transduction	protein kinase-related				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S			3	-0.162	50.5	4.97	18436743(specific to roots); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma		0	0	0	signalling.recept or kinases.misc
AT5G01950	gi7329668	putative protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	ATP binding / kinase/ protein serine/threonine kinase			30.2.8.1 signalling.recept or kinases.leucine rich repeat VIII-1	30.2.8.1	3	1	S		APH(1) FTH(1) LRR_1(5) LRRNT_2(1) MHC_1(1) Pkinase(1)	14	-0.191	106.23	7.25	17317660(Plasma Membrane proteome); 18431481(chloroplast); 18686298(tonoplast - phosphoproteome (leaves));		0.007	0.008	41	signalling.recept or kinases.leucine rich repeat VIII-1
AT3G46280	gi7799016	putative protein [Arabidopsis thaliana]	Signal transduction	protein kinase-related				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S			3	-0.162	50.5	4.97	18436743(specific to roots); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma		0	0	0	signalling.recept or kinases.misc

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AT1G51820	gi 9802784	Putative protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S		LRR_1(2) Pkinase(1) Pkinase_Tyr(1)	13	-0.14	98.1	6.47			0	0	0	signalling.recept or kinases.misc
AT1G67890	gi 16604649	putative protein kinase [Arabidopsis thaliana]	Signal transduction	PAS domain-containing protein tyrosine kinase family				30.6 signalling.MAP kinases	30.6		0	-		Kdo(1) PAS(1) PAS_3(1) PAS_4(1) Pkinase(1)	11	-0.621	85.22	7.6			0	0	0	signalling.MAP kinases
AT1G51850	gi 9802795	Putative protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S		LRR_1(2) Pkinase(1) Pkinase_Tyr(1)	14	-0.222	96.12	5.83	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.misc
AT1G67890	gi 16604649	putative protein kinase [Arabidopsis thaliana]	Signal transduction	PAS domain-containing protein tyrosine kinase family				30.6 signalling.MAP kinases	30.6		0	-		Kdo(1) PAS(1) PAS_3(1) PAS_4(1) Pkinase(1)	11	-0.621	85.22	7.6			0	0	0	signalling.MAP kinases
AT4G27290	gi 3269290	putative receptor like kinase [Arabidopsis thaliana]	Signal transduction	S-locus lectin protein kinase family protein				30.2.24 signalling.recept or kinases.S-locus glycoprotein like	30.2.24		1	S		APH(1) B_lectin(1) Kdo(1) PAN_2(1) Pkinase_Tyr(1)	17	-0.35	88.92	5.54			0	0	0	signalling.recept or kinases.S-locus glycoprotein like
AT2G13800	gi 4726119	putative receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	somatic embryogenesis receptor-like kinase 5				30.2.2 signalling.recept or kinases.leucine	30.2.2	1	1	S		LRR_1(3) LRRNT_2(1) Pkinase_Tyr(1)	6	-0.177	66.98	5.45			0	0	0	signalling.recept or kinases.leucine rich repeat II
AT2G37050	gi 4371296	putative receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat family protein	plasma membrane		30.2.1 signalling.recept or kinases.leucine rich repeat I	30.2.1	1	1	S		LRR_1(3) Pkinase(1) Pkinase_Tyr(1)	15	-0.202	103.49	6.17	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins		0.012	0.012	643	signalling.recept or kinases.leucine rich repeat I
AT1G29740	gi 9972372	Putative receptor-like serine/threonine kinase - partial protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat transmembrane protein kinase				30.2.8.2 signalling.recept or kinases.leucine rich repeat VIII	30.2.8.2	1	2	S		LRR_1(2) Pkinase(1)	27	-0.157	120.06	6.53			0.008	0.008	265	signalling.recept or kinases.leucine rich repeat VIII-2
AT4G34440	gi 3641836	putative serine/threonine protein kinase [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.22 signalling.recept or kinases.proline	30.2.22	1	1	C		Extensin_2(1) Pkinase(1) Protocadherin(1)	8	-0.626	70.9	6.07			0	0	0	signalling.recept or kinases.proline extensin like
AT5G60860	gi 15239462	RAB GTPase homolog A1F [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A1F	Ras-related GTP-binding protein, putative			30.5 signalling.G-proteins	30.5		0	-		Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.253	24.28	5.65	19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.313	0.226	6	signalling.G-proteins
AT3G53610	gi 15231847	RAB GTPase-8 [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog 8	Ras-related GTP-binding protein ARA-3			30.5 signalling.G-proteins	30.5		0	-		Arf(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.346	23.94	8.36	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture));		0.389	0.398	10	signalling.G-proteins
AT1G28550	gi 15218719	RAB GTPase-like protein A1I [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A1I	AtRABA1i (Rab GTPase homolog A1i); GTP binding			30.5 signalling.G-proteins	30.5		0	-		Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.304	24.27	5.64	17644812(plasma membrane - suspension cells); 19546170(mature pollen grains);		0.11	0.137	64	signalling.G-proteins
AT2G31680	gi 15225121	RAB GTPase-like protein ASD [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog ASD				30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.392	24.36	5.26	17407188(cotyledon); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 20706207(contaminants cell cycle		0	0	0	signalling.G-proteins



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AT1G06400	gi15221477	Ras-related protein RABA1a [Arabidopsis thaliana]	Signal transduction	Ras-related small GTP-binding family protein	Ras-related GTP-binding protein (ARA-2)			30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.305	23.93	6.45	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell		0.352	0.292	6	signalling.G-proteins
AT1G09630	gi15217568	Ras-related protein RABA2a [Arabidopsis thaliana]	Signal transduction	RAB GTPase 11C	RAB GTPase homolog 2A (ATRAB11C)	plasma membrane		30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.335	24.11	6.2	16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma		0.424	0.375	4	signalling.G-proteins
AT2G44610	gi15224916	Ras-related protein RABH1B [Arabidopsis thaliana]	Signal transduction	Ras-related small GTP-binding family protein	AtRABH1b-yeast ypt6 homologue (dual localized - cytosol & golgi)	golgi; cytosol	membrane fraction	30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.138	23.13	7.67	17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 19995728(propylastid (Brassica napus)); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 20061580(chlor		0.476	0.489	12	signalling.G-proteins
AT4G39890	gi15236081	Ras-related protein RABH1C [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog H1C	Ras-related GTP-binding family protein			30.5 signalling.G-proteins	30.5		0	S		Arf(1) ATP_bind_1(1) Miro(1) MMR_HSR1(1) Ras(1)	2	-0.28	23.68	6.61	19546170(mature pollen grains);		0.103	0.059	12	signalling.G-proteins
AT1G15530	gi15218220	receptor lectin kinase, putative [Arabidopsis thaliana]	Signal transduction	Concanavalin A-like lectin protein kinase family protein				30.2.99 signalling.receptor kinases.misc	30.2.99	1	2	M		APH(1) Lectin_legB(1) Pkinase_Tyr(1)	7	-0.131	73.15	5.09	15539469(vacuole); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension		0	0	0	signalling.receptor kinases.misc
AT1G51790	gi12321675	receptor protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.receptor kinases.misc; 30.11 signalling.light	30.2.99; 30.11	1	1	S		LRR_1(2) Pkinase(1) Pkinase_Tyr(1)	15	-0.174	97.78	5.6			0	0	0	signalling.receptor kinases.misc; signalling.light
AT1G56140	gi12321749	receptor protein kinase, putative [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat transmembrane protein kinase				30.2.8.2 signalling.receptor kinases.leucine rich repeat VIII-2	30.2.8.2	1	2	M		Adeno_E3_CR2(1) APH(1) DUF1191(1) LRR_1(4) Pkinase_Tyr(1) SKG6(1)	16	-0.122	113.76	6.37	16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome);		0	0	0	signalling.receptor kinases.leucine rich repeat VIII-2

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AT5G49760	gi 8978273	receptor protein kinase-like [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat family protein / protein kinase family protein			30.2.8.1 signalling.recept or kinases.leucine rich repeat VIII-1	30.2.8.1	1	2	S		LRR_1(3) LRRNT_2(1) Pkinase(1)	13	-0.129	104.71	5.87	1533949(vacuole); 16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0.09	0.092	67	signalling.recept or kinases.leucine rich repeat VIII-1
AT5G49760	gi 8978273	receptor protein kinase-like [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein	leucine-rich repeat family protein / protein kinase family protein			30.2.8.1 signalling.recept or kinases.leucine rich repeat VIII-1	30.2.8.1	1	2	S		LRR_1(3) LRRNT_2(1) Pkinase(1)	13	-0.129	104.71	5.87	1533949(vacuole); 16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0.09	0.092	67	signalling.recept or kinases.leucine rich repeat VIII-1
AT4G08850	gi 7267528	receptor protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat receptor-like protein kinase family protein	leucine-rich repeat family protein / protein kinase family protein	plasma membrane		30.2.12 signalling.recept or kinases.leucine rich repeat XII	30.2.12	3	2	-		APH(1) LRR_1(7) LRRNT_2(1) Pkinase(1)	14	-0.193	115.42	5.88	14506206(plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 19036721(detergent resistant plasma membrane		0.038	0.039	357	signalling.recept or kinases.leucine rich repeat XII
AT4G20450	gi 5262168	receptor protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	2	S		LRR_1(2) Pkinase(1) Pkinase_Tyr(1)	14	-0.3	100.69	5.45	19334764(plasma membrane (cell culture));		0	0	0	signalling.recept or kinases.misc
AT5G16900	gi 9755691	receptor protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S		APH(1) LRR_1(1) Pkinase(1) Pkinase_Tyr(1)	14	-0.148	97.25	6			0	0	0	signalling.recept or kinases.misc
AT1G66910	gi 12320925	receptor serine/threonine kinase PR5K, putative [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.20 signalling.recept or kinases.wheat LRK10 like	30.2.20	1	2	S		Pkinase(1) Pkinase_Tyr(1)	20	-0.127	74.24	5.72			0	0	0	signalling.recept or kinases.wheat LRK10 like
AT4G18250	gi 4375833	receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	receptor serine/threonine kinase, putative				30.2.15 signalling.recept or kinases.thaumati	30.2.15	1	1	C		Pkinase(1) Pkinase_Tyr(1) Thaumatin(2)	36	-0.221	95.27	6.63			0	0	0	signalling.recept or kinases.thaumatin like



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AT1G11350	gi4008010	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	S-domain-1 13				30.2.24 signalling.recept or kinases.S-locus glycoprotein like	30.2.24	1	1	S		B_lectin(1) PAN_1(1) PAN_2(1) Pkinase(1) RIO1(1) S_locus_glycop	21	-0.174	93.24	7.43			0	0	0	signalling.recept or kinases.S-locus glycoprotein like	
AT4G23250	gi4008012	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	kinases;protein kinases				30.2.17 signalling.recept or kinases.DUF26	30.2.17	2	3	S		Adeno_E3_CR2(1) Adipokin_hormo(1) ATP1G1_PLM_MAT8(1) DUF2273(1) DUF26(4) Herpes	26	-0.222	115.77	8.73	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.DUF26	
AT5G65240	gi10178186	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.2 signalling.recept or kinases.leucine rich repeat II	30.2.2	1	1	S		Adeno_E3_CR2(1) LRR_1(2) LRRNT_2(1) Pkinase(1) POR(1) SKG6(1)	10	-0.196	67.72	5.25	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension		0.015	0.015	264	signalling.recept or kinases.leucine rich repeat II	
AT3G46330	gi6522612	receptor-like protein kinase homolog [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	2	S		APH(1) LRR_1(1) Pkinase(1) Pkinase_Tyr(1)	14	-0.211	98.68	6.8			0	0	0	signalling.recept or kinases.misc	
AT4G23190	gi4127461	receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein				30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	S		DUF26(2) Kdo(1) Pkinase(1) Pkinase_Tyr(1)	16	-0.292	74.14	7.78			0	0	0	signalling.recept or kinases.DUF26	
AT3G14840	gi11994595	receptor-like serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat transmembrane protein kinase	leucine-rich repeat family protein	plasma membrane		30.2.8.2 signalling.recept or kinases.leucine rich repeat VIII-2	30.2.8.2	1	2	S		LRRNT_2(1)	5	0.39	12.49	4.87	10018929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane call		0	0	0	signalling.recept or kinases.leucine rich repeat VIII-2	
AT3G56100	gi269969409	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-LIKE KINASE; Flags: Precursor	Signal transduction	meristematic receptor-like kinase				30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	3	2	-		LRR_1(2) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	11	-0.013	77.33	7.93			0	0	0	signalling.recept or kinases.leucine rich repeat III	
AT1G51810	gi75334565	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51810; Flags: Precursor	Signal transduction	Leucine-rich repeat protein kinase family protein				30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	-		LRR_1(1) Pkinase(1) Pkinase_Tyr(1)	13	-0.161	82.82	5.62			0	0	0	signalling.recept or kinases.misc	
AT1G05810	gi114085	RecName: Full=Ras-related protein RABA5e; Short=AtRABA5e; AltName: Full=Ras-related protein Ara-1; Flags: Precursor	Signal transduction	RAB GTPase homolog ASE				30.5 signalling.G-proteins	30.5			0	C		Arf(1) ATP_bind_1(1) GTP_EFTU(1) Miro(1) MMR_HSR1(1) Ras(1)	4	-0.342	28.81	6.77	19114538(guard cells Arabidopsis leaf);		0	0	0	signalling.G-proteins
AT3G17840	gi118401662	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	receptor-like kinase 902	RLK902 (receptor-like kinase 902); ATP binding / kinase/ protein serine/threonine kinase	plasma membrane		30.2.3 signalling.recept or kinases.leucine rich repeat III	30.2.3	1	1	S		DUF1191(1) LRR_1(3) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	7	-0.066	70.41	6.15	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 18463617(suspension cells-phosphorylated		0.079	0.08	131	signalling.recept or kinases.leucine rich repeat III	

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AT1G61380	gi18407151	SD1-29 (S-DOMAIN-1 29); carbohydrate binding / kinase/ protein kinase [Arabidopsis thaliana]	Signal transduction	S-domain-1 29				30.2.24 signalling.recept or kinases.S-locus glycoprotein like	30.2.24	2	2	S		B_lectin(1) PAN_1(1) PAN_2(1) Pkinase_Tyr(1) S_locus_glycop	22	-0.133	89.9	8.21			0	0	0	signalling.recept or kinases.S-locus glycoprotein like
AT4G23270	gi3021279	serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein				30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	S		APH(1) DUF26(2) Kdo(1) Pkinase_Tyr(1)	15	-0.103	71.62	7.01	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.DUF26
AT4G11530	gi7267853	serine/threonine kinase-like protein (fragment) [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein kinase) 34				30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	1	S		Adeno_E3_CR2(1) APH(1) DUF26(2) Kdo(1) Pkinase_Tyr(1)	18	-0.108	74.03	6.13			0	0	0	signalling.recept or kinases.DUF26
AT4G23180	gi3021270	serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein				30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	-		APH(1) DUF26(2) Kdo(1) Pkinase_Tyr(1)	15	-0.17	74.28	7.45	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.DUF26
AT4G23280	gi3021267	serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein	protein kinase, putative and Duf26 domain			30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	S		APH(1) DUF26(2) Kdo(1)	15	-0.076	73.04	6.57	18431481(chloroplast);		0.014	0.014	87	signalling.recept or kinases.DUF26
AT4G23300	gi3021282	serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	cysteine-rich RLK (RECEPTOR-like protein				30.2.17 signalling.recept or kinases.DUF26	30.2.17	1	2	S		Adeno_E3_CR2(1) DUF26(2) Pkinase_Tyr(1)	17	-0.18	73.85	7.43	17293592(total seedlings 7# light and dark grown);		0	0	0	signalling.recept or kinases.DUF26
AT3G58690	gi7630064	serine/threonine-specific protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein	protein kinase family protein	plasma membrane		30.2.18 signalling.recept or kinases.extensin	30.2.18	1	1	S		APH(1) Pkinase_Tyr(1)	7	-0.16	43.95	8.79	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension		0	0	0	signalling.recept or kinases.extensin
AT1G56130	gi6056374	Similar to serine/threonine kinases [Arabidopsis thaliana]	Signal transduction	Leucine-rich repeat transmembrane protein kinase				30.2.8.2 signalling.recept or kinases.leucine rich repeat VIII-	30.2.8.2	1	2	S		APH(1) Form-deh_trans(1) LRR_1(2) Mid2(1) Pkinase(1)	16	-0.095	113.04	6.47	17644812(plasma membrane - suspension cells);		0	0	0	signalling.recept or kinases.leucine rich repeat VIII-2
AT1G61390	gi15219917	S-locus protein kinase, putative [Arabidopsis thaliana]	Signal transduction	S-locus lectin protein kinase family protein				30.2.24 signalling.recept or kinases.S-locus glycoprotein like	30.2.24	3	2	M		B_lectin(1) PAN_2(1) Pkinase_Tyr(1) S_locus_glycop(1) TIL(1)	20	-0.236	93.05	8.56			0	0	0	signalling.recept or kinases.S-locus glycoprotein like
AT4G33430	gi4490310	somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]	Signal transduction	BR11-associated receptor kinase	BAK1 (BR11-ASSOCIATED RECEPTOR KINASE); kinase	plasma membrane	endosome & plasma membrane	17.3.2.99 hormone metabolism.bras sinosteroid.signal transduction.other	17.3.2.99	1	1	S		APH(1) LRR_1(3) LRRNT_2(1) Pkinase(1)	7	-0.187	68.16	5.62	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19452453(14-3-3-interacting proteins); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma	12150928(extracellular -SUBA); ISI-000225780700005(plasma membrane - SUBA); 16723734(plasma membrane - SUBA); 16473966(plasma membrane - SUBA); 16123046(plasma membrane - SUBA); 12150928(plasma membrane - SUBA);	0.029	0.033	473	hormone metabolism.bras sinosteroid.signal transduction.other
AT1G53730	gi15220928	SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Signal transduction	STRUBBELIG-receptor family 6				30.2.5 signalling.recept or kinases.leucine rich repeat V	30.2.5	1	2	S		Cupin_4(1) LRR_1(1) LRR_2(1) LRRNT_2(1) Pkinase_Tyr(1)	6	-0.201	78.09	6.1	17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 18686298(tonoplast -		0	0	0	signalling.recept or kinases.leucine rich repeat V

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AT3G14350	gi30683104	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein binding / protein kinase / protein serine/threonine kinase / protein tyrosine kinase [Arabidopsis thaliana]	Signal transduction	STRUBBELIG-receptor family 7	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein serine/threonine kinase	plasma membrane		30.2.5 signalling.recept or kinases.leucine rich repeat V	30.2.5	1	1	S		LRRNT_2(1) Pkinase(1)	7	-0.231	77.64	6.23	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19253305(phosphoproteins (etiolated seedling)); 19334764(plasma membrane (cell		0	0	0	0	signalling.recept or kinases.leucine rich repeat V
AT1G70250	gi2194117	Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698) [Arabidopsis thaliana]	Signal transduction	receptor serine/threonine kinase, putative				30.2.15 signalling.recept or kinases.thaumat in like	30.2.15	1	0	S		Pkinase(1) Pkinase_Tyr(1) SCRL(1) Thaumatin(1) Toxin_5(1) Tryp_alpha_amy (1)	30	-0.1	87.51	6.1			0	0	0	0	signalling.recept or kinases.thaumat in like
AT1G26480	gi9797752	Strong similarity to GF14 mu from Arabidopsis thaliana gb AB011545 and is a member of the 14-3-3 protein PF00244 family	Signal transduction	general regulatory factor 12	14-3-3 protein GF14 iota (grf12)			30.7 signalling.14-3-3 proteins	30.7		0	-		14-3-3(1)	2	-0.724	30.55	4.83	16242667(mature Pollen); 16619310(14-3-3 proteins); 18436743(specific to flower); 19546170(mature pollen grains); 19888209(80S polysomal fraction);		0.108	0.115	203	0	signalling.14-3-3 proteins
AT1G18200	gi8671779	T10022.18 [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog A6B				30.5 signalling.G-proteins	30.5		0	-		Arf(1) ATP_bind_1(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.359	25.62	4.95			0	0	0	0	signalling.G-proteins
AT1G66150	gi15218941	TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	transmembrane kinase 1				30.2.9 signalling.recept or kinases.leucine rich repeat IX	30.2.9	1	1	S		Adeno_E3_CR2(1) APH(1) LRR_1(3) LRRNT_2(2) Pkinase(1) Pkinase_Tyr(1)	10	-0.131	102.39	5.97	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell culture)); 18686298(tonoplast -		0	0	0	0	signalling.recept or kinases.leucine rich repeat IX
AT1G16670	gi9989053	Unknown protein [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.8.2 signalling.recept or kinases.leucine	30.2.8.2		0	-		Pkinase(1) Pkinase_Tyr(1)	8	-0.318	43.29	8.02			0	0	0	0	signalling.recept or kinases.leucine rich repeat VIII.
AT4G17280	gi240255971	unknown protein [Arabidopsis thaliana]	Signal transduction	Auxin-responsive family protein				17.2.3 hormone metabolism.auxin.induced-regulated-responsive-	17.2.3	1	6	S		Cytochrom_B56(1) DUF2427(1) DUF568(1)	4	0.177	43.68	9.76	18436743(specific to roots);		0	0	0	0	hormone metabolism.auxin.induced-regulated-responsive-
AT2G23810	gi13272397	unknown protein [Arabidopsis thaliana]	Signal transduction	tetraspanin8	TET8 (TETRASPANNIN8)	plasma membrane		33.99 development.unspecified	33.99	1	4	S		Tetraspanin(1)	16	0.23	30.66	8.86	15060130(Plasma Membrane proteome); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf		0.077	0.078	115	0	development.unspecified
AT1G66880	gi10177797	unnamed protein product [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.20 signalling.recept or kinases.wheat LRK10 like	30.2.20	1	1	S		ABC1(1) APH(1) Pkinase(1) Pkinase_Tyr(1)	53	-0.301	144.43	5.78	17317660(Plasma Membrane proteome);		0	0	0	0	signalling.recept or kinases.wheat LRK10 like
AT5G43980	gi9758557	unnamed protein product [Arabidopsis thaliana]	Signal transduction	plasmodesmata-located protein 1			cell wall (sensu Magnoliophyta)	30.2.99 signalling.recept or kinases.misc	30.2.99	1	1	S		DUF26(2)	13	-0.188	32.61	8.34			0.033	0.046	103	0	signalling.recept or kinases.misc

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AT1G66880	gi10177797	unnamed protein product [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein				30.2.20 signalling.recept or kinases.wheat LRK10 like	30.2.20	1	1	S		ABC1(1) APH(1) Pkinase_Tyr(1)	53	-0.301	144.43	5.78	17317660(Plasma Membrane proteome);		0	0	0	signalling.recept or kinases.wheat LRK10 like
AT1G11330	gi15734724	Very similar to receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	S-locus lectin protein kinase family protein	S-locus lectin protein kinase family protein	plasma membrane		26.16 misc.myrosinase-s-lectin-jacalin	26.16	1	1	S		APH(1) B_lectin(1) PAN_1(1) PAN_2(1) Pkinase_Tyr(1) RIO1(1) S_locus_g	24	-0.247	94.15	8.27	16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18686298(tonoplast - phosphoproteom		0	0	0	misc.myrosinase-s-lectin-jacalin
AT2G23450	gi118400282	wall-associated receptor kinase-like 14 [Arabidopsis thaliana]	Signal transduction	Protein kinase superfamily protein	protein kinase family protein			30.2.25 signalling.recept or kinases.wall associated kinase	30.2.25	2	2	-		APH(1) Pkinase_Tyr(1)	25	-0.131	77.87	6.8			0	0	0	signalling.recept or kinases.wall associated kinase
AT5G47200	gi18809602	ras-related small GTP-binding protein-like [Arabidopsis thaliana]	Signal transduction	RAB GTPase homolog 1A	Ras-related GTP-binding protein, putative	not plastid		30.5 signalling.G-proteins	30.5		0	S		Arf(1) Miro(1) MMR_HSR1(1) Ras(1)	3	-0.29	22.31	5.27	15060130(Plasma Membrane proteome); 16247729(mature Pollen); 17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19423572(leaf (wt and clpr2-		0.644	0.623	1	signalling.G-proteins
AT3G57530	gi16706424	calcium-dependent protein kinase [Arabidopsis thaliana]	Signal transduction	calcium-dependent protein kinase 32	calmodulin-dependent protein kinase/kinase 32 (CPK32)	plasma membrane	nucleus	30.3 signalling.calcium	30.3	1	0	-		efhand(4) Pkinase_Tyr(1)	8	-0.507	60.94	5.99	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma		0	0	0	signalling.calcium
AT3G44310	gi116400	nitrilase I [Arabidopsis thaliana]	Signal transduction	nitrilase I	nitrilase I (NIT1 or NIT1) - dual localized in cytosol and nucleus	cytosol; nucleus		17.2.1 hormone metabolism.auxin.synthesis-degradation	17.2.1		0	-		CN_hydrolase(1)	7	-0.234	38.15	5.85	16538559(suspension (M&Skoog)); 16055689(Glutathionylated suspension cell); 15815986(Leaf); 17317660(Plasma Membrane proteome); 18538804(apoplast); 18538804(total leaf); 17828791(total leaf); 17293592(total seedlings 7# light and dark grown); 18431481(chloroplast); 18814325(cotyledons); 19200160(flowers-stage 12); 19429840(ubiquitinated or	15796778(cytosol -SUBA); 15796778(nucleus -SUBA);	0.624	0.597	2	hormone metabolism.auxin.synthesis-degradation

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AT4G35470	gi15237011	plant intracellular ras group-related LRR 4 [Arabidopsis thaliana]	Signal transduction	plant intracellular ras group-related LRR 4	leucine-rich repeat family protein	plasma membrane		35.1 not assigned.no ontology	35.1		0	-		LRR_1(5)	6	-0.265	61	5.52	14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane detergent resistant microdomains (DRM));		0.118	0.104	26	not assigned.no ontology
AT1G48480	gi4008006	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	receptor-like kinase 1	RKL1 (Receptor-like kinase 1); ATP binding / kinase protein serine/threonine kinase	plasma membrane		30.2.3 signalling.receptor kinases.leucine rich repeat III	30.2.3	1	2	S		DUF1191(1) LRR_1(2) LRRNT_2(1) Pkinase(1) Pkinase_Tyr(1)	7	-0.19	71.13	8.3	17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19200160(flowe r-stage 12); 19036721(detergent resistant plasma membrane (DRM) proteins		0.079	0.089	106	signalling.receptor kinases.leucine rich repeat III
AT3G53710	gi10441356	ARF GAP-like zinc finger-containing protein ZIGA2 [Arabidopsis thaliana]	Transcription	ARF-GAP domain 6				27.3.99 RNA.regulation of transcription.unclassified	27.3.99		0	M		ArfGap(1)	4	-0.938	49.72	6.77	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19253305(phosphoproteins (etiolated seedling)); 19376835(leaf		0.02	0.022	71	RNA.regulation of transcription.unclassified
AT3G61820	gi15228618	aspartyl protease-like protein [Arabidopsis thaliana]	Transcription	Eukaryotic aspartyl protease family protein	aspartyl protease family protein		cell wall (sensu Magnoliophyta)	27.3.99 RNA.regulation of transcription.unclassified	27.3.99	2	1	S		Asp(1)	12	0.004	51.46	8.75	18931141(peroxisomes-high&low purity (cell culture)); 19200160(flowe r-stage 12); 19429840(ubiquitinated or associated with ubiquitinated proteins (seedlings)); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0.232	0.267	313	RNA.regulation of transcription.unclassified
AT5G01310	gi15240948	basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana]	Transcription	APRATAXIN-like				27.3.6 RNA.regulation of transcription.bHLH.Basic Helix-	27.3.6		0	C		A1pp(1) AAA(1) HIT(1) HLH(1)	16	-0.535	101.39	8.48			0.025	0.027	227	RNA.regulation of transcription.bHLH.Basic Helix-Loop-Helix
AT2G34160	gi152696237	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At2g34160	Transcription	Alba DNA/RNA-binding protein	nucleic acid binding			35.2 not assigned.unknown	35.2		0	-		Alba(1)	0	-0.475	14.62	5.28	19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant));		0.685	0.66	1	not assigned.unknown

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AT1G20220	gi 8778978	Contains similarity to pigpen protein from <i>Mus musculus</i> gb AF224264 and contains protein of unknown function DUF78 PF 01918 domain. ESTs gb N38077, gb BE037702, gb AV442191, gb AV441368, gb Z17998, gb AV527266, gb AV520794, gb A1997847, gb AV543000	Transcription	Alba DNA/RNA-binding protein			cell wall (sensu Magnoliophyta)	27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	-		Alba(1)	1	-1.095	33.76	9.92	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19376835(leaf phosphoproteins)		0.108	0.064	12	RNA.regulation of transcription.putative transcription regulator
AT3G61260	gi 15233068	DNA-binding family protein / remorin family protein [Arabidopsis thaliana]	Transcription	Remorin family protein	DNA-binding family protein / remorin family protein	not plastid		27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	-		MAP7(1) Remorin_C(1) Remorin_N(1)	2	-0.765	23.14	5.55	13060130(plasma Membrane proteome); 15308754(plasma membrane (phosphorylated)); 15539469(vacuole); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 18463617(suspension cells-phosphorylated proteins); 19036721(sterol		0.557	0.537	7	RNA.regulation of transcription.putative transcription regulator
AT2G45820	gi 601843	DNA-binding protein [Arabidopsis thaliana]	Transcription	Remorin family protein	DNA-binding family protein / remorin family protein	plasma membrane		27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	-		MAP7(1) Remorin_C(1) Remorin_N(1)	2	-0.814	20.97	8.63	13060130(plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins);		0.353	0.337	10	RNA.regulation of transcription.putative transcription regulator
AT2G45820	gi 601843	DNA-binding protein [Arabidopsis thaliana]	Transcription	Remorin family protein	DNA-binding family protein / remorin family protein	plasma membrane		27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	-		MAP7(1) Remorin_C(1) Remorin_N(1)	2	-0.814	20.97	8.63	15060130(plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins);		0.353	0.337	10	RNA.regulation of transcription.putative transcription regulator
AT5G52470	gi 6003681	fibrillarin homolog [Arabidopsis thaliana]	Transcription	fibrillarin 1	fibrillarin 1 (FBR1) (FIB1) (SKIP7)	nucleus	nucleolus	27.4 RNA.RNA binding	27.4		0	M		Fibrillarin(1) FtsJ(1) Methyltransf_11(1)	3	-0.392	32.83	10.15	15496452(nucleolus); 17432890(leaf total membranes); 19200160(flower-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard	15827145(nucleus -SUBA); 10829025(nucleus -SUBA); 10806224(nucleus -SUBA);	0.282	0.351	93	RNA.RNA binding

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AT5G22650	gi 30688577	histone deacetylase HDT2 [Arabidopsis thaliana]	Transcription	histone deacetylase 2B	HD2B (HISTONE DEACETYLASE 2B)			27.3.55 RNA.regulation of transcription.HDA	27.3.55		0	-		Merozoite_SPAM(1) Nucleoplasmin(1)	1	-1.12	32.35	4.68	15144374(nucleus -SUBA);	0.111	0.061	1	RNA.regulation of transcription.HDA	
AT2G47210	gi 2275199	hypothetical protein [Arabidopsis thaliana]	Transcription	myb-like transcription factor family protein				27.3.25 RNA.regulation of transcription.MYB domain transcription	27.3.25		0	-		DMAP1(1) Myb_DNA-binding(1) PBC(1)	2	-0.725	49.82	9.26		0	0	0	RNA.regulation of transcription.MYB domain transcription factor family	
AT4G19610	gi 11079488	hypothetical protein [Arabidopsis thaliana]	Transcription	nucleotide binding;nucleic acid binding;RNA				27.4 RNA.RNA binding	27.4		0	-		RRM_1(5)	4	-0.777	91.57	6.66	15496452(nucleolus);	0	0	0	RNA.RNA binding	
AT2G07750	gi 15226161	putative DEAD-box ATP-dependent RNA helicase 33 [Arabidopsis thaliana]	Transcription	DEAD(H)-box RNA helicase family protein				27.1.2 RNA.processing.RNA helicase	27.1.2		0	C		DEAD(1) Helicase_C(1) PPI_Ypi1(1) ResIII(1)	14	-0.504	94.89	9.48		0	0	0	RNA.processing.RNA helicase	
AT3G03920	gi 6006850	putative GAR1 protein [Arabidopsis thaliana]	Transcription	H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein	glycine-rich protein		thylakoid membrane (sensu Viridiplantae)	27.4 RNA.RNA binding	27.4		0	M		Gar1(1)	1	-0.665	20.98	11.42	15322131(Thylakoid-stripped); 15496452(nucleolus); 19200160(flowe r-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasm a membrane (cell culture));	15496452(nucleus -SUBA);	0.104	0.105	94	RNA.RNA binding
AT3G60110	gi 7076764	putative protein [Arabidopsis thaliana]	Transcription	DNA-binding bromodomain-containing protein				27.3.42 RNA.regulation of transcription.Bromodomain	27.3.42		0	-		Bromodomain(1) Myb_DNA-binding(1) Pro_AI_protease(1) S-antigen(1)	6	-1.288	72.05	9.12		0	0	0	RNA.regulation of transcription.Bromodomain proteins	
AT5G08695	gi 13548328	putative protein [Arabidopsis thaliana]	Transcription	RNA-binding (RRM/RBD/RNP motifs) family protein				27.4 RNA.RNA binding	27.4			-		RRM_1(4) Smg4_UPF3(1)	8	-0.628	78.55	8.45		0	0	0	RNA.RNA binding	
AT3G01410	gi 6692261	putative RNase H [Arabidopsis thaliana]	Transcription	Polynucleotidyl transferase, ribonuclease H-like superfamily protein				27.1.19 RNA.processing.ribonucleases	27.1.19		0	-		RnaseH(1)	5	-0.423	31.67	8.85		0	0	0	RNA.processing.ribonucleases	
AGI no	gi 12323542	reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	Transcription																					
AT3G53460	gi 681902	RNA-binding protein cp29 [Arabidopsis thaliana]	Transcription	chloroplast RNA-binding protein 29	RNA binding protein CP29 A' (RNP29A')	plastid stroma	chloroplast	27.4 RNA.RNA binding	27.4		0	C		GRP(1) RRM_1(2)	2	-0.488	36.01	5.24	11826309(thylakoid peripheral&lumen); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 18538804(total leaf); 17848588(total seedling); 17828791(total leaf); 16648217(thylakoids); 18633119(young leaf); 18633119(stroma); 18431481(chloroplast); 18814325(cotyledons); 19200160(flowe r-stage 12); 20118260(leaf)	16633814(plastid -SUBA);	0.52	0.643	93	RNA.RNA binding

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AT1G61140	gi 2443887	Similar to transcription factor gb/Z46606 1658307 and others [Arabidopsis thaliana]	Transcription	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related	ATP binding / DNA binding / helicase / protein binding / zinc ion binding - EDA16 (embryo sac development arrest 16);			27.3.44 RNA.regulation of transcription.Chromatin Remodeling Factors	27.3.44		0	-		DEAD(1) FYVE(1) Helicase_C(1) Peptidase_M4_C(1) SNF2_N(1) zf-C3HC4(1)	29	-0.465	141.13	5.04			0	0	0	RNA.regulation of transcription.Chromatin Remodeling Factors
AT1G02080	gi 3258569	Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]	Transcription	transcription regulators	transcriptional regulator-related			27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	C		Gag_spuma(1) Not1(1) SATase_N(1)	37	-0.096	269.89	5.39	17432890(leaf total membranes); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis		0.074	0.075	548	RNA.regulation of transcription.putative transcription regulator
AT1G76010	gi 8778814	T4O12.22 [Arabidopsis thaliana]	Transcription	Alba DNA/RNA-binding protein	nucleic acid binding			27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	-		Alba(1) Collagen(1)	1	-1.21	37.38	9.78	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19253305(phosphoproteins (etiolated seedling)); 19816138(rosett		0.309	0.292	12	RNA.regulation of transcription.putative transcription regulator
AT1G02080	gi 42561615	transcriptional regulator-related [Arabidopsis thaliana]	Transcription	transcription regulators	transcriptional regulator-related			27.3.67 RNA.regulation of transcription.putative transcription regulator	27.3.67		0	C		Gag_spuma(1) Not1(1) SATase_N(1)	37	-0.096	269.89	5.39	17432890(leaf total membranes); 19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis		0.074	0.075	548	RNA.regulation of transcription.putative transcription regulator
AT1G09760	gi 15218274	U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]	Transcription	U2 small nuclear ribonucleoprotein A	U2 small nuclear ribonucleoprotein A' (U2 snRNP-A') - dually targeted to cytosol & nucleus	cytosol; nucleus	nucleoplasm & Cajal body & cytoplasm	27.1 RNA.processing	27.1		0	-			0	-0.239	28.04	5.82	15028209(Total chloroplast); 14617066(Nuclear proteome); 15496452(nucleolus); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 20706207(cell cycle interactome (cell	15133128(cytosol -SUBA); 15133128(nucleus -SUBA);	0.373	0.373	4	RNA.processing
AT3G15030	gi 8777486	unnamed protein product [Arabidopsis thaliana]	Transcription	TCP family transcription factor 4				27.3.29 RNA.regulation of transcription.TCP transcription	27.3.29		0	-		TCP(1)	2	-0.818	45.96	6.76			0	0	0	RNA.regulation of transcription.TCP transcription factor family
AT3G17450	gi 11994683	unnamed protein product [Arabidopsis thaliana]	Transcription	hAT dimerisation domain-containing protein				27.3.67 RNA.regulation of transcription.putative	27.3.67		0	-		DUF659(1) hATC(1) zf-C2HC_plant(2)	24	-0.635	100.53	6.17			0	0	0	RNA.regulation of transcription.putative transcription
AT3G21820	gi 11994649	unnamed protein product [Arabidopsis thaliana]	Transcription	histone-lysine N-methyltransferase ATXR2				27.3.69 RNA.regulation of transcription.SET-domain transcriptional	27.3.69		0	-		SET(1) zf-MYND(1)	24	-0.306	52.8	4.61	18463617(suspension cells-phosphorylated proteins);		0	0	0	RNA.regulation of transcription.SET-domain transcriptional regulator family
AT5G24450	gi 9758533	unnamed protein product [Arabidopsis thaliana]	Transcription	Transcription factor IIIc, subunit 5				27.3.67 RNA.regulation of transcription.putative	27.3.67		0	-			10	-0.705	63.64	4.86			0	0	0	RNA.regulation of transcription.putative transcription
AT2G06530	gi 18396352	vacuolar protein sorting-associated protein 2-1 [Arabidopsis thaliana]	Transcription	SNF7 family protein	VPS2.1	not plastid		27.3.71 RNA.regulation of transcription.SNF7	27.3.71		0	-		DUF177(1) Snf7(1)	0	-0.674	25.29	5.54	16400686(floem_sap B. napa); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19106119(plasma membrane detergent resistant microdomains	15141064(unclear -SUBA);	0.098	0.103	197	RNA.regulation of transcription.SNF7
AT5G22950	gi 15237175	vacuolar protein sorting-associated protein 24-1 [Arabidopsis thaliana]	Transcription	SNF7 family protein	VPS24.1			27.3.71 RNA.regulation of transcription.SNF7	27.3.71		0	-		MbeB_N(1) Snf7(1)	1	-0.665	26	5.58	19546170(mature pollen grains);		0	0	0	RNA.regulation of transcription.SNF7



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AT3G30842	gi 9294504	ABC transporter-like protein [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 10				34.16 transport.ABC transporters and multidrug resistance systems	34.16	11	11	-		AAA(1) ABC_tran(2) ABC2_membrane(2) DUF258(1) MMR_HSR1(1) NACHT(1) TatC(1)	13	-0.067	160.13	8.93			0.008	0	6	transport.ABC transporters and multidrug resistance systems
AT5G06530	gi 10178109	ABC transporter-like protein [Arabidopsis thaliana]	Transporters	ABC-2 type transporter family protein				34.16 transport.ABC transporters and multidrug resistance systems	34.16	6	5	-		ABC_tran(1) ABC2_membrane(1) DUF205(1)	6	0.051	82.93	9.26			0.013	0.015	204	transport.ABC transporters and multidrug resistance systems
AT5G57350	gi 15242103	AHA3: ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	Transporters	H(+)-ATPase 3	ATPase 3, plasma membrane-type	plasma membrane	plasma membrane	34.1.2 transport.p- and v-ATPases.H+-exporting ATPase	34.1.2	10	8	-		Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1)	9	0.052	104.45	6.73			0.249	0.244	18	transport.p- and v-ATPases.H+-exporting ATPase
AT3G47950	gi 30692952	AHA4: ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	Transporters	H(+)-ATPase 4	AHA4 (Arabidopsis H(+)-ATPase 4); ATPase	plasma membrane		34.1 transport.p- and v-ATPases	34.1	10	8	-		Cation_ATPase_N(1) E1-E2_ATPase(1) FmrO(1) Hydrolase(1)	6	0.128	105.72	6.08			0.067	0.068	148	transport.p- and v-ATPases
AT1G80660	gi 6730723	aha9, 5' partial; 1-2403 [Arabidopsis thaliana]	Transporters	H(+)-ATPase 9	AHA9 (H(+)-ATPase 9); hydrogen-exporting ATPase, phosphorylative mechanism			34.1.2 transport.p- and v-ATPases.H+-exporting ATPase	34.1.2	10	8	-		Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1) Hydrolase_3(1) PHO4(1) Sra(1) SU	8	0.005	105.21	5.99			0.149	0.154	173	transport.p- and v-ATPases.H+-exporting ATPase
AT1G44100	gi 608673	amino acid permease [Arabidopsis thaliana]	Transporters	amino acid permease 5				34.3 transport.amino acids	34.3	11	10	-		Aa_trans(1) CTP_transf_1(1) Ttp_Tyr_perm(1)	10	0.485	52.54	8.57			0	0	0	transport.amino acids

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AT4G21120	gi30685317	amino acid transporter 1 [Arabidopsis thaliana]	Transporters	amino acid transporter 1				34.3 transport.amino acids	34.3	14	14	-		7tm_1(1) 7tm_4(1) AA_permease(1) Aa_trans(1) Cons_hyph698(1) CopD(1) DIE2_ALG1	10	0.519	64.85	7.94	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane		0	0	0	transport.amino acids
AT1G64780	gi5880357	ammonium transporter [Arabidopsis thaliana]	Transporters	ammonium transporter 1;2				35.1 not assigned.no ontology	35.1	11	11	S		Ammonium_transp(1) CnDOT_TraJ(1) MFS_1(1) Oxidored_q1(1) Tetraspanin(1)	9	0.351	55.01	7.12	19245862(nuclear phosphoproteins (seedlings & cell culture));		0	0	0	not assigned.no ontology
AT2G38290	gi7140936	ammonium transporter [Arabidopsis thaliana]	Transporters	ammonium transporter 2	ATAMT2 (AMMONIUM TRANSPORTER 2); ammonium transmembrane transporter	plasma membrane	plasma membrane	34.5 transport.ammonium	34.5	11	11	-		7TMR-DISM_7TM(1) Ammonium_transp(1) DUF81(1) MFS_1(1) Oxidored_q1(1)	3	0.536	50.77	7.08	17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19114538(guard cell protein); 19036721(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(sterol dependent detergent resistant plasma membrane	16699542(plasma membrane - SUBA); 16649109(plasma membrane - SUBA); 12481062(plasma membrane - SUBA);	0	0	0	transport.ammonium
AT4G13510	gi15236300	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana]	Transporters	ammonium transporter 1;1	AMT1;1 (AMMONIUM TRANSPORTER 1); ammonium transmembrane transporter	plasma membrane	plasma membrane	34.5 transport.ammonium	34.5	10	9	S		Ammonium_transp(1) Chlorovi_GP_rps(1) MARVEL(1) MFS_1(1) Tetraspanin(1)	9	0.36	53.58	7.08	17317660(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(sterol dependent detergent resistant plasma membrane	17026539(plasma membrane - SUBA); 16917981(plasma membrane - SUBA);	0	0	0	transport.ammonium
AT4G18910	gi15234059	aquaporin NIP1-2 [Arabidopsis thaliana]	Transporters	NOD26-like intrinsic protein 1;2				34.19.3 transport.Major Intrinsic Proteins.NIP	34.19.3	6	6	-		DUF1109(1) MIP(1)	4	0.446	31.27	8.63	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome);		0	0	0	transport.Major Intrinsic Proteins.NIP
AT5G26340	gi15010580	AT5g26340/F9D12_17 [Arabidopsis thaliana]	Transporters	Major facilitator superfamily protein	carbohydrate transmembrane transporter/hexose:hydrogen symporter	plasma membrane		34.2 transporter.sugars	34.2	12	12	-		Branch_AA_trans(1) DUF791(1) DUF81(1) MFS_1(1) MreD(1) Sugar_tr(1)	7	0.52	57.42	8.98	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasma		0.032	0.037	248	transporter.sugars

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AT3G47730	gi22331647	ATATH1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	Transporters	ATP-binding cassette A2				34.16 transport.ABC transporters and multidrug resistance systems	34.16	6	6	M		ABC_tran(1) ABC2_membrane(1) NADH5_C(1)	15	0.083	108.69	8.04	19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell		0	0	0	transport.ABC transporters and multidrug resistance systems
AT5G61730	gi15240334	ATATH11; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	Transporters	ABC2 homolog 11				34.16 transport.ABC transporters and multidrug resistance systems	34.16	6	6	M		ABC_tran(1) ABC2_membrane(1)	13	0.113	104.5	7.85	17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins);		0	0	0	transport.ABC transporters and multidrug resistance systems
AT2G38940	gi15224985	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/inorganic phosphate transmembrane transporter/phosphate transmembrane transporter/sugar:hydrogen symporter [Arabidopsis thaliana]	Transporters	phosphate transporter 1;4	ATPT2 (PHOSPHATE TRANSPORTER 2)	plasma membrane		34.7 transport.phosphate	34.7	12	11	-		DUF112(1) MFS_1(1) Sugar_tr(1)	6	0.323	58.6	8.35	14760709(vacuolar proteome); 15060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins);		0	0	0	transport.phosphate
AT5G57110	gi8843813	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	Transporters	autoinhibited Ca2+ -ATPase, isoform 8	calcium-transporting ATPase/calmodulin binding (ACA8)	plasma membrane	plasma membrane	34.21 transport.calcium	34.21	9	6	-		Cation_ATPase_C(1) Cation_ATPase_N(1) E1-E2_ATPase(1) Gate(1) Hydrolase(1) Hydro	11	0.028	116.18	7.87	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins);	16267044(plasma membrane - SUBA); 16230331(plasma membrane - SUBA);	0.069	0.074	104	transport.calcium
AT3G46900	gi15232677	copper transporter 2 [Arabidopsis thaliana]	Transporters	copper transporter 2				34.12 transport.metal	34.12	2	3	-		Ctr(1)	3	0.38	17.06	6.63	16602701(GPI-anchored Plasma membrane suspension		0	0	0	transport.metal
AT1G11260	gi116520	glucose transporter [Arabidopsis thaliana]	Transporters	sugar transporter 1	sugar:hydrogen ion symporter (STP1)	plasma membrane		34.2 transporter.sugars	34.2	12	12	-		7tm_1(1) Branch_AA_trans(1) Cdic_mal_tran(1) DetM(1) DUF81(1) DUF895(1) MFS_1(1)	7	0.484	57.61	9.1	15060130(Plasma Membrane proteome); 15308754(plasma membrane (phosphorylated)); 15539469(vacuole); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19254160(leaf		0.146	0.154	203	transporter.sugars

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AT1G69480	gi112597793	hypothetical protein [Arabidopsis thaliana]	Transporters	EXS (ERD1/XPR1/SYG1) family				34.7 transport.phosphate	34.7	8	8	-		EXS(1) SPX(1)	12	-0.179	90.6	9.09	17317660(Plasma Membrane proteome);		0	0	0	transport.phosphate
AT1G69850	gi13377517	nitrate transporter NTL1 [Arabidopsis thaliana]	Transporters	nitrate transporter 1:2				34.4 transport.nitrate	34.4	12	12	-		HNOB(1) MFS_1(1) MVIN(1) Na_Ca_ex(1) OPT(1) PTR2(1) Sdh_cyt(1)	13	0.372	63.98	8.81	17317660(Plasma Membrane proteome); 19334764(plasma membrane (cell culture));		0	0	0	transport.nitrate
AT1G72150	gi15218382	PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana]	Transporters	PATELLIN 1	PATELLIN 1 cell plate trafficking (PATL1)	not plastid		34.99 transport.misc	34.99		0	-		CRAL_TRIO(1) CRAL_TRIO_N(1) EMP24_GP25L(1)	2	-0.535	64.05	4.82	15028209(Total chloroplast); 14760709(Vacuolar proteome); 15815986(seedling); 15815986(Leaf); 17317660(Plasma Membrane proteome); 18538804(apoplast); 18538804(total leaf); 17848588(cotyledon); 17848588(total seedling); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica napus body));		0.679	0.686	9	transport.misc
AT2G37280	gi15228112	PDR5 (PLEIOTROPIC DRUG RESISTANCE 5); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 5				34.16 transport.ABC transporters and multidrug resistance systems	34.16	13	13	-		AAA(1) ABC_tran(2) ABC2_membrane(2) Mg_chelatase(1) Oxidored_q3(1) PDR_assoc(1)	19	0.065	160.25	8.32	17317660(Plasma Membrane proteome);		0	0	0	transport.ABC transporters and multidrug resistance systems
AT1G59870	gi15218936	PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Arabidopsis thaliana]	Transporters	ABC-2 and Plant PDR ABC-type transporter family protein	PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCES), ABC transporter	plasma membrane	plasma membrane	34.16 transport.ABC transporters and multidrug resistance systems	34.16	13	13	C		ABC_tran(2) ABC2_membrane(2) DUF1282(1) DUF258(1) MFS_1(1) NACHT(1) PDR_assoc(1)	15	0.047	165.08	8.08	15028209(Total chloroplast); 12938931(Total chloroplast envelope); 15276431(Mitochondrial proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 15276431(mitochondrial membranes-suspension cells); 17317660(Plasma Membrane proteome);	16473969(plasma membrane - SUBA);	0.257	0.261	31	transport.ABC transporters and multidrug resistance systems
AT3G54140	gi15232435	peptide transporter PTR1 [Arabidopsis thaliana]	Transporters	peptide transporter 1	proton-dependent oligopeptide transport (POT) family protein	plasma membrane		34.13 transport.peptides and oligopeptides	34.13	11	10	-		MFS_1(1) PTR2(1)	11	0.142	64.04	8.58	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins	15500465(plasma membrane - SUBA);	0	0	0	transport.peptides and oligopeptides
AT5G49990	gi19758398	permease [Arabidopsis thaliana]	Transporters	Xanthine/uracil permease family protein				34.99 transport.misc	34.99	12	11	-		7tm_1(1) GHMP_kinases_N(1) MtrD(1) Xan_ur_permease(1)	6	0.498	57.32	9.57			0.074	0.083	159	transport.misc

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AT3G62150	gi15228695	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporters	P-glycoprotein 21	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances	plasma membrane		34.16 transport.ABC transporters and multidrug resistance systems	34.16	11	9	-		AAA(1) ABC_membrane(2) ABC_tran(2) BCCT(1) DUF1469(1) DUF2298(1) Dynamin_N(1) Ex	7	0.089	140.34	6.43	15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cells); 17644812(plasma membrane - suspension cells); 19260003(detergent resistant plasma membrane		0	0	0	transport.ABC transporters and multidrug resistance systems
AT5G43370	gi1523793	phosphate transporter [Arabidopsis thaliana]	Transporters	phosphate transporter 2				34.7 transport.phosphate	34.7	12	11	S		MFS_1(1) Sugar_tr(1)	6	0.35	57.65	9.12	17432890(leaf total membranes);		0	0	0	transport.phosphate
AT5G43350	gi15239848	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	Transporters	phosphate transporter 1;1				34.7 transport.phosphate	34.7	12	11	S		MFS_1(1) Sugar_tr(1)	6	0.351	57.62	9.11	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 18436743(specific to roots); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (DRM) proteins (Cell cultures));		0	0	0	transport.phosphate
AT4G35100	gi1688296	plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]	Transporters	plasma membrane intrinsic protein 3	PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	plasma membrane	plasma membrane	34.19.1 transport.Major Intrinsic Proteins.PIP	34.19.1	6	6	-		MIP(1) Ni_hydr_CYTB(1)	4	0.451	29.74	8.97	15215502(vacuolar proteome); 15060130(Plasma Membrane proteome); 15308754(plasma membrane (phosphorylated)); 16602701(GPI-anchored Plasma membrane suspension cells); 16618929(Plasma Membrane-LOPT-callus); 17293592(total seedlings 7 light and dark grown); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes);	16236160(plasma membrane - SUBA); 10737809(plasma membrane - SUBA);	0.461	0.471	16	transport.Major Intrinsic Proteins.PIP
AT2G18960	gi166746	plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]	Transporters	H(+)-ATPase 1	ATPase 1, plasma membrane-type	plasma membrane		34.1.2 transport.p- and v-ATPases.H+-exporting ATPase	34.1.2	10	10	-		Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1)	8	0.077	104.23	6.25	13660156(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 15539469(vacuole); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 17407188(cotyledon); 17293592(total seedlings 7 light and dark grown); 17644812(plasma membrane (phosphorylated));		0.495	0.494	9	transport.p- and v-ATPases.H+-exporting ATPase

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AT3G55740	gi 15228183	proline transporter 2 [Arabidopsis thaliana]	Transporters	proline transporter 2			plasma membrane	34.3 transport.amino acids	34.3	11	11	-		Aa_trans(1) Glycos_transf_4(1) IspA(1) Serpentine_recept(1) Transp_cyt_pur(1) YibE	3	0.653	48.09	9.18		15618414(plasma membrane - SUBA);	0	0	0	transport.amino acids
AT2G29940	gi 3420057	putative ABC transporter [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 3				34.16 transport.ABC transporters and multidrug resistance systems	34.16	12	11	-		AAA(1) ABC_tran(2) ABC2_membrane(2) DUF258(1) Dynamin_N(1) MMR_HSR1(1) PDR_assoc	13	0.053	159.87	8.74		19546170(mature pollen grains);	0	0	0	transport.ABC transporters and multidrug resistance systems
AT3G54820	gi 15233102	putative aquaporin PIP2-5 [Arabidopsis thaliana]	Transporters	plasma membrane intrinsic protein 2.5				34.19.1 transport.Major Intrinsic Proteins.PIP	34.19.1	6	6	-		DUF92(1) MIP(1)	4	0.506	30.59	8.99		18463617(suspension cells-phosphorylated proteins); 19106119(plasma membrane detergent resistant microdomains)	0.035	0.036	231	transport.Major Intrinsic Proteins.PIP
AT2G32830	gi 15225748	putative inorganic phosphate transporter 1-5 [Arabidopsis thaliana]	Transporters	phosphate transporter 1;5				34.7 transport.phosphate	34.7	12	10	-		MFS_1(1) Sugar_tr(1)	6	0.337	59.21	8.55			0	0	0	transport.phosphate
AT3G47960	gi 13877879	putative peptide transporter protein [Arabidopsis thaliana]	Transporters	Major facilitator superfamily protein	proton-dependent oligopeptide transport (POT) family protein		plasma membrane	34.13 transport.peptides and oligopeptides	34.13	12	12	-		7TM_GPCR_Srsx(1) DUF140(1) MFS_1(1) Nodulin-like(1) OPT(1) PTR2(1) UPF0014(1)	8	0.197	71.04	9.11		14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma	0	0	0	transport.peptides and oligopeptides
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporters	nitrate transporter 1.7	proton-dependent oligopeptide transport (POT) family protein		plasma membrane	34.13 transport.peptides and oligopeptides	34.13	11	10	-		MFS_1(1) PTR2(1)	9	0.246	68.42	8.84		14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 19376835(leaf	0	0	0	transport.peptides and oligopeptides
AT3G19930	gi 15230987	STP4 (SUGAR TRANSPORTER 4); carbohydrate transmembrane transporter/ monosaccharide transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	Transporters	sugar transporter 4	STP4 (SUGAR TRANSPORTER 4)		plasma membrane	34.2 transporter.sugars	34.2	12	11	-		BacA(1) C4dic_mal_tran(1) DUF1113(1) DUF791(1) DUF81(1) DUF895(1) Folate_carrier	7	0.559	57.1	8.36		15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma	0	0	0	transporter.sugars
AT1G71880	gi 15217601	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	Transporters	sucrose-proton symporter 1				34.2.1 transport.sugars.sucrose	34.2.1	12	12	-		BacA(1) MatE(1) MFS_1(1) PMP22_Claudin(1) PUCC(1) Sugar_tr(1)	7	0.472	54.86	9.04		15215502(Vacuolar proteome); 17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19334764(plasma membrane (cell culture)); 18686298(tonoplast - phosphoproteome (leaves));	0	0	0	transport.sugars.sucrose



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AT5G04930	gi18414733	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism [Arabidopsis thaliana]	Transporters	aminophospholipid ATPase 1				35.1 not assigned.ontology	35.1	10	10	-		Cation_ATPase_C(1) EI-E2_ATPase(1) Hydrolase(1) Hydrolase_3(1)	18	0.018	130.33	5.92	16618929(Plasma Membrane-LOPTT-callus); 17317660(Plasma Membrane proteome); 19452453(14-3-3-interacting proteins); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0	0	0	not assigned.ontology
AT3G53420	gi15231810	aquaporin PIP2-1 [Arabidopsis thaliana]	Transporters	plasma membrane intrinsic protein 2A	aquaporin (PIP2.1) - plasma membrane intrinsic protein 2A (PIP2A)	plasma membrane	plasma membrane	34.19.1 transport.Major Intrinsic Proteins.PIP	34.19.1	6	6	-		MIP(1)	4	0.506	30.47	8.6	10737809(nucleus -SUBA); 15060130(Plasma Membrane proteome); 15539469(vacuole); 17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 17432890(leaf total membranes); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(deterg	10737809(nucleus -SUBA); 17666025(plasma membrane - SUBA); 17306539(plasma membrane - SUBA); 16236160(plasma membrane - SUBA); 16183846(plasma membrane - SUBA); 16103374(plasma membrane - SUBA); 15743452(plasma membrane - SUBA); 15141064(plasma membrane - SUBA); 10737809(plasma membrane - SUBA);	0.373	0.363	2	transport.Major Intrinsic Proteins.PIP
AT4G38510	gi15010616	AT4g38510/F20M13_70 [Arabidopsis thaliana]	Transporters	ATPase, V1 complex, subunit B protein	probable H+-transporting ATPase	not plastid		34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	34.1.1		0	-		ATP-synt_ab(1) ATP-synt_ab_C(1) ATP-synt_ab_N(1)	2	-0.273	54.31	5.03	12938931(Total chloroplast envelope); 12766230(Total chloroplast envelope); 15215502(Vacuolar proteome); 15539469(vacuole); 16242667(mature Pollen); 15815986(Siliquae); 15815986(Leaf); 17151019(vacuole - suspension cell); 17432890(leaf total membranes); 18814325(cotyledons); 19546170(mature pollen grains); 19429840(ubiquitinated or associated with		0.661	0.69	22	transport.p- and v-ATPases.H+-transporting two-sector ATPase
AT1G08090	gi15223123	ATNRT2:1 (NITRATE TRANSPORTER 2:1); nitrate transmembrane transporter [Arabidopsis thaliana]	Transporters	nitrate transporter 2:1				34.4 transport.nitrate	34.4	11	11	-		DUF368(1) MFS_1(1) Sugar_tr(1)	10	0.312	57.71	8.85	17573350(endoplasmic reticulum -SUBA); 17583518(plasma membrane - SUBA); 17573350(plasma membrane - SUBA);		0	0	0	transport.nitrate



