Protein Group 1

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	25	61.83	408.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1342.6006	2683.1856	2683.0537	49.15	2	4.63	2.12	ALDFILGWHLDTTTFGDYPQIMK	LYK	rep3
1341.6643	2681.313	2683.0537	648.77	2	3.99	2.2	ALDFILGWHLDTTTFGDYPQIMK	LYT	rep1
594.3552	1780.0422	1779.85	108.01	3	4.73	2.84	CNNDNGDVAVDFFHR : +57.05000 (C1)	LYK	rep1
594.1501	1779.427	1779.85	237.66	3	4.54	2.38	CNNDNGDVAVDFFHR : +57.05000 (C1)	LYT	rep1
710.0968	1418.178	1417.6152	397	2	3.51	1.31	DFLSQGVRPSALK	LYK	rep3
710.4241	1418.8326	1417.6152	858.72	2	1.95	0.25	DFLSQGVRPSALK	LYT	rep1
345.8866	1034.6363	1034.2172	405.29	3	1.9	0.37	DIVGHRLPK	LYK	rep3
517.9009	1033.7862	1034.2172	416.72	2	1.64	0.61	DIVGHRLPK	LYT	rep1
1219.1339	3654.3783	3654.9197	148.13	3	3.97	2.19	DKYANPEIMIMENGYGEELGASDSVAVGTADHNR	LYT	rep3
797.5316	2389.5714	2389.6687	40.72	3	4.22	2.23	EKGVSQAGVQFYHDLIDELIK	LYK	rep1
797.4911	2389.4498	2389.6687	91.6	3	3.61	1.67	EKGVSQAGVQFYHDLIDELIK	LYT	rep2
776.9065	1551.7974	1552.6449	545.83	2	3.44	1.61	EYADFVFQEYGGK	LYT	rep2
776.9207	1551.8257	1552.6449	527.59	2	1.27	0.27	EYADFVFQEYGGK	LYK	rep2
576.7	1151.3843	1151.3146	60.58	2	2.91	1.3	FGLYYVDFK	LYK	rep1
576.6324	1151.2491	1151.3146	56.9	2	2.31	0.97	FGLYYVDFK	LYT	rep2
1008.079	3021.2135	3022.2141	331.09	3	5.8	3.3	GGKIGIAHSPAWFEAHDLADSQDGASIDR	LYT	rep1
626.0041	1249.9925	1250.4297	349.68	2	3.31	1.14	GPALWDIYCR : +57.05000 (C9)	LYK	rep1
626.5528	1251.0899	1250.4297	527.95	2	2.89	0.71	GPALWDIYCR : +57.05000 (C9)	LYT	rep2
1066.9229	2131.8301	2132.3813	258.5	2	4.41	0	GVSQAGVQFYHDLIDELIK	LYK	rep2
1067.5354	2133.0552	2132.3813	316.02	2	3.46	0	GVSQAGVQFYHDLIDELIK	LYT	rep2

772.6626	1543.3096	1543.8128	325.92	2	3.25	1.49	HLLSMQEAVCIDK : +57.05000 (C10)	LYK	rep2
772.9092	1543.8028	1543.8128	6.47	2	3.21	1.56	HLLSMQEAVCIDK : +57.05000 (C10)	LYT	rep3
797.8588	2390.5528	2390.6186	27.53	3	6.27	4.09	HWITFNEPWVFSHAGYDVGK	LYK	rep3
797.7006	2390.0782	2390.6186	226.06	3	5. 46	3.58	HWITFNEPWVFSHAGYDVGK	LYT	rep3
840.3149	2517.9213	2518.7917	345.56	3	4.84	2.85	HWITFNEPWVFSHAGYDVGKK	LYT	rep2
840.3801	2518.1169	2518.7917	267.92	3	4.72	2.9	HWITFNEPWVFSHAGYDVGKK	LYK	rep2
927.7281	2780.161	2779.9382	80.13	3	6.59	3.4	IGIAHSPAWFEAHDLADSQDGASIDR	LYK	rep3
927.5631	2779. 665	2779.9382	97.98	3	5.72	3.6	IGIAHSPAWFEAHDLADSQDGASIDR	LYT	rep2
430.9002	859.7847	860.0389	295.6	2	2.46	0.74	MSIAWPR	LYT	rep1
431.0847	860.1538	860.0389	133.62	2	2.29	0.76	MSIAWPR	LYK	rep2
751.2833	2250.8265	2251.5076	302.49	3	5.09	2.84	NAQNYAIGSKPLTAALNVYSR	LYK	rep2
751.8384	2252.4917	2251.5076	437.09	3	4.9	2.9	NAQNYAIGSKPLTAALNVYSR	LYT	rep2
1124.6803	3371.0174	3370.6047	122.44	3	5.96	3.1	NGITPFVTVFHWDTPQDLEDEYGGFLSER	LYK	rep3
1124.5702	3370.6871	3370.6047	24.44	3	4.42	2.05	NGITPFVTVFHWDTPQDLEDEYGGFLSER	LYT	rep2
476.2345	950.4533	950.0107	465.9	2	2.05	0.49	NLNTDAFR	LYT	rep1
475.9542	949.8927	950.0107	124.14	2	1.27	0.28	NLNTDAFR	LYK	rep2
902.9856	2705.9333	2706.9702	383.05	3	7.95	5.01	SGYEAYLVTHNLLISHAEAVEAYR	LYK	rep2
903.0879	2706.2402	2706.9702	269.68	3	6.39	3.79	SGYEAYLVT HNLLISHAEAVEAYR	LYT	rep3
945.8218	2834.4419	2835.1431	247.32	3	7.02	4.78	SGYEAYLVTHNLLISHAEAVEAYRK	LYK	rep3
945.741	2834.1994	2835.1431	332.83	3	5.43	3.64	SGYEAYLVTHNLLISHAEAVEAYRK	LYT	rep2
873.2347	2616.6807	2617.9233	474.64	3	5.51	3.42	VKHWITFNEPWVFSHAGYDVGK	LYK	rep3
874.1135	2619.3171	2617.9233	532.4	3	5.07	3	VKHWITFNEPWVFSHAGYDVGK	LYT	rep1
763.8975	1525.7793	1523.715	1354.83	2	1.81	0.31	WMQDSLITWESK	LYT	rep3
1180.7328	3539.1749	3539.8318	185.57	3	4.35	2.72	YANPEIMIMENGYGEELGASDSVAVGTADHNRK	LYT	rep3
1180.934	3539.7784	3539.8318	15.08	3	3.62	1.81	YANPEIMIMENGYGEELGASDSVAVGTADHNRK	LYK	rep1
390.2817	1167.8216	1167.3805	377.83	3	2.93	0.58	YKEDIQLMK	LYK	rep1
390.161	1167.4596	1167.3805	67.74	3	2.82	0.28	YKEDIQLMK	LYT	rep2

Matching Genes:

NP_187537.1 (PYK10 (phosphate starvation-response 3.1); hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana])

Protein Group 2

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	17	78.19	232.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
683.482	1364.9483	1365.5021	405.55	2	2.13	0.57	EEGHKIVGFHGR	LYK	rep3
683.594	1365.1724	1365.5021	241.42	2	1.87	0.53	EEGHKIVGFHGR	LYT	rep1
651.2762	1950.8053	1951.0593	130.21	3	4.16	1.67	FVYDKSPEEVTGEEHGK	LYK	rep1
651.2545	1950.7401	1951.0593	163.62	3	3.85	1.68	FVYDKSPEEVTGEEHGK	LYT	rep3
844.0955	1686.1753	1686.741	335.3 4	2	4.2	2.17	GANLWDDGSTHDAVTK	LYT	rep1
844.6134	1687.2112	1686.741	278.8	2	3.78	1.97	GANLWDDGSTHDAVTK	LYK	rep2
1290.7845	3869.3302	3870.344	261.95	3	5.99	3.85	GRVLPADPFVINHPDEHLVSVEGWYSPEGIIQGIK	LYK	rep3
1290.629	3868.8636	3870.344	382.49	3	5.85	3.68	GRVLPADPFVINHPDEHLVSVEGWYSPEGIIQGIK	LYT	rep1
698.8286	1395.6416	1395.6299	8.43	2	2.38	0.26	IFGSDGSVITMLR	LYK	rep2
364.8909	1091.6491	1091.2687	348.65	3	2.71	1.4	IGVHVRPLSN	LYK	rep3
364.9111	1091.7099	1091.2687	404.35	3	2.1	0.96	IGVHVRPLSN	LYT	rep2
1594.6333	3187.251	3188.6016	423.55	6.37	4.58		IIGFHGSAGGNLNSLGAYFAPLTTTTPLTPAK	LYK	rep3
1063.5367	3187.5868	3188.6016	318.26	3	4.91	2.73	IIGFHGSAGGNLNSLGAYFAPLTTTTPLTPAK	LYT	rep2
714.4014	2140.1806	2141.4314	584.08	3	4.98	2.7	IQLAAGIDGIQYVQFDYVK	LYK	rep3
1072.3069	2142.5982	2141.4314	544.87	2	2.02	0.59	IQLAAGIDGIQYVQFDYVK	LYT	rep3
1106.2474	3315.7188	3316.7744	318.25	3	4.73	2.49	KIIGFHGSAGGNLNSLGAYFAPLTTTTPLTPAK	LYK	rep1
1106.9022	3317.6832	3316.7744	274	3	4.18	1.9 8	KIIGFHGSAGGNLNSLGAYFAPLTTTTPLTPAK	LYT	rep3

688.4089	2062.2033	2062.2463	20.85	3	3.79	1.6	KTSDVIGSDEGTHFTLQVK	LYT	rep1
688.4073	2062.1986	2062.2463	23.16	3	2.13	0.34	KTSDVIGSDEGTHFTLQVK	LYK	rep1
782.1143	1562.2129	1562.7723	357.95	2	4.31	1.65	KVYVGQAQDGISAVK	LYK	rep3
782.1397	1562.2637	1562.7723	325.46	2	4.26	1.97	KVYVGQAQDGISAVK	LYT	rep1
1201.5432	2401.0708	2401.6365	235.52	2	2.51	1.33	QTSPPFGLEAGTVFELKEEGHK	LYT	rep2
1201.5642	2401.1128	2401.6365	218.03	2	2.25	0.93	QTSPPFGLEAGTVFELKEEGHK	LYK	rep1
1537.8743	3073.7329	3073.3281	131.72	2	4.66	2. 58	STLLGFEEFVLDYPSEYITAVDGTYDK	LYK	rep3
1537.3562	3072.6968	3073.3281	205.41	2	3.61	1.96	STLLGFEEFVLDYPSEYITAVDGTYDK	LYT	rep3
1484.6307	4450.8687	4450.9433	16.76	3	5.51	3.23	STLLGFEEFVLDYPSEYITAVDGTYDKIFGSDGSVITMLR	LYK	rep1
1484.6971	4451.068	4450.9433	28	3	5.18	2.95	STLLGFEEFVLDYPSEYITAVDGTYDKIFGSDGSVITMLR	LYT	rep2
967.626	1933.2364	1934.0734	432.76	2	3.71	1.8	TSDVIGSDEGTHFTLQVK	LYK	rep3
967.7779	1933.5401	1934.0734	275.73	2	3.59	1.82	TSDVIGSDEGTHFTLQVK	LYT	rep3
1219.4642	3655.3692	3657.1062	474.96	3	6.94	4.91	VLPADPFVINHPDEHLVSVEGWYSPEGIIQGIK	LYK	rep3
1219.8973	3656.6685	3657.1062	119.67	3	5.84	3.75	VLPADPFVINHPDEHLVSVEGWYSPEGIIQGIK	LYT	rep3
718.7205	1435.4253	1434.5994	575.75	2	3.46	1.38	VYVGQAQDGISAVK	LYT	rep3
718.1001	1434.1846	1434.5994	289.1	2	1.45	0.3	VYVGQAQDGISAVK	LYK	rep2

Matching Genes:

NP_001030710.1 (PBP1 (PYK10-BINDING PROTEIN 1) [Arabidopsis thaliana])

Protein Group 3

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	20	39.74	108.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1192.7984	2383.5811	2384.7139	475.01	2	2.4	0.99	AAGATWIQLDEPVLVMDLEGQK	LYT	rep2
1038.3452	2074.6748	2075.2915	297.14	2	4.1	2.57	ALAGQKDEALFSANAAALASR	LYK	rep1
714.4457	2140.3136	2140.571	120.28	3	2.57	0.82	ALGVDTVPVLVGPVSYLLLSK	LYT	rep2
1081.386	2160.7564	2161.6013	390.88	2	3.25	1.76	AMTVFWSAMAQSMTSRPMK	LYT	rep2
1081.4846	2160.9536	2161.6013	299.62	2	2.62	1.07	AMTVFWSAMAQSMTSRPMK	LYK	rep2
600.3817	1198.7478	1199.316	473.76	2	1.91	0.38	FALESFWDGK	LYT	rep1
706.7415	1411.4673	1411.609	100.36	2	2.5	1.02	GGIGVIQIDEAALR	LYT	rep3
706.7199	1411.4241	1411.609	130.98	2	2.4	1.18	GGIGVIQIDEAALR	LYK	rep2
591.698	1181.3804	1181.3454	29.59	2	2.55	0.84	GVTAFGFDLVR	LYT	rep2
724.705	1447.3943	1446.6753	497.04	2	2.33	1.02	HETCYQIALAIK : +57.05000 (C4)	LYK	rep2
802.3881	2404.1407	2404.6574	214.85	3	5.28	3.26	HETCYQIALAIKDEVEDLEK : +57.05000 (C4)	LYT	rep2
802.576	2404.7047	2404.6574	19.68	3	4.78	2.63	HETCYQIALAIKDEVEDLEK : +57.05000 (C4)	LYK	rep2
558.9937	1115.9717	1116.1838	190.03	2	2.17	0.34	IPSSEEIADR	LYT	rep
2559.2543	1115.9717	1116.1838	276.95	2	1.42	0.33	IPSSEEIADR	LYK	rep2
729.7913	1457.5669	1457.5914	16.8	2	2.24	0.81	IPSSEEIADRVNK	LYT	rep2
1635.276	4902.8045	4903.4007	121.58	3	3.52	2.03	ITNCGVQDSTQIHTHMCYSHFNDIIHSIIDMDADVITIENSR : +57.05000 (C4); +57.05000 (C17)	LYK	rep1
1634.9427	4901.8048	4903.4007	325.47	3	3.46	1.45	ITNCGVQDSTQIHTHMCYSHFNDIIHSIIDMDADVITIENSR : +57.05000 (C4); +57.05000 (C17)	LYT	rep3
1219.9036	2437.7915	2438.8708	442.54	2	3.64	1.74	KLNLPILPTTTIGSFPQTVELR	LYT	rep1
1220.3255	2438.6353	2438.8708	96.58	2	3.43	1.97	KLNLPILPTTTIGSFPQTVELR	LYK	rep2

997.5152	1993.0147	1993.1922	89.09	2	4.45	0.68	KSEHAFYLDWAVHSFR	LYK	r ep1
997.3142	1992.6128	1993.1922	290.7	2	4.39	0.68	KSEHAFYLDWAVHSFR	LYT	rep2
1155.7903	2309.565	2310.6977	490.23	2	1.83	0.5 3	LNLPILPTTTIGSFPQTVELR	LYK	rep2
1210.1385	2418.2613	2418.7102	185.61	2	3.45	1.65	NIWANDFAASLSTLQALEGIVGK	LYT	rep2
1210.136	2418.2564	2418.7102	187.62	2	1.26	0.16	NIWANDFAASLSTLQALEGIVGK	LYK	rep2
622.5341	1864.5787	1865.0194	236.3	3	3.87	0.93	SEHAFYLDWAVHSFR	LYT	rep2
622.6361	1864.8848	1865.0194	72.14	3	3.39	0.77	SEHAFYLDWAVHSFR	LYK	rep2
1005.8259	3014.4543	3014.2737	59.93	3	5.77	3.13	WFDTNYHYIVPELGPEVNFSYASHK	LYT	rep3
1005.4741	3013.3989	3014.2737	290.21	3	5.49	2.98	WFDTNYHYIVPELGPEVNFSYASHK	LYK	rep2
830.7138	1659.4119	1658.8186	357.67	2	3.72	1.84	YGAGIGPGVYDIHSPR	LYK	rep1
553.9995	1658.9751	1658.8186	94.32	3	3.35	1.84	YGAGIGPGVYDIHSPR	LYT	rep2
525.0808	1048.146	1048.2373	87.06	2	1.62	0.37	YTEVKPALK	LYK	rep1
524.7666	1047.5176	1048.2373	686.56	2	1.42	0.25	YTEVKPALK	LYT	rep1

Matching Genes:

NP_001078599.1 (ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE) [Arabidopsis thaliana])

Protein Group 4

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	18	52.88	162.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
696.2669	1390.5181	1390.5084	6.97	2	3.68	2.43	AHGGFSVFAGVGER	LYT	rep3
696.0594	1390.1031	1390.5084	291.51	2	3.26	1.99	AHGGFSVFAGVGER	LYK	rep3

933.571	1865.1263	1865.0559	37.73	2	1.58	0.36	DAEGQDVLLFIDNIFR	LYT	rep3
1261.3119	3780.9122	3782.1194	319.18	3	5.6	3.09	ENINSFQGLLDGKYDDLSEQSFYMVGGIDEVVAK	LYT	rep1
1262.2697	3783.7855	3782.1194	440.52	3	5.45	3.3	ENINSFQGLLDGKYDDLSEQSFYMVGGIDEVVAK	LYK	rep2
1270.4095	2538.8033	2539.7829	385.74	2	1.89	0.67	FEDQEGLPPIMTSLEVQDHPTR	LYT	rep1
532.0341	1593.0787	1592.8033	172.88	3	3.74	1.58	GEIKTEHYLPIHR	LYK	rep3
796.8714	1591.7271	1592.8033	675.69	2	2.76	1.12	GEIKTEHYLPIHR	LYT	rep1
1239.6942	3716.0592	3716.084	6.68	3	2.44	0.42	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	LYK	rep2
488.6842	975.3528	975.1464	211.67	2	2.56	0.81	IGLFGGAGVGK	LYT	rep2
488.6369	975.2581	975.1464	114.53	2	2.55	0.73	IGLFGGAGVGK	LYK	rep2
693.6851	1385.3545	1385.5918	171.23	2	2.38	0.96	IMNVLGEPIDER	LYT	rep2
1094.3938	2186.772	2186.4307	156.12	2	3.45	2.12	IPSAVGYQPTLASDLGALQER	LYT	rep2
1094.0428	2186.0699	2186.4307	165.01	2	1.33	0.1	IPSAVGYQPTLASDLGALQER	LYK	rep2
1282.2008	3843.5789	3844.2568	176.34	3	5.61	0.25	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	LYK	rep1
1282.1107	3843.3087	3844.2568	246.64	3	5.29	0.14	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	LYT	rep3
761.6341	1521.2525	1521.8097	366.15	2	3.41	1.58	KVLNTGAPITVPVGR	LYT	rep1
762.2516	1522.4876	1521.8097	445.46	2	3.12	1.21	KVLNTGAPITVPVGR	LYK	rep2
850.7705	1699.5254	1699.9586	254.82	2	4.16	2.17	LVLEVSHHLGQNVVR	LYK	rep1
850.7057	1699.3958	1699.9586	331.08	2	4.08	2.5	LVLEVSHHLGQNVVR	LYT	rep2
624.3185	1869.932	1868.0865	987.87	3	4.33	2.28	MLSPHILGEEHYNTAR	LYK	rep3
934.6748	1867.334	1868.0865	402.83	2	3.46	1.65	MLSPHILGEEHYNTAR	LYT	rep1
891.8325	2672.4741	2673.0139	201.95	3	3.36	1.67	NLQDIIAILGMDELSEDDKLTVAR	LYK	rep3
1031.1936	2060.3716	2061.2583	430.16	2	3.39	1.51	QISELGIYPAVDPLDSTSR	LYT	rep1
389.7349	1166.1811	1165.3061	750.85	3	3.03	1.3	TEHYLPIHR	LYT	rep3
389.3454	1165.0127	1165.3061	251.8	3	2.72	1.4	TEHYLPIHR	LYK	rep2
631.9947	1261.9737	1262.4387	368.37	2	2.5	1.23	TIAMDGTEGLVR	LYT	rep1
633.0215	1264.0274	1262.4387	1258.41	2	1.44	0.18	TIAMDGTEGLVR	LYK	rep3
713.5703	1425.125	1425.6341	357.11	2	4.43	2.63	VGLTGLTVAEYFR	LYK	rep2

713.5891	1425.1626	1425.6341	330.74	2	2.05	0.7	VGLTGLTVAEYFR	LYT	rep2

Matching Genes:

NP_5682 03.1 (ATP synthase beta chain 1, mitochondrial [Arabidopsis thaliana])

Protein Group 5

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	18	61.24	179.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
383.9609	1148.8593	1148.3569	437.51	3	3.08	0.68	AGIALSDKFVK	LYK	rep1
574.9402	1147.8648	1148.3569	428.56	2	2.92	0.53	AGIALSDKFVK	LYT	rep3
868.5367	1735.0577	1734.9337	71.44	2	3.7	1.72	DAPMFVVGVNEHEYK	LYK	rep3
1323.4948	3967.4608	3967.4325	7.12	3	6.06	3.69	DAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAK : +57.05000 (C26); +57.05000 (C30)	LYT	rep2
1323.1307	3966.3687	3967.432 5	268.13	3	4.69	2.83	DAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAK : +57.05000 (C26); +57.05000 (C30)	LYK	rep1
1017.0491	2032.0826	2033.3579	627.21	2	5.42	3	FGIVEGLMTTVHSITATQK	LYK	rep3
1017.4654	2032.9151	2033.3579	217.78	2	4.6	2.93	FGIVEGLMTTVHSITATQK	LYT	rep1
1086.847	2171.6783	2172.2712	272.97	2	2.49	1.05	GILGYTEDDVVSTDFVGDNR	LYT	rep2
417.4959	832.9762	832.9501	31.42	2	2.5	0.43	IGINGFGR	LYK	rep1
417.3536	832.6916	832.9501	310.34	2	2.04	0.13	IGINGFGR	LYT	rep1
393.1338	784.252	783.9653	365.67	2	2.16	0.34	IGRLVAR	LYK	rep3
465.2591	928.5026	928.13 12	400.14	2	2.82	1.19	KVVISAPSK	LYK	rep3
464.9182	927.8207	928.1312	334.54	2	2	0.61	KVVISAPSK	LYT	rep3

406.5302	811.0448	810.9646	98.88	2	1.86	0.42	LTGMSFR	LYT	rep2
881.9978	1761.98	1761.8511	73.19	2	3.15	1.87	LVSWYDNEWGYSSR	L YK	rep3
881.555	1761.0943	1761.8511	429.54	2	1.11	0.13	LVSWYDNEWGYSSR	LYT	rep2
985.9843	2954.9293	2954.1269	271.6	3	3.08	1.43	NPEDIPWAEAGADYVVESTGVFTDKDK	LYK	rep3
985.6543	2953.9394	2954.1269	63.48	3	1.68	0.48	NPEDIPWAEAGADYVVESTGVFTDKDK	LYT	rep1
1125.7771	2249.5386	2250.5136	433.24	2	2.3	0.23	SDLDIVSNASCTTNCLAPLAK : +57.05000 (C11); +57.05000 (C15)	LYT	rep1
1126.3684	2250.7212	2250.5136	92.25	2	2.2	0.36	SDLDIVSNASCTTNCLAPLAK : +57.05000 (C11); +57.05000 (C15)	LYK	rep2
560.1564	1677.4456	1677.0033	263.78	3	4.43	2.43	TLLFGEKPVTVFGIR	LYT	rep3
839.5547	1677.0938	1677.0033	53.97	2	4.3	2.22	TLLFGEKPVTVFG IR	LYK	rep1
750.292	1498.5684	1498.7266	105.53	2	2.77	1.66	VPTVDVSVVDLTVR	LYT	rep2
750.5342	1499.0528	1498.7266	217.66	2	2.7	1.14	VPTVDVSVVDLTVR	LYK	rep3
571.2775	1140.5393	1140.4014	121	2	3.43	1.68	VVDLIVHMSK	LYK	rep1
571.1421	1140.2686	1140.4014	116.42	2	2.1	0.9	VVDLIVHMSK	LYT	rep3
606.57	1211.1243	1211.4796	293.28	2	3.52	1.64	VVDLIVHMSKA	LYT	rep2
839.5197	2515.5355	2516.8772	533.08	3	3.5	1.75	VVISAPSKDAPMFVVGVNEHEYK	LYT	rep1
839.7096	2516.1053	2516.8772	306.68	3	2.08	0.6	VVISAPSKDAPMFVVGVNEHEYK	LYK	rep1
560.4716	1118.9275	1119.191	235.44	2	2.81	1.28	YDSVHGQWK	LYK	rep3
560.5179	1119.0201	1119.191	152.76	2	2. 6	1.23	YDSVHGQWK	LYT	rep3

Matching Genes:

NP_187062.1 (GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana])

Protein Group 6

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	18	61.24	176.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
383.9609	1148.8593	1148.3569	437.51	3	3.08	0.68	AGIALSDKFVK	LYK	rep1
574.9402	1147.8648	1148.3569	428.56	2	2.92	0.53	AGIALSDKFVK	LYT	rep3
868.5367	1735.0577	1734.9337	71.44	2	3.7	1.72	DAPMFVVGVNEHEYK	LYK	rep3
1323.4948	3967.4608	3967.4325	7.12	3	6.06	3.69	DAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAK : +57.05000 (C26); +57.05000 (C30)	LYT	rep2
1323.1307	3966.3687	3967.432 5	268.13	3	4.69	2.83	DAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAK : +57.05000 (C26); +57.05000 (C30)	LYK	rep1
1017.0491	2032.0826	2033.3579	627.21	2	5.42	3	FGIVEGLMTTVHSITATQK	LYK	rep3
1017.4654	2032.9151	2033.3579	217.78	2	4.6	2.93	FGIVEGLMTTVHSITATQK	LYT	rep1
1086.847	2171.6783	2172.2712	272.97	2	2.49	1.05	GILGYTEDDVVSTDFVGDNR	LYT	rep2
417.4959	832.9762	832.9501	31.42	2	2.5	0.43	IGINGFGR	LYK	rep1
417.3536	832.6916	832.9501	310.34	2	2.04	0.13	IGINGFGR	LYT	rep1
393.1338	784.252	783.9653	365.67	2	2.16	0.34	IGRLVAR	LYK	rep3
465.2591	928.5026	928.13 12	400.14	2	2.82	1.19	KVVISAPSK	LYK	rep3
464.9182	927.8207	928.1312	334.54	2	2	0.61	KVVISAPSK	LYT	rep3
406.5302	811.0448	810.9646	98.88	2	1.86	0.42	LTGMSFR	LYT	rep2
881.9978	1761.98	1761.8511	73.19	2	3.15	1.87	LVSWYDNEWGYSSR	L YK	rep3
881.555	1761.0943	1761.8511	429.54	2	1.11	0.13	LVSWYDNEWGYSSR	LYT	rep2
975.4181	2923.2308	2924.1008	297.53	3	3.02	1.08	NPEDIPWGEAGADFVVESTGVFTDKDK	LYK	rep3
1463.1165	2924.2173	2924.1008	39.84	2	1.19	0.11	NPEDIPWGEAGADFVVESTGVFTDKDK	LYT	rep3
1125.7771	2249.5386	2250.5136	433.24	2	2.3	0.23	SDLDIVSNASCTTNCLAPLAK : +57.05000 (C11); +57.05000 (C15)	LYT	rep1
1126.3684	2250.7212	2250.5136	92.25	2	2.2	0.36	SDLDIVSNASCTTNCLAPLAK : +57.05000 (C11); +57.05000 (C15)	LYK	rep2
560.1564	1677.4456	1677.0033	263.78	3	4.43	2.43	TLLFGEKPVTVFGIR	LYT	rep3

839.5547	1677.0938	1677.0033	53.97	2	4.3	2.22	TLLFGEKPVTV FGIR	LYK	rep1
750.292	1498.5684	1498.7266	105.53	2	2.77	1.66	VPTVDVSVVDLTVR	LYT	rep2
750.5342	1499.0528	1498.7266	217.66	2	2.7	1.14	VPTVDVSVVDLTVR	LYK	rep3
571.2775	1140.5393	1140.4014	121	2	3.43	1.68	VVDLIVHMSK	LYK	rep1
571.1421	1140.2686	1140.4014	116.42	2	2.1	0.9	VVDLIVHMSK	LYT	rep3
606.57	1211.1243	1211.4796	293.28	2	3.52	1.64	VVDLIVHMSKA	LYT	rep2
839.5197	2515.5355	2516.8772	533.08	3	3.5	1.75	VVISAPSKDAPMFVVGVNEHEYK	LYT	rep1
839.7096	2516.1053	2516.8772	306.68	3	2.08	0.6	VVISAPSKDAPMFVVGVNEHEYK	LYK	rep1
560.4716	1118.9275	1119.191	235.44	2	2.81	1.28	YDSVHGQWK	LYK	rep3
560.5179	1119.0201	1119.191	152.76	2	2.6	1.23	YDSVHGQWK	LYT	rep3

Matching Genes:

NP_172801.1 (GAPC-2; glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana])