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AT1G57990	gi15217805	ATPUP18; purine transmembrane transporter [Arabidopsis thaliana]	Transporters	purine permease 18	ATPUP18 (Arabidopsis thaliana purine permease 18)	plasma membrane	membrane	34.10 transport.nucleotides	34.1	10	10	-	-	DUF6(1) ER_lumen_receptor(1) FTSW_RODA_SPOVE(1) MARVEL(1) MFS_1(1) Na_Ca_ex(1) Psa	6	0.435	44.18	6.9	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19376835(leaf phosphoproteins);		0	0	0	transport.nucleotides
AT4G30190	gi15234666	H(+)-ATPase 2 [Arabidopsis thaliana]	Transporters	H(+)-ATPase 2	ATPase 2, plasma membrane-type (AHA2)	plasma membrane	plasma membrane	34.1.2 transport.p- and v-ATPases.H+-exporting ATPase	34.1.2	10	8	-	-	Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1) Hydrolase_3(1)	7	0.097	104.4	6.54	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 17293592(total seedlings 77 light and dark grown); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds)); 19452453(14-3-3-interacting proteins); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19106119(plasma membrane detergent resistant microdomains (DRM));	16831869(plasma membrane - SUBA); 15923333(plasma membrane - SUBA); 15722471(plasma membrane - SUBA); 11226186(plasma membrane - SUBA);	0.391	0.391	17	transport.p- and v-ATPases.H+-exporting ATPase
AT2G07560	gi15225747	H(+)-ATPase 6 [Arabidopsis thaliana]	Transporters	H(+)-ATPase 6				34.1 transport.p- and v-ATPases	34.1	10	9	-	-	Cation_ATPase_N(1) E1-E2_ATPase(1) FA_desaturase(1) Hydrolase(1) Oxidored_q3(1)	10	0.028	105.01	5.83	17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds)); 19452453(14-3-3-interacting proteins); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19106119(plasma membrane detergent resistant microdomains (DRM));		0.122	0.122	161	transport.p- and v-ATPases
AT3G60330	gi240255678	H(+)-ATPase 7 [Arabidopsis thaliana]	Transporters	H(+)-ATPase 7				34.1 transport.p- and v-ATPases	34.1	10	7	-	-	Cation_ATPase_C(1) Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1)	8	0.056	105.52	6.38	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19106119(plasma membrane detergent resistant microdomains (DRM));		0.048	0.049	161	transport.p- and v-ATPases
AT3G45060	gi15230589	high affinity nitrate transporter 2.6 [Arabidopsis thaliana]	Transporters	high affinity nitrate transporter 2.6				34.4 transport.nitrate	34.4	11	11	-	-	C4dic_mal_transporter(1) Cation_efflux(1) MFS_1(1) Sugar_tr(1)	8	0.385	58.64	8.84	15028209(Total chloroplast); 17317660(Plasma Membrane proteome);		0	0	0	transport.nitrate

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AT4G16370	gi 2244994	isp4 like protein [Arabidopsis thaliana]	Transporters	oligopeptide transporter	ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligopeptide transporter			34.13 transport.peptides and oligopeptides	34.13	10	16	-		OPT(1)	12	0.397	82.44	9.1	19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf		0.055	0.064	263	transport.peptides and oligopeptides
AT5G58270	gi 9187883	mitochondrial half-ABC transporter [Arabidopsis thaliana]	Transporters	ABC transporter of the mitochondrion 3	ABC transporter family protein - possibly also envelope	mitochondria	mitochondrion	34.16 transport.ABC transporters and multidrug resistance systems	34.16	6	5	M		AAA(1) ABC_membrane(1) ABC_tran(1) DUF1558(1) DUF31(1) Dynamin_N(1) KH_2(1) SMC_	4	-0.018	80.42	9.28	12938931(total chloroplast envelope); MitoDB(Mitochondrial proteome); 15276431(Mitochondrial proteome); 16618929(MITOPLASTID-LOPT-callus); 15276431(mitochondrial membranes-suspension cells); 18431481(chloroplast); 19995728(propagastid (Brassica napus)); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 16114538(whole	17517886(mitochondrion - SUBA); 11158531(mitochondrion - SUBA);	0.155	0.159	89	transport.ABC transporters and multidrug resistance systems
AT3G16340	gi 18401096	PDR1; ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 1				34.16 transport.ABC transporters and multidrug resistance systems	34.16	13	13	C		ABC_tran(2) ABC2_membrane(2) FHIPEP(1) ISN1(1) Oxidored_q3(1) PDR_assoc(1)	14	0.063	160.3	8.53	17317660(Plasma Membrane proteome);		0	0	0	transport.ABC transporters and multidrug resistance systems
AT2G26910	gi 15225814	PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 4				34.16 transport.ABC transporters and multidrug resistance systems	34.16	12	13	-		ABC_tran(2) ABC2_membrane(2) MFS_1(1) NACHT(1) PDR_assoc(1) TatC(1)	13	0.078	161.27	8.26	19376835(leaf phosphoproteins); 18686298(tonoplast phosphoproteome (leaves)); 19114538(guard cells Arabidopsis		0.014	0.014	175	transport.ABC transporters and multidrug resistance systems
AT1G02520	gi 15217785	P-glycoprotein 11 [Arabidopsis thaliana]	Transporters	P-glycoprotein 11	PGP11 (P-GLYCOPROTEIN 11); ATPase.	plasma membrane		34.16 transport.ABC transporters and multidrug resistance systems	34.16	12	10	-		AAA(1) ABC_membrane(2) ABC_tran(2) CimHS(1) DUF1558(1) Dynamin_N(1) SMC_N(1)	9	0.147	137.67	7.57	15308754(plasma membrane (phosphorylated)); 16618929(Plasma Membrane-LOPT-callus); 17317660(Plasma Membrane proteome); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasm		0	0	0	transport.ABC transporters and multidrug resistance systems
AT4G01820	gi 2739309	P-glycoprotein-like protein [Arabidopsis thaliana]	Transporters	P-glycoprotein 3				34.16 transport.ABC transporters and multidrug resistance systems	34.16	12	11	-		AAA(1) ABC_membrane(2) ABC_tran(2) DetM(1) Dynamin_N(1) Ferric_reduct(1) KH_2(1)	11	0.227	133.24	8.23	19376835(leaf phosphoproteins);		0	0	0	transport.ABC transporters and multidrug resistance systems
AT3G55320	gi 15233244	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporters	P-glycoprotein 20				34.16 transport.ABC transporters and multidrug resistance systems	34.16	11	13	-		ABC_membrane(2) ABC_tran(2) DUF1558(1) Dynamin_N(1) Viral_helicase(1)	16	0.092	155.16	5.85	17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19376835(leaf phosphoproteins)		0	0	0	transport.ABC transporters and multidrug resistance systems
AT4G32390	gi 15236781	phosphate translocator-related [Arabidopsis thaliana]	Transporters	Nucleotide-sugar transporter family protein				34.8 transport.metabolite transporters at the envelope membrane	34.8	10	9	S		DUF540(1) DUF6(1) TPT(1) UAA(1)	5	0.592	39.02	8.61	17660356(tonoplast (Brassica oleracea buds));		0	0	0	transport.metabolite transporters at the envelope membrane

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AT2G36380	gi 4581139	putative ABC transporter [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 6				34.16 transport.ABC transporters and multidrug resistance systems	34.16	12	12	M		7TMR- DISM_TTM(1) ABC_tran(2) ABC2_membran e(2) PDR_assoc(1)	16	0.051	164.21	7.52	16618929(Plasma Membrane-LOPTT-callus); 19334764(plasma membrane (cell culture)); 19114538(guard cells Arabidopsis leaf);		0	0	0	transport_ABC transporters and multidrug resistance systems
AT5G43340	gi 15239845	putative inorganic phosphate transporter 1-6 [Arabidopsis thaliana]	Transporters	phosphate transporter 1;6				34.7 transport.phosph ate	34.7	12	10	-		7tm_4(1) MFS_1(1) Sugar_tr(1)	7	0.457	56.25	9.05			0	0	0	transport.phosph ate
AT3G54700	gi 186511064	putative inorganic phosphate transporter 1-7 [Arabidopsis thaliana]	Transporters	phosphate transporter 1;7				34.7 transport.phosph ate	34.7	9	7	-		CTP_transf_1(1) MFS_1(1) Sugar_tr(1)	6	0.319	58.33	8.35	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma		0	0	0	transport.phosph ate
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis thaliana]	Transporters	nucleobase-ascorbate transporter 12	xanthine/uracil permease family protein	plasma membrane		34.99 transport.misc	34.99	12	11	C		CTP_transf_1(1) MFS_1(1) OPT(1) TatC(1) UbiA(1) Xan_ur_permeas e(1)	7	0.196	76.68	9.47	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma	16982705(plasma membrane - SUBA);	0	0	0	transport.misc
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis thaliana]	Transporters	nucleobase-ascorbate transporter 12	xanthine/uracil permease family protein	plasma membrane		34.99 transport.misc	34.99	12	11	C		CTP_transf_1(1) MFS_1(1) OPT(1) TatC(1) UbiA(1) Xan_ur_permeas e(1)	7	0.196	76.68	9.47	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma	16982705(plasma membrane - SUBA);	0	0	0	transport.misc
AT5G43360	gi 2149973	putative proton/phosphate cotransporter [Arabidopsis thaliana]	Transporters	phosphate transporter 1;3				34.7 transport.phosph ate	34.7	12	11	-		MadL(1) MFS_1(1) Sugar_tr(1)	6	0.388	57.26	9.11	15060130(Plasma Membrane proteome); 19334764(plasma membrane (cell culture));		0	0	0	transport.phosph ate

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AT2G37180	gi 15228096	RD28 (RESPONSIVE TO DESICCATION 28); water channel [Arabidopsis thaliana]	Transporters	Aquaporin-like superfamily protein	RD28 (plasma membrane intrinsic protein 2.3); water channel			34.19.1 transport.Major Intrinsic Proteins.PIP	34.19.1	6	6	-		MIP(1)	4	0.501	30.43	7.69	15060130(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19106119(plasma membrane detergent resistant microdomains (DRM)); 19334764(plasma membrane (cell		0.035	0.039	230	transport.Major Intrinsic Proteins.PIP
AT1G30410	gi 75333513	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABC12; Short=AtABC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName:	Transporters	multidrug resistance-associated protein 13				34.16 transport.ABC transporters and multidrug resistance systems	34.16	13	12	-		ABC_membrane(2) ABC_tran(2) BCCT(1) MMR_HSR1(1) SMC_N(1)	16	0.125	164.57	7.99			0.021	0.022	1176	transport.ABC transporters and multidrug resistance systems
AT2G24520	gi 12230479	RecName: Full=ATPase 5, plasma membrane-type; AltName: Full=Proton pump 5	Transporters	H(+)-ATPase 5				34.1 transport.p-and v-ATPases	34.1	10	10	-		Cation_ATPase_C(1) Cation_ATPase_N(1) E1-E2_ATPase(1) Hydrolase(1)	11	0.073	102.66	7.24	17317660(Plasma Membrane proteome); 19106119(plasma membrane detergent resistant microdomains (DRM)); 19114538(guard cells Arabidopsis		0	0	0	transport.p- and v-ATPases
AT3G51670	gi 15230555	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	Transporters	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein				34.99 transport.misc	34.99		0	-		CRAL_TRIO(1) CRAL_TRIO_N(1) EMP24_GP25L(1)	3	-0.45	46.51	8.41	17317660(Plasma Membrane proteome); 1764812(plasma membrane -suspension		0	0	0	transport.misc
AT5G56160	gi 145359309	sec14p-like phosphatidylinositol transfer-like protein [Arabidopsis thaliana]	Transporters	Sec14p-like phosphatidylinositol transfer family protein				34.99 transport.misc	34.99	1	1	-		CRAL_TRIO(1) CRAL_TRIO_N(1)	11	-0.516	66.26	6.74			0	0	0	transport.misc
AT1G66950	gi 5103820	Similar to gb Z70524 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF00005 ABC transporter family. ESTs gb N97039 and gb T43169 come from this gene [Arabidopsis thaliana]	Transporters	pleiotropic drug resistance 11				34.16 transport.ABC transporters and multidrug resistance systems	34.16	14	12	C		ABC_tran(2) ABC2_membrane(2) MMR_HSR1(1) PDR_assoc(1)	14	0.025	165.2	6.86			0	0	0	transport.ABC transporters and multidrug resistance systems
AT2G25600	gi 30682817	SPIK (Shaker Pollen Inward K+ channel); cyclic nucleotide binding / inward rectifier potassium channel/ potassium channel [Arabidopsis thaliana]	Transporters	Shaker pollen inward K+ channel	SPIK (SHAKER POLLEN INWARD K+ CHANNEL); cyclic nucleotide binding / inward rectifier potassium channel/			34.15 transport.potassium	34.15	4	5	-		Ank(3) cNMP_binding(1) Ion_trans(1) Ion_trans_2(1) TMC(1)	9	-0.118	99.22	6.32	19546170(mature pollen grains);		0.009	0.01	628	transport.potassium
AT1G61250	gi 2443878	Unknown protein [Arabidopsis thaliana]	Transporters	secretory carrier 3	SC3 (SECRETORY CARRIER 3); transmembrane transporter	plasma membrane		34.99 transport.misc	34.99	4	4	-		SCAMP(1) TatC(1)	3	0.185	32.61	8.87	13060130(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19036721(sterol dependent transport		0.166	0.122	5	transport.misc
AT5G61740	gi 10176867	unnamed protein product [Arabidopsis thaliana]	Transporters	ABC2 homolog 14	ATATH14 (ABC2 homolog 14); ATPase, coupled to transmembrane movement of substances	plasma membrane		34.16 transport.ABC transporters and multidrug resistance systems	34.16	4	4	-		ABC_tran(1) SMC_N(1)	12	-0.029	93.92	8.36	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 18463617(suspension cells-		0	0	0	transport.ABC transporters and multidrug resistance systems

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AT1G13210	gi15222212	ACA1 (autoinhibited Ca <sup>2+</sup> /ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding [Arabidopsis thaliana]	Unknown	autoinhibited Ca <sup>2+</sup> /ATPase II				35.1 not assigned.no ontology	35.1	10	9	M		Hydrolase(1)	17	-0.08	136.59	6.54	15276459(trichomes); 17317660(Plasma Membrane proteome); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins)		0	0	0	not assigned.no ontology
AT1G31810	gi186479105	actin binding [Arabidopsis thaliana]	Unknown	Formin Homology 14				35.1.20 not assigned.no ontology.formin homology 2 domain-containing	35.1.20		0	-		Aconitase_2_N(1) Act-Frag_cataly(1) CobT(1) CorA(1) DUF762(1) eIF-	18	-0.502	135.52	6.51	18463617(suspension cells-phosphorylated proteins);		0	0	0	not assigned.no ontology.formin homology 2 domain-containing protein
AT1G17620	gi11762174	At1g17620 [Arabidopsis thaliana]	Unknown	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	unknown protein	plasma membrane		35.2 not assigned.unknown	35.2	1	1	-		Hin1(1)	8	-0.017	28.29	10.05	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasma membrane detergent resistant microdomains (DRM));		0	0	0	not assigned.unknown
AT1G52320	gi15450411	At1g52320/F19K6_7 [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS				35.2 not assigned.unknown	35.2		0	-		DUF632(1) Filament(1) P4Ha_N(1)	3	-0.79	54.95	7.81	17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 18463617(suspension cells-phosphorylated proteins);		0	0	0	not assigned.unknown
AT1G73650	gi15809974	At1g73650/F25P22_7 [Arabidopsis thaliana]	Unknown	Protein of unknown function (DUF1295)	oxidoreductase, acting on the CH-CH group of donors	plasma membrane		35.2 not assigned.unknown	35.2	7	6	-		DUF1295(1) ICMT(1) Steroid_dh(1)	1	0.116	23.73	8.99	15060130(Plasma Membrane proteome); 15539469(vacuole); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf wt and clpr4-1 mutant); 19106119(plasma membrane detergent resistant microdomains		0.159	0.201	169	not assigned.unknown

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AT5G58090	gi16604491	AT5g58090.k21119_70 [Arabidopsis thaliana]	Unknown	O-Glycosyl hydrolases family 17 protein	glycosyl hydrolase family 17 protein	plasma membrane	anchored to membrane	35.1 not assigned.no ontology	35.1		0	M		Glyco_hydro_17 (1) X8(1)	8	-0.043	52.21	5.59		0.084	0.087	53	not assigned.no ontology	
AT1G51640	gi15217995	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding [Arabidopsis thaliana]	Unknown	exocyst subunit exo70 family protein G2				35.1 not assigned.no ontology	35.1		0	-		Exo70(1)	15	-0.379	76.2	8.02		0	0	0	not assigned.no ontology	
AT5G35570	gi10176802	axi 1 (auxin-independent growth promoter)-like protein [Arabidopsis thaliana]	Unknown	O- fucosyltransferase family protein	unknown protein Duf246 domain			35.2 not assigned.unknown	35.2	1	1	C		DUF246(1) Gemini_V1(1)	10	-0.487	72.91	6.79		0.012	0	21	not assigned.unknown	
AT1G78880	gi15219232	balbiani ring 1-related / BR1-related [Arabidopsis thaliana]	Unknown	Ubiquitin- specific protease family C19- related protein	balbiani ring 1- related / BR1- related	plasma membrane		35.1 not assigned.no ontology	35.1	2	2	-				7	-0.163	50.11	9.54		0	0	0	not assigned.no ontology
AT4G29360	gi7269834	beta-1, 3-glucanase-like protein [Arabidopsis thaliana]	Unknown	O-Glycosyl hydrolases family 17 protein			anchored to membrane	35.1 not assigned.no ontology	35.1		1	S		Glyco_hydro_17 (1) X8(1)	9	-0.027	57.66	5		0.021	0.021	166	not assigned.no ontology	
AT2G44790	gi1906000	blue copper-binding protein II [Arabidopsis thaliana]	Unknown	uclacyanin 2	UCC2 (UCLACYANIN 2); copper ion binding		anchored to membrane	35.1 not assigned.no ontology	35.1		2	S		Cu_bind_like(1)	3	0.017	20.35	5.83		0.099	0.103	53	not assigned.no ontology	

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AT4G23630	gi15236556	BT11 (VIRB2-INTERACTING PROTEIN 1) [Arabidopsis thaliana]	Unknown	VIRB2-interacting protein 1	BT11 (VIRB2-INTERACTING PROTEIN 1), RTLNB1 - cytosol & ER	cytosol; ER		35.1 not assigned.no ontology	35.1	4	3	-		Reticulon(1)	2	-0.068	30.53	8.32	150901501(plasma Membrane proteome); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17660356(tonoplast (Brassica oleracea buds)); 19200160(flower-stage 12); 17216043(leaf); 19253305(phosphoproteins (etiolated seedling)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins); 20166762(whole plant)	15494553(cytosol -SUBA);	0.145	0.189	83		not assigned.no ontology
AT4G11220	gi15237093	BT12 (VIRB2-INTERACTING PROTEIN 2) [Arabidopsis thaliana]	Unknown	VIRB2-interacting protein 2	reticulon family protein (RTLNB2)	cytosol		35.1 not assigned.no ontology	35.1	4	3	-		Reticulon(1)	2	-0.144	30.28	8.61	17317660(Plasma Membrane proteome); 17293592(total seedlings 7# light and dark grown); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica oleracea buds)); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis)	15494553(cytosol -SUBA);	0.122	0.153	79		not assigned.no ontology
AT1G51570	gi15217968	C2 domain-containing protein [Arabidopsis thaliana]	Unknown	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	C2 domain-containing protein			35.1.19 not assigned.no ontology.C2 domain-containing protein	35.1.19	3	3	-		C2(3) PRT_C(1)	10	-0.235	89.16	9.13	16287169(Cell Wall proteome); 16618929(ER-LOPIT-callus); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant))		0.121	0.117	82		not assigned.no ontology.C2 domain-containing protein
AT1G14870	gi15223920	cadmium resistance protein 2 [Arabidopsis thaliana]	Unknown	PLANT CADMIUM RESISTANCE 2				35.1 not assigned.no ontology	35.1	1	1	-		PLAC8(1)	16	-0.132	16.74	6.48	16618929(Plasma Membrane-LOPIT-callus); 17317660(Plasma Membrane proteome); 18436743(specific to roots);		0	0	0		not assigned.no ontology
AT4G37100	gi15235439	catalytic/ pyridoxal phosphate binding protein [Arabidopsis thaliana]	Unknown	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein				35.2 not assigned.unknown	35.2		0	C		Fez1(1)	8	-0.573	100.77	5.94	17317660(Plasma Membrane proteome);		0	0	0		not assigned.unknown
AT4G14385	gi18414206	chromatin modification-related protein EAF6 [Arabidopsis thaliana]	Unknown	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_processes unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Histone H4 acetyltransferase, NuA4 complex.				35.2 not assigned.unknown	35.2		0	-		NuA4(1)	0	-0.934	17.83	8.8	15539469(vacuole);		0	0	0		not assigned.unknown
AT3G20470	gi13687234	copa-like retroelement pol polyprotein [Arabidopsis thaliana]	Unknown	glycine-rich protein 5							1	S		GRP(1)	0	0.207	13.72	10			0	0	0		

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AT5G07300	gi7576168	copine-like protein [Arabidopsis thaliana]	Unknown	Calcium-dependent phospholipid-binding Copine family protein	BON2 (BONZAI 2)			35.1 not assigned.no ontology	35.1	2	0	-		C2(2) Copine(1) VWA(1)	5	-0.125	64.03	5.05	17644812(plasma membrane - suspension cells); 20706207(cell cycle interactome (cell culture)); 19114538(guard cell chloroplast); 15060130(Plasma Membrane proteome); 15539469(vacuole); 15815986(seedling); 15815986(Leaf); 17317660(Plasma Membrane proteome); 17828791(total leaf); 17293592(total seedlings 77 light and dark grown); 17028151(leaf defense proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica brassicae leaf))		0.06	0.066	538		not assigned.no ontology
AT4G20260	gi15235363	DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana]	Unknown	plasma-membrane associated cation-binding protein 1	DREPP plasma membrane polypeptide family	plasma membrane		35.1 not assigned.no ontology	35.1		0	-		DREPP(1)	0	-0.706	24.58	4.99	15060130(plasma membrane - SUBA); 17828791(total leaf); 17293592(total seedlings 77 light and dark grown); 17028151(leaf defense proteome); 17644812(plasma membrane - suspension cells); 17660356(tonoplast (Brassica brassicae leaf))	15060130(plasma membrane - SUBA);	0.711	0.792	32		not assigned.no ontology
AT4G00310	gi18411286	EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana]	Unknown	Putative membrane lipoprotein				35.2 not assigned.unknown	35.2		0	-			4	-0.848	33.19	5.74			0	0	0		not assigned.unknown
AT1G71820	gi7239509	EST gb AA712174 comes from this gene [Arabidopsis thaliana]	Unknown	SEC6	unknown protein Sec6 homology			35.2 not assigned.unknown	35.2		0	-		DHC_N1(1) HemN_C(1) Sec6(1)	13	-0.324	85.68	4.8			0.134	0.123	21		not assigned.unknown
AT1G61900	gi3367523	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_processes unknown; LOCATED IN: anchored to plasma membrane, plasma membrane, anchored to membrane; EXPRESSED IN: 23 plant structures; EXPRESSED			anchored to membrane	35.1 not assigned.no ontology	35.1		0	S			23	0.067	47.03	6.26	14517339(GPI anchored suspension cells); 17317660(Plasma Membrane proteome);		0	0	0		not assigned.no ontology
AT3G24255	gi8778279	F14D16.18 [Arabidopsis thaliana]	Unknown	RNA-directed DNA polymerase (reverse transcriptase)-related family				35.2 not assigned.unknown	35.2		0	-		GvpK(1)	9	-0.363	84.88	6.94			0	0	0		not assigned.unknown
AT1G28690	gi6691205	F1K23.11 [Arabidopsis thaliana]	Unknown	Tetratricopeptide repeat (TPR)-like superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5		0	M		ESAG6_7(1) PPR(5)	11	-0.173	58.14	8.75			0	0	0		not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein
AT1G28340	gi6560758	F3M18.23 [Arabidopsis thaliana]	Unknown	receptor like protein 4				35.1 not assigned.no ontology	35.1	2	1	S		Alba(1) LRR_1(2) LRRNT_2(1)	9	-0.139	68.42	8.57	16618929(UNKOWN-LOPT-callus); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell		0	0	0		not assigned.no ontology



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AT5G25250	gi15238749	Flotillin-like protein 1 [Arabidopsis thaliana]	Unknown	SPFH/Band 7/PHB domain-containing membrane-associated protein family				35.2 not assigned.unknown	35.2		0	-		Band_7(1) HrpE(1) TolA(1) tRNA_synt_lc_R2(1)	2	-0.394	52.31	5.83	15539469(vacuole); 17151019(vacuole - suspension cell); 19106119(plasma membrane detergent resistant microdomains (DRM)); 19334764(plasm		0	0	0	not assigned.unknown
AT4G00300	gi18411279	fringe-related protein [Arabidopsis thaliana]	Unknown	fringe-related protein				35.1 not assigned.no ontology	35.1	2	2	-		DUF604(1) DUF912(1) Fringe(1)	9	-0.284	88.86	8.9			0	0	0	not assigned.no ontology
AT5G16020	gi15237248	gamete-expressed 3 [Arabidopsis thaliana]	Unknown	gamete-expressed 3	stress protein-related			35.1 not assigned.no ontology	35.1	1	2	S		p47_phox_C(1) PQQ(1)	9	-0.257	73.34	5.34			0.014	0.014	106	not assigned.no ontology
AT2G42330	gi15227926	GC-rich sequence DNA-binding factor-like protein with Tufelin interacting domain [Arabidopsis thaliana]	Unknown	GC-rich sequence DNA-binding factor-like protein with Tufelin				35.1 not assigned.no ontology	35.1		0	-		G-patch(1) TFP11(1)	7	-0.546	86.53	7.94	19888209(80S polysomal fraction);		0	0	0	not assigned.no ontology
AT1G27090	gi15223426	glycine-rich protein [Arabidopsis thaliana]	Unknown	glycine-rich protein	glycine-rich protein- dually targeted to cytosol & nucleus	cytosol; nucleus		35.1.40 not assigned.no ontology.glycine rich proteins	35.1.40		0	-		OAR(1)	4	-0.825	46.02	5.26	19200160(flowe r-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19114538(guard cells Arabidopsis leaf);	15141064(cytosol -SUBA); 15141064(unclear -SUBA);	0.312	0.308	2	not assigned.no ontology.glycine rich proteins
AT1G26130	gi15222647	haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unknown	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase	haloacid dehalogenase-like -transport			35.1 not assigned.no ontology	35.1	10	10	M		E1-E2_ATPase(1) Hydrolase(1) Transposase_12(1)	22	-0.004	133.8	5.91	12938931(Total chloroplast envelope); 17317660(Plasma Membrane proteome);		0	0	0	not assigned.no ontology
AT4G39955	gi18420566	hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unknown	alpha/beta-Hydrolases superfamily protein				35.1 not assigned.no ontology	35.1		0	M		Abhydrolase_1(1) Abhydrolase_2(1) Peptidase_S15(1) Thioesterase(1)	8	-0.201	37.64	8.9	17317660(Plasma Membrane proteome); 19036721(steroid dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane		0	0	0	not assigned.no ontology
AT2G22180	gi15227160	hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	Unknown	hydroxyproline-rich glycoprotein family protein				35.1.41 not assigned.no ontology.hydroxyproline rich	35.1.41	1	1	-		Hin1(1)	3	-0.454	32.21	9.19	19546170(mature pollen grains);		0	0	0	not assigned.no ontology.hydroxyproline rich proteins
AT5G62740	gi15241939	Hypersensitive-induced response protein 1 [Arabidopsis thaliana]	Unknown	SPFH/Band 7/PHB domain-containing membrane-associated protein family	band 7 family protein			35.1 not assigned.no ontology	35.1		0	-		Band_7(1)	5	-0.101	31.43	5.29	13060130(Plasma Membrane proteome); 15539469(vacuole); 16618929(UNK NOWN-LOPIT-callus); 17317660(Plasma Membrane proteome); 17151019(vacuole - suspension cell); 17644812(plasma membrane - suspension cells); 17432890(leaf total membranes); 17660356(tonoplast (Brassica oleracea buds)); 19546170(mature pollen grains); 19036721(detergent resistant	15319477(plasma membrane - SUBA);	0.22	0.226	95	not assigned.no ontology

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AT2G28780	gi 3927826	hypothetical protein [Arabidopsis thaliana]	Unknown	unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: inflorescence meristem, root, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s:				35.2 not assigned.unknown	35.2	9	5	M		DUF893(1) DUF939(1) FUSC(1) LWQEQ(1) PAP2(1) SFT2(1)	19	0.1	87.99	8.86			0	0	0	not assigned.unknown
AT2G39690	gi 2795807	hypothetical protein [Arabidopsis thaliana]	Unknown	Protein of unknown function.				35.2 not assigned.unknown	35.2		0	-		DUF547(1)	9	-0.295	56.74	6.82			0	0	0	not assigned.unknown
AT4G15830	gi 2244939	hypothetical protein [Arabidopsis thaliana]	Unknown	ARM repeat superfamily protein				35.2 not assigned.unknown	35.2		0	-			6	-0.318	33.27	6.49			0	0	0	not assigned.unknown
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to salt stress; LOCATED IN: mitochondrion; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa -				35.2 not assigned.unknown	35.2		0	M			1	-1.174	35.92	7.62			0	0	0	not assigned.unknown
AT2G30480	gi 110741415	hypothetical protein [Arabidopsis thaliana]	Unknown	unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes -				35.2 not assigned.unknown	35.2		0	-			11	-1.138	71.09	5.21			0	0	0	not assigned.unknown
AT5G04420	gi 15237715	kelch repeat-containing protein [Arabidopsis thaliana]	Unknown	Galactose oxidase/kelch repeat superfamily protein	kelch repeat-containing protein			35.1 not assigned.no ontology	35.1		0	-		IncA(1) Kelch_1(1) Kelch_2(3)	5	-0.407	56.66	5.65	18463617(suspension cells-phosphorylated proteins); 19546170(mature pollen grains); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 19376835(leaf		0.029	0.031	411	not assigned.no ontology
AT2G42560	gi 15227965	late embryogenesis abundant domain-containing protein [Arabidopsis thaliana]	Unknown	late embryogenesis abundant domain-containing protein / LEA domain-containing protein	late embryogenesis abundant domain-containing protein			35.1.22 not assigned.no ontology.late embryogenesis abundant domain-containing protein	35.1.22		0	-		LEA_4(4)	0	-0.978	67.2	5.78	11402211,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15908592(Carboxylated seed protein); 17293592(total seedlings 77 light and dark grown); 18599647(seed proteome); 18436743(specific to seeds); 20702726(mature		0	0	0	not assigned.no ontology.late embryogenesis abundant domain-containing protein
AT3G15410	gi 2760084	leucine-rich repeat protein [Arabidopsis thaliana]	Unknown	Leucine-rich repeat (LRR) family protein	leucine-rich repeat family protein			35.1 not assigned.no ontology	35.1		0	M		LRR_1(3)	10	-0.111	64.11	6.01	19546170(mature pollen grains);		0.053	0.054	486	not assigned.no ontology
AT1G25570	gi 42562316	leucine-rich repeat protein-related [Arabidopsis thaliana]	Unknown	Di-glucose binding protein with Leucine-rich repeat domain				35.1 not assigned.no ontology	35.1	1	1	S		ATP-synt_8(1) LRR_1(1) LRRNT_2(1)	11	-0.022	68.97	5.23	15539469(vacuole); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma membrane (DRM) proteins		0	0	0	not assigned.no ontology

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AT5G42020	gi 1303695	luminal binding protein (BiP) [Arabidopsis thaliana]	Unknown	Heat shock protein 70 (Hsp70) family protein	luminal binding protein 2 precursor (BiP-2) (AtBP2)	ER	endoplasmic reticulum & endoplasmic reticulum lumen	29.6 protein.folding	29.6			1	S	Actin(1) HSP70(1) Hydantoinease_A(1) MrB_Mbl(1)	5	-0.467	73.56	5.11	15496452(nucleolus); 16358359(cell suspension (Gamborg)); 16502469(cell suspension-Cd-up); 16247729(mature Pollen); 15815986(Siliquae); 15815986(seedling); 15815986(Leaf); 1140221,12068122,15047896,16679420,17028149(seed-all-Jobpapers); 15908592(Carbo-related seed)	11226186(endoplasmic reticulum-SUBA);	0.512	0.533	34	protein.folding
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	Unknown	PLC-like phosphodiesterases superfamily protein				35.1 not assigned.no ontology	35.1			0	S		15	-0.294	44.33	4.99			0	0	0	not assigned.no ontology
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	Unknown	PLC-like phosphodiesterases superfamily protein				35.1 not assigned.no ontology	35.1			0	S		15	-0.294	44.33	4.99			0	0	0	not assigned.no ontology
ATMG00520	gi 13449330	maturase [Arabidopsis thaliana]	Unknown	Intron maturase, type II family protein				35.2 not assigned.unknown	35.2			0	-	Intron_maturase2(1) RVT_1(1)	9	-0.246	75.45	10.06			0	0	0	not assigned.unknown
AT5G44610	gi 18422461	microtubule-associated protein 18 [Arabidopsis thaliana]	Unknown	microtubule-associated protein 18				35.1 not assigned.no ontology	35.1			0	-	DREPP(1)	0	-0.888	18.55	4.92	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 18436743(specific to roots); 19334764(plasma membrane (cell culture));		0	0	0	not assigned.no ontology
AT1G48920	gi 15222009	nucleolin [Arabidopsis thaliana]	Unknown	nucleolin like 1	ATNUC-L1/PARL1 (PARALLEL 1); nucleic acid binding	nucleus		35.1 not assigned.no ontology	35.1			0	-	Collagen(1) DUF755(1) MPPN(1) RRM_1(2)	1	-1.173	58.77	5.12	15496452(nucleolus); 16618929(UNK NOWN-LOPIT-callus); 18463617(suspension cells-phosphorylated proteins); 19200160(flowers-stage 12); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19714877(interactomes 14-3-3 complexes (cell culture)); 19376835(leaf phosphoproteins); 20706207(cell cycle interactome (cell culture)); 20166762(leaf)	17286797(nucleus-SUBA);	0.158	0.161	298	not assigned.no ontology
AT5G20870	gi 15242078	O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana]	Unknown	O-Glycosyl hydrolases family 17 protein			anchored to membrane	35.1 not assigned.no ontology	35.1			0	S	Glyco_hydro_17(1) X8(1)	9	-0.151	54.57	8.26			0	0	0	not assigned.no ontology
AT2G32690	gi 21553811	outer membrane lipoprotein-like [Arabidopsis thaliana]	Unknown	glycine-rich protein 23								0	S	GRP(1)	1	0.134	16.86	9.87			0	0	0	
AT2G36050	gi 18404030	ovate family protein 15 [Arabidopsis thaliana]	Unknown	ovate family protein 15				35.1 not assigned.no ontology	35.1			0	C	DUF623(1)	4	-0.489	29.07	4.62			0	0	0	not assigned.no ontology
AT5G61800	gi 15240355	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unknown	Pentatricopeptide repeat (PPR) superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5			0	M	PPR(4)	13	-0.001	56.05	8.66			0	0	0	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein
AT5G43820	gi 240256396	pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	Unknown	Pentatricopeptide repeat (PPR) superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5			0	M	PPR(8)	15	-0.114	61.3	8.06			0	0	0	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein

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AT5G62810	gi 11094252	PEX14 [Arabidopsis thaliana]	Unknown	peroxin 14	PEX14 (PEROXISOME DEFECTIVE 2)	peroxisome	cytosol & peroxisome	35.1 not assigned.no ontology	35.1	1	1	-		Pex14_N(1)	0	-0.734	55.6	5.71	17317600(Plasma Membrane proteome); 17951448(peroxisome (leaves)); 18463617(suspension cells-phosphorylated proteins); 18931141(peroxisomes-high&low purity (cell culture)); 19546170(mature pollen grains); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma membrane (cell culture)); 19376835(leaf phosphoproteins)		0.148	0.157	347	not assigned.no ontology	
AT3G03530	gi 18396577	phospholipase C [Arabidopsis thaliana]	Unknown	non-specific phospholipase C4			plasma membrane	35.1 not assigned.no ontology	35.1		0	-		Phosphoesterase(1) Sulfatase(1)	8	-0.587	60.72	5.82	17317660(Plasma Membrane proteome); 18436743(specific to seeds); 19334764(plasma membrane (cell culture));		0	0	0	not assigned.no ontology	
AT1G09520	gi 18391032	protein binding / zinc ion binding [Arabidopsis thaliana]	Unknown	LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Zinc finger, PHD-type, conserved site (InterPro:IPR019786); BEST Arabidopsis thaliana protein match is: PHD				35.2 not assigned.unknown	35.2		0	C		IBR(1) PHD(1)	13	-0.475	28.03	8.77			0	0	0	not assigned.unknown	
AT5G50200	gi 13624657	putative component of high affinity nitrate transporter [Arabidopsis thaliana]	Unknown	nitrate transmembrane transporters				35.2 not assigned.unknown	35.2	1	1	S		DUF1328(1)	4	-0.13	23.4	9.28	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell culture));		0	0	0	not assigned.unknown	
AT1G36756	gi 7543898	putative protein [Arabidopsis thaliana]	Unknown	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10602.1); Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other				35.2 not assigned.unknown	35.2		0	M				3	-0.395	14.35	4.64			0	0	0	not assigned.unknown
AT3G57430	gi 6706414	putative protein [Arabidopsis thaliana]	Unknown	Tetratricopeptide repeat (TPR)-like superfamily protein	OTPR84 - PPR protein - editing ndhF, psbZ, ndhB	plastid		27.1.5* RNA.editing	27.1.5*		0	C		PPR(9)	22	-0.029	99.28	6.94			0	0	0	RNA.editing	

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AT3G60920	gi 8388608	putative protein [Arabidopsis thaliana]	Unknown	CONTAINS InterPro DOMAIN/s: Beige/BEACH (InterPro:IPR000409); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein / beige-related (TAIR:AT2G45540.1); Has 1795 Blast hits to 1563 proteins in 214 species: Archae - 2;				35.1 not assigned.no ontology	35.1	4	0	-			Beach(1)	30	-0.189	213.26	5.77			0	0	0	not assigned.no ontology
AT4G32285	gi 2864615	putative protein [Arabidopsis thaliana]	Unknown	ENTH/ANTH/VHS superfamily protein	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related			35.1.21 not assigned.no ontology. epsin N-terminal homology (ENTH) domain-containing protein	35.1.21		0	-		ANTH(1) DUF605(1) ENTH(1) IL1_propep(1) UCR_14kD(1)	5	-0.537	70.56	5.77	17517600(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19245862(nuclear phosphoproteins (seedlings & cell culture)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant)); 19752205(Plasma Membrane proteome); 14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma		0.068	0.051	23	not assigned.no ontology. epsin N-terminal homology (ENTH) domain-containing protein	
AT4G33700	gi 3549672	putative protein [Arabidopsis thaliana]	Unknown	CBS domain-containing protein with a domain of unknown function (DUF21)	CBS domain-containing protein	plasma membrane		35.1 not assigned.no ontology	35.1	5	3	S		CBS(1) DUF21(1)	6	0.183	47.11	5.73	14506206(Plasma Membrane proteome); 14506206(plasma membrane (phosphorylated)); 15308754(plasma membrane (phosphorylated)); 17317660(Plasma Membrane proteome); 19036721(detergent resistant plasma		0	0	0	not assigned.no ontology	
AT5G12290	gi 14586359	putative protein [Arabidopsis thaliana]	Unknown	dgd1 suppressor 1	digalactolipid-deficient DGD1 SUPPRESSOR 1 (DGS1)	mitochondria	mitochondrion			2	2	C		NCA2(1)	6	-0.244	68.9	6.62	MitoDB(Mitochondrial proteome); 16618929(MITOPLASTID-LOPIT-callus); 19546170(mature pollen grains); 19334764(plasma membrane (cell		0	0	0		
AT5G30520	gi 7413621	putative protein [Arabidopsis thaliana]	Unknown	unknown protein; Has 50 Blast hits to 50 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0				35.2 not assigned.unknown	35.2		0	M				2	0.31	13.24	4.98			0	0	0	not assigned.unknown

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AT3G44150	gi 7635460	putative protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_processes unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11800.1); Has 76 Blast				35.2 not assigned.unknown	35.2		0	S				8	0.027	27.09	9.23	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(sterol dependent detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasma membrane		0	0	0	not assigned.unknown
AGI no	gi 13548328	putative protein [Arabidopsis thaliana]	Unknown																						
AT4G06544	gi 7529254	putative protein [Arabidopsis thaliana]	Unknown																						
AT5G27650	gi 30690738	PWWP domain-containing protein [Arabidopsis thaliana]	Unknown	Tudor/PWWP/MBT superfamily protein				35.1 not assigned.no ontology	35.1		0	-		DUF1938(1) PWWP(1)	6	-0.693	118.1	6.34	19376835(leaf phosphoproteins);		0	0	0	not assigned.no ontology	
AT5G14770	gi 223635763	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial; Flags: Precursor	Unknown	Tetratricopeptide repeat (TPR)-like superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5		0	M		PPR(19)	19	-0.007	105.32	8.37	15269332(mitochondrion - SUBA);		0.016	0.018	447	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	
AT2G20310	gi 15225342	RPM1 interacting protein 13 [Arabidopsis thaliana]	Unknown	RPM1 interacting				35.2 not assigned.unknown	35.2		0	-				13	-0.796	47.94	5.39			0	0	0	not assigned.unknown
AT4G18060	gi 16974680	SH3 domain-containing protein 3 [Arabidopsis thaliana]	Unknown	SH3 domain-containing protein	SH3 domain-containing protein 3			35.1 not assigned.no ontology	35.1		0	M		BAR(1) SH3_1(1) SH3_2(1)	3	-0.572	39.53	6.4			0.051	0.053	18	not assigned.no ontology	
AT1G11820	gi 3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene [Arabidopsis thaliana]	Unknown	O-Glycosyl hydrolases family 17 protein	hydrolase, hydrolyzing O-glycosyl compounds			35.1 not assigned.no ontology	35.1		1	S		Glyco_hydro_17(1)	1	0.048	42.35	5.66	19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19525416(leaf (wt and clpr4-1 mutant));		0.122	0.13	35	not assigned.no ontology	
AT2G03510	gi 18395564	SPFH/Band 7/PHB domain-containing membrane-associated protein [Arabidopsis thaliana]	Unknown	SPFH/Band 7/PHB domain-containing membrane-associated protein family	band 7 family protein			35.1 not assigned.no ontology	35.1	1	1	-		Band_7(1)	3	-0.374	40.6	5.65	15496452(nucleolus); 16618929(ER-LOPIT-callus); 17151019(vacuole - suspension cell); 19200160(flowers-stage 12); 19546170(mature pollen grains); 19525416(leaf (wt and clpr4-1 mutant)); 19334764(plasma		0.199	0.233	61	not assigned.no ontology	
AT1G71040	gi 12323429	spore coat protein-like protein; 24980-21957 [Arabidopsis thaliana]	Unknown	Cupredoxin superfamily protein	LPR2 (LOW PHOSPHATE ROOT2); copper ion binding			35.1 not assigned.no ontology	35.1		0	-		Cu-oxidase(1) Cu-oxidase_2(1) Cu-oxidase_3(1)	3	-0.309	66.17	9.19	15593128(Cell Wall proteome); 17432890(leaf total membranes); 19525416(leaf (wt and clpr4-1		0.12	0.125	84	not assigned.no ontology	
AT1G17820	gi 9665060	Strong similarity to a hypothetical protein T18K17.13 gi 6598861 from Arabidopsis thaliana BAC T18K17 gb AC010556 and contains a PH PF00169 domain	Unknown	Putative integral membrane protein conserved region				35.2 not assigned.unknown	35.2		1	S		PH(1)	9	-0.518	90.11	9.08			0	0	0	not assigned.unknown	
AT3G01185	gi 5091549	T10024.18 [Arabidopsis thaliana]	Unknown	Protein of unknown function				35.2 not assigned.unknown	35.2		0	S		DUF784(1)	6	-0.089	16.81	7.56			0	0	0	not assigned.unknown	
AT2G19580	gi 15224802	TET2 (TETRASPANIN2) [Arabidopsis thaliana]	Unknown	tetraspanin2				33.99 development. unspecified	33.99	3	4	S		Tetraspanin(1)	14	0.363	30.13	8.81			0	0	0	development.unspecified	
AT2G31290	gi 15224649	ubiquitin thiolesterase [Arabidopsis thaliana]	Unknown	Ubiquitin carboxyl-terminal hydrolase family				35.2 not assigned.unknown	35.2		0	M		DUF860(1)	6	-0.526	48.7	9.2			0	0	0	not assigned.unknown	

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AT1G18180	gi145335854	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function (DUF1295)	oxidoreductase, acting on the CH-CH group of donors	plasma membrane		35.2 not assigned.unknown	35.2	7	6	S		DUF1295(1) ICMT(1) Steroid_dh(1)	3	0.337	35.2	9.44	15060130(Plasma Membrane proteome); 17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma		0	0	0	not assigned.unknown
AT1G45545	gi15220079	uncharacterized protein [Arabidopsis thaliana]	Unknown	Plant protein of unknown function (DUF827)	unknown protein DUF827 domain			35.2 not assigned.unknown	35.2		0	-		DUF683(1) DUF812(1) DUF827(1) Filament(1) LMP(1)	2	-0.765	84.45	5.11	19546170(mature pollen grains);		0	0	0	not assigned.unknown
AT1G53625	gi30695545	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; Has 29996 Blast hits to 6987 proteins in 655 species: Archae - 23; Bacteria - 6686; Metazoa - 10521; Fungi - 1178; Plants - 7439; Viruses - 681; Other Eukaryotes - 3468 (source:	unknown protein			35.2 not assigned.unknown	35.2		0	-				11	-0.525	8.51			0.101	0.11	27	not assigned.unknown
AT2G03350	gi18395537	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function.				35.2 not assigned.unknown	35.2		0	-		DUF538(1)	2	-0.274	20.17	9.57			0	0	0	not assigned.unknown
AT2G41810	gi15227439	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function.				35.2 not assigned.unknown	35.2		0	S		DUF642(1)	6	0.05	40.26	9.13			0.238	0.246	93	not assigned.unknown
AT3G13677	gi22331067	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; Has 24 Blast hits to 24 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI				35.2 not assigned.unknown	35.2		0	-			4	-0.317	19.63	9.51			0	0	0	not assigned.unknown
AT3G15480	gi18400781	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function				35.2 not assigned.unknown	35.2	3	4	S		Cic-like(1) Dis_P_DiS(1) DUF1218(1)	9	0.551	19.42	8.72	17317660(Plasma Membrane proteome);		0	0	0	not assigned.unknown
AT4G03180	gi15236259	uncharacterized protein [Arabidopsis thaliana]	Unknown	CONTAINS InterPro DOMAIN/s: rRNA processing (InterPro:IPR013730); Has 898 Blast hits to 687 proteins in 142 species: Archae - 2; Bacteria - 28; Metazoa - 200; Fungi - 99; Plants - 63; Viruses - 0; Other Eukaryotes - 506				35.2 not assigned.unknown	35.2		0	-		Bacillus_HBL(1) MAP7(1) rRNA_processing(1) SPT2(1)	0	-1.532	21.69	9.95			0	0	0	not assigned.unknown
AT4G12735	gi42572885	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: rosette leaf, cultured cell; BEST Arabidopsis thaliana protein match is:				35.2 not assigned.unknown	35.2		0	C			1	0.048	6.72	10.29	17317660(Plasma Membrane proteome);		0	0	0	not assigned.unknown

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AT4G15610	gi18414489	uncharacterized protein [Arabidopsis thaliana]	Unknown	Uncharacterised protein family (UPF0497)				35.1 not assigned.no ontology	35.1	4	4	-		DUF588(1)	5	0.73	20.53	9.68	18436743(specific to roots); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane)	10737809(unclear-SUBA);	0.052	0	56	not assigned.no ontology
AT5G08660	gi30682523	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function (DUF668)			mitochondrion	35.2 not assigned.unknown	35.2		0	-		DUF465(1) DUF668(1)	3	-0.465	72.5	8.84	MitoDB(Mitochondrial proteome); 17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19376835(leaf		0	0	0	not assigned.unknown
AT5G28920	gi30692070	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; Has 0 Blast hits to 0 proteins in 0 species (source: unknown)	unknown protein			35.2 not assigned.unknown	35.2		0	-			5	-0.49	46.44	9.55			0	0	0	not assigned.unknown
AT5G45540	gi15242429	uncharacterized protein [Arabidopsis thaliana]	Unknown	Protein of unknown function				35.2 not assigned.unknown	35.2	7	6	-		Drf_FH3(1) DUF594(1)	12	-0.165	93.23	7.05			0	0	0	not assigned.unknown
AT5G50540	gi18423175	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G50645.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 1738; Fungi - 3422; Plants -				35.2 not assigned.unknown	35.2	1	1	-			0	0.192	13.03	10.28			0	0	0	not assigned.unknown
AT5G53880	gi18423566	uncharacterized protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_processes unknown; LOCATED IN: mitochondrion, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages;				35.2 not assigned.unknown	35.2		0	-			5	-1.564	7.78	9.19	15060130(Plasma Membrane proteome); 15276431(Mitochondrial proteome); 15276431(mitochondrial membranes-suspension cells);		0	0	0	not assigned.unknown
AT1G01305	gi116830059	unknown [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_processes unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria -				35.2 not assigned.unknown	35.2			S			2	-0.111	15.84	10.14			0	0	0	not assigned.unknown
AT1G17147	gi116830105	unknown [Arabidopsis thaliana]	Unknown	VQ motif-containing				35.2 not assigned.unknown	35.2			-		VQ(1)	1	-0.515	10.9	4.89			0	0	0	not assigned.unknown
AT1G29380	gi116831287	unknown [Arabidopsis thaliana]	Unknown	Carbohydrate-binding X8 domain superfamily				35.1 not assigned.no ontology	35.1		0	S		GRP(1) X8(1)	8	-0.214	30.69	4.71			0	0	0	not assigned.no ontology
AT3G45460	gi116831268	unknown [Arabidopsis thaliana]	Unknown	IBR domain containing protein				35.2 not assigned.unknown	35.2		0	-		CI_4(1) IBR(1) Toxin_2(1) UPAR_LY6(1)	24	-0.229	44.78	8.34			0	0	0	not assigned.unknown
AT5G46680	gi21618238	unknown [Arabidopsis thaliana]	Unknown	Pentatricopeptide repeat (PPR-like) superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5		0	-		PPR(11) UBA_3(1)	14	-0.058	52.51	8.89			0	0	0	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein



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AT1G22250	gi30687784	unknown protein [Arabidopsis thaliana]	Unknown	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78170.1); Has 64 Blast hits to 64 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other				35.2 not assigned.unknown	35.2		0	-		E7(1)	8	-0.661	22.77	8.73			0	0	0	not assigned.unknown
AT2G05380	gi20466662	unknown protein [Arabidopsis thaliana]	Unknown	glycine-rich protein 3 short isoform				35.1.40 not assigned.no ontology.glycine rich proteins	35.1.40		1	S		GRP(1)	6	-0.495	11.59	8.24	19200160(flowe r-stage 12); 19329564(perox isomes (leaf)); 20166762(whole leaf);	16236160(uncle ar -SUBA); 10737809(uncle ar -SUBA);	0	0	0	not assigned.no ontology.glycine rich proteins
AT2G21990	gi15227126	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function.				35.2 not assigned.unknown	35.2		0	C		DUF617(1)	2	-0.421	27.64	9.3			0	0	0	not assigned.unknown
AT2G25270	gi26452742	unknown protein [Arabidopsis thaliana]	Unknown	unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G12400.1); Has 35333 Blast hits	unknown protein	plasma membrane		35.2 not assigned.unknown	35.2	5	5	S		Cation_efflux(1) DUF571(1) IncA(1) Tetraspannin(1) Tweety(1)	15	0.374	59.91	6.18	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 18463617(suspension cells-phosphorylated proteins); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0	0	0	not assigned.unknown
AT2G25800	gi3643603	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function				35.2 not assigned.unknown	35.2		0	C		DUF810(1)	12	-0.308	109.97	8.38	19334764(plasma membrane (cell culture));		0	0	0	not assigned.unknown
AT2G26570	gi15225334	unknown protein [Arabidopsis thaliana]	Unknown	Plant protein of unknown function (DUF827)	unknown protein	DUF827 domain		35.2 not assigned.unknown	35.2		0	-		AIP3(1) DASH_Spc19(1) DUF827(1) Endonuc-Msp(1) Laminin_I(1) Myosin_tail_1(1) Pr	2	-0.803	89.3	5.01	17317660(Plasma Membrane proteome); 18463617(suspension cells-phosphorylated proteins); 19376835(leaf phosphoproteins); 20706207(contaminants cell cycle		0.026	0.027	78	not assigned.unknown
AT2G27260	gi18401372	unknown protein [Arabidopsis thaliana]	Unknown	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family				35.2 not assigned.unknown	35.2	1	1	-		Hin1(1)	3	-0.363	27.58	9.59			0	0	0	not assigned.unknown
AT2G28310	gi30683843	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function				35.2 not assigned.unknown	35.2	1	1	M		DUF707(1)	5	-0.469	43.18	8.76			0	0	0	not assigned.unknown
AT2G40980	gi15226796	unknown protein [Arabidopsis thaliana]	Unknown	Protein kinase superfamily protein				35.2 not assigned.unknown	35.2		0	C		VirC1(1)	11	-0.331	69.11	5.32	17317660(Plasma Membrane proteome); 17216043(leaf); 19376835(leaf phosphoproteins); 18686298(tonoplast - phosphoproteom		0	0	0	not assigned.unknown
AT2G41800	gi15227437	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function, DUF642			cell wall (sensu Magnoliophyta)	35.2 not assigned.unknown	35.2		0	S		DUF642(1)	5	0.023	40.37	9.22	14595688(Cell Wall proteome); 16287169(Cell Wall proteome); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell culture)); 20706207(contaminants cell		0.378	0.369	26	not assigned.unknown

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName		
AT2G46150	gi15225931	unknown protein [Arabidopsis thaliana]	Unknown	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family				35.2 not assigned.unknown	35.2	1	1	C		Hin1(1) Transposase_25(1)	4	0.017	24.1	9.78	17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane		0	0	0	not assigned.unknown		
AT3G08600	gi18398173	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function (DUF1191)	unknown protein DUF538 domain			35.2 not assigned.unknown	35.2	1	1	M		Adeno_GP19K(1) DUF1191(1) GPS(1)	4	-0.092	34.73	9.58	17317660(Plasma Membrane proteome); 17644812(plasma membrane - suspension cells); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19106119(plasma membrane detergent		0.095	0.123	86	not assigned.unknown		
AT3G17350	gi15229029	unknown protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; BEST				35.2 not assigned.unknown	35.2		0	S				19	-0.082	33.58	5.83	19260003(detergent resistant plasma membrane (DRM) proteins (Cell cultures));		0	0	0	not assigned.unknown	
AT4G08760	gi15236604	unknown protein [Arabidopsis thaliana]	Unknown	BEST Arabidopsis thaliana protein match is: nucleolin like 1 (TAIR:AT1G48920.1); Has 36 Blast hits to 36 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0				35.2 not assigned.unknown	35.2		0	-					11	-0.507	58.89	9.49			0	0	0	not assigned.unknown
AT4G15950	gi28188681	unknown protein [Arabidopsis thaliana]	Unknown	RNA polymerase II, Rpb4, core protein				35.2 not assigned.unknown	35.2		0	-		RNA_poL_Rpb4(1)	5	-0.608	22.41	8.47			0	0	0	not assigned.unknown		
AT4G27595	gi1240256091	unknown protein [Arabidopsis thaliana]	Unknown	Plant protein of unknown function (DUF827)				35.1 not assigned.no ontology	35.1		0	C		ATG16(1) Cast(1) DUF1409(1) DUF724(1) DUF904(1) EzrA(1) Myosin_tail_1(1)	8	-0.884	138.95	5.04			0	0	0	not assigned.no ontology		
AT4G28100	gi18417127	unknown protein [Arabidopsis thaliana]	Unknown	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: anchored to plasma membrane, anchored to membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14			anchored to membrane	35.2 not assigned.unknown	35.2	1	2	S				16	0.044	33.1	8.93	14517339(GPI anchored suspension cells);		0	0	0	not assigned.unknown	
AT4G35730	gi79497106	unknown protein [Arabidopsis thaliana]	Unknown	Regulator of Vps4 activity in the MVB pathway protein			mitochondrion	35.2 not assigned.unknown	35.2		0	C		DUF292(1)	5	-0.741	52.2	8.13	MitoDB(Mitochondrial proteome); 19546170(mature		0	0	0	not assigned.unknown		
AT4G40020	gi15236102	unknown protein [Arabidopsis thaliana]	Unknown	Myosin heavy chain-related protein				35.2 not assigned.unknown	35.2		0	-		PTS_IIB fruc(1) Spb1_C(1)	4	-1.08	70.03	5.19	19546170(mature pollen grains);		0	0	0	not assigned.unknown		
AT5G06970	gi22326641	unknown protein [Arabidopsis thaliana]	Unknown	Protein of unknown function (DUF810)	unknown protein			35.2 not assigned.unknown	35.2		0	-		DUF810(1)	16	-0.287	124.53	5.88	19525416(leaf wt and clpr4-1 mutant); 19376835(leaf phosphoproteins)		0.015	0.015	355	not assigned.unknown		