Protein Group 7

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	12	66.77	157.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
694.8766	1387.7376	1388.5592	591.7	2	3.1	1.46	ASAGQFHHMFAGK	LYT	rep3
692.4921	2074.4527	2074.3367	55.95	3	5.79	3.34	ASAGQFHHMFAGKPHHVSK	LYK	rep3
692.5566	2074.6464	2074.3367	149.34	3	4.36	2.08	ASAGQFHHMFAGKPHHVSK	LYT	rep2
1249.5599	3745.6563	3746.9972	357.84	3	5.3	3.19	ASPGNIQSCDLHEGDWGTVGSIVFWNYVHDGEAK : +57.05000 (C9)	LYT	rep3
1250.0868	3747.2369	3746.9972	63.98	3	4.81	2.04	ASPGNIQSCDLHEGDWGTVGSIVFWNYVHDGEAK : +57.05000 (C9)	LYK	rep3
1254.0624	3759.1637	3761.0238	494.59	3	4.7	2.36	ATPGNIQSCDLHEGDWGTVGSIVFWNYVHDGEAK : +57.05000 (C9)	LYK	rep3

1253.9979	3758.9703	3761.0238	546	3	4.42	2.1	ATPGNIQSCDLHEGDWGTVGSIVFWNYVHDGEAK : +57.05000 (C9)	LYT	rep3
830.5576	1659.0996	1659.9214	495.04	2	3.83	2.38	FHHMFAGKPHHVSK	LYK	rep2
830.7055	1659.3953	1659.9214	316.93	2	3.28	2.02	FHHMFAGKPHHVSK	LYT	rep3
923.4713	1844.927	1846.0176	590.75	2	5.17	3.17	HGGPGSIVHWHLEYEK	LYK	rep3
616.3041	1845.8888	1846.0176	69.78	3	4.5	2.58	HGGPGSIVHWHLEYEK	LYT	rep2
619.5101	1855.5069	1855.9693	249.16	3	4.55	2.86	HGGSGSVVHWHFEYEK	LYK	rep2
619.3712	1855.0902	1855.9693	473.7	3	4.53	2.97	HGGSGSVVHWHFEYEK	LYT	rep2
549.3322	1644.973	1644.8733	60.62	3	4	0.44	IEAVDPEKNLITFR	LYK	rep1
549.41	1645.2066	1644.8733	202.66	3	3.31	0.48	IEAVDPEKNLITFR	LYT	rep2
830.2393	1658.4629	1658.9	263.48	2	2.15	1.05	IEAVEPEKNLITFR	LYT	rep2
554.141	1659.3995	1658.9	301.09	3	2.03	0.65	IEAVEPEKNLITFR	LYK	rep1
752.2364	2253.6859	2253.5168	75.01	3	5.22	2.88	INEEVAHPETLLQFAVEVSK	LYK	rep1
1127.2141	2252.4126	2253.51 68	489.99	2	2.88	1.4	INEEVAHPETLLQFAVEVSK	LYT	rep3
1144.9344	3431.7799	3432.7558	284.31	3	3.96	2.09	INEEVAHPETLLQFAVEVSKEIDEHLLAEE	LYK	rep1
1144. 933	3431.7755	3432.7558	285.59	3	3.31	1.79	INEEVAHPETLLQFAVEVSKEIDEHLLAEE	LYT	rep2
1327.6881	3980.0409	3982.309	569.56	3	6.49	4.24	ISDEVAHP ETLLQFCVEVSQEIDEHLLSEEEEVK : +57.05000 (C15)	LYK	rep3
1327.9388	3980.7931	3982.309	380.67	3	4.61	2.85	ISDEVAHPETLLQFCVEVSQEIDEHLLSEEEEVK : +57.05000 (C15)	LYT	rep3

Matching Genes:

NP_001031265.1 (MLP34 (MLP-LIKE PROTEIN 34) [Arabidopsis thaliana])

Protein Group 8

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	15	56.15	111.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error	Charge	Score	Score Delta	Peptide	Gro	Replic

			(ppm)					up	ate
886.8019	2657.3822	2657.9658	219.6	3	3.31	1.16	CNVLVNIEQQSPDIAQGVHGHLTK : +57.05000 (C1)	LYK	rep2
886.8911	2657.6499	2657.9658	118.88	3	3.3	1.74	CNVLVNIEQQSPDIAQGVHGHLTK : +57.05000 (C1)	LYT	rep3
845.1508	1688.2859	1688.8815	352.62	2	2.21	0.92	DDPDFTWEVVKPLK	LYT	rep3
615.8959	1229.7762	1230.5043	591.71	2	3.05	1.35	EHVIKPVIPAK	LYT	rep3
616.0539	1230.0921	1230.5043	334.97	2	2.8	1.15	EHVIKPVIPAK	LYK	rep2
1397.4005	4189.1781	4189.6351	109.09	3	4.11	2.47	EIGFISADVGLDADKCNVLVNIEQQSPDIAQGVHGHLTK : +57.05000 (C16)	LYT	rep2
1397.389	4189.1436	4189.6351	117.31	3	4.03	2.49	EIGFISADVGLDADKCNVLVNIEQQSPDIAQGVHGHLTK : +57.05000 (C16)	LYK	rep1
728.3991	1454.7825	1453.6077	808.23	2	3.79	1.63	FVIGGPHGDAGLTGR	LYK	rep3
728.1792	1454.3428	1453.6077	505.75	2	3.35	1.6	FVIGGPHGDAGLTGR	LYT	rep2
791.2668	1580.5179	1581.7805	798.24	2	3.21	0.97	FVIGGPHGDAGLTGRK	LYK	rep3
791.6436	1581.2715	1581.7805	321.78	2	3.16	1.24	FVIGGPHGDAGLTGRK	LYT	rep1
1203.2942	2404.5728	2405.6301	439.52	2	2.89	1.58	IIIDTYGGWGAHGGGAFSGKDPTK	LYT	rep3
802.4052	2404.192	2405.6301	597.82	3	1.32	0.22	IIIDTYGGWGAHGGGAFSGKDPTK	LYK	rep2
698.3312	2091.9701	2092.3223	168.33	3	4.54	2.5	KIIIDTYGGWGAHGGGAFSGK	LYK	rep3
698.36	2092.0565	2092.3223	127.02	3	3.98	2.12	KIIIDTYGGWGAHGGGAFSGK	LYT	rep3
1224.0038	3668.9879	3671.0901	572.64	3	6.79	0.1	KPEDIGAGDQGHMFGYATDETPELMPLTHVLATK	LYK	rep3
1224.6412	3670.9002	3671.0901	51.7 1	3	4.95	0.4	KPEDIGAGDQGHMFGYATDETPELMPLTHVLATK	LYT	rep3
422.4604	842.9051	842.9864	96.46	2	1.74	0.65	SVVAAGLAR	LYT	rep2
490.5493	979.0829	979.0537	29.85	2	2.05	0.91	TAAYGHFGR	LYK	rep3
490.4787	978.9418	979.0537	114.28	2	1.93	0.84	TAAYGHFGR	LYT	rep3
615.5623	1229.1089	1229.412	246.55	2	2.26	0.81	TCPWLRPDGK : +57.05000 (C2)	LYT	rep3
509.6957	1526.0637	1525.8351	149.87	3	3.74	0.89	TGTIPDKDILVLIK	LYK	rep2
883.9004	2648.6777	2649.8721	450.72	3	5.18	2.81	VHTVLISTQHDETVTNDEIAADLK	LYT	rep1
883.871	2648.5894	2649.8721	484.03	3	3.36	1.1	VHTVLISTQHDETVTNDEIAADLK	LYK	rep3
881.6313	1761.2469	1761.8957	368.28	2	2.85	0.99	YLDDNTIFHLNPSGR	LYK	rep2

881.7307	1761.4458	1761.8957	255.35	2	2.72	1.06	YLDDNTIFHLNPSGR	LYT	rep3

Matching Genes:

NP_181225.1 (MAT3 (METHIONINE ADENOSYLTRANSFERASE 3); methionine adenosyltransferase [Arabidopsis thaliana])

Protein Group 9

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	16	50	75.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
552.0013	1101.9869	1101.2439	674.66	2	1.73	0.44	AGWGVMTSHR	LYK	rep1
551.5285	1101.0413	1101.2439	183.96	2	1.58	0.34	AGWGVMTSHR	LYT	rep3
775.5354	1549.0552	1549.8199	493.43	2	2.59	1.17	AVGNVNNIIGPALIGK	LYT	rep2
775.7251	1549.4346	1549.8199	248.63	2	1.7	0.45	AVGNVNNIIGPALIGK	LYK	rep2
1585.1583	4752.4515	4753.2663	171.42	3	3.21	1.71	AVGNVNNIIGPALIGKDPTQQTAIDNFMVHELDGTQNEWGWCK : +57.05000 (C42)	LYT	rep2
1585.1017	4752.2816	4753.2663	207.17	3	2.74	1.38	AVGNVNNIIGPALIGKDPTQQTAIDNFMVHELDGTQNEWGWCK : +57.05000 (C42)	LYK	rep1
1074.3453	3220.0125	3221.4612	449.69	3	6.36	4.17	DPTQQTAIDNFMVHELDGTQNEWGWCK : +57.05000 (C26)	LYK	rep1
1074.7582	3221.2511	3221.4612	65.23	3	4.57	2.6	DPTQQTAIDNFMVHELDGTQNEWGWCK : +57.05000 (C26)	LYT	rep1
840.9145	1679.8133	1680.8209	599.49	2	3.38	1.27	GNPTVEVDIHTSNGIK	LYT	rep1
518.0979	1034.1802	1034.1739	6.07	2	3.11	1.36	HIANLAGNPK	LYK	rep3
517.9981	1033.9805	1034.1739	187.04	2	1.78	0.55	HIANLAGNPK	LYT	rep2
1003.023	2004.0303	2004.3011	135.12	2	2.89	1.32	IVLPVPAFNVINGGSHAGNK	LYK	rep2
1002.7207	2003.4258	2004.3011	436.72	2	1.97	0.92	IVLPVPAFNVINGGSHAGNK	LYT	rep2

410.9557	1229.8438	1229.4169	347.25	3	2.89	0.75	KAGWGVMTSHR	LYK	rep3
410.8776	1229.6094	1229.4169	156.61	3	2.61	0.5	KAGWGVMTSHR	LYT	rep2
927.8659	1853.7161	1853.2615	245.32	2	1.47	0.4	LAMQEFMILPVGAASFK	LYT	rep2
771.9559	2312.8443	2312.8242	8.7	3	3.04	1.12	LAMQEFMILPVGAASFKEAMK	LYK	rep3
771.6283	2311.8614	2312.8242	416.29	3	1.87	0.35	LAMQEFMILPVGAASFKEAMK	LYT	rep3
751.7813	1501.5469	1499.8228	1149.57	2	2.15	1.07	LGANAILAVSLAVCK : +57.05000 (C14)	LYK	rep3
606.8026	1211.5896	1212.4261	689.94	2	3.07	1.29	MGVEVYHHLK	LYK	rep2
607.0243	1212.033	1212.4261	324.26	2	3.06	1.38	MGVEVYHHLK	LYT	rep2
1001.4683	3001.3813	3001.1838	65.8	3	3	1.37	SFVAEYPIVSIE DPFDQDDWEHYAK	LYT	rep1
1501.3711	3000.7266	3001.1838	152.35	2	1.87	0.56	SFVAEYPIVSIEDPFDQDDWEHYAK	LYK	rep2
1126.5865	2251.1573	2252.4409	569.89	2	2.85	1	SGETEDTFIADLAVGLSTGQIK	LYK	rep3
1126.8814	2251.7471	2252.4409	308.02	2	1.31	0.13	SGETEDTFIADLAVGLSTGQIK	LYT	rep1
1163.0677	2324.1197	2324.3826	113.1	2	3.68	1.4	YGQDATNVGDEGGFAPNIQENK	LYT	rep1
1036.4672	3106.378	3107.311	300.26	3	4.49	2.62	YGQDATNVGDEGGFAPNIQENKEGLELLK	LYK	rep1
1036.3373	3105.9884	3107.311	425.66	3	4.3	1.99	YGQDATNVGDEGGFAPNIQENKEGLELLK	LYT	rep2

Matching Genes:

NP_181192.1 (LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase [Arabidopsis thaliana])

Protein Group 10

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	15	29.65	102.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
514.8502	1541.5272	1540.7486	505.3	3	3.91	1.5	ARFEELNMDLFR	LYT	rep2
771.6419	1541.2681	1540.7486	337.15	2	3.42	1.57	ARFEELNMDLFR	LYK	rep3

838.6761	1675.3365	1675.6749	201.98	2	3.11	1.34	ATAGDTHLGGEDFDNR	LYT	rep1
838.4655	1674.9153	1675.6749	453.31	2	3.09	1.66	ATAGDTHLGGEDFDNR	LYK	rep1
616.1834	1230.3511	1230.3071	35.76	2	1.52	0.49	FSDSSVQSDMK	LYT	rep2
863.955	2588.8414	2588.8157	9.92	3	2.19	0.53	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYT	rep1
863.8718	2588.592	2588.8157	86.41	3	1.7	0.5	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYK	rep2
830.6215	1659.2273	1659.8848	396.07	2	3.39	1.6	IINEPTAAAIAYGLDK	LYT	rep1
894.5905	1787.1653	1788.0577	499.09	2	3.68	2.05	IINEPTAAAIAYGLDKK	LYT	rep1
894.6775	1787.3394	1788.0577	401.74	2	3.09	1.74	IINEPTAAAIAYGLDKK	LYK	rep1
912.1868	1822.3579	1823.1255	421	2	3.45	1.79	IQAGPADKPMIYVEYK	LYK	rep2
608.6407	1822.8988	1823.1255	124.35	3	1.69	0.06	IQAGPADKPMIYVEYK	LYT	rep1
1575.388	3148.7603	3149.3447	185.57	2	3.97	2.65	KIEDSIEQAIQWLEGNQLAEADEFEDK	LYT	rep1
1050.5717	3148.6915	3149.3447	207.42	3	1.61	0.07	KIEDSIEQAIQWLEGNQLAEADEFEDK	LYK	rep3
901.6586	1801.3015	1801.0383	146.16	2	3.66	1.96	MDKSTVHDVVLVGGSTR	LYT	rep2
601.2782	1800.8111	1801.0383	126.15	3	1.54	0.37	MDKSTVHDVVLVGGSTR	LYK	rep1
550.451	1648.3297	1645.9881	1422.58	3	3.63	1.8	MKELESICNPIIAK : +57.05000 (C8)	LYT	rep3
639.9811	1277.9466	1278.4846	420.84	2	3.06	1.48	MVNHFVQEFK	LYK	rep3
640.4624	1278.9092	1278.4846	332.12	2	2.97	1.31	MVNHFVQEFK	LYT	rep2
717.9392	1433.8628	1434.671	563.32	2	3.01	1.05	MVNHFVQEFKR	LYK	rep1
717.9734	1433.9312	1434.671	515.67	2	2.68	1.24	MVNHFVQEFKR	LYT	rep3
602.4823	1804.4234	1804.0439	210.36	3	2.71	0.51	NQVAMNPVNTVFDAKR	LYK	rep1
602.3204	1803.9378	1804.0439	58.82	3	2.2	0.58	NQVAMNPVNTVFDAKR	LYT	rep1
714.1084	1426.2012	1426.5806	265.91	2	3.12	1.08	STVHDVVLVGGSTR	LYT	rep1
714.0083	1426.001	1426.5806	406.25	2	2.74	0.78	STVHDVVLVGGSTR	LYK	rep1
719.4934	1436.9712	1436.6169	246.62	2	3.96	2.09	VQQLLQDFFNGK	LYT	rep1
718.9771	1435.9385	1436.6169	472.23	2	2.31	0.95	VQQLLQDFFNGK	LYK	rep2

Matching Genes:

NP_195870.1 (HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding [Arabidopsis thaliana])

Protein Group 11

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	40.98	145.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
336.8035	1007.3869	1007.1453	239.9	3	2.89	0.46	ARYDEIIK	LYK	rep2
336.8	1007.3765	1007.1453	229.53	3	2.48	0.44	ARYDEIIK	LYT	rep2
433.893	1298.6555	1298.5355	92.43	3	3.09	0.58	EHALLAFTLGVK	LYK	rep1
649.9554	1297.8951	1298.5355	493.21	2	2.86	1.15	EHALLAFTLGVK	LYT	rep2
545.9435	1634.807	1634.8834	46.76	3	3.93	1.8	FHINIVVIGHVDSGK	LYK	rep2
546.0201	1635.0369	1634.8834	93.91	3	3.74	1.9	FHINIVVIGHVDSGK	LYT	rep2
913.0785	2736.212	2737.1289	334.98	3	5.21	3.28	FHINIVVIGHVDSGKSTTTGHLIYK	LYK	rep3
913.1637	2736.4676	2737.1289	241.6	3	3.72	2.22	FHINIVVIGHVDSGKSTTTGHLIYK	LYT	rep1
1273.4076	3817.1993	3819.3041	551.1	3	7.03	4.39	GAANFTSQVIIMNHPGQIGNGYAPVLDCHTSHIAVK : +57.05000 (C28)	LYK	rep3
1274.3656	3820.0733	3819.3041	201.4	3	5.55	3.39	GAANFTSQVIIMNHPGQIGNGYAPVLDCHTSHIAVK :+57.05000 (C28)	LYT	rep3
513.5882	1025.1607	1025.207	45.2	2	2.64	1.33	IGGIGTVPVGR	LYT	rep1
513.4573	1024.899	1025.207	300.48	2	1.97	0.81	IGGIGTVPVGR	LYK	rep2
1140.8059	2279.5962	2280.6724	471.85	2	4.02	2.26	MTPTKPMVVETFSEYPPLGR	LYK	rep3
1141.1609	2280.3062	2280.6724	160.55	2	3.48	1.84	MTPTKPMVVETFSEYPPLGR	LYT	rep2
458.0985	914.1813	914.1045	83.98	2	1.58	0.35	QTVAVGVIK	LYT	rep2
457.9198	913.824	914.1045	306.89	2	1.04	0.12	QTVAVGVIK	LYK	rep2

560.8445	1119.6734	1120.2604	523.98	2	2.47	1.08	STTTGHLIYK	LYK	rep2
560.9275	1119.8394	1120.2604	375.78	2	2.45	1.11	STTTGHLIYK	LYT	rep3
1262.3023	2522.5889	2522.7988	83.21	2	3.01	1.29	SVEMHHESLLEALPGDNVGFNVK	LYT	rep1
1261.6155	2521.2154	2522.7988	627.66	2	2.52	0.99	SVEMHHESLLEALPGDNVGFNVK	LYK	rep1
1253.8904	2505.7652	2506.9873	487.49	2	4.53	2.68	VETGMIKPGMVVTFAPTGLTTEVK	LYT	rep1
1253.5916	2505.1675	2506.9873	725.88	2	4.05	2.07	VETGMIKPGMVVTFAPTGLTTEVK	LYK	rep3
484.7415	1451.2009	1451.6105	282.16	3	3.71	1.77	YYCTVIDAPGHR : +57.05000 (C3)	LYK	rep1
484.74	1451.1965	1451.6105	285.18	3	3.24	1.62	YYCTVIDAPGHR : +57.05000 (C3)	LYT	rep2
652.4357	1954.2835	1955.2042	470.88	3	2	0.68	YYCTVIDAPGHRDFIK : +57.05000 (C3)	LYK	rep1

Matching Genes:

NP_001030993.1 (calmodulin binding / translation elongation factor [Arabidopsis thaliana])

Protein Group 12

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	45.55	117.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
845.1508	1688.2859	1688.8815	352.62	2	2.21	0.92	DDPDFTWEVVKPLK	LYT	rep3
651.9922	1301.9688	1302.5672	459.45	2	2.92	0.53	EHVIKPIIPEK	LYK	rep3
651.9019	1301.7881	1302.5672	598.15	2	2.75	0.7 7	EHVIKPIIPEK	LYT	rep1
728.3991	1454.7825	1453.6077	808.23	2	3.79	1.63	FVIGGPHGDAGLTGR	LYK	rep3
728.1792	1454.3428	1453.6077	505 .75	2	3.35	1.6	FVIGGPHGDAGLTGR	LYT	rep2
791.2668	1580.5179	1581.7805	798.24	2	3.21	0.97	FVIGGPHGDAGLTGRK	LYK	rep3

791.6436	1581.2715	1581.7805	321.78	2	3.16	1.24	FVIGGPHGDAGLTGRK	LYT	rep1
1203.2942	2404.5728	2405.6301	439.52	2	2.89	1.58	IIIDTYGGWGAHGGGAFSGKDPTK	LYT	rep3
802.4052	2404.192	2405.6301	597.82	3	1.32	0.22	IIIDTYGGWGAHGGGAFSGKDPTK	LYK	rep2
698.3312	2091.9701	2092.3223	168.33	3	4.54	2.5	KIIIDTYGGWGAHGGGAFSGK	LYK	rep3
698.36	2092.0565	2092.3223	127.02	3	3.98	2.12	KIIIDTYGGWGAHGGGAFSGK	LYT	rep3
1229.2357	3684.6837	3685.0769	106.7	3	7.66	5.51	RPEDIGAGDQGHMFGYATDETPELMPLSHVLATK	LYK	rep3
1229.1156	3684.3233	3685.0769	204.49	3	6.2	4.42	RPEDIGAGDQGHMFGYATDETPELMPLSHVLATK	LYT	rep2
490.5493	979.0829	979.0537	29.85	2	2.05	0.91	TAAYGHFGR	LYK	rep3
490.4787	978.9418	979.0537	114.28	2	1.93	0.84	TAAYGHFGR	LYT	rep3
571.6226	1141.2295	1141.2845	48.2	2	2.04	0.53	TIFHLNPSGR	LYK	rep2
571.6031	1141.1905	1141.2845	82.42	2	1.96	0.91	T IFHLNPSGR	LYT	rep3
736.0699	1470.1241	1470.7601	432.47	2	2.1	0.89	TNMVMVFGEITTK	LYT	rep2
793.6173	2377.8285	2378.5613	308.09	3	4.17	2.52	VHTVLISTQHDETVTNDEIAR	LYT	rep1
793.7158	2378.124	2378.5613	183.84	3	3.92	2.24	VHTVLISTQHDETVTNDEIAR	LYK	rep2
807.3811	2419.1198	2417.6855	593.25	3	4.21	2.1	VLVNIEQQSPDIAQGVHGHFTK	LYK	rep3
1209.4173	2416.8189	2417.6855	358.46	2	4.04	2.52	VLVNIEQQSPDIAQGVHGHFTK	LYT	r ep3
888.7388	1775.4619	1775.9656	283.57	2	3.1	1.77	YLDDKTIFHLNPSGR	LYT	rep2
888.5652	1775.1148	1775.9656	479.05	2	3.08	1 .39	YLDDKTIFHLNPSGR	LYK	rep1

Matching Genes:

NP_001078345.1 (MAT2/SAM-2 (S-adenosylmethionine synthetase 2) [Arabidopsis thaliana])

Protein Group 13

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	63.97	141.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
953.2391	2856.6939	2857.2551	196.41	3	6.23	3.01	ALSDHHVLLEGTLLKPNMVTPGSDSPK	LYK	rep3
953.2686	2856.7822	2857.2551	165.52	3	4.88	2.17	ALSDHHVLLEGTLLKPNMVTPGSDSPK	LYT	rep2
763.605	1525.1944	1525.6225	280.66	2	2.79	1.03	ANSEATLGTYKGDAK	LYT	rep1
763.6763	1525.3369	1525.6225	187.2	2	2.74	1.25	ANSEATLGTYKGDAK	LYK	rep1
1456.0122	2910.0088	2910.3948	132.63	2	1.83	0.66	ELLFTAPGALPCLSGVILFEETLYQK : +57.05000 (C12)	LYT	rep3
970.5138	2908.5179	2910.3948	644.91	3	1.32	0.03	ELLFTAPGALPCLSGVILFEETLYQK : +57.05000 (C12)	LYK	rep3
745.5463	1489.0769	1488.6485	287.77	2	3.42	1.57	GILAADESTGTIGKR	LYT	rep1
745.0983	1488.1809	1488.6485	314.11	2	2.99	1.08	GILAADESTGTIGKR	LYK	rep1
741.8514	2222.5308	2223.3247	357.06	3	4.42	2.28	IGENEPSEHSIHENAYGLAR	LYK	rep3
1112.2039	2222.3921	2223.3247	419.45	2	3.49	1.81	IGENEPSEHSIHENAYGLAR	LYT	rep1
438.3591	1312.0537	1311.4928	427.72	3	3.78	1.43	KPWSLSFSFGR	LYT	rep3
438.5678	1312.68	1311.4928	905.2	3	3.18	1.13	KPWSLSFSFGR	LYK	rep2
807.9768	1613.938	1614.7657	512.59	2	2.04	0.02	LASINVENVETNRR	LYK	rep3
539.3883	1615.1414	1614.7657	232.67	3	1.75	0.4	LASINVENVETNRR	LYT	rep2
399.9986	1196.9723	1196.3153	549.2	3	2.98	1.14	LGDGAAESLHVK	LYK	rep1
399.8619	1196.5622	1196.3153	206.35	3	2.86	1.32	LGDGAAESLHVK	LYT	rep3
808.1398	1614.264	1614.7657	310.75	2	3.77	2.22	RLASINVENVETNR	LYT	rep3
808.0476	1614.0796	1614.7657	424.9	2	3.37	1.39	RLASINVENVETNR	LYK	rep2
1165.3269	2328.6382	2329.5718	400.74	2	2.61	1.04	TVPAAVPAIVFLSGGQSEEEATR	LYT	rep2
869.4382	2605.2912	2605.7314	168.94	3	4.15	0.65	VDKGTVELAGTDGETTTQGLDGLGDR	LYT	rep2
8 69.6916	2606.0515	2605.7314	122.82	3	3.4	0.49	VDKGTVELAGTDGETTTQGLDGLGDR	LYK	rep1
669.4868	1336.958	1336.499	343.46	2	2.58	1.11	VSPEVIAEHTVR	LYK	rep3
446.5277	1336.5597	1336.499	45.37	3	2.21	0.89	VSPEVIAEHTVR	LYT	rep1
1045.8964	3134.6656	3136.5436	598.73	3	3.54	1.31	YAVICQENGLVPIVEPEILVDGSHDIQK : +57.05000(C5)	LYK	rep3

1046.0453	3135.1124	3136.5436	456.29	3	2.72	1.43	YAVICQENGLVPIVEPEILVDGSHDIQK : +57.05000 (C5)	LYT	rep1

Matching Genes:

NP_190861.1 (fructose-bisphosphate aldolase, putative [Arabidopsis thaliana])

Protein Group 14

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	14	38.6	72.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1360.6526	2719.2896	2719.8662	212	2	4.12	1.9	AHGTAVGLPSEDDMGNSEVGHNALGAGR	LYT	rep1
907.4272	2719.2583	2719.8662	223.52	3	3.81	2.33	AHGTAVGLPSEDDMGNSEVGHNALGAGR	LYK	rep1
774.6839	1547.3521	1547.6267	177.44	2	2.18	0.89	ALEYEDFDKFDR	LYK	rep1
1153.972	2305.9283	2305.5469	165.43	2	3.73	2.02	DVLDGSSVGFVETLEADLVALR	LYK	rep3
741.737	1481.4583	1481.6212	109.96	2	2.91	1.37	FGHVTFFWNGNR	LYT	rep3
494.8489	1481.5233	1481.6212	66.05	3	2.88	0.73	FGHVTFFWNGNR	LYK	rep2
659.4039	1975.1883	1975.1953	3.54	3	2.48	0.84	GIYVVTADHGNAEDMVKR	LYT	rep1
659.1625	1974.4639	1975.1953	370.27	3	2.03	0.6	GIYVVTADHGNAEDMVKR	LYK	rep2
470.3806	1408.1182	1407.5358	413.8	3	1.77	0.4	GWDAQVLGEAPHK	LYK	rep2
704.7517	1407.4878	1407.5358	34.05	2	1.17	0.18	GWDAQVLGEAPHK	LYT	rep3
620.2842	1238.5528	1238.397	125.82	2	2.44	0.95	HGAPDTWTLIK	LYT	rep3
620.4702	1238.9248	1238.397	426.26	2	2.18	1	HGAPDTWTLIK	LYK	rep2
394.2063	1179.5954	1179.3774	184.84	3	2.21	0.42	IRVHILTDGR	LYT	rep2
394.2375	1179.6892	1179.3774	264.33	3	2.13	0.47	IRVHILTDGR	LYK	rep2
768.7211	2303.1397	2303.5327	170.6	3	2.04	0.37	KEPGANDQYLPPFVIVDESGK	LYT	rep3

880.3944	2638.1598	2637.1404	386.55	3	6.23	3.87	LQILTSHTLKPVPIAIGGPGLAQGVR	LYK	rep3
879.8768	2636.607	2637.1404	202.25	3	5.38	3.17	LQILTSHTLKPVPIAI GGPGLAQGVR	LYT	rep1
522.3303	1563.9675	1563.7222	156.89	3	3.07	0.57	RGWDAQVLGEAPHK	LYK	rep2
522.0721	1563.193	1563.7222	338.42	3	2.53	0.56	RGWDAQVLGEAPHK	LYT	rep3
456.514	911.0124	910.0328	1076.45	2	1.76	0.26	VHILTDGR	LYK	rep3
455.7619	909.5082	910.0328	576.47	2	1.32	0.24	VHILTDGR	LYT	rep3
614.8561	1841.5448	1841.1009	241.06	3	3.78	1.83	YAGMLQYDGELKLPSR	LYK	rep1
614.6123	1840.8134	1841.1009	156.16	3	2.7	1.23	YAGMLQYDGELKLPSR	LYT	rep2
907.0024	2717.9838	2717.9514	11.94	3	4.7	3.1	YVSESFETNTLHLVGLLSDGGVHSR	LYT	rep3
907.0797	2718.2157	2717.9514	97.23	3	3.01	1.6	YVSESFETNTLHLVGLLSDGGVHSR	LYK	rep2

Matching Genes:

NP_563852.1 (2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative [Arabidopsis thaliana])

Protein Group 15

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	34.54	81.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
795.5668	2383.6768	2382.6396	435.32	3	5.19	3.02	EAYLVSHNLLNAHAEAVEVFR	LYK	rep2
795.1874	2382.5387	2382.6396	42.38	3	4.31	2.02	EAYLVSHNLLNAHAEAVEVFR	LYT	rep3
576.7	1151.3843	1151.3146	60.58	2	2.91	1.3	FGLYYVDFK	LYK	rep1
576.6324	1151.2491	1151.3146	56.9	2	2.31	0.97	FGLYYVDFK	LYT	rep2
626.0041	1249.9925	1250.4297	349.68	2	3.31	1.14	GPALWDIYCR : +57.05000 (C9)	LYK	rep1
626.5528	1251.0899	1250.4297	527.95	2	2.89	0.71	GPALWDIYCR : +57.05000 (C9)	LYT	rep2

595.2228	1782. 6449	1783.1313	272.78	3	2.92	1.57	HLLAMNEAICIDKVR : +57.05000 (C10)	LYK	rep1
607.109	1818.3035	1818.0472	140.99	3	3.69	1.57	IGIAHSPAWFEPHDLK	LYT	rep1
909.7252	1817.4348	1818.0472	336.83	2	3.67	1.72	IGIAHSPAWFEPHDLK	LYK	rep2
954.6282	2860.861	2861.0976	82.7	3	4.86	2.89	IGIAHSPAWFEPHDLKDSNDAPTVSR	LYT	rep2
954.8585	2861.5521	2861.0976	158.83	3	4.83	3.13	IGIAHSPAWFEPHDLKDSNDAPTVSR	LYK	rep1
893.8068	1785.5979	1785.874	154.59	2	2.28	0.9	LGTTDSVDVGTADHNRK	LYT	rep1
893.5917	1785.1678	1785.874	395.47	2	2.19	0.92	LGTTDSVDVGTADHNRK	LYK	rep2
476.2345	95 0.4533	950.0107	465.9	2	2.05	0.49	NLNTDAFR	LYT	rep1
475.9542	949.8927	950.0107	124.14	2	1.27	0.28	NLNTDAFR	LYK	rep2
1078.3753	2154.7349	2155.4831	347.13	2	4.3	2.12	NVDHSAIGSMPLTAALPVYAK	LYK	rep1
719.8094	2156.4049	2155.4831	427.62	3	1.48	0.35	NVDHSAIGSMPLTAALPVYAK	LYT	rep3
1184.1438	2366.272	2365.6091	280.22	2	3.01	1.78	NWITFNEPWVFAHAGYDLGK	LYK	rep1
789.4596	2365.3553	2365.6091	107.29	3	1.81	0.63	NWITFNEPWVFAHAGYDLGK	LYT	rep3
865.1199	2592.3361	2592.9136	222.69	3	3.63	0.97	VKNWITFNEPWVFAHAGYDLGK	LYK	rep3
864.9205	2591.7381	2592.9136	453.33	3	2.47	1.06	VKNWITFNEPWVFAHAGYDLGK	LYT	rep2
1339.8677	2677.7198	2679.0869	510.3	2	2.34	0.81	VLDFMLGWHLEPTTSGDYPQIMK	LYT	rep1
1340.763	2679.5103	2679.0869	158.03	2	0.77	0.12	VLDFMLGWHLEPTTSGDYPQIMK	LYK	rep2
390.2817	1167.8216	1167.3805	377.83	3	2.93	0.58	YKEDIQLMK	LYK	rep1
390.161	1167.4596	1167.3805	67.74	3	2.82	0.28	YKEDIQLMK	LYT	rep2

Matching Genes:

NP_176801.1 (beta-glucosidase (PSR3.2) [Arabidopsis thaliana])

Protein Group 16

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	11	76.82	142.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
720.5511	1439.0865	1439.5532	324.23	2	2.9	1.38	EIDDENMAVTFR	LYT	rep1
621.0298	1240.044	1240.4347	314.97	2	3.72	1.62	GLEGHVMEQLK	LYK	rep1
621.138	1240.2603	1240.4347	140.59	2	3.63	1.39	GLEGHVMEQLK	LYT	rep3
879.1857	1756.3557	1756.9809	355.84	2	5.13	2.49	IWNYTCDGKPEVFK : +57.05000 (C6)	LYK	rep1
879.2616	1756.5076	1756.9809	269.41	2	4.3	2.35	IWNYTCDGKPEVFK : +57.05000 (C6)	LYT	rep3
785.012	1568.0083	1568.6913	435.35	2	1.91	0.62	QNDDMPEPSNYMK	LYT	rep1
798.6231	1595.2305	1595.7395	318.97	2	3.59	1.68	REIDDENMAVTFR	LYK	rep1
798.3887	1594.7618	1595.7395	612.72	2	3.02	1.24	REIDDENMAVTFR	LYT	rep3
1140.1302	3417.3673	3418.6592	377.9	3	6.1	3.19	SENHLFPDAIGHHIQGVTIHDGEWDSHGAIK	LYK	rep3
1140.2902	3417.847	3418.6592	237.57	3	5	2.59	SENHLFPDAIGHHIQGVTIHDGEWDSHGAIK	LYT	rep2
657.9783	1313.941	1314.4704	402.82	2	1.5	0.42	SLAADMDDHVLK	LYT	rep3
659.2798	1316.544	1314.4704	1577.47	2	1.15	0.14	SLAADMDDHVLK	LYK	rep1
693.659	1385.3023	1385.5487	177.84	2	4.09	1.89	SLAADMDDHVLKA	LYK	rep1
693.3592	1384.7027	1385.5487	610.6	2	3.7	1.5	SLAADMDDHVLKA	LYT	rep1
474.253	946.4904	947.067	608.81	2	1.94	0.44	SPDDIICK : +57.05000 (C7)	LYT	rep2
700.8826	1399.7495	1399.6383	79.49	2	5.38	2.43	VYDVIFQFIQK	LYK	rep1
701.343	1400.6704	1399.6383	737.44	2	4.68	2.42	V YDVIFQFIQK	LYT	rep2
1254.3524	3760.0338	3761.0564	271.89	3	6.31	4.08	WRSENHLFPDAIGHHIQGVTIHDGEWDSHGAIK	LYK	rep3
1254.4694	3760.3846	3761.0564	178.61	3	4.7	2.8	WRSENHLFPDAIGHHIQGVTIHDGEWDSHGAIK	LYT	rep3

Matching Genes:

NP_565264.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 17

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	47.33	119.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
832.4383	1662.8609	1662.844	10.16	2	3.26	1.71	DDADFTWEVVKPLK	LYT	rep1
832.2387	1662.4617	1662.844	229.89	2	1.39	0.27	DDADFTWEVVKPLK	LYK	rep2
645.0327	1288.0498	1288.5405	380.8	2	2.8	0.99	EHVIKPVIPEK	LYK	rep3
645.0393	1288.063	1288.5405	370.57	2	2.63	1.16	EHVIKPVIPEK	LYT	rep3
728.3991	1454.7825	1453.6077	808.23	2	3.79	1.63	FVIGGPHGDAGLTGR	LYK	rep3
728.1792	1454.3428	1453.6077	505.75	2	3.35	1.6	FVIGGPHGDAGLTGR	LYT	rep2
791.2668	1580.5179	1581.7805	798.24	2	3.21	0.97	FVIGGPHGDAGLTGRK	LYK	rep3
791.6436	1581.2715	1581.7805	321.78	2	3.16	1.24	FVIGGPHGDAGLTGRK	LYT	rep1
1203.2942	2404.5728	2405.6301	439.52	2	2.89	1.58	IIIDTYGGWGAHGGGAFSGKDPTK	LYT	rep3
802.4052	2404.192	2405.6301	597.82	3	1.32	0.22	III DTYGGWGAHGGGAFSGKDPTK	LYK	rep2
698.3312	2091.9701	2092.3223	168.33	3	4.54	2.5	KIIIDTYGGWGAHGGGAFSGK	LYK	rep3
698.36	2092.0565	2092.3223	127.02	3	3.98	2.12	KIIIDTYGGWGAHGGGAFSGK	LYT	rep3
1224.1554	3669.4427	3671.0901	448.74	3	5.28	0	KPEEVGAGDQGHMFGYATDETPELMPLTHVLATK	LYT	rep1
1224.2521	3669.7327	3671.0901	369.73	3	5.01	0.17	KPEEVGAGDQGHMFGYATDETPELMPLTHVLATK	LYK	rep2
437.5625	873.1094	873.0125	111.01	2	1.44	0.34	SIVASGLAR	LYT	rep2
490.5493	979.0829	979.0537	29.85	2	2.05	0.91	TAAYGHFGR	LYK	rep3
490.4787	978.9418	979.0537	114.28	2	1.93	0.84	TAA YGHFGR	LYT	rep3

571.6226	1141.2295	1141.2845	48.2	2	2.04	0.53	TIFHLNPSGR	LYK	rep2
571.6031	1141.1905	1141.2845	82.42	2	1.96	0.91	TIFHLNPSGR	LYT	rep3
736.0699	1470.1241	1470.7601	432.47	2	2.1	0.89	TNMVMVFGEITTK	LYT	rep2
883.9004	2648.6777	2649.8721	450.72	3	5.18	2.81	VHTVLISTQHDETVTNDEIAADLK	LYT	rep1
883.871	2648.5894	2649.8721	484.03	3	3.36	1.1	VHTVLISTQHDETVTNDEIAADLK	LYK	rep3
1192.6863	2383.357	2383.6689	130.88	2	3.74	1.87	VLVNIEQQSPDIAQGVHGHLTK	LYT	rep1
1192.3416	2382.6675	2383.6689	420.12	2	3.36	1.96	VLVNIEQQSPDIAQGVHGHLTK	LYK	rep1

Matching Genes:

NP_188365.1 (MTO3 (S-adenosylmethionine synthase 3); methionine adenosyltransferase [Arabidopsis thaliana])

Protein Group 18

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	12	29.2	73.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
576.7	1151.3843	1151.3146	60.58	2	2.91	1.3	FGLYYVDFK	LYK	rep1
576.6324	1151.2491	1151.3146	56.9	2	2.31	0.97	FGLYYVDFK	LYT	rep2
469.6875	1406.039	1405.5997	312.54	3	2.44	0.1	FYHDLIDELLK	LYT	rep3
703.8228	1405.6299	1405.5997	21.48	2	1.17	0.14	FYHDLIDELLK	LYK	rep1
711.9137	2132.7176	2132.4245	137.43	3	4.79	0.26	GVSQAGVKFYHDLIDELLK	LYT	rep3
1066.8892	2131.7627	2132.4245	310.36	2	4.39	0	GVSQAGVKFYHDLIDELLK	LYK	rep1
595.2228	1782.6449	1783.1313	272.78	3	2.92	1.57	HLLAMNEAICIDKVR : +57.05000 (C10)	LYK	rep1
607.109	1818.3035	1818.0472	140.99	3	3.69	1.57	IGIAHSPAWFEPHDLK	LYT	rep1
909.7252	1817.4348	1818.0472	336.83	2	3.67	1.72	IGIAHSPAWFEPHDLK	LYK	rep2
963.5861	2887.7347	2889.1509	490.17	3	4.47	2.69	IGIAHSPAWFEPHDLKDSNDVPTVSR	LYT	rep3

963.7473	2888.2185	2889.1509	322.72	3	4.19	2.39	IGIAHSPAWFEPHDLKDSNDVPTVSR	LYK	rep1
476.2345	950.4533	950.0107	465.9	2	2.05	0.49	NLNTDAFR	LYT	rep1
475.9542	949.8927	950.0107	124.14	2	1.27	0.28	NLNTDAFR	LYK	rep2
1076.8777	2151.7398	2152.4158	314.06	2	2.63	0.6	NVDHSAIGSQPLTAALPVYAK	LYT	rep1
785.0887	2352.2428	2351.5825	280.77	3	2.18	0.57	NWITFNEPWVFAHAGYDVGK	LYT	rep3
897.3314	2688.9708	2689.9429	361.37	3	5.48	3.27	SGYEAYLVSHNLLNAHAEAVEVFR	LYK	rep2
897.5004	2689.4776	2689.9429	172.95	3	4.99	2.53	SGYEA YLVSHNLLNAHAEAVEVFR	LYT	rep1
860.5209	2578.5391	2578.887	134.87	3	2.88	1.68	VKNWITFNEPWVFAHAGYDVGK	LYT	rep3
390.2817	1167.8216	1167.3805	377.83	3	2.93	0.58	YKEDIQLMK	LYK	rep1
390.161	1167.4596	1167.3805	67.74	3	2.82	0.28	YKEDIQLMK	LYT	rep2

Matching Genes:

NP_176802.1 (glycosyl hydrolase family 1 protein [Arabidopsis thaliana])

Protein Group 19

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	11	69.2	69.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
806.6753	1611.335	1611.8865	342.12	2	4.15	2.01	ALLDDPVFRPLVEK	LYK	rep3
807.0657	1612.1158	1611.8865	142.25	2	3.01	1.76	ALLDDPVFRPLVEK	LYT	rep2
656.3063	1310.597	1309.4768	855.43	2	2.69	0.86	DIVALSGAHTLGR	LYT	rep1
929.7812	1857.5467	1858.1031	299.48	2	2.62	1.37	ELLSGEKEGLLQLVSDK	LYK	rep1
1212.9825	3635.9242	3637.0349	305.4	3	4.64	2.8	EQFPTISFADFHQLAGVVAVEVTGGPDIPFHPGR	LYK	rep3
1213.6439	3637.9083	3637.0349	240.14	3	2.84	1.39	EQFPTISFADFHQLAGVVAVEVTGGPDIPFHPGR	LYT	rep3
636.6277	1906.8596	1907.0593	104.73	3	4.61	2.01	FDAEQAHGANSGIHIALR	LYK	rep3

636.495	1906.4615	1907.0593	313.47	3	3.89	2.15	FDAEQAHGANSGIHIALR	LYT	rep3
546.3912	1636.1502	1635.7639	236.18	3	3.85	1.21	LAWHSAGTFDCQSR : +57.05000 (C11)	LYT	rep1
546.2661	1635.7749	1635.7639	6.71	3	2.89	0.83	LAWHSAGTFDCQSR : +57.05000 (C11)	LYK	rep2
1448.5753	4342.7025	4344.8994	505.63	3	3.8	1.8	LLDPIREQFPTISFADFHQLAGVVAVEVTGGPDIPFHPGR	LYK	rep3
461.9553	1382.8423	1382.5497	211.66	3	1.77	0.31	LPDATKGCDHLR : +57.05000 (C8)	LYK	rep1
462.0024	1382.9837	1382.5497	313.9	3	1.24	0.04	LPDATKGCDHLR : +57.05000 (C8)	LYT	rep1
690.6708	2068.9889	2069.3518	175.39	3	3.57	1.7	QMGLSDKDIVALSGAHTLGR	LYT	rep3
690.8693	2069.5843	2069.3518	112.36	3	3.19	1.57	QMGLSDKDIVALSGAHTLGR	LYK	rep1
1141.3753	2280.7349	2280.4563	122.17	2	3.93	2.15	SGFEGAWTSNPLIFDNSYFK	LYK	rep2
1140.7412	2279.4668	2280.4563	433.88	2	2.54	0.75	SGFEGAWTSNPLIFDNSYFK	LYT	rep2
689.7015	2066.0811	2065.1843	434.26	3	3.45	1.92	YAADEDAFFADYAEAHMK	LYT	rep2
689.4061	2065.1949	2065.1843	5.13	3	2.18	0.56	YAADEDAFFADYAEAHMK	LYK	rep1

Matching Genes:

NP_001030991.2 (APX1 (ASCORBATE PEROXIDASE 1, MATERNAL EFFECT EMBRYO ARREST 6); L-ascorbate peroxidase [Arabidopsis thaliana])

Protein Group 20

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	12	33.21	52.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1360.6526	2719.2896	2719.8662	212	2	4.12	1.9	AHGTAVGLPSEDDMGNSEVGHNALGAGR	LYT	rep1
907.4272	2719.2583	2719.8662	223.52	3	3.81	2.33	AHGTAVGLPSEDDMGNSEVGHNALGAGR	LYK	rep1
966.1727	2895.4947	2896.3574	297.86	3	5.79	3.29	EGNLQILTSHTLKPVPIAIGGPGLSAGVR	LYK	rep3
966.7714	2897.2906	2896.3574	322.2	3	1.63	0.28	EGNLQILTSHTLKPVPIAIGGPGLSAGVR	LYT	rep1
741.737	1481.4583	1481.6212	109.96	2	2.91	1.37	FGHVTFFWNGNR	LYT	rep3

494.8489	1481.5233	1481.6212	66.05	3	2.88	0.73	FGHVTFFWNGNR	LYK	rep2
1422.077	4263.2076	4262.769	102.88	3	5.52	3.44	FRQDIETPGLANVAATVMNLHGFVAPSDYETSLIEVVEK	LYK	rep1
1421.6866	4262.0365	4262.769	171.85	3	4.39	2.45	FRQDIETPGLANVAATVMNLHGFVAPSDYETSL IEVVEK	LYT	rep2
573.6947	1718.0606	1717.9308	75.59	3	4.03	1.56	GTVHLIGLLSDGGVHSR	LYT	rep3
859.3158	1716.616	1717.9308	765.32	2	1.75	0.33	GTVHLIGLLSDGGVHSR	LYK	rep3
470.3806	1408.1182	1407.5358	413.8	3	1.77	0.4	GWDAQVLGEAPHK	LYK	rep2
704.7517	1407.4878	1407.5358	34.05	2	1.17	0.18	GWDAQVLGEAPHK	LYT	rep3
394.2063	1179.5954	1179.3774	184.84	3	2.21	0.42	IRVHILTDGR	LYT	rep2
394.2375	1179.6892	1179.3774	264.33	3	2.13	0.47	IRVHILTDGR	LYK	rep2
510.5836	1019.1515	1018.2145	920.3	2	1.7	0.39	LADHPKLPK	LYT	rep1
522.3303	1563.9675	1563.7222	156.89	3	3.07	0.57	RGWDAQVLGEAPHK	LYK	rep2
522.0721	1563.193	1563.7222	338.42	3	2.53	0.56	RGWDAQVLGEAPHK	LYT	rep3
652.5635	1303.1114	1303.386	210.69	2	1.78	0.37	TSGEYLAHNGVR	LYT	rep2
456.514	911.0124	910.0328	1076.45	2	1.76	0.26	VHILTDGR	LYK	rep3
455.7619	909.5082	910.0328	576.47	2	1.32	0.24	VHILTDGR	LYT	rep3
614.8561	1841.5448	1841.1009	241.06	3	3.78	1.83	YAGMLQYDGELKLPSR	LYK	rep1
614.6123	1840.8134	1841.1009	156.16	3	2.7	1.23	YAGMLQYDGELKLPSR	LYT	rep2

Matching Genes:

NP_187471.1 (2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative [Arabidopsis thaliana])

Protein Group 21

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	13	33.05	120.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

1631.7174	4892.1287	4892.3857	52.53	3	3.63	1.91	EHGKPTLLGFEEFELDYPSEYITAVDGTYDAIFGNEPIVNMLR	LYK	rep1
1631.579	4891.7135	4892.3857	137.41	3	3.56	1.75	EHGKPTLLGFEEFELDYPSEYITAVDGTYDAIFGNEPIVNMLR	LYT	rep2
534.9366	1067.8575	1068.2734	389.38	2	2.56	1.12	FGVHVAPITK	LYK	rep2
357.1976	1068.5692	1068.2734	276.91	3	2.33	0.7	FGVHVAPITK	LYT	rep1
554.1166	1106.2176	1106.2768	53.58	2	2.05	0.5	FTLQVQDKK	LYK	rep2
553.9046	1105.7935	1106.2768	436.92	2	1.93	0.49	FTLQVQDKK	LYT	rep2
1173.1802	2344.3448	2345.6658	563.17	2	4.23	2.68	IIGFHGFAGNHVNSIGAYFVPK	LYK	rep3
782.842	2345.5026	2345.6658	69.54	3	4.15	2.16	IIGFHGFAGNHVNSIGAYFVPK	LYT	rep2
774.6418	1547.2679	1547.713	287.61	2	1.77	0.63	IYASYGGEGIQYVK	LYT	rep2
825.4037	2473.1876	2473.8386	263.17	3	4.79	2.49	KIIGFHGFAGNHVNSIGAYFVPK	LYK	rep3
825.4722	2473.393	2473.8386	180.12	3	3.79	1.65	KIIGFHGFAGNHVNSIGAYFVPK	LYT	rep2
1034.7937	2067.5718	2068.2956	349.96	2	4.47	2.3	KVSVGQAQDGIGAVSFVYDK	LYT	rep2
1034.7991	2067.5826	2068.2956	344.77	2	4.32	2.62	KVSVGQAQDGIGAVSFVYDK	LYK	rep2
751.2559	2250.7441	2251.3747	280.11	3	2.04	0.54	LEGAGSEAGTLWDDGAFDGVRK	LYT	rep1
777.4976	1552.9795	1553.8038	530.5	2	2.13	0.6	NFGVDTVVTTLIFK	LYT	rep2
604.7083	1207.4009	1207.255	120.87	2	1.72	0.58	NGSQVVFGDER	LYT	rep2
1496.4678	2990.92	2991.1807	87.15	2	3.08	1.5	TLLGFEEFELESDEYITSVEGYYEK	LYK	rep3
1496.0061	2989.9966	2991.1807	395.84	2	1.11	0.09	TLLGFEEFELESDEYITSVEGYYEK	LYT	rep3
1025.35	3073.0264	3073.4224	128.81	3	4.06	1.7	VQLTFDEIIYSIQVTYDGATALQSQLR	LYK	rep3
590.7557	1769.2437	1769.056	106.11	3	1.67	0.17	VSIPFGIGAGTAFEFKK	LYK	rep2
590.734	1769.1785	1769.056	69.26	3	1.64	0	VSIPFGIGAGTAFEFKK	LYT	rep3

Matching Genes:

NP_188267.1 (jacalin lectin family protein [Arabidopsis thal iana])

Protein Group 22

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	12	44.27	111.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1235.3673	3703.0785	3703.111	8.78	3	3.38	1.51	CPEEIGAGDQGHMFGYATDETPELMPLSHVLATK : +57.05000 (C1)	LYT	rep1
845.1508	1688.2859	1688.8815	352.62	2	2.21	0.92	DDPDFTWEVVKPLK	LYT	rep3
645.0327	1288.0498	1288.5405	380.8	2	2.8	0.99	EHVIKPVIPEK	LYK	rep3
645.0393	1288.063	1288.5405	370.57	2	2.63	1.16	EHVIKPVIPEK	LYT	rep3
728.3991	1454.7825	1453.6077	808.23	2	3.79	1.63	FVIGGPHGDAGLTGR	LYK	rep3
728.1792	1454.3428	1453.6077	505.75	2	3.35	1.6	FVIGGPHGDAGLTGR	LYT	rep2
791.2668	1580.5179	1581.7805	798.24	2	3.21	0.97	FVIGGPHGDAGLTGRK	LYK	rep3
791.6436	1581.2715	1581.7805	321.78	2	3.16	1.24	FVIGGPHGDAGLTGRK	LYT	rep1
1203.2942	2404.5728	2405.6301	439.52	2	2.89	1.58	IIIDTYGGWGAHGGGAFSGKDPTK	LYT	rep3
802.4052	2404.192	2405.6301	597.82	3	1.32	0. 22	IIIDTYGGWGAHGGGAFSGKDPTK	LYK	rep2
698.3312	2091.9701	2092.3223	168.33	3	4.54	2.5	KIIIDTYGGWGAHGGGAFSGK	LYK	rep3
698.36	2092.0565	2092.3223	127.02	3	3.98	2.12	KIIIDTYGGWGAHGGGAFSGK	LYT	rep3
490.5493	979.0829	979.0537	29.85	2	2.05	0.91	TAAYGHFGR	LYK	rep3
490.4787	978.9418	979.0537	114.28	2	1.93	0.84	TAAYGHFGR	LYT	rep3
571.6226	1141.2295	1141.2845	48.2	2	2.04	0.53	TIFHLNPSGR	LYK	rep2
571.6031	1141.1905	1141.2845	82.42	2	1.96	0.91	TIFHLNPSGR	LYT	rep3
736.0699	1470.1241	1470.7601	432.47	2	2.1	0.89	TNMVMV FGEITTK	LYT	rep2
793.6173	2377.8285	2378.5613	308.09	3	4.17	2.52	VHTVLISTQHDETVTNDEIAR	LYT	rep1
793.7158	2378.124	2378.5613	183.84	3	3.92	2.24	VHTVLISTQHDETVTNDEIAR	LYK	rep2
807.3811	2419.1198	2417.6855	593.25	3	4.21	2.1	VLVNIEQQSPDIAQGVHGHFTK	LYK	rep3
1209.4173	2416.8189	2417.6855	358.46	2	4.04	2.52	VLVNIEQQSPDIAQGVHGHFTK	LYT	rep3

Matching Genes:

NP_171751.1 (SAM1 (S-adenosylmethionine synthetase 1); methionine adenosyltransferase [Arabidopsis thaliana])

Protein Group 23

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	11	36.83	25.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
369.6198	1105.8358	1105.249	530.89	3	1.59	0.5	ADVYKPSLGR	LYT	rep1
479.1128	956.2099	956.0984	116.55	2	2.14	0.15	FEWISFK	LYT	rep1
1071.263	2140.5103	2141.4377	433.09	2	3.66	2.03	GQLVVIPQGFAYVVQSHGNK	LYT	rep1
668.9903	1335.9649	1336.499	399.65	2	3.26	1.75	ISYVVQGTGISGR	LYT	rep1
538.7234	1613.1467	1613.6948	339.67	3	1.26	0.35	QPYESEEWRHPR	LYT	rep1
1491.1305	4470.368	4470.9287	125.41	3	6.24	4	RGDVFANTPGSAHWIYNSGEQPLVIIALLDIANYQNQLDR	LYT	rep1
1040.6673	2079.3189	2080.1853	416.5	2	3.39	1.84	SEAGQIEYWDHNHPQLR	LYT	rep1
830.4138	2488.218	2487.6096	244.56	3	5.63	3.45	VFHLAGNNQQGGFGGSQQQQEQK	LYT	rep1
927.8002	1853.5848	1854.1161	286.56	2	1.88	0.78	VTSVNSYTLPILEYVR	LYT	rep1
981.1286	1960.2415	1961.1475	461.98	2	3.59	2.12	YNMNANEILYCTGGQGR : +57.05000 (C11)	LYT	rep1
1031.1187	2060.2217	2060.3567	65.5	2	4.31	1.27	YVIEQGGLYLPTFFTSPK	LYT	rep1

Matching Genes:

NP_194581.1 (CRU3 (CRUCIFERIN 3); nutrient reservoir [Arabidopsis thaliana])

Protein Group 24

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	41.61	47.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1382.2958	4143.8639	4143.5284	80.96	3	6.13	4.19	ALEAFHCDPAAWGVNVQPYSGSPANFAAYTALLQPHDR : +57.05000 (C7)	LYK	rep3
1382.3173	4143.9283	4143.5284	96.52	3	5.81	4.16	ALEAFHCDPAAWGVNVQPYSGSPANFAAYTALLQPHDR : +57.05000 (C7)	LYT	rep3
1374.6168	4120.827	4120.5991	55.33	3	2.43	0.75	GQPEGAVYDFEDKINFAVFPALQGGPHNHQIGALAVALK	LYT	rep3
1003.7291	3008.1639	3009.3879	406.74	3	4.74	2.33	GYQIVTNGTENHLVLWDLRPLGLTGNK	LYK	rep3
1004.0861	3009.2347	3009.3879	50.92	3	3.14	1.06	GYQIVTNGTENHLVLWDLRPLGLTGNK	LYT	rep3
1131.0547	2260.0938	2261.5227	631.83	2	4.57	2.79	IMGLDLPSGGHLTHGYYTSGGK	LYK	r ep3
1195.104	2388.1924	2389.6955	629	2	3.82	1.68	IMGLDLPSGGHLTHGYYTSGGKK	LYK	rep3
1195.2698	2388.524	2389.6955	490.26	2	2.86	1.38	IMGLDLPSGGHLTHGYYTSGGKK	LYT	rep2
1342.7239	2683.4322	2684.1142	254.12	2	3.37	1.65	INFAVFPALQGGPHNHQIGALAVALK	LYK	rep2
1342.9427	2683.8697	2684.1142	91.12	2	2.87	1.08	INFAVFPALQGGPHNHQIGALAVALK	LYT	rep3
1335.4991	4003.474	4004.5391	265.99	3	5.58	2.97	VGALLLCDMAHISGLVAAQEAANPFEYCDVVTTTTHK : +57.05000 (C7); +57.05000 (C28)	LYT	rep1
1335.6337	4003.8775	4004.5391	165.22	3	5.17	3.05	VGALLLCDMAHISGLVAAQEAANPFEYCDVVTTTTHK : +57.05000 (C7); +57.05000 (C28)	LYK	rep2

646.0892	1935.2442	1935.0997	74.68	3	1.99	0.55	VNFTTGYIDYD KLEEK	LYK	rep1
996.7157	1991.4158	1992.1333	360.17	2	2.48	0.93	YYGGNEFIDEIENLCR : +57.05000 (C15)	LYT	rep2

Matching Genes:

NP_193129.1 (SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4); glycine hydroxymethyltransferase [Arabidopsis thaliana])