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT5G19230	gi15239685	unknown protein [Arabidopsis thaliana]	Unknown	Glycoprotein membrane precursor GPI-anchored			anchored to membrane	35.2 not assigned.unknown	35.2	2	1	S		SCP(1)	6	0.244	20.51	5.85	12805588(GBI-anchored-callus); 17317660(Plasma Membrane proteome); 19260003(detergent resistant plasma membrane (DRM) proteins)		0	0	0	not assigned.unknown
AT5G19240	gi15239686	unknown protein [Arabidopsis thaliana]	Unknown	Glycoprotein membrane precursor GPI-anchored				35.2 not assigned.unknown	35.2		0	S			4	0.084	21.34	6.57	18436743(specific to leaves);		0	0	0	not assigned.unknown
AT5G28237	gi26452400	unknown protein [Arabidopsis thaliana]	Unknown	Pyridoxal-5'-phosphate-dependent enzyme family	tryptophan synthase, beta subunit, putative			35.1 not assigned.no ontology	35.1		0	M		PALP(1)	11	-0.169	50.65	6.58			0.054	0.057	223	not assigned.no ontology
AT5G42370	gi113430796	unknown protein [Arabidopsis thaliana]	Unknown	Calcineurin-like metallo-phosphoesterase superfamily protein				35.2 not assigned.unknown	35.2	1	1	S			8	-0.201	50.34	9.07			0	0	0	not assigned.unknown
AT5G56170	gi115241141	unknown protein [Arabidopsis thaliana]	Unknown	LORELEI-LIKE-GPI-ANCHORED PROTEIN 1			anchored to membrane	35.1 not assigned.no ontology	35.1		0	S			8	0.117	18.46	6.26			0	0	0	not assigned.no ontology
AT5G62630	gi114423506	Unknown protein [Arabidopsis thaliana]	Unknown	hipl2 protein precursor	HIPL2 (HIPL2 PROTEIN PRECURSOR); catalytic		anchored to membrane	35.2 not assigned.unknown	35.2		0	S		Metallothio_5(1)	28	-0.37	75.62	4.86	12805588(GBI-anchored-callus); 17317660(Plasma Membrane proteome);		0.029	0.033	437	not assigned.unknown
AT1G42470	gi112322632	unknown protein, 5' partial [Arabidopsis thaliana]	Unknown	Patched family protein				35.1 not assigned.no ontology	35.1	12	11	-		DUF805(1) Herpes_LMP2(1) Ion_trans(1) MARVEL(1) Patched(1) Trp_Tyr_perm(1)	48	0.183	140.09	7.8	17317660(Plasma Membrane proteome); 19546170(mature pollen grains); 19036721(detergent resistant plasma membrane (DRM) proteins (Cell cultures)); 19334764(plasma membrane (cell		0	0	0	not assigned.no ontology
AT1G69290	gi112325092	unknown protein; 45065-49536 [Arabidopsis thaliana]	Unknown	Pentatricopeptide repeat (PPR) superfamily protein				35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	35.1.5		0	C		PPR(4) RasGAP(1)	9	-0.133	73.89	7.57			0	0	0	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein
AT3G42170	gi112325234	unknown protein; 6859-4829 [Arabidopsis thaliana]	Unknown	BED zinc finger; hAT family dimerisation domain							0	-		ApoC-I(1) hATC(1) zf-BED(1)	14	-0.436	78.82	5.2			0.148	0.152	150	
AT2G15025	gi9294045	unnamed protein product [Arabidopsis thaliana]	Unknown	Beta-galactosidase related protein				35.2 not assigned.unknown	35.2			-			5	0.288	20.71	4.73			0	0	0	not assigned.unknown
AT5G22450	gi9757826	unnamed protein product [Arabidopsis thaliana]	Unknown	unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G19390.1); Has 30201 Blast hits				35.2 not assigned.unknown	35.2		0	C		Prog_receptor(1)	10	-0.731	126.09	8.97	19334764(plasma membrane (cell culture));		0.013	0.014	901	not assigned.unknown
AT5G58160	gi8777317	unnamed protein product [Arabidopsis thaliana]	Unknown	actin binding				35.1.20 not assigned.no ontology.formin homology 2 domain-containing	35.1.20	1	0	-		CAF1(1) Drf_FH1(1) FH2(1) PLU-1(1) PTEN_C2(1) STAG(1)	16	-0.386	146.47	6.62	19546170(mature pollen grains);		0	0	0	not assigned.no ontology.formin homology 2 domain-containing protein
AT5G39970	gi10176989	unnamed protein product [Arabidopsis thaliana]	Unknown	catalytics			anchored to membrane	35.1 not assigned.no ontology	35.1		0	S		DUF26(1)	28	-0.199	75.62	5.12			0	0	0	not assigned.no ontology
AT1G15780	gi112320923	wall-associated kinase, putative [Arabidopsis thaliana]	Unknown	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants -				35.2 not assigned.unknown	35.2		0	-		DUF1602(1) KIX(1)	5	-0.767	146.35	9.27	18814325(cotyledons);		0	0	0	not assigned.unknown

AGI accession	GI accession	Protein description	Functional categories	STD Annot.	Lab Annot.	Curated Loc.	TAIR Loc.	MapManBin	sep.MapManBin	Aramemnon	TMHMM	TargetP	Predotar	PFAM	Cys	Calc.gravy	Calc.MW	Calc.PI	ProteomicsPub.	GFP/YFP loc.	Coverage	Coverage_ctp	Coverage_start	sep.BinName
AT1G67270	gi240254330	Zinc-finger domain of monoamine-oxidase A repressor R1 protein [Arabidopsis thaliana]	Unknown	Zinc-finger domain of monoamine-oxidase A repressor R1 protein				35.2 not assigned.unknown	35.2		0	-		zf-4CXXC_R1(1)	22	-0.481	61.12	8.54			0.018	0.019	433	not assigned.unknown

Supplementary Table S3-2 Differentially expressed plasma membrane proteins between the lag and log phase

ATG	GI	Protein description	Functional categories	Peptide count	Peptides used	Confidence	Anova (p)	Log/Lag fold	Normalized abundance				Log phase			
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT2G34040	gi 18403429	Apoptosis inhibitory protein 5 (API5) [Arabidopsis thaliana]	Cell growth/division	5	5	113.26	0.028	5.707	52958.62	60572.25	300917.7	365282.3	1309203	946536.3	1023042	1171052
AT1G52540	gi 5903051	Contains PF00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from	Cell growth/division	2	2	82.03	0.002	4.944	12837.88	17326.71	21413.46	27366.25	93798.8	97193.19	105883.2	93392.13
AT1G29030	gi 10764848	F1K23.1 [Arabidopsis thaliana]	Cell growth/division	2	2	32.93	0.029	4.030	213668.4	261794.4	332150	452402.8	1661747	1409326	1324452	682656.3
AT1G52740	gi 15219078	histone H2A protein 9 [Arabidopsis thaliana]	Cell growth/division	1	1	29.6	0.012	3.804	21384.85	30613.95	37642.25	51841.07	142356.1	140548.3	152446.2	102888.6
AT5G22880	gi 1617013	histone H2B like protein [Arabidopsis thaliana]	Cell growth/division	1	1	16.44	0.002	4.396	23148.18	24537.72	18689.89	21642.26	116997.3	120102.8	90691.89	59138.02
AT1G18680	gi 15221835	HNH endonuclease domain-containing protein [Arabidopsis thaliana]	Cell growth/division	1	1	20.28	0.029	4.001	213541.3	261572.2	331641.9	450478.8	1642470	1395684	1313966	677659.1
AT3G51690	gi 4895169	putative helicase [Arabidopsis thaliana]	Cell growth/division	3	3	36.97	0.003	3.659	185223	214788.3	114683.9	134093.5	523209.3	693224.4	642946.9	514471.9
AT3G49670	gi 15229189	receptor-like kinase BAM2 [Arabidopsis thaliana]	Cell growth/division	3	3	74.68	0.005	1.546	429839.5	343814.7	394539	399005.7	582478.5	546722.6	577901.5	716155.1
AT1G08130	gi 8778834	T6D22.23 [Arabidopsis thaliana]	Cell growth/division	1	1	16.58	0.002	8.712	52634.63	58384.37	31337.25	28002.79	362556.7	346878.8	431060.3	343620.7
AT3G45600	gi 15231187	tetraspanin3 [Arabidopsis thaliana]	Cell growth/division	2	2	115.08	0.034	1.575	80095.69	39587.33	36354.55	42737.92	91923.85	62201.85	75445.04	83586.89
AT2G23810	gi 13272397	unknown protein [Arabidopsis thaliana]	Cell growth/division	4	4	149.58	0.002	3.614	124292.2	195735	178931.5	207397.6	670017.1	632354.7	640062.4	610221.5
AT5G64940	gi 8843758	ABC transporter-like [Arabidopsis thaliana]	Cell structure	1	1	16.15	0.021	0.134	648197.3	444863	285371.3	219497.9	28844.14	55859.66	40291.64	89451
AT5G09810	gi 15242516	actin 7 [Arabidopsis thaliana]	Cell structure	2	2	129.25	0.045	0.466	432766.5	583271.4	322770	311244	174283.1	169655.4	157914.6	266868
AT1G35720	gi 142920	annexin [Arabidopsis thaliana]	Cell structure	5	5	170.74	0.006	12.162	11029.35	11991.79	36273.61	50842.49	347230.1	314655.4	314792.9	362766
AT1G35720	gi 222424855	AT1G35720 [Arabidopsis thaliana]	Cell structure	3	3	67.41	0.000	4.557	224858.4	259814.7	258078.9	230963	1111686	1112867	1189944	1022820
AT1G66250	gi 12323569	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis thaliana]	Cell structure	3	3	80.13	0.010	0.173	108319.5	244265.1	489473.4	202174.2	31374.33	64362.71	41939.4	43446.7
AT3G47050	gi 15232713	beta-glucosidase [Arabidopsis thaliana]	Cell structure	2	2	89.76	0.022	1.742	72817.01	124733.1	90876.34	88418	172481.1	162875	180319.1	140845.2
AT1G62790	gi 15221585	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	Cell structure	1	1	25.14	0.008	19.845	200.0622	447.2628	634.0794	1109.134	13465.83	14259.74	12644.09	7070.32
AT5G20230	gi 16203	blue copper-binding protein [Arabidopsis thaliana]	Cell structure	2	2	120.02	0.002	6.229	37212.9	32888.91	39676.24	45706.89	301278.5	240075	261630.8	165582.9
AT2G03505	gi 22325443	carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	Cell structure	1	1	24.57	0.040	22.266	115.6664	437.8718	352.0099	1171.191	15865.03	14907.54	13332.88	2136.021
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	Cell structure	1	1	43.29	0.021	11.085	421.6592	339.6749	3654.146	2503.688	21589.96	19635.06	17552.66	17923.09

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT5G53870	gi 15238868	early nodulin-like protein 1 [Arabidopsis thaliana]	Cell structure	3	3	52.49	0.025	8.049	38693.34	27358.82	120770.3	153631.3	1014531	685424.4	519189.5	521023.5
AT4G31840	gi 15236544	early nodulin-like protein 15 [Arabidopsis thaliana]	Cell structure	1	1	62.17	0.045	2.804	34952.18	84729.85	102901.9	140391.9	289826.4	256611.4	229935.3	241323.5
AT4G27520	gi 15234164	early nodulin-like protein 2 [Arabidopsis thaliana]	Cell structure	2	2	166.95	0.024	5.939	16470.17	31271.25	108603.3	122275.1	413137.2	410144	357285.2	474053.6
AT1G75680	gi 15222328	endoglucanase 10 [Arabidopsis thaliana]	Cell structure	1	1	50.5	0.040	0.661	275171.1	294910.5	188025	197639.6	138560.8	188857.3	165202.9	139338.1
AT1G74790	gi 5882745	F25A4.24 [Arabidopsis thaliana]	Cell structure	9	9	400.44	0.019	3.164	813898.7	1201352	1851973	2204543	5423506	4581272	4884219	4319354
AT1G01980	gi 15217586	FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	Cell structure	4	4	94.32	0.003	3.237	148367.1	225179.8	227196.6	279152.8	732708.5	654805.5	716475	744518.1
AT5G55730	gi 15240570	fasciclin-like arabinogalactan protein 1	Cell structure	2	2	164.48	0.014	1.983	2113567	2038306	1441616	1499307	3293015	3321055	3456631	3992506
AT5G44130	gi 15241423	fasciclin-like arabinogalactan protein 13 [Arabidopsis thaliana]	Cell structure	4	4	129.41	0.001	3.940	210258.8	249471.5	149175.1	158467	696453.9	853078.1	782401.7	691725.2
AT2G45470	gi 18406799	FASCICLIN-like arabinogalactan protein 8 [Arabidopsis thaliana]	Cell structure	5	5	304.63	0.003	1.808	1013088	780897.3	669354	829650.3	1536464	1419989	1382891	1613168
AT1G03870	gi 18379157	fasciclin-like arabinogalactan protein 9	Cell structure	4	4	230.68	0.012	2.692	1596383	1322134	728189.1	611410.4	2931175	3210902	3115501	2206867
AT4G12730	gi 13377778	fasciclin-like arabinogalactan-protein 2	Cell structure	9	9	406.93	0.000	2.433	3018998	2870243	2833070	2705210	7342547	6160291	6885888	7414654
AT2G33120	gi 600710	formerly called HAT24; synaptobrevin-related protein [Arabidopsis	Cell structure	2	2	118.79	0.025	1.884	108814.2	159471.7	186461.1	230720.8	325136.1	309761.4	336859.2	319506.8
AT1G29660	gi 15220512	GDSL esterase/lipase [Arabidopsis thaliana]	Cell structure	1	1	26.96	0.014	10.203	6247.002	10167.16	28826.29	30184.66	258318.5	168098.3	196884.4	146226.3
AT5G42100	gi 15238298	glucan endo-1,3-beta-glucosidase 10 [Arabidopsis thaliana]	Cell structure	2	2	87.49	0.017	0.262	341289.6	217844.9	100744.3	145444.1	51649.77	58705.26	53386.31	46877.02
AT2G01630	gi 18379267	glucan endo-1,3-beta-glucosidase 3 [Arabidopsis thaliana]	Cell structure	1	1	65.88	0.047	4.588	2103.663	3226.936	9534.79	15334.46	40418.96	37907.57	34661.22	25573.26
AT4G28365	gi 7485901	hypothetical protein F20O9.30 - Arabidopsis	Cell structure	1	1	22.48	0.013	2.529	12360139	12721040	38681522	37203069	51376047	43740644	66001088	94262265
AT5G15350	gi 15242279	Lamin-like protein [Arabidopsis thaliana]	Cell structure	2	2	57.14	0.038	2.669	370314	465443.1	1102406	1353406	2266263	2083059	2230440	2203959
AT5G51480	gi 15242108	Monocopper oxidase-like protein SKS2 [Arabidopsis thaliana]	Cell structure	3	3	108.53	0.011	2.275	131477.2	181613.5	250739.2	266713.2	472611.1	432712.2	455591.3	528223.8
AT2G13820	gi 15225509	Non-specific lipid-transfer protein-like protein [Arabidopsis thaliana]	Cell structure	2	2	45.72	0.030	3.299	31303.67	49336.56	104438.9	144826.2	268522.8	278055.4	279486	262269.1
AT1G53840	gi 15220958	pectinesterase 1 [Arabidopsis thaliana]	Cell structure	3	3	101.13	0.007	3.493	83137.28	86295.08	61089.25	87773.41	299857.3	318480.6	311332.2	182250.7
AT5G17820	gi 15238030	peroxidase 57 [Arabidopsis thaliana]	Cell structure	1	1	40.85	0.035	3.083	46444.5	21155.72	6916.314	7029.876	71547.28	76612.85	67649.78	35617.03

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT4G28300	gi 7269684	predicted proline-rich protein [Arabidopsis	Cell structure	1	1	18.02	0.023	2.547	43618.12	45371.82	98817.75	116224.2	191295.2	183026.9	201770.7	198280
AT4G21450	gi 3080389	putative membrane associated protein	Cell structure	2	2	56.94	0.004	2.883	38346.8	56585.77	63436.81	69039.37	161794.6	169605.7	155806.2	168500.4
AT4G34830	gi 5123699	putative protein [Arabidopsis thaliana]	Cell structure	1	1	25.46	0.025	2.960	205542.8	188611.5	375627.3	384991.9	1124967	769096.6	873607.5	650760.6
AT4G00340	gi 75319455	RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase SD2-2; AltName: Full=Receptor-like kinase 4; AltName: Full=S-domain-2 (SD2) receptor kinase 2; Short=SD2-2; Flags:	Cell structure	4	4	88.12	0.012	2.326	158994.1	126918.1	204810.4	239807.7	458648.1	424579.2	424630.5	391694.3
AT4G20830	gi 30685222	Reticuline oxidase-like protein [Arabidopsis	Cell structure	24	24	679.12	0.000	2.818	1301968	1337389	1355050	1409439	3917834	3506996	3696122	4106231
AT2G21280	gi 18399648	Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis	Cell structure	1	1	27.29	0.032	5.948	1669.985	3236.029	11963.29	14211.88	46788.52	50341.6	51905.99	35846.26
AT2G25060	gi 4559346	similar to early nodulins [Arabidopsis thaliana]	Cell structure	3	3	170.36	0.006	2.184	130191.8	197627.8	224740.3	271341.8	388581.5	401420.5	390241.9	619108.3
AT3G52400	gi 5701797	syntaxin protein [Arabidopsis thaliana]	Cell structure	2	2	115.25	0.007	4.070	31836.04	49603.6	64195.42	83038.04	241346.7	226816.1	238835.9	223619.8
AT3G11820	gi 15229865	syntaxin-121 [Arabidopsis thaliana]	Cell structure	5	5	195.76	0.012	4.679	62830.39	86531.84	155546.8	193818.1	679802.1	553447.6	560588.2	539698.4
AT3G09740	gi 18398623	syntaxin-71 [Arabidopsis thaliana]	Cell structure	7	7	215.59	0.001	1.535	605018.7	643478.4	495455.1	564672.9	962077.6	926763.7	826801.8	828831.2
AT1G04820	gi 15220329	tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana]	Cell structure	2	2	63.05	0.015	0.170	47990.61	49323.76	31720.59	44962.14	2734.968	5328.811	4229.923	17238.04
AT5G19770	gi 15241168	tubulin alpha-3/alpha-5 chain [Arabidopsis thaliana]	Cell structure	2	2	25.06	0.020	0.252	33917.1	19389.08	19641.68	20917.3	4122.882	3012.154	8473.985	8088.226
AT5G04885	gi 26451217	unknown protein [Arabidopsis thaliana]	Cell structure	7	7	284.06	0.001	1.591	477803.6	391107.8	471661.5	473768.5	780003.1	592947.4	699975.4	813624
AT3G03790	gi 6006862	unknown protein [Arabidopsis thaliana]	Cell structure	5	5	39.08	0.016	2.467	1016979	1095295	2090587	2376454	4266656	3479544	4055561	4432227
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	12	12	395.95	0.000	10.559	223307	270253.6	220628	260299.5	2842021	2519789	2709660	2218034
AT5G64080	gi 10176956	unnamed protein product [Arabidopsis thaliana]	Cell structure	1	1	51.59	0.030	5.498	13149.4	17500.5	86036.58	130748.3	319201.9	338383.4	297996.2	404744.4
AT2G27130	gi 18401329	xylogen-like protein 11 [Arabidopsis thaliana]	Cell structure	1	1	41.42	0.027	7.450	2191.367	3441.621	8496.1	11103.82	49303.24	54888.38	60694.89	23110.02
AT4G01700	gi 15234281	class II chitinase-like protein [Arabidopsis	Disease/defence	9	9	733.58	0.000	14.211	2671078	4206820	3051041	3304807	54669743	49710945	49863172	33820364
AT4G02600	gi 15235429	MLO-like protein 1 [Arabidopsis thaliana]	Disease/defence	2	2	39.87	0.005	0.461	125238	142371.6	98504.79	108269.7	58438.85	53818.11	40334.28	66010.22
AT2G43610	gi 15224319	putative chitinase [Arabidopsis thaliana]	Disease/defence	3	3	110.13	0.002	77.206	2477.167	4002.407	1896.466	2411.269	195596.8	336609.2	248884.3	51749.82
AT2G32680	gi 15225727	receptor like protein 23 [Arabidopsis thaliana]	Disease/defence	1	1	21.91	0.000	0.209	96182.48	169470.1	106323.4	141921.6	18355.78	41829.77	20096.71	27072.27

ATG	GI	Protein description	Functional categories	Peptide count	Peptides used	Confidence	Anova (p)	Log/Lag fold	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Lag 1	Lag 2	Lag 3	Lag 4
AT4G19530	gi 15235064	TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	Disease/defence	1	1	22.01	0.044	9.567	632.6529	1061.78	1288.382	4460.442	20208.45	25340.12	19661.68	5998.454
AT4G32840	gi 15233959	6-phosphofructokinase 6 [Arabidopsis thaliana]	Energy	2	2	28.72	0.024	0.619	30146.05	40837.59	29756.73	34114.6	23875.44	23490.03	20199.16	15914.19
ATCG00120	gi 7525018	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	Energy	3	3	88.54	0.002	15.731	2574.548	1796.368	5787.923	3944.197	52626.12	59534.61	71551.7	38148.66
AT2G36530	gi 15227987	bifunctional enolase 2/transcriptional activator [Arabidopsis thaliana]	Energy	3	3	67.87	0.003	3.236	32446.86	40977.98	55329.57	67687.84	160045.4	139274.6	150185	186195.3
AT3G55440	gi 414550	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	Energy	2	2	56.79	0.015	6.220	8407.057	12745.97	33310.36	42673.11	146973.9	156525.5	171119.2	129616.5
AT1G79550	gi 15219412	phosphoglycerate kinase [Arabidopsis thaliana]	Energy	1	1	43.79	0.016	0.059	175585.5	102802.8	34711.16	67918.15	1559.269	11960.37	2702.22	6433.028
AT5G08680	gi 22326673	ATP synthase subunit beta-3 [Arabidopsis thaliana]	Intracellular traffic	2	2	25.7	0.007	0.139	47479.05	38854.66	27565.43	28345.97	3386.576	3878.007	4822.661	7714.578
AT5G17920	gi 15238686	5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase [Arabidopsis thaliana]	Metabolism	10	10	321.93	0.020	0.248	1076153	888861	593390.8	563805.4	135429.8	179083.7	142740.3	316277.5
AT2G38280	gi 18404701	AMP deaminase [Arabidopsis thaliana]	Metabolism	1	1	22.27	0.034	3.367	62330.48	96232.63	272852.5	264349	609346.8	572880.3	557870.5	602470.2
AT5G64370	gi 9759413	beta-ureidopropionase [Arabidopsis thaliana]	Metabolism	1	1	38.67	0.041	9.104	3507.056	2941.645	3494.09	1246.94	10140.09	16081.02	19471.31	56183.24
AT4G35790	gi 7486399	hypothetical protein F4B14.60 - Arabidopsis thaliana	Metabolism	3	3	118.68	0.005	5.878	6552.449	11079.45	20230.65	24115.58	77429.74	92726.5	101094.6	93063.03
AT5G20980	gi 30688090	methionine synthase 3 [Arabidopsis thaliana]	Metabolism	3	3	57.84	0.039	0.352	179663.6	186856.6	152810.4	135566.7	26965.93	56273.73	49033.09	98497.28
AT4G09320	gi 16396	nucleoside diphosphate kinase [Arabidopsis thaliana]	Metabolism	1	1	67.28	0.039	0.211	465.7005	681.571	2778.259	5235.744	0	0	0	1928.938
AT3G03780	gi 14532772	putative methionine synthase [Arabidopsis thaliana]	Metabolism	7	7	233.32	0.029	0.455	478057.9	459006.7	455297.8	413522.5	147337.6	189309.8	156654.5	328242.8
AT4G27270	gi 3269288	putative protein [Arabidopsis thaliana]	Metabolism	1	1	35.49	0.019	2.859	7659.234	10892.37	20429.05	28089.22	43213.69	46723.47	44044.85	57798.55
AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	Metabolism	5	5	215.73	0.008	2.577	358076.1	565136.4	654257.9	755910.9	1476676	1338094	1329234	1868179
AT4G36750	gi 15234512	Quinone reductase family protein [Arabidopsis thaliana]	Metabolism	3	3	206.97	0.000	2.591	74853.87	79164.67	75407.17	85751.01	207086.7	194615.3	189780.9	225148.4
AT1G32440	gi 8920620	Strong similarity to a pyruvate kinase isozyme G, chloroplast precursor from Nicotiana tabacum gb Z28374. It contains a pyruvate kinase domain PF 00224. EST gb AI996399 comes from this gene	Metabolism	2	2	26.56	0.000	2.239	1474455	1406151	1553994	1370670	3731270	2846779	3388719	3029292
AT1G73370	gi 15219457	sucrose synthase 6 [Arabidopsis thaliana]	Metabolism	2	2	24.66	0.021	28.675	1375.226	1873.792	23063.44	25204.23	469956.3	379282.7	408983.9	219023.8



ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT1G66980	gi 9755449	Unknown protein [Arabidopsis thaliana]	Metabolism	2	2	86.4	0.014	3.061	154364.6	266629	404551.9	409495.9	942512.8	811925.9	837172.6	1188332
AT3G02740	gi 15232960	aspartyl protease-like protein [Arabidopsis	Protein destination and storage	2	2	58.14	0.003	2.429	59155.69	69765.1	93423.18	101621.3	196111.4	167797.4	210795.9	212075.5
AT3G52500	gi 16209647	AT3g52500/F22O6_120 [Arabidopsis thaliana]	Protein destination and storage	4	4	118.75	0.004	2.509	192587.5	135629.1	183810.4	169113.8	419671.2	432643.3	366283.7	490448.3
AT5G58870	gi 18424166	cell division protease ftsH-9 [Arabidopsis thaliana]	Protein destination and storage	1	1	31.28	0.004	2.199	249195.4	325987.7	249087.6	289860.6	682329.3	670597.2	596053.1	501516.3
AT1G05840	gi 6850312	Contains similarity to nucellin from Hordeum vulgare gb U87148. ESTs gb T22068, gb F14251, gb F14237, gb F14242 come from this gene [Arabidopsis	Protein destination and storage	1	1	44.99	0.014	8.926	3975.65	7165.984	16040.71	23670.27	108005.7	128607.8	137992.1	79304.85
AT4G12570	gi 15235410	E3 ubiquitin-protein ligase UPL5 [Arabidopsis	Protein destination and storage	3	3	28.41	0.015	2.598	16093.97	23825.61	48319.9	46447.68	71391.63	75005.28	79973.24	123540.1
AT1G63500	gi 6633851	F2K11.13 [Arabidopsis thaliana]	Protein destination and storage	3	3	90.5	0.008	2.822	21316.87	33838.12	37896.07	45495.94	90725.95	106365.7	107189.3	86650.22
AT1G56410	gi 15223533	heat shock protein-70 cognate protein	Protein destination and storage	1	1	21.34	0.012	0.149	31915.63	51778.36	17130.55	19954.12	2701.899	4932.462	2209.139	8126.091
AT1G69840	gi 15222481	Hypersensitive-induced response protein 2 [Arabidopsis thaliana]	Protein destination and storage	12	12	536.28	0.003	4.195	489122.3	680756	944421	1046410	3445288	3079490	3135914	3598683
AT3G63260	gi 15229398	protein kinase family protein [Arabidopsis	Protein destination and storage	5	5	136	0.024	4.447	19315.13	29771.25	78834.71	89059.65	248251.1	248451.8	256242.2	211981.1
AT3G22750	gi 18403507	protein kinase family protein [Arabidopsis	Protein destination and storage	2	2	28.62	0.016	5.598	51300.94	63783.6	157808.8	181492.1	799771.2	568021.5	626311.1	549622.3
AT3G46140	gi 15231346	protein kinase-related protein [Arabidopsis	Protein destination and storage	1	1	24.66	0.001	0.147	2691515	3040726	2457192	2205566	372878.5	346157.4	285747	520735.9
AT2G03530	gi 4335747	putative integral membrane protein [Arabidopsis	Protein destination and storage	1	1	47.36	0.041	8.658	735.7644	1271.214	7498.06	8268.515	54751.03	36356.68	39600.07	23177.26
AT4G35230	gi 3080427	putative protein [Arabidopsis thaliana]	Protein destination and storage	3	3	84.79	0.023	3.821	29821.82	54646.97	90198.76	121635.4	287999.7	299650	303594.6	240897.9
AT4G13190	gi 4753653	putative protein [Arabidopsis thaliana]	Protein destination and storage	2	2	44.7	0.036	3.307	32211.45	45435.09	120427.5	154132.3	316535.6	264536.3	281892.5	301612.6
AT3G53780	gi 7629998	putative protein [Arabidopsis thaliana]	Protein destination and storage	1	1	51.82	0.022	2.863	1954.992	4731.034	2036.559	4973.248	11502.5	8705.995	7564.863	11438.77
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	2	2	49.63	0.020	4.060	13385.31	14927.02	36168.97	41646.07	128339	99899.29	101624	101013.3
AT1G34750	gi 15218759	putative protein phosphatase 2C 10 [Arabidopsis	Protein destination and storage	3	3	65.7	0.033	3.703	9600.543	18171.47	27599	35538.62	95980.04	92642.26	88105.44	59929.45
AT1G22280	gi 18395099	putative protein phosphatase 2C 9 [Arabidopsis thaliana]	Protein destination and storage	3	3	110.72	0.014	6.984	3095.811	5248.77	13167.96	18557.78	70077.53	69608.31	75574.72	64601.26
AT3G17410	gi 22331138	putative serine/threonine protein kinase [Arabidopsis thaliana]	Protein destination and storage	4	4	164.75	0.006	4.406	52538.14	54726.6	92897.44	112833.4	384838.3	323148.1	355541	315675.6
AT1G55490	gi 15222729	RuBisCO large subunit-binding protein subunit beta [Arabidopsis thaliana]	Protein destination and storage	1	1	17.14	0.027	2.980	280032.6	254009.8	860443.3	879161.5	1756775	1454989	1718562	1845596
AT1G61360	gi 15219912	S-like receptor protein kinase [Arabidopsis	Protein destination and storage	2	2	59.41	0.022	3.148	15926.33	22572.03	44712.35	60307.4	114332.3	103732.2	116730.9	116984.8

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT2G05920	gi 18396193	Subtilase-like protein [Arabidopsis thaliana]	Protein destination and storage	5	5	130.18	0.014	1.991	191591.3	354549.5	230682	277079.6	540353.4	544450.5	534927.5	478326.5
AT1G01740	gi 15223469	tetratricopeptide repeat domain-containing protein kinase [Arabidopsis	Protein destination and storage	1	1	40.56	0.033	4.094	1889.974	2256.964	3229.08	6239.215	15174.25	15036.53	16834.29	8689.442
AT5G57950	gi 9758364	unnamed protein product [Arabidopsis thaliana]	Protein destination and storage	1	1	27.75	0.007	2.562	1080774	1106906	2942676	2999444	3854254	3723336	5277108	7972695
AT5G23720	gi 10176839	unnamed protein product [Arabidopsis thaliana]	Protein destination and storage	2	2	20.37	0.006	2.674	1254915	1017619	2598934	2356251	4399433	3669783	4890634	6367129
AT4G00330	gi 6049872	weak similarity to receptor protein kinase [Arabidopsis thaliana]	Protein destination and storage	2	2	33.72	0.014	5.367	19612.43	25735.26	57411.9	70490.44	264130.6	227365.8	222269.3	215991.2
AT2G36160	gi 15227588	40S ribosomal protein S14-1 [Arabidopsis thaliana]	Protein synthesis	2	2	72.33	0.017	7.825	4129.583	5123.661	9042.835	16005.54	85108.18	70640.35	70653.3	42007.01
AT3G11510	gi 15229775	40S ribosomal protein S14-2 [Arabidopsis thaliana]	Protein synthesis	2	2	85.01	0.015	6.910	8626.703	11790.22	19919.91	27531.49	150230.3	121006.2	121740.8	75986.27
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	Protein synthesis	2	2	85.95	0.030	1.689	312381.1	230588.1	415411.5	490318	599922.4	582370.4	620810.9	643950.1
AT3G04230	gi 15229252	40S ribosomal protein S16-2 [Arabidopsis thaliana]	Protein synthesis	2	2	41.99	0.009	3.802	31594.17	17930.36	39090.5	32832.41	140166.4	124633.8	111877.3	85087.31
AT2G04390	gi 15228141	40S ribosomal protein S17-1 [Arabidopsis thaliana]	Protein synthesis	8	8	300.06	0.001	2.798	1854488	1737759	1917029	2076402	6199698	5219279	5048004	4760261
AT3G02080	gi 15232844	40S ribosomal protein S19-1 [Arabidopsis thaliana]	Protein synthesis	4	4	95.75	0.004	10.811	24794.94	30374.58	47655.93	58944.22	537987.2	441543.9	438953.6	330461.6
AT5G61170	gi 15240154	40S ribosomal protein S19-3 [Arabidopsis thaliana]	Protein synthesis	3	3	50.96	0.007	10.269	11102.81	17301.45	32745.88	40500.81	309238.1	265626.9	270738.6	198284
AT2G41840	gi 15227443	40S ribosomal protein S2-3 [Arabidopsis thaliana]	Protein synthesis	2	2	55.5	0.027	6.819	2713.972	4643.715	9901.716	15566.49	71803.61	62313.17	51350.67	38360.19
AT5G02960	gi 15242574	40S ribosomal protein S23-2 [Arabidopsis thaliana]	Protein synthesis	3	3	98.15	0.002	3.488	171289.8	110790	122560.3	96682.82	475764.1	503510.8	488629.4	280771.4
AT3G04920	gi 15229845	40S ribosomal protein S24-1 [Arabidopsis thaliana]	Protein synthesis	3	3	108.52	0.000	9.242	403829.1	263584.7	188274.5	142165	2886338	2625763	2479799	1229837
AT5G28060	gi 15241125	40S ribosomal protein S24-2 [Arabidopsis thaliana]	Protein synthesis	1	1	62.95	0.032	3.645	226938.9	224997	46361.15	76129.65	597448.5	648301.6	602914	245020.7
AT2G21580	gi 15226590	40S ribosomal protein S25-2 [Arabidopsis thaliana]	Protein synthesis	4	4	160.71	0.000	5.744	898587.2	741361.1	631022.4	708536	5291492	4230975	4333354	3259046
AT4G34555	gi 18418472	40S ribosomal protein S25-3 [Arabidopsis thaliana]	Protein synthesis	5	5	279.38	0.001	6.107	1011282	875822.4	787990.2	921066.4	6767679	5459774	5701618	4033777
AT4G39200	gi 15234970	40S ribosomal protein S25-4 [Arabidopsis thaliana]	Protein synthesis	6	6	301.65	0.001	6.153	1015104	884244	807493.8	948433.2	6954403	5595632	5829425	4112557
AT2G40510	gi 15226694	40S ribosomal protein S26-2 [Arabidopsis thaliana]	Protein synthesis	2	2	114.52	0.032	5.410	10607.6	19208.16	40110.68	60651.21	209186.9	195085	177213.9	124976.7
AT1G23410	gi 15220742	40S ribosomal protein S27a-1 [Arabidopsis thaliana]	Protein synthesis	2	2	56.52	0.039	3.248	44675.65	65226.58	194621.3	242091.4	469915.6	363592.3	361269.7	580816.8
AT2G31610	gi 15225107	40S ribosomal protein S3-1 [Arabidopsis thaliana]	Protein synthesis	5	5	197.91	0.020	4.306	67013.58	106500.8	210111.5	238275.7	796038.6	614426	660818.8	606701.2
AT4G34670	gi 15236171	40S ribosomal protein S3a-2 [Arabidopsis thaliana]	Protein synthesis	4	4	110.7	0.002	3.118	239242.7	318137.6	163658.6	206433.1	778114.7	887508.4	704499.1	521772.4
AT4G31700	gi 15236042	40S ribosomal protein S6-1 [Arabidopsis thaliana]	Protein synthesis	1	1	23.96	0.037	4.725	1487.26	1917.338	2961.559	6414.409	9748.699	20761.62	21130.27	8751.215

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT5G20290	gi 15241316	40S ribosomal protein S8-1 [Arabidopsis thaliana]	Protein synthesis	5	5	289.42	0.001	11.593	19660.4	20258.88	24783.64	21886.91	297780.9	290237.8	261622.1	154163.9
AT5G39850	gi 15242498	40S ribosomal protein S9-2 [Arabidopsis thaliana]	Protein synthesis	3	3	80.41	0.008	5.979	9436.346	12139.25	17484.42	23125.27	100344.5	105015.9	99009.47	67434.81
AT2G37190	gi 15228098	60S ribosomal protein L12-1 [Arabidopsis thaliana]	Protein synthesis	2	2	76.69	0.010	2.052	58386.4	92619.57	66487.64	70980.75	165531	144060.6	128205.2	154215
AT4G27090	gi 15236981	60S ribosomal protein L14-2 [Arabidopsis thaliana]	Protein synthesis	4	4	188.62	0.017	8.121	28894.47	40781.02	91011.45	106324.3	690077.9	591103.3	561943.6	325385.3
AT1G29970	gi 12324168	60S ribosomal protein L18A, putative; 23187-20334 [Arabidopsis	Protein synthesis	2	2	48.47	0.005	0.035	120381.7	146908.1	15473.45	34599.18	2403.58	4870.381	2267.234	1681.888
AT3G05560	gi 15230008	60S ribosomal protein L22-2 [Arabidopsis thaliana]	Protein synthesis	3	3	81.15	0.011	7.180	21473.9	24692.51	57496.82	78545.15	409128.2	302137.6	316806.7	280093.8
AT5G27770	gi 15241051	60S ribosomal protein L22-3 [Arabidopsis thaliana]	Protein synthesis	3	3	68.89	0.011	7.671	20987.21	26243.39	54804.27	71221.92	425167.3	321267.8	310315.5	272333.1
AT3G53020	gi 15231730	60S ribosomal protein L24-2 [Arabidopsis thaliana]	Protein synthesis	2	2	112.26	0.019	0.282	4055084	4162440	1417316	1337998	996307.8	763498.1	736282.3	599303.3
AT3G49910	gi 15229631	60S ribosomal protein L26-1 [Arabidopsis thaliana]	Protein synthesis	5	5	171.49	0.009	18.268	11204.78	2944.953	9622.362	11076.33	187764.5	202972.7	171868	74015.92
AT2G19730	gi 15224835	60S ribosomal protein L28-1 [Arabidopsis thaliana]	Protein synthesis	5	5	193.15	0.018	2.339	673794	1185455	1148065	1375140	2793664	2347849	2609751	2499715
AT5G56710	gi 15241902	60S ribosomal protein L31-3 [Arabidopsis thaliana]	Protein synthesis	1	1	34	0.026	6.116	7341.346	13002.74	24118.15	29189.07	168093.6	93779.29	112216	76352.84
AT4G18100	gi 15236757	60S ribosomal protein L32-1 [Arabidopsis thaliana]	Protein synthesis	4	4	77.53	0.011	8.026	33000.56	22637.68	20446.77	35603.95	281693.4	273702	247474.9	93600.44
AT3G55170	gi 15233198	60S ribosomal protein L35-3 [Arabidopsis thaliana]	Protein synthesis	2	2	84.29	0.027	3.887	235098	281019.3	358489	482922.1	1693264	1450382	1387948	744831.5
AT2G43460	gi 15224284	60S ribosomal protein L38 [Arabidopsis thaliana]	Protein synthesis	1	1	79.48	0.001	2.609	193637.2	166359	162162	151346.8	465753.3	405055.5	410615.2	475921.7
AT5G02870	gi 186519603	60S ribosomal protein L4-2 [Arabidopsis thaliana]	Protein synthesis	3	3	25.02	0.013	0.352	358974.8	336565.3	190596.9	196130.4	82673.2	104557.5	95671.73	98275.48
AT2G01250	gi 15226212	60S ribosomal protein L7-2 [Arabidopsis thaliana]	Protein synthesis	6	6	108.79	0.009	2.320	242093.8	270909.5	205782.8	198265.8	600856.5	592781.4	617581.6	316509.9
AT3G13580	gi 15231288	60S ribosomal protein L7-4 [Arabidopsis thaliana]	Protein synthesis	3	3	112.54	0.006	6.710	59649.9	43445.56	19861.54	25301.91	298305.3	290890	296453.3	109176.7
AT1G33120	gi 18398753	60S ribosomal protein L9-1 [Arabidopsis thaliana]	Protein synthesis	6	6	168.79	0.003	3.736	207430.9	243589.1	293646	278808.5	1140705	958462.5	980647.1	744269.9
AT4G10450	gi 15235114	60S ribosomal protein L9-2 [Arabidopsis thaliana]	Protein synthesis	5	5	108.15	0.022	4.588	61425.06	71400.36	225188.5	226064.6	767500	634965.2	685118.9	592050.2
AT5G58420	gi 17979233	AT5g58420/mqj2_10 [Arabidopsis thaliana]	Protein synthesis	4	4	50.49	0.006	3.788	69964.61	68392.12	158611.6	163063.8	427240.2	387519.5	457034.4	470876.3
AT5G60390	gi 295789	elongation factor 1-alpha [Arabidopsis thaliana]	Protein synthesis	4	4	101.56	0.005	1.649	259664.3	261940.4	227867	256683.6	429126.1	378188.8	352538	499753.8
AT1G27400	gi 9802532	F17L21.19 [Arabidopsis thaliana]	Protein synthesis	1	1	29.69	0.041	3.670	17659.64	28260.75	39926.7	70309.19	180849.1	147834.6	141565.9	102789.1
AT1G5898	gi 656627	RF12 [Arabidopsis thaliana]	Protein synthesis	2	2	53.99	0.005	3.305	21863.93	22437.89	17422.86	24192	84256.55	81036.7	69468.47	49160.91
AT3G48930	gi 166867	ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]	Protein synthesis	1	1	37.64	0.044	9.567	632.6529	1061.78	1288.382	4460.442	20208.45	25340.12	19661.68	5998.454
AT3G60770	gi 7329687	ribosomal protein S13-like [Arabidopsis thaliana]	Protein synthesis	4	4	115.94	0.009	5.320	68663.68	80185.61	107249.9	131340.1	637058.6	530010.1	556785.4	337166.2

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT3G61110	gi 6850878	ribosomal protein S27 [Arabidopsis thaliana]	Protein synthesis	1	1	23.32	0.015	3.606	1046.045	847.8239	2357.831	2394.504	5731.027	6271.387	6138.965	5821.672
AT5G10360	gi 2224751	ribosomal protein S6 [Arabidopsis thaliana]	Protein synthesis	1	1	27.52	0.042	17.779	282.911	729.8724	1528.406	1770.974	30029.58	21670.27	21413.12	3553.394
AT1G22780	gi 13877525	S18.A ribosomal protein [Arabidopsis thaliana]	Protein synthesis	6	6	306.95	0.005	2.579	693741.7	767979.6	660495.8	763903.7	2095734	2081636	1927734	1337340
AT1G07960	gi 1532175	similar to protein disulfide isomerase [Arabidopsis thaliana]	Protein synthesis	1	1	21.49	0.040	2.659	41180.83	52901.26	120316.8	141567.7	270199.9	182404	284354.7	209402.2
AT4G00100	gi 3193323	similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]	Protein synthesis	4	4	126.65	0.007	5.087	66769.41	78508.82	103487.6	124845.7	569978.6	487096	517158.5	326172.6
AT4G02230	gi 337779	T2H3.3 [Arabidopsis]	Protein synthesis	1	1	22.96	0.047	0.160	6629.218	7761.194	10457.42	20068.47	3218.466	1518.257	1833.026	600.3017
AT5G42980	gi 15239136	thioredoxin H3 [Arabidopsis thaliana]	Protein synthesis	1	1	24.18	0.039	0.338	74533.38	45083.75	39649.59	24372.41	10986.22	26353.6	12795.42	11929.77
AT4G11420	gi 15233360	translation initiation factor eIF-3 subunit 10 [Arabidopsis thaliana]	Protein synthesis	2	2	16.49	0.000	3.148	881340.2	871711.3	875130.6	914681.9	2936643	2567929	2960164	2688988
AT1G14320	gi 17682	Wilm's tumor suppressor homologue [Arabidopsis thaliana]	Protein synthesis	1	1	86.52	0.004	0.080	431111.2	197482.4	176774.8	141537.3	17047.03	26104.43	24002.15	8820.995
AT2G42590	gi 1840607	14-3-3-like protein GF14 mu [Arabidopsis thaliana]	Signal transduction	2	2	62.89	0.034	4.473	87913.37	108330.2	406014.5	350453.3	1393653	943634	981045.8	943047.1
AT1G71830	gi 15081616	At1g71830/F14O23_24 [Arabidopsis thaliana]	Signal transduction	2	2	22.03	0.009	8.686	2599.387	2472.828	5075.879	8867.423	39121.21	45587	50469.32	29983.06
AT3G07390	gi 18426884	AT3g07390/F21O3_10 [Arabidopsis thaliana]	Signal transduction	3	3	218.4	0.016	2.972	1939383	2969238	4055418	4563976	10927693	10253940	10243969	8775563
AT3G56090	gi 13358191	AT3g56090 [Arabidopsis thaliana]	Signal transduction	1	1	83.78	0.041	4.293	5126.328	6633.501	28216.76	36360.27	84212.1	75816.95	55819.38	111885.6
AT4G38580	gi 409755	ATFP6 [Arabidopsis]	Signal transduction	1	1	58.69	0.030	5.192	3050.704	6138.409	10371.81	13186.32	60748.83	39029.38	37346.16	32902.38
AT5G62390	gi 15241803	BCL-2-associated athanogene 7 [Arabidopsis]	Signal transduction	2	2	66.23	0.004	0.204	381121.5	266933.4	212663.6	143411.3	46635.46	62629.37	54327.67	40896.92
AT4G29900	gi 4914414	Ca <sup>2+</sup> -transporting ATPase-like protein [Arabidopsis]	Signal transduction	3	3	48.39	0.013	2.781	17033.05	13435.41	29936.54	32821.07	50601.08	69918.68	70089.97	68689.92
AT1G05150	gi 15220436	Calcium-binding tetratricopeptide family protein [Arabidopsis]	Signal transduction	3	3	62.44	0.027	2.860	34418.58	60106.01	85687	95676.51	223422.8	198629	171358.5	195667.3
AT2G32450	gi 15225686	Calcium-binding tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	Signal transduction	3	3	73.52	0.001	15.285	179653	222752.6	250409.4	277768.1	4102392	3289374	4066458	2765910
AT5G19450	gi 15239742	calcium-dependent protein kinase 19 [Arabidopsis thaliana]	Signal transduction	2	2	57.54	0.009	3.412	38486.69	47394.86	48161.08	69730.93	226798.5	146039.6	166338	156174.8

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Lag 1	Lag 2	Lag 3	Lag 4
AT4G04720	gi 15234435	calcium-dependent protein kinase 21 [Arabidopsis thaliana]	Signal transduction	1	1	72.75	0.044	4.806	2641.331	3749.629	22773.37	24865.45	68872.25	63584.79	64794.56	62428
AT4G23650	gi 15236560	calcium-dependent protein kinase 6 [Arabidopsis	Signal transduction	2	2	99.23	0.047	0.296	177036.4	194314.1	75382.16	82189.98	35699.48	29992.64	48243.16	42829.75
AT4G04700	gi 5706728	contains similarity to eukaryotic protein kinase domain (Pfam: PF00069, score=272.9, E=4.1e-78,	Signal transduction	1	1	30.84	0.007	14.815	335.3046	240.887	419.5314	1017.917	6224.807	10941.41	6874.703	5791.253
AT2G40300	gi 15225679	ferritin 4 [Arabidopsis thaliana]	Signal transduction	1	1	71.03	0.029	1.977	77946.69	70780.43	69716.51	62751.21	107501	157567.1	110478.1	180406.4
AT5G01600	gi 15241018	ferritin heavy chain [Arabidopsis thaliana]	Signal transduction	6	6	317.76	0.013	2.085	521289.3	842076.2	397019.6	396899.6	1057651	1279658	955293.2	1206368
AT4G17530	gi 2245111	GTP-binding RAB1C like protein [Arabidopsis	Signal transduction	1	1	56.23	0.001	log no	16125.11	6407.042	1223.699	1850.299	0	0	0	0
AT4G34460	gi 15236122	guanine nucleotide-binding protein subunit beta [Arabidopsis thaliana]	Signal transduction	1	1	25.25	0.011	2.472	8509.961	10570.95	6914.644	6986.75	14745.79	21794.85	24315.14	20681.34
AT3G28450	gi 15233004	leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	7	7	320.04	0.005	2.678	195929.9	253166.5	339674.1	355674	765039.1	755030	798897.5	745980.4
AT3G23750	gi 15229508	leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	3	3	47.92	0.047	1.748	93859.44	73609.06	143337.1	184009.3	226752.4	198924.5	185928.5	253467.1
AT2G01820	gi 15226361	leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	7	7	356.48	0.010	0.391	2195235	2364953	1391492	1260629	674633	734101.3	734470.9	674351.9
AT2G01210	gi 15226197	leucine-rich repeat transmembrane protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	2	2	63.56	0.007	2.571	1086179	1117724	2960338	3026074	3915627	3778700	5335846	8029893
AT3G08510	gi 15231929	phosphoinositide phospholipase C 2	Signal transduction	22	22	575.25	0.002	7.365	469263.8	547546.4	787831.6	958763.5	5562939	5067266	5313485	4409653
AT5G58670	gi 2769704	phosphoinositol-specific phospholipase C delta [Arabidopsis thaliana]	Signal transduction	1	1	28.49	0.002	5.887	12677.41	10166.84	10187.79	4541.175	48087.32	67317.86	66358.84	39433.98
AT3G51740	gi 15231029	probably inactive leucine-rich repeat receptor-like protein kinase IMK2 [Arabidopsis thaliana]	Signal transduction	2	2	77.92	0.010	0.191	150226.7	155898.3	68472.29	56047.15	16819.96	24627.08	24380.97	16608.59
AT5G38260	gi 15240865	protein kinase family protein [Arabidopsis	Signal transduction	3	3	42.55	0.029	3.549	43888.11	58529.84	132725.7	161021.6	397964	344747.7	350326.1	313023.5
AT5G10290	gi 8953410	protein serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	2	2	55.15	0.027	3.992	5513.175	8271.242	22923.87	24707.25	63551.92	59519.81	68176.51	53892.12
AT5G35735	gi 18421491	putative auxin-responsive protein [Arabidopsis	Signal transduction	1	1	27.02	0.050	5.571	1265.431	1211.986	4731.071	10059.52	34269.64	24295.12	20272.38	17370.67
AT3G08680	gi 15231955	putative inactive receptor kinase [Arabidopsis	Signal transduction	1	1	27.22	0.020	2.415	6177.886	7526.216	5636.832	10486.84	10880.18	18858.64	22926.19	19373.25
AT3G02880	gi 15233013	putative inactive receptor kinase [Arabidopsis	Signal transduction	11	11	503.18	0.013	2.799	823056.1	1083854	1831293	2160316	4167359	3736605	4120976	4487322

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									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT3G17840	gi 18401662	putative inactive receptor kinase RLK902 [Arabidopsis thaliana]	Signal transduction	2	2	82.5	0.002	0.152	72223.78	96939.08	26226.22	27282.16	10946.6	12915.39	6951.926	2926.443
AT3G24660	gi 15230141	putative kinase-like protein TMKL1 [Arabidopsis	Signal transduction	1	1	45.21	0.005	0.120	46054.84	26201.79	16558.47	13866.92	4009.585	2773.011	1504.363	4010.286
AT2G13800	gi 4726119	putative receptor-like protein kinase [Arabidopsis	Signal transduction	3	3	62.72	0.000	2.301	128287.9	114198.3	132791.7	136759.2	270030	291927.8	294082.7	322002.3
AT3G46060	gi 15231322	Ras-related protein ARA-3 [Arabidopsis thaliana]	Signal transduction	2	2	37.77	0.021	3.971	15333.4	16320.7	44210.53	55816.57	141561.2	124770	123434.7	133085.9
AT1G56140	gi 12321749	receptor protein kinase, putative [Arabidopsis	Signal transduction	3	3	52.83	0.013	2.166	231603	354068.1	395788	462467.3	786388.5	710685.8	853022.7	778007.5
AT5G49760	gi 8978273	receptor protein kinase-like [Arabidopsis thaliana]	Signal transduction	6	6	170.6	0.026	1.567	936571.8	1436305	1500836	1530416	2105798	2066188	2144979	2151930
AT1G66910	gi 12320925	receptor serine/threonine kinase PR5K, putative [Arabidopsis thaliana]	Signal transduction	2	2	37.54	0.041	2.973	38573.47	52892.19	135825.4	162526.1	319777.6	266405.3	291682	281111.7
AT5G65240	gi 10178186	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	64.3	0.009	4.488	34327.13	31838.4	74296.81	91501.27	296638.8	220868.4	254236.1	269246.7
AT1G11350	gi 4008010	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	60.93	0.012	3.687	9885.917	15017.33	24022.61	33913.34	75742.17	73304.59	75881.38	80488.27
AT1G48480	gi 4008006	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	3	3	115.1	0.005	0.115	88238.05	53200.02	31203.63	34014.32	6338.302	13064.37	2218.613	2087.142
AT3G14840	gi 11994595	receptor-like serine/threonine kinase	Signal transduction	9	9	195.14	0.029	2.426	496781.2	554499.5	1219342	1428174	2256023	2082301	2285300	2351007
AT3G58690	gi 7630064	serine/threonine-specific protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	2	2	29.83	0.036	3.467	34195.02	42845.94	120532.9	146694.6	340121.4	281045	293795.7	278753
AT4G33430	gi 4490310	somatic embryogenesis receptor-like kinase-like protein [Arabidopsis	Signal transduction	3	3	103.65	0.030	3.929	6928.846	8063.984	17557.17	31943.36	62212.63	69129.64	69105.43	52954.42
AT1G26480	gi 9797752	Strong similarity to GF14 mu from Arabidopsis thaliana gb AB011545 and is a member of the 14-3-3 protein PF00244 family	Signal transduction	2	2	60.18	0.003	0.277	128998.9	219948.3	144137.4	164980.5	24791.41	52679.47	48338.77	56649.57
AT3G61820	gi 15228618	aspartyl protease-like protein [Arabidopsis	Transcription	1	1	19.04	0.037	72.938	44.26616	87.97342	0	538.3695	14490.29	12775.34	15398.62	6248.451
AT2G45820	gi 601843	DNA-binding protein [Arabidopsis thaliana]	Transcription	4	4	143.03	0.008	3.602	145876.9	190825.1	283196	334894.6	977334.8	731622.2	732712.2	997885.4
AT3G03920	gi 6006850	putative GAR1 protein [Arabidopsis thaliana]	Transcription	2	2	43.42	0.003	5.263	25482.46	34110.03	28343.42	42342.94	214998	168591.1	158470.4	143597.6
AT3G60110	gi 7076764	putative protein [Arabidopsis thaliana]	Transcription	1	1	28.59	0.040	3.210	24849.47	31774.23	110446	130807.8	252673.1	179145.9	188824.7	335660
AT3G61260	gi 15233068	remorin-like protein [Arabidopsis thaliana]	Transcription	3	3	110.37	0.006	3.438	12354.78	34015.99	30246.23	45505.05	69307.16	84343.6	84496.82	181737.2
AT1G76010	gi 8778814	T4O12.22 [Arabidopsis thaliana]	Transcription	2	2	54.64	0.014	2.656	25122.56	27247.24	53933.91	54822.6	102990.5	104029	98594.03	122328.4
AT3G21820	gi 11994649	unnamed protein product [Arabidopsis thaliana]	Transcription	1	1	18.18	0.025	2.960	205542.8	188611.5	375627.3	384991.9	1124967	769096.6	873607.5	650760.6

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									Lag phase				Log phase			
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT5G61730	gi 15240334	ABC transporter A family member 9 [Arabidopsis thaliana]	Transporters	2	2	103.47	0.004	0.200	180715.4	123787.7	96674.32	94620.83	21165.94	32494.87	27174.67	18222.55
AT2G36910	gi 15228052	ABC transporter B family member 1 [Arabidopsis thaliana]	Transporters	2	2	47.05	0.006	2.076	86251.86	89774.96	101062.1	92653.32	154971.7	209924.3	166900.8	235702.7
AT2G47000	gi 15226477	ABC transporter B family member 4 [Arabidopsis thaliana]	Transporters	7	7	457.51	0.002	0.581	1281539	1185468	1013496	1066973	679551.3	682763	680264.6	601649.7
AT1G59870	gi 15218936	ABC transporter G family member 36 [Arabidopsis thaliana]	Transporters	17	17	646.98	0.010	2.494	691998.5	832398.8	1175790	1160984	2629398	2345013	2478826	2178002
AT3G30842	gi 9294504	ABC transporter-like protein [Arabidopsis thaliana]	Transporters	4	4	74.02	0.026	2.780	131132.9	192857.6	345323.2	331571.2	805484.6	596283.4	618148.3	762863.2
AT4G13510	gi 15236300	ammonium transporter 1;1 [Arabidopsis thaliana]	Transporters	2	2	176.54	0.046	0.147	1901023	2033647	463361.4	301063.3	148346.9	203144.6	158688.9	179854.5
AT2G38290	gi 15224479	ammonium transporter 2 [Arabidopsis thaliana]	Transporters	1	1	34.66	0.023	5.289	2404.594	5124.612	9032.655	14857.39	46889.04	41966.92	36730.08	40588.05
AT4G18910	gi 15234059	aquaporin NIP1-2 [Arabidopsis thaliana]	Transporters	1	1	35.42	0.029	0.018	47895.86	41980.72	3612.098	20162.27	1541.95	495.5371	0	0
AT3G53420	gi 15231810	aquaporin PIP2-1 [Arabidopsis thaliana]	Transporters	2	2	59.68	0.005	6.359	12843.45	11887.63	29597.11	31203.41	144651.6	122455.1	112520	164305.6
AT5G26340	gi 15010580	AT5g26340/F9D12_17 [Arabidopsis thaliana]	Transporters	2	2	73.68	0.020	1.553	167604.6	202738.5	117731.9	124231.4	215652.2	294504.4	242362.8	198502
AT5G57110	gi 8843813	Ca <sup>2+</sup> -transporting ATPase-like protein [Arabidopsis thaliana]	Transporters	5	5	265.18	0.015	0.518	995388.2	498921.5	589568	741047.4	399505.6	364193.7	330328	370383.4
AT1G11260	gi 16520	glucose transporter [Arabidopsis thaliana]	Transporters	2	2	178.78	0.002	0.312	595155.7	520376.7	395546.6	477671.1	151750.8	154523.7	168082	145912
AT4G30190	gi 15234666	H(+)-ATPase 2 [Arabidopsis thaliana]	Transporters	25	25	1142.58	0.004	2.305	3668821	4210741	4999887	5313832	11395366	9937792	10330563	10264620
AT5G57350	gi 15242103	H(+)-ATPase 3 [Arabidopsis thaliana]	Transporters	10	10	490.8	0.004	2.372	1833239	1796694	2554252	2542419	5680478	4697519	4695155	5626998
AT2G07560	gi 15225747	H(+)-ATPase 6 [Arabidopsis thaliana]	Transporters	9	9	332.72	0.002	2.019	663824.9	605345.4	646698.1	750563.5	1462924	1336186	1345763	1239903
AT3G60330	gi 240255678	H(+)-ATPase 7 [Arabidopsis thaliana]	Transporters	6	6	205.76	0.001	2.538	697862.6	710598.7	756766	784031	2117540	1795193	1656739	1914438
AT1G80660	gi 15220197	H(+)-ATPase 9 [Arabidopsis thaliana]	Transporters	7	7	358.06	0.000	1.746	959154.7	895243.2	891089.2	928867.5	1628514	1583247	1540429	1664370
AT3G45060	gi 15230589	high affinity nitrate transporter 2.6 [Arabidopsis thaliana]	Transporters	1	1	86.78	0.024	0.296	64803.11	65705.02	24457.01	29395.18	19048.55	13660.72	16307.37	5490.583
AT2G38940	gi 15224985	inorganic phosphate transporter 1-4 [Arabidopsis thaliana]	Transporters	5	5	276.26	0.032	3.460	372962.1	553140.6	1455192	1563756	3770441	3149670	3120949	3608515
AT3G54140	gi 15232435	peptide transporter PTR1 [Arabidopsis thaliana]	Transporters	1	1	33.11	0.027	2.996	3065.898	3074.561	5886	7772.679	6582.422	18318.29	10669.43	23754.16
AT1G02520	gi 15217785	P-glycoprotein 11 [Arabidopsis thaliana]	Transporters	5	5	156.47	0.000	0.456	1043305	1026129	850111.5	941471.5	450731.2	452247.4	395793.5	461210.8
AT4G01820	gi 2739309	P-glycoprotein-like protein [Arabidopsis thaliana]	Transporters	3	3	183.23	0.001	0.370	710869.7	560564.4	484743.7	598884.1	224484.3	224062.6	214495.7	207967.4
AT5G43370	gi 1523793	phosphate transporter [Arabidopsis thaliana]	Transporters	13	13	695.8	0.007	4.004	2189473	2320874	4262053	4462328	15233595	12087936	13339021	12337781