Protein Group 25

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	48.84	67.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
934.3297	2799.9657	2801.1252	413.97	3	5.27	2.7	GEHKQPAYLALQPFGTVPAVVDGDYK	LYK	rep3
934.4188	2800.233	2801.1252	318.53	3	3.48	1.22	GEHKQPAYLALQPFGTVPAVVDGDYK	LYT	rep2
730.125	1458.2344	1458.5397	209.28	2	3.5	1.75	HVSAWWDDISSR	LYT	rep3
730.1294	1458.2432	1458.5397	203.26	2	3.37	2	HVSAWWDDISSR	LYK	rep2
971.6397	1941.2637	1941.1173	75.43	2	4.5	2.71	HVSAWWDDISSRPAWK	LYK	rep2
971.2998	1940.584	1941.1173	274.73	2	4.32	2.89	HVSAWWDDISSRPAWK	LYT	rep1
794.19	1586.3643	1586.7125	219.46	2	3.8	1.81	KHVSAWWDDISSR	LYK	rep1
793.9278	1585.8399	1586.7125	549.96	2	3.61	1.64	KHVSAWWDDISSR	LYT	rep3
506.0856	1515.2332	1514.7276	333.78	3	3.16	1.04	LAGVLDVYEAHLSK	LYT	rep1
506.2029	1515.5853	1514.7276	566.24	3	3.09	0.83	LAGVLDVYEAHLSK	LYK	rep2
522.0811	1042.1465	1042.2775	125.62	2	2.39	0.38	RALVTLIEK	LYT	rep2
522.1006	1042.1856	1042.2775	88.14	2	2.03	0.21	RALVTLIEK	LYK	rep2
1037.0236	3108.0472	3108.5547	163.25	3	5.13	2.99	SKYLAGDFVSLADLAHLPFTDYLVGPIGK	LYT	rep2
552.6543	1103.293	1102.2468	949.14	2	1.87	0.57	VYGPHFASPK	LYK	rep1
551.7752	1101.5347	1102.2468	646.05	2	1.73	0.41	VYGPHFASPK	LYT	rep1

629.938	1257.8604	1258.4331	455.09	2	2.2	0.62	VYGPHFASPKR	LYK	rep1
630.0066	1257.9976	1258.4331	346.06	2	2.18	0.57	VYGPHFASPKR	LYT	rep2
965.9805	2894.9179	2893.3042	557.75	3	3.12	1.39	YLAGDFVSLADLAHLPFTDYLVGPIGK	LYK	rep3
1447.0784	2892.1411	2893.3042	401.98	2	1.42	0.5	YLAGDFVSLADLAHLPFTDYLVGPIGK	LYT	rep3

Matching Genes:

NP_180643.1 (ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase)

Protein Group 26

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	34.48	80.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
771.7852	1541.5547	1541.67	74.79	2	2.91	1.51	AEYDEAGPGIVHRK	LYT	rep3
771.7912	1541.5667	1541.67	67.04	2	2.86	1.18	AEYDEAGPGIVHRK	LYK	rep1
1053.3295	3156.9649	3157.6082	203.73	3	1.72	0.3	CPEVLFQPSFVGMEAAGIHETTYNSIMK : +57.05000 (C1)	LYT	rep3
1154.3876	3460.1392	3460.9693	239.83	3	4.91	1.01	FRCPEVLFQPSFVGMEAAGIHETTYNSIMK : +57.05000 (C3)	LYT	rep2
1154.1586	3459.4522	3460.9693	438.33	3	2.73	0.69	FRCPEVLFQPSFVGMEAAGIHETTYNSIMK : +57.05000 (C3)	LYK	rep1
619.6364	1237.2571	1237.4608	164.6	2	2.45	0.47	HHGVMVGMNQK	LYK	rep3
413.6602	1237.9572	1237.4608	401.12	3	2.15	0.13	HHGVMVGMNQK	LYT	rep2
657.1161	1968.3248	1968.2623	31.74	3	2.34	0.72	IAPEEHPVLLTE APLNPK	LYT	rep3
506.2698	1515.7858	1515.6791	70.45	3	3.9	1.8	IWHHTFYNELR	LYK	rep3
758.6241	1515.2325	1515.6791	294.66	2	3.14	1.22	IWHHTFYNELR	LYT	rep1
1051.3451	3151.0118	3152.5259	480.27	3	5.31	0.39	TTGIVLDSGDGVSHTVPIYEGFSLPHAILR	LYT	rep2
1051.6451	3151.9119	315 2.5259	194.74	3	5	0.25	TTGIVLDSGDGVSHTVPIYEGFSLPHAILR	LYK	rep1
960.0453	1918.075	1919.0838	525.7	2	4.12	2.36	YPIEHGVVSNWDDMEK	LYT	rep1

1139.9122	3416.7132	3416.7483	10.26	3	5.07	2.85	YPIEHGVVSNWDDMEKIWHHTFYNELR	LYT	rep2
1140.1549	3417.4412	3416.7483	202.81	3	5.03	2.94	YPIEHGVVSNWDD MEKIWHHTFYNELR	LYK	rep1

Matching Genes:

NP_175350.1 (ACT8 (ACTIN 8); structural constituent of cytoskeleton [Arabidopsis thaliana])

Protein Group 27

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	37.34	45.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
726.7167	2177.1265	2176.3915	337.74	3	4.58	2.05	CAHHNNHHEGFMNFMHR : +57.05000 (C1)	LYK	rep3
726.1698	2175.4859	2176.3915	416.09	3	2.81	1.49	CAHHNNHHEGFMNFMHR : +57.05000 (C1)	LYT	rep2
630.4407	1258.8658	1259.483	490.05	2	2.17	0.44	FHWKPTCGVK : +57.05000 (C7)	LYK	rep2
631.0579	1260.1001	1259.483	490.01	2	2.12	0.22	FHWKPTCGVK : +57.05000 (C7)	LYT	rep3
1122.1092	2242.2027	2242.4746	121.27	2	2.02	0.78	GFFEVTHDISNLTCADFLR : +57.05000 (C14)	LYT	rep3
509.9577	1526.8496	1525.7505	720.4	3	3.32	1.63	GPILLEDYHLVEK	LYT	rep1
548.1882	1641.5412	1641.8515	188.97	3	2.59	0.97	HAEKYPTPPAVCSGK : +57.05000 (C12)	LYK	rep2
548.1862	1641.535	1641.8515	192.76	3	1.77	0.12	HAEKYPTPPAVCSGK : +57.05000 (C12)	LYT	rep3
606.9702	1817.8872	1817.1072	429.26	3	3.32	1.02	HRLGPNYLQLPVNAPK	LYT	rep1
606.5256	1816.5534	1817.1072	304.74	3	1.52	0.2	HRLGPNYLQLPVNAPK	LYK	rep1
1173.0807	3516.2186	3515.9165	85.92	3	3.06	1.2	ILDFFSHHPESLNMFTFLFDDIGIPQDYR	LYT	rep2
1173.2762	3516.8053	3515.9165	252.78	3	1.36	0.15	ILDFFSHHPESLNMFTFLFDDIGIPQDYR	LYK	rep2
763.5303	1525.045	1523.7809	829.57	2	2.52	0.87	LGPNYLQLPVNAPK	LYT	rep3
762.8079	1523.6001	1523.7809	118.61	2	1.77	0.42	LGPNYLQLPVNAPK	LYK	rep2
945.1427	2832.4046	2831.97	153.49	3	2.98	1.42	VGGTNHSHATQDLYDSIAAGNYPEWK	LYT	rep3

1170.3031	3507.8858	3507.7729	32.18	3	4.26	1.91	YRPASSYNSPFFTTNSGAPVWNNNSSMTVGPR	LYT	rep1
1169.8199	3506.4364	3507.7729	381.03	3	3.56	1.45	YRPASSYNSPFFTTNSGAPVWNNNSSMTVGPR	LYK	rep2

Matching Genes:

NP_001031791.1 (CAT2 (CATALASE 2); catalase [Arabidopsis thaliana])

Protein Group 28

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	32.63	75.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
600.2312	1198.4468	1198.4224	20.41	2	1.86	0.47	AVFPSIVGRPR	LYT	rep1
600.2521	1198.4886	1198.4224	55.25	2	1.82	0.76	AVFPSIVGRPR	LYK	rep1
1055.9095	3164.7052	3163.6559	331.66	3	5.7	3.09	CPEVLFQPSLIGMEAPGIHETTYNSIMK : +57.05000 (C1)	LYT	rep3
1055.0746	3162.2003	3163.6559	460.11	3	5.59	3.14	CPEVLFQPSLIGMEAPGIHETTYNSIMK : +57.05000 (C1)	LYK	rep2
1156.392	3466.1524	3467.017	249.36	3	4.44	1.79	FRCPEVLFQPSLIGMEAPGIHETTYNSIMK : +57.05000 (C3)	LYT	rep2
573.1067	1144.1978	1144.3736	153.67	2	1.96	0.47	HTGVMVGMGQK	LYT	rep1
506.2698	1515.7858	1515.6791	70.45	3	3.9	1.8	IWHHTFYNELR	LYK	rep3
758.6241	1515.2325	1515.6791	294.66	2	3.14	1.22	IWHHTFYNELR	LYT	rep1
738.7589	1475.5022	1475.5221	13.45	2	2.26	0.76	SEYDESGPSIVHR	LYT	rep3
802.683	1603.3504	1603.6951	214.93	2	2.13	0.91	SEYDESGPSIVHRK	LYK	rep2
1051.7975	3152.369	3152.5259	49.77	3	5.25	0.18	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	LYK	rep1
1051.5966	3151.7662	315 2.5259	240.97	3	4.92	0.04	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	LYT	rep2
967.0988	1932.1819	1933.1106	480.4	2	2.68	0.77	YPIEHGIVSNWDDMEK	LYT	rep 1

Matching Genes:

NP_196543.1 (ACT7 (actin 7) [Arabidopsis thaliana])

Protein Group 29

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	19.57	49.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1058.343	2114.6704	2116.4087	821.31	2	4.77	2.6	GHVFEEMQRPGTPLYNIK	LYK	rep3
1058.6516	2115.2876	2116.4087	529.69	2	4.18	2.57	GHVFEEMQRPGTPLYNIK	LYT	rep2
781.0096	2340.0055	2339.6116	168.36	3	1.83	0.76	GVQYLNEIKDSVVAGFQWASK	LYK	rep1
595.5259	1189.0362	1189.3926	299.65	2	1.87	0.21	IMDYKHNIR	LYT	rep1
520.454	1038.8924	1039.2768	369.94	2	2.69	0.54	IRPVLTVNK	LYT	rep2
520.8167	1039.6177	1039.2768	327.99	2	2.39	0.71	IRPVLTVNK	LYK	rep2
761.2166	2280.6262	2281.6823	462.88	3	4.55	2.39	KIWAFGPETTGPNMVVDMCK : +57.05000 (C19)	LYT	rep1
761.1459	2280.4141	2281.6823	555.81	3	1.43	0.07	KIWAFGPETTGPNMVVDMCK : +57.05000 (C19)	LYK	rep1
1030.37	3088.0865	3088.5901	163.04	3	2.16	0.74	LLEPVYMVEIQAPEGALGGIYSVLNQKR	LYT	rep1
904.6308	1807.2459	1807.9659	398.26	2	3.85	2.25	NATLTNEKEVDAHPIR	LYT	rep2
603.9844	1808.9296	1807.9659	533.04	3	3.44	1.86	NATLTNEKEVDAHPIR	LYK	rep1
654.5242	1307.0327	1307.4844	345.41	2	2.39	0.9	NMSVIAHVDHGK	LYK	rep1
772.5315	1543.0474	1543.7926	482.74	2	2.64	0.99	RGFVQFCYEPIK : +57.05000 (C7)	LYK	rep1
772.6875	1543.3594	1543.7926	280.63	2	1.68	0.3	RGFVQFCYEPIK : +57.05000 (C7)	LYT	rep1

1200.6326	2399.2495	2399.5806	137.94	2	3.26	1.64	YRVENLYEGPLDDQYANAIR	LYT	rep2
1200.5608	2399.106	2399.5806	197.77	2	2.67	1.27	YRVENLYEGPLDDQYANAIR	LYK	rep1

Matching Genes:

NP_849818.1 (LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana])

Protein Group 30

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	18.83	54.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
508.9644	1523.8696	1523.6548	140.99	3	3.9	0.24	ARFEELNNDLFR	LYT	rep3
763.6714	1525.3272	1523.6548	1097.63	2	1.45	0.33	ARFEELNNDLFR	LYK	rep2
602.045	1202.0743	1202.2799	171.04	2	2.97	0.47	GRLSQEEIDR	LYK	rep3
601.8449	1201.6741	1202.2799	503.87	2	2.43	0.35	GRLSQEEIDR	LYT	rep1
887.6296	2659.8654	2661.7966	725.52	3	2.14	0.41	GVNPDEAVAYGAAVQGGILSGEGGDETK	LYT	rep1
830.6215	1659.2273	1659.8848	396.07	2	3.39	1.6	IINEPTAAAIAYGLDK	LYT	rep1
894.5905	1787.1653	1788.0577	499.09	2	3.68	2.05	IINEPTAAAIAYGLDKK	LYT	rep1
894.6775	1787.3394	1788.0577	401.74	2	3.09	1.74	IINEPTAAAIAYGLDKK	LYK	rep1
636.6647	1906.9705	1907.1391	88.41	3	2.99	1.15	IKDAVVTVPAYFNDAQR	LYK	rep2
636.6281	1906.8607	1907.1391	146.01	3	1.93	0.61	IKDAVVTVPAYFNDAQR	LYT	rep1
602.3731	1202.7305	1201.4629	1055.07	2	2.14	0.48	KLVPYQIVNK	LYT	rep3
601.4549	1200.8941	1201.4629	473.42	2	1.83	0.48	KLVPYQIVNK	LYK	rep2
1052.295	2102.5743	2103.4498	416.23	2	4.44	2.86	LKEVEAVCNPIITAVYQR : +57.05000 (C8)	LYT	rep1
702.0964	2103.2658	2103.4498	87.44	3	2.67	1.03	LKEVEAVCNPIITAVYQR : +57.05000 (C8)	LYK	rep2

768.9619	1535.9082	1536.6119	457.95	2	3.68	1.5	NGHVEIIANDQGNR	LYK	rep2
768.8575	1535.6993	1536.6119	593.95	2	3.52	1.76	NGHVEIIANDQGNR	LYT	rep1

Matching Genes:

NP_198206.1 (luminal binding protein 1 (BiP-1) (BP1) [Arabidopsis thaliana])

Protein Group 31

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	18.64	74.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
762.5843	1523.1529	1522.7098	290.96	2	3.56	0.06	ARFEELNIDLFR	LYK	rep1
762.5401	1523.0645	1522.7098	232.91	2	3.17	0.01	ARFEELNIDLFR	LYT	rep3
838.6761	1675.3365	1675.6749	201.98	2	3.11	1.34	ATAGDTHLGGEDFDNR	LYT	rep1
838.4655	1674.9153	1675.6749	453.31	2	3.09	1.66	ATAGDTHLGGEDFDNR	LYK	rep1
863.955	2588.8414	2588.8157	9.92	3	2.19	0.53	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYT	rep1
863.8718	2588.592	2588.8157	86.41	3	1.7	0.5	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYK	rep2
830.6215	1659.2273	1659.8848	396.07	2	3.39	1.6	IINEPTAAAIAYGLDK	LYT	rep1
894.5905	1787.1653	1788.0577	499.09	2	3.68	2.05	IINEPTAAAIAYGLDKK	LYT	rep1
894.6775	1787.3394	1788.0577	401.74	2	3.09	1.74	IINEPTAAAIAYGLDKK	LYK	rep1
1066.5057	3196.4937	3196.42	23.08	3	3.61	1.43	KIEDSIEAAIEWLEANQLAECDEFEDK : +57.05000 (C21)	LYK	rep3
550.451	1648.3297	1645.9881	1422.58	3	3.63	1.8	MKELESICNPIIAK : +57.05000 (C8)	LYT	rep3
639.9811	1277.9466	1278.4846	420.84	2	3.06	1.48	MVNHFVQEFK	LYK	rep3
640.4624	1278.9092	1278.4846	332.12	2	2.97	1.31	MVNHFVQEFK	LYT	rep2
717.9392	1433.8628	1434.671	563.32	2	3.01	1.05	MVNHFVQEFKR	LYK	rep1

717.9734	1433.9312	1434.671	515.67	2	2.68	1.24	MVNHFVQEFKR	LYT	rep3

Matching Genes:

NP_187555.1 (heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) [Arabidopsis thaliana])

Protein Group 32

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	34.64	34.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
636.0758	1905.2039	1904.2002	527.13	3	5.02	2.65	HVLVILTDMSSYADALR	LYT	rep3
1152.7831	3455.3258	3455.7959	136.04	3	6.39	3.55	IFNGSGKPIDNGPPILPEAYLDISGSSINPSER	LYK	rep3
1152.4882	3454.441	3455.7959	392.06	3	5.82	3.26	IFNGSGKPIDNGPPILPEAYLDISGSSINPSER	LYT	rep3
727.434	2179.2784	2178.5216	347.41	3	5.19	3.28	IPLFSAAGLPHNEIAAQICR : +57.05000 (C19)	LYT	rep1
727.464	2179.3685	2178.5216	388.76	3	5.19	3.29	IPLFSAAGLPHNEIAAQICR : +57.05000 (C19)	LYK	rep3
675.1935	2022.557	2023.1719	303.93	3	2.56	0.67	KDHSDVSNQLYANYAIGK	LYT	rep3
1377.0018	4127.982	4128.6333	157.75	3	4.7	2.82	KGSITQIPILTMPNDDITHPTPDLTGYITEGQIYIDR	LYT	rep1
1376.8944	4127.6598	4128.6333	235.8	3	3.66	1.95	KGSITQIPILTMPNDDITHPTPDLTGYITEGQIYIDR	LYK	rep1
615.5054	1228.9952	1229.3452	284.75	2	2.61	0.71	RGQVLEVDGEK	LYK	rep1
615.5827	1229.1497	1229.3452	159.0	2	2.44	0.76	RGQVLEVDGEK	LYT	rep2
1206.4017	3616.1817	3617.9858	498.65	3	2.3	0.54	TENLIQEDHGEDNFAIVFAAMGVNMETAQFFK	LYK	rep3

Matching Genes:

NP_973871.1 ((VACUOLAR ATP SYNTHASE SUBUNIT B3); ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism / hydrogen-exporting ATPase, phosphorylative mechanism [Arabidopsis thaliana])

Protein Group 33

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	28.54	64.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
534.2093	1066.4029	1066.2558	137.88	2	2.11	0.34	DLALIIHGSK	LYK	rep2
533.9639	1065.9121	1066.2558	322.35	2	1.75	0.48	DLALIIHGSK	LYT	rep1
896.2537	1790.4917	1789.9874	281.75	2	4.31	2.47	FKDIFQEVYEASWK	LYT	rep2
597.538	1789.5904	1789.9874	221.79	3	4.15	1.7	FKDIFQEVYEASWK	LYK	rep1
497.7909	993.5662	993.0373	532.63	2	1.87	0.93	HAFGDQYR	LYK	rep1
497.7672	993.5187	993.0373	484.81	2	1.6	0.71	HAFGDQYR	LYT	rep3
626.6272	1251.2388	1251.4974	206.65	2	2.26	0.73	LIDDMVAYALK	LYT	rep2
644.7974	1287.5791	1287.5493	23.17	2	1.83	0.62	LITPFVELDIK	LYT	rep2
749.2167	1496.4178	1496.8238	271.26	2	1.76	0.71	LVPGWTKPICIGR : +57.05000 (C10)	LYK	rep3
748.6848	1495.354	1496.8238	981.91	2	1.45	0.49	LVPGWTKPICIGR : +57.05000 (C10)	LYT	rep2
887.7714	1773.5271	1774.0993	322.52	2	3.88	2	NILNGTVFREPIICK : +57.05000 (C14)	LYK	rep1
888.1635	1774.3113	1774.0993	119.49	2	3.36	1.77	NILNGTVFREPIICK : +57.05000 (C14)	LYT	rep2
799.088	1596.1604	1595.7195	276.34	2	4.34	2.51	SKYDAAGIWYEHR	LYT	rep3
799.1072	1596.1988	1595.7195	300.36	2	3.87	1.01	SKYDAAGIWYEHR	LYK	rep2
679.2493	1356.4829	1355.4591	755.35	2	2.88	1.68	TIEAEAAHGTVTR	LYK	rep3
678.5169	1355.0181	1355.4591	325.35	2	2.83	1.4	TIEAEAAHGTVTR	LYT	rep2
559.4082	1116.8008	1117.2615	412.3	2	2.83	0.85	YFDLGLPHR	LYT	rep3

559.3822	1116.7488	1117.2615	458.84	2	2.68	0.84	YFDLGLPHR	LYK	rep2

Matching Genes:

NP_176768.1 (isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative [Arabidopsis thaliana])

Protein Group 34

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	43.96	54.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
964.4705	2890.3879	2888.1579	772.1	3	3.31	1.42	ALDWGPGGGPDLIVDDGGDATLLIHEGVK	LYK	rep2
963.1738	2886.498	2888.1579	574.74	3	2.56	0.97	ALDWGPGGGPDLIVDDGGDATLLIHEGVK	LYT	rep2
565.3562	1128.6968	1129.359	586.34	2	2.19	0.62	DIIMVDHMR	LYT	rep3
565.7847	1129.5537	1129.359	172.44	2	1.7	0.02	DIIMVDHMR	LYK	rep2
788.0707	2361.1886	2361.574	163.2	3	3.11	1.28	DQSDYVSIPIEGPYKPPHYR	LYK	rep1
787.9305	2360.7681	2361.574	341.22	3	2.72	0.87	DQSDYVSIPIEGPYKPPHYR	LYT	rep2
513.6719	102 5.3282	1025.1874	137.34	2	1.77	0.6	HSLPDGLMR	LYT	rep2
513.6179	1025.2202	1025.1874	32.08	2	1.53	0.44	HSLPDGLMR	LYK	rep2
1262.3226	3783.9444	3784.3387	104.18	3	4.94	2.63	LMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK : +57.05000 (C6); +57.05000 (C17)	LYK	rep1
1262.0262	3783.0553	3784.3387	339.14	3	3.88	1.6	LMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK : +57.05000 (C6);	LYT	rep3

							+57.05000 (C17)		
739.3221	1476.6285	1475.6499	663.14	2	2.41	1.14	LVGVSEETTTGVKR	LYT	rep1
738.6745	1475.3333	1475.6499	214.55	2	2.27	1.01	LVGVSEETTTGVKR	LYK	rep1
1064.7548	3191.2408	3190.578	207.73	3	4.92	2.99	NNAIVCNIGHFDNEIDMLGLETYPGVKR : +57.05000 (C6)	LYT	rep2
1064.6537	3190.9376	3190.578	112.69	3	4.61	3.06	NNAIVCNIGHFDNEIDMLGLETYPGVKR : +57.05000 (C6)	LYK	rep1
630.5091	1259.0025	1259.395	311.68	2	2.96	1.16	SKFDNLYGCR : +57.05000 (C9)	LYT	rep1
630.2233	1258.4309	1259.395	765.5	2	2.18	0.92	SKFDNLYGCR : +57.05000 (C9)	LYK	rep2
426.0969	850.1781	850.0636	134.68	2	1.97	0.64	VALLHLGK	LYT	rep2
426.0254	850.0352	850.0636	33.47	2	1.67	0.33	VALLHLGK	LYK	rep2

Matching Genes :

NP_001031627.1 (HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase [Arabidopsis thaliana])

Protein Group 35

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	55.44	30.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
773.796	2318.3646	2318.6238	111.78	3	5.3	3.15	IMEKLPGHHGPTNTGVVHHEK	LYK	rep3
773.557	2317.6475	2318.6238	421.04	3	2.69	0.85	IMEKLPGHHGPTNTGVVHHEK	LYT	rep1
649.2074	1944.5987	1945.1539	285.43	3	3.27	1.15	LPGHHGPTNTGVVHHEKK	LYK	rep1
649.2762	1944.8053	1945.1539	179.25	3	3.26	0.86	LPGHHGPTNTGVVHHEKK	LYT	rep3
965.662	2893.9625	2895.0356	370.69	3	4.16	1.93	LPGHHGSHQTGTNTAYGTNTNVVHHEK	LYT	rep2
965.6353	2893.8823	2895.0356	398.39	3	4.13	2.26	LPGHHGSHQTGTNTAYGTNTNVVHHEK	LYK	rep1
1128.0609	3381.1593	3382.6518	441.25	3	2.96	1.07	VMEKLPGHHGSHQTGTNTAYGTNTNVVHHEK	LYK	rep3
727.2654	2178.7727	2179.385	280.97	3	2.98	1.26	VMEQLPGHHGATGTGGVHHEK	LYT	rep1

727.277	2178.8075	2179.385	265	3	2.9	1.14	VMEQLPGHHGATGTGGVHHEK	LYK	rep1
769.9822	2306.9231	2307.5578	275.09	3	3.57	1.56	VMEQLPGHHGATGTGGVHHEKK	LYK	rep3
1138.7167	3413.1265	3414.6077	433.76	3	4.74	2.73	VMEQLPGHHGSHQTGTNTTYGTTNTGGVHHEK	LYK	rep1
1138.8275	3413.4591	3414 .6077	336.37	3	4.45	2.63	VMEQLPGHHGSHQTGTNTTYGTTNTGGVHHEK	LYT	rep2

Matching Genes:

NP_190666.1 (LTI30/XERO2 (LOW TEMPERATURE-INDUCED 30) [Arabidopsis thaliana])

Protein Group 36

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	18.91	30.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
585.8231	1754.4459	1754.8168	211.35	3	2.36	0.84	ADDLTGINDEEHAAKR	LYT	rep3
586.0504	1755.1278	1754.8168	177.23	3	1.49	0.36	ADDLTGINDEEHAAKR	LYK	rep2
974.0921	1946.1685	1947.0737	464.92	2	3.54	2.05	ANGENSAKNPSTISTTVQK	LYT	rep1
649.8236	1946.4473	1947.0737	321.7	3	1.38	0.43	ANGENSAKNPSTISTTVQK	LYK	rep1
912.6889	1823.3621	1824.0102	355.34	2	2.49	1.15	DLVNHPNFDAIIAAGTR	LYK	rep1
896.2061	1790.3965	1790.8475	251.84	2	3.49	1.67	EASQAYEEYHEAVHK	LYT	rep3
895.9212	17 89.8267	1790.8475	570.02	2	2.92	0.71	EASQAYEEYHEAVHK	LYK	rep2
739.0879	1476.1602	1476.5948	294.36	2	1.6	0.27	EFEAAHAGFEQLK	LYT	rep3
391.567	781.1184	780.8752	311.54	2	2.35	0.19	GDALHIR	LYK	rep3
806.6219	1611.2281	1611.8049	357.89	2	2.55	1.17	LTTSLNNLVDTHRK	LYK	rep2
806.3745	1610.7334	1611.8049	664.77	2	2.46	1.27	LTTSLNNLVDTHRK	LYT	rep1

610.2024	1218.3892	1218.3891	0.04	2	2.77	0.69	RNSMLEAIER	LYT	rep1
652.4441	1302.8726	1303.4509	443.68	2	3.11	0.97	RQNMLDEIER	LYT	rep1
652.7095	1303.4034	1303.4509	36.49	2	2.65	0.7	RQNMLDEIER	LYK	rep2
1286.3643	2570.7129	2571.8485	441.55	2	2.71	1.45	SSGGYNAGLEGLLKPADGVCGCFNK : +57.05000 (C20); +57.05000 (C22)	LYT	rep1

Matching Genes:

NP_188216.2 ((TSA1-LIKE); unknown protein [Arabidopsis thaliana])

Protein Group 37

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	31.53	49.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
858.5389	2572.5933	2573.8254	478.7	3	6.55	3.81	ASFQNVGLDRPSDLVALSGGHTFGK	LYK	rep3
858.6265	2572.8559	2573.8254	376.68	3	5.21	2.88	ASFQNVGLDRPSDLVALSGGHTFGK	LYT	rep2
922.7173	2765.1284	2765.1775	17.76	3	1.99	0.3	DSLQAFFALANTNLPAPFFTLPQLK	LYK	rep3
674.2176	1346.4195	1345.531	660.32	2	5.06	2.63	FFNAFVEAMNR	LYK	rep1
673.5645	1345.1133	1345.531	310.42	2	4.1	2.37	FFNAFVEAMNR	LYT	rep3
794.2461	1586.4766	1586.819	215.75	2	3.82	1.63	MGNITPLTGTQGQIR	LYT	rep2
794.1053	1586.1949	1586.819	393.3	2	2.36	0.83	MGNITPLTGTQGQIR	LYK	rep1
617.491	1232.9663	1233.4656	404.79	2	1.45	0.33	MKAAVETACPR : +57.05000 (C9)	LYT	rep1
607.0564	1212.0972	1211.3754	595.87	2	2.52	1.01	NQCQFIMDR : +57.05000 (C3)	LYT	rep2
606.3299	1210.6441	1211.3754	603.7	2	1.6	0.58	NQCQFIMDR : +57.05000 (C3)	LYK	rep2
974.5792	2920.7142	2921.364	222.43	3	2.68	0.79	RDSLQAFFALANTNLPAPFFTLPQLK	LYK	rep1
568.3727	1702.0946	1701.9233	100.61	3	2.79	1.3	TPTVFDNKYYVNLK	LYK	rep1

568.4823	1702.4234	1701.9233	293.84	3	2.55	1.17	TPTVFDNKYYVNLK	LYT	rep2

Matching Genes:

NP_850652.1 (peroxidase 32 (PER32) (P32) (PRXR3) [Arabidopsis thaliana])

Protein Group 38

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	9	16.54	69.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
838.6761	1675.3365	1675.6749	201.98	2	3.11	1.34	ATAGDTHLGGEDFDNR	LYT	rep1
838.4655	1674.9153	1675.6749	453.31	2	3.09	1.66	ATAGDTHLGGEDFDNR	LYK	rep1
863.955	2588.8414	2588.8157	9.92	3	2.19	0.53	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYT	rep1
863.8718	2588.592	2588.8157	86.41	3	1.7	0.5	GEGPAIGIDLGTTYSCVGVWQHDR : +57.05000 (C16)	LYK	rep2
830.6215	1659.2273	1659.8848	396.07	2	3.39	1.6	IINEPTAAAIAYGLDK	LYT	rep1
894.5905	1787.1653	1788.0577	499.09	2	3.68	2.05	IINEPTAAAIAYGLDKK	LYT	rep1
894.6775	1787.3394	1788.0577	401.74	2	3.09	1.74	IINEPTAAAIAYGLDKK	LYK	rep1
639.9811	1277.9466	1278.4846	420.84	2	3.06	1.48	MVNHFVQEFK	LYK	rep3
640.4624	1278.9092	1278.4846	332.12	2	2.97	1.31	MVNHFVQEFK	LYT	rep2

717.9392	1433.8628	1434.671	563.32	2	3.01	1.05	MVNHFVQEFKR	LYK	rep1
717.9734	1433.9312	1434.671	515.67	2	2.68	1.24	MVNHFVQEFKR	LYT	rep3
602.4823	1804.4234	1804.0439	210.36	3	2.71	0.51	NQVAMNPVNTVFDAKR	LYK	rep1
602.3204	1803.9378	1804.0439	58.82	3	2.2	0.58	NQVAMNPVNTVFDAKR	LYT	rep1
712.2078	1422.3999	1421.664	517.62	2	1.56	0.29	PMIVVEYKGEEK	LYK	rep3
719.4934	1436.9712	1436.6169	246.62	2	3.96	2.09	VQQLLQDFFNGK	LYT	rep1
718.9771	1435.9385	1436.6169	472.23	2	2.31	0.95	VQQLLQDFFNGK	LYK	rep2

Matching Genes:

NP_1958 69.1 (heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) [Arabidopsis thaliana])

Protein Group 39

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	41.86	56.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
943.1652	2826.472	2826.0937	133.85	3	4.58	2.79	HTGAGILSMANSGPNTNGSQFFICTDK : +57.05000 (C24)	LYT	rep3
1413.6006	2825.1856	2826.0937	321.35	2	3.46	1.94	HTGAGILSMANSGPNTNGSQFFICTDK : +57.05000 (C24)	LYK	rep2
1205.8961	3614.6649	3613.9572	195.81	3	4.48	2.64	HTGAGILSMANSGPNTNGSQFFICTDKTSWLDGK : +57.05000 (C24)	LYK	rep1
1205.3168	3612.9268	3613.9572	285.11	3	4.42	2.41	HTGAGILSMANSGPNTNGSQFFICTDKTSWLDGK : +57.05000 (C24)	LYT	rep2
506.9988	1011.982	1012.2099	225.17	2	2.64	1.27	HVVFGQVVK	LYK	rep3
506.9467	1011.8777	1012.2099	328.16	2	2.28	1.09	HVVFGQVVK	LYT	rep3
542.5409	1624.5992	1623.9436	403.72	3	2.98	0.07	HVVFGQVVKGLDVVK	LYT	rep2
813.2819	1624.5481	1623.9436	372.27	2	1.69	0.14	HVVFGQVVKGLDVVK	LYK	rep2
985.3523	2953.0334	2954.2667	417.45	3	7.28	4.68	KHTGAGILSMANSGPNTNGSQFFICTDK : +57.05000 (C25)	LYK	rep3

985.5203	2953.5373	2954.2667	246.88	3	5.12	3.44	KHTGAGILSMANSGPNTNGSQFFICTDK : +57.05000 (C25)	LYT	rep1
470.9024	939.7892	939.1589	671.13	2	2.46	0.75	LGKPLHFK	LYK	rep3
470.4074	938.7992	939.1589	383	2	1.29	0.17	LGKPLHFK	LYT	rep2
764.2752	1526.5347	1526.762	148.84	2	1.82	0.42	VFFDMSLSGTPIGR	LYK	rep2
764.2764	1526.5371	1526.762	147.24	2	1.77	0.62	VFFDMSLSGTPIGR	LYT	rep1

Matching Genes:

NP_195213.1 (ROC5 (ROTAMASE CYP 5); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana])

Protein Group 40

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	35.27	35.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
509.1214	1016.2271	1016.1805	45.88	2	2.3	0.76	AMIGQVAGGGR	LYT	rep2
899.7385	2696.1921	2696.9287	273.13	3	5.73	3.65	GVAMNPVEHPHGGGNHQHIGHASTVR	LYK	rep3
899.8647	2696.5708	2696.9287	132.72	3	4.2	2.2	GVAMNPVEHPHGGGNHQHIGHASTVR	LYT	rep3
951.8729	2852.5953	2853.115	182.14	3	3.15	1.61	GVAMNPVEHPHGGGNHQHIGHASTVRR	LYK	rep1
951.7012	2852.08	2853.115	362.74	3	2.2	0.88	GVAMNPVEHPHGGGNHQHIGHASTVRR	LYT	rep2
647.0866	1292.1575	1292.4462	223.34	2	2.59	1.11	GVVTEIIHDPGR	LYT	rep1
646.8516	1291.6875	1292.4462	586.96	2	1.39	0.24	GVVTEIIHDPGR	LYK	rep2
691.2596	1380.5035	1379.6964	584.95	2	3.04	0.99	KATLVVGNVLPLR	LYT	rep1
690.6278	1379.24	1379.6964	330.78	2	1.45	0.06	KATLVVGNVLPLR	LYK	rep2

988.1659	1974.3162	1975.1539	424.12	2	3.52	2.04	SIPEGAVVCNVEHHVGDR : +57.05000 (C9)	LYK	rep1
988.1149	1974.2141	1975.1539	475.79	2	2.99	1.4	SIPEGAVVCNVEHHVGDR : +57.05000 (C9)	LYT	rep3
984.6569	2950.9471	2952.2466	440.16	3	3.89	1.83	VRGVAMNPVEHPHGGGNHQHIGHASTVR	LYK	rep3
354.2559	1059.7441	1059.2284	486.88	3	1.98	0.46	VTFRHPFR	LYT	rep1
531.168	1060.3203	1059.2284	1030.91	2	1.92	0.22	VTFRHPFR	LYK	rep1

Matching Genes:

NP_179393.1 (EMB2296 (EMBRYO DEFECTIVE 2296); structural constituen t of ribosome [Arabidopsis thaliana])

Protein Group 41

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	35.24	37.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1175.4304	2348.8452	2349.5615	304.85	2	1.9	0.58	ELVKDDAWLDGEFISTVQQR	LYT	rep3
1443.2195	2884.4234	2884.4304	2.44	2	3.62	1.46	GIMLGADQPVILHMLDIPPAAEALNGVK	LYT	rep1
592.1202	1773.3372	1773.9714	357.51	3	4.58	2.44	KLSSALSAASSACDHIR : +57.05000 (C13)	LYT	rep2
592.2274	1773.6588	1773.9714	176.26	3	4.54	2.23	KLSSALSAASSACDHIR : +57.05000 (C13)	LYK	rep1
823.6116	1645.2076	1645.7985	359.08	2	3.38	1.78	LSSALSAASSACDHIR : +57.05000 (C12)	LYT	rep1
549.6132	1645.816	1645.7985	10.61	3	2.56	1.2	LSSALSAASSACDHIR : +57.05000 (C12)	LYK	rep2
681.2234	1360.4312	1360.667	173.29	2	4.79	2	MELIDAAFPLLK	LYT	rep2
681.0581	1360.1006	1360.667	416.24	2	3.5	1.22	MELID AAFPLLK	LYK	rep2
1133.6028	2265.19	2266.4375	550.43	2	4.99	2.96	NVIIWGNHSSSQYPDVNHAK	LYK	rep3
1134.1729	2266.3301	2266.4375	47.38	2	4.77	2.99	NVIIWGNHSSSQYPDVNHAK	LYT	rep2
667.6772	2000.0083	2000.4173	204.5	3	2.75	0.93	VLVTGAAGQIGYALVPMIAR	LYT	rep2

Matching Genes:

NP_171936.1 (malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana])

Protein Group 42

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	34.06	27.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
738.3621	1474.7085	1475.5653	580.63	2	3.28	0.83	DLLYKDHNSDQK	LYK	rep3
738.7715	1475.5274	1475.5653	25.7	2	2.52	0.33	DLLYKDHNSDQK	LYT	rep2
1410.8192	4229.4342	4229.6758	57.12	3	6.54	4.5	EDLIASLTVNDKGDLLNASYYHIVNPLFNTAVGAEVSHK	LYT	rep1
1410.5936	4228.7574	4229.6758	217.12	3	5.23	3.51	EDLIASLTVNDKGDLLNASYYHIVNPLFNTAVGAEVSHK	LYK	rep2
977.5278	2929.56	2930.2429	233.05	3	5.88	3.71	GDLLNASYYHIVNPLFNTAVGAEVSHK	LYT	rep3
977.4979	2929.4703	2930.2429	263.67	3	4.77	2.99	GDLLNASYYHIVNPLFNTAVGAEVSHK	LYK	rep2
582.0393	1162.063	1162.3404	238.67	2	2.38	1.08	GPGLYTEIGKK	LYK	rep2
581.9488	1161.8819	1162.3404	394.52	2	2.34	0.74	GPGLYTEIGKK	LYT	rep3
760.9322	1519.8487	1518.7196	743.44	2	3.73	1.32	KGDLLLGDVAFQSR	LYK	rep2
759.9248	1517.834	1518.7196	583.1	2	2.96	0.94	KGDLLLGDVAFQSR	LYT	rep1
975.638	1949.2603	1949.2224	19.44	2	4.18	2.18	VNSAGIASALIQHEWKPK	LYK	rep3
975.2571	1948.4986	1949.2224	371.34	2	3.51	2.1	VNSAGIASALIQHEWKPK	LYT	rep2

Matching Genes:

NP_186777.1 (porin, putative [Arabidopsis thaliana])

Protein Group 43

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	10	35.41	56.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
695.083	1388.1504	1388.5707	302.64	2	2.49	0.92	ELDYLVGAVANPK	LYK	rep3
489.7561	1466.2448	1465.808	298.04	3	4.55	2.17	FLKPSVAGFLMQK	LYK	rep3
489.5607	1465.6587	1465.808	101.83	3	3.84	1.3	FLKPSVAGFLMQK	LYT	rep3
573.3002	1716.877	1716.8054	41.72	3	1.43	0.31	FYAEEEKNDPEFAK	LYT	rep3
791.3812	2371.1202	2370.707	174. 29	3	1.89	0.28	GVSLLLPTDVVIADKFAPDANSK	LYK	rep1
678.4752	2032.4022	2032.2682	65.94	3	2.24	0.09	KLAALADVYVNDAFGTAHR	LYT	rep1
1075.5376	107 4.5298	1074.2781	234.31	1	2.28	0.65	KPFAAIVGGSK	LYT	rep3
537.885	1073.7544	1074.2781	487.43	2	1.75	0.25	KPFAAIVGGSK	LYK	rep3
635.8317	1904.4715	1904.0953	197.57	3	3.75	2.04	LAALADVYVNDAFGTAHR	LYK	rep1
636.0225	1905.0439	1904.0953	498.18	3	2.09	0.87	LAALADVYVNDAFGTAHR	LYT	rep2
955.5889	2863.7431	2863.2566	169.93	3	1.8	0.45	MSHISTGGGASLELLEGKPLPGVLALDEA	LYT	rep2
634.6123	1267.209	1265.5322	1325	2	3.19	1.7	VVLCSHLGRPK : +57.05000 (C4)	LYT	rep3
633.5482	1265.0808	1265.5322	356.65	2	3.02	1.41	VVLCSHLGRPK : +57.05000 (C4)	LYK	rep3
358.3953	1072.16 23	1072.3053	133.33	3	2.26	0.67	YSLKPLVPR	LYT	rep3
358.5236	1072.5472	1072.3053	225.6	3	2.06	0.87	YSLKPLVPR	LYK	rep2

Matching Genes:

NP_178073.1 (PGK (PHOSPHOGLYCERATE KINASE) [Arabidopsis thaliana])

Protein Group 44

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	46.67	46.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1221.847	2441.6783	2442.7717	447.63	2	2.59	1.29	AGEALYALGAYFATTTTPVTPAKK	LYT	rep1
947.7298	1893.4439	1893.1791	139.88	2	2.51	1.36	ASELLHQFGVHVMPLTN	LYK	rep2
946.974	1891.9324	1893.1791	658.5	2	1.88	0.55	ASELLHQFGVHVMPLTN	LYT	rep3
669.8052	1337.5948	1337.4886	79.35	2	2.31	0.91	EEGHKIVGFHGK	LYT	rep1
1426.0245	4275.0501	4276.5952	361.29	3	5.13	2.92	GAENIVGGEHGKPTLLGFEEFEIDYPSEYITAVEGTYDK	LYK	rep2
1426.1774	4275.5086	4276.5952	254.07	3	4.82	3.17	GAENIVGGEHGKPTLLGFEEFEIDYPSEYITAVEGTYDK	LYT	rep3
1043.3113	2084.607	2085.3293	346.4	2	4.77	3	KVHVGQGQDGVSSINVVYAK	LYK	rep3
696.1031	2085.286	2085.3293	20.79	3	4.75	2.5	KVHVGQGQDGVSSINVVYAK	LYT	rep1
393.5314	785.0472	784.9086	176.5	2	2.06	0	LVGFHGR	LYK	rep3
657.1935	1968.557	1968.998	224.01	3	2.56	1.15	VEAGGGAGGASWDDGVHDGVR	LYT	rep1
657.3512	1969.0301	1968.998	16.29	3	1.3	0.24	VEAGGGAGGASWDDGVHDGVR	LYK	rep2
979.0247	1956.0337	1957.1565	573.67	2	3.61	2.25	VHVGQGQDGVSSINVVYAK	LYK	rep2
978.9491	1955.8826	1957.1565	650.88	2	1.49	0.55	VHVGQGQDGVSSINVVYAK	LYT	rep3

Matching Genes:

NP_001030711.1 (jacalin lectin family protein [Arabidopsis thaliana])

Protein Group 45

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	52.32	60.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1168.8676	3503.5792	3504.7056	321.39	3	5.52	2.67	DENHLFPDAIGHHIQGVTVHDGEWDSHEAIK	LYK	rep3
1168.8781	3503.6107	3504.7056	312.4	3	3.81	1.61	DENHLFPDAIGHHIQGVTVHDGEWDSHEAIK	LYT	rep3
621.0298	1240.044	1240.4347	314.97	2	3.72	1.62	GLEGHVMEQLK	LYK	rep1
621.138	1240.2603	1240.4347	140.59	2	3.63	1.39	GLEGHVMEQLK	LYT	rep3
538.9132	1075.8108	1076.3174	470.63	2	2.19	0.39	ITMIWEKR	LYT	rep2
538.8972	1075.7788	1076.3174	500.34	2	1.81	0.02	ITMIWEKR	LYK	rep1
879.1857	1756.3557	1756.9809	355.84	2	5.13	2.49	IWNYTCDGKPEVFK : +57.05000 (C6)	LYK	rep1
879.2616	1756.5076	1756.9809	269.41	2	4.3	2.35	IWNYTCDGKPEVFK : +57.05000 (C6)	LYT	rep3
707.5858	1413.156	1413.602	315.5	2	2.01	0.5	SVVADMDEHVLKA	LYK	rep1
707.8329	1413.6502	1413.602	34.06	2	1.35	0.14	SVVADMDEHVLKA	LYT	rep1
1282.8646	3845.5704	3847.103	398.38	3	6.42	4.36	WRDENHLFPDAIGHHIQGVTVHDGEWDSHEAIK	LYK	rep3
1282.8966	3845.6663	3847.103	373.44	3	5.33	3.63	WRDENHLFPDAIGHHIQGVTVHDGEWDSHEAIK	LYT	rep1

Matching Genes:

NP_565265.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 46

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	63.37	61.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
599.4961	1196.9766	1197.3912	346.27	2	2.84	1.16	GVGGTGKPLHFK	LYK	rep3
599.391	1196.7664	1197.3912	521.83	2	2.44	0.88	GVGGTGKPLHFK	LYT	rep3

1397.896	2793.7764	2794.138	129.42	2	3.72	1.57	HTGPGILSMANAGANTNGSQFFICTVK : +57.05000 (C24)	LYK	rep3
932.2632	2793.7661	2794.138	133.12	3	3.36	1.54	HTGPGILSMANAGANTNGSQFFICTVK : +57.05000 (C24)	LYT	rep3
813.1731	1624.3306	1624.8852	341.34	2	3.31	0.84	HVVFGQVVEGLDVVK	LYT	rep1
542.5947	1624.7607	1624.8852	76.64	3	3.22	0.05	HVVFGQVVEGLDVVK	LYK	rep3
733.9283	1465.8409	1465.7201	82.4	2	3.02	1.25	IVMELYTDKTPR	LYK	rep1
733.8836	1465.7515	1465.7201	21.44	2	1.84	0.45	IVMELYTDKTPR	LYT	rep2
974.6825	2921.024	2922.3109	440.38	3	7.53	5.03	KHTGPGILSMANAGANTNGSQFFICTVK : +57.05000 (C25)	LYK	rep3
974.813	2921.4155	2922.3109	306.42	3	6.95	4.56	KHTGPGILSMANAGANTNGSQFFICTVK : +57.05000 (C25)	LYT	rep1
813.8361	2438.4847	2440.759	931.81	3	1.7	0.6	TDWLDGKHVVFGQVVEGLDVVK	LYT	rep3
1278.0138	3831.0179	3832.0775	276.51	3	2.81	1.5	VIPNFMCQGGDFTAGNGTGGESIYGSKFEDENFER : +57.05000 (C7)	LYK	rep1
1278.318	3831.9305	3832.0775	38.36	3	1.48	0.41	VIPNFMCQGGDFTAGNGTGGESIYGSKFEDENFER : +57.05000 (C7)	LYT	rep2

Matching Genes:

NP_195585.1 (ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana])

Protein Group 47

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	52.58	49.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
600.4198	1798.2359	1797.9516	158.16	3	2.13	0.62	AAVGAPDHLGDCPFSQR : +57.05000 (C12)	LYT	rep1

811.9911	2432.9498	2433.5937	264.61	3	2.11	0.79	DSNDGSEHALLVELEALENHLK	LYT	rep1
1225.1126	2448.2095	2449.8122	654.23	2	4.88	2.61	IHLINLSDKPQWFLDISPQGK	LYK	rep3
817.5967	2449.7666	2449.8122	18.65	3	1.75	0.6	IHLINLSDKPQWFLDISPQGK	LYT	rep2
713.5885	1425.1614	1425.6821	365.23	2	3.89	1.89	LYHLQVALGHFK	LYT	rep3
713.4141	1424.8125	1425.6821	609.94	2	3.86	1.98	LYHLQVALGHFK	LYK	rep2
593.6028	1185.19	1185.2511	51.56	2	1.58	0.54	SHDGPFIAGER	LYT	rep3
883.709	2648.1035	2648.8442	279.65	3	5.01	2.3	SKDSNDGSEHALLVELEALENHLK	LYK	rep3
883.8149	2648.4213	2648.8442	159.65	3	4.85	2.81	SKDSNDGSEHALLVELEALENHLK	LYT	rep3
972.974	1943.9324	1945.1694	635.94	2	3.52	1.79	SWSVPESFPHVHNYMK	LYK	rep3
973.2818	1944.5479	1945.1694	319.53	2	3.05	1.34	SWSVPESFPHVHNYMK	LYT	rep3
550.3504	1098.6851	1099.2826	543.52	2	1.8	0.55	VSAVDLSLAPK	LYT	rep1

Matching Genes:

NP_173387.1 (DHAR1 (DEHYDROASCORBATE REDUCTASE); glutathione dehydrogenase (ascorbate) [Arabidopsis thaliana])

Protein Group 48

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	31.34	40.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
964.4705	2890.3879	2888.1579	772.1	3	3.31	1.42	ALDWGPGGGPDLIVDDGGDATLLIHEGVK	LYK	rep2
963.1738	2886.498	2888.1579	574.74	3	2.56	0.97	ALDWGPGGGPDLIVDDGGDATLLIHEGVK	LYT	rep2
565.3562	1128.6968	1129.359	586.34	2	2.19	0.62	DIIMVDHMR	LYT	rep3
565.7847	1129.5537	1129.359	172.44	2	1.7	0.02	DIIMVDHMR	LYK	rep2

783.7955	2348.3631	2349.5632	510.78	3	1.97	0.68	DQSDYVSIPVEGPYKPVHYR	LYT	rep1
513.6719	1025.3282	1025.1874	137.34	2	1.77	0.6	HSLPDGLMR	LYT	rep2
513.6179	1025.2202	1025.1874	32.08	2	1.53	0.44	HSLPDGLMR	LYK	rep2
1262.3226	3783.9444	3784.3387	104.18	3	4.94	2.63	LMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK : +57.05000 (C6); +57.05000 (C17)	LYK	rep1
1262.0262	3783.0553	3784.3387	339.14	3	3.88	1.6	LMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK : +57.05000 (C6); +57.05000 (C17)	LYT	rep3
739.3221	1476.6285	1475.6499	663.14	2	2.41	1.14	LVGVSEETTTGVKR	LYT	rep1
738.6745	1475.3333	1475.6499	214.55	2	2.27	1.01	LVGVSEETTTGVKR	LYK	rep1
1064.7548	3191.2408	3190.578	207.73	3	4.92	2.99	NNAIVCNIGHFDNEIDMLGLETYPGVKR : +57.05000 (C6)	LYT	rep2
1064.6537	3190.9376	3190.578	112.69	3	4.61	3.06	NNAIVCNIGHFDNEIDMLGLETYPGVKR : +57.05000 (C6)	LYK	rep1
630.5091	1259.0025	1259.395	311.68	2	2.96	1.16	SKFDNLYGCR : +57.05000 (C9)	LYT	rep1
630.2233	1258.4309	1259.395	765.5	2	2.18	0.92	SKFDNLYGCR : +57.05000 (C9)	LYK	rep2

Matching Genes:

NP_189023.1 (SAHH2 (S-ADENOSYL-L-HOMOCYSTEINE (SAH) HYDROLASE 2); adenosylhomocysteinase [Arabidopsis thaliana])

Protein Group 49

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	35.27	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
509.1214	1016.2271	1016.1805	45.88	2	2.3	0.76	AMIGQVAGGGR	LYT	rep2
899.7385	2696.1921	2696.9287	273.13	3	5.73	3.65	GVAMNPVEHPHGGGNHQHIGHASTVR	LYK	rep3
899.8647	2696.5708	2696.9287	132.72	3	4.2	2.2	GVAMNPVEHPHGGGNHQHIGHASTVR	LYT	rep3
951.8729	2852.5953	2853.115	182.14	3	3.15	1.61	GVAMNPVEHPHGGGNHQHIGHASTVRR	LYK	rep1

951.7012	2852.08	2853.115	362.74	3	2.2	0.88	GVAMNPVEHPHGGGNHQHIGHASTVRR	LYT	rep2
647.0866	1292.1575	1292.4462	223.34	2	2.59	1.11	GVVTEIIHDPGR	LYT	rep1
646.8516	1291.6875	1292.4462	586.96	2	1.39	0.24	GVVTEIIHDPGR	LYK	rep2
691.2596	1380.5035	1379.6964	584.95	2	3.04	0.99	KATLVVGNVLPLR	LYT	rep1
690.6278	1379.24	1379.6964	330.78	2	1.45	0.06	KATLVVGNVLPLR	LYK	rep2
995.1333	1988.251	1989.1806	467.31	2	1.55	0.46	SIPEGAVICNVEHHVGDR : +57.05000 (C9)	LYT	rep3
344.1205	1029.3382	1029.2023	132.04	3	1.99	0.63	VAFRHPFR	LYT	rep1
984.6569	2950.9471	2952.2466	440.16	3	3.89	1.83	VRGVAMNPVEHPHGGGNHQHIGHASTVR	LYK	rep3

Matching Genes:

NP_195336.1 (60S ribosomal protein L8 (RPL8C) [Arabidopsis thaliana])

Protein Group 50

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	51.55	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
598.6167	1792.8266	1792.9946	93.7	3	1.85	0.14	FVYAHFPINASIGGDGK	LYK	rep3
598.6774	1793.0086	1792.9946	7.81	3	1.66	0.29	FVYAHFPINASIGGDGK	LYT	rep1
621.158	1240.3003	1240.456	125.53	2	1.92	0.6 4	HLNLDFQLIK	LYK	rep2
624.1321	1869.3728	1868.1029	679.76	3	4.22	0.71	HLNLDFQLIKDPETGK	LYK	rep2
623.755	1868.2415	1868.1029	7 4.22	3	3.47	0.7	HLNLDFQLIKDPETGK	LYT	rep1
650.0015	1297.9873	1298.4891	386.44	2	1.83	0.42	KFLDGIYVSEK	LYT	rep1
680.7506	1359.4856	1359.6406	113.99	2	2.01	0.29	KVEMLDGVTIVR	LYT	rep1
680.7332	1359.4507	1359.6406	139.66	2	1.92	0.58	KVEMLDGVTIVR	LYK	rep2

612.1354	1222.2552	1222.3976	116.5	2	2.05	0.57	LKIDSWFGTR	LYT	rep1
694.597	2080.7677	2080.3779	187.34	3	2.08	0.36	MRFV YAHFPINASIGGDGK	LYK	rep2
694.4889	2080.4432	2080.3779	31.38	3	1.91	0.38	MRFVYAHFPINASIGGDGK	LYT	rep1
792.538	1583.0603	1582.7637	187.44	2	3.32	1.53	TALSHVDNLISGVTR	LYK	rep2
792.1719	1582.3282	1582.7637	275.15	2	2.78	1.58	TALSHVDNLISGVTR	LYT	rep1
639.09	1 914.2464	1914.12 67	62.55	3	4.91	2.64	VKDEIVLDGNDIELVSR	LYT	rep1
639.0712	1914.19	1914.1267	33.08	3	4.52	2.35	VKDEIVLDGNDIELVSR	LYK	rep2

Matching Genes:

NP_564417.1 (60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana])

Protein Group 51

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	8	64.24	88.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
619.2793	1236.543	1235.4181	910.56	2	2.97	1.11	GLDGHVMEHLK	LYK	rep3
618.5367	1235.0577	1235.4181	291.74	2	2.4	0.73	GLDGHVMEHLK	LYT	rep2
538.9132	1075.8108	1076.3174	470.63	2	2.19	0.39	ITMIWEKR	LYT	rep2
538.8972	1075.7788	1076.3174	500.34	2	1.81	0.02	ITMIWEKR	LYK	rep1
720.6922	1439.3687	1439.6427	190.33	2	1.87	0.87	QMVVDIEGHVNKA	LYK	rep1
480.7535	1439.237	1439.6427	281.83	3	1.7	0.3	QMVVDIEGHVNKA	LYT	rep3
464.7783	1391.3113	1391.6045	210.68	3	2.97	1.13	RGLDGHVMEHLK	LYT	rep1
464.9263	1391.7555	1391.6045	108.53	3	2.91	1	RGLDGHVMEHLK	LYK	rep3
778.4324	1554.8492	1555.6738	530.1	2	3.12	1.17	RNDDFPEPSGYMK	LYT	rep1

778.6319	1555.2481	1555.6738	273.67	2	3.08	0.85	RNDDFPEPSGYMK	LYK	rep1
1143.4564	3427.3458	3428.6157	370.39	3	6.91	4.24	SENHVFADAIGHHIQNVVVHEGEHDSHGSIR	LYK	rep3
1143.5712	3427.69	3428.6157	269.99	3	5.85	3.87	SENHVFADAIGHHIQNVVVHEGEHDSHGSIR	LYT	rep3
632.6192	1263.2227	1262.3291	707.9	2	1.83	0.27	SWDYTYDGKK	LYK	rep1
422.0433	1263.1063	1262.3291	615.73	3	1.69	0.35	SWDYTYDGKK	LYT	rep3
693.8006	1385.5855	1383.6356	1409.24	2	2.32	0.92	VFDIIYEFIPK	LYK	rep3

Matching Genes:

NP_194098.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 52

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	29.49	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
481.132	960.2483	960.0455	211.31	2	1.48	0.32	DIVDAHYK	LYK	rep1
480.881	959.7463	960.0455	311.66	2	1.44	0.19	DIVDAHYK	LYT	rep3
1139.7389	3416.1932	3416.803	178.46	3	4.28	1.63	HAAAEIFANPDVIAEVPWYGIEQEYTLLQK	LYK	rep2
543.1937	1626.5577	1626.6919	82.49	3	3.41	1.35	HKEHISAYGEGNER	LYK	rep3
1114.6171	3340.8277	3342.6824	554.84	3	4.12	2	ITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTK	LYT	rep3
1126.5791	2251.1426	2252.4541	582.24	2	5.1	2.99	LTGHHETADINTFLWGVANR	LYK	rep3
751.6394	2251.8947	2252.4541	248.33	3	3.91	1.75	LTGHHETADINTFLWGVANR	LYT	rep1
804.2198	2409.6361	2408.6404	413.39	3	5.25	2.44	RLTGHHETADINTFLWGVANR	LYT	rep3
803.6918	2408.0518	2408.6404	244.34	3	4.13	1.92	RLTGHHETADINTFLWGVANR	LYK	rep1