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT2G18960	gi 166746	plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]	Transporters	22	22	899.77	0.007	2.680	1738922	1856424	2795836	2987780	6838125	5993026	5937399	6369499
AT2G36380	gi 4581139	putative ABC transporter [Arabidopsis thaliana]	Transporters	3	3	85.88	0.008	2.386	104112.6	184925	193666.8	190148.5	389707.3	412476.9	427943.4	374976.7
AT2G29940	gi 3420057	putative ABC transporter [Arabidopsis thaliana]	Transporters	2	2	56.74	0.014	1.972	75944.4	132738.4	102858.1	99332.91	215462.3	198386.8	215663.9	180849.2
AT5G43340	gi 15239845	putative inorganic phosphate transporter 1-6 [Arabidopsis thaliana]	Transporters	5	5	138.58	0.031	4.661	7916.238	16426.91	37167.07	53527.19	143335.8	134018.2	143492.2	115337.5
AT3G54700	gi 186511064	putative inorganic phosphate transporter 1-7 [Arabidopsis thaliana]	Transporters	5	5	193.18	0.002	2.758	192758.2	163879	202442.3	181703.7	529373.4	598208	462179.2	453665.4
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis	Transporters	1	1	68.46	0.020	0.076	114140	136135.5	25421.14	31226.92	5884.63	4717.016	10027.79	2790.396
AT3G47960	gi 13877879	putative peptide transporter protein [Arabidopsis	Transporters	1	1	59.92	0.032	0.467	24193.47	33636.13	31974.35	27922.23	8520.879	13511.76	25356.27	7546.021
AT5G43360	gi 2149973	putative proton/phosphate cotransporter [Arabidopsis thaliana]	Transporters	5	5	243.36	0.002	3.183	1089932	1040739	1471486	1594684	4468752	3797934	4314277	3962833
AT5G56160	gi 145359309	sec14p-like phosphatidylinositol transfer-like protein	Transporters	3	3	27.37	0.034	3.940	68650.28	75598.11	299703.9	328842.7	887611.3	646125	685561.2	825778.5
AT1G66950	gi 5103820	Similar to gb Z70524 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF 00005 ABC transporter family. ESTs gb N97039 and gb T43169 come from this gene [Arabidopsis thaliana]	Transporters	10	10	409	0.009	2.843	260027	430134.2	459923.2	471109.6	1248080	1174662	1170860	1015704
AT3G19930	gi 15230987	sugar transport protein 4 [Arabidopsis thaliana]	Transporters	1	1	101.52	0.014	0.148	658495.1	318312.1	169136.5	215341.6	44127.26	79064.56	53587.75	24316.27
AT1G61250	gi 2443878	Unknown protein [Arabidopsis thaliana]	Transporters	2	2	47.31	0.002	2.827	29239.79	44041.28	40725.29	41366.58	113031.5	109807.3	118585	97891.49
AT5G61740	gi 10176867	unnamed protein product [Arabidopsis thaliana]	Transporters	2	2	41.22	0.003	0.230	76679.82	78620.17	75317.6	92618.22	12771.79	16298.27	12949.82	32309.59
AT3G56190	gi 15228848	alpha-soluble NSF attachment protein 2	Unknown	2	2	119.25	0.006	0.085	144465.8	125109.8	91408.51	80293.66	4913.401	7806.036	14905.93	9918.619
AT1G73650	gi 15809974	At1g73650/F25P22_7 [Arabidopsis thaliana]	Unknown	1	1	35.62	0.006	2.903	22574.77	24148.86	39672.82	35740.63	77158.65	104387.7	87309.14	85756.27
AT5G58090	gi 16604491	AT5g58090/k21119_70 [Arabidopsis thaliana]	Unknown	1	1	62.5	0.014	3.140	46057.28	59704.63	79915.83	100347.4	245497.1	229726.4	239720.4	183133.7
AT4G29360	gi 7269834	beta-1, 3-glucanase-like protein [Arabidopsis	Unknown	1	1	25.32	0.000	7.314	143874.6	145186.2	168795.3	152857.3	1105406	992454.7	1164027	1204783
AT2G44790	gi 1906000	blue copper-binding protein II [Arabidopsis thaliana]	Unknown	3	3	92.44	0.009	3.536	160686.2	164835.5	295445.2	268979.4	908113.5	808084.3	786603.4	643821
AT4G14385	gi 18414206	chromatin modification-related protein EAF6 [Arabidopsis thaliana]	Unknown	2	2	23.09	0.022	3.138	18754.81	30808.98	100706.6	94921.92	153804.1	150786.5	208797.7	256016.9



ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT5G07300	gi 7576168	copine-like protein [Arabidopsis thaliana]	Unknown	1	1	16.04	0.000	0.095	64612.67	53384.1	25319.04	25478.93	4602.657	6114.68	3057.595	2331.276
AT1G61900	gi 3367523	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	Unknown	3	3	96.32	0.023	1.628	47907.79	58650.88	77723.23	85525.44	103603.4	110226.5	99084.72	126435
AT5G25250	gi 15238749	Flotillin-like protein 1 [Arabidopsis thaliana]	Unknown	3	3	61.43	0.003	3.016	130597.9	165602.1	98207.38	123469.7	467317.5	379089.3	380377.6	335312.2
AT5G56590	gi 15241268	glucan endo-1,3-beta-glucosidase 13 [Arabidopsis thaliana]	Unknown	4	4	115.26	0.016	4.615	10445.61	18175.67	36300.1	41402.47	130619	111178.2	141841	107004.9
AT4G31140	gi 15235840	glucan endo-1,3-beta-glucosidase 5 [Arabidopsis thaliana]	Unknown	3	3	101.27	0.001	2.811	48241.95	50655.6	62653.65	84715.12	152097.7	168737.8	180104.8	191405.3
AT4G39955	gi 18420566	hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unknown	1	1	22.59	0.027	12.744	147.0339	647.0596	3113.13	2890.462	23309.53	22936.57	21964.31	18418.3
AT2G22180	gi 15227160	hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	Unknown	1	1	26.54	0.002	11.455	7958.793	9881.647	6606.736	1667.784	78917.24	87355.56	84662.31	48221.03
AT5G62740	gi 15241939	Hypersensitive-induced response protein 1 [Arabidopsis thaliana]	Unknown	6	6	200.13	0.008	5.455	145895.7	194013.5	379702.2	437731.9	1792219	1458259	1476211	1586998
AT3G01290	gi 18395770	Hypersensitive-induced response protein 3 [Arabidopsis thaliana]	Unknown	11	11	511.43	0.001	4.251	1110267	1577592	1170864	1259513	5827895	5213200	5303214	5414199
AT4G15830	gi 2244939	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	17.12	0.040	0.190	16965.12	24713.6	43228.68	67434.98	8481.855	7649.596	8706.42	4078.553
AT1G21880	gi 18395044	LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana]	Unknown	2	2	82.6	0.025	3.100	42530.37	94377.24	145911.5	178467.7	340713.4	359224.2	332601.2	397566.3
AT2G17120	gi 18398317	LysM domain-containing GPI-anchored protein 2 [Arabidopsis thaliana]	Unknown	6	6	160.14	0.005	3.133	725842.1	880409.9	1007355	1196135	3333433	2869489	3106582	2627508
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	Unknown	5	5	150.96	0.018	3.064	63476.23	96432.33	168833.3	205706.7	419655.1	373684.4	414330.4	429713.3
AT4G12420	gi 15234551	Monocopper oxidase-like protein SKU5 [Arabidopsis thaliana]	Unknown	14	14	571.33	0.012	2.194	4805512	6126681	8555365	9097620	16567401	13514398	15361075	17286366
AT5G06320	gi 15239999	NDR1/HIN1-Like protein 3 [Arabidopsis thaliana]	Unknown	3	3	210.68	0.005	2.042	734079.2	820342.4	728579.7	755257	1429678	1412146	1367812	1993028
AT1G42470	gi 42562545	Niemann-Pick C1 protein [Arabidopsis thaliana]	Unknown	2	2	42.56	0.010	0.233	66318.71	71743.54	47059.22	34982.24	8313.164	16302.23	11908.15	14704.5
AT1G48920	gi 15222009	nucleolin [Arabidopsis thaliana]	Unknown	2	2	59.07	0.029	5.090	11327.83	4059.008	12240.94	16176.38	70248.4	63508.73	57796.88	31407.6
AT5G43820	gi 240256396	pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	Unknown	3	3	39.17	0.023	3.202	331082.6	342382.4	1000375	1051643	2241438	1986833	2112841	2386329
AT4G20260	gi 15235363	plasma-membrane associated cation-binding protein 1 [Arabidopsis	Unknown	2	2	127.23	0.011	3.796	57839.85	56718.58	124207	174627.5	428652.2	306073.3	317703.5	516861.8

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance				Log phase			
									Lag phase		Lag phase		Lag phase		Lag phase	
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT2G20310	gi 15225342	RPM1 interacting protein 13 [Arabidopsis thaliana]	Unknown	1	1	23.65	0.028	3.069	43729	64720.37	93999.07	113925.4	314168.5	208867.7	238728.2	209078
AT4G18060	gi 16974680	SH3 domain-containing protein 3 [Arabidopsis	Unknown	2	2	113.74	0.025	0.012	159277.5	108657.4	18321.71	18112.38	184.3942	589.7993	1294.512	1445.712
AT1G11820	gi 3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from	Unknown	1	1	31.69	0.021	3.982	710.6146	2009.214	5609.795	3561.498	8876.948	12686.34	15801.33	9980.369
AT1G71040	gi 12323429	spore coat protein-like protein; 24980-21957 [Arabidopsis thaliana]	Unknown	4	4	89.5	0.035	0.213	895429.4	999884.5	222139.3	248764.2	140121.9	131971.8	123528	107765.1
AT3G01185	gi 5091549	T10O24.18 [Arabidopsis thaliana]	Unknown	1	1	17.65	0.012	9.734	6564.084	8036.852	24620.36	30471.74	193710	176197.6	174744.7	133739.7
AT5G28920	gi 30692070	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	27.19	0.015	1.998	156478.8	115017.5	95211.3	101475.4	216238.8	225033.4	238294.2	255797.3
AT4G15610	gi 18414489	uncharacterized protein [Arabidopsis thaliana]	Unknown	2	2	43.32	0.011	4.208	11371.7	15617.19	28932.75	32492.65	105643.6	80559.84	82095.54	103737.4
AT4G03180	gi 15236259	uncharacterized protein [Arabidopsis thaliana]	Unknown	2	2	15.43	0.039	8.906	643.2603	876.983	11182.96	18541.59	81852.01	58120.84	66178.02	72125.69
AT2G41800	gi 15227437	uncharacterized protein [Arabidopsis thaliana]	Unknown	3	3	68.92	0.002	4.383	11793.84	9979.52	13649.49	14474.45	47652.37	44110.28	41513.48	85436.52
AT1G18180	gi 145335854	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	33.06	0.004	1.827	9757.308	10752.66	9608.467	8120.323	14893.56	20035.9	17337.56	17596.64
AT5G45540	gi 15242429	uncharacterized protein [Arabidopsis thaliana]	Unknown	2	2	27.8	0.007	0.291	113268.9	167224.8	84843.02	83796.57	29385.05	32958.04	35916.78	32302.11
AT3G13677	gi 22331067	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	23.15	0.025	0.016	48802.2	2979.276	4541.559	569.1187	452.6313	357.7913	127.2256	0
AT1G45545	gi 15220079	uncharacterized protein [Arabidopsis thaliana]	Unknown	3	3	27.84	0.001	0.178	717707.8	347520.7	298582	395927.9	105599.1	75327.94	76916.2	55824.34
AT1G01305	gi 116830059	unknown [Arabidopsis thaliana]	Unknown	1	1	18.6	0.006	22.449	4231.656	7672.921	25729.03	25254.19	398075.4	339068.5	371376.8	303265.5
AT5G62630	gi 14423506	Unknown protein [Arabidopsis thaliana]	Unknown	8	8	347.03	0.001	2.705	1543946	1657352	1535376	1648866	4903802	4254574	4440297	3677173
AT5G42370	gi 13430796	unknown protein [Arabidopsis thaliana]	Unknown	1	1	21.45	0.032	8.334	294.31	1568.901	4322.928	3662.319	22886.46	21485.1	19581.04	18121.39
AT4G15950	gi 28188681	unknown protein [Arabidopsis thaliana]	Unknown	1	1	18.57	0.006	22.449	4231.656	7672.921	25729.03	25254.19	398075.4	339068.5	371376.8	303265.5
AT2G25800	gi 3643603	unknown protein [Arabidopsis thaliana]	Unknown	3	3	23.19	0.019	1.513	41128.69	52668.7	38305.04	48669.54	77019.05	65126.77	63219.98	68118.09
AT1G69290	gi 12325092	unknown protein; 45065-49536 [Arabidopsis	Unknown	2	2	111.33	0.011	7.582	6773.221	12797.81	22279.61	38195.63	139994.8	165042.1	176033.4	125865.9
AT1G77630	gi 12323377	unknown protein; 84247-85908 [Arabidopsis	Unknown	2	2	85.06	0.020	3.642	26868.87	50164.41	86922.17	123575.7	249382.7	263161.6	258649.4	276093.2
AT5G39970	gi 10176989	unnamed protein product [Arabidopsis thaliana]	Unknown	1	1	55.12	0.025	5.794	2541.171	2808.356	9466.95	11500.76	46137.58	37340.62	39915.52	29088.44
AT3G17350	gi 11994552	unnamed protein product [Arabidopsis thaliana]	Unknown	1	1	35.91	0.036	4.230	1289.52	2270.599	4790.144	6783.747	20556.33	14799.61	13878.13	14775.84

ATG	GI	Protein description	Funtional categories	Peptide co	Peptides us	Confidence	Anova (p)	Log/Lag fo	Normalized abundance							
									Lag phase				Log phase			
									Lag 1	Lag 2	Lag 3	Lag 4	Log 1	Log 2	Log 3	Log 4
AT1G6727 0	gi 240254 330	Zinc-finger domain of monoamine-oxidase A repressor R1 protein [Arabidopsis thaliana]	Unknown	2	2	28.96	0.006	22.574	4231.656	7770.067	25729.03	26085.36	404913.9	347626.6	380153.3	307887.7















Supplementary Table 3-5 ABA- responsive plasma membrane proteins at the lag phase

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	cell growth/division	3	3	53.7	0.010	2.553	35355.26	46964.37	26211.13	35408.54	51102.04	80090.44	141862.5	94414.11
AT1G74790	gi 5882745	F25A4.24 [Arabidopsis thaliana]	Cell growth/division	14	14	596.4	0.006	3.722	2384101	2887773	1254664	1217958	9152270	3969586	5284392	10416788
AT3G13210	gi 10172609	probable cell cycle control protein; crooked neck-like protein [Arabidopsis thaliana]	cell growth/division	4	4	36.13	0.037	0.325	258096.7	214119.6	301843.4	287899.7	145007.3	81631.79	104477.4	14340.92
AT3G45600	gi 15231187	TET3 (TETRASPANIN3) [Arabidopsis thaliana]	Cell growth/division	5	5	216.24	0.001	4.100	96577.34	86834.94	41790.65	46091.19	290059.6	198974.2	286443.8	336840.1
AT4G28050	gi 15234374	TET7 (TETRASPANIN7) [Arabidopsis thaliana]	Cell growth/division	1	1	41.74	0.040	1.827	69154.39	67510.49	42302	35207.38	70076.25	83142.44	146873.4	91310.79
AT5G03340	gi 11265361	transitional endoplasmic reticulum ATPase - Arabidopsis thaliana	cell growth/division	4	4	141.37	0.028	2.867	63444.93	95737.68	61039.78	36186.57	106609.2	96361.6	234366.2	297863.4
AT4G20890	gi 15233429	TUB9; GTP binding / GTPase/ structural molecule [Arabidopsis thaliana]	Cell growth/division	8	8	268.25	0.019	3.645	294079.3	155036.2	113634.7	55298.8	258372.7	495213.3	615847.7	883086.8
AT1G68560	gi 4163997	alpha-xylosidase precursor [Arabidopsis thaliana]	Cell structure	8	8	131.46	0.021	3.356	148086.4	181682.8	173371.9	157128.4	266134.9	389311.7	1199660	360785.6
AT5G15500	gi 15242318	ankyrin repeat family protein [Arabidopsis thaliana]	cell structure	2	2	77.3	0.003	193.462	0	77.92422	82.08243	3.497537	4536.114	2355.677	3324.159	21415.85
AT5G65020	gi 15238320	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis	cell structure	3	3	30.58	0.004	0.359	534256.2	436942.7	551609.9	576423.6	265051	160615	234725.2	93319.82
AT5G42100	gi 15238298	ATBG_PAP; glucan endo-1,3-beta-D-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Cell structure	2	2	52.61	0.016	4.049	42931.86	30715.19	27368.79	39548.41	55760.39	130750.1	293174.7	89462.62
AT1G53840	gi 15220958	ATPME1; pectinesterase [Arabidopsis thaliana]	Cell structure	5	5	263.45	0.006	2.591	113616.1	95110.36	51013.75	51040.61	158216.3	181017.9	190861.4	275168.9
AT3G14300	gi 15231826	ATPMEPCRRC; pectinesterase [Arabidopsis thaliana]	cell structure	4	4	30.77	0.004	2.233	31946.46	34183.35	17947.43	16621.54	49967.27	55583.47	60408.22	58891.65
AT1G66250	gi 12323569	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis thaliana]	cell structure	4	4	318.73	0.003	4.441	96967.28	105137.9	64863.89	74518.68	226257.6	239346.7	705747.4	345052.5
AT3G13560	gi 9280308	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	cell structure	6	6	236.6	0.002	3.299	104658.4	139880.6	69957.47	70028.22	236785.1	250780.9	339402.7	441679.6
AT4G37410	gi 15235541	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis	cell structure	2	2	39.23	0.014	53.099	210.0016	90.25661	227.5982	139.7015	2204.914	30854.5	646.1037	1741.314
AT1G70710	gi 2440033	endo-1,4-beta-glucanase [Arabidopsis thaliana]	cell structure	1	1	34.93	0.038	2.450	10374.5	35324.55	15354.44	13465.58	39214.98	42311.09	76301.38	24712.96
AT4G20830	gi 30685222	FAD-binding domain-containing protein [Arabidopsis	Cell structure	30	30	1379.42	0.000	3.193	939938.5	840542.2	928898	1189352	2233074	2795949	4231613	3188738
AT4G12730	gi 13377778	fasciclin-like arabinogalactan-protein 2 [Arabidopsis	cell structure	16	16	1084.46	0.002	4.072	6262584	5652025	4443170	5250667	12349044	18155938	38302992	19174614
AT5G55730	gi 15240570	FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1) [Arabidopsis thaliana]	Cell structure	18	18	1011.03	0.008	3.438	5461346	6614710	3646262	3312602	9183737	11551089	29227544	15475397
AT5G44130	gi 15241423	FLA13 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 13 PRECURSOR) [Arabidopsis thaliana]	Cell structure	3	3	74.29	0.020	7.435	55388.75	44068.1	106613.8	111557.3	98359.06	638548.9	1079743	544788.3
AT2G04780	gi 18395849	FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) [Arabidopsis thaliana]	cell structure	4	4	230.58	0.005	2.500	232988.4	257436.9	156102.1	143630.5	481246.4	498240.8	317251.3	678443.7
AT2G45470	gi 18406799	FLA8 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 8) [Arabidopsis thaliana]	Cell structure	8	8	455.95	0.006	4.857	2137491	2858283	2324713	1854588	4949487	8016853	23536013	8062388
AT1G03870	gi 18379157	FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) [Arabidopsis thaliana]	Cell structure	1	1	95.34	0.001	3.359	324018	308846.3	242228.5	267998.2	601812.9	777825	1175724	1284231
AT2G01630	gi 18379267	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana]	Cell structure	5	5	184.47	0.002	3.180	32760.69	42270.76	61228.54	47292.12	89216.98	158997.5	196140	139420.6
AT5G20940	gi 22326918	glycosyl hydrolase family 3 protein [Arabidopsis	cell structure	4	4	90.71	0.007	0.401	34104.31	22389.87	23621.47	40010.05	18737.4	11347.3	10654.02	7440.804
AT5G04885	gi 30680681	glycosyl hydrolase family 3 protein [Arabidopsis	Cell structure	31	31	1192.08	0.044	3.372	2339540	3013211	2391262	2291267	3685003	6515655	19511383	4126903
AT2G30870	gi 15224582	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase [Arabidopsis	Cell structure	3	3	36.65	0.043	3.307	15487.11	16311.63	15937.48	15753.3	18959.76	57270.02	27643.87	106090
AT5G48450	gi 8777375	pectinesterase-like protein [Arabidopsis thaliana]	cell structure	3	3	82.19	0.047	3.133	57643.56	80176.23	52458.59	62173.35	111284	108186.6	461659.5	109793.8
AT3G49120	gi 405611	peroxidase [Arabidopsis thaliana]	cell structure	1	1	19.09	0.016	29.079	778.2809	870.1893	1592.623	713.3825	8519.828	3536.022	5964.848	96971.5
AT5G17820	gi 15238030	peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana]	Cell structure	10	10	365.77	0.000	5.572	68435.05	65899.67	99982.76	97531.49	288806.4	740522.4	459755.1	360098.1
AT1G42550	gi 240254220	PMI1 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	cell structure	7	7	69.45	0.009	2.518	531247.4	516149.8	362570.3	336989.8	1159439	1373277	578005.5	1287330
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis	Cell structure	10	10	357.38	0.004	2.467	668464.9	659748.7	330674.5	426120.2	1106451	991782.3	1493831	1551970
AT2G13820	gi 15225509	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Cell structure	3	3	147.08	0.015	2.381	136422.9	157553.3	200576.9	138698.7	202375.2	406029.4	584578	314959.7
AT3G58100	gi 6735322	putative protein [Arabidopsis thaliana]	cell structure	2	2	83	0.003	3.221	73760.89	77534.5	51987.57	38026.01	143784	134403.5	275166	223852.8
AT4G03230	gi 4262151	putative receptor kinase [Arabidopsis thaliana]	cell structure	5	5	48.82	0.008	0.150	14124.08	21479.21	34232.69	27398.26	6610.108	4357.949	3000.544	628.137
AT5G51480	gi 15242108	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	12	12	438.04	0.002	2.467	671452.3	663614.9	791673	763655.9	1189508	1806769	2511795	1621973

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT4G12420	gi 15234551	SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	24	24	1160.82	0.001	3.146	9709144	10185538	7744547	6905005	18914504	20852434	39612040	29311732
AT3G46550	gi 15231453	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding [Arabidopsis thaliana]	Cell structure	3	3	153.43	0.018	2.086	50044.31	55821.34	32671.28	41917.78	99237.32	105045.9	51888.38	120280.1
AT4G27520	gi 21592865	unknown [Arabidopsis thaliana]	Cell structure	10	10	593.07	0.000	12.296	277848.9	373172.3	244604	199938.3	3330893	1665380	1872909	6602183
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	3	3	133.93	0.009	10.180	17577.89	10568.22	25261.78	37241.92	51927.79	415642.6	114174.3	341065.2
AT5G64080	gi 10176956	unnamed protein product [Arabidopsis thaliana]	Cell structure	3	3	116.17	0.009	1.914	49624.63	62168.16	98615.23	70644.14	104247.7	135425.5	129970	168354
AT3G49750	gi 15229606	AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana]	Disease/defence	2	2	122.16	0.045	1.919	25400.55	17743.36	16798.76	16965.88	20264.23	56392.38	39911.03	31026.03
AT4G01700	gi 15234281	chitinase, putative [Arabidopsis thaliana]	Disease/defence	5	5	194.39	0.001	4.890	527122.6	603628.8	263384.1	218405.2	2227176	1744739	2189237	1723755
AT1G20440	gi 388259	cor47 [Arabidopsis thaliana]	disease/defence	1	1	37.28	0.034	8.237	8604.131	6138.325	10134.93	12476.92	10817.6	33446.36	100910	162521.8
AT1G30360	gi 18397470	ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Disease/defence	20	20	830.72	0.006	2.041	440348.9	364627.2	202460.5	242193.3	572272.7	631300.2	669549.5	676969.5
AT2G43610	gi 15224319	glycoside hydrolase family 19 protein [Arabidopsis thaliana]	Disease/defence	3	3	107.6	0.005	5.875	65464.8	107553.5	35483.53	30490.72	448512.1	142628	267179.5	545803
AT4G23670	gi 15236566	major latex protein-related / MLP-related [Arabidopsis thaliana]	disease/defence	1	1	30.37	0.004	57.463	376.8966	810.0279	593.9834	591.8711	2132.979	37289.26	60389.61	36536.15
AT5G22060	gi 535588	putative [Arabidopsis thaliana]	Disease/defence	3	3	49.97	0.036	3.867	22108.1	42093.28	24028.79	10676.26	55689.19	37994.36	210030.3	78730.37
AT1G20780	gi 42562204	SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	disease/defence	4	4	39.37	0.008	3.149	7370.983	9576.577	5366.751	5310.486	10301.1	19998.28	25690.72	30996.4
AT3G53990	gi 30693971	universal stress protein (USP) family protein [Arabidopsis thaliana]	disease/defence	3	3	69.19	0.041	5.706	10880.62	23458.97	8399.222	7834.078	20080.68	21101.45	129020.9	118345.7
ATCG00480	gi 7525040	ATP synthase CF1 beta subunit [Arabidopsis thaliana]	Energy	8	8	311.23	0.037	2.274	604160.1	874539.6	1464724	1194300	3873168	1285190	2288835	1963640
AT3G55440	gi 414550	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	Energy	5	5	142.4	0.036	4.390	133533.6	146579.3	180109	105063.8	148182	502026.7	1298991	532354.6
AT4G32840	gi 15233959	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase [Arabidopsis thaliana]	Energy	2	2	21.26	0.007	0.292	83019.07	30499.78	33576.06	46574.85	17216.32	15494.01	16216.86	7531.093
AT3G56190	gi 15228848	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein [Arabidopsis thaliana]	Intracellular traffic	6	6	318.61	0.019	1.583	102769.3	95614.04	66510.3	59472.35	118492.8	115558.7	123323	155940.4
AT5G08680	gi 22326673	ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana]	Intracellular traffic	6	6	111.6	0.011	2.450	51357.17	77320.32	141336.9	102372.3	215935.5	153188.2	302223	240822
AT5G64370	gi 9759413	beta-ureidopropionase [Arabidopsis thaliana]	Intracellular traffic	5	5	125.32	0.043	2.580	24659.28	20323.07	98908.54	106130.9	138268.3	117346.7	225651.1	163675.6
AT5G08080	gi 18415701	SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor [Arabidopsis thaliana]	Intracellular traffic	9	9	499.52	0.001	1.906	482120.1	437745.1	389086	359476.4	617519.2	816386	781904.3	964792.8
AT5G12370	gi 14586367	putative protein [Arabidopsis thaliana]	intracellular traffic	4	4	44.27	0.001	0.563	75678.87	70580.96	64884.82	84215.11	45191.16	43014.06	45603.99	32619.15
AT3G10380	gi 18398855	SEC8 (SUBUNIT OF EXOCYST COMPLEX 8) [Arabidopsis thaliana]	intracellular traffic	3	3	17.39	0.019	2.417	6536.946	8690.576	3898.285	3363.572	11322.64	17803.51	8317.977	16906.3
AT1G21380	gi 18394983	VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana]	intracellular traffic	1	1	67.78	0.014	5.270	38055.95	34330.52	7895.326	6075.315	72997.62	73898.94	217480.5	90749.37
AT5G58060	gi 15242933	YKT61 [Arabidopsis thaliana]	intracellular traffic	1	1	47.37	0.046	2.745	24101.24	28244.89	35606.62	18047.4	50388.44	33249.02	149727.9	57565.1
AT4G35790	gi 18419668	ATPLDELTA; phospholipase D [Arabidopsis thaliana]	Metabolism	9	9	327.18	0.010	4.986	182006.7	170344.3	149105.5	152247.1	502011.2	496263.3	362761.6	1898147
AT5G17920	gi 55670112	Chain A, A. Thaliana Cobalamine Independent Methionine Synthase	metabolism	15	15	195.48	0.029	0.485	53699.28	63984.37	72236.49	86183.89	40990.66	38457.89	40329.6	14263.71
AT1G43710	gi 15218445	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	metabolism	2	2	19.66	0.004	6.696	39838.17	38895.1	34792.98	41122.28	128324.4	165211.6	609873.9	132069.9
AT1G34430	gi 8778253	F12K21.24 [Arabidopsis thaliana]	Metabolism	5	5	152.56	0.005	2.912	163783.8	105068.8	163843.3	116610.7	232454.1	467776.2	583690.5	315707.5
AT5G58480	gi 30697080	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	2	2	28.78	0.023	2.228	14169.5	5809.306	3548.873	6302.85	16557.81	12581.13	19762.32	17570.9
AT5G56590	gi 15241268	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	5	5	273.42	0.002	2.530	80202.64	71498.59	40991.05	57501.42	130283.3	192038	128440.3	182175.9
AT4G31140	gi 15235840	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	9	9	358.5	0.002	3.278	309728.9	247987.3	201533.7	227496.7	1193521	471455	738400.7	831179.1
AT2G18730	gi 4185139	putative diacylglycerol kinase [Arabidopsis thaliana]	metabolism	4	4	45.01	0.000	3.774	60568.62	70952.05	56557.53	46683.88	171215.8	168314.5	302376.4	244018.6
AT3G03780	gi 14532772	putative methionine synthase [Arabidopsis thaliana]	Metabolism	10	10	129.81	0.014	2.107	4414.223	6169.629	10315.09	8631.775	11438.24	14028.72	20570.11	16181.34
AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	metabolism	15	15	969.89	0.004	4.569	2627457	3978652	3440056	2532646	8016140	7913873	26940901	14602277
AT5G55480	gi 15240520	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	Metabolism	25	25	1445.8	0.003	4.028	5918647	8991709	6379965	4762929	17507867	16225465	45293030	25918229
AT3G54200	gi 15232445	unknown protein [Arabidopsis thaliana]	Metabolism	2	2	145.13	0.001	1.827	310320.7	258697.6	223784.3	255490.3	434959.8	410915.7	549721	519757.7
AT1G35710	gi 14596041	Unknown protein [Arabidopsis thaliana]	metabolism	2	2	47.91	0.005	3.322	51509.04	64987.48	42009.56	30968.08	81574.56	133920.7	218687.1	195311.5
AT1G11910	gi 1354272	aspartic proteinase [Arabidopsis thaliana]	protein destination and	3	3	83.15	0.040	5.240	4949.528	4474.806	14324.49	12816.52	16963.07	17730.58	121233	35670.95

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT3G02740	gi 15232960	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination and	7	7	230.35	0.005	2.793	188182.2	124362.8	110933.2	126281.2	353694	320554.2	240973.4	620342.6
AT5G10080	gi 15238055	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination and	8	8	186.17	0.024	0.494	21905.06	13599.69	16340.3	24967.19	7832.618	7546.931	6318.813	16265.23
AT3G52500	gi 16209647	AT3g52500/F22O6_120 [Arabidopsis thaliana]	protein destination and	2	2	30.7	0.022	4.289	76607.14	61054.47	56465.14	57692.1	97809.22	299211.7	554101.6	128855.4
AT1G63500	gi 240254311	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Protein destination and storage	9	9	313.29	0.030	2.270	122490.5	103834.1	72583.49	68762.77	121670.3	155402.6	199804	357684.3
AT1G69840	gi 15222481	band 7 family protein [Arabidopsis thaliana]	Protein destination and	10	10	413.18	0.003	2.411	648346	720659.4	633666.8	575937.2	1005790	1225416	1995014	1990116
AT1G65240	gi 4646203	Belongs to PF00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	protein destination and storage	5	5	127.94	0.031	3.857	81823.32	77214.27	76377.07	61397.73	153918	115507.1	672187.9	203294.1
AT5G46570	gi 15237465	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	5	5	98.24	0.005	3.484	3406.344	2594.114	1142.244	1963.336	5501.289	6832.271	6688.757	12699.33
AT4G00710	gi 22328189	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	7	7	242.69	0.041	1.644	111062.5	77951.72	59987.43	49063.21	112210.7	95322	153362.6	129016.6
AT1G05690	gi 42561724	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	protein destination and storage	3	3	30.68	0.006	2.803	5448.502	4507.788	4095.852	3664.486	6844.525	13082.62	19567.48	10167.47
AT5G47850	gi 15238823	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase [Arabidopsis thaliana]	protein destination and storage	3	3	24.62	0.010	5.351	3439.937	2820.025	1550.942	2111.575	4814.473	9040.967	28659.69	10581.17
AT3G26940	gi 15231654	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	3	3	35.53	0.011	0.315	80442.5	84582.64	103550.3	126162.9	25154.68	18499.51	67678.13	12816.94
AT1G05840	gi 6850312	Contains similarity to nucellin from Hordeum vulgare gb U87148. ESTs gb T22068, gb F14251, gb F14237, gb F14242 come from this gene [Arabidopsis thaliana]	protein destination and storage	3	3	137.78	0.004	9.029	38102.17	32216.23	8976.801	7590.392	117423	90500.56	306795	269769.9
AT1G03230	gi 18379072	extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana]	Protein destination and storage	5	5	180.39	0.002	5.163	40098.56	40557.68	11363.31	15653.54	117811	136833.3	121645.4	179647.2
AT1G12470	gi 8778633	F5O11.22 [Arabidopsis thaliana]	protein destination and	2	2	26.2	0.038	0.340	173559.5	157510.9	149435.5	131221.1	117559.5	62225.35	10013.82	18205.68
AT3G58880	gi 15231588	F-box family protein [Arabidopsis thaliana]	protein destination and	2	2	28.49	0.015	0.352	20995.89	21059.46	52021.57	41682.36	11643.68	15953.45	13421.93	6787.873
AT2G17760	gi 25347778	hypothetical protein At2g17760 [imported] - Arabidopsis thaliana	protein destination and storage	5	5	207.43	0.005	7.241	32780.15	42472.63	14847.18	20731.89	218987.2	70329.07	123718.7	389499.8
AT1G79560	gi 4835753	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this gene [Arabidopsis thaliana]	protein destination and storage	2	2	23.62	0.006	7.573	747.0303	1752.538	1131.791	1502.314	8671.931	9923.178	2613.379	17666.85
AT5G51770	gi 15242183	protein kinase family protein [Arabidopsis thaliana]	Protein destination and	2	2	46.08	0.046	0.438	7283.182	5949.364	4542.459	16499.7	3676.976	4075.064	3497.387	3747.571
AT2G23200	gi 15227790	protein kinase family protein [Arabidopsis thaliana]	protein destination and	3	3	34.02	0.003	0.217	34485.41	24444.74	22498.88	29909.06	3932.414	13326.9	3497.792	3352.55
AT1G07870	gi 15223024	protein kinase family protein [Arabidopsis thaliana]	protein destination and	4	4	72.13	0.019	2.483	10539.06	9030.855	7140.038	6541.863	9404.756	23619.07	21556.17	27991.86
AT2G39360	gi 15225078	protein kinase family protein [Arabidopsis thaliana]	protein destination and	7	7	170.83	0.002	6.983	10468.94	11580.12	8341.844	9019.788	31634.08	40391.37	70413.48	132785.5
AT5G24010	gi 15237872	protein kinase family protein [Arabidopsis thaliana]	protein destination and	8	8	279.09	0.023	2.192	115070.4	125210.1	80503.57	70595.94	110800.9	277360.3	212470.9	257148.4
AT4G02630	gi 15235432	protein kinase family protein [Arabidopsis thaliana]	Protein destination and	10	10	189.03	0.001	2.833	76276.27	71286.54	72748.63	96353.4	159275.3	193581.9	304057.1	240268.6
AT5G03320	gi 15242720	protein kinase, putative [Arabidopsis thaliana]	Protein destination and	3	3	56.46	0.044	0.466	58406.23	58395.79	62696.29	51117.4	43276.58	27367.39	28538.17	8227.585
AT5G56460	gi 15241220	protein kinase, putative [Arabidopsis thaliana]	protein destination and	4	4	36.85	0.044	0.271	37875.96	29601.41	28159.44	32340.57	3401.164	3781.499	27156.12	369.4654
AT3G46290	gi 15231393	protein kinase, putative [Arabidopsis thaliana]	protein destination and	10	10	277.64	0.015	2.284	136407.2	172172.2	124416.8	98959.75	202849.9	296315	222519.4	493506
AT4G28400	gi 18417190	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	protein destination and storage	3	3	58.69	0.009	0.122	66089.14	63387.27	70795.98	44576.62	3118.146	23549.17	608.1357	2703.816
AT2G07180	gi 19423982	putative protein kinase [Arabidopsis thaliana]	protein destination and	2	2	28.27	0.010	2.166	176253.9	123505.6	123104.7	122237	205460.9	315385.8	219050.4	440768.6
AT2G39110	gi 3928095	putative protein kinase [Arabidopsis thaliana]	protein destination and	3	3	44.32	0.025	0.339	139262.9	121914.5	98586.54	121763.3	63892.58	46636.85	42999.29	9537.538
AT2G28000	gi 21554572	putative rubisco subunit binding-protein alpha subunit [Arabidopsis thaliana]	protein destination and storage	5	5	75.89	0.035	0.586	76812.2	73443.93	51367.2	65623.97	49815.13	44958.65	40389.21	21486.08
AT2G16600	gi 15227259	ROC3; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	protein destination and storage	2	2	124.41	0.025	2.811	206001.7	222509	99828.79	91548.59	234586.1	287002.8	556788.4	663998.2
AT2G05920	gi 62321128	serine protease like protein [Arabidopsis thaliana]	Protein destination and	6	6	123.99	0.010	1.878	73787.83	50276.89	73478.75	66625.43	80609.64	127174.6	154178.8	134028.7
AT2G47060	gi 79324935	serine/threonine protein kinase, putative [Arabidopsis	Protein destination and	4	4	50.97	0.044	0.380	5495.92	4278.38	6606.481	12170.55	5597.543	2810.144	1357.601	1091.229
AT3G17410	gi 22331138	serine/threonine protein kinase, putative [Arabidopsis	Protein destination and	7	7	163.27	0.011	3.140	18259	34524.24	43768.19	29010.74	89376.89	47575.73	104393.1	152940.9
AT4G32300	gi 2864613	S-receptor kinase -like protein [Arabidopsis thaliana]	Protein destination and	4	4	145.99	0.014	1.794	79036.51	96460.17	55855.76	63187.57	93116.36	132551.4	135674.8	167204
AT1G27750	gi 6693023	T22C5.20 [Arabidopsis thaliana]	Protein destination and	5	5	48.84	0.009	0.130	20874.88	22655.82	47150	33693.92	3925.215	3295.187	8477.732	491.3094
AT5G56380	gi 10177837	unnamed protein product [Arabidopsis thaliana]	protein destination and	3	3	32.19	0.050	0.402	94973.21	89358.9	69023.55	70911.72	59026.65	24655.96	39781.08	6878.597

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	protein synthesis	5	5	73.83	0.008	0.423	49673.89	41040.76	79609.8	70252.2	32133.03	30546.42	22858.69	16109.16
AT2G04390	gi 15228141	40S ribosomal protein S17 (RPS17A) [Arabidopsis thaliana]	Protein synthesis	11	11	433.34	0.018	2.153	1159707	980241.1	1302234	1115215	1311945	3013339	3384506	2100582
AT3G02080	gi 15232844	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	Protein synthesis	4	4	91.09	0.018	3.146	29169.8	28015.72	33584.86	38091.52	61445.47	46002.17	124648	173360.8
AT5G61170	gi 15240154	40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana]	Protein synthesis	4	4	93.94	0.005	7.153	2510.208	3944.43	4315.553	2971.436	7438.193	25324.78	47902.96	17624.02
AT5G35530	gi 15238533	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	protein synthesis	7	7	170.96	0.020	2.109	34923.06	31480.69	31319.17	33504.33	43992.34	53617.33	117972.6	61203.99
AT4G29390	gi 15233565	40S ribosomal protein S30 (RPS30B) [Arabidopsis thaliana]	Protein synthesis	2	2	67.87	0.046	44.252	247.7371	0	231.4723	261.8929	18736.86	8817.337	430.1072	4811.272
AT3G04840	gi 15229364	40S ribosomal protein S3A (RPS3aA) [Arabidopsis thaliana]	Protein synthesis	4	4	109.35	0.032	2.331	147981.3	165393.1	68431.33	72235.84	360589.8	185109.3	164701.8	348133.1
AT5G46430	gi 15237436	60S ribosomal protein L32 (RPL32B) [Arabidopsis thaliana]	Protein synthesis	5	5	62.17	0.008	2.922	5152.077	4991.683	5326.058	7278.724	9201.712	22356.73	23579.91	11327.19
AT2G47610	gi 15226635	60S ribosomal protein L7A (RPL7aA) [Arabidopsis thaliana]	protein synthesis	1	1	28.74	0.006	0.115	28340.35	24374.01	7556.062	8581.904	1714.57	2129.543	543.535	3521.389
AT1G33120	gi 18398753	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	Protein synthesis	10	10	530.99	0.001	2.916	826002.4	460674.1	586992.9	479312.1	2097974	1425576	1855855	1482509
AT2G37270	gi 15228111	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	3	3	172.83	0.004	3.111	229655.8	269015.1	169395	164409.5	489585.4	369418.2	907731.3	823208.8
AT5G60390	gi 295789	elongation factor 1-alpha [Arabidopsis thaliana]	Protein synthesis	7	7	223.92	0.011	3.620	28099.62	54731.18	25008.23	10081.8	74169.78	75804.84	142321.2	134566.8
AT1G56070	gi 6056373	elongation factor EF-2 [Arabidopsis thaliana]	protein synthesis	5	5	259.45	0.041	2.778	264880.2	375729.2	214224.9	153903.6	305624	440984.5	1150867	904403.2
AT1G20620	gi 8778617	F5M15.5 [Arabidopsis thaliana]	protein synthesis	4	4	56.11	0.019	7.687	1340.47	3400.854	19412.83	10669.15	21848.22	34745.86	96684.9	114420.1
AT2G33370	gi 2341028	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene [Arabidopsis thaliana]	protein synthesis	5	5	104.29	0.017	2.536	61221.1	59827.39	43634.86	52002.46	117343.4	104268.3	248758.5	79183.73
AT2G36170	gi 18404062	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana]	protein synthesis	4	4	164.28	0.034	2.264	51721.6	33377.12	16014.97	16160.63	49977.98	77224.97	47444.02	90841.57
AT4G34050	gi 21595512	caffeoyl-CoA O-methyltransferase-like protein [Arabidopsis thaliana]	secondary metabolism	2	2	29.61	0.020	11.810	9981.147	16550.72	12132.51	5998.141	44831.33	21004.84	122163.2	339467.3
AT1G74020	gi 1754983	strictosidine synthase [Arabidopsis thaliana]	secondary metabolism	2	2	50.5	0.015	28.865	724.5191	887.8359	865.9172	244.101	7996.033	7866.914	1644.759	61074.35
AT4G34460	gi 42573173	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/nucleotide binding / protein binding [Arabidopsis thaliana]	Signal transduction	4	4	30.93	0.001	7.059	5417.786	5323.534	13741.5	9556.312	28716.5	67438.74	62862.35	81273.03
AT3g07390	gi 18426884	AT3g07390/F21O3_10 [Arabidopsis thaliana]	Signal transduction	6	6	392.18	0.025	3.007	7593197	9251779	3590460	2708386	20035781	7934571	16682821	24931393
AT5G01600	gi 15241018	ATFER1; ferric iron binding / iron ion binding [Arabidopsis thaliana]	Signal transduction	7	7	345.01	0.013	14.323	57002.14	57981.92	299105.2	235392.7	566354.8	2115198	5962658	658111.1
AT1G11300	gi 145335397	ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	signal transduction	6	6	61.03	0.038	0.392	30167.4	36601.25	68693.34	81912.79	19377.39	37198.17	18576.81	9992.946
AT3G08510	gi 15231929	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	Signal transduction	19	19	527.44	0.012	3.695	224218	165307.4	184849.3	185688.5	306102.8	797321	429569.4	1275306
AT4G18760	gi 15234009	AtRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	Signal transduction	7	7	607.34	0.003	2.693	1250734	1397556	1204128	1084824	2187059	2506980	5129159	3473689
AT5G35735	gi 18421491	auxin-responsive family protein [Arabidopsis thaliana]	Signal transduction	1	1	22.07	0.003	6.054	4488.918	9745.48	12627.91	8046.737	34290.83	24685.77	57648.8	94730.82
AT4G39400	gi 15235059	BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	11	11	45.06	0.003	4.585	36504.58	70298.66	53589.59	32227.84	277771.3	105180.9	188004.3	312150.5
AT4G29900	gi 4914414	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	Signal transduction	5	5	169.82	0.017	3.409	140470	190535.5	151672.4	120888.1	223949.3	314263.7	952257	567245.5
AT5G24430	gi 22136058	calcium dependent protein kinase-like protein [Arabidopsis thaliana]	signal transduction	3	3	66.27	0.030	2.594	26644.93	33330.62	21380.54	22089.1	31554.25	47794.37	70143.44	118845.3
AT2G32450	gi 15225686	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	7	7	232.92	0.031	2.458	32151.78	25928.26	11854.17	12279.95	33213.36	42588.02	85655.12	40593.27
AT1G05150	gi 15220436	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	10	10	301.83	0.002	3.088	53032.31	56705.44	37995.35	34822.48	88780.19	121586	201784.7	151535.7
AT3G57530	gi 6706424	calcium-dependent protein kinase [Arabidopsis thaliana]	signal transduction	5	5	50.4	0.040	0.514	354051.7	278831.7	234605.2	208009.8	160238.8	105164	220150.5	66776.16
AT1G52540	gi 5903051	Contains PF00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene [Arabidopsis thaliana]	signal transduction	6	6	149.2	0.003	4.004	64724.14	69466.89	85152.22	81066.05	140550.7	236058	468940.7	357300.4
AT4G21940	gi 15234656	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	4	4	69.26	0.033	2.229	32704.18	31400.18	17921.36	16309.26	27962.04	66318.47	50730.06	74222.57
AT3G10620	gi 8567796	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative [Arabidopsis thaliana]	signal transduction	2	2	29.38	0.031	0.481	99645.71	71145.72	111766.9	106094.7	59784.13	44565.76	63055.57	19360.33
AT1G43890	gi 8778652	F9C16.3 [Arabidopsis thaliana]	signal transduction	1	1	#N/A	0.045	2.186	23703.04	26061.53	30602.59	23651.6	26459.79	63604.07	92331.58	45025.98
AT4G09000	gi 1255987	GF14chi isoform [Arabidopsis thaliana]	signal transduction	6	6	114.88	0.003	5.103	7370.693	16369.85	20652.13	7272.175	43317.96	41775.99	80350.56	98197.03

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT4G28490	gi 15235312	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2	2	36.74	0.015	0.164	16969.23	20225.46	41567.08	41577.47	947.9721	5422.585	12325.74	998.3473
AT3G51740	gi 15231029	IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	20	20	773.79	0.018	2.415	585830.6	774847.1	699488.4	562511.1	933216.2	1559886	2722990	1116645
AT2G19230	gi 240254475	kinase [Arabidopsis thaliana]	signal transduction	3	3	65.71	0.017	0.377	61505.19	51017.75	39759.03	43092.59	33525.64	13951.35	6993.107	19131.81
AT1G51800	gi 15218033	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	4	4	100.57	0.032	3.800	414824.2	964018.8	920453.1	858166.4	5458865	875699.7	2719066	2945018
AT2G14510	gi 15225949	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	7	7	76.69	0.027	0.193	36696.44	20756.4	67882.26	74818.81	16310.58	18002.58	2732.047	1501.884
AT3G53590	gi 15231843	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	2	2	33.27	0.042	0.252	9749.412	14489.12	18074.3	22738.14	3563.647	11803.95	259.0584	777.1362
AT2G31880	gi 15225153	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3	3	34.97	0.005	5.007	15095.46	14157.01	5105.479	8392.473	51733.85	26560.98	95051.41	40724.58
AT2G26730	gi 15225780	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3	3	119.67	0.003	4.440	64251.98	74805.22	62910.84	50365.51	153002.9	193423.4	548095.3	225752.4
AT3G08680	gi 15231955	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	4	4	100.29	0.004	3.901	71933.28	73787.13	43990.74	38258.54	130806.6	150417.4	358002.4	250130.3
AT1G06840	gi 15222211	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	10	10	243.91	0.005	2.907	120760.9	123237.3	91173.57	83281.81	171810	239577.1	394767	410317.9
AT3G02880	gi 15233013	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	30	30	1685.4	0.001	2.261	3898685	4101136	3250624	3321486	5436870	8993915	9277394	9241469
AT5G16590	gi 15237379	LRR1; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	17	17	658.58	0.005	2.272	429098.8	409463	279244.6	274055.6	520576.2	734550.1	931525.6	975126.4
AT1G21880	gi 18395044	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	7	7	377.89	0.030	2.304	174110.6	199089.9	256990.6	187826.7	252202.2	328281.9	794754.9	509763
AT2G17120	gi 18398317	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	6	6	176.11	0.003	2.854	742678.9	544549	322206.1	409223.7	1453072	1095819	1175719	2035644
AT5G06320	gi 15239999	NHL3 [Arabidopsis thaliana]	Signal transduction	7	7	395.45	0.000	3.097	1279918	987566.4	1366484	1417664	3987186	2902012	3585615	5170107
AT1G27460	gi 18396347	NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding [Arabidopsis thaliana]	signal transduction	3	3	23.42	0.043	1.765	351710.2	402570.3	240957.1	264253.9	687593.4	354961.8	442606.6	737700.7
AT1G73080	gi 15219370	PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	6	6	80.4	0.017	0.450	145749.8	256092.8	212128.3	208792.8	117445.3	104103.1	105218.2	43506.02
AT1G77630	gi 30699276	peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	Signal transduction	13	13	645.92	0.007	4.860	275102.6	459171.4	464234.5	301300.5	1078348	778118.1	3536482	1896179
AT5G58670	gi 18424132	PLC1 (PHOSPHOLIPASE C 1); phospholipase C [Arabidopsis thaliana]	Signal transduction	6	6	230.9	0.000	14.061	68897.62	65786.05	52020.56	48604.06	386182	565725	1038449	1318265
AT2G33580	gi 15226133	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	signal transduction	5	5	170.36	0.003	6.958	19068.33	23694.29	12429.56	13046.57	43249.8	82660.38	230926.5	117987.4
AT4G23200	gi 15236421	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	5	5	52.94	0.000	4.087	197546.5	153476.5	119622.5	103213	489188.5	427702.9	788658.9	639545.9
AT1G70520	gi 15223169	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	9	9	279.79	0.013	2.105	198411.5	218992.5	138290.2	148390.4	218927.8	348352.6	456814.7	457825.8
AT3G24550	gi 13877617	protein kinase-like protein [Arabidopsis thaliana]	signal transduction	25	25	942.22	0.003	1.714	1414149	1817612	2135422	1813788	2469814	3142168	3338787	3358154
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	signal transduction	10	10	558.33	0.000	4.179	178601	220628.3	179826.8	134860.6	530037.2	615762.1	1016932	820576.8
AT5G24390	gi 15238518	RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	signal transduction	2	2	25.33	0.002	7.400	5564.568	7284.399	7126.307	5767.059	26248.88	20864.49	85466.49	57906.74
AT5G59840	gi 15238542	Ras-related GTP-binding family protein [Arabidopsis thaliana]	signal transduction	3	3	109.33	0.023	0.381	316370.4	293963.9	344547	414799.2	181019.8	156735.7	145371	39141.92
AT1G15530	gi 15218220	receptor lectin kinase, putative [Arabidopsis thaliana]	Signal transduction	7	7	172.1	0.010	3.386	116932	129518.1	81770.23	87514.43	174746.5	243308.3	638705.2	350801.1
AT1G51790	gi 12321675	receptor protein kinase, putative [Arabidopsis thaliana]	signal transduction	5	5	51.57	0.019	0.491	204175.2	164591.7	262279.5	326461.1	177543.3	110039.7	106089.1	76220.8
AT4G23250	gi 4008012	receptor-like protein kinase [Arabidopsis thaliana]	signal transduction	7	7	187.8	0.040	1.965	13133.25	19629.93	7755.861	8395.551	15145.22	21238.06	32126.63	27589.12
AT4G23190	gi 4127461	receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	signal transduction	11	11	281.83	0.000	4.452	34985.59	43316.24	21368.23	20739.52	101754.5	120407.9	128907.7	184973.5
AT3G56100	gi 269969409	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-LIKE KINASE; Flags: Precursor	signal transduction	4	4	65.85	0.011	5.763	362.2148	1403.031	1358.948	1401.405	2342.418	5680.523	12202.55	5855.606
AT1G51810	gi 75334565	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51810; Flags:	signal transduction	2	2	57.63	0.025	3.650	2049.909	1721.723	5420.447	8345.978	27566.51	17330.15	11436.9	7676.614

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT3G17840	gi 18401662	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	10	10	416.58	0.018	1.986	391795.8	354011.8	226638.4	232663.9	701251.9	417818.9	801174.3	473204.9
AT4G23270	gi 3021279	serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	8	8	123.77	0.002	2.378	106912.2	110243	96285.9	78441.77	157173.4	274560.9	278873.9	221198.3
AT4G23180	gi 3021270	serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction	7	7	110.46	0.028	0.287	102830.1	94770.56	107186.2	93549.92	59471.79	39128.73	4775.047	10899.49
AT1G53730	gi 15220928	SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Signal transduction	4	4	74.93	0.034	2.704	21855.14	26106.4	13066.91	12328.11	34210.85	50102.84	24102.93	89974.03
AT4G17280	gi 240255971	unknown protein [Arabidopsis thaliana]	signal transduction	3	3	49.43	0.017	13.939	2724.772	4279.985	2565.884	941.3964	33431.24	8899.315	7332.058	96864.02
AT2G23810	gi 13272397	unknown protein [Arabidopsis thaliana]	signal transduction	4	4	157.4	0.001	3.687	215424.5	193092.9	201879.5	175345.8	746386	478503.2	533494	1138764
AT1G11330	gi 5734724	Very similar to receptor-like protein kinase [Arabidopsis thaliana]	signal transduction	4	4	70.24	0.015	0.504	25474.54	31466.89	35888.12	36907.48	13731.15	25855.25	9869.773	15930.6
AT2G34160	gi 52696237	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At2g34160	transcription	2	2	32.27	0.022	0.372	130661.9	92184.35	125684.4	97923.7	61062.58	45837.02	46690.49	12499.66
AT1G02080	gi 42561615	transcriptional regulator-related [Arabidopsis thaliana]	transcription	7	7	41.32	0.033	4.339	109745	73663.29	66081.3	60046.89	125842.9	302985.5	140230.9	773916.6
AT3G15030	gi 8777486	unnamed protein product [Arabidopsis thaliana]	transcription	1	1	19.19	0.024	0.180	24751.63	18571.72	19139.23	23366.45	2640.64	12278.98	216.6614	318.394
AT5G57350	gi 15242103	AHA3; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	Transporter	11	11	329.9	0.001	14.746	666.0543	1265.472	235.1467	280.0548	4628.913	11456.22	8850.822	11143.94
AT3G47950	gi 30692952	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	Transporter	13	13	272.02	0.012	10.306	19272.21	24746.08	10931.66	8618.009	34103.62	110972.4	90542.1	419521.7
AT1G80660	gi 6730723	aha9, 5' partial; 1-2403 [Arabidopsis thaliana]	Transporter	9	9	183.27	0.003	0.147	41665.09	25939.72	17790.15	57183.76	6426.93	8975.018	1929.967	3557.703
AT1G44100	gi 608673	amino acid permease [Arabidopsis thaliana]	Transporter	1	1	73.91	0.011	5.941	25564.84	34183.48	7112.917	4989.537	95705.26	93083.09	51058.89	187005.7
AT4G13510	gi 15236300	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana]	Transporter	3	3	278.26	0.017	2.629	1554280	1588017	859380.5	564330	2348237	1963656	4430984	3259471
AT3G47730	gi 22331647	ATATH1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	Transporter	10	10	277.27	0.007	3.006	35213.09	52699.54	20375.55	31701.86	80355.64	95798.15	170224	74421.78
AT2G38940	gi 15224985	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	Transporter	11	11	757.44	0.004	3.404	1125111	966554.1	1824168	1744054	2491431	5776419	6320077	4677790
AT5G57110	gi 8843813	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	Transporter	23	23	993.38	0.006	2.586	1177413	1631098	1055178	995031.7	1872377	2619236	4317602	3754611
AT1G69480	gi 12597793	hypothetical protein [Arabidopsis thaliana]	Transporter	7	7	177.39	0.000	7.413	18419.45	18244.4	19205.87	16586.89	137301.6	103363.7	67602.34	228852.8
AT1G72150	gi 15218382	PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana]	Transporter	9	9	268.56	0.003	14.003	59567.88	98641.35	27115.09	18396.55	328817	294055.8	764477	1465283
AT2G37280	gi 15228112	PDR5 (PLEIOTROPIC DRUG RESISTANCE 5); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporter	3	3	30.2	0.045	16.381	1418.889	2924.114	3696.228	2368.85	99058.16	51350.61	2235.117	17846.61
AT5G49990	gi 9758398	permease [Arabidopsis thaliana]	Transporter	3	3	80.09	0.036	5.314	23289.23	22348.01	31891.38	30499.52	33974.24	140183.1	331773	68125.42
AT5G43350	gi 15239848	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	Transporter	11	11	588.36	0.010	3.027	186809.1	284095.4	464996	397922.2	607762	964760.3	1670786	794208
AT4G35100	gi 1688296	plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]	Transporter	1	1	32.4	0.017	6.183	25925.42	36507.9	50172.12	32422.57	88893.43	125934.1	583972.9	97920.44
AT2G29940	gi 3420057	putative ABC transporter [Arabidopsis thaliana]	Transporter	7	7	99.19	0.002	4.120	283506.5	365471.5	406402.6	350468.2	1940728	744511.7	2005190	1101601
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporter	5	5	146.75	0.014	10.432	6989.681	8830.893	17076.52	15353.21	93498.41	82327.6	21368.85	306151.9
AT1G71880	gi 15217601	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	Transporter	3	3	72.98	0.000	0.075	26912.55	20423.21	32055.06	27538.24	944.1972	4009.881	1448.252	1579.507
AT2G39350	gi 15225076	ABC transporter family protein [Arabidopsis thaliana]	transporters	8	8	122.37	0.001	11.524	22216.95	18409.18	9186.243	9549.21	148663.4	89659.33	96660.89	349121
AT3G47780	gi 4741195	ABC transporter-like protein [Arabidopsis thaliana]	transporters	3	3	64.43	0.046	0.514	306575.5	328107.5	255065.7	228194.3	217315.3	97773.71	197565.9	61421.04
AT5G04930	gi 18414733	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism [Arabidopsis thaliana]	transporters	6	6	73.04	0.008	2.694	9686.233	18138.01	11706.32	11754.83	20150.43	27565.07	39614.84	50810.08
AT1G08090	gi 15223123	ATNRT2;1 (NITRATE TRANSPORTER 2;1); nitrate transmembrane transporter [Arabidopsis thaliana]	transporters	3	3	30.27	0.025	0.411	37882.33	24725.1	17734.56	17285.75	14491.65	9776.479	4519.872	11299.86