Matching Genes:

NP_176794.1 (ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2); glutamate-ammonia ligase)

Protein Group 53

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	9	24.88	36.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1032.698	2063.3804	2064.176	385.44	2	2.38	0.4	APTNDRFDDLFFYGIDSA	LYT	rep2
996.708	1991.4004	1992.1577	380.13	2	3.36	1.92	FEYVNGSQVVVGDEHGKK	LYT	rep2
996.5525	1991.0894	1992.1577	536.26	2	3.22	1.72	FEYVNGSQVVVGDEHGKK	LYK	rep2
639.7741	1277.5325	1278.418	692.61	2	2.1	0.71	HLYVFDIESR	LYT	rep2
1090.4913	3268.4505	3267.7034	228.65	3	2.86	0.96	IVGFYGFAGNNLHSLGAYFAPLTNVTPLNAK	LYK	rep1
776.5347	1551.0537	1551.6169	362.97	2	2.52	1.12	LDKFGGEEETPSSR	LYK	rep1
518.2197	1551.6357	1551.6169	12.1	3	2.39	0.52	LDKFGGEEETPSSR	LYT	rep2
762.021	1522.0264	1522.7049	445.62	2	2.42	0.84	LNTLDSYNIVDKK	LYT	rep1
508.7598	1523.2558	1522.7049	361.77	3	1.99	0.49	LNTLDSYNIVDKK	LYK	rep2
837.6578	2509.95	2508.707	495.48	3	2.88	1.24	SFEADPFVINHPEEHLVSVEGR	LYK	rep2
836.9237	2507.7476	2508.707	382.42	3	1.66	0.44	SFEADPFVINHPEEHLVSVEGR	LYT	rep1
545.9337	1634.7777	1634.7759	1.08	3	2.8	1.15	WFHCSTPGDSLTAR : +57.05000 (C4)	LYT	rep3
545.8763	1634.6056	1634.7759	104.2	3	2.38	0.63	WFHCSTPGDSLTAR : +57.05000 (C4)	LYK	rep1
564.9771	16 91.9077	1691.8486	34.91	3	2.22	0.47	WTQVETFGVRPSER	LYK	rep1
846.7283	1691.441	1691.8486	240.96	2	2.2	0.39	WTQVETFGVRPSER	LYT	rep3

Matching Genes:

NP_188262.1 (jacalin lectin family protein [Arabidopsis thaliana])

Protein Group 54

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	27.98	26.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
412.9845	1235.93	1236.3843	367.4	3	2.28	0.86	FHGHSPAVVTGK	LYK	rep3
1101.6267	2201.2378	2202.4812	564.53	2	4.99	3.09	FHGHSPAVVTGKPIDLGGSLGR	LYK	rep3
735.1243	2202.3493	2202.4812	59.87	3	4.22	2.1	FHGHSPAVVTGKPIDLGGSLGR	LYT	rep2
1471.6869	4412.0372	4411.8773	36.24	3	3.94	2.36	HKDATGSLNDFNGGDAMNSDELLIHECDVLIPCALGGVLNK : +57.05000 (C27); +57.05000 (C33)	LYT	rep1
1471.5551	4411.6417	4411.8773	53.4	3	2.37	0.64	HKDATGSLNDFNGGDAMNSDELLIHECDVLIPCALGGVLNK : +57.05000 (C27); +57.05000 (C33)	LYK	rep1
1185.7631	3554.2657	3553.9863	78.61	3	7.18	0.91	IHDLIGIHTDVPAPDMGTNAQTMAWILDEYSK	LYT	rep1
1185.3639	3553.0682	3553.9863	258.33	3	6.14	1.82	IHDLIGIHTDVPAPDMGTNAQTMAWILDEYSK	LYK	rep2
786.816	2357.4246	2356.6191	341.81	3	4.4	2.45	YHPEVDPDEVNALAQLMTWK	LYT	rep1

787.0388	2358.093	2356.6191	625.41	3	2.12	0.87	YHPEVDPDEVNALAQLMTWK	LYK	rep1

Matching Genes:

NP_196361.1 (GDH2 (GLUTAMATE DEHYDROGENASE 2); oxidoreductase [Arabidopsis thaliana])

Protein Group 55

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	11.87	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
661.1839	1320.3521	1320.4548	77.8	2	2.28	0.99	HFSVEGQLEFK	LYT	rep2
661.1051	1320.1946	1320.4548	197.06	2	2.02	0.88	HFSVEGQLEFK	LYK	rep2
925.2707	1848.5257	1849.098	309.52	2	3 .8	2.02	HSEFISYPISLWIEK	LYT	rep3
925.2107	1848.4058	1849.098	374.35	2	3.36	1.51	HSEFISYPISLWIEK	LYK	rep2
799.1385	1596.2613	1596.7888	330.38	2	4.4	1.93	IKEVSHEWDLVNK	LYT	rep1
660.2267	1977.6566	1977.271	195.01	3	2.74	0.87	KHSEFISYPISLWIEK	LYT	rep2
989.4375	1976.8594	1977.271	208.15	2	2.57	1.27	KHSEFISYPISLWIEK	LYK	rep1
1132.6903	3395.0474	3395.8916	248.58	3	2.66	1.25	LDGQPELFIHIIPDKTNNTLTIIDSGIGMTK	LYK	rep1
1132.6981	3395.0709	3395.8916	241.68	3	1.42	0.29	LDGQPELFIHIIPDKTNNTLTIIDSGIGMTK	LYT	rep1
606.8289	1211.6421	1209.3556	1890.71	2	2.33	0.62	RAPFDLFDTK	LYT	rep3
605.5838	1209.1519	1209.3556	168.43	2	1.91	0.55	RAPFDLFDTK	LYK	rep2
651.3446	1951.0103	1950.2471	391.38	3	4.08	2.41	SKLDGQPELFIHIIPDK	LYK	rep2
650.8898	1949.6458	1950.2471	308.28	3	3.71	2.07	SKLDGQPELFIHIIPDK	LYT	rep3

Matching Genes:

NP_200412.1 (HSP81-3 (Heat shock protein 81-3); ATP binding [Arabidopsis thaliana])

Protein Group 56

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	27.54	43.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
728.0441	2181.1087	2181.5068	182.49	3	4.35	1.33	AKLNNHGTLGALLQHEVLPR	LYT	rep2
775.4502	1548.8848	1549.6938	522.06	2	3.77	1.59	ASYLHHFDEFKR	LYT	rep2
517.491	1549.4494	1549.6938	157.72	3	3.56	1.62	ASYLHHFDEFKR	LYK	rep3
567.185	1132.3543	1132.3143	35.29	2	2.26	0.76	GPGLFTDIGKK	LYK	rep2
723.0677	1444.1197	1444.5975	330.79	2	4.06	2.21	KGGVHAADVATQYK	LYT	rep3
482.5144	1444.5197	1444.5975	53.85	3	3.23	1.54	KGGVHAADVATQYK	LYK	rep2
1043.3899	2084.7642	2085.3279	270.3	2	3.18	1.81	LEVQYFHDHATVTAAAALK	LYT	rep3
696.1222	2085.3431	2085.3279	7.3	3	2.41	0.73	LEVQYFHDHATVTAAAALK	LYK	rep2
991.7688	1981.522	1982.2556	370.08	2	4.57	2.65	LNNHGTLGALLQHEVLPR	LYT	rep1
991.6654	1981.3152	1982.2556	474.4	2	4.41	2.72	LNNHGTLGALLQHEVLPR	LYK	rep3

Matching Genes:

NP_201551.1 (porin, putative [Arabidopsis thaliana])

Protein Group 57

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	34.46	48.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
683.482	1364.9483	1365.5021	405.55	2	2.13	0.57	EEGHKIVGFHGR	LYK	rep3
683.594	1365.1724	1365.5021	241.42	2	1.87	0.53	EEGHKIVGFHGR	LYT	rep1
651.2762	1950.8053	1951.0593	130.21	3	4.16	1.67	FVYDKSPEEVTGEEHGK	LYK	rep1
651.2545	1950.7401	1951.0593	163.62	3	3.85	1.68	FVYDKSPEEVTGEEHGK	LYT	rep3
1325.4064	3973.1956	3972.4763	181.08	3	4.17	2.35	GSTIPTDPFVINHPEEHLVSIEIWYKPDGLIQGLR	LYK	rep3
1324.7335	3971.1771	3972.4763	327.06	3	3.65	1.97	GSTIPTDPFVINHPEEHLVSIEIWYKPDGLIQGLR	LYT	rep3
698.8286	1395.6416	1395.6299	8.43	2	2.38	0.26	IFGSDGSVITMLR	LYK	rep2
539.5023	1076.989	1077.2419	234.75	2	1.56	0.54	IGVHVRPVSN	LYT	rep3
538.9649	1075.9141	1077.2419	1232.62	2	1.55	0.25	IGVHVRPVSN	LYK	rep3
782.1143	1562.2129	1562.7723	357.95	2	4. 31	1.65	KVYVGQAQDGISAVK	LYK	rep3
782.1397	1562.2637	1562.7723	325.46	2	4.26	1.97	KVYVGQAQDGISAVK	LYT	rep1
718.7205	1435.4253	1434.5994	575.75	2	3.46	1.38	VYVGQAQDGISAVK	LYT	rep3
718.1001	1434.1846	1434.5994	289.1	2	1.45	0.3	VYVGQAQDGISAVK	LYK	rep2

Matching Genes:

NP_188264.1 (jacalin lectin family protein [Arabidopsis thaliana])

Protein Group 58

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	18.93	40.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
762.6133	1523.211	1523.7214	335	2	3.55	1.56	ALLHSSHMYHEAK	LYT	rep1

762.4065	1522.7974	1523.7214	606.43	2	3.5	1.55	ALLHSSHMYHEAK	LYK	rep2
442.9578	1325.8498	1324.5314	995.41	3	2.68	0.89	GKHIIVATGSDVK	LYK	rep3
442.7521	1325.2329	1324.5314	529.68	3	2.35	0.63	GKHIIVATGSDVK	LYT	rep1
873.0405	2616.0981	2616.8887	302.1	3	4.49	2.58	HGHVDYDKVPGVVYTYPEVASVGK	LYT	rep2
872.8621	2615.5627	2616.8887	506.69	3	4.24	2.29	HGHVDYDKVPGVVYTYPEVASVGK	LYK	rep2
570.5539	1139.0921	1139.3069	188.53	2	2.32	0.64	HIIVATGSDVK	LYK	rep2
570.7027	1139.3897	1139.3069	72.69	2	1.96	0.53	HIIVATGSDVK	LYT	rep3
1174.6688	3520.983	3519.9497	293.55	3	5.86	3.4	ILGVHIMSPNAGELIHEAVLAINYDASSEDIAR	LYT	rep1
1174.0533	3519.1366	3519.9497	231.01	3	3.93	2.06	ILGVHIMSPNAGELIHEAVLAINYDASSEDIAR	LYK	rep2
741.0751	1480.1346	1480.7168	393.19	2	3.27	0	VCHAHPTMSEAIK : +57.05000 (C2)	LYK	rep3
494.5421	1480.6029	1480.7168	76.92	3	2.9	0	VCHAHPTMSEAIK : +57.05000 (C2)	LYT	rep1

Matching Genes:

NP_566570.3 (LPD2 (LIPOAMIDE DEHYDROGENASE 2); FAD binding / dihydrolipoyl dehydrogenase/ disulfide oxidoreductase/ oxidoreductase [Arabidopsis thaliana])

Protein Group 59

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	36.31	41.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
949.3625	2845.0642	2845.2444	63.33	3	3.98	1.84	ALSDHHVLLEGTLLKPNMVTPGSESAK	LYT	rep1
960.3762	2878.1052	2877.2444	299.16	3	2.74	0.38	ALSDHHVLLEGTLLKPNMVTPGSESAK : +32.00000 (M18)	LYK	rep3
745.5463	1489.0769	1488.6485	287.77	2	3.42	1.57	GILAADESTGTIGKR	LYT	rep1
745.0983	1488.1809	1488.6485	314.11	2	2.99	1.08	GILAADESTGTIGKR	LYK	rep1
438.3591	1312.0537	1311.4928	427.72	3	3.78	1.43	KPWSLSFSFGR	LYT	rep3

438.5678	1312.68	1311.4928	905.2	3	3.18	1.13	KPWSLSFSFGR	LYK	rep2
1165.3269	2328.6382	2329.5718	400.74	2	2.61	1.04	TVPAAVPAIVFLSGGQSEEEATR	LYT	rep2
869.8262	2606.455	2604.7466	655.91	3	1.87	0.16	VDKGTVELAGTNGETTTQGLDGLGDR	LYK	rep3
1045.8964	3134.6656	3136.5436	598.73	3	3.54	1.31	YAVICQENGLVPIVEPEILVDGSHDIQK : +57.05000 (C5)	LYK	rep3
1046.0453	3135.1124	3136.5436	456.29	3	2.72	1.43	YAVICQENGLVPIVEPEILVDGSHDIQK : +57.05000 (C5)	LYT	rep1

Matching Genes:

NP_181187.1 (fructose-bisphosphate aldolase, putative [Arabidopsis thaliana])

Protein Group 60

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	13.72	26.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1083.1534	3246.4369	3247.6477	372.84	3	2.68	0.82	AGLPLQDLEFVQFHPTGIYGAGCLITEGSR : +57.05000 (C23)	LYT	rep1
1083.2611	3246.7598	3247.6477	273.38	3	1.89	0.4	AGLPLQDLEFVQFHPTGIYGAGCLITEGSR : +57.05000 (C23)	LYK	rep1
647.111	1938.3094	1938.2412	35.19	3	2.14	0.65	DHIYLHLNHLPPEVLK	LYK	rep2
647.2245	1938.65	1938.2412	210.91	3	1.24	0.24	DHIYLHLNHLPPEVLK	LYT	rep3
838.7821	2513.3228	2513.9043	231.29	3	5.09	2.93	GVGPHKDHIYLHLNHLPPEVLK	LYK	rep3
839.2942	2514.8591	2513.9043	379.81	3	4.03	1.79	GVGPHKDHIYLHLNHLPPEVLK	LYT	rep2
63 9.3941	1276.7725	1277.3437	447.21	2	2.5	1.16	HTLGYWEDEK	LYT	rep1
512.0315	1533.071	1532.6616	267.12	3	3.62	1.51	HTLGYWEDEKVR	LYT	rep2
821.2362	1640.4568	1640.9114	277.01	2	4.26	2.64	TGHALLHTLYGQAMK	LYK	rep2
821.1858	1640.356	1640.9114	338.45	2	4.23	2.57	TGHALLHTLYGQAMK	LYT	rep3
540.5086	1079.0015	1079.2335	214.97	2	1.56	0.41	WHMYDTVK	LYK	rep2

Matching Genes:

NP_201477.1 (SDH1-1 (Succinate dehydrogenase 1-1) [Arabidopsis thaliana])

Protein Group 61

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	23.15	39.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1264.3015	2526.5874	2526.8486	103.36	2	2.78	1.19	ESSIPLITVFDKDPNNHPYVIK	LYT	rep2
1443.6166	4327.8263	4328.7607	215.88	3	4.41	2.34	GQGLSFLLGDAENSQGAFQYFGLEESQVPLIIIQTADDKK	LYT	rep1
1443.1818	4326.5218	4328.7607	517.22	3	2.98	1.17	GQGLSFLLGDAENSQGAFQYFGLEESQVPLIIIQTADDKK	LYK	rep3
722.8788	2165.6129	2165.4586	71.24	3	4.25	2.2	HDFIVVEFYAPWCGHCK : +57.05000 (C13); +57.05000 (C16)	LYT	rep3
722.871	2165.5894	2165.4586	60.41	3	2.31	0.69	HDFIVVEFYAPWCGHCK : +57.05000 (C13); +57.05000 (C16)	LYK	rep2
543.7386	1085.4615	1085.3871	68.54	2	2.46	1.02	KVVVVGIFPK	LYT	rep1
534.9871	1601.9377	1599.7878	1343.85	3	3.01	1.25	LFKPFDEQFVDSK	LYK	rep2
800.5995	1599.1834	1599.7878	377.83	2	2.47	0.67	LFKPFDEQFVDSK	LYT	rep1
795.5784	1589.1411	1589.7115	358.8	2	3.2	1.72	LRSELDFAHTSDAK	LYK	rep1
795.593	1589.1704	1589.7115	340.37	2	2.41	1.15	LRSELDFAHTSDAK	LYT	rep3

661.2603	1320.5049	1320.3669	104.51	2	1.62	0.25	SELDFAHTSDAK	LYT	rep1

Matching Genes :

NP_173594.1 (ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase [Arabidopsis thaliana])

Protein Group 62

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	24.11	41.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
706.7616	2117.2613	2117.2388	10.65	3	2.45	0.99	ALEEEIEDIGGHLNAYTSR	LYK	rep2
706.8041	2117.3888	2117.2388	70.85	3	1.9	0.25	ALEEEIEDIGGHLNAYTSR	LYT	rep2
1105.6615	3313.961	3314.6077	195.09	3	3.93	2.38	EMQEVEGQTDEVVLDHLHATAFQYTPLGR	LYT	rep1
1105.7982	3314.3712	3314.6077	71.34	3	3.81	1.83	EMQEVEGQTDEVVLDHLHATAFQYTPLGR	LYK	rep2
1127.4505	2252.8853	2253.4558	253.17	2	4.13	2.43	FESDETNGTAHFLEHMIFK	LYK	rep1
1127.9163	2253.8169	2253.4558	160.26	2	3.1	1.79	FESDETNGTAHFLEHMIFK	LYT	rep3
392.4537	1174.3375	1174.3096	23.83	3	1.58	0.18	IDAVDASTVKR	LYK	rep2
392.7632	1175.2663	1174.3096	814.69	3	1.36	0.33	IDAVDASTVKR	LYT	rep2
588.7635	1175.5113	1173.3696	1825.21	2	2.55	0.85	RIPTAELFAR	LYK	rep3
587.6647	1173.3138	1173.3696	47.61	2	2.45	0.79	RIPTAELFAR	LYT	rep3
671.7792	2012.314	2012.2539	29.89	3	1.68	0.48	SSLLLHMDGTSPIAEDIGR	LYK	rep2

1156.6101	2311.2046	2311.5647	155.76	2	4.91	3.39	YASPHPILASHNHILSAPETR	LYK	rep3
1156.3011	2310.5865	2311.5647	423.19	2	4.51	3.03	YASPHPILASHNHILSAPETR	LYT	rep2

Matching Genes:

NP_186858.1 (MPPBETA; metalloendopeptidase [Arabidopsis thaliana])

Protein Group 63

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	18.93	37.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
762.6133	1523.211	1523.7214	335	2	3.55	1.56	ALLHSSHMYHEAK	LYT	rep1
762.4065	1522.7974	1523.7214	606.43	2	3.5	1.55	ALLHSSHMYHEAK	LYK	rep2
442.9578	1325.8498	1324.5314	995.41	3	2.68	0.89	GKHIIVATGSDVK	LYK	rep3
442.7521	1325.2329	1324.5314	529.68	3	2.35	0.63	GKHIIVATGSDVK	LYT	rep1
864.2358	2589.684	2590.8545	451.76	3	6.05	3.52	HGHVDYDKVPGVVYTHPEVASVGK	LYK	rep3
864.2925	2589.854	2590.8545	386.17	3	5.3	3.27	HGHVDYDKVPGVVYTHPEVASVGK	LYT	rep3
570.5539	1139.0921	1139.3069	188.53	2	2.32	0.64	HIIVATGSDVK	LYK	rep2
570.7027	1139.3897	1139.3069	72.69	2	1.96	0.53	HIIVATGSDVK	LYT	rep3
1169.1449	3504.4112	3503.9502	131.58	3	2.53	1	ILGVHIMAPNAGELIHEAVLAINYDASSEDIAR	LYT	rep1
1168.5638	3502.6681	3503.9502	365.91	3	1.42	0.07	ILGVHIMAPNAGELIHEAVLAINYDASSEDIAR	LYK	rep2

494.4634	1480.3668	1480.7168	236.31	3	2.99	0	VCHAHPTMSEALK : +57.05000 (C2)	LYT	rep2
494.7794	1481.3146	1480.7168	403.75	3	2.72	0	VCHAHPTMSEALK : +57.05000 (C2)	LYK	rep1

Matching Genes:

NP_175237.1 (dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1) [Arabidopsis thaliana])

Protein Group 64

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	18.91	20.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
729.1424	1456.2691	1457.5068	849.22	2	1.39	0.44	DVHDHIEYGTSGK	LYT	rep1
1175.991	2349.9663	2350.7222	321.52	2	4.08	1.96	FLGPSLFHYYQKPLNIVEGK	LYK	rep3
1176.1131	2350.2105	2350.7222	217.67	2	3.43	1.68	FLGPSLFHYYQKPLNIVEGK	LYT	rep3
869.4672	2605.378	2604.9675	157.58	3	4.89	3.06	LLQHATTIYLHHAIGDFAEALAAK	LYT	rep3
869.7934	2606.3567	2604.9675	533.29	3	3.65	1.87	LLQHATTIYLHHAIGDFAEALAAK	LYK	rep1
555.4427	1663.3048	1663.8188	308.93	3	1.96	0.48	QEHCAEVGSHLIQR : +57.05000 (C4)	LYK	rep2
607.974	1820.8985	1820.0051	490.87	3	5.16	2.28	RQEHCAEVGSHLIQR : +57.05000 (C5)	LYK	rep3
711.6002	2131.7772	2131.3584	196.49	3	2.55	0.55	YPLPQGEIHHVVNPDPYR	LYK	rep3

Matching Genes:

NP_568064.1 (AGT2 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 2); alanine-glyoxylate transaminase [Arabidopsis thaliana])

Protein Group 65

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	16.93	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
711.8185	2132.432	2132.456	11.29	3	2.31	0.32	AHVIVMGATNRPNSIDPALR	LYK	rep2
711.8114	2132.4107	2132.456	21.25	3	2.23	0.68	AHVIVMGATNRPNSIDPALR	LYT	rep3
1505.9667	4514.8765	4513.9028	215.72	3	3.51	1.44	EKMDVIDLEDDSIDAEILNSMAVTNEHFHTALGNSNPSALR	LYT	rep2
1505.3246	4512.9503	4513.9028	211.02	3	1.66	0.41	EKMDVIDLEDDSIDAEILNSMAVTNEHFHTALGNSNPSALR	LYK	rep1
609.5605	1825.6582	1825.9766	174.36	3	2.13	0.31	ELQETVQYPVEHPEK	LYT	rep1
946.3816	2836.1213	2834.1989	678.28	3	3.47	1.31	ISKDTHGYVGADLAALCTEAALQCIR : +57.05000 (C17); +57.05000 (C24)	LYT	rep1
474.4469	946.8782	947.1362	272.41	2	2.15	0.69	KGDLFLVR	LYT	rep2
474.5837	947.1518	947.1362	16.42	2	1.66	0.47	KGDLFLVR	LYK	rep2
785.0607	1568.1057	1568.7386	403.44	2	3.51	1.8	KYQAFAQTLQQSR	LYT	rep1
785.553	1569.0904	1568.7386	224.21	2	2.55	1.28	KYQAFAQTLQQSR	LYK	rep2
794.0554	1586.0952	1586.9451	535.5	2	2.81	0.87	RIVSQLLTLMDGLK	LYT	rep1

Matching Genes:

NP_187595.1 (CDC48 (CELL DIVISION CYCLE 48); ATPase [Arabidopsis thaliana])

Protein Group 66

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	31.78	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

1320.9483	2639.8809	2640.0068	47.7	2	3.67	2.05	ADVYKPQLGYISTLNSYDLPILR	LYT	rep1
764.8832	2291.6261	2292.4734	369.61	3	3.02	1.09	FNTLETTLTHSSGPASYGRPR	LYT	rep1
1154.792	2307.5684	2308.5608	429.87	2	1.46	0.41	FQWVEFKTNANAQINTLAGR	LYK	rep1
750.8533	1499.691	1500.666	649.74	2	3.08	1.28	IEVWDHHAPQLR	LYT	rep1
1207.3692	2412.7227	2412.6738	20.26	2	3.12	1.28	NPRPFYLAGNNPQGQVWLQGR	LYT	rep1
1207.3902	2412.7647	2412.6738	37.66	2	0.88	0.09	NPRPFYLAGNNPQGQVWLQGR	LYK	rep1
1464.2721	4389.7928	4390.751	218.22	3	3.52	1.78	SGDTIATTPGVAQWFYNDGQEPLVIVSVFDLASHQNQLDR	LYT	rep1
718.7464	1435.4771	1435.7218	170.44	2	1.8	0.31	VQGPFGVIRPPLR	LYT	rep1

Matching Genes:

NP_199225.1 (CRA1 (CRUCIFERINA); nutrient reservoir [Arabidopsis thaliana])

Protein Group 67

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	23.6	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1134.6122	3400.8131	3401.7718	281.83	3	4.43	2.16	ITEIAGVVVSFDPKPIPGDWNGAGAHCNYSTK : +57.05000 (C27)	LYT	rep3
1126.5791	2251.1426	2252.4541	582.24	2	5.1	2.99	LTGHHETADINTFLWGVANR	LYK	rep3
751.6394	2251.8947	2252.4541	248.33	3	3.91	1.75	LTGHHETADINTFLWGVANR	LYT	rep1
804.2198	2409.6361	2408.6404	413.39	3	5.25	2.44	RLTGHHETADINTFLWGVANR	LYT	rep3
803.6918	2408.0518	2408.6404	244.34	3	4.13	1.92	RLTGHHETADINTFLWGVANR	LYK	rep1
1163.8993	3488.6744	3488.7397	18.73	3	4.18	0.01	WNYDGSSTGQAPGEDSEVILYPQAIFKDPFR	LYT	rep2

Matching Genes:

NP_198576.1 (ATGSR1 (Arabidopsis thaliana glutamine synthase clone R1); glutamate-ammonia ligase)

Protein Group 68

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	21.49	39.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1032.698	2063.3804	2064.176	385.44	2	2.38	0.4	APTNDRFDDLFFYGIDSA	LYT	rep2
996.708	1991.4004	1992.1577	380.13	2	3.36	1.92	FEYVNGSQVVVGDEHGKK	LYT	rep2
996.5525	1991.0894	1992.1577	536.26	2	3.22	1.72	FEYVNGSQVVVGDEHGKK	LYK	rep2
647.0669	1292.1182	1292.4447	252.61	2	2.88	1.41	HLYVFDLETR	LYT	rep2
647.1592	1292.3028	1292.4447	109.81	2	2.63	0.82	HLYVFDLETR	LYK	rep2
776.5347	1551.0537	1551.6169	362.97	2	2.52	1.12	LDKFGGEEETPSSR	LYK	rep1
518.2197	1551.6357	1551.6169	12.1	3	2.39	0.52	LDKFGGEEETPSSR	LYT	rep2
762.021	1522.0264	1522.7049	445.62	2	2.42	0.84	LNTLDSYNIVDKK	LYT	rep1
508.7598	1523.2558	1522.7049	361.77	3	1.99	0.49	LNTLDSYNIVDKK	LYK	rep2
545.9337	1634.7777	1634.7759	1.08	3	2.8	1.15	WFHCS TPGDSLTAR : +57.05000 (C4)	LYT	rep3
545.8763	1634.6056	1634.7759	104.2	3	2.38	0.63	WFHCSTPGDSLTAR : +57.05000 (C4)	LYK	rep1
564.9771	1691.9077	1691.8486	34.91	3	2.22	0.47	WTQVETFGVRPSER	LYK	rep1
846.7283	1691.441	1691.8486	240.96	2	2.2	0.39	WTQVETFGVRPSER	LYT	rep3

Matching Genes:

NP_001030709.1 (ATMLP-470 (MYROSINASE-BINDING PROTEIN-LIKE PROTEIN-470) [Arabidopsis thaliana])

Protein Group 69

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	37.75	33.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
942.2828	2823.825	2824.121	104.8	3	5.37	2.91	HTGPGILSMANAGANTNGSQFFICTEK : +57.05000 (C24)	LYT	rep2
942.0829	2823.2252	2824.121	317.2	3	2.01	0.24	HTGPGILSMANAGANTNGSQFFICTEK : +57.05000 (C24)	LYK	rep2
827.0634	1652.1111	1651.9139	119.37	2	4. 86	3.17	HVVFGQVVEGLNVVR	LYK	rep2
551.532	1651.5725	1651.9139	206.7	3	4.54	1.63	HVVFGQVVEGLNVVR	LYT	rep1
984.5961	2950.7647	2952.293 9	517.96	3	5.8	3.65	KHTGPGILSMANAGANTNGSQFFICTEK : +57.05000 (C25)	LYT	rep2
984.7023	2951.0833	2952.2939	410.04	3	4.85	2.99	KHTGPGILSMANAGANTNGSQFFICTEK : +57.05000 (C25)	LYK	rep1
738.1184	1474.2212	1474.6838	313.67	2	2.42	0.75	TSKPVVIADCGQIS : +57.05000 (C10)	LYK	rep2
737.7096	1473.4036	1474.6838	868.11	2	2.28	1.03	TSKPVVIADCGQIS : +57.05000 (C10)	LYT	rep1

Matching Genes:

NP_001077901.1 (ROC3 (rotamase CyP 3) [Arabidopsis thaliana])

Protein Group 70

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	48.82	30.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
808.9261	2423.755	2423.7268	11.62	3	2.2	0.75	AILNESSEFVGDKVAYALAQGLK	LYT	rep2
930.8149	2789.4213	2789.1526	96.36	3	4.09	1.82	ELGGQADVDGFLVGGASLKPEFIDIIK	LYT	rep2
931.1654	2790.4727	2789.1526	473.32	3	3.32	1.39	ELGGQADVDGFLVGGASLKPEFIDIIK	LYK	rep2

478.2046	954.3936	954.0858	322.6	2	2.01	0.27	FFVGGNWK	LYT	rep1
1043.1444	3126.4098	3126.5552	46.51	3	2.82	0.96	KGGAFTGEVSAEMLVNLDIPWVILGHSER	LYT	rep3
1042.9977	3125.9696	3126.5552	187.3	3	2.31	0.79	KGGAFTGEVSAEMLVNLDIPWVILGHSER	LYK	rep3
889.7273	1777.439	1777.9398	281.68	2	3.87	2.2	VASPAQAQEVHDELRK	LYT	rep1
889.6378	1777.26	1777.9398	382.33	2	3.57	1.4	VASPAQAQEVHDELRK	LYK	rep1
1152.8655	2303.7154	2304.6086	387.6	2	3.38	1.8	VTNWSNVVIAYEPVWAIGTGK	LYT	rep1
1153.1924	2304.3692	2304.6086	103.9	2	1.5	0.37	VTNWSNVVIAYEPVWAIGTGK	LYK	rep2

Matching Genes:

NP_191104.1 (ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase [Arabidopsis thaliana])

Protein Group 71

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	14.8	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1067.0833	2132.1509	2131.3957	354.35	2	2.95	1.52	ATGQEYAEFLHEFMCAVK : +57.05000 (C15)	LYK	rep2
711.3339	2130.9781	2131.3957	195.91	3	2.78	1.14	ATGQEYAEFLHEFMCAVK : +57.05000 (C15)	LYT	rep3
789.203	2364.5855	2364.6626	32.59	3	1.86	0.53	DAHYLTGLLPPVILSQDVQER	LYK	rep2
695.605	1389.1944	1389.6018	293.19	2	3.63	1.84	KPQGLYISLNEK	LYT	rep3
696.076	1390.1363	1389.6018	384.62	2	2.95	1.23	KPQGLYISLNEK	LYK	rep2
763.4725	2287.3941	2287.582	82.14	3	4.36	2.26	RATGQEYAEFLHEFMCAVK : +57.05000 (C16)	LYK	rep1
763.358	2287.0506	2287.582	232.3	3	3.39	1.06	RATGQEYAEFLHEFMCAVK : +57.05000 (C16)	LYT	rep2
1292.6146	3874.8204	3876.3271	388.7	3	5.39	3.44	VRDDMLLAASEA LAAQVTEEHYANGLIYPPFSNIR	LYT	rep3
1292.766	3875.2745	3876.3271	271.56	3	4.63	2.78	VRDDMLLAASEALAAQVTEEHYANGLIYPPFSNIR	LYK	rep2

Matching Genes:

NP_196728.1 (ATNADP-ME2 (NADP-MALIC ENZYME 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor [Arabidopsis thaliana])

Protein Group 72

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	38.71	21.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1528.2159	4581.6244	4581.2524	81.18	3	3.86	2.58	ANVPVAEVNVPVIGGHAGVTILPLFSQATPQANLSSDILTALTKR	LYT	rep1
1527.6251	4579.8519	4581.2524	305.71	3	1.61	0.26	ANVPVAEVNVPVIGGHAGVTILPLFSQATPQANLSSDILTALTKR	LYK	rep1
674.4392	1346.8628	1347.608	552.97	2	3.14	0.93	KLFGVTTLDVVR	LYT	rep1
1003.3827	3007.1246	3008.3552	409.07	3	4.57	2.54	LNPLVSSLSLYDIANTPGVAADVGHINTR	LYT	rep1
1003.5995	3007.775	3008.3552	192.87	3	2.19	0.92	LNPLVSSLSLYDIANTPGVAADVGHINTR	LYK	rep2
898.1186	1794.2215	1793.2303	552.71	2	2.37	0.79	VAILGAAGGIGQPLALLMK	LYT	rep2
1010.7312	3029.1701	3028.5597	201.56	3	4.22	2.17	YCPHALINMISNPVNSTVPIAAEIFKK : +57.05000 (C2)	LYK	rep1
1514.7085	3027.4014	3028.5597	382.46	2	3.39	1.66	YCPHALINMISNPVNSTVPIAAEIFKK : +57.05000 (C2)	LYT	rep1

Matching Genes:

NP_564625.1 (malate dehydrogenase (NAD), mitochondrial [Arabidopsis thaliana])

Protein Group 73

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	19.74	27.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
393.214	1176.6185	1176.3321	243.43	3	2.72	0.87	HRLGDLFYR	LYT	rep2
393.0869	1176.2371	1176.3321	80.81	3	2.51	0.76	HRLGDLFYR	LYK	rep1
570.0897	1707.2457	1705.9601	753.6	3	3.77	1.32	KHFPSVNWLISYSK	LYK	rep2
570.1155	1707.323	1705.9601	798.9	3	3.36	1.26	KHFPSVNWLISYSK	LYT	rep2
1283.4244	3847.2498	3847.3022	13.62	3	2.04	0.66	NGSVTIVGAVSPPGGDFSDPVTSATLSIVQVFWGLDKK	LYK	rep1
601.8159	1802.4243	1802.0062	232	3	2.92	0.48	NIIHFYNLANQAVER	LYT	rep3
602.0497	1803.1256	1802.0062	621.17	3	2.78	0.04	NIIHFYNLANQAVER	LYK	rep1
773.2832	1544.5508	1545.7668	786.68	2	2.38	0.85	TTLVANTSNMPVAAR	LYT	rep1
668.8466	1335.6775	1335.5141	122.33	2	1.59	0.5	VGHDNLIGEIIR	LYK	rep2
668.585	1335.1543	1335.5141	269.42	2	1.14	0.02	VGHDNLIGEIIR	LYT	rep2
1228.1731	2454.3306	2455.6826	550.56	2	2.32	1.01	YSTALESFYEKFDPDFINIR	LYK	rep1

Matching Genes:

NP_001031299.1 (VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism [Arabidopsis thaliana])

Protein Group 74

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	21.37	34.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
974.1543	1946.293	1947.1667	448.72	2	2.56	0.82	HTAFFSNYRPQFYLR	LYK	rep3
974.2744	1946.5332	1947.1667	325.34	2	2.05	0.56	HTAFFSNYRPQFYLR	LYT	rep1
590.6725	1768.994	1768.9119	46.39	3	5.2	2.95	HYAHVDCPGHADYVK : +57.05000 (C7)	LYT	rep3

590.6534	1768.9369	1768.9119	14.1	3	5.2	2.86	HYAHVDCPGHADYVK : +57.05000 (C7)	LYK	rep1
604.1041	1809.2889	1809.0019	158.63	3	3.9	1.9	NKPHVNVGTIGHVDHGK	LYK	rep3
604.2853	1809.8324	1809.0019	459.05	3	1.81	0.18	NKPHVNVGTIGHVDHGK	LYT	rep1
1186.5997	3556.7757	3556.1252	182.92	3	3.08	1	QVGVPSLVCFLNKVDVVDDPELLELVEMELR : +57.05000 (C9)	LYK	rep3
735.9926	2204.9542	2204.5972	161.95	3	3	1.34	VLDKPFLMPIEDVFSIQGR	LYT	rep3
735.882	2204.6224	2204.5972	11.45	3	2.66	1.21	VLDKPFLMPIEDVFSIQGR	LYK	rep2

Matching Genes:

NP_192202.1 (elongation factor Tu, putative / EF-Tu, putative [Arabidopsis thaliana])

Protein Group 75

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	24.43	26.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
711.8361	2132.4847	2133.2432	355.54	3	4.41	2.35	GSFETIHIQDSTGHEFATR	LYK	rep2
712.1031	2133.286	2133.2432	20.07	3	4.28	2.21	GSFETIHIQDSTGHEFATR	LYT	rep3
556.9143	1111.813	1112.3263	461.43	2	1.83	0.47	GTKPWVSLPK	LYT	rep1
800.3339	2397.9781	2398.5559	240.89	3	4.45	2.09	HKGSFETIHIQDSTGHEFATR	LYT	rep2
416.4721	830.9285	828.9817	2348.45	2	1.75	0.22	HWMLDK	LYT	rep1
415.4707	828.9258	828.9817	67.38	2	1.13	0.15	HWMLDK	LYK	rep2
726.0447	1450.0738	1450.6468	395.05	2	2.06	0.58	LGGAFAPKPSSGPHK	LYT	rep1
484.6642	1450.9691	1450.6468	222.13	3	2.03	0.68	LGGAFAPKPSSGPHK	LYK	rep2
490.5507	1468.6287	1468.8119	124.73	3	2.97	0.5	SRECLPLVLIIR : +57.05000 (C4)	LYK	rep1

Matching Genes:

NP_200650.1 (40S ribosomal protein S4 (RPS4D) [Arabidopsis thaliana])

Protein Group 76

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	22.65	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
794.4672	2380.378	2379.6575	302.8	3	2.1	0.67	FLHDPSKDTGFVGSALSSNMIR	LYK	rep1
994.6689	2980.9834	2982.2795	434.62	3	4.92	3.2	GFNLQHVADGLYGSHLHVYSWPGGEIK	LYT	rep3
994.8301	2981.4668	2982.2795	272.53	3	4.81	3.11	GFNLQHVADGLYGSHLHVYSWPGGEIK	LYK	rep1
482.6285	1444.8621	1443.6761	821.52	3	1.67	0.14	HKTMISTSWGAPK	LYT	rep2
1137.7045	3410.0899	3411.6907	469.2	3	3.84	1.84	LPMPFVGDELHHSGWNSCSSCHGDASVDRR : +57.05000 (C18); +57.05000 (C21)	LYK	rep1
1137.9286	3410.7623	3411.6907	272.13	3	2.8	1.13	LPMPFVGDELHHSGWNSCSSCHGDASVDRR : +57.05000 (C18); +57.05000 (C21)	LYT	rep2
809.6925	2426.054	2426.6511	246.05	3	4.82	2.7	WEKPGHSPLYGYDFWYQPR	LYK	rep3

809.7035	2426.087	2426.6511	232.47	3	3.73	1.99	WEKPGHSPLYGYDFWYQPR	LYT	rep3

Matching Genes:

NP_193139.1 (selenium-binding protein, putative [Arabidopsis thaliana])

Protein Group 77

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	25.06	27.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1295.513	2589.0103	2588.9702	15.48	2	2.8	0.67	AQEMFAHLLFGADTNVVQPMNVR	LYT	rep1
599.9724	1796.8938	1797.2192	181.06	3	5.24	1.63	FVIQTLAPLGCLPIVR : +57.05000 (C11)	LYK	rep2
600.1675	1797.479	1797.2192	144.56	3	3.48	1.25	FVIQTLAPLGCLPIVR : +57.05000 (C11)	LYT	rep2
566.5301	1131.0445	1131.3749	292.03	2	1.81	0.55	IGPMLNEMAR	LYT	rep2
519.397	1555.1674	1553.7191	932.17	3	2.99	0.52	LKNDISALYSSGASK	LYT	rep1
778.1834	1554.3511	1553.7191	406.77	2	2.75	0.86	LKNDISALYSSGASK	LYK	rep2
1246.9109	2491.8062	2492.7493	378.32	2	2.8	1.34	NSPASAPFQFTVFDFYNAVLTR	LYK	rep3
1247.3513	2492.687	2492.7493	24.96	2	2.57	1.01	NSPASAPFQFTVFDFYNAVLTR	LYT	rep2
684.4795	1366.9434	1366.5683	274.44	2	1.65	0.76	TLVAQGFWPYGK	LYK	rep2

Matching Genes:

NP_175802.1 (myrosinase-associated protein, putative [Arabidopsis thaliana])

Protein Group 78

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	18.24	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1453.1505	4356.4281	4355.9447	110.96	3	5.02	2.97	AGVGIDNVDLSAATEFGCLVVNAPTANTIAAAEHGIALMAAMAR : +57.05000 (C18)	LYT	rep1
1452.5614	4354.6607	4355.9447	294.76	3	4.61	1.2	AGVGIDNVDLSAATEFGCLVVNAPTANTIAAAEHGIALMAAMAR : +57.05000 (C18)	LYK	rep3
1157.2985	3468.8719	3469.9289	304.6 3	3	4.94	2.81	AHAIGVDLVSFDEALATADFISLHMPLTPTTSK	LYT	rep1
1157.444	3469.3084	3469.9289	178.83	3	4.68	2.98	AHAIGVDLVSFDEALATADFISLHMPLTPTTSK	LYK	rep2
583.0768	1164.138	1163.3716	658.78	2	1.76	0.26	NKYVGVSLVGK	LYT	rep1
442.4991	1324.474	1324.4468	20.53	3	2.78	0.98	VIAHDPYAPADR	LY T	rep3

442.6995	1325.0751	1324.4468	474.41	3	1.86	0.38	VIAHDPYAPADR	LYK	rep1
365.5682	1093.6812	1093.2814	365.76	3	2.43	0.58	VKDGVPHLTK	LYK	rep3

Matching Genes:

NP_195146.1 (EDA9 (embryo sac development arrest 9); NAD binding / amino acid binding / cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor / phosphoglycerate dehydrogenase [Arabidopsis thaliana])

Protein Group 79

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	29.97	26.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
699.7305	1397.4453	1397.6239	127.75	2	2.24	0.51	AILLWTLEPGER	LYK	rep2
601.73	1201.4444	1201.3351	90.98	2	1.76	0.24	DALLANEATKR	LYT	rep1
601.7185	1201.4214	1201.3351	71.88	2	1.3	0.04	DALLANEATKR	LYK	rep2
580.8943	1159.773	1160.1984	366.63	2	2.1	0.57	HYNDEDVIR	LYT	rep2
581.2737	1160.5318	1160.1984	287.38	2	1.53	0.51	HYNDEDVIR	LYK	rep2
614.7721	1841.2928	1841.9392	350.93	3	2.63	1.1	SLEEDVAHHTTGDFRK	LYK	rep3
737.9052	2210.692	2210.5603	59.55	3	3.29	1.2	STIQCLTRPELYFVDVLR : +57.05000 (C5)	LYK	rep1
1105.8931	2209.7705	2210.5603	357.28	2	2.45	0.94	STIQCLTRPELYFVDVLR : +57.05000 (C5)	LYT	rep2
748.6698	2242.9859	2243.4839	221.95	3	2.27	0.48	TAFEGWGTNEDLIISILAHR	LYK	rep3
748.8495	2243.525	2243.4839	18.32	3	1.37	0.18	TAFEGWGTNEDLIISILAHR	LYT	rep1

514.0721	1026.1285	1026.1518	22.79	2	2.47	0.56	TSTQLLHAR	LYK	rep3
514.0074	1025.9991	1026.1518	148.89	2	0.87	0.01	TSTQLLHAR	LYT	rep3

Matching Genes:

NP_174810.1 (ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis thaliana])

Protein Group 80

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	24.4	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
692.5402	1383.0647	1383.4961	311.78	2	1.93	0.84	AHIQMVNDNGER	LYT	rep1
1249.3346	3744.9803	3745.1008	32.18	3	2.58	0.87	CTENLDDPSDADVYKPSLGYISTLNSYNLPILR : +57.05000 (C1)	LYT	rep1
756.8281	2267.4609	2268.5151	464.72	3	2.29	0.73	FSTIETTLTHSSPMSYGRPR	LYT	rep1
817.6325	1633.2493	1633.8076	341.72	2	3.51	1.95	HAIGEQFEWIEFK	LYT	rep1
750.8533	1499.691	1500.66 6	649.74	2	3.08	1.28	IEVWDHHAPQLR	LYT	rep1
803.7999	2408.3763	2408.6836	127.57	3	3.33	1.41	NLRPFLIAGNNPQGQEWLQGR	LYT	rep1

Matching Genes:

NP_171884.1 (CRU2 (CRUCIFERIN 2); nutrient reservoir [Arabidopsis thaliana])

Protein Group 81

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	7	52.14	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
553.1361	1104.2566	1104.3276	64.29	2	2.36	0.9	IAGFSTHLMK	LYT	rep3
553.0646	1104.1136	1104.3276	193.84	2	2.21	0.82	IAGFSTHLMK	LYK	rep2
421.2736	1260.7974	1260.514	224.8	3	1. 49	0.28	IAGFSTHLMKR	LYT	rep1
684.5432	1367.0708	1367.6393	415.63	2	2.28	0.6	ILEEVAIIPSKR	LYT	rep1
617.9366	1233.8575	1234.4302	463.94	2	2.11	0.71	MTLDFHTNKK	LYT	rep3
617.9357	1233.8557	1234.4302	465.33	2	1.56	0.33	MTLDFHTNKK	LYK	rep2
449.9357	1346.7835	1346.6036	133.6	3	3.7	1.21	NKIAGFSTHLMK	LYT	rep1
1294.0145	3879.0201	3880.3994	355.45	3	2.77	0.83	VDKETLEMLASLGMSDTSGISAVEPQQAMAPIAAFGGR	LYT	rep1
1315.7469	3944.2174	3944.3994	46.16	3	1.96	0.27	VDKETLEMLASLGMSDTSGISAVEPQQAMAPIAAFGGR : +32.00000 (M8); +32.00000 (M14)	LYK	rep3

Matching Genes:

NP_001031325.1 (structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 82

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	4	16.98	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1307.0897	3918.2457	3918.4016	39.78	3	5.37	2.72	IHDENSSLYNTPPCFGIYMCGLVFEDLLEQGGLK : +57.05000 (C14); +57.05000 (C20)	LYK	rep3
663.1337	1986.3775	1987.1811	404.4	3	2.83	0.8	KADLLYNAIEESNGFFR	LYT	rep1
993.6402	1985.2647	1987.1811	964.41	2	0.88	0.07	KADLLYNAIEESNGFFR	LYK	rep2
644.8297	1931.4657	1931.1826	146.56	3	4.96	2.56	YLHICANETIHGVEFK : +57.05000 (C5)	LYK	rep3
878.0253	2631.0523	2630.9805	27.32	3	3.46	1.68	YLHICANETIHGVEFKDYPVPK : +57.05000 (C5)	LYK	rep1
877.9619	2630.8623	2630.9805	44.92	3	3.32	1.98	YLHICANETIHGVEFKDYPVPK : +57.05000 (C5)	LYT	rep2

Matching Genes:

NP_195288.1 (PSAT (phosphoserine aminotransferase); phosphoserine transaminase [Arabidopsis thaliana])

Protein Group 83

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	41.51	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
460.4371	918.8586	918.055	875.3	2	1.57	0.26	LFTERPR	LYT	rep3
932.1943	2793.5595	2793.1484	147.18	3	2.63	1.05	NISQYAIMAIGMQVEDHQFDPVASK	LYT	rep2
360.5297	1078.5655	1078.313	234.2	3	2.74	0.76	RVLIALHEK	LYT	rep2
360.6243	1078.8493	1078.313	497.4	3	2.72	0.67	RVLIALHEK	LYK	rep1
386.3024	1155.8838	1155.3111	495.68	3	2.44	1.09	VFGHPASIATR	LYT	rep2

386.2049	1155.5912	1155.3111	242.41	3	1.87	0.79	VFGHPASIATR	LYK	rep2
483.183	964.3503	964.0773	283.17	2	1.69	0.4	VLDVYEAR	LYT	rep2
1048.234	3141.6785	3142.6157	298.21	3	5.29	3.04	YLAGETFTLTDLHHIPAIQYLLGTPTKK	LYK	rep3
1048.4222	3142.2432	3142.6157	118.52	3	3.49	1.46	YLAGETFTLTDLHHIPAIQYLLGTPTKK	LYT	rep2

Matching Genes:

NP_192161.1 (ATGSTF2 (Arabidopsis thaliana Glutathione S-transferase (class phi) 2); glutathione transferase)

Protein Group 84

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	30.66	27.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1004.7046	2007.3936	2008.2418	422.37	2	3.24	1.47	ENAITVGTQHALDPLTTVK	LYT	rep1
1004.9601	2007.9046	2008.2418	167.92	2	1.35	0.04	ENAITVGTQHALDPLTTVK	LYK	rep2
582.0393	1162.063	1162.3404	238.67	2	2.38	1.08	GPGLYTEIGKK	LYK	rep2
581.9488	1161.8819	1162.3404	394.52	2	2.34	0.74	GPGLYTEIGKK	LYT	rep3
591.9964	1181.9771	1182.292	266.34	2	2.69	0.96	HFNAGFNFTK	LYT	rep1
592.0439	1182.0721	1182.292	186.01	2	2.42	0.88	HFNAGFNFTK	LYK	rep2
942.8151	2825.4217	2827.1179	599.97	3	3.62	1.8	LNASYYQIVSPSTVVGAEISHNFTTK	LYT	rep1
943.2666	2826.7763	2827.1179	120.82	3	2.82	1.23	LNASYYQIVSPSTVVGAEISHNFTTK	LYK	rep1
1009.0032	2015.9908	2017.26	629.19	2	4.37	2.73	VNNAGVANALIQHEWRPK	LYK	rep3
1009.2616	2016.5076	2017.26	372.98	2	3.71	2.4	VNNAGVANALIQHEWRPK	LYT	rep3

Matching Genes:

NP_197013.1 (porin, putative / voltage-dependent anion-selective channel protein, putative [Arabidopsis thaliana])

Protein Group 85

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	29.14	27.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
621.0298	1240.044	1240.4347	314.97	2	3.72	1.62	GLEGHVMEQLK	LYK	rep1
621.138	1240.2603	1240.4347	140.59	2	3.63	1.39	GLEGHVMEQLK	LYT	rep3
1162.172	3483.4925	3483.6514	45.6	3	6. 04	3.76	NENHVFPDAIGHHIQNVTVHEGEHDSHGSIR	LYK	rep3
1266.5206	3796.5384	3798.0351	394.08	3	6.41	3.84	WKNENHVFPDAIGHHIQNVTVHEGEHDSHGSIR	LYK	rep3
1266.661	3796.9596	3798.0351	283.2	3	4.66	2.82	WKNENHVFPDAIGHHIQNVTVHEGEHDSHGSIR	LYT	rep2

Matching Genes:

NP_194099.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 86

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	34.77	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
549.08	1644.2164	1643.8689	211.4	3	2.04	0.52	LGDDEFGHMLAGILR	LYK	rep1
789.9221	1577.8286	1578.6024	490.15	2	2.02	0.9	NGVDDQGINFDTGAR	LYT	rep1
732.7582	2195.2511	2195.5056	115.94	3	3.17	1.39	NPSADMLLRPDELNLDLIR	LYT	rep3

732.891	2195.6495	2195.5056	65.54	3	2.81	0.82	NPSADMLLRPDELNLDLIR	LYK	rep3
1216.7167	3647.1265	3647.9714	231.6	3	3.34	1.66	TFKGAVDPFHVNAVDTTGAGDSFVGALLNQIVDDR	LYT	rep1
1095.9916	3284.9513	3285.626	205.35	3	4.45	2.6	VSDVELEFLTGSNKIDDETALTLWHPNLK	LYK	rep1
1095.8236	3284.4473	3285.626	358.72	3	2.03	0.53	VSDVELEFLTGSNKIDDETALTLWHPNLK	LYT	rep3

Matching Genes:

NP_180697.1 (pfkB-type carbohyd rate kinase family protein [Arabidopsis thaliana])

Protein Group 87

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	19.27	21.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
772.6874	1543.3592	1542.781	374.76	2	2.68	0.66	DGVVLLWDLAEGKK	LYT	rep3
773.1377	1544.2598	1542.781	958.53	2	1.47	0.09	DGVVLLWDLAEGKK	LYK	rep1
774.3114	2319.9107	2319.6469	113.74	3	4.5	2.68	KLYSLEANSVIHALCFSPNR : +57.05000 (C15)	LYT	rep3
774.1971	2319.568	2319.6469	34.03	3	3.35	1.53	KLYSLEANSVIHALCFSPNR : +57.05000 (C15)	LYK	rep2
731.6813	2192.0203	2191.4742	49.32	3	3.33	2.05	LYSLEANSVIHALCFSPNR : +57.05000 (C14)	LYT	rep2
1096.867	2191.7183	2191.474	111.49	2	2.75	1.11	LYSLEANSVIHALCFSPNR : +57.05000 (C14)	LYK	rep2
703.7318	2108.172	2108.2588	41.18	3	1.7	0.58	YTISEGGEGHRDWVSCVR : +57.05000 (C16)	LYT	rep3
725.0037	1447.9917	1448.6497	454.21	2	2.72	0.86	YWLCAATEHGIK : +57.05000 (C4)	LYT	rep3
483.9981	1448.9708	1448.6497	221.67	3	1.84	0.5	YWLCAATEHGIK : +57.05000 (C4)	LYK	rep2

Matching Genes:

NP_173248.1 (ATARCA (Arabidopsis thaliana Homolog of the Tobacco ArcA); nucleotide binding)

Protein Group 88

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	25.08	15.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
708.2448	1414.4739	1414.6764	143.14	2	1.96	0.43	GREPLFLPCTPK : +57.05000 (C9)	LYT	rep1
497.1955	1488.563	1488.7829	147.73	3	3.21	1.04	HGKVPGLAVVIVGSR	LYK	rep3
497.3528	1489.0351	1488.7829	169.34	3	2.53	0.84	HGKVPGLAVVIVGSR	LYT	rep1
994.8933	2981.6565	2982.3193	222.27	3	4.77	3.24	HINEEHILGAISIDKDVDGFHPLNIGK	LYT	rep2
994.8588	2981.5528	2982.3193	257.02	3	4.23	2.65	HINEEHILGAISIDKDVDGFHPLNIGK	LYK	rep1
774.2056	2319.5932	2319.668	32.22	3	4.87	1.37	VHELNSNPDVHGILVQLPLPK	LYK	rep3
774.0587	2319.1527	2319.668	222.14	3	3.11	1.02	VHELNSNPDVHGILVQLPLPK	LYT	rep3

Matching Genes:

NP_187837.1 (tetrahydrofolate dehydrogenase/ cyclohydrolase, putative [Arabidopsis thaliana])

Protein Group 89

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.96	5	19.36	62.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
600.2312	1198.4468	1198.4224	20.41	2	1.86	0.47	AVFPSIVGRPR	LYT	rep1

600.2521	1198.4886	1198.4224	55.25	2	1.82	0.76	AVFPSIVGRPR	LYK	rep1
567.023	1132.0303	1132.1849	136.56	2	1.74	0.24	GYSFTTTAER	LYK	rep3
573.1067	1144.1978	1144.3736	153.67	2	1.96	0.47	HTGVMVGMGQK	LYT	rep1
506.2698	1515.7858	1515.6791	70.45	3	3.9	1.8	IWHHTFYNELR	LYK	rep3
758.6241	1515.2325	1515.6791	294.66	2	3.14	1.22	IWHHTFYNELR	LYT	rep1
1051.7975	3152.369	3152.5259	49.77	3	5.25	0.18	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	LYK	rep1
1051.5966	3151.7662	3152.5259	240.97	3	4.92	0.04	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	LYT	rep2

Matching Genes:

NP_001031504.1 (ACT1 (ACTIN 1); structural constituent of cytoskeleton [Arabidopsis thaliana])

Protein Group 90

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	17.34	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
904.8352	2711.4821	2711.1133	136.06	3	4.29	2.52	AIAIMSHPIPNTNDSHSVQVIIPQK	LYT	rep1
904.4822	2710.4231	2711.1133	254.59	3	3.64	1.66	AIAIMSHPIPNTNDSHSVQVIIPQK	LYK	rep2
732.1591	2193.4537	2193.4889	16.07	3	4.78	2.62	KSDMYVFCCSYSHNVAPK : +57.05000 (C8); +57.05000 (C9)	LYK	rep2
732.0355	2193.0831	2193.4889	185.03	3	3.38	1.35	KSDMYVFCCSYSHNVAPK : +57.05000 (C8); +57.05000 (C9)	LYT	rep3
1261.8021	3782.3829	3783.1189	194.55	3	5.5	2.92	YGLDGNTIDFIGHAVALHTNDQHLDQPAFDTVMR	LYT	rep2
1261.4486	3781.3223	3783.1189	474.88	3	5.09	3.02	YGLDGNTIDFIGHAVALHTNDQHLDQPAFDTVMR	LYK	rep2

Matching Genes:

NP_191551.1 (ATGDI2 (RAB GDP DISSOCIATION INHIBITOR 2); RAB GDP-dissociation inhibitor [Arabidopsis thaliana])

Protein Group 91

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	24.93	25.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
735.1372	1468.2588	1467.6561	410.66	2	3.52	0.15	AMGHHVTVISSSNK	LYK	rep2
734.6177	1467.2198	1467.6561	297.31	2	3.06	0.61	AMGHHVTVISSSNK	LYT	rep3
798.9151	1595.8145	1595.8291	9.15	2	4.01	0.1	AMGHHVTVISSSNKK	LYK	rep3
676.5537	1351.0918	1351.6234	393.28	2	1.74	0.58	GGILGLGGVGHMGVK	LYT	rep3
1053.4017	3157.1817	3156.6862	156.96	3	2.58	0.75	IPEGMAVEQAAPLLCAGVTVYSPLSHFGLK : +57.05000 (C15)	LYK	rep3
1090.9506	3269.8282	3269.7331	29.07	3	2.69	0.81	MSELADSLDYVIDTVPVHHALEPYLSLLK	LYT	rep3
1090.8319	3269.4723	3269.7331	79.79	3	1.66	0.34	MSELADSLDYVIDTVPVHHALEPYLSLLK	LYK	rep1