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT1G57990	gi 15217805	ATPUP18; purine transmembrane transporter [Arabidopsis thaliana]	transporters	1	1	35.37	0.006	3.500	22180.22	24211.76	18803.61	14467.59	39639.83	56675.56	53591.21	128935.2
AT3G16340	gi 18401096	PDR1; ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	16	16	375.22	0.001	4.236	121667.4	123135.2	156778.6	138225.9	647155.2	337446.6	465438.6	836370.5
AT2G26910	gi 15225814	PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	4	4	92.32	0.049	0.312	22960.39	9370.507	20726.07	22061.88	7305.856	7858.31	7338.02	943.9019
AT3G55320	gi 15233244	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	4	4	33.71	0.004	2.350	145729.4	140870.2	115880.6	78377.64	245613.7	367322.2	206478.2	310690.6
AT4G32390	gi 15236781	phosphate translocator-related [Arabidopsis thaliana]	transporters	1	1	22.1	0.020	0.361	154376.5	130655.5	189841.2	229289.2	87798.41	67721.41	78261	20076.1
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis thaliana]	transporters	5	5	182.55	0.008	2.111	21212.03	15268.19	15065.32	13488.97	31153.27	22796.06	34689.75	48666.14
AT2G37180	gi 15228096	RD28 (RESPONSIVE TO DESICCATION 28); water channel [Arabidopsis thaliana]	transporters	1	1	32.94	0.012	6.556	3575.109	938.5811	4587.352	2398.036	8087.5	13439.06	43025.04	10832.58
AT1G30410	gi 75333513	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABCC.12; Short=AtABCC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName: Full=Multidrug resis	transporters	1	1	24.76	0.042	0.259	128272.6	130355.5	186018.1	183830.5	53931.36	46495.72	58891.53	3741.155
AT3G51670	gi 15230555	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	transporters	3	3	37.95	0.010	0.298	52292.16	39351.38	30746.76	36590.84	7152.228	13513.53	22221.84	4534.618
AT1G13210	gi 15222212	ACA.1 (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding [Arabidopsis thaliana]	unknown	5	5	120.35	0.006	4.244	5957.747	7845.609	3112.98	3133.405	26926.92	10651.09	32510.04	15009.3
AT1G31810	gi 186479105	actin binding [Arabidopsis thaliana]	unknown	6	6	40.01	0.017	0.359	37561.97	32652	48174.46	51105.23	21344.97	23165.18	5388.126	11008.51
AT1G52320	gi 15450411	At1g52320/F19K6_7 [Arabidopsis thaliana]	unknown	1	1	26.37	0.020	14.224	136.688	537.5428	126.9332	102.3614	1961.522	3929.599	301.7461	6659.008
AT1G51640	gi 15217995	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding [Arabidopsis thaliana]	unknown	4	4	40.25	0.007	0.398	103444.4	87795.04	102441.8	93390.07	61205.33	30597.76	43210.84	19084.05
AT4G23630	gi 15236556	BTII (VIRB2-INTERACTING PROTEIN 1) [Arabidopsis thaliana]	unknown	4	4	76.77	0.045	0.245	22100.44	20125.76	23315.57	17679.55	2508.839	6459.841	281.1044	11131.63
AT1G51570	gi 15217968	C2 domain-containing protein [Arabidopsis thaliana]	unknown	4	4	41.26	0.048	20.300	72.31868	5517.35	3014.466	3627.424	6815.965	32567.01	190155.7	18762.75
AT4G20260	gi 15235363	DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana]	Unknown	5	5	230.1	0.005	9.997	350161.1	233149.4	275255	339152.4	755074.4	1486961	4308560	5423014
AT4G00310	gi 18411286	EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana]	unknown	2	2	16.66	0.010	0.438	25088.33	13190.83	19092.61	33294.42	8508.611	11649.66	9843.935	9708.922
AT1G71820	gi 7239509	EST gb AA712174 comes from this gene [Arabidopsis thaliana]	Unknown	4	4	57.31	0.024	2.383	42734.27	51993.65	17638.23	19642.66	50095.98	70430.97	95623.61	98404.54
AT1G61900	gi 3367523	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	Unknown	8	8	181.86	0.002	1.972	89234.8	98335.82	67748.26	59741	147352.8	184049.5	160072.1	129703.6
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	58.73	0.001	9.428	113066.2	81498.55	33239.17	45018.55	972891.7	536752.9	316037.5	746522.5
AT2G30480	gi 110741415	hypothetical protein [Arabidopsis thaliana]	unknown	5	5	57.47	0.012	3.978	1745491	3572262	4870899	4721024	23830966	6167759	17312456	12000007
AT3G15410	gi 2760084	leucine-rich repeat protein [Arabidopsis thaliana]	unknown	3	3	33.73	0.047	0.378	15556.56	18348.02	52712.53	48634.34	11344.72	12408.38	17440.4	9882.141
AT5G42020	gi 1303695	luminal binding protein (BiP) [Arabidopsis thaliana]	unknown	3	3	109.75	0.034	0.068	36.32165	5003.107	1548.496	2198.125	0	599.9009	0	0
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	unknown	10	10	241.38	0.000	2.920	130538.1	136433.9	112113.2	103826.6	229685.9	350648.2	432100.5	397660
AT5G61800	gi 15240355	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	unknown	3	3	38.41	0.016	0.511	85102.49	72909.66	67302.27	88825.67	55035.68	39724.49	44864.37	20840.99
AT4G33700	gi 3549672	putative protein [Arabidopsis thaliana]	unknown	1	1	66.71	0.032	3.512	57023.85	49410.88	26480.68	18320.49	64325.09	71767.21	273239.6	121750.9
AT5G30520	gi 7413621	putative protein [Arabidopsis thaliana]	unknown	2	2	29.11	0.034	0.235	15352.92	6548.102	4497.945	4462.137	3193.122	2068.138	322.8711	1670.753
AT4G06544	gi 7529254	putative protein [Arabidopsis thaliana]	unknown	2	2	29.32	0.007	0.463	52256.86	50524.25	40320.88	34588.16	22920.45	18261.99	28631.1	12483.84
AT3G44150	gi 7635460	putative protein [Arabidopsis thaliana]	unknown	4	4	88.65	0.039	1.981	151755.9	134418.2	71406.96	86994.08	151092.4	152023.1	297255	280335
AT3G60920	gi 8388608	putative protein [Arabidopsis thaliana]	unknown	5	5	41.15	0.007	1.716	175446.4	196415.1	231213.1	223746.2	428635.1	295241.4	417920	276943.9
AT4G34440	gi 3641836	putative serine/threonine protein kinase [Arabidopsis	unknown	4	4	47.71	0.018	0.128	152097.5	122126.7	21477.67	26528.6	8761.548	10331.88	16213.15	5998.847
AT5G14770	gi 223635763	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial; Flags: Precursor	unknown	4	4	52.61	0.011	0.326	4024.987	4288.127	4904.896	10514.94	2304.068	2843.177	1368.178	1217.607
AT1G11820	gi 3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene [Arabidopsis	Unknown	1	1	39.56	0.046	1.958	44536.03	38054.25	16294.65	26227.71	52856.92	51175.08	45710.95	95173.24



ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	ABA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	ABA1	ABA2	ABA3	ABA4
AT2G19580	gi 15224802	TET2 (TETRASPANIN2) [Arabidopsis thaliana]	unknown	1	1	34.41	0.047	2.579	3760.951	2957.039	739.6652	1230.068	3307.36	6177.918	8581.761	4334.593
AT2G31290	gi 15224649	ubiquitin thiolesterase [Arabidopsis thaliana]	unknown	3	3	35.91	0.034	0.408	71957.69	62374.13	69191.46	160115.6	25644.06	50564.44	52778.12	19261.76
AT1G17147	gi 116830105	unknown [Arabidopsis thaliana]	unknown	2	2	30.92	0.012	0.144	36991.45	40340.3	30130.76	49674.97	4807.257	6942.502	10268.18	549.9105
AT3G45460	gi 116831268	unknown [Arabidopsis thaliana]	unknown	4	4	34.18	0.010	6.686	2100.909	1691.205	3873.233	6332.434	7083.143	15573.26	43069.16	27870.48
AT2G41800	gi 15227437	unknown protein [Arabidopsis thaliana]	Unknown	1	1	22.8	0.003	7.111	39402.05	32150.97	41603.77	32993.28	118851.1	177820.1	601814.2	140819.2
AT5G19240	gi 15239686	unknown protein [Arabidopsis thaliana]	unknown	1	1	40.86	0.007	2.203	15189.5	10657.68	5912.326	7370.023	24252.28	20513.4	21081.31	20356.75
AT3G17350	gi 15229029	unknown protein [Arabidopsis thaliana]	Unknown	2	2	51.72	0.001	4.325	22939.31	18607.94	9637.12	9348.871	48283.2	60033.44	95604.38	57867.07
AT2G40980	gi 15226796	unknown protein [Arabidopsis thaliana]	unknown	2	2	27.8	0.003	8.886	512.524	945.4107	1195.989	752.7715	3146.924	3757.584	16854.04	6514.268
AT5G56170	gi 15241141	unknown protein [Arabidopsis thaliana]	unknown	2	2	83.41	0.011	3.311	105441	146381.3	86966.75	80235.01	192385.6	200726.6	606428.3	387679.5
AT3G08600	gi 18398173	unknown protein [Arabidopsis thaliana]	Unknown	3	3	118.32	0.030	2.172	102407.7	69029.74	38105.66	25725.18	108290.2	135966.7	110840.1	155851
AT2G27260	gi 18401372	unknown protein [Arabidopsis thaliana]	unknown	3	3	90.26	0.027	2.812	2291.923	3227.747	578.5081	736.8678	4153.42	6574.073	4212.721	4276.756
AT4G35730	gi 79497106	unknown protein [Arabidopsis thaliana]	unknown	3	3	27.98	0.007	0.404	11165.23	11341.6	12917.6	13110.57	4791.997	5292.82	7181.759	2335.55
AT4G28100	gi 18417127	unknown protein [Arabidopsis thaliana]	Unknown	4	4	148.07	0.023	3.154	156807.4	129427.3	47812.62	55921.46	377444.6	174643.3	189389.2	488660.6
AT4G08760	gi 15236604	unknown protein [Arabidopsis thaliana]	unknown	4	4	58.87	0.003	0.196	38686.64	53531.88	37338.23	34278.83	6486.909	17059.56	5441.712	3042.072
AT2G21990	gi 15227126	unknown protein [Arabidopsis thaliana]	unknown	4	4	30.87	0.002	2.344	18663.04	16923.49	14506.53	12709.52	25792.63	32289.42	47047.83	42074.71
AT2G25800	gi 3643603	unknown protein [Arabidopsis thaliana]	Unknown	7	7	232.21	0.015	3.628	125648.5	183003.9	45394.94	35135.5	344514	203606.3	452657.4	411185.2
AT2G26570	gi 15225334	unknown protein [Arabidopsis thaliana]	unknown	7	7	51.73	0.031	0.367	17445.67	17836.88	45330.02	50425.97	9153.219	12731.78	17201.96	8988.522
AT2G28310	gi 30683843	unknown protein [Arabidopsis thaliana]	unknown	7	7	33.09	0.007	3.126	215215.5	215154.8	132730.7	105562.3	316299.3	432489.6	870786.5	470899.5
AT5G06970	gi 22326641	unknown protein [Arabidopsis thaliana]	unknown	10	10	212.99	0.039	1.757	126733	148485.2	164901.1	161800.7	330743	168227.8	360515.9	198376.1
AT5G58160	gi 8777317	unnamed protein product [Arabidopsis thaliana]	unknown	4	4	32.36	0.044	0.304	166964.9	142318.2	224368.6	237434.5	85336.48	83698.6	58021.18	7637.823

Supplementary Table 3-5 CA-responsive plasma membrane proteins at the lag phase

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	cell growth/division	3	3	53.7	0.009	2.754	35355.25981	46964.36651	26211.13398	35408.54423	156128.4112	86805.0686	100521.9646	53016.04182
AT1G74790	gi 5882745	F25A4.24 [Arabidopsis thaliana]	Cell growth/division	14	14	596.4	0.009	3.899	2384101.429	2887772.561	1254664.27	1217958.398	13440749.52	7668429.878	5097149.728	3988276.338
AT5G57970	gi 15242914	methyladenine glycosylase family protein [Arabidopsis thaliana]	cell growth/division	1	1	23.48	0.002	0.317	263039.4759	249429.7978	198988.3249	173817.5673	52767.21449	45967.45181	67717.59191	113867.5652
AT3G13210	gi 10172609	probable cell cycle control protein; crooked neck-like protein [Arabidopsis thaliana]	cell growth/division	4	4	36.13	0.001	0.308	258096.6582	214119.5921	301843.3837	287899.7394	72650.2338	52730.87666	75242.38209	126645.9172
AT4G29090	gi 2583130	putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	Cell growth/division	5	5	42.13	0.028	0.259	30675.13566	19650.95333	68200.09963	81235.1439	5388.505358	9851.753728	28127.75491	8283.816097
AT1G31970	gi 15222526	(STRESS RESPONSE SUPPRESSOR 1); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]	cell growth/division	3	3	28.79	0.022	2.317	72390.11873	84690.03239	125723.6123	108299.8007	256871.7786	222218.2741	316452.2554	110501.2417
AT3G45600	gi 15231187	TET3 (TETRASPANIN 3) [Arabidopsis thaliana]	Cell growth/division	5	5	216.24	0.004	2.480	96577.34365	86834.94412	41790.65443	46091.19005	187438.997	171308.1957	166395.7382	147775.7055
AT4G28050	gi 15234374	TET7 (TETRASPANIN 7) [Arabidopsis thaliana]	Cell growth/division	1	1	41.74	0.010	2.171	69154.38983	67510.48758	42301.99857	35207.37944	151331.354	130632.1177	90869.53155	92155.56999
AT5G03340	gi 11265361	transitional endoplasmic reticulum ATPase - [Arabidopsis thaliana]	cell growth/division	4	4	141.37	0.027	2.154	63444.93357	95737.68313	61039.78125	36186.57414	82341.72681	152476.7773	125537.4316	191961.6548
AT5G37140	gi 15240114	tRNA-splicing endonuclease positive effector-related [Arabidopsis thaliana]	cell growth/division	3	3	22.97	0.036	0.414	77545.16671	72489.21613	174876.5788	185855.1708	38987.04403	40160.42421	85258.29006	47020.17433

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G68560	gi 4163997	alpha-xylosidase precursor [Arabidopsis thaliana]	Cell structure	8	8	131.46	0.000	1.964	148086.3838	181682.8093	173371.9371	157128.3936	343507.9496	365262.996	314545.2735	273352.5958
AT5G65020	gi 15238320	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding	cell structure	3	3	30.58	0.007	0.377	534256.173	436942.7493	551609.9218	576423.5632	210881.4698	91208.61918	187376.7731	302458.2764
AT1G75680	gi 15222328	ATG9B7 (Arabidopsis thaliana glycosyl hydrolase 9B7); catalytic/hydrolase, hydrolyzing O-glycosyl compounds	Cell structure	13	13	538.42	0.005	3.127	1614117.055	1375666.28	681350.0836	576980.1838	4599417.11	2914604.835	2930082.834	2839637.255
AT1G53840	gi 15220958	ATPME1; pectinesterase [Arabidopsis thaliana]	Cell structure	5	5	263.45	0.004	2.954	113616.1126	95110.36386	51013.74681	51040.61153	300525.5228	264666.9224	187296.4891	165562.5988
AT3G14300	gi 15231826	ATPMEPCRC; pectinesterase [Arabidopsis thaliana]	cell structure	4	4	30.77	0.019	2.858	31946.45565	34183.35058	17947.42797	16621.54364	120702.3022	74026.47178	57519.00815	35554.37059
AT1G01980	gi 15217586	ATSEC1A; FAD binding / catalytic/electron carrier/oxidoreductase [Arabidopsis thaliana]	Cell structure	5	5	148.34	0.017	3.494	151342.9344	169160.7532	214210.8002	201673.5342	1233768.3	510584.9329	581236.4322	247413.9746
AT1G66250	gi 12323569	beta-1,3-glucanase precursor, putative; 34016-35272 [Arabidopsis thaliana]	cell structure	4	4	318.73	0.001	4.532	96967.2835	105137.9046	64863.88929	74518.68379	491488.7055	322920.4228	525333.9822	208034.0884
AT3G13560	gi 9280308	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	cell structure	6	6	236.6	0.003	3.220	104658.3648	139880.634	69957.46799	70028.21882	396042.2925	375251.9855	283208.53	183568.9188
AT5G20230	gi 16203	blue copper-binding protein [Arabidopsis thaliana]	cell structure	3	3	215.36	0.004	4.990	657292.1851	549990.4574	357812.3411	367555.9458	4651279.716	2357815.591	1353514.55	1282200.505
AT1G32860	gi 6910583	CDS [Arabidopsis thaliana]	cell structure	6	6	178.93	0.000	4.374	123597.0816	132478.0243	164050.2262	143462.7194	428863.6469	678642.9654	932669.5783	424915.7035

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G20130	gi 15231052	CYP705A22; electron carrier/ heme binding / iron ion binding / monooxygenase / oxygen binding [Arabidopsis thaliana]	cell structure	5	5	39.74	0.032	0.627	348071.6518	352510.4424	526796.6917	504010.6153	226472.7895	206653.4991	370387.0352	281733.9219
AT4G37410	gi 15235541	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase / oxygen binding [Arabidopsis thaliana]	cell structure	2	2	39.23	0.006	9.751	210.0016294	90.2566144	227.5981788	139.7015152	4189.493972	810.5231139	879.5398194	629.8621455
AT4G20830	gi 30685222	FAD-binding domain- containing protein [Arabidopsis thaliana]	Cell structure	30	30	1379.42	0.011	3.314	939938.5263	840542.1574	928898.0292	1189352.323	5036110.909	2747950.159	3832681.676	1302970.358
AT4G12730	gi 13377778	fasciclin-like arabinogalactan- protein 2 [Arabidopsis thaliana]	cell structure	16	16	1084.46	0.003	4.684	6262583.661	5652025.448	4443170.015	5250667.255	38773263.67	25465221.93	27029245.85	9943687.997
AT5G55730	gi 15240570	FLA1 (FASCICLIN- LIKE ARAB INO GALACTAN 1) [Arabidopsis thaliana]	Cell structure	18	18	1011.03	0.003	4.356	5461346.488	6614709.695	3646261.577	3312602.066	31995736.02	19378723.56	21649675.76	9894211.356
AT5G44130	gi 15241423	FLA13 (FASCICLIN- LIKE ARABINO GALA CTAN PROTEIN 13 PRECURSOR) [Arabidopsis thaliana]	Cell structure	3	3	74.29	0.011	5.997	55388.75466	44068.10123	106613.7761	111557.3134	412117.8533	476128.8573	884964.6369	131727.2292
AT2G04780	gi 18395849	FLA7 (FASCICLIN- LIKE ARABINO GAL ACTAN 7) [Arabidopsis thaliana]	cell structure	4	4	230.58	0.002	4.585	232988.4186	257436.9001	156102.1015	143630.4683	1468575.838	920484.0075	801925.2422	431730.7666
AT2G45470	gi 18406799	FLA8 (FASCICLIN- LIKE ARABINO GALA CTAN PROTEIN 8) [Arabidopsis thaliana]	Cell structure	8	8	455.95	0.000	4.904	2137491.312	2858283.004	2324712.88	1854587.776	13355541.61	11321167.54	13596150.6	6721130.353

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G03870	gi 18379157	FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) [Arabidopsis glycosyl	Cell structure	1	1	95.34	0.006	5.125	324018.0056	308846.2678	242228.4736	267998.1919	2767042.334	1179628.977	1398948.162	512590.5581
AT2G01630	gi 18379267	hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis glycosyl	Cell structure	5	5	184.47	0.019	2.889	32760.69338	42270.75585	61228.53926	47292.1188	91619.4883	91437.67573	262790.8525	84519.82561
AT5G18220	gi 15238768	hydrolase family 17 protein [Arabidopsis thaliana] glycosyl	cell structure	2	2	24.94	0.040	5.351	548.1558771	2458.934329	189.9493336	31.20479461	3624.960511	7707.877994	1654.088602	4286.852579
AT5G04885	gi 30680681	hydrolase family 3 protein [Arabidopsis thaliana] glycosyl	Cell structure	31	31	1192.08	0.001	3.898	2339539.706	3013211.181	2391261.99	2291267.347	10838064.79	9563828.905	13866728.13	4850725.741
AT5G20940	gi 22326918	hydrolase family 3 protein [Arabidopsis thaliana] glycosyl	cell structure	4	4	90.71	0.003	0.344	34104.31407	22389.87112	23621.47413	40010.04633	12539.64636	6085.030798	10831.35715	11920.53712
AT4G03340	gi 304281941	glycosyltransferase family 14 protein [Arabidopsis	cell structure	3	3	24.71	0.005	0.208	76503.24271	71830.06947	151742.9555	138481.7557	15675.32499	8861.401077	25685.29767	41010.48305
AT2G30870	gi 15224582	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase	Cell structure	3	3	36.65	0.037	2.003	15487.11035	16311.63056	15937.48289	15753.30449	41082.29325	33307.52718	37914.47497	14845.01232
AT5G61130	gi 30697478	PDCB1 (PLASMODESMATA CALLOSE-BINDING PROTEIN 1); callose binding / polysaccharide binding [Arabidopsis thaliana]	cell structure	1	1	28.32	0.039	2.750	16218.53616	11570.79176	3379.382316	5068.463969	40251.25325	26118.18934	19318.0904	13958.3098

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G48450	gi 8777375	pectinesterase-like protein [Arabidopsis thaliana]	cell structure	3	3	82.19	0.016	2.592	57643.56425	80176.22873	52458.58562	62173.35006	83579.49925	138833.0969	277725.3963	154301.777
AT5G17820	gi 15238030	peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana]	Cell structure	10	10	365.77	0.000	4.456	68435.05154	65899.66722	99982.76349	97531.4879	445868.1491	426893.0843	383948.0864	222136.737
AT4G31840	gi 15236544	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	Cell structure	6	6	433.84	0.011	9.082	150420.7744	182955.343	564233.8437	399272.5393	5369840.063	3939648.348	1826188.797	643108.4021
AT5G25090	gi 15238698	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	cell structure	4	4	138.06	0.012	4.647	56069.88052	45352.11385	87458.37656	72675.61834	545578.3641	376682.7733	182616.6935	110476.606
AT1G42550	gi 240254220	PMT1 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	cell structure	7	7	69.45	0.010	3.827	531247.3602	516149.816	362570.3018	336989.7894	2488933.958	2148324.227	1430457.091	617188.1363
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	Cell structure	10	10	357.38	0.019	3.265	668464.9232	659748.7202	330674.4714	426120.1919	3099919.9	1644969.897	1324781.833	738551.6662
AT1G62790	gi 15221585	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Cell structure	3	3	52.09	0.004	5.813	1903.977747	5678.834897	4151.840077	6680.154537	45923.08139	23792.08141	25548.74145	11776.04546
AT2G13820	gi 15225509	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Cell structure	3	3	147.08	0.001	6.295	136422.8945	157553.2523	200576.9167	138698.7231	1678170.954	1039434.673	855569.2208	412836.5115
AT2G34730	gi 3132472	putative myosin heavy chain [Arabidopsis thaliana]	cell structure	4	4	52.19	0.010	3.444	16494.8056	29679.82795	66159.463	31445.87287	191019.4255	87763.10064	134804.9876	81660.85089
AT2G33240	gi 20196856	putative myosin heavy chain [Arabidopsis thaliana]	cell structure	7	7	50.25	0.038	2.385	641972.3061	520467.4634	1308018.639	964583.628	3741698.834	1296093.43	1682297.009	1471430.085
AT3G58100	gi 6735322	putative protein [Arabidopsis thaliana]	cell structure	2	2	83	0.024	2.665	73760.89396	77534.49738	51987.5702	38026.00591	74007.8058	220677.4535	220084.3075	128222.5183

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G03230	gi 4262151	putative receptor kinase [Arabidopsis thaliana]	cell structure	5	5	48.82	0.008	0.222	14124.08069	21479.21007	34232.68962	27398.26047	7966.424948	2755.465765	1948.243585	8882.785496
AT2G25060	gi 4559346	similar to early nodulins [Arabidopsis thaliana]	cell structure	5	5	435.73	0.022	7.254	84671.78569	98274.04636	479955.2628	394691.7751	3157241.134	2271701.477	1871395.734	371195.719
AT5G51480	gi 15242108	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	12	12	438.04	0.019	4.868	671452.3304	663614.9222	791673.0087	763655.8941	7132956.408	2965571.88	3058562.616	912883.4793
AT4G12420	gi 15234551	SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana]	Cell structure	24	24	1160.82	0.006	3.338	9709143.761	10185537.98	7744547.451	6905005.333	44874310.32	28038125.01	29075630.82	13310863.38
AT3G46550	gi 15231453	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding [Arabidopsis thaliana]	Cell structure	3	3	153.43	0.002	3.734	50044.30964	55821.33541	32671.27859	41917.77712	237274.123	183345.8908	164616.6437	88626.29692
AT4G27520	gi 21592865	unknown [Arabidopsis thaliana]	Cell structure	10	10	593.07	0.004	4.441	277848.9214	373172.2698	244604.0084	199938.3091	1889759.255	1364735.037	486346.6116	1124586.06
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	3	3	133.93	0.036	2.532	17577.89187	10568.22121	25261.78302	37241.92157	87756.57086	66749.16352	44439.84661	30538.64512
AT5G64080	gi 10176956	unnamed protein product [Arabidopsis thaliana]	Cell structure	3	3	116.17	0.010	6.263	49624.62937	62168.15878	98615.23473	70644.1441	815740.0182	605300.988	178055.391	161111.9914
AT3G49750	gi 15229606	AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana]	Disease/defence	2	2	122.16	0.005	3.227	25400.55323	17743.36131	16798.7606	16965.87733	93394.01369	53229.01299	70180.44498	31383.15771
AT4G01700	gi 15234281	chitinase, putative [Arabidopsis thaliana]	Disease/defence	5	5	194.39	0.029	2.513	527122.5865	603628.8048	263384.128	218405.2428	1463966.305	1126277.108	530269.5531	931590.7667
AT1G20440	gi 388259	cor47 [Arabidopsis thaliana]	disease/defence	1	1	37.28	0.000	3.807	8604.13116	6138.324996	10134.93329	12476.91601	43351.65029	33360.77118	35382.94214	30114.48822
AT1G32090	gi 15222569	early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Disease/defence	11	11	267	0.005	1.988	216827.0913	198672.844	186553.2874	231507.7348	537304.5437	335032.4491	489181.728	295254.5755

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G30360	gi 18397470	ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Disease/defence	20	20	830.72	0.008	2.355	440348.8692	364627.1768	202460.4516	242193.2933	1056046.74	563254.9646	702242.9801	620937.137
AT2G43610	gi 15224319	glycoside hydrolase family 19 protein [Arabidopsis thaliana]	Disease/defence	3	3	107.6	0.013	2.566	65464.80364	107553.4574	35483.52572	30490.7151	169286.3308	122497.0934	145736.1655	175853.6342
AT3G09440	gi 15232682	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) [Arabidopsis thaliana]	disease/defence	10	10	302.84	0.046	3.491	7297.951694	11565.61507	3312.565874	2260.799714	47667.58052	11782.06089	12857.62076	13003.56394
AT3G11010	gi 6016693	putative disease resistance protein [Arabidopsis thaliana]	disease/defence	1	1	18.91	0.044	8.682	0	2944.132982	233.437846	0	2197.865877	7190.601414	6392.588784	11806.94005
AT4G23260	gi 3021278	putative protein [Arabidopsis thaliana]	disease/defence	5	5	114.62	0.024	0.473	53415.49093	59574.23492	81561.00318	71849.72928	50667.35549	14853.66303	34889.83624	25467.92595
AT5G43470	gi 32364507	resistance protein Hod3 [Arabidopsis thaliana]	disease/defence	4	4	32.31	0.046	0.316	25402.30267	31903.08863	76770.02955	63192.06286	3774.87953	10350.87705	27011.81498	21199.80985
AT5G47910	gi 3242789	respiratory burst oxidase protein D [Arabidopsis thaliana]	disease/defence	4	4	86.13	0.002	4.047	91499.83651	92517.81869	40250.5946	49450.48841	334428.7067	229453.0335	377751.094	166090.969
AT4G02450	gi 3193303	T14P8.5 [Arabidopsis thaliana]	disease/defence	2	2	51.31	0.013	2.069	24947.99172	27825.02679	19834.40474	21452.35468	70238.71847	54280.92642	30655.70059	39397.9135
AT3G53990	gi 30693971	universal stress protein (USP) family protein [Arabidopsis thaliana]	disease/defence	3	3	69.19	0.004	4.180	10880.62418	23458.96734	8399.22186	7834.078365	29632.59352	58963.51148	76463.55524	46330.3972
ATCG00120	gi 7525018	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	Energy	9	9	327.59	0.036	6.815	29811.48202	36828.84987	95223.08943	100732.5988	582302.769	566231.0796	580961.3586	60049.44877
ATCG00480	gi 7525040	ATP synthase CF1 beta subunit [Arabidopsis thaliana]	Energy	8	8	311.23	0.026	2.406	604160.0793	874539.5778	1464724.294	1194300.392	3311939.462	2013036.863	3306257.739	1324579.975
AT3G55440	gi 414550	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	Energy	5	5	142.4	0.001	3.369	133533.5665	146579.3366	180108.9968	105063.78	357704.4074	543328.0396	668744.0029	334561.0092



ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G32840	gi 15233959	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase [Arabidopsis thaliana]	Energy	2	2	21.26	0.003	0.281	83019.07364	30499.78432	33576.06424	46574.84657	15188.47354	14530.1927	10529.56353	14107.2341
AT1G79550	gi 15219412	PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase [Arabidopsis thaliana]	Energy	1	1	46	0.000	2.015	21208.28631	28060.4843	19485.27973	20813.91695	51667.63294	39608.42824	41839.75603	47398.12838
AT5G09600	gi 2864622	putative protein [Arabidopsis thaliana]	Energy	2	2	24.1	0.032	0.405	71489.07343	55967.37006	135117.355	138339.4767	19758.69201	46933.94842	55296.87236	40300.72813
ATCG00490	gi 1944432	ribulosebiphosphate carboxylase [Arabidopsis thaliana]	Energy	4	4	42.96	0.006	0.219	4006.783194	7950.137495	4897.675038	14114.32534	1039.8193	2751.144226	1353.962646	1638.499993
AT3G56190	gi 15228848	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein [Arabidopsis thaliana]	Intracellular traffic	6	6	318.61	0.002	2.689	102769.2717	95614.03797	66510.29907	59472.34589	277506.2202	237839.1691	203548.2878	153395.8545
AT5G08680	gi 22326673	ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana]	Intracellular traffic	6	6	111.6	0.009	4.799	51357.16658	77320.31743	141336.9227	102372.275	934737.6424	326543.995	312795.1565	213013.9168
AT3G11820	gi 15229865	SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/protein anchor [Arabidopsis thaliana]	Intracellular traffic	10	10	285.07	0.001	2.492	158265.5079	127006.1451	119779.7881	135395.5525	432590.3725	369711.3015	316060.6496	228211.0656
AT5G08080	gi 18415701	SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor [Arabidopsis thaliana]	Intracellular traffic	9	9	499.52	0.002	2.737	482120.053	437745.0578	389085.9741	359476.3545	1552918.393	1227081.231	1111704.32	675289.0891

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G09740	gi 18398623	SYP71 (SYNTAXIN OF PLANTS 71); protein transporter [Arabidopsis thaliana]	Intracellular traffic	9	9	328.23	0.008	2.467	342832.4355	348123.3278	157493.181	141205.14	613957.8082	665409.4527	647920.8068	514334.8893
AT1G17620	gi 11762174	[Arabidopsis thaliana] formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	intracellular traffic	4	4	139.41	0.032	3.182	137012.7342	110229.1208	216163.1794	239108.4448	700212.7377	701793.3963	655387.418	177730.5716
AT2G33120	gi 600710	putative protein [Arabidopsis thaliana]	intracellular traffic	5	5	232.83	0.006	2.238	129491.0269	111530.6215	105264.9696	96531.23944	377827.2813	243032.2848	196628.3356	173734.2933
AT5G12370	gi 14586367	SEC8 (SUBUNIT OF EXOCYST COMPLEX 8) [Arabidopsis thaliana]	intracellular traffic	4	4	44.27	0.028	0.664	75678.86689	70580.95669	64884.82255	84215.10914	72087.13408	39184.50472	40536.21525	44303.77763
AT3G10380	gi 18398855	unknown protein [Arabidopsis thaliana]	intracellular traffic	3	3	17.39	0.019	2.168	6536.945832	8690.576338	3898.285257	3363.57196	8759.740295	10992.48544	16311.03789	12696.82663
AT3G52400	gi 5701797	unknown protein [Arabidopsis thaliana]	intracellular traffic	3	3	125.61	0.002	2.528	129227.9141	104933.9186	84408.94423	69472.38825	323702.6043	266546.6806	207475.4894	183388.7215
AT5G11890	gi 15239804	unknown protein [Arabidopsis thaliana]	intracellular traffic	5	5	169.92	0.028	3.106	45520.7197	51237.27412	40405.45504	43163.39108	301209.2564	108191.3908	74540.85134	76165.75998
AT1G45688	gi 18401556	unknown protein [Arabidopsis thaliana]	intracellular traffic	4	4	59.28	0.042	2.003	10466.15204	6724.477156	10087.38358	12748.41849	24344.22352	25251.24997	20639.31527	9929.545719
AT1G76850	gi 12322227	unknown protein [Arabidopsis thaliana]	intracellular traffic	4	4	39.75	0.048	0.444	10190.86846	10157.74755	18889.45659	28111.85178	10504.10286	4360.221635	7015.427624	7994.506975
AT5G62630	gi 14423506	Unknown protein [Arabidopsis thaliana]	intracellular traffic	12	12	559.6	0.044	2.845	1921180.906	2246193.435	645807.3136	623379.3533	6492703.487	4436442.465	1964910.597	2570627.24
AT5G36880	gi 145323645	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative [Arabidopsis thaliana]	metabolism	3	3	75.91	0.050	0.124	10672.4355	8170.286486	47703.98908	47339.37171	120.7879795	3121.685219	8250.26105	2602.873828
AT5G11520	gi 15239078	ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana]	metabolism	2	2	37.51	0.032	0.234	40187.45839	34324.10797	60824.3081	62682.0458	1209.167162	9587.021797	17457.17573	18142.66152

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G58090	gi 16604491	AT5g58090/k21119_70 [Arabidopsis thaliana]	metabolism	10	10	274.36	0.009	2.650	113013.8163	67364.26236	45021.06163	44049.91392	260324.9093	159367.1315	128689.5096	165678.878
AT4G35790	gi 18419668	ATPLDDELTA; phospholipase D [Arabidopsis thaliana]	Metabolism	9	9	327.18	0.003	2.019	182006.7107	170344.3284	149105.5255	152247.0789	444408.13	339667.3019	299672.1172	236098.9756
AT4G29360	gi 7269834	beta-1, 3-glucanase-like protein [Arabidopsis thaliana]	metabolism	5	5	146.35	0.017	4.629	63379.70646	66065.58295	27193.70132	21924.25304	431078.3525	178392.5143	132753.3607	84287.10677
AT5G17920	gi 55670112	Chain A, A. Thaliana Cobalamine Independent Methionine Synthase [Arabidopsis thaliana]	metabolism	15	15	195.48	0.014	0.285	53699.27765	63984.37075	72236.48819	86183.89131	5126.093285	16288.35131	35604.52714	21548.35033
AT3G25860	gi 9279589	emb1075 (embryo defective 1075); S-acetyltransferase [Arabidopsis thaliana]	metabolism	7	7	334.78	0.008	2.267	157934.3709	143930.5601	173723.0631	155944.0561	347692.5454	288541.2107	230749.3218	564881.9854
AT1G43710	gi 15218445	emb1075 (embryo defective 1075); carboxy-lyase/catalytic/ [Arabidopsis thaliana]	metabolism	2	2	19.66	0.008	3.753	39838.16817	38895.10373	34792.97769	41122.27708	69307.76163	204847.3607	223357.7709	82840.25232
AT1G34430	gi 8778253	F12K21.24 [Arabidopsis thaliana]	Metabolism	5	5	152.56	0.005	3.175	163783.8293	105068.8396	163843.3101	116610.7247	656847.3861	507742.2623	347440.4396	232237.9433
AT5G54500	gi 15239652	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as [Arabidopsis thaliana]	Metabolism	5	5	71.75	0.009	2.475	20187.88807	22945.07776	13256.86227	10280.51813	53198.60027	50008.88224	28038.60857	33748.63552
AT4G31140	gi 15235840	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	9	9	358.5	0.000	2.385	309728.9412	247987.308	201533.7212	227496.6504	486715.9189	627461.3994	700182.7723	539225.2968

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G56590	gi 15241268	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Metabolism	5	5	273.42	0.008	2.791	80202.63767	71498.59219	40991.05232	57501.42009	229997.2807	202275.874	177468.5523	88573.50733
AT4G16155	gi 7159284	lipoamide dehydrogenase [Arabidopsis thaliana]	metabolism	6	6	192.74	0.002	2.449	76587.70374	61429.71082	65888.77791	87297.3531	225996.6547	154062.889	118757.8513	214292.024
AT4G23850	gi 15236634	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase [Arabidopsis thaliana]	metabolism	6	6	72.91	0.032	2.244	8506.143122	14988.07997	5136.109209	4084.494726	12790.85899	23892.05952	21913.23568	14801.59134
AT4G11850	gi 15234335	PLDGAMMA1; phospholipase D [Arabidopsis thaliana]	metabolism	6	6	93.34	0.008	0.482	129121.6388	130152.7905	171968.1231	208949.7304	111364.5416	54254.11764	76178.3771	66503.38147
AT2G18730	gi 4185139	putative diacylglycerol kinase [Arabidopsis thaliana]	metabolism	4	4	45.01	0.005	3.423	60568.61983	70952.05198	56557.52908	46683.88163	107785.0213	325884.2897	231738.9171	138257.3794
AT3G03780	gi 14532772	putative methionine synthase [Arabidopsis thaliana]	Metabolism	10	10	129.81	0.020	3.333	4414.223141	6169.628679	10315.09205	8631.775244	49719.72366	12607.73107	19706.2912	16404.15106
AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	metabolism	15	15	969.89	0.000	4.585	2627457.395	3978652.394	3440056.437	2532645.523	20899975.84	13271776.67	13701332.92	9795523.474
AT4G13940	gi 32967699	S-adenosyl-L-homocystein hydrolase [Arabidopsis thaliana]	metabolism	7	7	134.66	0.042	0.566	59548.25336	25825.11924	30921.72098	31471.80363	24426.38896	21499.87145	15833.12952	21861.23596
AT5G55480	gi 15240520	SVL1 (SHV3-LIKE 1); glycerophosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	Metabolism	25	25	1445.8	0.000	4.189	5918646.937	8991708.691	6379964.962	4762928.982	33553056.61	25921991.25	30003866.7	19668268.58
AT1G66970	gi 30697435	SVL2 (SHV3-LIKE 2); glycerophosphodiesterase/ kinase [Arabidopsis thaliana]	Metabolism	3	3	95.95	0.018	3.767	5269.287532	12154.39196	10246.70142	3260.576877	11339.48396	30172.82511	32156.14481	42854.85209

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G58070	gi 15242942	TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter [Arabidopsis thaliana]	Metabolism	2	2	51.22	0.017	2.915	2228.041259	4671.078731	1557.863176	7378.765428	11232.1605	14868.35925	12015.95812	8036.832518
AT3G54200	gi 15232445	unknown protein [Arabidopsis thaliana]	Metabolism	2	2	145.13	0.007	2.855	310320.6513	258697.6187	223784.3211	255490.257	1234176.505	667691.1075	701985.7607	389257.0372
AT1G45000	gi 15219503	26S proteasome regulatory complex subunit p42D, putative [Arabidopsis thaliana]	protein destination a	5	5	43.25	0.017	0.284	297104.3762	199195.5069	176042.9213	177611.9159	15947.25608	36627.18086	90803.54798	98272.34653
AT1G04730	gi 15219798	AAA-type ATPase family protein [Arabidopsis thaliana]	protein destination a	6	6	42.6	0.017	0.448	354239.1093	277837.3843	378057.1467	638882.9064	183152.8185	115971.8159	266895.3719	172622.482
AT3G56450	gi 15228924	ALPHA-SNAP1; binding / soluble NSF attachment protein [Arabidopsis thaliana]	protein destination a	2	2	92.18	0.006	3.420	4073.615315	3000.296487	4118.077115	2805.371845	6875.979376	22136.56666	9782.280389	9071.888409
AT2G02800	gi 15227042	PK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Protein destination a	3	3	76.02	0.012	2.027	18119.35632	14565.38075	10214.76986	8841.376238	33795.02852	22617.79902	28960.55032	19513.41
AT3G02740	gi 15232960	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination a	7	7	230.35	0.003	2.493	188182.1841	124362.8499	110933.2178	126281.1728	399966.6783	439479.7964	296660.0418	234356.4689
AT5G10080	gi 15238055	aspartyl protease family protein [Arabidopsis thaliana]	Protein destination a	8	8	186.17	0.003	0.265	21905.06212	13599.69181	16340.29895	24967.18878	2521.5966	3697.713879	6242.878562	7923.756702
AT1G62290	gi 22330379	aspartyl protease family protein [Arabidopsis thaliana]	protein destination a	2	2	21.56	0.037	0.407	10593.06084	11539.46804	27865.99002	23511.81826	8223.249701	4564.864772	12098.18546	5036.490085
AT3G09830	gi 222423927	AT3G09830 [Arabidopsis thaliana]	Protein destination a	4	4	41.21	0.042	2.579	12045.40018	14214.87011	12020.63307	25294.27232	58307.2522	39460.99022	50589.32983	15621.7574

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G52500	gi 16209647	AT3g52500/F22O6_120 [Arabidopsis thaliana]	protein destination a	2	2	30.7	0.001	2.720	76607.14261	61054.46833	56465.14461	57692.10146	115057.7755	186921.6417	208967.7896	173966.1125
AT1G63500	gi 240254311	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Protein destination a	9	9	313.29	0.002	2.291	122490.5275	103834.1497	72583.49037	68762.77143	247747.2934	205503.0559	178673.5277	210452.4716
AT1G69840	gi 15222481	band 7 family protein [Arabidopsis thaliana]	Protein destination a	10	10	413.18	0.000	2.181	648345.9694	720659.4494	633666.7873	575937.1938	1678062.272	1372302.542	1394128.58	1178491.917
AT1G65240	gi 4646203	Belongs to PF 00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	protein destination a	5	5	127.94	0.001	2.581	81823.32406	77214.26981	76377.06647	61397.72683	131380.2987	235810.7949	235035.2119	163937.2303
AT5G46570	gi 15237465	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination a	5	5	98.24	0.004	2.673	3406.343569	2594.114033	1142.244444	1963.3364	6658.633687	6542.653415	5509.189467	5632.128876
AT4G00710	gi 22328189	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination a	7	7	242.69	0.002	2.509	111062.4512	77951.71511	59987.43309	49063.21297	221733.8943	172921.7573	161378.3693	191932.5407
AT1G05690	gi 42561724	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	protein destination a	3	3	30.68	0.024	2.708	5448.50223	4507.788027	4095.852418	3664.485925	20053.79757	14116.86085	8264.281504	5535.82032

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G47850	gi 15238823	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase [Arabidopsis thaliana]	protein destination a	3	3	24.62	0.001	4.118	3439.937172	2820.024792	1550.942245	2111.574904	6440.5539	11802.78236	14354.74144	8267.019631
AT3G26940	gi 15231654	(CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	protein destination a	3	3	35.53	0.007	0.264	80442.49715	84582.64159	103550.3144	126162.9095	57293.09541	10179.41892	21629.55131	15236.72136
AT3G18190	gi 15229595	chaperonin, putative [Arabidopsis thaliana]	protein destination a	4	4	31.1	0.002	0.417	66747.61727	57446.85525	59522.25359	45274.40977	18176.65639	18253.61309	22736.11738	36335.35925
AT1G53430	gi 8671883	Contains similarity to receptor-like serine/threonine kinase from Arabidopsis thaliana gb AF024648 and contains multiple leucine rich PF 00560 repeats and protein kinase PF 00069	protein destination a	5	5	52.07	0.045	3.036	53013.40785	32394.34505	11928.13957	29385.57119	90113.77114	140157.1081	120045.6065	34404.05489
AT1G03230	gi 18379072	extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana]	Protein destination a	5	5	180.39	0.034	2.700	40098.5613	40557.67612	11363.30723	15653.54342	42216.43849	69694.88348	60027.40619	118752.9453
AT1G12470	gi 8778633	F5O11.22 [Arabidopsis thaliana]	protein destination a	2	2	26.2	0.000	0.414	173559.5487	157510.9411	149435.464	131221.0691	75506.80355	50058.01807	52185.06969	75766.73784
AT3G58880	gi 15231588	F-box family protein [Arabidopsis thaliana]	protein destination a	2	2	28.49	0.038	0.417	20995.89248	21059.46092	52021.56583	41682.36189	26303.00016	9454.819094	9900.910979	10934.69977

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G60040	gi 15232242	F-box family protein [Arabidopsis thaliana]	protein destination a	4	4	32.32	0.002	0.212	32531.64081	28330.07062	64009.6648	61158.60354	8875.092194	6017.989036	8668.962393	15835.11602
AT5G25860	gi 15239511	F-box family protein [Arabidopsis thaliana]	protein destination a	3	3	19.28	0.001	2.824	19831.53311	27905.75056	31881.08277	23847.83379	89492.54645	53838.47985	84140.10474	64735.07949
AT4G23940	gi 18416240	FtsH protease, putative [Arabidopsis thaliana]	protein destination a	4	4	41.53	0.021	3.092	348296.8001	637049.7866	756364.9262	706133.8667	3242238.91	1311890.397	2156737.067	857657.0934
AT4G37910	gi 4467097	heat shock protein 70 like protein [Arabidopsis thaliana]	protein destination a	5	5	166.07	0.010	3.682	22750.75169	24156.8262	85341.66944	75171.21461	220824.6268	255799.4017	160890.9446	126189.7349
AT2G17760	gi 25347778	hypothetical protein At2g17760 [imported] - Arabidopsis	protein destination a	5	5	207.43	0.015	3.678	32780.14587	42472.62556	14847.17903	20731.89419	206467.2353	66879.4224	75276.26704	59054.30457
AT1G79560	gi 4835753	is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this PP2A	protein destination a	2	2	23.62	0.027	2.652	747.0302784	1752.538285	1131.790678	1502.314211	1505.122413	4660.729881	4445.587019	3002.887901
AT1G69960	gi 15222511	(SERINE/THREONINE PHOSPHATASE 2A); protein serine/threonine phosphatase [Arabidopsis thaliana]	protein destination a	1	1	17.64	0.025	2.428	184.5213595	991.0174372	248.2455247	415.4539964	1094.109348	1003.88239	1110.572469	1257.782758
AT5G10080	gi 110741881	predicted GPI-anchored protein [Arabidopsis thaliana]	Protein destination a	8	8	186.17	0.020	0.435	5810.554086	6491.722879	11317.58288	15836.61763	4249.012386	4224.084817	4686.159759	3985.278521
AT3G54030	gi 15232406	protein kinase family protein [Arabidopsis thaliana]	Protein destination a	7	7	247.34	0.003	2.431	141170.4448	121560.4476	91377.73489	89157.80506	372665.0549	198404.3873	278602.8874	228119.1036



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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G02630	gi 15235432	protein kinase family protein [Arabidopsis thaliana]	Protein destination a	10	10	189.03	0.024	3.186	76276.27257	71286.53915	72748.63204	96353.40148	513045.5367	154345.7671	227602.7451	113953.2835
AT5G41260	gi 15237604	protein kinase family protein [Arabidopsis thaliana]	Protein destination a	6	6	127.12	0.001	0.297	5265.929276	4953.014143	2612.809059	5388.299882	1308.81605	1027.521197	1359.716474	1710.934455
AT5G51770	gi 15242183	protein kinase family protein [Arabidopsis thaliana]	Protein destination a	2	2	46.08	0.008	0.286	7283.182095	5949.364279	4542.4592	16499.69556	2398.098805	3059.28752	2072.169118	2270.340716
AT1G54610	gi 15221868	protein kinase family protein [Arabidopsis thaliana]	protein destination a	2	2	25.13	0.040	2.409	718667.5902	921395.4609	1847317.85	1534654.286	5409331.128	2367303.727	2618469.784	1704772.071
AT2G39360	gi 15225078	protein kinase family protein [Arabidopsis thaliana]	protein destination a	7	7	170.83	0.011	3.946	10468.94483	11580.11995	8341.843892	9019.787602	21473.35781	45685.79452	71193.73387	17162.58133
AT2G23200	gi 15227790	protein kinase family protein [Arabidopsis thaliana]	protein destination a	3	3	34.02	0.005	0.461	34485.40871	24444.73681	22498.87529	29909.059	10743.81518	8602.515236	13779.28211	18178.12951
AT5G24010	gi 15237872	protein kinase family protein [Arabidopsis thaliana]	protein destination a	8	8	279.09	0.003	2.395	115070.4287	125210.1372	80503.57235	70595.93957	254751.1835	230843.7421	283193.6711	168394.8877
AT5G57610	gi 15242791	protein kinase family protein [Arabidopsis thaliana]	protein destination a	2	2	46.54	0.002	0.378	29351.97393	25314.51373	41275.34909	45630.62629	14584.87951	9050.427817	16202.43026	13687.10857
AT5G01020	gi 30679085	protein kinase family protein [Arabidopsis thaliana]	protein destination a	4	4	31.48	0.012	0.255	13491.32594	13242.77864	22943.18372	26509.05574	1526.601851	3070.864664	9309.847043	5502.261363
AT2G28940	gi 30684071	protein kinase family protein [Arabidopsis thaliana]	protein destination a	3	3	40.21	0.037	0.416	9316.047226	7605.727334	6061.617291	4707.722989	3923.154113	1688.528193	1076.81485	4833.259032
AT5G03320	gi 15242720	protein kinase, putative [Arabidopsis thaliana]	Protein destination a	3	3	56.46	0.005	0.347	58406.22627	58395.78976	62696.28843	51117.40013	9747.321564	15014.06618	21596.0776	33774.69333
AT3G46290	gi 15231393	protein kinase, putative [Arabidopsis thaliana]	protein destination a	10	10	277.64	0.002	3.181	136407.1967	172172.1992	124416.8099	98959.74981	689891.9576	346801.426	347560.6796	308140.4816
AT5G56460	gi 15241220	protein kinase, putative [Arabidopsis thaliana]	protein destination a	4	4	36.85	0.000	0.158	37875.95958	29601.4076	28159.43691	32340.56544	4711.927847	5317.718786	7975.491129	2183.409729

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G17220	gi 18398350	protein kinase, putative [Arabidopsis thaliana]	protein destination a	3	3	27.81	0.021	0.297	50875.7118	38272.46117	116590.4192	156463.482	32005.34265	22756.42428	26868.65546	26121.33072
AT4G28400	gi 18417190	phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	protein destination a	3	3	58.69	0.003	0.439	66089.14306	63387.26788	70795.97864	44576.61697	29804.55091	17502.86472	32995.25575	27079.51617
AT4G04910	gi 7267250	putative component of vesicle-mediated transport [Arabidopsis thaliana]	Protein destination a	8	8	163.15	0.002	2.374	97374.88835	138550.5675	117194.1401	110098.7293	317507.0738	294122.1811	318171.0831	170004.2617
AT3G48820	gi 7576220	putative protein [Arabidopsis thaliana]	protein destination a	3	3	40.25	0.041	2.612	2204647.088	3019281.547	5304215.239	3958953.12	18224068.26	6594408.6	8200518.134	4819743.96
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination a	6	6	166.72	0.008	2.093	54726.62652	37724.44249	22871.72833	25124.52864	81669.83704	74872.11157	72992.77674	64464.12886
AT2G39110	gi 3928095	putative protein kinase [Arabidopsis thaliana]	protein destination a	3	3	44.32	0.010	0.409	139262.854	121914.4751	98586.54186	121763.2878	24378.35057	61831.6758	37415.17873	73527.26921
AT2G29000	gi 3461842	putative receptor-like protein kinase [Arabidopsis thaliana]	protein destination a	2	2	60.34	0.004	0.160	16441.40272	14028.99063	30664.35513	23888.83018	902.0559439	2459.10883	3871.013827	6351.120054
AT2G16600	gi 15227259	ROC3; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	protein destination a	2	2	124.41	0.021	2.330	206001.7401	222509.0447	99828.7941	91548.59068	540834.0379	361354.7823	282720.1254	259625.2632
AT2G47060	gi 79324935	serine/threonine protein kinase, putative [Arabidopsis thaliana]	Protein destination a	4	4	50.97	0.010	0.348	5495.919938	4278.380185	6606.481225	12170.54535	2769.193804	1641.179895	3325.680724	2210.620469
AT4G32300	gi 2864613	S-receptor kinase -like protein [Arabidopsis thaliana]	Protein destination a	4	4	145.99	0.001	2.636	79036.51291	96460.172	55855.75681	63187.56956	255634.7718	196251.927	170609.6547	153887.8481

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G70490	gi 4056469	Strong similarity to gb M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967, gb AA712956, gb T46403, gb T46050, gb A1100391	protein destination a	5	5	237.72	0.000	2.609	188372.0543	235678.206	222974.9311	147812.532	584212.2831	422127.4528	592254.9683	474957.753
AT1G27750	gi 6693023	T22C5.20 [Arabidopsis thaliana]	Protein destination a	5	5	48.84	0.011	0.169	20874.8818	22655.82209	47150.00167	33693.91716	1014.785406	5134.402212	1609.405865	13289.15904
AT5G56380	gi 10177837	unnamed protein product [Arabidopsis thaliana]	protein destination a	3	3	32.19	0.012	0.307	94973.20779	89358.89758	69023.55091	70911.71692	8889.761573	14054.87268	26810.85343	49808.38071
AT2G42360	gi 15227929	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	protein destination a	1	1	22.4	0.000	20.035	533.8160327	1105.324274	841.4803589	1145.21033	26218.10758	21988.90811	18991.95692	5442.913043
AT5G01520	gi 15241003	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	protein destination a	1	1	18.92	0.014	0.313	11816.13716	12243.11985	26471.50876	27379.18078	6133.212024	5552.955902	9756.132494	2930.987555
AT2G36160	gi 15227588	40S ribosomal protein S14 (RPS14A) [Arabidopsis thaliana]	Protein synthesis	4	4	114.74	0.022	3.857	9938.004057	9171.533065	3321.874579	974.4080887	18680.66871	25616.33214	24167.4103	21803.46817
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	protein synthesis	5	5	73.83	0.039	0.439	49673.88931	41040.75653	79609.80209	70252.2032	10587.37383	48371.54687	18449.82529	28312.49627
AT2G04390	gi 15228141	40S ribosomal protein S17 (RPS17A) [Arabidopsis thaliana]	Protein synthesis	11	11	433.34	0.026	5.638	1159707.381	980241.0758	1302233.523	1115214.942	12323670.67	6996404.02	5140415.791	1233900.018
AT3G02080	gi 15232844	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	Protein synthesis	4	4	91.09	0.005	2.616	29169.79733	28015.71962	33584.86466	38091.51637	110947.4952	88057.39201	93564.73794	44572.67284

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G61170	gi 15240154	40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana]	Protein synthesis	4	4	93.94	0.035	9.874	2510.208299	3944.429643	4315.552721	2971.436401	5103.972788	56691.66571	65102.34155	8781.271657
AT2G21580	gi 15226590	40S ribosomal protein S25 (RPS25B) [Arabidopsis thaliana]	Protein synthesis	8	8	357.24	0.041	5.862	34713.48274	22604.00379	37707.93171	41223.94281	335913.0299	230927.6103	203200.0526	28666.67821
AT4G39200	gi 15234970	40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana]	Protein synthesis	12	12	550.46	0.023	4.259	95998.53008	90817.21497	130386.0294	122775.085	428576.7508	703471.1188	624088.3288	117741.4594
AT3G43980	gi 15229840	40S ribosomal protein S29 (RPS29A) [Arabidopsis thaliana]	Protein synthesis	3	3	70.59	0.050	4.846	5981.460852	10401.57305	16504.99288	24303.65892	84231.15915	94434.29613	86741.63336	11715.34477
AT5G35530	gi 15238533	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	protein synthesis	7	7	170.96	0.000	2.269	34923.05786	31480.69484	31319.16926	33504.33342	67224.57478	76209.79115	95218.35559	59107.62928
AT4G29390	gi 15233565	40S ribosomal protein S30 (RPS30B) [Arabidopsis thaliana]	Protein synthesis	2	2	67.87	0.029	45.980	247.7370832	0	231.4722529	261.892944	2290.742514	2183.997453	18768.32602	10832.69292
AT3G04840	gi 15229364	40S ribosomal protein S3A (RPS3aA) [Arabidopsis thaliana]	Protein synthesis	4	4	109.35	0.007	2.732	147981.3068	165393.1134	68431.3303	72235.83795	368634.1456	233800.4265	257360.8331	380450.615
AT5G62300	gi 7671404	40S ribosomal protein [Arabidopsis thaliana]	protein synthesis	7	7	123.58	0.045	6.165	15376.67964	16115.92774	61966.69262	57498.82544	432978.7461	277160.8056	185539.1122	34993.12685
AT2G37190	gi 15228098	60S ribosomal protein L12 (RPL12A) [Arabidopsis thaliana]	Protein synthesis	2	2	39.97	0.009	2.347	48154.31957	43907.80136	28591.96702	23497.00125	107263.2175	77504.98086	54304.98331	99197.96867
AT1G27400	gi 15223501	60S ribosomal protein L17 (RPL17A) [Arabidopsis thaliana]	Protein synthesis	6	6	197.27	0.032	6.632	15247.60618	9119.324566	8971.172587	22705.48694	132496.7573	115852.7343	110378.1811	12935.68727
AT1G67430	gi 15220431	60S ribosomal protein L17 (RPL17B) [Arabidopsis thaliana]	Protein synthesis	5	5	171.17	0.037	10.638	3262.292814	2290.221039	456.4755323	2438.107385	27251.51686	27766.33493	32892.15093	1952.924575

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G19730	gi 15224835	60S ribosomal protein L28 (RPL28A) [Arabidopsis thaliana]	Protein synthesis	5	5	382.69	0.021	6.114	695410.9568	621778.2549	2341502.762	2449071.608	16188888.72	10201691.21	8831512.604	2123283.361
AT4G29410	gi 15233567	60S ribosomal protein L28 (RPL28C) [Arabidopsis thaliana]	protein synthesis	5	5	203.8	0.015	3.256	284147.3417	195262.4726	146780.6421	138148.8643	1203954.024	543269.6287	373420.9416	367853.1158
AT5G56710	gi 15241902	60S ribosomal protein L31 (RPL31C) [Arabidopsis thaliana]	Protein synthesis	5	5	99.68	0.019	2.510	186384.446	171721.1255	118665.8824	131196.4368	706740.6743	275865.0374	289697.8899	253739.0164
AT5G46430	gi 15237436	60S ribosomal protein L32 (RPL32B) [Arabidopsis thaliana]	Protein synthesis	5	5	62.17	0.001	3.419	5152.076855	4991.683337	5326.057904	7278.724266	15252.26291	30878.0914	13034.8971	18606.71713
AT2G39390	gi 15225083	60S ribosomal protein L35 (RPL35B) [Arabidopsis thaliana]	Protein synthesis	7	7	111.26	0.027	2.109	31818.45506	31285.47845	21419.6943	24376.92008	79020.19099	53051.99611	29309.03896	68317.94664
AT2G43460	gi 15224284	60S ribosomal protein L38 (RPL38A) [Arabidopsis thaliana]	Protein synthesis	5	5	155.12	0.020	6.717	83956.25742	86564.83834	245413.3943	215525.9606	2024293.976	1002789.536	1005583.34	208938.4884
AT2G47610	gi 15226635	60S ribosomal protein L7A (RPL7aA) [Arabidopsis thaliana]	protein synthesis	1	1	28.74	0.023	0.244	28340.34576	24374.01362	7556.06225	8581.903989	4344.589374	7109.549299	1744.911521	3614.707324
AT1G33120	gi 18398753	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	Protein synthesis	10	10	530.99	0.002	3.460	826002.3501	460674.1235	586992.873	479312.0534	3136079.998	1378004.685	2233004.253	1393156.103
AT4G10450	gi 15235114	60S ribosomal protein L9 (RPL90D) [Arabidopsis thaliana]	Protein synthesis	6	6	227.92	0.027	2.488	96400.46933	54994.64535	128298.6564	84467.63596	175633.6913	290971.3751	325941.2055	113423.6408
AT1G43170	gi 15218306	(ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	6	6	137.26	0.035	2.512	38396.22906	44845.54394	135772.6923	91293.20274	264011.7886	116402.8032	259564.4718	139615.2445

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G37270	gi 15228111	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	3	3	172.83	0.000	4.883	229655.8383	269015.0812	169395.0366	164409.5166	1374919.509	1068985.613	928063.6013	692776.3091
AT5G60390	gi 295789	elongation factor 1-alpha [Arabidopsis thaliana]	Protein synthesis	7	7	223.92	0.012	3.607	28099.61559	54731.18231	25008.23358	10081.79753	68979.18968	78542.95291	125443.0768	152428.1785
AT1G56070	gi 6056373	elongation factor EF-2 [Arabidopsis thaliana]	protein synthesis	5	5	259.45	0.008	2.134	264880.188	375729.2201	214224.8887	153903.6297	667146.3374	473070.7508	488551.2205	524220.4744
AT4G02930	gi 1149571	mitochondrial elongation factor Tu [Arabidopsis thaliana]	protein synthesis	4	4	85.45	0.003	0.416	139263.4625	106728.2582	170868.6677	194574.177	47522.65716	77044.23406	52467.40477	77114.33795
AT1G22780	gi 15219950	PFL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana]	Protein synthesis	12	12	542.04	0.018	6.494	430221.4222	481632.9063	1154229.366	1079251.516	9203409.317	5520669.071	4635745.214	1064763.612
AT5G20180	gi 15241288	ribosomal protein L36 family protein [Arabidopsis thaliana]	protein synthesis	1	1	23.37	0.003	2.168	6780.355749	4850.841333	4562.262763	5723.573193	16445.34985	10075.41928	12120.78648	8867.858246
AT2G33370	gi 2341028	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene	protein synthesis	5	5	104.29	0.005	4.373	61221.09873	59827.39038	43634.85514	52002.45691	492472.5166	154584.1955	141760.0217	158683.2452
AT1G74020	gi 1754983	strictosidine synthase [Arabidopsis thaliana]	secondary metabolis	2	2	50.5	0.008	5.341	724.5191498	887.835861	865.917215	244.1009513	7361.686364	2205.146898	2283.256483	2691.055897
AT1G74010	gi 15221105	strictosidine synthase family protein [Arabidopsis thaliana]	secondary metabolis	2	2	22.54	0.030	4.158	106486.471	40844.04509	41888.32959	22136.22004	300938.8065	342239.8218	171117.2466	64528.35622

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G34460	gi 42573173	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding [Arabidopsis thaliana]	Signal transduction	4	4	30.93	0.022	3.799	5417.785605	5323.533823	13741.4973	9556.311628	47056.64147	11509.90567	22692.05269	48060.3854
AT1G35160	gi 14532442	At1g35160/T32 G9_30 [Arabidopsis thaliana]	signal transduction	7	7	73.03	0.010	0.039	10653.46035	652.0527751	1000.759714	1003.892835	191.4650997	42.24588567	99.74513304	190.7190377
AT3g07390	gi 18426884	AT3g07390/F21 O3_10 [Arabidopsis thaliana]	Signal transduction	6	6	392.18	0.006	3.765	7593196.749	9251779.006	3590459.969	2708386.358	32673499.36	21328136.86	15865686.66	17274327.64
AT5G01600	gi 15241018	ATFER1; ferric iron binding / iron ion binding [Arabidopsis thaliana]	Signal transduction	7	7	345.01	0.028	6.671	57002.13539	57981.92089	299105.2233	235392.6675	959344.9864	758178.4792	2375270.419	239979.4106
AT2G40300	gi 15225679	ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding [Arabidopsis thaliana]	Signal transduction	7	7	243.62	0.019	5.342	32062.78253	25658.79743	147382.7555	120162.2271	342074.7039	438728.5906	802445.4545	154297.1922
AT4G38580	gi 15233937	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding [Arabidopsis thaliana]	Signal transduction	5	5	152.3	0.000	2.184	35741.15882	31896.67827	30715.45754	26583.44487	55228.56747	67447.81206	72014.10775	78151.33044
AT4G35860	gi 15233367	ATGB2 (GTP-BINDING 2); GTP binding [Arabidopsis thaliana]	signal transduction	1	1	28.24	0.000	3.636	6996.661749	5138.112526	3747.31685	4276.520607	23038.22031	19255.66428	15621.83264	15378.33422
AT2G17820	gi 18398532	ATFK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase [Arabidopsis thaliana]	signal transduction	3	3	39.4	0.044	0.317	7337.945918	5109.302365	18686.28663	23172.76577	5296.885319	3252.076371	5504.570853	3136.366948

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G11300	gi 145335397	ATP binding / carbohydrate binding / kinase / protein kinase / protein serine/threonine kinase / protein tyrosine kinase / sugar binding [Arabidopsis thaliana]	signal transduction	6	6	61.03	0.016	0.386	30167.40465	36601.25258	68693.34147	81912.78986	24702.16422	16677.70322	25287.96478	17217.54418
AT5G49780	gi 240256419	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	signal transduction	6	6	42.75	0.002	0.293	76562.45385	87904.05257	97962.58252	98651.80675	18617.25337	17487.17801	21277.50197	48554.99098
AT3G08510	gi 15231929	ATRAB8C; GTP binding [Arabidopsis thaliana]	Signal transduction	19	19	527.44	0.001	2.498	224218.0032	165307.4433	184849.2975	185688.5058	623693.2041	426289.9986	517449.4494	331476.0562
AT5G03520	gi 15242773	ATRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding [Arabidopsis thaliana]	Signal transduction	3	3	58.42	0.031	2.855	1455590.513	1887189.814	2838842.185	2172191.191	11783891.35	3789889.748	5305822.52	2968938.848
AT5G20020	gi 1668706	AtRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	signal transduction	1	1	31.67	0.020	2.448	24456.8008	22315.82607	21360.89911	19022.4195	100168.7633	34621.80763	41547.47071	36986.77741
AT4G18760	gi 15234009	auxin-responsive family protein [Arabidopsis thaliana]	Signal transduction	7	7	607.34	0.006	3.572	1250734.205	1397555.679	1204128.459	1084823.897	8014769.185	3358538.649	4149198.553	2112043.991
AT3G25290	gi 18404500	auxin-responsive protein, putative [Arabidopsis thaliana]	Signal transduction	8	8	204.79	0.020	3.559	229421.1963	200806.2721	57447.08952	77043.83063	894805.7527	269218.5344	458077.703	387980.0561
AT4G12980	gi 15235545		signal transduction	4	4	113.93	0.005	3.369	49807.27016	37943.03667	37258.65731	47804.74804	221307.4127	130231.0175	164085.1073	66618.32193



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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G39400	gi 15235059	BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	signal transduction	11	11	45.06	0.012	2.132	36504.58257	70298.65763	53589.59332	32227.84355	75963.12683	89964.12604	106071.8688	138735.3837
AT1G55610	gi 15222751	BRL1 (BRI 1 LIKE); kinase [Arabidopsis thaliana]	signal transduction	4	4	30.1	0.004	0.112	4542.106638	5284.838402	14162.95019	14603.73318	602.4897151	339.9695213	2088.473904	1275.179912
AT3G61050	gi 1769895	CaLB protein [Arabidopsis thaliana]	signal transduction	5	5	28.51	0.034	0.219	139684.172	96509.04433	114386.823	236248.6196	2941.416008	20852.63864	44650.7088	60319.19095
AT5G24430	gi 22136058	calcium dependent protein kinase-like protein [Arabidopsis thaliana]	signal transduction	3	3	66.27	0.001	2.115	26644.92796	33330.61884	21380.54056	22089.09686	61716.42932	53407.35021	59308.88448	44389.92849
AT1G05150	gi 15220436	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	10	10	301.83	0.001	2.922	53032.30899	56705.43543	37995.35347	34822.47903	110736.884	160930.8484	168458.7643	93226.08628
AT2G32450	gi 15225686	calcium-binding EF hand family protein [Arabidopsis thaliana]	Signal transduction	7	7	232.92	0.038	2.275	32151.78416	25928.25943	11854.17251	12279.94716	25673.53688	65207.45018	53292.34994	42889.26678
AT3G57530	gi 6706424	calcium-dependent protein kinase [Arabidopsis thaliana]	signal transduction	5	5	50.4	0.004	0.402	354051.6812	278831.747	234605.1804	208009.8137	106955.3575	65160.31772	111671.5075	148509.1476
AT2G41410	gi 16213	calmodulin like protein [Arabidopsis thaliana]	signal transduction	4	4	50.46	0.012	3.041	6570.481268	6033.566007	2432.448612	3647.07044	20297.43894	15672.93938	13466.34667	7380.809916

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G52540	gi 5903051	Contains PF 00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene	signal transduction	6	6	149.2	0.012	2.708	64724.14416	69466.89492	85152.2166	81066.05037	109577.4285	221664.2833	339323.8407	143004.9324
AT4G21940	gi 15234656	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis	Signal transduction	4	4	69.26	0.012	2.315	32704.18293	31400.1809	17921.35941	16309.25544	80816.66349	60272.03099	47026.39683	39530.52383
AT3G10620	gi 8567796	diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative [Arabidopsis	signal transduction	2	2	29.38	0.002	0.364	99645.70594	71145.72364	111766.9314	106094.6556	21707.54786	34902.95455	44717.30473	40293.51928
AT2G03150	gi 42568895	emb1579 (embryo defective 1579); binding / calcium ion binding [Arabidopsis	signal transduction	6	6	45.65	0.000	0.281	85378.74756	75901.88311	87238.6231	85774.43082	26759.29148	13755.14063	22013.19828	31310.53449
AT1G43890	gi 8778652	F9C16.3 [Arabidopsis thaliana]	signal transduction	#N/A	#N/A	#N/A	0.000	2.805	23703.04044	26061.52633	30602.58904	23651.60304	74542.17389	73976.3848	86007.11304	57243.0202
AT3G51550	gi 15230520	FER (FERONIA); kinase/ protein kinase [Arabidopsis	signal transduction	16	16	584.4	0.002	2.842	388064.5802	486161.2554	282244.3268	226153.7897	1386470.47	880937.4966	867949.4253	794213.133
AT4G17530	gi 2245111	GTP-binding RAB1C like protein [Arabidopsis thaliana]	Signal transduction	4	4	210.26	0.003	3.752	62346.16293	66329.84065	99675.45384	85435.50246	462650.1547	236433.169	321706.5963	156658.0612

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G28490	gi 15235312	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	2	2	36.74	0.001	0.167	16969.23303	20225.45815	41567.08435	41577.47059	7098.895718	5667.098486	3954.661333	3434.550005
AT3G51740	gi 15231029	IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	20	20	773.79	0.000	3.077	585830.623	774847.0983	699488.423	562511.0686	2590894.879	1818388.652	2254741.294	1406803.025
AT2G19230	gi 240254475	kinase [Arabidopsis thaliana]	signal transduction	3	3	65.71	0.004	0.176	61505.19428	51017.74846	39759.03292	43092.59103	7346.26181	2829.02686	4043.37042	20174.52199
AT1G34300	gi 15218576	lectin protein kinase family protein [Arabidopsis thaliana]	signal transduction	10	10	163.59	0.016	1.728	100372.6085	126816.5097	200037.7525	177473.3728	297519.1976	239567.8209	287743.9554	219841.6599
AT5G60270	gi 15239260	lectin protein kinase family protein [Arabidopsis thaliana]	signal transduction	3	3	72.82	0.041	2.355	65759.69166	53965.77772	143941.14	106269.1175	280799.0987	183625.5101	300862.287	106086.5307
AT3G23750	gi 15229508	leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Signal transduction	4	4	57.76	0.007	2.146	4419.568468	9773.643816	4885.507386	4556.658107	11656.22995	10590.18702	14068.63085	14404.59582
AT2G01820	gi 15226361	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	Signal transduction	12	12	570.37	0.019	2.705	1642343.571	2490016.103	837190.524	771572.1999	5723206.479	2414793.607	3322200.082	4067434.638
AT1G51800	gi 15218033	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	4	4	100.57	0.030	2.637	414824.1928	964018.7816	920453.1153	858166.4184	1415717.35	1861017.388	3839278.416	1210343.408
AT2G14510	gi 15225949	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	7	7	76.69	0.006	0.130	36696.44144	20756.40277	67882.25883	74818.81356	1648.64163	6793.748487	10710.3478	6865.693386

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G28970	gi 15227015	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	3	3	55.97	0.001	0.292	26927.92007	24947.00196	24625.93569	24400.37108	10071.14586	4584.173856	5654.405695	9175.147948
AT3G08680	gi 15231955	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	4	4	100.29	0.010	2.380	71933.28469	73787.13432	43990.74269	38258.54059	86692.73958	134622.8227	190029.0207	131291.7788
AT3G28450	gi 15233004	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	10	10	459.77	0.030	2.613	711073.0156	641586.3374	321925.9092	345783.1165	2482985.678	941573.6597	807730.2595	1047232.956
AT3G02880	gi 15233013	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	30	30	1685.4	0.004	3.266	3898684.97	4101136.156	3250623.5	3321486.486	19371898.25	10482056.01	11742145.13	5993100.687
AT1G06840	gi 15222211	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	Signal transduction	10	10	243.91	0.003	3.517	120760.9477	123237.3117	91173.56955	83281.811	617282.2427	219661.6923	350939.9551	283635.2337
AT2G31880	gi 15225153	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3	3	34.97	0.006	4.386	15095.46359	14157.00532	5105.479357	8392.472891	87178.92009	32276.31243	39308.06664	28736.55762
AT2G26730	gi 15225780	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	3	3	119.67	0.000	2.933	64251.97556	74805.22186	62910.84249	50365.51067	156447.4277	155419.5015	266421.8488	161756.0304
AT5G16590	gi 15237379	LRR1, ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	17	17	658.58	0.002	2.784	429098.7851	409463.0105	279244.622	274055.5744	1125718.707	973813.7954	1150680.015	624368.3872
AT1G21880	gi 18395044	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	7	7	377.89	0.002	3.730	174110.6221	199089.8886	256990.5726	187826.7304	953892.5769	1131295.465	525671.4569	440607.6282

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G17120	gi 18398317	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) [Arabidopsis thaliana]	Signal transduction	6	6	176.11	0.004	2.784	742678.9253	544548.9873	322206.1454	409223.7097	1971823.958	1237902.658	1411232.247	998094.3732
AT5G06320	gi 15239999	NHL3 [Arabidopsis thaliana]	Signal transduction	7	7	395.45	0.010	3.514	1279918.015	987566.3541	1366484.151	1417663.698	7683222.381	4276119.164	4000649.314	1790978.036
AT1G73080	gi 15219370	PEPRT (PEPT receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	6	6	80.4	0.024	0.606	145749.8382	256092.7917	212128.2549	208792.7827	142999.903	141482.506	86588.77557	127171.8469
AT1G77630	gi 30699276	peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	Signal transduction	13	13	645.92	0.000	5.973	275102.6086	459171.4184	464234.4505	301300.4706	2678636.177	2732643.525	2205693.794	1341688.745
AT5G58670	gi 18424132	PLC1 (PHOSPHOLIPASE C 1); phospholipase C [Arabidopsis thaliana]	Signal transduction	6	6	230.9	0.001	3.216	68897.61536	65786.04688	52020.5586	48604.05753	275920.4391	172728.4543	187071.0662	120955.7993
AT1G70520	gi 15223169	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	9	9	279.79	0.002	2.978	198411.5455	218992.4544	138290.2393	148390.3601	692781.0385	515331.6256	573877.6871	314697.3804
AT4G23200	gi 15236421	protein kinase family protein [Arabidopsis thaliana]	Signal transduction	5	5	52.94	0.001	3.339	197546.488	153476.5228	119622.4655	103212.9639	661137.4751	479980.7239	425833.4913	349425.2067
AT3G24550	gi 13877617	protein kinase-like protein [Arabidopsis thaliana]	signal transduction	25	25	942.22	0.001	2.641	1414148.903	1817612.187	2135421.609	1813787.864	6523927.086	3898008.449	4745258.306	3800194.82
AT2G02220	gi 15227264	PSKRT (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	4	4	43.4	0.041	1.660	29690.10464	44447.03924	28621.4764	23228.67138	43095.24986	60470.77885	37399.13007	68185.84138

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	signal transduction	10	10	558.33	0.001	3.969	178601.017	220628.3412	179826.7691	134860.5587	841944.7831	709945.6214	872566.1234	409026.4119
AT3G46280	gi 7799016	putative protein [Arabidopsis thaliana]	signal transduction	9	9	310.42	0.038	4.913	420336.776	464820.0062	101279.4537	117818.5995	2508601.194	1908239.349	469199.1053	539059.5998
AT1G67890	gi 16604649	putative protein kinase [Arabidopsis thaliana]	signal transduction	3	3	37.2	0.001	0.120	6769.812346	5938.533838	16464.22011	13795.26888	1767.91602	727.1547724	1093.755602	1565.449043
AT1G51850	gi 9802795	Putative protein kinase [Arabidopsis thaliana]	signal transduction	13	13	503.28	0.012	2.660	541788.8056	685425.7904	391009.4155	341678.8282	2248480.789	1098643.528	889198.7466	977182.1687
AT2G37050	gi 4371296	putative receptor-like protein kinase [Arabidopsis thaliana]	signal transduction	6	6	67.69	0.032	1.918	16208.37018	15906.22461	9428.529782	10354.81039	39628.59614	18003.52333	21551.08761	20376.57968
AT1G29740	gi 9972372	Putative receptor-like serine/threonine kinase - partial protein [Arabidopsis thaliana]	signal transduction	5	5	70.93	0.000	0.322	124306.6538	132517.4149	174867.4831	165911.7226	31224.0479	46366.349	63231.22056	51380.00529
AT4G34440	gi 3641836	putative serine/threonine protein kinase [Arabidopsis thaliana]	signal transduction	4	4	47.71	0.027	0.132	152097.4509	122126.7404	21477.66909	26528.59793	3409.699229	11728.50248	4235.540579	23107.98633
AT4G17170	gi 15235981	RABBITC (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase [Arabidopsis thaliana]	Signal transduction	1	1	32.96	0.042	2.191	6565.422903	4987.418308	2047.385568	4679.657827	15361.13663	9858.253615	8758.829705	6073.52537
AT5G24390	gi 15238518	RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	signal transduction	2	2	25.33	0.000	6.578	5564.567648	7284.398844	7126.306864	5767.058671	41296.14739	57684.91189	43143.78597	27219.31886
AT5G59840	gi 15238542	Ras-related GTP-binding family protein [Arabidopsis thaliana]	signal transduction	3	3	109.33	0.002	0.389	316370.3654	293963.8721	344547.0371	414799.1832	94257.74596	91772.82304	179811.2879	167227.3855
AT1G15530	gi 15218220	receptor lectin kinase, putative [Arabidopsis thaliana]	Signal transduction	7	7	172.1	0.032	2.604	116931.9884	129518.0682	81770.23286	87514.4328	108540.921	321407.5867	412924.2619	239865.5283

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G56140	gi 12321749	receptor protein kinase, putative [Arabidopsis thaliana]	Signal transduction	12	12	349.11	0.002	0.356	65859.93672	44948.8386	36478.9037	50383.01997	16366.63338	11584.21401	20825.2379	21542.01935
AT5G49760	gi 8978273	receptor protein kinase-like [Arabidopsis thaliana]	signal transduction	11	11	171.76	0.018	0.608	242174.4228	193774.8506	240287.433	244620.4507	179386.6891	111207.9666	97923.18511	171458.5562
AT4G08850	gi 7267528	receptor protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	16	16	760.08	0.018	2.642	2327789.352	2557465.604	1226736.296	1067945.748	7820518.034	4340620.311	2978125.793	3826754.631
AT5G16900	gi 9755691	receptor protein kinase-like protein [Arabidopsis thaliana]	signal transduction	4	4	66.98	0.001	2.111	41121.82911	32630.34459	35548.94387	27391.17651	63774.82902	90574.99414	75959.04796	58254.40374
AT4G18250	gi 4375833	receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction	4	4	36.31	0.003	0.437	161928.725	154840.771	166343.8526	171077.539	101794.6173	44528.4916	57196.72444	82438.94683
AT3G46330	gi 6522612	receptor-like protein kinase homolog [Arabidopsis thaliana]	signal transduction	4	4	63.84	0.014	0.382	83702.15289	91206.27257	126383.0575	106855.1569	17001.32349	25996.76389	57508.33192	55208.75905
AT4G23190	gi 4127461	receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	signal transduction	11	11	281.83	0.002	3.243	34985.59055	43316.23941	21368.22786	20739.52187	108603.5862	115155.7899	102140.3079	64640.60076
AT3G14840	gi 11994595	receptor-like serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	24	24	733.2	0.006	2.498	845008.5867	1071341.839	515193.4171	373069.6165	1893481.42	1658101.991	1707647.855	1747925.695
AT3G56100	gi 269969409	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-	signal transduction	4	4	65.85	0.009	4.790	362.2148097	1403.030516	1358.948079	1401.405209	3295.705375	7205.124881	8141.948294	3035.149308

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G17840	gi 18401662	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	10	10	416.58	0.049	2.617	391795.7979	354011.825	226638.3875	232663.918	1606675.399	451102.1985	676751.9678	419361.166
AT1G61380	gi 18407151	SD1-29 (S-DOMAIN-1 29); carbohydrate binding / kinase/ protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	44.39	0.017	0.293	19743.32173	17467.11368	55239.93342	52272.31528	7006.358747	11310.93903	14177.15528	9969.650338
AT4G23270	gi 3021279	serine/threonine kinase [Arabidopsis thaliana]	Signal transduction	8	8	123.77	0.005	4.670	106912.2454	110243.0295	96285.89933	78441.76558	752329.6259	470300.857	440303.5758	167321.9333
AT4G23180	gi 3021270	serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction	7	7	110.46	0.010	0.294	102830.0599	94770.56262	107186.1554	93549.92044	8178.728538	31008.33135	36335.62708	41460.39437
AT1G61390	gi 15219917	S-locus protein kinase, putative [Arabidopsis thaliana]	Signal transduction	3	3	44.7	0.030	11.126	627.57803	1319.062472	9576.277792	9949.155484	98621.42048	64807.25003	68590.00802	6870.004249
AT3G14350	gi 30683104	SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Signal transduction	2	2	51.49	0.012	2.415	26439.66969	29440.25265	17104.90944	15968.77795	69496.49299	58272.30735	57788.72161	29225.94133
AT1G70250	gi 2194117	Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698) [Arabidopsis thaliana]	signal transduction	2	2	25.36	0.009	0.291	3817.80428	4131.04725	6089.99391	7937.512612	2699.760005	1309.452205	647.3601013	1734.974582
AT1G66150	gi 15218941	TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	4	4	63.95	0.001	2.612	63112.3187	52865.47437	57397.89172	52512.27344	182983.8361	159879.7781	149613.2399	97500.92055



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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G16670	gi 9989053	Unknown protein [Arabidopsis thaliana]	Signal transduction	3	3	39.62	0.004	0.454	125232.7482	171798.2775	148520.6313	151550.4488	61258.91392	40927.7423	78849.12178	89958.63182
AT2G23810	gi 13272397	unknown protein [Arabidopsis thaliana]	signal transduction	4	4	157.4	0.009	2.697	215424.548	193092.9118	201879.5063	175345.8356	890744.0579	558287.2366	346974.3533	323277.2111
AT5G43980	gi 9758557	unnamed protein product [Arabidopsis thaliana]	Signal transduction	4	4	47.27	0.030	2.296	48954.85167	66274.80563	119827.0071	132586.9051	325548.9597	162619.5767	218392.3909	137654.0867
AT1G66880	gi 10177797	unnamed protein product [Arabidopsis thaliana]	signal transduction	3	3	66.02	0.006	0.433	81453.43064	71280.87646	53629.2709	63469.17059	18428.16176	34896.34619	22024.7583	41466.36102
AT5G01310	gi 15240948	basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana]	transcription	4	4	46	0.029	2.504	83439.61773	82425.34203	140170.1249	92026.35652	284876.1063	394035.5051	205836.1668	111847.9661
AT2G34160	gi 52696237	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana	transcription	2	2	32.27	0.007	0.430	130661.9125	92184.34952	125684.3719	97923.70076	37952.6383	28091.87207	57629.48973	68222.68072
AT3G61260	gi 15233068	DNA-binding family protein / remorin family protein [Arabidopsis thaliana]	Transcription	3	3	76.87	0.001	2.539	80395.86397	54272.94539	55978.86134	66483.38569	195976.7132	183784.149	155609.4107	117569.7128
AT2G45820	gi 601843	DNA-binding protein [Arabidopsis thaliana]	transcription	4	4	106.25	0.016	2.665	78588.07086	47271.2434	35909.52519	37326.04008	226307.9193	117454.6934	78963.59362	107852.2561
AT5G52470	gi 6003681	fibrillarin homolog [Arabidopsis thaliana]	transcription	3	3	39.67	0.008	0.206	246651.1148	231470.0235	110850.7582	101782.4782	46796.80467	12609.88737	24105.36746	59092.31997
AT3G53460	gi 681902	RNA-binding protein cp29 [Arabidopsis thaliana]	transcription	3	3	24.97	0.045	0.406	70505.78161	66693.71369	30520.12838	28181.35908	11233.73503	11804.97898	19562.63004	36866.37558
AT1G02080	gi 3258569	Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]	transcription	7	7	49.49	0.015	0.328	113702.4943	111100.6302	94557.9881	88244.95845	10166.70496	25654.50676	35796.63469	61974.21873
AT1G02080	gi 42561615	transcriptional regulator-related [Arabidopsis thaliana]	transcription	7	7	41.32	0.027	1.943	109745.0033	73663.28576	66081.29616	60046.8945	179697.334	208454.9726	115019.6653	98262.77442

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G15030	gi 8777486	unnamed protein product [Arabidopsis thaliana]	transcription	1	1	19.19	0.020	0.456	24751.63332	18571.7194	19139.23157	23366.44958	13248.3683	5180.608836	5852.296248	14832.9192
AT5G24450	gi 9758533	unnamed protein product [Arabidopsis thaliana]	transcription	3	3	40.51	0.002	0.322	95481.99575	89035.38255	151406.9402	124622.2024	22821.73925	28612.14964	51740.28938	44962.69869
AT3G30842	gi 9294504	ABC transporter-like protein [Arabidopsis thaliana]	Transporter	3	3	78.13	0.046	2.322	674081.9977	983208.0467	1231424.364	1599452.448	4512381.916	1723145.075	2754817.791	1432471.974
AT3G47950	gi 30692952	AHA4; ATPase/hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	Transporter	13	13	272.02	0.024	2.268	19272.20982	24746.07533	10931.65713	8618.00915	22622.74527	36640.89197	48442.73158	36448.37651
AT1G80660	gi 6730723	aha9, 5' partial; 1-2403 [Arabidopsis thaliana]	Transporter	9	9	183.27	0.002	0.147	41665.0937	25939.71645	17790.14592	57183.76107	5911.02131	2112.467966	7628.39407	5325.314268
AT2G38290	gi 7140936	ammonium transporter [Arabidopsis thaliana]	Transporter	2	2	52.22	0.021	2.242	16979.35253	11844.76176	6099.114203	9305.585971	26044.93725	22353.864	34843.26065	15920.60549
AT4G13510	gi 15236300	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana]	Transporter	3	3	278.26	0.018	2.419	1554280.336	1588016.902	859380.4652	564330.0205	3458689.995	1850084.146	2404128.745	3332783.591
AT5g26340	gi 15010580	AT5g26340/F9D12_17 [Arabidopsis thaliana]	Transporter	4	4	136.15	0.006	3.362	138013.5087	135516.903	52639.81458	57314.31829	409011.0704	403608.6351	207572.5734	269261.0722
AT3G47730	gi 22331647	AT1AT1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	Transporter	10	10	277.27	0.050	2.753	35213.0928	52699.54104	20375.54595	31701.86203	32809.88506	125605.7006	137506.8895	89428.92326
AT5G61730	gi 15240334	AT1AT1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	Transporter	10	10	291.65	0.002	3.202	179827.7156	213942.0207	141620.0067	126319.0854	751679.7106	478555.3309	584729.6216	303559.0415

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G38940	gi 15224985	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/inorganic phosphate transmembrane transporter/phosphate transmembrane transporter/sugar:hydrogen symporter	Transporter	11	11	757.44	0.026	2.812	1125110.624	966554.0866	1824167.551	1744053.827	6287768.842	3802356.098	4215552.818	1608380.187
AT5G57110	gi 8843813	Ca2+-transporting ATPase-like protein [Arabidopsis glucose transporter [Arabidopsis thaliana]	Transporter	23	23	993.38	0.002	2.672	1177412.636	1631098.187	1055177.561	995031.6924	4671831.462	2418705.457	3077415.978	2812569.93
AT1G11260	gi 16520	hypothetical protein [Arabidopsis thaliana]	Transporter	4	4	254.6	0.003	2.636	465089.0442	427223.7074	263605.993	260611.2083	1136752.035	787011.2138	1120523.981	689746.9388
AT1G69480	gi 12597793	PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Arabidopsis thaliana]	Transporter	7	7	177.39	0.023	3.908	18419.45027	18244.39674	19205.86537	16586.88727	100295.0934	120074.8924	38679.90831	24145.77308
AT1G59870	gi 15218936	PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	Transporter	3	3	104.27	0.018	0.036	18510.95698	4814.690894	1336.881918	2122.39728	422.0307233	472.5035217	72.67404344	6.880801345

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT5G43350	gi 15239848	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	Transporter	11	11	588.36	0.028	2.809	186809.1455	284095.3641	464996.0028	397922.1656	1335851.158	658610.2085	1316322.11	436017.8319
AT4G35100	gi 1688296	plasma membrane intrinsic protein PIP3 [Arabidopsis	Transporter	1	1	32.4	0.011	2.347	25925.41795	36507.90191	50172.12497	32422.56931	81247.17276	51237.6538	127267.736	80589.14556
AT2G18960	gi 166746	plasma membrane proton pump H+ ATPase [Arabidopsis	Transporter	21	21	495.99	0.030	0.644	423568.2341	378421.9956	330958.3661	401755.3612	192341.1382	175633.5684	266065.6256	353732.2476
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporter	5	5	146.75	0.012	3.965	6989.681487	8830.893307	17076.52447	15353.20616	57232.11453	69060.71615	47599.69514	17430.57614
AT3G19930	gi 15230987	STP4 (SUGAR TRANSPORTER 4); carbohydrate transmembrane transporter/ monosaccharide transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Transporter	2	2	114.11	0.039	2.429	255952.7205	310587.8637	126632.6925	128283.2355	885141.9911	343307.427	303679.8611	463294.8191

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G71880	gi 15217601	SUC1 (sucrose-proton symporter 1); carbohydrate transmembrane transporter/sucrose:hydrogen symporter/sugar:hydrogen symporter [Arabidopsis thaliana]	Transporter	3	3	72.98	0.046	3.252	26912.55244	20423.21443	32055.05593	27538.24406	177001.5943	81424.02603	61303.86357	28035.53984
AT3G47780	gi 4741195	ABC transporter-like protein [Arabidopsis thaliana]	transporters	3	3	64.43	0.000	0.406	306575.4779	328107.5424	255065.7317	228194.3131	95584.03552	102469.3398	121657.7209	134467.3031
AT5G04930	gi 18414733	ALAT1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism [Arabidopsis thaliana]	transporters	6	6	73.04	0.001	2.728	9686.232872	18138.00926	11706.32424	11754.82943	41302.70016	30267.3068	38123.11613	30220.01407
AT4G38510	gi 15010616	AT4g38510/F20M13_70 [Arabidopsis thaliana]	transporters	1	1	17.13	0.028	0.498	1811.819494	1229.425686	1215.588717	2567.921658	1284.58657	706.90985	632.3337055	775.2527485
AT5G58270	gi 9187883	mitochondrial half-ABC transporter [Arabidopsis thaliana]	transporters	1	1	24.18	0.036	2.258	58937.24415	55676.12585	59827.33855	96159.90353	259424.6531	114230.1849	155941.4677	81370.24147
AT3G16340	gi 18401096	PDR1; ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	16	16	375.22	0.000	3.037	121667.3799	123135.1748	156778.5528	138225.8548	448906.6451	503331.5935	352284.0738	334613.8138
AT2G26910	gi 15225814	(PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	4	4	92.32	0.011	0.287	22960.3874	9370.50675	20726.07183	22061.87774	6592.351192	2180.623947	5067.035628	7732.774454

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT3G55320	gi 15233244	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	4	4	33.71	0.006	3.326	145729.3567	140870.1555	115880.608	78377.64479	351247.0677	669794.4808	371167.5146	207081.2621
AT4G32390	gi 15236781	phosphate translocator-related [Arabidopsis thaliana]	transporters	1	1	22.1	0.000	0.313	154376.5022	130655.488	189841.1523	229289.1797	54758.71811	42940.27764	62211.64969	60651.75401
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis thaliana]	transporters	5	5	182.55	0.014	3.141	21212.03205	15268.18948	15065.31617	13488.96674	96510.6337	34223.29354	47633.33022	25923.70638
AT1G30410	gi 75333513	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABCC.12; Short=AtABCC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName: Full=Multidrug [Arabidopsis thaliana]	transporters	1	1	24.76	0.000	0.220	128272.5957	130355.4856	186018.109	183830.4997	23653.68103	24118.3294	53376.90169	37011.9818
AT2G24520	gi 12230479	RecName: Full=ATPase 5, plasma membrane-type; AltName: Full=Proton pump 5 [Arabidopsis thaliana]	transporters	5	5	85.95	0.006	43.035	87.61036549	129.2089327	1936.486464	341.4118489	58576.69028	2394.672276	23345.99799	23041.78367
AT3G51670	gi 15230555	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	transporters	3	3	37.95	0.008	0.288	52292.15797	39351.3799	30746.76083	36590.83818	4500.994561	7177.838725	11536.02848	22578.18351

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G25600	gi 30682817	SPINK (Shaker1 Pollen Inward K+ channel); cyclic nucleotide binding / inward rectifier potassium channel/ potassium channel [Arabidopsis thaliana]	transporters	1	1	15.14	0.018	0.202	150569.0185	160167.829	225890.2625	151785.4815	4252.647778	21014.26452	64223.46076	49583.77801
AT1G13210	gi 15222212	(autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin actin binding [Arabidopsis thaliana]	unknown	5	5	120.35	0.001	4.056	5957.746604	7845.609074	3112.979602	3133.405352	16670.9799	23238.08428	17159.06845	24245.67068
AT1G31810	gi 186479105	At1g52320/F19K6_7 [Arabidopsis thaliana]	unknown	6	6	40.01	0.001	0.383	37561.97039	32651.99943	48174.4611	51105.23127	22530.24558	14059.0425	13485.36996	14840.51649
AT1G52320	gi 15450411	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding [Arabidopsis thaliana]	unknown	4	4	40.25	0.004	0.421	103444.4395	87795.03859	102441.8042	93390.07156	55994.54639	25638.72646	28944.0119	52332.18485
AT1G78880	gi 15219232	balbiani ring 1-related / BR1-related [Arabidopsis thaliana]	unknown	1	1	23.11	0.029	2.086	3350.139232	2640.561473	1341.593327	1778.37579	6519.854467	4478.958518	5110.436163	2897.114868
AT4G23630	gi 15236556	BT11 (VIRB2-INTERACTING PROTEIN 1) [Arabidopsis thaliana]	unknown	4	4	76.77	0.024	0.324	22100.44441	20125.76439	23315.57076	17679.54683	7469.267593	6999.895232	1476.173075	10988.73766
AT4G11220	gi 15237093	BT12 (VIRB2-INTERACTING PROTEIN 2) [Arabidopsis thaliana]	unknown	2	2	57.46	0.018	0.256	64454.99709	60537.85977	36439.61185	29165.6308	3832.153724	4842.494664	18827.29944	21346.66325

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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT4G20260	gi 15235363	DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana]	Unknown	5	5	230.1	0.002	2.987	350161.0629	233149.387	275255.0446	339152.4303	1229608.01	805268.1845	1003935.929	538241.188
AT4G00310	gi 18411286	(EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana]	unknown	2	2	16.66	0.001	0.287	25088.32513	13190.82977	19092.6096	33294.42478	7471.604063	6627.251248	5379.742332	6556.989284
AT1G71820	gi 7239509	EST gb AA712174 comes from this gene [Arabidopsis thaliana]	Unknown	4	4	57.31	0.024	2.899	42734.26817	51993.64555	17638.22868	19642.6609	167184.9871	58323.96414	91911.55187	65323.21068
AT1G61900	gi 3367523	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	Unknown	8	8	181.86	0.017	4.744	89234.80264	98335.81771	67748.25547	59740.99702	792638.923	314164.3658	273914.4015	113912.4235
AT3G24255	gi 8778279	F14D16.18 [Arabidopsis thaliana]	unknown	5	5	24.31	0.028	0.357	225742.1042	231706.8717	361916.9598	244826.0385	26764.56613	60276.99131	156282.1344	137052.349
AT1G28340	gi 6560758	F3M18.23 [Arabidopsis thaliana]	unknown	3	3	44.56	0.003	2.206	29951.28323	40830.05975	23709.8494	25719.6452	68302.97624	56803.95037	88551.24806	51501.99673
AT1G27090	gi 15223426	glycine-rich protein [Arabidopsis thaliana]	Unknown	5	5	377.84	0.009	2.316	337323.286	300887.459	177869.5804	190125.4498	808093.1425	445694.9477	431445.5769	644881.511
AT1G26130	gi 15222647	haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	unknown	4	4	28.41	0.009	0.429	168450.7382	132230.8327	243233.3069	266890.0197	93414.34669	56490.88735	115416.9081	82870.84139
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	58.73	0.000	20.651	113066.2124	81498.5523	33239.172	45018.55405	2629250.478	1307516.678	942137.7551	755195.8972
AT2G30480	gi 110741415	hypothetical protein [Arabidopsis thaliana]	unknown	5	5	57.47	0.006	3.567	1745491.456	3572261.631	4870899.128	4721023.514	16196067.97	8765745.1	18987488.05	9229635.351
AT5G04420	gi 15237715	kelch repeat-containing protein [Arabidopsis thaliana]	unknown	2	2	20.11	0.022	2.038	115860.0727	84400.39641	116041.3436	97680.31959	342310.2612	131038.7526	182347.8859	188042.5119
AT3G15410	gi 2760084	leucine-rich repeat protein [Arabidopsis thaliana]	unknown	3	3	33.73	0.040	0.323	15556.55675	18348.02334	52712.52537	48634.34346	10554.39619	6927.752671	20514.55455	5697.359408



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									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G25570	gi 42562316	leucine-rich repeat protein-related [Arabidopsis thaliana]	Unknown	9	9	198.9	0.036	2.601	266553.0668	356919.8923	106244.5768	114554.6665	423315.5198	780683.9267	698023.9935	293883.1474
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	unknown	10	10	241.38	0.004	4.302	130538.0587	136433.9337	112113.1976	103826.5973	906976.6371	478226.0314	465557.5138	226947.4443
ATMG00520	gi 13449330	maturase [Arabidopsis thaliana]	unknown	5	5	46.1	0.046	0.405	24931.18115	30783.85752	69420.58628	60933.63069	8303.304126	19780.90257	26568.9452	20740.94169
AT5G61800	gi 15240355	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	unknown	3	3	38.41	0.001	0.470	85102.49309	72909.65502	67302.26936	88825.66785	35797.34178	26298.41757	46304.1762	39234.61942
AT1G09520	gi 18391032	protein binding / zinc ion binding [Arabidopsis thaliana]	Unknown	2	2	26.65	0.017	0.410	73324.53442	64037.74147	57159.83921	39393.52708	26211.68598	24278.70521	10402.08394	34918.74812
AT4G32285	gi 2864615	putative protein [Arabidopsis thaliana]	unknown	6	6	66.25	0.012	0.245	6579.09245	6899.522615	16569.02321	13277.04961	881.5795595	2055.128808	4167.15724	3524.673298
AT3G57430	gi 6706414	putative protein [Arabidopsis thaliana]	unknown	3	3	31.22	0.007	0.303	29745.7284	28541.37541	68026.51491	62292.28752	11064.92953	9214.143911	19210.01563	17662.56662
AT5G30520	gi 7413621	putative protein [Arabidopsis thaliana]	unknown	2	2	29.11	0.020	0.226	15352.92269	6548.101793	4497.945282	4462.136701	2787.021343	2424.048058	492.3869077	1264.814411
AT3G60920	gi 8388608	putative protein [Arabidopsis thaliana]	unknown	5	5	41.15	0.028	3.714	175446.4012	196415.101	231213.0921	223746.169	1613947.933	733074.2437	447235.2096	276231.4512
AT4G06544	gi 7529254	putative protein [Arabidopsis thaliana]	unknown	2	2	29.32	0.001	0.216	52256.8566	50524.24711	40320.88112	34588.15618	11318.62449	8875.880476	4647.183622	13619.37681
AT3G44150	gi 7635460	putative protein [Arabidopsis thaliana]	unknown	4	4	88.65	0.005	2.318	151755.9469	134418.1675	71406.96018	86994.0847	325229.5622	227192.2893	214101.6523	263982.4965
AT5G14770	gi 223635763	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial	unknown	4	4	52.61	0.001	0.233	4024.987143	4288.126646	4904.896351	10514.93897	1347.739095	1506.559018	1067.352793	1610.825997

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT1G11820	gi 3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene	Unknown	1	1	39.56	0.018	2.060	44536.02624	38054.24682	16294.65345	26227.71143	67828.7078	76710.25913	63745.84456	49495.30932
AT1G17820	gi 9665060	Strong similarity to a hypothetical protein T18K17.13 gi 6598861 from Arabidopsis thaliana BAC T18K17 gb AC010556 and contains a ubiquitin	unknown	2	2	19.53	0.010	2.450	1110689.829	1677690.196	2561534.051	2604701.995	7110320.591	3927776.808	4752189.848	3697492.065
AT2G31290	gi 15224649	thiolesterase [Arabidopsis thaliana]	unknown	3	3	35.91	0.028	0.398	71957.68835	62374.13002	69191.46482	160115.5981	49871.24812	18891.08827	48721.20903	27253.28798
AT1G17147	gi 116830105	unknown [Arabidopsis thaliana]	unknown	2	2	30.92	0.003	0.304	36991.45415	40340.30158	30130.7567	49674.96774	16011.89027	10092.57696	5925.39046	15735.12168
AT3G45460	gi 116831268	unknown [Arabidopsis thaliana]	unknown	4	4	34.18	0.001	11.194	2100.908736	1691.205314	3873.233117	6332.434429	68283.51814	38220.58358	24084.44809	26107.80564
AT5G46680	gi 21618238	unknown [Arabidopsis thaliana]	unknown	2	2	34.36	0.002	6.672	75.26002933	228.0362933	263.4266613	89.74416686	647.621197	970.3447156	1705.653931	1056.510083
AT5G42370	gi 13430796	unknown protein [Arabidopsis thaliana]	Unknown	4	4	104.74	0.017	6.186	566.134222	4173.107267	5674.387926	5689.418928	37650.88106	26951.36665	24693.58947	10317.74787
AT2G46150	gi 15225931	unknown protein [Arabidopsis thaliana]	Unknown	1	1	61.77	0.025	2.133	34466.12468	30233.60961	13517.26063	12568.99321	44838.29775	63756.77604	46503.75744	38570.22464
AT5G19230	gi 15239685	unknown protein [Arabidopsis thaliana]	Unknown	1	1	130.13	0.042	2.825	59930.36483	51655.89515	24408.93879	31711.18978	194237.6155	155264.4087	52556.35375	71738.20524
AT3G08600	gi 18398173	unknown protein [Arabidopsis thaliana]	Unknown	3	3	118.32	0.014	2.742	102407.6945	69029.7378	38105.66466	25725.18386	211508.3651	170506.8297	135117.6665	128069.2799
AT4G28100	gi 18417127	unknown protein [Arabidopsis thaliana]	Unknown	4	4	148.07	0.033	5.031	156807.4239	129427.3478	47812.61676	55921.46173	1246745.806	256584.6735	187286.938	271398.8384
AT2G25800	gi 3643603	unknown protein [Arabidopsis thaliana]	Unknown	7	7	232.21	0.033	2.707	125648.4899	183003.8776	45394.94473	35135.5037	369447.7943	170727.274	237645.5752	275577.1413

ATG	Accession	Description	Functional categories	Peptide count	Peptides used for	Confidence score	Anova (p)*	CA/control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA1	CA2	CA3	CA4
AT2G26570	gi 15225334	unknown protein [Arabidopsis thaliana]	unknown	7	7	51.73	0.005	0.231	17445.67451	17836.88083	45330.0242	50425.97225	8857.736875	5877.982231	10090.99715	5478.20509
AT2G21990	gi 15227126	unknown protein [Arabidopsis thaliana]	unknown	4	4	30.87	0.022	10.186	18663.0383	16923.49198	14506.52997	12709.51557	277568.6386	36404.6048	291681.4121	34025.00785
AT4G40020	gi 15236102	unknown protein [Arabidopsis thaliana]	unknown	2	2	25.38	0.015	3.948	45999.44937	54122.67993	55111.25932	56197.11815	436509.0017	147833.8601	169060.205	81395.06444
AT4G08760	gi 15236604	unknown protein [Arabidopsis thaliana]	unknown	4	4	58.87	0.005	0.335	38686.64227	53531.88437	37338.22557	34278.83068	14131.84091	6644.033203	12295.91273	21806.06827
AT5G19240	gi 15239686	unknown protein [Arabidopsis thaliana]	unknown	1	1	40.86	0.019	2.368	15189.50335	10657.68362	5912.325507	7370.023139	12974.35527	28182.1372	27766.37003	23718.89258
AT2G27260	gi 18401372	unknown protein [Arabidopsis thaliana]	unknown	3	3	90.26	0.005	5.769	2291.92289	3227.747265	578.5081434	736.8677576	10143.90196	13573.21584	10049.71812	5664.867539
AT4G27595	gi 240256091	unknown protein [Arabidopsis thaliana]	unknown	6	6	43.55	0.013	0.412	24019.63505	26906.11326	11534.35056	26110.8486	8451.330153	6533.991929	8254.057936	13230.89156
AT5G28237	gi 26452400	unknown protein [Arabidopsis thaliana]	unknown	5	5	43.54	0.005	0.309	41449.76983	40685.10534	69666.97538	72773.76696	15047.54918	8581.982482	20804.15594	24848.04998
AT2G28310	gi 30683843	unknown protein [Arabidopsis thaliana]	unknown	7	7	33.09	0.003	2.971	215215.5481	215154.7658	132730.7018	105562.261	679206.1112	457108.6435	497092.0871	353163.3557
AT1G22250	gi 30687784	unknown protein [Arabidopsis thaliana]	unknown	2	2	19.58	0.012	0.089	10243.9321	4968.721225	2153.375183	1827.696579	325.3945501	48.390351	967.293304	372.2559227
AT5G58160	gi 8777317	unnamed protein product [Arabidopsis thaliana]	unknown	4	4	32.36	0.001	0.226	166964.8734	142318.1968	224368.5571	237434.4733	24504.38287	37334.94267	72167.02971	40608.83051
AT2G15025	gi 9294045	unnamed protein product [Arabidopsis thaliana]	unknown	1	1	21.85	0.008	0.331	85480.2396	77024.75779	59905.75175	63301.70861	9955.285596	17829.64217	22785.32322	43874.3722
AT5G39970	gi 10176989	unnamed protein product [Arabidopsis thaliana]	unknown	5	5	179.23	0.033	2.839	105341.3983	104906.4149	33226.40311	25762.61784	282522.9822	220914.5653	113572.3805	147287.2193

Supplementary Table 3-5 Common CA- and ABA responsive plasma membrane proteins at the lag phase

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	cell growth/division	0.008866467	2.754	0.01029625	2.553	35355.26	46964.37	26211.13	35408.54	51102.04	80090.44	141862.5	94414.11	156128.4	86805.07	100522	53016.04
AT3G13210	gi 10172609	probable cell cycle control protein; crooked neck-like protein [Arabidopsis thaliana]	cell growth/division	0.00081038	0.308	0.036506355	0.325	258096.7	214119.6	301843.4	287899.7	145007.3	81631.79	104477.4	14340.92	72650.23	52730.88	75242.38	126645.9
AT5G03340	gi 11265361	transitional endoplasmic reticulum ATPase - Arabidopsis thaliana	cell growth/division	0.027193751	2.154	0.027966233	2.867	63444.93	95737.68	61039.78	36186.57	106609.2	96361.6	234366.2	297863.4	82341.73	152476.8	125537.4	191961.7
AT1G68560	gi 4163997	alpha-xylosidase precursor [Arabidopsis thaliana]	cell structure	0.000135377	1.964	0.021437243	3.356	148086.4	181682.8	173371.9	157128.4	266134.9	389311.7	1199660	360785.6	343507.9	365263	314545.3	273352.6
AT5G65020	gi 15238320	ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis thaliana]	cell structure	0.00650566	0.377	0.004058842	0.359	534256.2	436942.7	551609.9	576423.6	265051	160615	234725.2	93319.82	210881.5	91208.62	187376.8	302458.3
AT1G53840	gi 15220958	ATPME1; pectinesterase [Arabidopsis thaliana]	cell structure	0.004352505	2.954	0.006023405	2.591	113616.1	95110.36	51013.75	51040.61	158216.3	181017.9	190861.4	275168.9	300525.5	264666.9	187296.5	165562.6
AT3G14300	gi 15231826	ATPMEPCRC; pectinesterase [Arabidopsis thaliana]	cell structure	0.019149133	2.858	0.00448453	2.233	31946.46	34183.35	17947.43	16621.54	49967.27	55583.47	60408.22	58891.65	120702.3	74026.47	57519.01	35554.37
AT1G66250	gi 12323569	beta-1,3-glucanase precursor, putative; 34016-35272	cell structure	0.000922393	4.532	0.002702824	4.441	96967.28	105137.9	64863.89	74518.68	226257.6	239346.7	705747.4	345052.5	491488.7	322920.4	525334	208034.1
AT3G13560	gi 9280308	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	cell structure	0.003001581	3.220	0.00162546	3.299	104658.4	139880.6	69957.47	70028.22	236785.1	250780.9	339402.7	441679.6	396042.3	375252	283208.5	183568.9
AT4G37410	gi 15235541	CYP81F4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	cell structure	0.005766967	9.751	0.013697598	53.099	210.0016	90.25661	227.5982	139.7015	2204.914	30854.5	646.1037	1741.314	4189.494	810.5231	879.5398	629.8621
AT1G74790	gi 5882745	F25A4.24 [Arabidopsis thaliana]	cell structure	0.008640836	3.899	0.006109917	3.722	2384101	2887773	1254664	1217958	9152270	3969586	5284392	10416788	13440750	7668430	5097150	3988276
AT4G20830	gi 30685222	FAD-binding domain-containing protein [Arabidopsis thaliana]	cell structure	0.011016599	3.314	0.000291252	3.193	939938.5	840542.2	928898	1189352	2233074	2795949	4231613	3188738	5036111	2747950	3832682	1302970
AT4G12730	gi 13377778	fasciclin-like arabinogalactan-protein 2 [Arabidopsis thaliana]	cell structure	0.0029303	4.684	0.001705762	4.072	6262584	5652025	4443170	5250667	12349044	18155938	38302992	19174614	38773264	25465222	27029246	9943688
AT5G55730	gi 15240570	FLA1 (FASCICLIN-LIKE ARABINOOGALACTAN 1) [Arabidopsis thaliana]	cell structure	0.002818972	4.356	0.007785344	3.438	5461346	6614710	3646262	3312602	9183737	11551089	29227544	15475397	31995736	19378724	21649676	9894211
AT5G44130	gi 15241423	FLA13 (FASCICLIN-LIKE ARABINOOGALACTAN PROTEIN 13 PRECURSOR) [Arabidopsis thaliana]	cell structure	0.011104151	5.997	0.020080587	7.435	55388.75	44068.1	106613.8	111557.3	98359.06	638548.9	1079743	544788.3	412117.9	476128.9	884964.6	131727.2
AT2G04780	gi 18395849	FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) [Arabidopsis thaliana]	cell structure	0.002379997	4.585	0.005165762	2.500	232988.4	257436.9	156102.1	143630.5	481246.4	498240.8	317251.3	678443.7	1468576	920484	801925.2	431730.8
AT2G45470	gi 18406799	FLA8 (FASCICLIN-LIKE ARABINOOGALACTAN PROTEIN 8) [Arabidopsis thaliana]	cell structure	0.000161884	4.904	0.006088062	4.857	2137491	2858283	2324713	1854588	4949487	8016853	23536013	8062388	13355542	11321168	13596151	6721130
AT1G03870	gi 18379157	FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) [Arabidopsis thaliana]	cell structure	0.005878549	5.125	0.000830107	3.359	324018	308846.3	242228.5	267998.2	601812.9	777825	1175724	1284231	2767042	1179629	1398948	512590.6
AT2G01630	gi 18379267	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana]	cell structure	0.018754031	2.889	0.00164121	3.180	32760.69	42270.76	61228.54	47292.12	89216.98	158997.5	196140	139420.6	91619.49	91437.68	262790.9	84519.83
AT4G31140	gi 15235840	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure	0.000364178	2.385	0.001648452	3.278	309728.9	247987.3	201533.7	227496.7	1193521	471455	738400.7	831179.1	486715.9	627461.4	700182.8	539225.3
AT5G56590	gi 15241268	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	cell structure	0.008451838	2.791	0.002080619	2.530	80202.64	71498.59	40991.05	57501.42	130283.3	192038	128440.3	182175.9	229997.3	202275.9	177468.6	88573.51
AT5G20940	gi 22326918	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	cell structure	0.002687644	0.344	0.007383232	0.401	34104.31	22389.87	23621.47	40010.05	18737.4	11347.3	10654.02	7440.804	12539.65	6085.031	10831.36	11920.54
AT5G04885	gi 30680681	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	cell structure	0.001433085	3.898	0.044243516	3.372	2339540	3013211	2391262	2291267	3685003	6515655	19511383	4126903	10838065	9563829	13866728	4850726
AT2G30870	gi 15224582	GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase	cell structure	0.037480978	2.003	0.043266665	3.307	15487.11	16311.63	15937.48	15753.3	18959.76	57270.02	27643.87	106090	41082.29	33307.53	37914.47	14845.01

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT5G48450	gi 8777375	pectinesterase-like protein [Arabidopsis thaliana]	cell structure	0.015835076	2.592	0.046718988	3.133	57643.56	80176.23	52458.59	62173.35	111284	108186.6	461659.5	109793.8	83579.5	138833.1	277725.4	154301.8
AT5G17820	gi 15238030	peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana]	cell structure	0.000283039	4.456	0.00035049	5.572	68435.05	65899.67	99982.76	97531.49	288806.4	740522.4	459755.1	360098.1	445868.1	426893.1	383948.1	222136.7
AT1G42550	gi 24025422	PMI1 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	cell structure	0.010092737	3.827	0.008540801	2.518	531247.4	516149.8	362570.3	336989.8	1159439	1373277	578005.5	1287330	2488934	2148324	1430457	617188.1
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	cell structure	0.018649273	3.265	0.003987639	2.467	668464.9	659748.7	330674.5	426120.2	1106451	991782.3	1493831	1551970	3099920	1644970	1324782	738551.7
AT2G13820	gi 15225509	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	cell structure	0.001265763	6.295	0.015137253	2.381	136422.9	157553.3	200576.9	138698.7	202375.2	406029.4	584578	314959.7	1678171	1039435	855569.2	412836.5
AT4G03230	gi 4262151	putative receptor kinase [Arabidopsis thaliana]	cell structure	0.007980695	0.222	0.007898938	0.150	14124.08	21479.21	34232.69	27398.26	6610.108	4357.949	3000.544	628.137	7966.425	2755.466	1948.244	8882.785
AT5G51480	gi 15242108	SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase [Arabidopsis thaliana]	cell structure	0.019261046	4.868	0.001630512	2.467	671452.3	663614.9	791673	763655.9	1189508	1806769	2511795	1621973	7132956	2965572	3058563	912883.5
AT3G46550	gi 15231453	SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding [Arabidopsis thaliana]	cell structure	0.001762999	3.734	0.018397318	2.086	50044.31	55821.34	32671.28	41917.78	99237.32	105045.9	51888.38	120280.1	237274.1	183345.9	164616.6	88626.3
AT5G12370	gi 14586367	putative protein [Arabidopsis thaliana]	cell structure	0.02819615	0.664	0.000975066	0.563	75678.87	70580.96	64884.82	84215.11	45191.16	43014.06	45603.99	32619.15	72087.13	39184.5	40536.22	44303.78
AT4G01700	gi 15234281	chitinase, putative [Arabidopsis thaliana]	disease/defence	0.028538851	2.513	0.000681545	4.890	527122.6	603628.8	263384.1	218405.2	2227176	1744739	2189237	1723755	1463966	1126277	530269.6	931590.8
AT1G20440	gi 388259	cor47 [Arabidopsis thaliana]	disease/defence	0.00019206	3.807	0.034419268	8.237	8604.131	6138.325	10134.93	12476.92	10817.6	33446.36	100910	162521.8	43351.65	33360.77	35382.94	30114.49
AT1G30360	gi 18397470	ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	disease/defence	0.008362891	2.355	0.006089171	2.041	440348.9	364627.2	202460.5	242193.3	572272.7	631300.2	669549.5	676969.5	1056047	563255	702243	620937.1
AT2G43610	gi 15224319	glycoside hydrolase family 19 protein [Arabidopsis thaliana]	disease/defence	0.012570816	2.566	0.005342499	5.875	65464.8	107553.5	35483.53	30490.72	448512.1	142628	267179.5	545803	169286.3	122497.1	145736.2	175853.6
AT3G53990	gi 30693971	universal stress protein (USP) family protein [Arabidopsis thaliana]	disease/defence	0.00373732	4.180	0.04140711	5.706	10880.62	23458.97	8399.222	7834.078	20080.68	21101.45	129020.9	118345.7	29632.59	58963.51	76463.56	46330.4
ATCG00480	gi 7525040	ATP synthase CF1 beta subunit [Arabidopsis thaliana]	energy	0.025925559	2.406	0.037156702	2.274	604160.1	874539.6	1464724	1194300	3873168	1285190	2288835	1963640	3311939	2013037	3306258	1324580
AT3G55440	gi 414550	cytosolic triose phosphate isomerase [Arabidopsis thaliana]	energy	0.001012809	3.369	0.036360846	4.390	133533.6	146579.3	180109	105063.8	148182	502026.7	1298991	532354.6	357704.4	543328	668744	334561
AT4G32840	gi 15233959	PFK6 (PHOSPHOFRUCTOKINASE 6); 6-phosphofructokinase	energy	0.002509532	0.281	0.006897226	0.292	83019.07	30499.78	33576.06	46574.85	17216.32	15494.01	16216.86	7531.093	15188.47	14530.19	10529.56	14107.23
AT3G56190	gi 15228848	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein [Arabidopsis thaliana]	intracellular traffic	0.001688225	2.689	0.019225894	1.583	102769.3	95614.04	66510.3	59472.35	118492.8	115558.7	123323	155940.4	277506.2	237839.2	203548.3	153395.9
AT5G08680	gi 22326673	ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana]	intracellular traffic	0.008640758	4.799	0.01095614	2.450	51357.17	77320.32	141336.9	102372.3	215935.5	153188.2	302223	240822	934737.6	326544	312795.2	213013.9
AT1G71820	gi 7239509	EST gb AA712174 comes from this gene [Arabidopsis thaliana]	intracellular traffic	0.023906287	2.899	0.024269867	2.383	42734.27	51993.65	17638.23	19642.66	50095.98	70430.97	95623.61	98404.54	167185	58323.96	91911.55	65323.21
AT3G10380	gi 18398855	SEC8 (SUBUNIT OF EXOCYST COMPLEX 8) [Arabidopsis thaliana]	intracellular traffic	0.0186531	2.168	0.018804938	2.417	6536.946	8690.576	3898.285	3363.572	11322.64	17803.51	8317.977	16906.3	8759.74	10992.49	16311.04	12696.83
AT5G08080	gi 18415701	SYPI32 (SYNTAXIN OF PLANTS 132); SNAP receptor [Arabidopsis thaliana]	intracellular traffic	0.002030401	2.737	0.001281205	1.906	482120.1	437745.1	389086	359476.4	617519.2	816386	781904.3	964792.8	1552918	1227081	1111704	675289.1
AT4G35790	gi 18419668	ATPLDELTA; phospholipase D [Arabidopsis thaliana]	metabolism	0.00282113	2.019	0.010083229	4.986	182006.7	170344.3	149105.5	152247.1	502011.2	496263.3	362761.6	1898147	444408.1	339667.3	299672.1	236099
AT5G17920	gi 55670112	Chain A, A. Thaliana Cobalamine Independent Methionine Synthase	metabolism	0.01384735	0.285	0.028770716	0.485	53699.28	63984.37	72236.49	86183.89	40990.66	38457.89	40329.6	14263.71	5126.093	16288.35	35604.53	21548.35
AT1G43710	gi 15218445	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	metabolism	0.007797383	3.753	0.004269387	6.696	39838.17	38895.1	34792.98	41122.28	128324.4	165211.6	609873.9	132069.9	69307.76	204847.4	223357.8	82840.25
AT1G34430	gi 8778253	F12K21.24 [Arabidopsis thaliana]	metabolism	0.004938575	3.175	0.004695692	2.912	163783.8	105068.8	163843.3	116610.7	232454.1	467776.2	583690.5	315707.5	656847.4	507742.3	347440.4	232237.9
AT2G18730	gi 4185139	putative diacylglycerol kinase [Arabidopsis thaliana]	metabolism	0.004825667	3.423	0.000227909	3.774	60568.62	70952.05	56557.53	46683.88	171215.8	168314.5	302376.4	244018.6	107785	325884.3	231738.9	138257.4

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT3G03780	gi 14532772	putative methionine synthase [Arabidopsis thaliana]	metabolism	0.020084185	3.333	0.01377351	2.107	4414.223	6169.629	10315.09	8631.775	11438.24	14028.72	20570.11	16181.34	49719.72	12607.73	19706.29	16404.15
AT5G55480	gi 15240520	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis	metabolism	0.000175602	4.189	0.0025886	4.028	5918647	8991709	6379965	4762929	17507867	16225465	45293030	25918229	33553057	25921991	30003867	19668269
AT5G10080	gi 15238055	aspartyl protease family protein [Arabidopsis thaliana]	protein destination and storage	0.003108248	0.265	0.024279533	0.494	21905.06	13599.69	16340.3	24967.19	7832.618	7546.931	6318.813	16265.23	2521.597	3697.714	6242.879	7923.757
AT3G02740	gi 15232960	aspartyl protease family protein [Arabidopsis thaliana]	protein destination and storage	0.002684036	2.493	0.005085828	2.793	188182.2	124362.8	110933.2	126281.2	353694	320554.2	240973.4	620342.6	399966.7	439479.8	296660	234356.5
AT3G52500	gi 16209647	AT3g52500/F22O6_120 [Arabidopsis thaliana]	protein destination and storage	0.000553518	2.720	0.022378681	4.289	76607.14	61054.47	56465.14	57692.1	97809.22	299211.7	554101.6	128855.4	115057.8	186921.6	208967.8	173966.1
AT1G63500	gi 24025431	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	protein destination and storage	0.001514896	2.291	0.0299311	2.270	122490.5	103834.1	72583.49	68762.77	121670.3	155402.6	199804	357684.3	247747.3	205503.1	178673.5	210452.5
AT1G69840	gi 15222481	band 7 family protein [Arabidopsis thaliana]	protein destination and storage	0.000102968	2.181	0.003421029	2.411	648346	720659.4	633666.8	575937.2	1005790	1225416	1995014	1990116	1678062	1372303	1394129	1178492
AT1G65240	gi 4646203	Belongs to PF00026 Eukaryotic aspartyl protease family [Arabidopsis thaliana]	protein destination and storage	0.001064861	2.581	0.030734926	3.857	81823.32	77214.27	76377.07	61397.73	153918	115507.1	672187.9	203294.1	131380.3	235810.8	235035.2	163937.2
AT5G46570	gi 15237465	BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	0.004448284	2.673	0.005109065	3.484	3406.344	2594.114	1142.244	1963.336	5501.289	6832.271	6688.757	12699.33	6658.634	6542.653	5509.189	5632.129
AT4G00710	gi 22328189	BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana]	protein destination and storage	0.002295754	2.509	0.040593265	1.644	111062.5	77951.72	59987.43	49063.21	112210.7	95322	153362.6	129016.6	221733.9	172921.8	161378.4	191932.5
AT1G05690	gi 42561724	BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	protein destination and storage	0.024075403	2.708	0.006298383	2.803	5448.502	4507.788	4095.852	3664.486	6844.525	13082.62	19567.48	10167.47	20053.8	14116.86	8264.282	5535.82
AT5G47850	gi 15238823	CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase [Arabidopsis	protein destination and storage	0.001308778	4.118	0.010171657	5.351	3439.937	2820.025	1550.942	2111.575	4814.473	9040.967	28659.69	10581.17	6440.554	11802.78	14354.74	8267.02
AT3G26940	gi 15231654	CDG1 (CONSTITUTIVE DIFFERENTIAL GROWTH 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	0.0070955	0.264	0.010956152	0.315	80442.5	84582.64	103550.3	126162.9	25154.68	18499.51	67678.13	12816.94	57293.1	10179.42	21629.55	15236.72
AT1G12470	gi 8778633	F5O11.22 [Arabidopsis thaliana]	protein destination and storage	0.000418197	0.414	0.037842762	0.340	173559.5	157510.9	149435.5	131221.1	117559.5	62225.35	10013.82	18205.68	75506.8	50058.02	52185.07	75766.74
AT3G58880	gi 15231588	F-box family protein [Arabidopsis thaliana]	protein destination and storage	0.037768414	0.417	0.014730777	0.352	20995.89	21059.46	52021.57	41682.36	11643.68	15953.45	13421.93	6787.873	26303	9454.819	9900.911	10934.7
AT2G17760	gi 25347778	hypothetical protein At2g17760 [imported] - Arabidopsis thaliana	protein destination and storage	0.015371903	3.678	0.005259717	7.241	32780.15	42472.63	14847.18	20731.89	218987.2	70329.07	123718.7	389499.8	206467.2	66879.42	75276.27	59054.3
AT1G79560	gi 4835753	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this gene [Arabidopsis	protein destination and storage	0.027046873	2.652	0.005517288	7.573	747.0303	1752.538	1131.791	1502.314	8671.931	9923.178	2613.379	17666.85	1505.122	4660.73	4445.587	3002.888
AT5G51770	gi 15242183	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.007848928	0.286	0.046113612	0.438	7283.182	5949.364	4542.459	16499.7	3676.976	4075.064	3497.387	3747.571	2398.099	3059.288	2072.169	2270.341
AT2G23200	gi 15227790	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.005354675	0.461	0.002540675	0.217	34485.41	24444.74	22498.88	29909.06	3932.414	13326.9	3497.792	3352.55	10743.82	8602.515	13779.28	18178.13
AT2G39360	gi 15225078	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.011310561	3.946	0.00154263	6.983	10468.94	11580.12	8341.844	9019.788	31634.08	40391.37	70413.48	132785.5	21473.36	45685.79	71193.73	17162.58
AT4G23200	gi 15236421	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.000821816	3.339	0.000382084	4.087	197546.5	153476.5	119622.5	103213	489188.5	427702.9	788658.9	639545.9	661137.5	479980.7	425833.5	349425.2
AT4G02630	gi 15235432	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.024200796	3.186	0.000604692	2.833	76276.27	71286.54	72748.63	96353.4	159275.3	193581.9	304057.1	240268.6	513045.5	154345.8	227602.7	113953.3

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT5G24010	gi 15237872	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.002532512	2.395	0.02340643	2.192	115070.4	125210.1	80503.57	70595.94	110800.9	277360.3	212470.9	257148.4	254751.2	230843.7	283193.7	168394.9
AT1G70520	gi 15223169	protein kinase family protein [Arabidopsis thaliana]	protein destination and storage	0.001821279	2.978	0.012883152	2.105	198411.5	218992.5	138290.2	148390.4	218927.8	348352.6	456814.7	457825.8	692781	515331.6	573877.7	314697.4
AT5G56460	gi 15241220	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	0.000434948	0.158	0.043586992	0.271	37875.96	29601.41	28159.44	32340.57	3401.164	3781.499	27156.12	369.4654	4711.928	5317.719	7975.491	2183.41
AT5G03320	gi 15242720	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	0.004969538	0.347	0.043502604	0.466	58406.23	58395.79	62696.29	51117.4	43276.58	27367.39	28538.17	8227.585	9747.322	15014.07	21596.08	33774.69
AT3G46290	gi 15231393	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	0.002061653	3.181	0.014621412	2.284	136407.2	172172.2	124416.8	98959.75	202849.9	296315	222519.4	493506	689892	346801.4	347560.7	308140.5
AT4G28400	gi 18417190	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis	protein destination and storage	0.002945555	0.439	0.008684123	0.122	66089.14	63387.27	70795.98	44576.62	3118.146	23549.17	608.1357	2703.816	29804.55	17502.86	32995.26	27079.52
AT2G39110	gi 3928095	putative protein kinase [Arabidopsis thaliana]	protein destination and storage	0.009612178	0.409	0.024999003	0.339	139262.9	121914.5	98586.54	121763.3	63892.58	46636.85	42999.29	9537.538	24378.35	61831.68	37415.18	73527.27
AT2G16600	gi 15227259	ROC3; peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	protein destination and storage	0.021419103	2.330	0.024931819	2.811	206001.7	222509	99828.79	91548.59	234586.1	287002.8	556788.4	663998.2	540834	361354.8	282720.1	259625.3
AT4G23270	gi 3021279	serine/threonine kinase [Arabidopsis thaliana]	protein destination and storage	0.00470252	4.670	0.001502121	2.378	106912.2	110243	96285.9	78441.77	157173.4	274560.9	278873.9	221198.3	752329.6	470300.9	440303.6	167321.9
AT5G58160	gi 8777317	unnamed protein product [Arabidopsis thaliana]	protein destination and storage	0.000902492	0.226	0.043942915	0.304	166964.9	142318.2	224368.6	237434.5	85336.48	83698.6	58021.18	7637.823	24504.38	37334.94	72167.03	40608.83
AT5G56380	gi 10177837	unnamed protein product [Arabidopsis thaliana]	protein destination and storage	0.011594205	0.307	0.049748012	0.402	94973.21	89358.9	69023.55	70911.72	59026.65	24655.96	39781.08	6878.597	8889.762	14054.87	26810.85	49808.38
AT3G15030	gi 8777486	unnamed protein product [Arabidopsis thaliana]	protein destination and storage	0.019841222	0.456	0.023566831	0.180	24751.63	18571.72	19139.23	23366.45	2640.64	12278.98	216.6614	318.394	13248.37	5180.609	5852.296	14832.92
AT5G64080	gi 10176956	unnamed protein product [Arabidopsis thaliana]	protein destination and storage	0.010210487	6.263	0.008626686	1.914	49624.63	62168.16	98615.23	70644.14	104247.7	135425.5	129970	168354	815740	605301	178055.4	161112
AT2G47060	gi 79324935	serine/threonine protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	0.009639001	0.348	0.044282827	0.380	5495.92	4278.38	6606.481	12170.55	5597.543	2810.144	1357.601	1091.229	2769.194	1641.18	3325.681	2210.62
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	protein synthesis	0.039050969	0.439	0.007864365	0.423	49673.89	41040.76	79609.8	70252.2	32133.03	30546.42	22858.69	16109.16	10587.37	48371.55	18449.83	28312.5
AT2G04390	gi 15228141	40S ribosomal protein S17 (RPS17A) [Arabidopsis thaliana]	protein synthesis	0.0259505	5.638	0.018486765	2.153	1159707	980241.1	1302234	1115215	1311945	3013339	3384506	2100582	12323671	6996404	5140416	1233900
AT3G02080	gi 15232844	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	protein synthesis	0.005038934	2.616	0.017913075	3.146	29169.8	28015.72	33584.86	38091.52	61445.47	46002.17	124648	173360.8	110947.5	88057.39	93564.74	44572.67
AT5G61170	gi 15240154	40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana]	protein synthesis	0.034577426	9.874	0.004737205	7.153	2510.208	3944.43	4315.553	2971.436	7438.193	25324.78	47902.96	17624.02	5103.973	56691.67	65102.34	8781.272
AT5G35530	gi 15238533	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	protein synthesis	0.00025622	2.269	0.020410896	2.109	34923.06	31480.69	31319.17	33504.33	43992.34	53617.33	117972.6	61203.99	67224.57	76209.79	95218.36	59107.63
AT4G29390	gi 15233565	40S ribosomal protein S30 (RPS30B) [Arabidopsis thaliana]	protein synthesis	0.029285406	45.980	0.045542914	44.252	247.7371	0	231.4723	261.8929	18736.86	8817.337	430.1072	4811.272	2290.743	2183.997	18768.33	10832.69
AT3G04840	gi 15229364	40S ribosomal protein S3A (RPS3aA) [Arabidopsis thaliana]	protein synthesis	0.0068682	2.732	0.031876637	2.331	147981.3	165393.1	68431.33	72235.84	360589.8	185109.3	164701.8	348133.1	368634.1	233800.4	257360.8	380450.6
AT5G46430	gi 15237436	60S ribosomal protein L32 (RPL32B) [Arabidopsis thaliana]	protein synthesis	0.001226818	3.419	0.007505213	2.922	5152.077	4991.683	5326.058	7278.724	9201.712	22356.73	23579.91	11327.19	15252.26	30878.09	13034.9	18606.72
AT2G47610	gi 15226635	60S ribosomal protein L7A (RPL7aA) [Arabidopsis thaliana]	protein synthesis	0.023483795	0.244	0.005789152	0.115	28340.35	24374.01	7556.062	8581.904	1714.57	2129.543	543.535	3521.389	4344.589	7109.549	1744.912	3614.707
AT1G33120	gi 18398753	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	protein synthesis	0.002361834	3.460	0.000538524	2.916	826002.4	460674.1	586992.9	479312.1	2097974	1425576	1855855	1482509	3136080	1378005	2233004	1393156
AT2G37270	gi 15228111	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	protein synthesis	0.000148962	4.883	0.004301399	3.111	229655.8	269015.1	169395	164409.5	489585.4	369418.2	907731.3	823208.8	1374920	1068986	928063.6	692776.3
AT5G60390	gi 295789	elongation factor 1-alpha [Arabidopsis thaliana]	protein synthesis	0.012339614	3.607	0.011334713	3.620	28099.62	54731.18	25008.23	10081.8	74169.78	75804.84	142321.2	134566.8	68979.19	78542.95	125443.1	152428.2
AT1G56070	gi 6056373	elongation factor EF-2 [Arabidopsis thaliana]	protein synthesis	0.007534703	2.134	0.04053359	2.778	264880.2	375729.2	214224.9	153903.6	305624	440984.5	1150867	904403.2	667146.3	473070.8	488551.2	524220.5
AT2G33370	gi 2341028	Strong similarity to 60S ribosomal protein L17 (gb X01694). EST gb AA042332 comes from this gene [Arabidopsis thaliana]	protein synthesis	0.004792107	4.373	0.016883569	2.536	61221.1	59827.39	43634.86	52002.46	117343.4	104268.3	248758.5	79183.73	492472.5	154584.2	141760	158683.2
AT1G74020	gi 1754983	strictosidine synthase [Arabidopsis thaliana]	secondary metabolism	0.007663948	5.341	0.015423187	28.865	724.5191	887.8359	865.9172	244.101	7996.033	7866.914	1644.759	61074.35	7361.686	2205.147	2283.256	2691.056

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT4G34460	gi 42573173	AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding	signal transduction	0.022089939	3.799	0.000932513	7.059	5417.786	5323.534	13741.5	9556.312	28716.5	67438.74	62862.35	81273.03	47056.64	11509.91	22692.05	48060.39
AT3g07390	gi 18426884	AT3g07390/F21O3_10 [Arabidopsis thaliana]	signal transduction	0.005684849	3.765	0.024958623	3.007	7593197	9251779	3590460	2708386	20035781	7934571	16682821	24931393	32673499	21328137	15865687	17274328
AT5G01600	gi 15241018	ATFER1; ferric iron binding / iron ion binding [Arabidopsis thaliana]	signal transduction	0.02776079	6.671	0.012824719	14.323	57002.14	57981.92	299105.2	235392.7	566354.8	2115198	5962658	658111.1	959345	758178.5	2375270	239979.4
AT1G11300	gi 14533539	ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	signal transduction	0.015768514	0.386	0.037554862	0.392	30167.4	36601.25	68693.34	81912.79	19377.39	37198.17	18576.81	9992.946	24702.16	16677.7	25287.96	17217.54
AT3G08510	gi 15231929	ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	signal transduction	0.00097076	2.498	0.011518657	3.695	224218	165307.4	184849.3	185688.5	306102.8	797321	429569.4	1275306	623693.2	426290	517449.4	331476.1
AT3G49750	gi 15229606	AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana]	signal transduction	0.004552876	3.227	0.044614414	1.919	25400.55	17743.36	16798.76	16965.88	20264.23	56392.38	39911.03	31026.03	93394.01	53229.01	70180.44	31383.16
AT4G18760	gi 15234009	AtRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	signal transduction	0.006270216	3.572	0.003098327	2.693	1250734	1397556	1204128	1084824	2187059	2506980	5129159	3473689	8014769	3358539	4149199	2112044
AT4G39400	gi 15235059	BR11 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	signal transduction	0.012098889	2.132	0.002687031	4.585	36504.58	70298.66	53589.59	32227.84	277771.3	105180.9	188004.3	312150.5	75963.13	89964.13	106071.9	138735.4
AT5G24430	gi 22136058	calcium dependent protein kinase-like protein [Arabidopsis thaliana]	signal transduction	0.000953038	2.115	0.029883148	2.594	26644.93	33330.62	21380.54	22089.1	31554.25	47794.37	70143.44	118845.3	61716.43	53407.35	59308.88	44389.93
AT1G05150	gi 15220436	calcium-binding EF hand family protein [Arabidopsis thaliana]	signal transduction	0.001306445	2.922	0.00196457	3.088	53032.31	56705.44	37995.35	34822.48	88780.19	121586	201784.7	151535.7	110736.9	160930.8	168458.8	93226.09
AT2G32450	gi 15225686	calcium-binding EF hand family protein [Arabidopsis thaliana]	signal transduction	0.037789174	2.275	0.03055347	2.458	32151.78	25928.26	11854.17	12279.95	33213.36	42588.02	85655.12	40593.27	25673.54	65207.45	53292.35	42889.27
AT3G57530	gi 6706424	calcium-dependent protein kinase [Arabidopsis thaliana]	signal transduction	0.0040256	0.402	0.039767823	0.514	354051.7	278831.7	234605.2	208009.8	160238.8	105164	220150.5	66776.16	106955.4	65160.32	111671.5	148509.1
AT1G52540	gi 5903051	Contains PF00069 Eukaryotic protein kinase domain. ESTs gb W43822, gb T20475 and gb AA586152 come from this gene	signal transduction	0.012194021	2.708	0.003005094	4.004	64724.14	69466.89	85152.22	81066.05	140550.7	236058	468940.7	357300.4	109577.4	221664.3	339323.8	143004.9
AT4G21940	gi 15234656	CPK15; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	0.012048791	2.315	0.032594747	2.229	32704.18	31400.18	17921.36	16309.26	27962.04	66318.47	50730.06	74222.57	80816.66	60272.03	47026.4	39530.52
AT3G10620	gi 8567796	diadenosine 5',5''-P1,P4-tetraphosphate hydrolase, putative [Arabidopsis thaliana]	signal transduction	0.001600696	0.364	0.031450649	0.481	99645.71	71145.72	111766.9	106094.7	59784.13	44565.76	63055.57	19360.33	21707.55	34902.95	44717.3	40293.52
AT4G28490	gi 15235312	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	0.000917724	0.167	0.015123231	0.164	16969.23	20225.46	41567.08	41577.47	947.9721	5422.585	12325.74	998.3473	7098.896	5667.098	3954.661	3434.55
AT3G51740	gi 15231029	IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	signal transduction	0.000354603	3.077	0.01752178	2.415	585830.6	774847.1	699488.4	562511.1	933216.2	1559886	2722990	1116645	2590895	1818389	2254741	1406803
AT2G19230	gi 24025447	kinase [Arabidopsis thaliana]	signal transduction	0.003782084	0.176	0.01712563	0.377	61505.19	51017.75	39759.03	43092.59	33525.64	13951.35	6993.107	19131.81	7346.262	2829.027	4043.37	20174.52
AT2G14510	gi 15225949	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.00574959	0.130	0.027301992	0.193	36696.44	20756.4	67882.26	74818.81	16310.58	18002.58	2732.047	1501.884	1648.642	6793.748	10710.35	6865.693
AT1G51800	gi 15218033	leucine-rich repeat protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.030198212	2.637	0.031591673	3.800	414824.2	964018.8	920453.1	858166.4	5458865	875699.7	2719066	2945018	1415717	1861017	3839278	1210343
AT2G31880	gi 15225153	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.006313535	4.386	0.004931157	5.007	15095.46	14157.01	5105.479	8392.473	51733.85	26560.98	95051.41	40724.58	87178.92	32276.31	39308.07	28736.56



ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT2G26730	gi 15225780	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.000475894	2.933	0.003260345	4.440	64251.98	74805.22	62910.84	50365.51	153002.9	193423.4	548095.3	225752.4	156447.4	155419.5	266421.8	161756
AT3G08680	gi 15231955	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.009573085	2.380	0.003676223	3.901	71933.28	73787.13	43990.74	38258.54	130806.6	150417.4	358002.4	250130.3	86692.74	134622.8	190029	131291.8
AT1G06840	gi 15222211	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.002556713	3.517	0.004545218	2.907	120760.9	123237.3	91173.57	83281.81	171810	239577.1	394767	410317.9	617282.2	219661.7	350940	283635.2
AT3G02880	gi 15233013	leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana]	signal transduction	0.004286553	3.266	0.001413547	2.261	3898685	4101136	3250624	3321486	5436870	8993915	9277394	9241469	19371898	10482056	11742145	5993101
AT5G16590	gi 15237379	LRR1; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	0.00156476	2.784	0.004886919	2.272	429098.8	409463	279244.6	274055.6	520576.2	734550.1	931525.6	975126.4	1125719	973813.8	1150680	624368.4
AT1G21880	gi 18395044	LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) [Arabidopsis thaliana]	signal transduction	0.002106947	3.730	0.030455699	2.304	174110.6	199089.9	256990.6	187826.7	252202.2	328281.9	794754.9	509763	953892.6	1131295	525671.5	440607.6
AT2G17120	gi 18398317	LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) [Arabidopsis thaliana]	signal transduction	0.003979389	2.784	0.003377774	2.854	742678.9	544549	322206.1	409223.7	1453072	1095819	1175719	2035644	1971824	1237903	1411232	998094.4
AT5G06320	gi 15239999	NHL3 [Arabidopsis thaliana]	signal transduction	0.010326971	3.514	0.000250747	3.097	1279918	987566.4	1366484	1417664	3987186	2902012	3585615	5170107	7683222	4276119	4000649	1790978
AT1G73080	gi 15219370	PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	0.023728896	0.606	0.017069677	0.450	145749.8	256092.8	212128.3	208792.8	117445.3	104103.1	105218.2	43506.02	142999.9	141482.5	86588.78	127171.8
AT1G77630	gi 30699276	peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	signal transduction	0.000170394	5.973	0.007094073	4.860	275102.6	459171.4	464234.5	301300.5	1078348	778118.1	3536482	1896179	2678636	2732644	2205694	1341689
AT5G58670	gi 18424132	PLC1 (PHOSPHOLIPASE C 1); phospholipase C [Arabidopsis thaliana]	signal transduction	0.000975205	3.216	0.000129865	14.061	68897.62	65786.05	52020.56	48604.06	386182	565725	1038449	1318265	275920.4	172728.5	187071.1	120955.8
AT3G24550	gi 13877617	protein kinase-like protein [Arabidopsis thaliana]	signal transduction	0.000720712	2.641	0.002844619	1.714	1414149	1817612	2135422	1813788	2469814	3142168	3338787	3358154	6523927	3898008	4745258	3800195
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	signal transduction	0.000542469	3.969	0.00020767	4.179	178601	220628.3	179826.8	134860.6	530037.2	615762.1	1016932	820576.8	841944.8	709945.6	872566.1	409026.4
AT4G34440	gi 3641836	putative serine/threonine protein kinase [Arabidopsis thaliana]	signal transduction	0.026549376	0.132	0.017661417	0.128	152097.5	122126.7	21477.67	26528.6	8761.548	10331.88	16213.15	5998.847	3409.699	11728.5	4235.541	23107.99
AT5G24390	gi 15238518	RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	signal transduction	0.0000347	6.578	0.001562751	7.400	5564.568	7284.399	7126.307	5767.059	26248.88	20864.49	85466.49	57906.74	41296.15	57684.91	43143.79	27219.32
AT5G59840	gi 15238542	Ras-related GTP-binding family protein [Arabidopsis thaliana]	signal transduction	0.002359798	0.389	0.022908885	0.381	316370.4	293963.9	344547	414799.2	181019.8	156735.7	145371	39141.92	94257.75	91772.82	179811.3	167227.4
AT1G15530	gi 15218220	receptor lectin kinase, putative [Arabidopsis thaliana]	signal transduction	0.03168842	2.604	0.009594533	3.386	116932	129518.1	81770.23	87514.43	174746.5	243308.3	638705.2	350801.1	108540.9	321407.6	412924.3	239865.5
AT4G23190	gi 4127461	receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	signal transduction	0.001765793	3.243	0.000479318	4.452	34985.59	43316.24	21368.23	20739.52	101754.5	120407.9	128907.7	184973.5	108603.6	115155.8	102140.3	64640.6
AT3G56100	gi 26996940	RecName: Full=Probable leucine-rich repeat receptor-like protein kinase IMK3; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 3; AltName: Full=Protein MERISTEMATIC RECEPTOR-LIKE KINASE; Flags: Precursor	signal transduction	0.009103272	4.790	0.011140848	5.763	362.2148	1403.031	1358.948	1401.405	2342.418	5680.523	12202.55	5855.606	3295.705	7205.125	8141.948	3035.149
AT3G17840	gi 18401662	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	0.049152937	2.617	0.017676093	1.986	391795.8	354011.8	226638.4	232663.9	701251.9	417818.9	801174.3	473204.9	1606675	451102.2	676752	419361.2
AT4G23180	gi 3021270	serine/threonine kinase-like protein [Arabidopsis thaliana]	signal transduction	0.010341946	0.294	0.028067076	0.287	102830.1	94770.56	107186.2	93549.92	59471.79	39128.73	4775.047	10899.49	8178.729	31008.33	36335.63	41460.39
AT4G12420	gi 15234551	SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana]	signal transduction	0.005623149	3.338	0.001151762	3.146	9709144	10185538	7744547	6905005	18914504	20852434	39612040	29311732	44874310	28038125	29075631	13310863
AT4G32300	gi 2864613	S-receptor kinase-like protein [Arabidopsis thaliana]	signal transduction	0.001008749	2.636	0.014203607	1.794	79036.51	96460.17	55855.76	63187.57	93116.36	132551.4	135674.8	167204	255634.8	196251.9	170609.7	153887.8

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT3G45600	gi 15231187	TET3 (TETRASPANIN3) [Arabidopsis thaliana]	signal transduction	0.004464106	2.480	0.000930836	4.100	96577.34	86834.94	41790.65	46091.19	290059.6	198974.2	286443.8	336840.1	187439	171308.2	166395.7	147775.7
AT1G43890	gi 8778652	F9C16.3 [Arabidopsis thaliana]	signal transduction	0.0000628	2.805	0.04507274	2.186	23703.04	26061.53	30602.59	23651.6	26459.79	63604.07	92331.58	45025.98	74542.17	73976.38	86007.11	57243.02
AT2G34160	gi 52696237	Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At2g34160	transcription	0.006620001	0.430	0.02190972	0.372	130661.9	92184.35	125684.4	97923.7	61062.58	45837.02	46690.49	12499.66	37952.64	28091.87	57629.49	68222.68
AT1G27750	gi 6693023	T22C5.20 [Arabidopsis thaliana]	transcription	0.011203569	0.169	0.009346459	0.130	20874.88	22655.82	47150	33693.92	3925.215	3295.187	8477.732	491.3094	1014.785	5134.402	1609.406	13289.16
AT1G02080	gi 42561615	transcriptional regulator-related [Arabidopsis thaliana]	transcription	0.02728035	1.943	0.03295325	4.339	109745	73663.29	66081.3	60046.89	125842.9	302985.5	140230.9	773916.6	179697.3	208455	115019.7	98262.77
AT3G47780	gi 4741195	ABC transporter-like protein [Arabidopsis thaliana]	transporters	0.000221793	0.406	0.046062713	0.514	306575.5	328107.5	255065.7	228194.3	217315.3	97773.71	197565.9	61421.04	95584.04	102469.3	121657.7	134467.3
AT3G47950	gi 30692952	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	transporters	0.02426179	2.268	0.012353224	10.306	19272.21	24746.08	10931.66	8618.009	34103.62	110972.4	90542.1	419521.7	22622.75	36640.89	48442.73	36448.38
AT1G80660	gi 6730723	aha9, 5' partial; 1-2403 [Arabidopsis thaliana]	transporters	0.002338819	0.147	0.003463061	0.147	41665.09	25939.72	17790.15	57183.76	6426.93	8975.018	1929.967	3557.703	5911.021	2112.468	7628.394	5325.314
AT5G04930	gi 18414733	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	transporters	0.00058729	2.728	0.007527788	2.694	9686.233	18138.01	11706.32	11754.83	20150.43	27565.07	39614.84	50810.08	41302.7	30267.31	38123.12	30220.01
AT4G13510	gi 15236300	AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana]	transporters	0.017818748	2.419	0.017242958	2.629	1554280	1588017	859380.5	564330	2348237	1963656	4430984	3259471	3458690	1850084	2404129	3332784
AT3G47730	gi 22331647	ATATH1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana]	transporters	0.04970008	2.753	0.006594315	3.006	35213.09	52699.54	20375.55	31701.86	80355.64	95798.15	170224	74421.78	32809.89	125605.7	137506.9	89428.92
AT2G38940	gi 15224985	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen	transporters	0.02611075	2.812	0.003783117	3.404	1125111	966554.1	1824168	1744054	2491431	5776419	6320077	4677790	6287769	3802356	4215553	1608380
AT5G57110	gi 8843813	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	transporters	0.001630893	2.672	0.005580193	2.586	1177413	1631098	1055178	995031.7	1872377	2619236	4317602	3754611	4671831	2418705	3077416	2812570
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	transporters	0.000239054	20.651	0.000831408	9.428	113066.2	81498.55	33239.17	45018.55	972891.7	536752.9	316037.5	746522.5	2629250	1307517	942137.8	755195.9
AT1G69480	gi 12597793	hypothetical protein [Arabidopsis thaliana]	transporters	0.023179141	3.908	0.000313486	7.413	18419.45	18244.4	19205.87	16586.89	137301.6	103363.7	67602.34	228852.8	100295.1	120074.9	38679.91	24145.77
AT2G30480	gi 11074141	hypothetical protein [Arabidopsis thaliana]	transporters	0.00582765	3.567	0.011813515	3.978	1745491	3572262	4870899	4721024	23830966	6167759	17312456	12000007	16196068	8765745	18987488	9229635
AT3G16340	gi 18401096	PDR1; ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	0.0000701	3.037	0.000513034	4.236	121667.4	123135.2	156778.6	138225.9	647155.2	337446.6	465438.6	836370.5	448906.6	503331.6	352284.1	334613.8
AT2G26910	gi 15225814	PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	transporters	0.010670974	0.287	0.049236715	0.312	22960.39	9370.507	20726.07	22061.88	7305.856	7858.31	7338.02	943.9019	6592.351	2180.624	5067.036	7732.774
AT3G55320	gi 15233244	PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	transporters	0.006374261	3.326	0.004098064	2.350	145729.4	140870.2	115880.6	78377.64	245613.7	367322.2	206478.2	310690.6	351247.1	669794.5	371167.5	207081.3
AT4G32390	gi 15236781	phosphate translocator-related [Arabidopsis thaliana]	transporters	0.000247264	0.313	0.020365546	0.361	154376.5	130655.5	189841.2	229289.2	87798.41	67721.41	78261	20076.1	54758.72	42940.28	62211.65	60651.75

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT5G43350	gi 15239848	PHT1;1 (PHOSPHATE TRANSPORTER 1;1); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen	transporters	0.027768981	2.809	0.009933905	3.027	186809.1	284095.4	464996	397922.2	607762	964760.3	1670786	794208	1335851	658610.2	1316322	436017.8
AT4G35100	gi 1688296	plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]	transporters	0.011454609	2.347	0.016988635	6.183	25925.42	36507.9	50172.12	32422.57	88893.43	125934.1	583972.9	97920.44	81247.17	51237.65	127267.7	80589.15
AT2G27810	gi 3860251	putative membrane transporter [Arabidopsis thaliana]	transporters	0.013791752	3.141	0.007668455	2.111	21212.03	15268.19	15065.32	13488.97	31153.27	22796.06	34689.75	48666.14	96510.63	34223.29	47633.33	25923.71
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis	transporters	0.012203933	3.965	0.013902346	10.432	6989.681	8830.893	17076.52	15353.21	93498.41	82327.6	21368.85	306151.9	57232.11	69060.72	47599.7	17430.58
AT1G30410	gi 75333513	RecName: Full=ABC transporter C family member 12; Short=ABC transporter ABCC.12; Short=AtABCC12; AltName: Full=ATP-energized glutathione S-conjugate pump 13; AltName: Full=Glutathione S-conjugate-transporting ATPase 13; AltName: Full=Multidrug resis	transporters	0.000399123	0.220	0.041587141	0.259	128272.6	130355.5	186018.1	183830.5	53931.36	46495.72	58891.53	3741.155	23653.68	24118.33	53376.9	37011.98
AT3G51670	gi 15230555	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis	transporters	0.008149469	0.288	0.009723372	0.298	52292.16	39351.38	30746.76	36590.84	7152.228	13513.53	22221.84	4534.618	4500.995	7177.839	11536.03	22578.18
AT1G71880	gi 15217601	SUC1 (Sucrose-proton symporter 1); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana]	transporters	0.046006021	3.252	0.000137961	0.075	26912.55	20423.21	32055.06	27538.24	944.1972	4009.881	1448.252	1579.507	177001.6	81424.03	61303.86	28035.54
AT1G13210	gi 15222212	ACA.1 (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding [Arabidopsis thaliana]	unknown	0.001152458	4.056	0.006237088	4.244	5957.747	7845.609	3112.98	3133.405	26926.92	10651.09	32510.04	15009.3	16670.98	23238.08	17159.07	24245.67
AT1G31810	gi 18647910	actin binding [Arabidopsis	unknown	0.000888691	0.383	0.017252112	0.359	37561.97	32652	48174.46	51105.23	21344.97	23165.18	5388.126	11008.51	22530.25	14059.04	13485.37	14840.52
AT1G52320	gi 15450411	Atlg52320/F19K6_7 [Arabidopsis thaliana]	unknown	0.039584353	10.724	0.020306552	14.224	136.688	537.5428	126.9332	102.3614	1961.522	3929.599	301.7461	6659.008	3951.551	174.6975	3316.339	2246.371
AT1G51640	gi 15217995	ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein binding [Arabidopsis thaliana]	unknown	0.004024468	0.421	0.007109977	0.398	103444.4	87795.04	102441.8	93390.07	61205.33	30597.76	43210.84	19084.05	55994.55	25638.73	28944.01	52332.18
AT4G23630	gi 15236556	BTI1 (VIRB2-INTERACTING PROTEIN 1) [Arabidopsis	unknown	0.023911254	0.324	0.045353956	0.245	22100.44	20125.76	23315.57	17679.55	2508.839	6459.841	281.1044	11131.63	7469.268	6999.895	1476.173	10988.74
AT4G20260	gi 15235363	DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana]	unknown	0.00184897	2.987	0.004996966	9.997	350161.1	233149.4	275255	339152.4	755074.4	1486961	4308560	5423014	1229608	805268.2	1003936	538241.2
AT4G00310	gi 18411286	EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana]	unknown	0.001220057	0.287	0.009712471	0.438	25088.33	13190.83	19092.61	33294.42	8508.611	11649.66	9843.935	9708.922	7471.604	6627.251	5379.742	6556.989
AT1G61900	gi 3367523	ESTs gb AA728658 and gb N95943 come from this gene [Arabidopsis thaliana]	unknown	0.017338883	4.744	0.002397629	1.972	89234.8	98335.82	67748.26	59741	147352.8	184049.5	160072.1	129703.6	792638.9	314164.4	273914.4	113912.4
AT1G03230	gi 18379072	extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana]	unknown	0.033626959	2.700	0.001964168	5.163	40098.56	40557.68	11363.31	15653.54	117811	136833.3	121645.4	179647.2	42216.44	69694.88	60027.41	118752.9
AT3G15410	gi 2760084	leucine-rich repeat protein [Arabidopsis thaliana]	unknown	0.040302409	0.323	0.046789499	0.378	15556.56	18348.02	52712.53	48634.34	11344.72	12408.38	17440.4	9882.141	10554.4	6927.753	20514.55	5697.359
AT4G36945	gi 4006878	MAP3K-like protein kinase [Arabidopsis thaliana]	unknown	0.003502434	4.302	0.000492494	2.920	130538.1	136433.9	112113.2	103826.6	229685.9	350648.2	432100.5	397660	906976.6	478226	465557.5	226947.4

ATG	GI	Description	Functional categories	Anova (p)* CA	CA/Control	Anova (p)* ABA	ABA/Control	NA1	NA2	NA3	NA4	ABA1	ABA2	ABA3	ABA4	CA1	CA2	CA3	CA4
AT5G61800	gi15240355	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	unknown	0.001284071	0.470	0.01638821	0.511	85102.49	72909.66	67302.27	88825.67	55035.68	39724.49	44864.37	20840.99	35797.34	26298.42	46304.18	39234.62
AT4G06544	gi7529254	putative protein [Arabidopsis thaliana]	unknown	0.000772867	0.216	0.007450992	0.463	52256.86	50524.25	40320.88	34588.16	22920.45	18261.99	28631.1	12483.84	11318.62	8875.88	4647.184	13619.38
AT5G30520	gi7413621	putative protein [Arabidopsis thaliana]	unknown	0.019918537	0.226	0.03391013	0.235	15352.92	6548.102	4497.945	4462.137	3193.122	2068.138	322.8711	1670.753	2787.021	2424.048	492.3869	1264.814
AT4G26690	gi4455192	putative protein [Arabidopsis thaliana]	unknown	0.000215283	4.585	0.004056707	4.569	2627457	3978652	3440056	2532646	8016140	7913873	26940901	14602277	20899976	13271777	13701333	9795523
AT3G58100	gi6735322	putative protein [Arabidopsis thaliana]	unknown	0.024175158	2.665	0.00285531	3.221	73760.89	77534.5	51987.57	38026.01	143784	134403.5	275166	223852.8	74007.81	220677.5	220084.3	128222.5
AT3G44150	gi7635460	putative protein [Arabidopsis thaliana]	unknown	0.004829822	2.318	0.038877858	1.981	151755.9	134418.2	71406.96	86994.08	151092.4	152023.1	297255	280335	325229.6	227192.3	214101.7	263982.5
AT3G60920	gi8388608	putative protein [Arabidopsis thaliana]	unknown	0.027938344	3.714	0.006841021	1.716	175446.4	196415.1	231213.1	223746.2	428635.1	295241.4	417920	276943.9	1613948	733074.2	447235.2	276231.5
AT5G14770	gi22363576	RecName: Full=Pentatricopeptide repeat-containing protein At5g14770, mitochondrial; Flags: Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene [Arabidopsis thaliana]	unknown	0.001175976	0.233	0.010691913	0.326	4024.987	4288.127	4904.896	10514.94	2304.068	2843.177	1368.178	1217.607	1347.739	1506.559	1067.353	1610.826
AT1G11820	gi3157949	Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene [Arabidopsis thaliana]	unknown	0.018020285	2.060	0.04596545	1.958	44536.03	38054.25	16294.65	26227.71	52856.92	51175.08	45710.95	95173.24	67828.71	76710.26	63745.84	49495.31
AT4G28050	gi15234374	TET7 (TETRASPANIN7) [Arabidopsis thaliana]	unknown	0.009623506	2.171	0.040167783	1.827	69154.39	67510.49	42302	35207.38	70076.25	83142.44	146873.4	91310.79	151331.4	130632.1	90869.53	92155.57
AT2G31290	gi15224649	ubiquitin thiolesterase [Arabidopsis thaliana]	unknown	0.028463439	0.398	0.033878068	0.408	71957.69	62374.13	69191.46	160115.6	25644.06	50564.44	52778.12	19261.76	49871.25	18891.09	48721.21	27253.29
AT1G17147	gi11683010	unknown [Arabidopsis thaliana]	unknown	0.002773344	0.304	0.012235072	0.144	36991.45	40340.3	30130.76	49674.97	4807.257	6942.502	10268.18	549.9105	16011.89	10092.58	5925.39	15735.12
AT4G27520	gi21592865	unknown [Arabidopsis thaliana]	unknown	0.004422903	4.441	0.000435685	12.296	277848.9	373172.3	244604	199938.3	3330893	1665380	1872909	6602183	1889759	1364735	486346.6	1124586
AT3G45460	gi11683126	unknown [Arabidopsis thaliana]	unknown	0.000666683	11.194	0.009839627	6.686	2100.909	1691.205	3873.233	6332.434	7083.143	15573.26	43069.16	27870.48	68283.52	38220.58	24084.45	26107.81
AT2G26570	gi15225334	unknown protein [Arabidopsis thaliana]	unknown	0.005490746	0.231	0.03083868	0.367	17445.67	17836.88	45330.02	50425.97	9153.219	12731.78	17201.96	8988.522	8857.737	5877.982	10091	5478.205
AT4G08760	gi15236604	unknown protein [Arabidopsis thaliana]	unknown	0.004547694	0.335	0.002706858	0.196	38686.64	53531.88	37338.23	34278.83	6486.909	17059.56	5441.712	3042.072	14131.84	6644.033	12295.91	21806.07
AT1G78830	gi17644159	unknown protein [Arabidopsis thaliana]	unknown	0.035826198	2.532	0.008852001	10.180	17577.89	10568.22	25261.78	37241.92	51927.79	415642.6	114174.3	341065.2	87756.57	66749.16	44439.85	30538.65
AT2G23810	gi13272397	unknown protein [Arabidopsis thaliana]	unknown	0.009037008	2.697	0.000780545	3.687	215424.5	193092.9	201879.5	175345.8	746386	478503.2	533494	1138764	890744.1	558287.2	346974.4	323277.2
AT2G25800	gi3643603	unknown protein [Arabidopsis thaliana]	unknown	0.032733124	2.707	0.01484064	3.628	125648.5	183003.9	45394.94	35135.5	344514	203606.3	452657.4	411185.2	369447.8	170727.3	237645.6	275577.1
AT4G28100	gi18417127	unknown protein [Arabidopsis thaliana]	unknown	0.033234327	5.031	0.023371245	3.154	156807.4	129427.3	47812.62	55921.46	377444.6	174643.3	189389.2	488660.6	1246746	256584.7	187286.9	271398.8
AT2G28310	gi30683843	unknown protein [Arabidopsis thaliana]	unknown	0.002584389	2.971	0.006952309	3.126	215215.5	215154.8	132730.7	105562.3	316299.3	432489.6	870786.5	470899.5	679206.1	457108.6	497092.1	353163.4
AT2G27260	gi18401372	unknown protein [Arabidopsis thaliana]	unknown	0.005318754	5.769	0.027301926	2.812	2291.923	3227.747	578.5081	736.8678	4153.42	6574.073	4212.721	4276.756	10143.9	13573.22	10049.72	5664.868
AT2G21990	gi15227126	unknown protein [Arabidopsis thaliana]	unknown	0.022325791	10.186	0.001930965	2.344	18663.04	16923.49	14506.53	12709.52	25792.63	32289.42	47047.83	42074.71	277568.6	36404.6	291681.4	34025.01
AT5G19240	gi15239686	unknown protein [Arabidopsis thaliana]	unknown	0.018791015	2.368	0.006902706	2.203	15189.5	10657.68	5912.326	7370.023	24252.28	20513.4	21081.31	20356.75	12974.36	28182.14	27766.37	23718.89
AT3G08600	gi18398173	unknown protein [Arabidopsis thaliana]	unknown	0.013950289	2.742	0.030212133	2.172	102407.7	69029.74	38105.66	25725.18	108290.2	135966.7	110840.1	155851	211508.4	170506.8	135117.7	128069.3
AT3G54200	gi15232445	unknown protein [Arabidopsis thaliana]	unknown	0.007369491	2.855	0.000794259	1.827	310320.7	258697.6	223784.3	255490.3	434959.8	410915.7	549721	519757.7	1234177	667691.1	701985.8	389257

Supplementary Table 3-6 ABA-responsive plasma membrane proteins at the log phase

AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	ABA/Control	Normalized abundance							
									Control				ABA			
									Control 1	Control 2	Control 3	Control 4	ABA 1	ABA 2	ABA 3	ABA 4
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	Cell growth/division	1	1	43.29	0.047	0.474	19751.42992	15921.75455	14632.26757	16743.36613	8405.663083	8555.409545	10950.00469	3866.123613
AT5G62690	gi 13605867	AT5g62700/MRG21_12 [Arabidopsis thaliana]	Cell structure	2	2	92.1	0.032	2.984	99923.63539	83280.47788	81132.25221	160033.9161	427540.7597	247420.5871	379305.9524	211905.9297
AT1G75680	gi 15222328	endoglucanase 10 [Arabidopsis thaliana]	Cell structure	4	4	194.44	0.014	1.558	237262.7875	253581.6403	256642.3997	230229.9132	423302.4458	312557.2606	444997.8603	342837.3629
AT4G12420	gi 15234551	Monocopper oxidase-like protein SKU5 [Arabidopsis thaliana]	Cell structure	1	1	20.13	0.006	2.750	4850.81378	3403.6616	5231.417916	4787.332959	10985.50987	12254.15598	10799.65178	16219.98341
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	Cell structure	1	1	33.82	0.048	2.070	43944.8662	60717.81335	53364.13248	59249.24808	123382.5001	67043.20766	144187.4243	115245.0564
AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis thaliana]	Cell structure	1	1	82.52	0.014	0.515	39538.69922	37370.08703	37645.01276	43956.95027	15656.93568	26813.33181	16217.23525	22937.06579
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	8	8	334.59	0.000	0.222	1681666.071	1277627.222	1440141.604	1298024.813	328036.2672	356121.2876	321440.0913	258862.1575
AT4G01700	gi 15234281	class II chitinase-like protein [Arabidopsis thaliana]	Disease/defence	11	11	798.53	0.000	0.088	47986591.05	39169540.89	40601692.48	30262350.42	3546518.033	4565102.383	2555156.731	3236386.654
AT1G30360	gi 18397470	Early-responsive to dehydration stress protein (ERD4) [Arabidopsis thaliana]	Disease/defence	2	2	48.96	0.003	2.564	26452.55378	32898.11243	33155.64895	40438.68786	84196.14389	86821.95439	63560.60122	106270.6303
AT1G73370	gi 15219457	sucrose synthase 6 [Arabidopsis thaliana]	Metabolism	1	1	26.39	0.001	0.074	340428.9978	255873.3454	283597.6943	164308.2186	15560.43475	29071.56599	16324.99214	16600.85312
AT1G03230	gi 18379072	aspartyl protease-like protein [Arabidopsis thaliana]	Protein destination and storage	6	6	309.79	0.008	0.363	104081.0938	148588.2972	123678.2118	60038.41848	56011.00137	37588.05506	46781.96011	17961.52815
AT2G03530	gi 4335747	putative integral membrane protein [Arabidopsis thaliana]	Protein destination and storage	1	1	47.36	0.032	0.160	48400.54851	29616.71775	32927.76163	20580.08569	7471.355957	2424.07946	10780.93881	345.9532115
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	2	2	76.1	0.034	2.596	25339.89635	26122.77947	28045.70576	31798.06904	75715.79193	52708.36441	116551.1431	43948.48999
AT2G36160	gi 15227588	40S ribosomal protein S14-1 [Arabidopsis thaliana]	Protein synthesis	1	1	40.92	0.000	0.080	9891.822026	16291.04048	13223.79502	8740.658537	595.8772965	1278.236446	1350.817428	631.6817243
At3g60240	gi 7576200	protein synthesis initiation factor-like [Arabidopsis thaliana]	protein synthesis	2	2	36.07	0.009	0.271	398463.075	258875.9426	284689.6027	263364.4102	78778.16172	125498.2875	74181.90675	48550.34667
AT3G57030	gi 6911873	putative protein [Arabidopsis thaliana]	Secondary metabolism	2	2	63.67	0.025	0.181	16358.67313	16531.96434	10550.43521	9633.500185	2132.230631	1239.404266	5594.265124	640.2210453
At1g35160	gi 14532442	At1g35160/T32G9_30 [Arabidopsis thaliana]	signal transduction	1	1	30.36	0.042	2.178	5083.322095	1763.294333	4221.120805	7160.655065	6796.303714	5997.63865	14592.11367	12318.51947
AT5G19450	gi 15239742	calcium-dependent protein kinase 19 [Arabidopsis thaliana]	Signal transduction	2	2	26.82	0.025	0.298	160326.4326	89333.11572	98398.57956	109617.6832	35814.78247	49765.93047	35749.92077	14894.67349
AT4G04700	gi 5706728	contains similarity to eukaryotic protein kinase domain (Pfam: PF00069, score=272.9, E=4.1e-78, N=1) [Arabidopsis thaliana]	Signal transduction	1	1	50.44	0.003	0.183	15480.31682	24060.58014	19092.23805	15826.90253	3611.568826	4282.423519	1965.339688	3790.52533
AT3G08510	gi 15231929	phosphoinositide phospholipase C 2 [Arabidopsis thaliana]	Signal transduction	3	3	127.87	0.006	0.307	340064.3987	283528.9074	295266.4291	222582.9588	118855.5659	60696.73448	126050.686	45302.06906
AT5G16590	gi 15237379	putative inactive receptor kinase [Arabidopsis thaliana]	Signal transduction	2	2	83.36	0.002	1.868	56767.27875	60912.03233	64605.02459	74068.8913	119888.5963	123758.7469	110700.396	124588.5499
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	115.15	0.001	0.379	130616.6101	85100.50796	94812.33383	73469.17702	57228.40039	33474.9812	29921.16399	24766.91723
AT3G46060	gi 15231322	Ras-related protein ARA-3 [Arabidopsis thaliana]	Signal transduction	1	1	18.85	0.024	2.703	2546.609819	1334.557727	1010.261063	1680.14474	5373.252557	3670.324685	5576.105367	3145.889527
AT1G48480	gi 4008006	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	48.76	0.001	0.170	312281.8522	236668.3392	258119.4407	158733.4395	38848.1505	48971.40504	38352.66718	37979.38494
AT3G61820	gi 15228618	aspartyl protease-like protein [Arabidopsis thaliana]	Transcription	1	1	19.04	0.003	0.060	12629.03527	9968.968036	12400.44119	5542.031573	289.5957348	1034.791972	664.9780124	443.3121886
AT5G06530	gi 10178109	ABC transporter-like protein [Arabidopsis thaliana]	Transporter	1	1	24.14	0.002	1260.093	63.77882491	101.2232652	6.586130625	5.096136591	92643.98726	34256.80381	82681.02285	13056.86293
AT1G64780	gi 5880357	ammonium transporter [Arabidopsis thaliana]	Transporter	1	1	29.73	0.047	0.348	25498.75463	31451.9582	29505.65657	12214.42733	3661.8128	14874.78684	7611.836934	8180.920673
AT4G13510	gi 15236300	ammonium transporter 1;1 [Arabidopsis thaliana]	Transporter	2	2	137.26	0.009	0.430	37072.47943	34980.76647	34751.71029	17121.8138	16693.30049	17404.16492	9998.623119	9199.704087
AT4G18910	gi 15234059	aquaporin NIP1-2 [Arabidopsis thaliana]	Transporter	1	1	74.18	0.042	0.162	271832.7953	123831.7596	140484.055	149658.8394	7243.301324	53903.74436	22020.91432	28030.82087
AT5G43350	gi 15239848	inorganic phosphate transporter 1-1 [Arabidopsis thaliana]	Transporter	12	12	728	0.006	0.324	10155822.37	7056317.777	8206147.327	8381829.658	3242055.487	3378642.792	2527315.571	1805368.581

AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	ABA/Control	Normalized abundance							
									Control				ABA			
									Control 1	Control 2	Control 3	Control 4	ABA 1	ABA 2	ABA 3	ABA 4
AT1G72150	gi 15218382	patellin-1 [Arabidopsis thaliana]	Transporter	1	1	38.21	0.028	62.163	1142.667567	848.7709878	769.3452534	671.6684982	99109.85717	15292.3419	96789.53402	2178.895403
AT3G47960	gi 13877879	putative peptide transporter protein [Arabidopsis thaliana]	Transporter	2	2	49.14	0.001	4.168	31938.80838	28367.69698	33688.68979	24160.06192	157485.3135	122462.2433	133911.0468	78644.64946
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporter	1	1	26.09	0.018	12.453	479.8262827	412.106665	253.7967793	424.8073679	6123.016894	2650.054784	9223.289754	1562.051797
AT4G16370	gi 2244994	isp4 like protein [Arabidopsis thaliana]	transporters	1	1	46.72	0.001	9.073	3511.976968	3202.440452	3768.709584	4642.055341	28429.56207	46295.57853	22673.36544	39839.50659
AT5G25250	gi 15238749	Flotillin-like protein 1 [Arabidopsis thaliana]	Unknown	2	2	68.51	0.017	0.160	8763.115131	12108.20239	12995.62424	10543.19988	584.802337	3935.833989	2161.648969	439.09168
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	56.14	0.018	79.300	1113.271657	1617.936283	1882.16726	31399.53892	958172.1243	461105.3779	1209692.774	226857.3832
AT4G20260	gi 15235363	plasma-membrane associated cation-binding protein 1 [Arabidopsis thaliana]	Unknown	2	2	148.39	0.013	5.144	231983.5353	202109.8651	178293.5675	233758.6491	1030874.718	548487.2831	1897296.298	876194.2453
AT2G41810	gi 15227439	uncharacterized protein [Arabidopsis thaliana]	Unknown	3	3	150.67	0.031	0.354	28234.71567	30638.91846	26180.88042	37673.39666	9681.407839	20815.62016	6995.243633	6004.870597
AT1G42470	gi 12322632	unknown protein, 5' partial [Arabidopsis thaliana]	Unknown	2	2	37.35	0.049	4.470	2506.598499	4332.285281	3820.807481	4814.542838	29825.90732	14868.4674	17578.91595	6900.219403

Supplementary Table 3-6 CA-responsive plasma membrane proteins at the log phase

AGI	Accession	Protein Description	Functional category	Peptide count	Peptides used for	Confidence score	Anova (p)	CA/Control	Normalized abundance				CA			
									Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	Cell	1	1	43.29	0.02	0.63	19751.4	15921.8	14632.3	16743.4	12276.1	12938	8498.92	8338.59
AT1G74790	gi 5882745	F25A4.24 [Arabidopsis thaliana]	Cell	10	10	531.63	0.02	0.63	5695056	4420901	4746665	4447882	2814501	2523738	3576477	3249990
AT3G49670	gi 15229189	receptor-like kinase BAM2 [Arabidopsis thaliana]	Cell	1	1	35.6	0.01	0.35	25236.8	24438.5	21606.3	15303	8880.97	6702.57	6385.23	8781.4
AT5G46700	gi 15237490	Tetraspanin family protein [Arabidopsis thaliana]	Cell	1	1	66.78	0	0.31	61687.2	49141.5	54020.9	68226.2	20078.6	21285	16099.8	15826.2
AT3G45600	gi 15231187	tetraspanin3 [Arabidopsis thaliana]	Cell	2	2	44.88	0.01	0.52	38444.7	27533.3	29049.4	40119.6	20607.5	16722.3	17506.8	15561.9
AT2G23810	gi 13272397	unknown protein [Arabidopsis thaliana]	Cell	5	5	194.4	0.01	0.61	639592	509572	542209	590989	362742	352597	372048	296353
AT5G39970	gi 10176989	unnamed protein product [Arabidopsis thaliana]	Cell	1	1	55.12	0.04	0.54	39824.4	28650.5	31178.4	24741.6	13669.4	14986.1	18515.2	20122.4
AT5G62690	gi 13605867	AT5g62700/MRG21_12 [Arabidopsis thaliana]	Cell structure	2	2	92.1	0.01	0.57	99923.6	83280.5	81132.3	160034	58924.1	57960.4	54327.5	70121.4
AT3G47000	gi 15232707	beta-glucosidase [Arabidopsis thaliana]	Cell structure	1	1	78.37	0	1.95	12641.6	14486.1	15546	17326.2	25931.4	31294.7	29744.7	29939.5
AT3G22600	gi 18403453	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis	Cell structure	1	1	46.46	0.02	0.49	6522.5	6568.53	6262.58	12790.3	2335.65	4951.79	2477.65	5990.06
AT5G20230	gi 16203	blue copper-binding protein [Arabidopsis thaliana]	Cell structure	3	3	130.8	0	0.31	411484	311845	359056	242401	93804.2	87121.9	145863	82270.9
AT1G75680	gi 15222328	endoglucanase 10 [Arabidopsis thaliana]	Cell structure	4	4	194.44	0	0.56	237263	253582	256642	230230	144261	124989	138701	144942
AT1G03870	gi 18379157	fasciclin-like arabinogalactan protein 9 [Arabidopsis thaliana]	Cell structure	1	1	38.5	0	0.48	11079.1	9597.11	7891.21	5529.62	4055.3	4952.43	4285.87	2926.56
AT2G45470	gi 10880493	fasciclin-like arabinogalactan protein FLA8 [Arabidopsis thaliana]	Cell structure	1	1	22.41	0.01	2.17	12170.5	10807.4	13636.7	9965.88	18056.8	20704.3	35939.8	26342
AT4G12420	gi 15234551	Monocopper oxidase-like protein SKU5 [Arabidopsis thaliana]	Cell structure	1	1	20.13	0.04	1.75	4850.81	3403.66	5231.42	4787.33	8542.12	9461.26	7249.56	6812.5
AT1G53840	gi 15220958	pectinesterase 1 [Arabidopsis thaliana]	Cell structure	5	5	293.11	0	0.45	298684	325294	269728	249267	122633	163069	116246	108578
AT5G17820	gi 15238030	peroxidase 57 [Arabidopsis thaliana]	Cell structure	1	1	57.66	0.04	1.77	66345.9	66137.9	56306.1	32386.1	101008	90219.6	106380	93999.1
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	Cell structure	1	1	33.82	0.02	0.64	43944.9	60717.8	53364.1	59249.2	34422.8	41583.6	26279.7	36367.5
no	gi 2895512	putative pectin methylesterase [Arabidopsis	Cell structure	1	1	50.52	0	16.41	1838.59	364.687	864.215	470.194	13942.5	14634.6	15319.6	14143
AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis thaliana]	Cell structure	1	1	82.52	0.02	0.59	39538.7	37370.1	37645	43957	21880.4	16249.3	27558.1	27337
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	8	8	334.59	0	1.96	1681666	1277627	1440142	1298025	2727940	2635776	3143522	2675079
AT4G01700	gi 15234281	class II chitinase-like protein [Arabidopsis	Disease/defence	11	11	798.53	0.02	0.52	4.8E+07	3.9E+07	4.1E+07	3E+07	1.8E+07	1.9E+07	2.5E+07	2.1E+07
AT2G02130	gi 15226878	defensin-like protein 1 [Arabidopsis thaliana]	Disease/defence	1	1	13.78	0.01	0.49	29198.9	20621.8	21584.7	22029.7	11304.4	14009	8801.11	11184
AT1G30360	gi 18397470	Early-responsive to dehydration stress protein (ERD4) [Arabidopsis thaliana]	Disease/defence	2	2	48.96	0.02	1.69	26452.6	32898.1	33155.6	40438.7	61098	57074.1	55423.3	50693.3
AT5G22060	gi 535588	putative [Arabidopsis thaliana]	Disease/defence	4	4	182.98	0.02	0.34	86740.9	88043.1	88980.1	127416	44754.1	40668.1	20905.8	27095.7
ATCG00120	gi 7525018	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	Energy	3	3	108.72	0.02	0.34	50744.7	50741.9	60357.8	36094.2	11608.9	18167.5	13728.1	24540.6
AT2G33120	gi 600710	formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	Intracellular traffic	2	2	47.15	0.01	0.53	57623.5	54388.9	54242.9	37725.2	28285.4	30507.4	24816.3	25717.3
AT4G35790	gi 7486399	hypothetical protein F4B14.60 - Arabidopsis	Metabolism	4	4	232.3	0.01	1.84	105882	116789	114578	125762	243533	205076	208869	195105
AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	Metabolism	1	1	22.57	0.03	0.56	185940	159502	133130	204067	71652.8	69557.9	101573	135483
AT1G73370	gi 15219457	sucrose synthase 6 [Arabidopsis thaliana]	Metabolism	1	1	26.39	0.02	0.52	340429	255873	283598	164308	122730	137816	169856	112326
At4g29410	gi 15233567	60S ribosomal protein L28-2 [Arabidopsis thaliana]	Protein destination and	1	1	24.46	0.01	0.61	184235	176574	185204	123532	120893	85852.1	112252	91476.7
AT1G03230	gi 18379072	aspartyl protease-like protein [Arabidopsis thaliana]	Protein destination and	6	6	309.79	0.01	3.11	104081	148588	123678	60038.4	305129	356118	353486	341184
AT5G02490	gi 15241847	heat shock protein 70 [Arabidopsis thaliana]	Protein destination and	9	9	389.77	0.02	0.53	320524	325830	322090	613724	223830	184739	199969	224305
AT1G56410	gi 15223533	heat shock protein-70 cognate protein [Arabidopsis thaliana]	Protein destination and	7	7	283.55	0.03	0.53	288823	295804	292247	564361	202861	165400	186744	203474
AT1G63500	gi 240254311	Protein kinase protein with tetratricopeptide repeat domain [Arabidopsis thaliana]	Protein destination and	3	3	90.95	0	1.67	54526.5	60378.5	58381	50585.1	97612.6	82209.5	105305	88344.6

AGI	Accession	Protein Description	Functional category	Peptide count	Peptides used for	Confidence score	Anova (p)	CA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
AT2G03530	gi 4335747	putative integral membrane protein [Arabidopsis thaliana]	Protein destination and	1	1	47.36	0.03	0.43	48400.5	29616.7	32927.8	20580.1	13397.8	15567.6	13388.8	14758.5
AT3G53780	gi 7629998	putative protein [Arabidopsis thaliana]	Protein destination and	1	1	51.82	0.04	0.66	10997	5254.78	6324.74	9078.75	8246.18	4304.35	3060.95	5150.24
AT4G35230	gi 3080427	putative protein [Arabidopsis thaliana]	Protein destination and	1	1	58.31	0.04	1.55	30035.3	38302.2	42235.5	39892.9	59005.5	69853	46909.5	58027.2
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination and	2	2	76.1	0	1.88	25339.9	26122.8	28045.7	31798.1	46724.7	59270	51392.5	52073.4
AT2G42960	gi 15228043	putative receptor-like protein kinase [Arabidopsis thaliana]	Protein destination and	1	1	37.53	0.04	0.65	1796.41	2291.37	903.193	1974.9	969.116	1976.38	383.598	1190.56
AT3G17410	gi 22331138	putative serine/threonine protein kinase [Arabidopsis thaliana]	Protein destination and	3	3	146.09	0	1.61	104330	109495	106742	102896	166941	164899	187859	161868
AT1G48210	gi 15221111	serine/threonine protein kinase [Arabidopsis thaliana]	Protein destination and	2	2	50.21	0	1.56	84370.7	74839.2	82918.2	79097.2	124871	115866	146277	115510
AT2G36160	gi 15227588	40S ribosomal protein S14-1 [Arabidopsis thaliana]	Protein synthesis	1	1	40.92	0.02	2.14	9891.82	16291	13223.8	8740.66	21042.4	25196.4	27199.7	29649.6
AT1G04270	gi 1107485	40S ribosomal protein S15 [Arabidopsis thaliana]	Protein synthesis	1	1	42.1	0.04	2.98	24392.8	29164.1	15764.4	26819.8	70721.6	57711.2	108639	49765.6
AT2G41840	gi 15227443	40S ribosomal protein S2-3 [Arabidopsis thaliana]	Protein synthesis	1	1	26.88	0.03	0.57	16772.7	13079.8	9658.45	18260.8	8894.21	6317.75	8659.83	9156.35
AT2G37270	gi 15228111	40S ribosomal protein S5-1 [Arabidopsis thaliana]	Protein synthesis	1	1	68.72	0.02	2.42	56354.5	53849.9	43799.8	17117.4	98883.2	94380.2	153704	67613.8
AT5G60390	gi 295789	elongation factor 1-alpha [Arabidopsis thaliana]	Protein synthesis	4	4	150.67	0	1.60	151884	141967	141518	183683	216990	239306	255482	275736
At3g60240	gi 7576200	protein synthesis initiation factor-like [Arabidopsis thaliana]	Protein synthesis	2	2	36.07	0.01	0.57	398463	258876	284690	263364	182944	182757	180834	143941
AT3G57030	gi 6911873	putative protein [Arabidopsis thaliana]	Secondary metabolism	2	2	63.67	0.02	0.60	16358.7	16532	10550.4	9633.5	7081.62	11010.4	7034.92	6909.68
AT5G19450	gi 15239742	calcium-dependent protein kinase 19 [Arabidopsis thaliana]	Signal transduction	2	2	26.82	0.04	0.59	160326	89333.1	98398.6	109618	65567.1	73105.4	66075.8	65638.5
AT4G04720	gi 15234435	calcium-dependent protein kinase 21 [Arabidopsis thaliana]	Signal transduction	1	1	72.75	0.01	1.61	60907	49960.9	52238.7	56652.1	96722.2	86948.8	99244.6	70138.7
AT4G04700	gi 5706728	contains similarity to eukaryotic protein kinase domain (Pfam: PF00069, score=272.9, E=4.1e-78, N=1) [Arabidopsis thaliana]	Signal transduction	1	1	50.44	0.01	2.34	15480.3	24060.6	19092.2	15826.9	45247.7	39257.7	49857.2	39991.6
AT3G08510	gi 15231929	phosphoinositide phospholipase C 2 [Arabidopsis thaliana]	Signal transduction	3	3	127.87	0.01	1.67	340064	283529	295266	222583	478957	488904	613434	329043
AT3G51740	gi 15231029	probably inactive leucine-rich repeat receptor-like protein kinase IMK2 [Arabidopsis thaliana]	Signal transduction	1	1	34.83	0.05	0.65	15425.1	15775.2	12560	16660.6	8708.51	7254.66	10274.4	12940.6
AT3G02880	gi 15233013	putative inactive receptor kinase [Arabidopsis thaliana]	Signal	5	5	250.14	0.01	1.76	1318158	1273001	1124708	699464	1924059	1904928	2345797	1577910
AT5G16590	gi 15237379	putative inactive receptor kinase [Arabidopsis thaliana]	Signal	2	2	83.36	0.01	1.65	56767.3	60912	64605	74068.9	112436	96873.4	113796	100377
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	2	2	115.15	0.01	0.48	130617	85100.5	94812.3	73469.2	47704.5	48860.7	44290.1	42433.9
AT3G46280	gi 7799016	putative protein [Arabidopsis thaliana]	Signal	3	3	125.02	0	0.30	114592	99298.4	113175	63099	37077.2	30978.5	24798.2	23802.6
AT1G51820	gi 9802784	Putative protein kinase [Arabidopsis thaliana]	Signal	1	1	57.81	0.01	0.22	9104.28	15149.3	10885.7	6718.69	1149.73	2075.38	2679.64	3169.11
AT3G46060	gi 15231322	Ras-related protein ARA-3 [Arabidopsis thaliana]	Signal	1	1	18.85	0.04	1.69	2546.61	1334.56	1010.26	1680.14	4140.28	3157.82	1837.95	1956.68
At1g35160	gi 14532442	At1g35160/T32G9_30 [Arabidopsis thaliana]	Signal	1	1	30.36	0.02	0.42	5083.32	1763.29	4221.12	7160.66	2085.68	1122.09	2358.03	2126.52
At3g57530	gi 6706424	calcium-dependent protein kinase [Arabidopsis thaliana]	Signal transduction	1	1	33.19	0.01	1.56	35309.8	28609	36805	35917.6	50928.7	54281.1	58353.8	49868.5
AT5G58670	gi 2769704	phosphoinositol-specific phospholipase C delta [Arabidopsis thaliana]	Signal transduction	2	2	47.2	0.01	1.59	69983.4	90963.5	94743.6	64051.3	133160	130788	126908	117836
AT4G35470	gi 15237011	plant intracellular ras group-related LRR 4 [Arabidopsis thaliana]	Signal transduction	2	2	41.65	0.03	2.09	7266.04	11350.8	7958.96	9655.83	19423.1	19491.9	23831.7	12945.5
AT1G48480	gi 4008006	receptor-like protein kinase [Arabidopsis thaliana]	Signal	2	2	48.76	0.03	0.59	312282	236668	258119	158733	129207	140913	178319	118166



AGI	Accession	Protein Description	Functional category	Peptide count	Peptides used for	Confidence score	Anova (p)	CA/Control	Normalized abundance							
									Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
AT1G56140	gi 6056376	Similar to serine/threonine kinases [Arabidopsis thaliana]	Signal transduction	1	1	50.74	0.01	0.54	2676.65	4092.94	5698.46	11308.2	893.994	1890.74	3066.97	6957.03
AT3G61820	gi 15228618	aspartyl protease-like protein [Arabidopsis thaliana]	Transcription	1	1	19.04	0.03	0.53	12629	9968.97	12400.4	5542.03	4875.99	5212.39	7005.54	4569.75
AT2G45820	gi 601843	DNA-binding protein [Arabidopsis thaliana]	Transcription	1	1	32.19	0	0.63	117667	152274	127702	181616	81519.5	98730.9	79482.8	101715
At5g22650	gi 30688577	histone deacetylase HDT2 [Arabidopsis thaliana]	Transcription	3	3	86.49	0.01	0.53	65786.5	51278.3	38694.9	56748.8	25201.7	33317	19750.4	34180.3
AT4G19610	gi 11079488	hypothetical protein [Arabidopsis thaliana]	Transcription	1	1	23.28	0.01	0.54	32457.7	24175.3	26003.1	36751.1	17832.6	14896	17070.4	15128.9
AT5G08695	gi 13548328	putative protein [Arabidopsis thaliana]	Transcription	1	1	21.85	0.01	0.54	32457.7	24175.3	26003.1	36751.1	17832.6	14896	17070.4	15128.9
AT1G61140	gi 2443887	Similar to transcription factor gb Z46606 1658307 and others [Arabidopsis thaliana]	Transcription	1	1	20.27	0.01	5.14	5383.16	8999.25	6784.1	3467.64	27087.6	48370.2	19902.2	31229.3
AT1G59870	gi 15218936	ABC transporter G family member 36 [Arabidopsis thaliana]	Transporter	2	2	52.88	0.02	1.62	54903.3	40022.3	47090.8	62239.9	77405.3	82565.1	85426.8	84502.2
AT5G06530	gi 10178109	ABC transporter-like protein [Arabidopsis thaliana]	Transporter	1	1	24.14	0.04	11.69	63.7788	101.223	6.58613	5.09614	200.654	715.715	674.941	474.843
AT4G21120	gi 30685317	amino acid transporter 1 [Arabidopsis thaliana]	Transporter	1	1	39.76	0.01	0.62	21588.9	23810.7	24625.5	21813.5	13249.5	15013.1	12873.6	15648.8
AT1G64780	gi 5880357	ammonium transporter [Arabidopsis thaliana]	Transporter	1	1	29.73	0.04	1.95	25498.8	31452	29505.7	12214.4	62268.5	41491.6	47790.6	40916.1
AT4G13510	gi 15236300	ammonium transporter 1;1 [Arabidopsis thaliana]	Transporter	2	2	137.26	0.01	2.19	37072.5	34980.8	34751.7	17121.8	88755.5	53272.5	80180.6	49162.1
AT4G18910	gi 15234059	aquaporin NIP1-2 [Arabidopsis thaliana]	Transporter	1	1	74.18	0.02	0.47	271833	123832	140484	149659	103474	73366.3	95247.1	46939.4
AT5G43350	gi 15239848	inorganic phosphate transporter 1-1 [Arabidopsis thaliana]	Transporter	12	12	728	0	0.50	1E+07	7056318	8206147	8381830	4395782	4028838	4762642	3582049
AT2G38940	gi 15224985	inorganic phosphate transporter 1-4 [Arabidopsis thaliana]	Transporter	2	2	50.34	0.01	0.55	434430	362529	410803	417453	294728	203092	191656	203412
AT1G72150	gi 15218382	patellin-1 [Arabidopsis thaliana]	Transporter	1	1	38.21	0.05	1.61	1142.67	848.771	769.345	671.668	1249.76	1701.13	1172.93	1392.76
AT3G54820	gi 15233102	putative aquaporin PIP2-5 [Arabidopsis thaliana]	Transporter	1	1	44.21	0.01	2.19	5185.68	3860.76	3550.59	3760.45	11280.7	11655.6	5398.03	7450.89
AT3G47960	gi 13877879	putative peptide transporter protein [Arabidopsis thaliana]	Transporter	2	2	49.14	0.02	0.58	31938.8	28367.7	33688.7	24160.1	17860.5	19816.1	14465.4	16568.9
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporter	1	1	26.09	0.02	2.91	479.826	412.107	253.797	424.807	1141.5	1916.23	862.712	645.072
AT3G19930	gi 15230987	sugar transport protein 4 [Arabidopsis thaliana]	Transporter	2	2	146.23	0	0.59	84526.8	80689.6	69523	70791.1	44195.3	44040.2	49425.3	43056.3
AT4G16370	gi 2244994	isp4 like protein [Arabidopsis thaliana]	Transporters	1	1	46.72	0.04	0.52	3511.98	3202.44	3768.71	4642.06	1773.8	2835.2	1486.96	1839.46
AT4G38580	gi 4097553	ATFP6 [Arabidopsis thaliana]	Unknown	2	2	75.26	0.01	1.83	61642.1	40790.5	41802.5	39223.7	88602.2	73725.7	103222	70990.7
AT2G44790	gi 1906000	blue copper-binding protein II [Arabidopsis thaliana]	Unknown	4	4	187.19	0	0.38	899704	715694	721951	613372	252568	268246	336370	259876
no	gi 3687234	copa-like retroelement pol polyprotein [Arabidopsis thaliana]	Unknown	1	1	25.52	0	1.95	12641.6	14486.1	15546	17326.2	25931.4	31294.7	29744.7	29939.5
AT5G25250	gi 15238749	Flotillin-like protein 1 [Arabidopsis thaliana]	Unknown	2	2	68.51	0.01	2.98	8763.12	12108.2	12995.6	10543.2	36661.4	33983.6	25710.2	36006.4
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	56.14	0	108.61	1113.27	1617.94	1882.17	31399.5	850402	887019	1173137	1000625
AT4G20260	gi 15235363	plasma-membrane associated cation-binding protein 1 [Arabidopsis thaliana]	Unknown	2	2	148.39	0.01	2.18	231984	202110	178294	233759	510463	469443	502595	361718
AT2G41800	gi 15227437	uncharacterized protein [Arabidopsis thaliana]	Unknown	2	2	70.72	0.04	2.15	29778.4	27668.2	25983.5	56731.7	76992.1	84702.8	74567.7	64627.1
AT2G41810	gi 15227439	uncharacterized protein [Arabidopsis thaliana]	Unknown	3	3	150.67	0.01	2.14	28234.7	30638.9	26180.9	37673.4	72493.7	60952.9	73376.1	55811.8
AT3G15480	gi 18400781	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	28.91	0.01	0.28	10180.8	4331.72	6004.48	1847.28	1761.15	2269.58	1648.42	525.312
AT4G12735	gi 42572885	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	78.93	0	19.52	1887.94	2364.1	616.057	3663.04	32540.6	41142.9	46099.5	46770.3
AT5G62630	gi 14423506	Unknown protein [Arabidopsis thaliana]	Unknown	9	9	379.88	0.02	0.57	2980569	2372389	2609064	2360091	1247579	1232969	1811650	1557660
AT1G42470	gi 12322632	unknown protein, 5' partial [Arabidopsis thaliana]	Unknown	2	2	37.35	0	0.13	2506.6	4332.29	3820.81	4814.54	341.8	509.812	404.793	750.013
AT3G17350	gi 11994552	unnamed protein product [Arabidopsis thaliana]	Unknown	1	1	35.91	0.01	0.62	17920.6	11545.9	11198.3	13119.4	9238.54	8520.36	8185.37	7487.43

Supplementary Table 3-6 Common CA- and ABA-responsive plasma membrane proteins at the log phase

AGI	GI	Protein description	Functional categories	Anova (p)/AB	ABA/Control	Anova (p)/CA	CA/Control
AT2G21130	gi 2443757	cyclophilin [Arabidopsis thaliana]	Cell	0.047	0.474	0.020	0.629
AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis thaliana]	Cell structure	0.014	0.515	0.020	0.588
AT4G01700	gi 15234281	class II chitinase-like protein [Arabidopsis thaliana]	Disease/defence	0.000	0.088	0.020	0.521
AT1G73370	gi 15219457	sucrose synthase 6 [Arabidopsis thaliana]	Metabolism	0.001	0.074	0.020	0.521
AT3G61820	gi 15228618	aspartyl protease-like protein [Arabidopsis thaliana]	Protein destination and storage	0.003	0.060	0.030	0.535
AT2G03530	gi 4335747	putative integral membrane protein [Arabidopsis thaliana]	Protein destination and storage	0.032	0.160	0.030	0.435
At3g60240	gi 7576200	protein synthesis initiation factor-like [Arabidopsis thaliana]	protein synthesis	0.009	0.271	0.010	0.571
AT3G57030	gi 6911873	putative protein [Arabidopsis thaliana]	Secondary metabolism	0.025	0.181	0.020	0.602
AT5G19450	gi 15239742	calcium-dependent protein kinase 19 [Arabidopsis thaliana]	Signal transduction	0.025	0.298	0.040	0.592
AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	0.001	0.379	0.010	0.476
AT1G48480	gi 4008006	receptor-like protein kinase [Arabidopsis thaliana]	Signal transduction	0.001	0.170	0.030	0.588
AT4G18910	gi 15234059	aquaporin NIP1-2 [Arabidopsis thaliana]	Transporter	0.042	0.162	0.020	0.465
AT5G43350	gi 15239848	inorganic phosphate transporter 1-1 [Arabidopsis thaliana]	Transporter	0.006	0.324	0.000	0.495
AT1G78830	gi 17644159	unknown protein [Arabidopsis thaliana]	Cell structure	0.000	0.222	0.000	1.960
AT1G03230	gi 18379072	aspartyl protease-like protein [Arabidopsis thaliana]	Protein destination and storage	0.008	0.363	0.010	3.110
AT2G36160	gi 15227588	40S ribosomal protein S14-1 [Arabidopsis thaliana]	Protein synthesis	0.000	0.080	0.020	2.140
AT4G04700	gi 5706728	contains similarity to eukaryotic protein kinase domain (Pfam: PF00069, score=272.9, E=4.1e-78, N=1) [Arabidopsis thaliana]	Signal transduction	0.003	0.183	0.010	2.340
AT3G08510	gi 15231929	phosphoinositide phospholipase C 2 [Arabidopsis thaliana]	Signal transduction	0.006	0.307	0.010	1.670
AT1G64780	gi 5880357	ammonium transporter [Arabidopsis thaliana]	Transporter	0.047	0.348	0.040	1.950
AT4G13510	gi 15236300	ammonium transporter 1;1 [Arabidopsis thaliana]	Transporter	0.009	0.430	0.010	2.190

AGI	GI	Protein description	Functional categories	Anova (p)/AB	ABA/Control	Anova (p)/CA	CA/Control
AT5G25250	gi 15238749	Flotillin-like protein 1 [Arabidopsis thaliana]	Unknown	0.017	0.160	0.010	2.980
AT2G41810	gi 15227439	uncharacterized protein [Arabidopsis	Unknown	0.031	0.354	0.010	2.140
AT5G62690	gi 13605867	AT5g62700/MRG21_12 [Arabidopsis	Cell structure	0.032	2.984	0.010	0.568
AT1G75680	gi 15222328	endoglucanase 10 [Arabidopsis thaliana]	Cell structure	0.014	1.558	0.000	0.565
AT4G25240	gi 4454012	Pollen-specific protein precursor like [Arabidopsis thaliana]	Cell structure	0.048	2.070	0.020	0.637
At1g35160	gi 14532442	At1g35160/T32G9_30 [Arabidopsis thaliana]	signal transduction	0.042	2.178	0.020	0.422
AT3G47960	gi 13877879	putative peptide transporter protein [Arabidopsis thaliana]	Transporter	0.001	4.168	0.020	0.581
AT4G16370	gi 2244994	isp4 like protein [Arabidopsis thaliana]	transporters	0.001	9.073	0.040	0.524
AT1G42470	gi 12322632	unknown protein, 5' partial [Arabidopsis thaliana]	Unknown	0.049	4.470	0.000	0.130
AT4G12420	gi 15234551	Monocopper oxidase-like protein SKU5 [Arabidopsis thaliana]	Cell structure	0.006	2.750	0.040	1.750
AT1G30360	gi 18397470	Early-responsive to dehydration stress protein (ERD4) [Arabidopsis thaliana]	Disease/defence	0.003	2.564	0.020	1.690
AT1G06700	gi 7523708	Putative protein kinase [Arabidopsis thaliana]	Protein destination and storage	0.034	2.596	0.000	1.880
AT5G16590	gi 15237379	putative inactive receptor kinase [Arabidopsis thaliana]	Signal transduction	0.002	1.868	0.010	1.650
AT3G46060	gi 15231322	Ras-related protein ARA-3 [Arabidopsis thaliana]	Signal transduction	0.024	2.703	0.040	1.690
AT5G06530	gi 10178109	ABC transporter-like protein [Arabidopsis thaliana]	Transporter	0.002	1260.093	0.040	11.690
AT1G72150	gi 15218382	patellin-1 [Arabidopsis thaliana]	Transporter	0.028	62.163	0.050	1.610
AT1G69870	gi 12325237	putative peptide transporter; 37139-33250 [Arabidopsis thaliana]	Transporter	0.018	12.453	0.020	2.910
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	0.018	79.300	0.000	108.610
AT4G20260	gi 15235363	plasma-membrane associated cation-binding protein 1 [Arabidopsis thaliana]	Unknown	0.013	5.144	0.010	2.180

Supplementary Table 3-7 ABA-responsive plasma membrane proteins at the stationary phase

AGI	GI	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	ABA/Control	Normalized abundance							
									Control				ABA			
									Control 1	Control 2	Control 3	Control 4	ABA 1	ABA 2	ABA 3	ABA 4
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis]	Signal transduction	1	1	61.74	0.001	74.888	4368.123	11089.25	13942.35	7730.133	775972.2	583855.3	832092.7	588646.8
AT3G44310	gi 16400	nitrilase I [Arabidopsis]	Signal transduction	2	2	45.17	0.017	5.280	2044.885	4234.238	3219.134	10064.66	19784.57	31544.75	6797.215	45164.33
AT5G52650	gi 8953720	unnamed protein product [Arabidopsis]	Transcription	1	1	40.15	0.012	0.166	23256.7	17698.52	7831.248	25209.02	7099.411	2370.939	1406.188	1413.525
AT1G32860	gi 6910583	CDS [Arabidopsis]	Cell structure	1	1	35.25	0.018	0.280	13176.54	10416.84	9335.003	11895.82	5105.209	2211.421	3828.024	1423.841
AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis]	Cell structure	2	2	155.53	0.021	0.311	28244.35	17045.02	73019.86	39132.37	9623.537	11583.19	16532.74	11251.59

Supplementary Table 3-7 CA-responsive plasma membrane proteins at stationary phase

Accession	AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	CA/Control	Normalized abundance							
										Control				CA			
										Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
gi 6715648	AT1G01050	gi 6715648	T25K16.5 [Arabidopsis thaliana]	Intracellular traffic	1	1	51.95	0.006733	0.200736	5223.405	10225.01	30286.56	11866.33	1822.796	3080.107	3994.1	2665.673
gi 15220329	AT1G04820	gi 15220329	tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana]	Cell growth/division	2	2	34.37	0.009603	0.440985	64008.17	74482.04	43270.72	115223.7	37010.26	36386.54	12859.34	44709.64
gi 16314	AT1G06760	gi 16314	histone H1-1 [Arabidopsis thaliana]	Cell growth/division	1	1	42.08	0.036769	0.360969	3913.321	5801.893	3338.835	4332.138	1879.504	2657.501	375.6414	1363.225
gi 7523712	AT1G06840	gi 7523712	Hypothetical protein [Arabidopsis thaliana]	Signal transduction	1	1	17.02	0.044007	0.236382	18532.72	5940.275	10142.47	36383.82	4024.577	3940.717	4228.029	4589.652
gi 18395044	AT1G21880	gi 18395044	LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana]	Signal transduction	2	2	119.14	0.020209	1.89943	499701.2	273315.8	324098.8	474300.3	883200.1	387277.6	882893.5	831424.6
gi 15220698	AT1G23290	gi 15220698	60S ribosomal protein L27a-2 [Arabidopsis thaliana]	Protein synthesis	1	1	17.81	0.000616	CA no	622.1012	2347.813	3014.878	9577.068	0	0	0	0
gi 6910583	AT1G32860	gi 6910583	CDS [Arabidopsis thaliana]	Cell structure	1	1	35.25	0.008347	2.435386	13176.54	10416.84	9335.003	11895.82	21939.39	29287.44	30105.11	27832.31
gi 1429207	AT1G35720	gi 1429207	annexin [Arabidopsis thaliana]	Cell growth/division	1	1	36.54	0.019677	0.534845	90964.44	107510	145880.7	81221.56	34898.05	77504.57	66226.75	48988.28
gi 8778533	AT1G48210	gi 8778533	F21D18.6 [Arabidopsis thaliana]	Protein destination and storage	2	2	102.17	0.002319	1.577966	93577.37	101368.8	93741.8	104074.4	150421.6	146448.4	167417.7	155477.8
gi 3377517	AT1G69850	gi 3377517	nitrate transporter NTL1 [Arabidopsis thaliana]	Transporter	2	2	82.11	0.030882	0.631216	86756.29	50713.53	87705.13	91382.64	43531.08	42841.27	61652.2	51791.64
gi 15219412	AT1G79550	gi 15219412	phosphoglycerate kinase [Arabidopsis thaliana]	Energy	2	2	66.04	0.0058	0.357713	26996.36	47762.88	60549.98	55874.55	14011.34	18933.97	20648.16	14795.5
gi 15226197	AT2G01210	gi 15226197	leucine-rich repeat transmembrane protein kinase-like protein [Arabidopsis thaliana]	Signal transduction	1	1	46.32	0.032823	2.116961	1926984	3761621	2781668	1586756	6898459	5091155	5191411	4109309
gi 4544402	AT2G16250	gi 4544402	putative LRR receptor protein kinase [Arabidopsis thaliana]	Signal transduction	1	1	30.73	0.029619	1.570098	104747.1	71109.13	65271.75	93521.97	132094.4	109204.2	144536.9	139597.9
gi 18395770	AT3G01290	gi 18395770	Hypersensitive-induced response protein 3 [Arabidopsis thaliana]	Signal transduction	1	1	29.33	0.040214	0.216648	9492.741	8308.013	4943.915	4106.837	557.5327	1469.098	2624.779	1165.908
gi 15233013	AT3G02880	gi 15233013	putative inactive receptor kinase [Arabidopsis thaliana]	Signal transduction	1	1	54.55	0.021534	0.538945	6505.192	5907.938	3477.213	10607.95	3258.137	3464.629	2797.692	4760.674
gi 166706	AT3G04120	gi 166706	cystolic glyceraldehyde-3-phosphate dehydrogenase	Energy	1	1	44.44	0.010662	0.259687	20540.64	35290.35	50738.85	52181.98	9968.411	11438.66	10263.88	9554.896
gi 30683104	AT3G14350	gi 30683104	STRUBBELIG-receptor family 7 protein [Arabidopsis thaliana]	Signal transduction	1	1	36.77	0.030779	1.838941	3103.647	1861.199	3139.923	4065.018	7093.848	4788.452	4020.253	6476.965

Accession	AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	CA/Control	Normalized abundance							
										Control				CA			
										Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
gi 22331138	AT3G17410	gi 22331138	putative serine/threonine protein kinase [Arabidopsis thaliana]	Protein destination and storage	2	2	119.08	0.001202	1.350947	113491.9	124635.9	122264.5	117039.7	154590	158117.8	174932.7	157344.8
gi 15231187	AT3G45600	gi 15231187	tetraspanin3 [Arabidopsis thaliana]	Cell growth/division	1	1	26.89	0.033139	0.628259	13307.7	14105.99	19273.74	16024.02	7184.362	11700.44	9176.921	11337.31
gi 166867	AT3G48930	gi 166867	ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]	Protein synthesis	1	1	19.9	0.044177	0.15119	274.6825	1000.012	1152.878	960.3071	0	512.2142	0	0
gi 15231847	AT3G53610	gi 15231847	RAB GTPase-8 [Arabidopsis thaliana]	Signal transduction	1	1	58.38	0.022908	0.549711	46840.83	54969.79	30549.36	90659.82	29038.64	39345.52	11171.58	43040.64
gi 15232435	AT3G54140	gi 15232435	peptide transporter PTR1 [Arabidopsis thaliana]	Transporter	2	2	138.65	0.012164	0.557423	108495.1	112111.8	113721.4	122515.8	53671.04	77306.7	71438.16	52239.35
gi 15228848	AT3G56190	gi 15228848	alpha-soluble NSF attachment protein 2 [Arabidopsis thaliana]	Intracellular traffic	1	1	29.98	0.004321	2.464417	5152.213	6536.492	8925.455	6348.901	14109.06	11547.92	22001.18	18790.06
gi 6049881	AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis thaliana]	Cell structure	2	2	155.53	0.021349	0.436577	28244.35	17045.02	73019.86	39132.37	18272.08	10248.58	22968.99	17245.71
gi 15234281	AT4G01700	gi 15234281	class II chitinase-like protein [Arabidopsis thaliana]	Disease/defence	2	2	134.9	0.02107	0.077421	202464.8	384629.9	1516114	164105.7	26555.66	64915.76	41341.02	42725.24
gi 16396	AT4G09320	gi 16396	nucleoside diphosphate kinase [Arabidopsis thaliana]	Intracellular traffic	1	1	18.87	0.025426	0.316828	422.4525	1612.325	3137.786	1124.464	276.5499	381.6715	820.9325	515.9184
gi 15234551	AT4G12420	gi 15234551	Monocopper oxidase-like protein SKU5 [Arabidopsis thaliana]	Cell structure	1	1	24.21	0.003249	0.167757	8343.912	7289.115	7393.167	8303.699	1770.548	656.3075	1678.042	1150.924
gi 13377778	AT4G12730	gi 13377778	fasciclin-like arabinogalactan-protein 2 [Arabidopsis thaliana]	Cell structure	4	4	102.55	0.002467	0.396173	146027.9	152866	60808.69	223865.7	57089.07	77061.6	25774.26	71269.03
gi 2245111	AT4G17530	gi 2245111	GTP-binding RAB1C like protein [Arabidopsis thaliana]	Signal transduction	1	1	80.11	0.009442	0.364378	11504.28	27426.36	2410.651	28764.12	3868.409	5836.501	814.4193	15025.55
gi 15235064	AT4G19530	gi 15235064	TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	Disease/defence	1	1	17.43	0.044177	0.15119	274.6825	1000.012	1152.878	960.3071	0	512.2142	0	0
gi 30685222	AT4G20830	gi 30685222	Reticuline oxidase-like protein [Arabidopsis thaliana]	Cell structure	1	1	50.41	0.012187	0.517311	28988.64	36891.56	16209.72	24974.04	10337.82	20987	8147.332	15913.2
gi 15236560	AT4G23650	gi 15236560	calcium-dependent protein kinase 6 [Arabidopsis thaliana]	Signal transduction	1	1	32.61	0.04097	0.610428	10153.5	6289.938	7937.18	7027.822	5011.893	3965.65	3857.765	6337.296
gi 4455192	AT4G26690	gi 4455192	putative protein [Arabidopsis thaliana]	Metabolism	1	1	51.91	0.010344	0.615988	614878.5	369796.6	331537.6	644254.6	350925.1	256050.5	250985.7	349662.9
gi 8953410	AT5G10290	gi 8953410	protein serine/threonine kinase-like protein [Arabidopsis thaliana]	Signal transduction	1	1	36.28	0.049431	0.500556	914.4611	477.0455	3643.827	1552.844	289.7392	239.9764	1373.645	1394.394

Accession	AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	CA/Control	Normalized abundance							
										Control				CA			
										Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
gi 9755770	AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Unknown	1	1	61.74	0.000175	91.9621	4368.123	11089.25	13942.35	7730.133	689943.3	826624.9	960897	937074.5
gi 15241168	AT5G19770	gi 15241168	tubulin alpha-3/alpha-5 chain [Arabidopsis thaliana]	Cell growth/division	2	2	63.43	0.024403	0.134505	5145.361	4725.955	29631.53	20849.51	2873.429	669.3024	2924.587	1650.383
gi 535588	AT5G22060	gi 535588	putative [Arabidopsis thaliana]	Disease/defence	2	2	56.67	0.021398	0.47706	12795.82	22839.86	23294.56	27943.61	7465.954	6360.936	11950.87	15666.32
gi 15238298	AT5G42100	gi 15238298	glucan endo-1,3-beta-glucosidase 10 [Arabidopsis thaliana]	Cell structure	1	1	31.11	0.028257	0.280807	17348.12	8635.406	8111.05	8013.175	2084.898	2812.696	4360.845	2565.726
gi 1523793	AT5G43370	gi 1523793	phosphate transporter [Arabidopsis thaliana]	Transporter	2	2	74.81	0.024779	0.466681	629690.2	910529.6	809338.7	1360602	400329	586347.1	270970	473813.9
gi 15241423	AT5G44130	gi 15241423	fasciclin-like arabinogalactan protein 13 [Arabidopsis thaliana]	Cell structure	1	1	36.04	0.003827	0.300929	140276.1	155404.4	42550.25	106858.7	29108.83	52142.22	17280.63	35408.46
gi 8978273	AT5G49760	gi 8978273	receptor protein kinase-like [Arabidopsis thaliana]	Signal transduction	1	1	74.19	0.028633	0.584281	82772.77	63362.81	72422.57	115159.8	41385.51	55337.63	35797.61	62464.39
gi 15238868	AT5G53870	gi 15238868	early nodulin-like protein 1 [Arabidopsis thaliana]	Cell structure	2	2	115.98	0.024139	0.617841	235978.4	8356.416	89594.26	221008.9	177185.4	4680.401	33882.93	127114.6
gi 15239652	AT5G54500	gi 15239652	flavodoxin-like quinone reductase 1 [Arabidopsis thaliana]	Metabolism	2	2	65.43	0.03135	0.552671	184945.3	194206	233679.6	337737.8	114764.7	154883.5	123227.1	132476
gi 7525018	ATCG00120	gi 7525018	ATP synthase CF1 alpha subunit [Arabidopsis thaliana]	Energy	3	3	150.37	0.028914	1.594581	192783	75451.15	69608.99	63471.04	254756.4	175391.8	120488.9	89290.82
gi 20196856	At2g33240	gi 20196856	putative myosin heavy chain [Arabidopsis thaliana]	cell structure	2	2	20.74	0.02036	2.912006	351243.2	552616	477373.4	152216.4	1367769	1044900	1137559	915184.4
gi 7576220	At3g48820	gi 7576220	putative protein [Arabidopsis thaliana]	protein destination and storage	1	1	22.05	0.027031	3.039233	666518.2	1345827	1001001	592580.2	4017382	2120833	3099217	1721820
gi 15237248	At5g16020	gi 15237248	gamete-expressed 3 [Arabidopsis thaliana]	unknown	1	1	17.67	0.008409	3.064953	243867.1	358599.6	350884.2	195252.9	1088553	717569.9	943827.3	770466.8
gi 30688577	At5g22650	gi 30688577	histone deacetylase HDT2 [Arabidopsis thaliana]	transcription	1	1	25.31	0.024595	0.017587	153.0426	525.4663	9337.005	3175.853	0	0	0	231.9903
gi 6692674	AT1G06700	gi 6692674	F12K11.1 [Arabidopsis thaliana]	Protein destination and storage	1	1	42.62	0.013555	1.715684	30725.64	27843.5	19617.98	23234.6	53711.04	37439.78	43816.67	39040.11
gi 9802532	AT1G27400	gi 9802532	F17L21.19 [Arabidopsis thaliana]	Protein synthesis	1	1	30.88	0.023958	1.537213	9353.885	7238.581	4719.726	6814.133	11634.07	11640.44	9843.065	10118.55
gi 14334818	AT1G57720	gi 14334818	putative elongation factor 1B gamma [Arabidopsis thaliana]	Protein synthesis	1	1	33.67	0.022016	0.017636	2231.669	5852.288	2935.682	4873.771	0	0	280.2956	0
gi 11994683	AT3G17450	gi 11994683	unnamed protein product [Arabidopsis thaliana]	Transcription	2	2	22.06	0.033576	1.569005	3319994	4413363	3578528	2015238	6883936	5867541	4457558	3701292
gi 26451217	AT3G19130	gi 26451217	unknown protein [Arabidopsis thaliana]	Cell growth/division	1	1	27.06	0.002236	1.544406	122094.4	79835.84	75765.83	60622.07	173241.6	133332.2	112167.3	103759.5

Accession	AGI	Accession	Protein description	Functional categories	Peptide count	Peptides used for quantitation	Confidence score	Anova (p)	CA/Control	Normalized abundance							
										Control				CA			
										Control 1	Control 2	Control 3	Control 4	CA 1	CA 2	CA 3	CA 4
gi 16400	AT3G44310	gi 16400	nitrilase I [Arabidopsis thaliana]	Signal transduction	2	2	45.17	0.008566	0.231807	2044.885	4234.238	3219.134	10064.66	529.8979	1221.79	1333.75	1449.376
gi 42572885	AT4G12735	gi 42572885	uncharacterized protein [Arabidopsis thaliana]	Unknown	1	1	76.53	0.008166	14.81695	4883.867	835.1235	1165.199	6146.737	47205.13	39302.79	55585.53	50985.18
gi 15235439	AT4G37100	gi 15235439	catalytic/ pyridoxal phosphate binding protein [Arabidopsis thaliana]	Unknown	1	1	33.37	0.017192	1.907637	2190.935	3149.275	4232.356	6267.527	5932.932	5814.16	9753.614	8716.44
gi 166765	AT5G02500	gi 166765	heat shock protein HSP70-1 [Arabidopsis thaliana]	Protein destination and storage	1	1	68.23	0.025324	0.483494	13599.95	22175.57	27182.16	21839.28	6281.454	6415.977	12487.76	15813.62
gi 13605831	AT5G02870	gi 13605831	AT5g02870/F9G14_180 [Arabidopsis thaliana]	Protein synthesis	1	1	22.15	0.014612	0.555203	35925.49	27892.9	31316.69	22267.47	14606.98	19093.18	19967.76	11514.33
gi 15240969	AT5G38650	gi 15240969	Proteasome maturation factor UMP1 [Arabidopsis thaliana]	Protein destination and storage	1	1	15.56	0.013244	0.384532	20962.27	32474.99	43081.95	44028.9	12801.11	12063.61	17756.23	11424.23
gi 15238845	AT5G47930	gi 15238845	40S ribosomal protein S27-3 [Arabidopsis thaliana]	Protein synthesis	1	1	38.23	0.03137	0.080509	5983.823	6289.397	1198.173	13483.06	891.4005	445.5452	499.0585	334.0639
gi 8953720	AT5G52650	gi 8953720	unnamed protein product [Arabidopsis thaliana]	Protein synthesis	1	1	40.15	0.047837	0.189354	23256.7	17698.52	7831.248	25209.02	4776.549	7872.662	850.5059	511.6064



Supplementary Table 3-7 Both CA- and ABA-responsive plasma membrane proteins at the stationary phase

AGI	GI	Protein description	Functional category	Anova (p)/ABA	ABA/Control	Anova (p)/CA	CA/Control
AT5G17460	gi 9755770	hypothetical protein [Arabidopsis thaliana]	Signal transduction	0.000526977	74.8876284	0.00017478	91.9621037
AT3G44310	gi 16400	nitrilase I [Arabidopsis	Signal transduction	0.016553325	5.27993112	0.00856619	0.2318066
AT5G52650	gi 8953720	unnamed protein product [Arabidopsis thaliana]	Transcription	0.011840862	0.16609206	0.04783698	0.18935376
AT1G32860	gi 6910583	CDS [Arabidopsis thaliana]	Cell structure	0.017604565	0.28039521	0.00834733	2.4353858
AT4G00340	gi 6049881	Similar to receptor-like protein kinase precursor; F5I10.19 [Arabidopsis thaliana]	Cell structure	0.021237741	0.31116971	0.02134908	0.4365769

Supplementary Table S4-1 Overlapping of microassay and proteome data at lag phase.

ATG	Protein description	Functional categories	Proteins ratios	Log <sub>10</sub> <sup>[protein ratio]</sup>	mRNA ratios	Log <sub>10</sub> <sup>[transcript ratio]</sup>	PTMs
At4g29090	putative non-LTR retroelement reverse transcriptase	cell growth/division	0.26	-0.59	0.10	-1.02	
At3g51670	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	transporters	0.29	-0.54	0.18	-0.73	
At5g56380	unnamed protein product	protein destination and storage	0.31	-0.51	0.35	-0.45	
At4g27595	unknown protein	unknown	0.41	-0.39	0.38	-0.42	
At4g28490	HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	signal transduction	0.17	-0.78	0.45	-0.35	
At5g10080	aspartyl protease family protein	protein destination and storage	0.27	-0.58	0.47	-0.33	
At5g09600	putative protein	energy	0.40	-0.39	0.47	-0.33	
At1g09520	protein binding / zinc ion binding	unknown	0.41	-0.39	0.49	-0.31	
At3g24255	F14D16.18	unknown	0.36	-0.45	0.49	-0.31	
At4g03230	putative receptor kinase	cell structure	0.22	-0.65	0.53	-0.28	
At1g04730	AAA-type ATPase family protein	protein destination and storage	0.45	-0.35	0.53	-0.27	
At2g17820	ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase	signal transduction	0.32	-0.50	2.26	0.35	phosphoprotein
At3g15030	unnamed protein product	transcription	0.46	-0.34	2.71	0.43	
At5g56460	protein kinase, putative	protein destination and storage	0.16	-0.80	4.81	0.68	phosphoprotein
At5g01520	zinc finger (C3HC4-type RING finger) family protein	protein destination and storage	0.31	-0.50	66.98	1.83	
At4g20830	FAD-binding domain-containing protein	cell structure	3.31	0.52	0.21	-0.69	phosphoprotein
At3g25290	auxin-responsive family protein	signal transduction	3.56	0.55	0.21	-0.68	
At5g55730	FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1)	cell structure	4.36	0.64	0.30	-0.53	GPI anchored
At2g01630	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	cell structure	2.89	0.46	0.44	-0.36	GPI anchored
At5g25090	plastocyanin-like domain-containing protein	cell structure	4.65	0.67	0.45	-0.35	GPI anchored
At3g47950	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	transporters	2.27	0.36	0.51	-0.29	phosphoprotein
At5g61130	PDCB1 (PLASMODESMATA CALLOSE-BINDING PROTEIN 1); callose binding / polysaccharide binding	cell structure	2.75	0.44	0.51	-0.29	GPI anchored
At1g43710	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding	metabolism	3.75	0.57	0.56	-0.25	
At1g79560	Is a member of PF 00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this gene	protein destination and storage	2.65	0.42	0.57	-0.25	
At4g25240	Pollen-specific protein precursor like	cell structure	3.27	0.51	0.61	-0.22	GPI anchored
At5g55480	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	metabolism	4.19	0.62	0.62	-0.21	GPI anchored and phosphoprotein

ATG	Protein description	Functional categories	Proteins ratios	Log <sub>10</sub> <sup>[protein ratio]</sup>	mRNA ratios	Log <sub>10</sub> <sup>[transcript ratio]</sup>	PTMs
At3g17840	RLK902; ATP binding / kinase/ protein serine/threonine kinase	signal transduction	2.62	0.42	0.62	-0.21	phosphoprotein
At4g29410	60S ribosomal protein L28 (RPL28C)	protein synthesis	3.26	0.51	0.66	-0.18	phosphoprotein
At1g53840	ATPME1; pectinesterase	cell structure	2.95	0.47	0.67	-0.18	phosphoprotein
At2g13820	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	cell structure	6.29	0.80	0.67	-0.17	GPI anchored and phosphoprotein
At4g35100	plasma membrane intrinsic protein PIP3	transporters	2.35	0.37	0.68	-0.17	GPI anchored and phosphoprotein
At5g04885	glycosyl hydrolase family 3 protein	cell structure	3.90	0.59	0.69	-0.16	GPI anchored
At1g34430	F12K21.24	metabolism	3.18	0.50	0.72	-0.14	phosphoprotein
At5g35530	40S ribosomal protein S3 (RPS3C)	protein synthesis	2.27	0.36	0.73	-0.13	
At1g74020	strictosidine synthase	secondary metabolism	5.34	0.73	1.61	0.21	
At1g15530	receptor lectin kinase, putative	signal transduction	2.60	0.42	1.89	0.28	
At4g40020	unknown protein	unknown	3.95	0.60	1.94	0.29	
At2g27260	unknown protein	unknown	5.77	0.76	2.02	0.31	
At5g43980	unnamed protein product	signal transduction	2.30	0.36	2.06	0.31	
At4g17530	GTP-binding RAB1C like protein	signal transduction	3.75	0.57	2.13	0.33	
At3g61260	DNA-binding family protein / remorin family protein	transcription	2.54	0.40	2.15	0.33	
At2g39360	protein kinase family protein	protein destination and storage	3.95	0.60	2.16	0.33	
At4g08850	receptor protein kinase-like protein	protein destination and storage	2.64	0.42	2.16	0.33	
At3g46290	protein kinase, putative	protein destination and storage	3.18	0.50	2.34	0.37	
At3g51550	FER (FERONIA); kinase/ protein kinase	signal transduction	2.84	0.45	2.39	0.38	
At2g38940	ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	transporters	2.81	0.45	2.47	0.39	
At5g17460	hypothetical protein	unknown	20.65	1.31	2.51	0.40	
At5g60270	lectin protein kinase family protein	signal transduction	2.36	0.37	2.53	0.40	
At2g41410	calmodulin like protein	signal transduction	3.04	0.48	2.57	0.41	
At4g32300	S-receptor kinase -like protein	signal transduction	2.64	0.42	2.63	0.42	
At2g42360	zinc finger (C3HC4-type RING finger) family protein	protein destination and storage	20.03	1.30	2.67	0.43	
At1g63500	ATP binding / binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	protein destination and storage	2.29	0.36	2.68	0.43	
At3g54200	unknown protein	metabolism	2.86	0.46	3.07	0.49	
At5g58670	PLC1 (PHOSPHOLIPASE C 1); phospholipase C	signal transduction	3.22	0.51	3.52	0.55	
At1g69480	hypothetical protein	transporters	3.91	0.59	3.79	0.58	
At5g44130	FLA13 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 13 PRECURSOR)	cell structure	6.00	0.78	3.95	0.60	
At4g31140	glycosyl hydrolase family 17 protein	cell structure	2.39	0.38	4.25	0.63	
At5g17820	peroxidase 57 (PER57) (P57) (PRXR10)	cell structure	4.46	0.65	4.27	0.63	
At5g57110	Ca <sup>2+</sup> -transporting ATPase-like protein	transporters	2.67	0.43	4.91	0.69	

ATG	Protein description	Functional categories	Proteins ratios	Log <sub>10</sub> <sup>[protein ratio]</sup>	mRNA ratios	Log <sub>10</sub> <sup>[transcript ratio]</sup>	PTMs
At5g58070	TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter	metabolism	2.91	0.46	5.16	0.71	
At4g38580	ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding	signal transduction	2.18	0.34	5.81	0.76	
At1g45688	unknown protein	intracellular traffic	2.00	0.30	5.95	0.77	
At3g45600	TET3 (TETRASPANIN3)	signal transduction	2.48	0.39	6.12	0.79	
At1g53430	Contains similarity to receptor-like serine/threonine kinase from Arabidopsis thaliana gb AF024648 and contains multiple leucine rich PF 00560 repeats and protein kinase PF 00069 domain. ESTs gb T04455, gb N38129 come from this gene	protein destination and storage	3.04	0.48	6.25	0.80	
At5g26340	AT5g26340/F9D12_17	transporters	3.36	0.53	6.88	0.84	
At1g30360	ERD4 (early-responsive to dehydration 4)	disease/defence	2.35	0.37	7.52	0.88	
At4g27520	unknown	cell structure	4.44	0.65	9.76	0.99	
At5g06320	NHL3	signal transduction	3.51	0.55	9.92	1.00	
At3g53990	universal stress protein (USP) family protein	disease/defence	4.18	0.62	11.65	1.07	
At1g69870	putative peptide transporter; 37139-33250	transporters	3.97	0.60	16.87	1.23	
At1g20440	cor47	disease/defence	3.81	0.58	374.40	2.57	

ATG	Note	Proteins ratios	mRNA ratios	Protein description	Functional categories	Note
At2g17820	phosphoprotein	0.316536005	2.2644336	ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase [Arabidopsis thaliana]	signal transduction	phosphoprotein
At3g15030		0.455722159	2.7103732	unnamed protein product [Arabidopsis thaliana]	transcription	
At5g56460	phosphoprotein	0.157750918	4.8103433	protein kinase, putative [Arabidopsis thaliana]	protein destination and storage	phosphoprotein
At5g01520		0.312839234	66.981964	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	protein destination and storage	
At4g20830	phosphoprotein	3.313825187	0.20581397	FAD-binding domain-containing protein [Arabidopsis thaliana]	cell structure	phosphoprotein
At3g25290		3.559441461	0.20995402	auxin-responsive family protein [Arabidopsis thaliana]	signal transduction	
At5g55730	GPI anchored	4.356117465	0.29664287	FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1) [Arabidopsis thaliana]	cell structure	GPI anchored
At2g01630	GPI anchored	2.889467465	0.43723223	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana]	cell structure	GPI anchored
At5g25090	GPI anchored	4.646632028	0.4461005	plastocyanin-like domain-containing protein [Arabidopsis thaliana]	cell structure	GPI anchored
At3g47950	phosphoprotein	2.267726773	0.5133308	AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana]	transporters	phosphoprotein
At5g61130	GPI anchored	2.749823765	0.5133353	PDCB1 (PLASMODESMATA CALLOSE-BINDING PROTEIN 1); callose binding / polysaccharide binding [Arabidopsis thaliana]	cell structure	GPI anchored
At1g43710		3.752723405	0.56317514	emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	metabolism	
At1g79560		2.651965953	0.5687288	Is a member of PF00004 ATPases associated with various cellular activities (AAA) family. ESTs gb T43031, gb R64750, gb AA394742 and gb AI100347 come from this gene [Arabidopsis thaliana]	protein destination and storage	

ATG	Note	Proteins ratios	mRNA ratios	Protein description	Functional categories	Note
At4g25240	GPI anchored	3.265321905	0.60521334	Pollen-specific protein precursor like [Arabidopsis thaliana]	cell structure	GPI anchored
At5g55480	GPI anchored and phosphoprotein	4.189388461	0.61562085	SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	metabolism	GPI anchored and phosphoprotein
At3g17840	phosphoprotein	2.617097957	0.6179531	RLK902; ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	signal transduction	phosphoprotein
At4g29410	phosphoprotein	3.255749957	0.6551995	60S ribosomal protein L28 (RPL28C) [Arabidopsis thaliana]	protein synthesis	phosphoprotein
At1g53840	phosphoprotein	2.954015918	0.6674815	ATPME1; pectinesterase [Arabidopsis thaliana]	cell structure	phosphoprotein
At2g13820	GPI anchored and phosphoprotein	6.294512615	0.6730967	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	cell structure	GPI anchored and phosphoprotein
At4g35100	GPI anchored and phosphoprotein	2.346730803	0.6765681	plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]	transporters	GPI anchored and phosphoprotein
At5g04885	GPI anchored	3.898181883	0.6948865	glycosyl hydrolase family 3 protein [Arabidopsis thaliana]	cell structure	GPI anchored
At1g34430	phosphoprotein	3.175399134	0.7164539	F12K21.24 [Arabidopsis thaliana]	metabolism	phosphoprotein
At5g35530		2.2690435	0.7339936	40S ribosomal protein S3 (RPS3C) [Arabidopsis thaliana]	protein synthesis	