Matching Genes:

NP_001031788.1 (CAD5 (CI NNAMYL ALCOHOL DEHYDROGENASE 5) [Arabidopsis thaliana])

Protein Group 92

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	30.8	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1149.8724	3446.5938	3446.7939	58.05	3	5.3	2.78	AGAHKQEAHLALNPFGQIPALEDGDLTLFESR	LYK	rep3
1149.6075	3445.7992	3446.7939	288.61	3	5.27	2.84	AGAHKQEAHLALNPFGQIPALEDGDLTLFESR	LYT	rep2
1057.5653	3169.6724	3169.512	50.64	3	5.64	2.82	SEFLAGDSFTLADLHHLPAIHYLLGTDSK	LYK	rep3

1057.3514	3169.0308	3169.512	151.79	3	3.36	1.57	SEFLAGDSFTLADLHHLPAIHYLLGTDSK	LYT	rep2
643.8067	1285.5977	1286.5301	724.78	2	1.65	0.73	VHGVPMSTATMR	LYT	rep1
644.0513	1286.0869	1286.5301	344.48	2	1.29	0.36	VHGVPMSTATMR	LYK	rep2
483.183	964.3503	964.0773	283.17	2	1.69	0.4	VLDVYEAR	LYT	rep2

Matching Genes:

NP_850479.1 (ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); glutathione transferase [Arabidopsis thaliana])

Protein Group 93

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.95	5	12.78	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
726.7167	2177.1265	2176.3915	337.74	3	4.58	2.05	CAHHNNHHEGFMNFMHR : +57.05000 (C1)	LYK	rep3
726.1698	2175.4859	2176.3915	416.09	3	2.81	1.49	CAHHNNHHEGFMNFMHR : +57.05000 (C1)	LYT	rep2
1122.1092	2242.2027	2242.4746	121.27	2	2.02	0.78	GFFEVTHDISNLTCADFLR : +57.05000 (C14)	LYT	rep3
606.9702	1817.8872	1817.1072	429.26	3	3.32	1.02	HRLGPNYLQLPVNAPK	LYT	rep1
606.5256	1816.5534	1817.1072	304.74	3	1.52	0.2	HRLGPNYLQLPVNAPK	LYK	rep1
763.5303	1525.045	1523.7809	829.57	2	2.52	0.87	LGPNYLQLPVNAPK	LYT	rep3
762.8079	1523.6001	1523.7809	118.61	2	1.77	0.42	LGPNYLQLPVNAPK	LYK	rep2
429.4125	1285.2141	1284.4689	580.22	3	1.79	0.48	RWVEILSEPR	LYT	rep3

Matching Genes:

NP_001031073.1 (CAT3 (CATALASE 3); catalase [Arabidopsis thaliana])

Protein Group 94

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	12.52	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
561.3221	1680.943	1680.9952	31.1	3	3.56	2.07	GILLGAVHGIVESLFR	LYT	rep3
561.2804	1680.8177	1680.9952	105.6	3	1.66	0.6	GILLGAVHGIVESLFR	LYK	rep2
1127.0717	3378.1915	3378.914	213.84	3	5.91	4.01	IFSHMKPNSILGLSHGFLLGHLQSSGLDFPK	LYK	rep3
1127.1488	3378.4229	3378.914	145.35	3	5.47	3.52	IFSHMKPNSILGLSHGFLLGHLQSSGLDFPK	LYT	rep2
1021.4418	3061.3018	3060.3672	305.41	3	4.67	2.28	KGHSYSEIINESVIESVDSLNPFMHAR	LYK	rep1
1021.3716	3061.0913	3060.3672	236.6	3	3.71	1.71	KGHSYSEIINESVIESVDSLNPFMHAR	LYT	rep3

Matching Genes:

NP_001078309.1 (ketol-acid reductoisomerase [Arabidopsis thaliana])

Protein Group 95

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	17.77	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
592.1202	1773.3372	1773.9714	357.51	3	4.58	2.44	KLSSALSAASSACDHIR : +57.05000 (C13)	LYT	rep2
592.2274	1773.6588	1773.9714	176.26	3	4.54	2.23	KLSSALSAASSACDHIR : +57.05000 (C13)	LYK	rep1
823.6116	1645.2076	1645.7985	359.08	2	3.38	1.78	LSSALSAASSACDHIR : +57.05000 (C12)	LYT	rep1
549.6132	1645.816	1645.7985	10.61	3	2.56	1.2	LSSALSAASSACDHIR : +57.05000 (C12)	LYK	rep2
827.6715	2479.991	2480.7002	285.86	3	3.37	1.45	NVIIWGNHSSTQYPDVNHATVK	LYT	rep3

667.6772	2000.0083	2000.4173	204.5	3	2.75	0.93	VLVTGAAGQIGYALVPMIAR	LYT	rep2

Matching Genes:

NP_199147.1 (malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana])

Protein Group 96

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.22	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1147.899	2293.7823	2294.5788	347.16	2	4.34	2.4	AFVEQYYHILHQSPGLVHR	LYK	rep1
765.7128	2294.1148	2294.5788	202.22	3	3.77	1.86	AFVEQYYHILHQSPGLVHR	LYT	rep3
1345.681	4034.0196	4036.2663	556.64	3	6.62	4.12	LTAPPAEPAARPEASAHENVPNSSHVDVEDDGHSIYVR	LYK	rep3
735.074	1468.1324	1468.6654	362.94	2	3.01	1.22	NFGAIKHEGIQVR	LYK	rep1
735.1712	1468.3267	1468.6654	230.62	2	2.2	0.18	NFGAIKHEGIQVR	LYT	rep1

Matching Genes:

NP_200906.2 (nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana])

Protein Group 97

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	33.48	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
800.7798	1599.544	1599.7561	132.59	2	3.58	1.76	FNGGGHVNHSIFWK	LYK	rep3
800.8535	1599.6914	1599.7561	40.41	2	3.33	1.74	FNGGGHVNHSIFWK	LYT	rep1
857.7185	2570.132	2570.7385	235.91	3	1.87	0.62	HHQAYVTNYNNALEQLDQAVNK	LYT	rep3
1110.2443	3327.7093	3328.5742	259.84	3	5.56	2.88	HHQAYVTNYNNALEQLDQAVNKGDASTVVK	LYT	rep3
1110.2025	3327.5841	3328.5742	297.47	3	4.7	2.58	HHQAYVTNYNNALEQLDQAVNKGDASTVVK	LYK	rep2
1060.5897	3178.7457	3179.4634	225.72	3	2.69	1.21	NLAPSSEGGGEPPKGSLGSAIDAHFGSLEGLVK	LYT	rep1
1060.5094	3178.5047	3179.4634	301.51	3	1.73	0.19	NLAPSSEGGGEPPKGSLGSAIDAHFGSLEGLVK	LYK	rep2

Matching Genes:

NP_001030670.1 (MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); manganese superoxide dismutase [Arabidopsis thaliana])

Protein Group 98

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	18.43	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
749.7449	1497.4742	1497.6555	121.09	2	2.16	1.03	ATTHPVVSDKLSDK	LYT	rep2
749.746	1497.4764	1497.6555	119.62	2	1.79	0.51	ATTHPVVSDKLSDK	LYK	rep1
684.6586	2050.9522	2051.3481	193	3	3.86	1.42	GPGTTIEFSITLIEQLFGK	LYK	rep3
636.0721	1270.1285	1270.5024	294.35	2	2.76	1.49	KATGYPVFMEK	LYT	rep2
636.1138	1270.2119	1270.5024	228.63	2	1.56	0.6	KATGYPVFMEK	LYK	rep2
809.7064	2426.0958	2426.671	237.05	3	4.74	1.9	RGGADVTVASVETQVGVDACHGIK : +57.05000 (C20)	LYT	rep1
809.6388	2425.8929	2426.671	320.65	3	3.79	1.49	RGGADVTVASVETQVGVDACHGIK : +57.05000 (C20)	LYK	rep1

Matching Genes:

NP_001030698.1 (catalytic [Arabidopsis thaliana])

Protein Group 99

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	6.93	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1082.8177	3245.4298	3245.7392	95.35	3	6.87	4.41	AVLDAATIAGLHPLHLIHETTATALAYGIYK	LYT	rep3
1082.8805	3245.618	3245.7392	37.35	3	5.46	3.38	AVLDAATIAGLHPLHLIHETTATALAYGIYK	LYK	rep1
1134.5043	3400.4893	3401.9255	422.17	3	4.67	2.61	RAVLDAATIAGLHPLHLIHETTATALAYGIYK	LYK	rep1
1134.8182	3401.4312	3401.9255	145.3	3	3.87	2.12	RAVLDAATIAGLHPLHLIHETTATALAYGIYK	LYT	rep3
770.2467	2307.7166	2307.6142	44.37	3	1.92	0.82	VREFQVHESFPFSISLAWK	LYK	rep1

Matching Genes:

NP_178110.3 (heat shock protein 70, putative / HSP70, putative [Arabidopsis thaliana])

Protein Group 100

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	21.94	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
561.8291	1121.6426	1122.2795	567.52	2	2.35	0.62	AVNALEQHIK	LYT	rep2
561.8268	1121.638	1122.2795	571.65	2	1.73	0.21	AVNALEQHIK	LYK	rep2

1012.9108	3035.7088	3036.407	229.93	3	5.13	3.25	EGVSTAVSHGLWLNIPDYDAPTQLVKPK	LYT	rep2
1012.7661	3035.2749	3036.407	372.84	3	4.51	2.27	EGVSTAVSHGLWLNIPDYDAPTQLVKPK	LYK	rep2
590.2775	1767.8089	1767.8988	50.83	3	2.07	0.41	IHVPEGYDYELYNR	LYK	rep2
590.0986	1767.2724	1767.8988	354.3	3	1.68	0.43	IHVPEGYDYELYNR	LYT	rep1
109 1.4969	3271.4674	3272.7436	389.97	3	3.88	1.2	NLDFLEMWRPFLQPYHLIIVQDGDPSK	LYK	rep3
1091.6644	3271.9698	3272.7436	236.45	3	3.56	1.37	NLDFLEMWRPFLQPYHLIIVQDGDPSK	LYT	rep2

Matching Genes:

NP_197069.1 (RGP2 (Reversibly glycosylated polypeptide-3); DNA binding / alpha-1,4-glucan-protein synthase (UDP-forming) [Arabidopsis thaliana])

Protein Group 101

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	17.81	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
490.4415	1468.3009	1468.6409	231.46	3	4.08	0.22	AMGHHVTVISSSDK	LYK	rep3
490.6365	1468.8861	1468.6409	167.01	3	3.8	0.12	AMGHHVTVISSSDK	LYT	rep3
533.1659	1596.4742	1596.8138	212.69	3	4.04	0.22	AMGHHVTVISSSDKK	LYK	rep3
676.5537	1351.0918	1351.6234	393.28	2	1.74	0.58	GGILGLGGVGHMGVK	LYT	rep3
1206.0658	3615.1739	3616.249	297.29	3	3.37	1.34	IPEGMAVEQAAPLLCAGVTVYSPLSHFGLMASGLK : +57.05000 (C15)	LYK	rep3

Matching Genes:

NP_188576.1 (CAD4 (CINNAMYL ALCOHOL DEHYDROGENASE 4); cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana])

Protein Group 102

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	30.57	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1189.8358	3566.484	3565.8589	175.3	3	5.4	2.99	AEDSPAVTSTPLVVTEHPVEPTTELPVEHPEEK	LYK	rep3
1189.4532	3565.3363	3565.8589	146.56	3	3.8	2.16	AEDSPAVTSTPLVVTEHPVEPTTELPVEHPEEK	LYT	rep1
513.0127	1024.0098	1024.2174	202.69	2	1.43	0.46	GLFDFLGKK	LYT	rep1
1494.1014	4479.2808	4479.8393	124.67	3	3.19	1.11	LPGHHDEKAEDSPAVTSTPLVVTEHPVEPTTELPVEHPEEK	LYK	rep1
1134.1058	3399.294	3400.6257	391.6	3	2.98	1.27	TAEDDVPVSTTIPVPVSESVVEHDHPEEEKK	LYT	rep1
1134.0302	3399.067	3400.6257	458.37	3	2.4	0.87	TAEDDVPVSTTIPVPVSESVVEHDHPEEEKK	LYK	rep2

Matching Genes:

NP_173468.1 (COR47 (cold regulated 47) [Arabidopsis thaliana])

Protein Group 103

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	13.05	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1431.8108	2861.606	2863.0605	508.04	2	3.72	1.8	ATNGDTFLGGEDFDNALLDFLVNEFK	LYK	rep3
1264.9879	3791.9403	3792.0908	39.7	3	1.77	0.59	ATNGDTFLGGEDFDNALLDFLVNEFKTTEGIDLAK	LYT	rep1
1229.6253	2457.2349	2456.8828	143.31	2	1.87	0.53	ELLLLDVTPLSLGIETLGGVFTR	LYT	rep2

687.8888	2060.6429	2061.2151	277.59	3	2.14	0.62	NTADTTIYSIEKSLGEYR	LYT	rep3
539.0298	1614.0659	1613.8225	150.81	3	3.49	1.27	SRFETLVNHLIER	LYK	rep1
539.0123	1614.0135	1613.8225	118.36	3	3.34	0.71	SRFETLVNHLIER	LYT	rep3

Matching Genes:

NP_196521.1 (mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP binding / unfolded protein binding [Arabidopsis thaliana])

Protein Group 104

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	6	18.9	20.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
854.1445	2559.4101	2559.8386	167.39	3	1.75	0.26	EKLVDTNGAGDAFVGGFLSQLVHGK	LYT	rep1
690.5606	1379.1055	1378.5796	381.5	2	2.06	0.38	HLPMYDEMSQK	LYT	rep3
607.5786	1213.1416	1213.3874	202.58	2	1.79	0.07	KPENWALVEK	LYT	rep3
607.5501	1213.0845	1213.3874	249.66	2	1.73	0.31	KPENWALVEK	LYK	rep3
527.9148	1053.814	1054.3298	489.24	2	1.65	0.5	KYPVIPLPK	LYK	rep2
527.898	1053.7803	1054.3298	521.2	2	1.25	0.23	KYPVIPLPK	LYT	rep3
821.0049	2459.9912	2460.7922	325.53	3	2.91	0.93	LNNAILAEDKHLPMYDEMSQK	LYK	rep1
821.0458	2460.1139	2460.7922	275.67	3	2.39	0.43	LNNAILAEDKHLPMYDEMSQK	LYT	rep2
768.4415	2302.3011	2302.5513	108.64	3	2.83	1.29	LVDTNGAGDAFVGGFLSQLVHGK	LYT	rep3
768.4794	2302.4146	2302.5513	59.34	3	2.72	0.97	LVDTNGAGDAFVGGFLSQLVHGK	LYK	rep2

Matching Genes:

NP_187593.1 (ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana])

Protein Group 105

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	19.81	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
913.8881	2738.6407	2739.1399	182.24	3	2.25	0.83	IALIGLGQSVSSPVAFHSLGEAVATVSK	LYT	rep1
1046.9374	3137.7887	3137.626	51.85	3	4.48	2.44	MGSYLAVAAASANPPHFIHLVYKPPNGSVK	LYK	rep3
1047.1727	3138.4947	3137.626	276.88	3	4.29	2.46	MGSYLAVAAASANPPHFIHLVYKPPNGSVK	LYT	rep1
1014.745	3041.2115	3042.3266	366.54	3	2.62	0.87	VDAHLSGLLAQVSSEEDFTGKPGQSTVLR	LYT	rep1
1014.8704	3041.5876	3042.3266	242.92	3	2.25	0.89	VDAHLSGLLAQVSSEEDFTGKPGQSTVLR	LYK	rep1
971.4931	1940.9705	1941.2457	141.78	2	3.61	2.14	VQWMHIDMAGPVWNEK	LYT	rep1

Matching Genes:

NP_179997.1 (cytosol aminopeptidase [Arabidopsis thaliana])

Protein Group 106

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	19.63	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1086.9635	3257.867	3256.7222	351.54	3	6.39	4.04	IPVLIHNGKPVNESIIQVQYIDEVWSHK	LYT	rep3
1086.0372	3255.0882	3256.7222	501.71	3	5.08	2.95	IPVLIHNGKPVNESIIQVQYIDEVWSHK	LYK	rep2
545.6943	1634.0595	1632.9756	663.79	3	3.58	1.41	NKSPLLLQMNPIHK	LYT	rep3

545.1158	1632.3241	1632.9756	398.97	3	3.22	0.8	NKSPLLLQMNPIHK	LYK	rep2
507.3972	1519.168	1518.8724	194.6	3	2.96	1.19	SPLLLQMNPIHKK	LYK	rep2
507.2971	1518.8677	1518.8724	3.11	3	2.87	1.37	SPLLLQMNPIHKK	LYT	rep3

Matching Genes:

NP_565178.1 (ATGSTU19 (GLUTATHIONE TRANSFERASE 8); glutathione transferase [Arabidopsis thaliana])

Protein Group 107

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	46.98	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
952.4606	1902.9056	1904.066	609.45	2	4.28	2.09	EAFSLFDKDGDGCITTK : +57.05000 (C13)	LYT	rep1
952.8371	1903.6585	1904.066	214.02	2	2.15	0.71	EAFSLFDKDGDGCITTK : +57.05000 (C13)	LYK	rep2
1346.6083	4036.8014	4038.4009	396.08	3	4.84	2.64	SLGQNPTEAELQDMINEVDADGNGTIDFPEFLNLMAK	LYK	rep3
604.9989	1811.9732	1809.9803	1101.06	3	3.68	1.28	VFDKDQNGFISAAELR	LYT	rep1
905.637	1809.2583	1809.9803	398.9	2	3.29	1.14	VFDKDQNGFISAAELR	LYK	rep3

Matching Genes:

NP_176814.1 (CAM4 (CALMODULIN 4); calcium ion binding [Arabidopsis thaliana])

Protein Group 108

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	11.64	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1114.3627	3340.0645	3341.7878	515.66	3	5.36	2.58	DHVLNHLSIPAACFTHPEISMVGLTEPQAR : +57.05000 (C13)	LYK	rep3
1296.017	3885.0274	3886.4148	356.98	3	7.3	4.69	MIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTR	LYT	rep1
1296.5409	3886.5992	3886.4148	47.45	3	7.24	4.57	MIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTR	LYK	rep1

Matching Genes:

NP_567487.1 (dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2) [Arabidopsis thaliana])

Protein Group 109

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	16.26	31.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
791.9083	2372.7015	2371.6371	448.82	3	4.17	2.35	DLVLLSGAHTIGVSHCSSFTNR : +57.05000 (C16)LYT	rep1	
792.2274	2373.6588	2371.6371	852.46	3	3.05	0.53	DLVLLSGAHTIGVSHCSSFTNR : +57.05000 (C16)	LYK	rep3
774.8387	2321.4928	2322.6289	489.16	3	5.59	3.01	IVQDFVSNHVSNAPSLAAALIR	LYK	rep3
775.4047	2323.1905	2322.6289	241.8	3	3.84	1.49	IVQDFVSNHVSNAPSLAAALIR	LYT	rep1
417.3369	1248.9873	1248.4405	437.92	3	2.77	1.15	MHFHDCFVR : +57.05000 (C6)	LYT	rep3
626.0274	1250.0391	1248.4405	1280.44	2	2.36	0.83	MHFHDCFVR : +57.05000 (C6)	LYK	rep3

Matching Genes:

NP_172018.1 (RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase [Arabidopsis thaliana])

Protein Group 110

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	34.05	34.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
535.732	1069.4483	1068.2303	1140.15	2	1.98	0.41	EKLPGYHPK	LYK	rep3
535.387	1068.7583	1068.2303	494.28	2	1.93	0.38	EKLPGYHPK	LYT	rep1
513.0127	1024.0098	1024.2174	202.69	2	1.4 3	0.46	GLFDFLGKK	LYT	rep1
907.4315	2719.2711	2720.0503	286.47	3	2.71	0.77	KPEDGSAVAAAPVVVPPPVEEAHPVEK	LYK	rep2
907.4443	2719.3095	2720.0503	2 72.33	3	2.67	0.65	KPEDGSAVAAAPVVVPPPVEEAHPVEK	LYT	rep3
632.3482	1262.6807	1263.4016	570.6	2	2.53	1.36	VHISEPEPEVK	LYT	rep3
632.6136	1263.2115	1263.4016	150.5	2	2.29	1.06	VHISEPEPEVK	LYK	rep2
700.8933	2099.6565	2100.3376	324.32	3	3.73	1.88	VHISEPEPEVKHESLLEK	LYK	rep1
700.9617	2099.8615	2100.3376	226.68	3	3.51	1.65	VHISEPEPEVKHESLLEK	LYT	rep2

Matching Genes:

NP_177745.1 (ERD14 (EARLY RESPONSE TO DEHYDRATION 14) [Arabidopsis thaliana])

Protein Group 111

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	9.25	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
765.5428	2293.6051	2293.5884	7.27	3	5.17	2.36	HDFIVVEFYAPWCGHCQK : +57.05000 (C13); +57.05000 (C16)	LYK	rep2
765.1467	2292.4167	2293.5884	510.85	3	4.28	1.7	HDFIVVEFYAPWCGHCQK : +57.05000 (C13); +57.05000 (C16)	LYT	rep1

529.2235	1584.6471	1584.8164	106.85	3	4.29	1.9	LFKPFDELFVDSK	LYT	rep1
1011.3025	2020.5894	2022.3157	853.64	2	2.9	0	NVLIEFYAPWCGHCQK : +57.05000 (C11); +57.05000 (C14)	LYT	rep1
1011.6129	2021.2102	2022.3157	546.64	2	2.27	0	NVLIEFYAPWCGHCQK : +57.05000 (C11); +57.05000 (C14)	LYK	rep2

Matching Genes:

NP_177875.1 (ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase [Arabidopsis thaliana])

Protein Group 112

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	13.47	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
736.3215	2205.9411	2206.487	247.42	3	3.47	1.33	ILSQDKEHFAEMAVDAVFR	LYK	rep1
736.3036	2205.8873	2206.487	271.82	3	3.07	1.64	ILSQDKEHFAEMAVDAVFR	LYT	rep2
764.7	1527.3843	1527.798	270.76	2	3	1. 52	KIIGHGINCFVNR : +57.05000 (C9)	LYK	rep2
510.2162	1527.6251	1527.798	113.17	3	2.77	1.07	KIIGHGINCFVNR : +57.05000 (C9)	LYT	rep2
382.9681	1145.8809	1145.2732	530.67	3	2.06	0.32	KSHAIEAFSR	LYK	rep1
1107.8739	3320.5982	3321.6599	319.62	3	2.27	0.61	QLIYNFPEELFADAGILAIEHADFEGIER	LYK	rep3
509.5738	1017.1319	1017.1003	31.07	2	1.54	0.43	SHAIEAFSR	LYT	rep1

Matching Genes:

NP_197589.1 (chaperonin, putative [Arabidopsis tha liana])

Protein Group 113

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	14.54	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1212.8031	3635.3858	3636.8672	407.31	3	3.99	2.31	GNAAFSSGDFNSAVNHFTDAINLTPTNHVLFSNR	LYT	rep1
622.4075	1242.7994	1243.5287	586.49	2	1.51	0.35	HMQNPMIMNK	LYT	rep1
712.347	2134.0177	2133.3262	324.14	3	3.37	1.8	LGAAHLGLNQFDEAVEAYSK	LYT	rep1
676.8507	2027.5286	2028.1484	305.59	3	3.42	1.92	SAAHASLNHYDEALSDAKK	LYT	rep3

Matching Genes:

NP_176461.1 (stress-inducible protein, putative [Arabidopsis thaliana])

Protein Group 114

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	15.97	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
746.0665	2235.1761	2234.6113	252.75	3	5.98	3.94	HAVGLVRPVSIAFEVIHSFR	LYK	rep3
745.9797	2234.9157	2234.6113	136.23	3	4.8	3.15	HAVGLVRPVSIAFEVIHSFR	LYT	rep2
1332.8214	3995.4408	3995.4242	4.15	3	6.18	4.26	SGVYTDSHCGSTPMDVNHAVLAVGYGVEDGVPYWLIK : +57.05000 (C9)	LYT	rep2
1332.6876	3995.0394	3995.4242	96.31	3	5.45	3.72	SGVYTDSHCGSTPMDVNHAVLAVGYGVEDGVPYWLIK : +57.05000 (C9)	LYK	rep1

Matching Genes:

NP_001032106.1 (AALP (ARABIDOPSIS ALEURAIN-LIKE PROTEASE); cysteine-type peptidase [Arabidopsis thaliana])

Protein Group 115

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.59	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1105.1752	3312.502	3313.7743	383.94	3	4.86	2.83	DHVLNHLSIPAACFTHPEISMVGLTEPQAK : +57.05000 (C13)	LYK	rep3
1296.017	3885.0274	3886.4148	356.98	3	7.3	4.69	MIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTR	LYT	rep1
1296.5409	3886.5992	3886.4148	47.45	3	7.24	4.57	MIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTR	LYK	rep1

Matching Genes:

NP_001078165.1 (LPD1 (LIPOAMIDE DEHYDROGENASE 1) [Arabidopsis thaliana])

Protein Group 116

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	14.53	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
788.6923	1575.3689	1575.7695	254.22	2	3.45	2.1	GKWSSPLIDNPAYK	LYT	rep1
619.6114	1855.8109	1855.1073	379.27	3	1.99	0.33	LSHVYTAILKPDNEVR	LYK	rep3
743.9503	2228.8275	2229.4556	281.72	3	2.13	0.29	SGEYVEHHLKFPPSVPYDK	LYT	rep1
1068.9132	3203.7161	3204.4934	242.55	3	4.57	2.54	YLRPQEAGWTPQGFDSESPYSIMFGPDK	LYK	rep2
1069.0131	3204.0157	3204.4934	149.07	3	4.17	2.31	YLRPQEAGWTPQGFDSESPYSIMFGPDK	LYT	rep2

Matching Genes:

NP_200987.1 (calnexin 1 (CNX1) [Arabidopsis thaliana])

Protein Group 117

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	8.04	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1264.7943	3791.3595	3792.1487	208.12	3	5.35	3.06	AKGNAAFSSGDFTTAINHFTEAIALAPTNHVLFSNR	LYT	rep1
1264.3043	3789.8895	3792.1487	595.75	3	4.38	2.36	AKGNAAFSSGDFTTAINHFTEAIALAPTNHVLFSNR	LYK	rep3
1198.8793	3593.6143	3592.8974	199.53	3	4.47	2.28	GNAAFSSGDFTTAINHFTEAIALAPTNHVLFSNR	LYT	rep3
1198.2303	3591.6676	3592.8974	342.31	3	3.67	2.08	GNAAFSSGDFTTAINHFTEAIALAPTNHVLFSNR	LYK	rep2
616.0124	1230.0091	1229.5021	412.37	2	2.29	0.57	HMQNPMVMNK	LYT	rep1
615.8992	1229.7827	1229.5021	228.29	2	1.3	0.15	HMQNPMVMNK	LYK	rep2

Matching Genes:

NP_172691.1 (stress-inducible protein, putative [Arabidopsis thaliana])

Protein Group 118

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	15.73	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

873.9756	1745.9356	1746.9242	565.91	2	2.81	1.52	GHSLQYFTTHTDLVK	LYT	rep3
583.4121	1747.2129	1746.9242	165.24	3	2.77	1.41	GHSLQYFTTHTDLVK	LYK	rep2
952.1649	1902.3142	1903.1106	418.44	2	3.49	1.88	GHSLQYFTTHTDLVKR	LYK	rep1
951.9129	1901.8101	1903.1106	683.35	2	3.44	1.5	GHSLQYFTTHTDLVKR	LYT	rep2
1200.9926	3599.9542	3600.9585	278.89	3	3.49	1.27	TAWEELIDRVEQTGVDALEINFSCPHGMPER : +57.05000 (C24)	LYK	rep1
754.611	2260.8094	2261.4747	294.18	3	2.32	0.73	TLRPEPCVEGYSTPGGYSYK : +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_188408.1 (dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein [Arabidopsis thaliana])

Protein Group 119

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	20.1	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
489.5175	1465.5289	1465.637	73.73	3	2.25	0.71	DKDLAHIEEHMK	LYT	rep3
965.9958	2894.9641	2895.2588	101.79	3	1.91	0.32	EDLSKLYFGNFQILDINGSTCFLTR	LYT	rep2
470.2724	1407.7937	1407.4527	242.26	3	1.78	0.41	GGDVSWHIHDER	LYT	rep3
772.5227	1543.0298	1543.7308	454.1	2	3.06	1.4	KTALYDFHVAHGGK	LYK	rep3
657.8036	1970.3873	1970.3678	9.9	3	3.05	0.67	SLLALQGPLAAPVLQHLTK	LYT	rep1
657.9628	1970.8648	1970.3678	252.26	3	1.84	0.63	SLLALQGPLAAPVLQHLTK	LYK	rep1

Matching Genes:

NP_172650.1 (aminomethyltransferase, putative [Arabidopsis thaliana])

Protein Group 120

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	16.15	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1293.8387	2585.6617	2586.4597	308.55	2	3.51	1.18	DAAADEEDDDDVDLFGEETEEEK	LYK	rep3
375.935	1124.7815	1124.2954	432.38	3	2.95	0.74	KLDEHLLTR	LYT	rep2
375.9863	1124.9355	1124.2954	569.34	3	2.56	0.6	KLDEHLLTR	LYK	rep1
499.1906	996.3656	996.1225	244.1	2	2.26	0.55	LDEHLLTR	LYT	rep1
499.1895	996.3633	996.1225	241.77	2	1.7	0.1	LDEHLLTR	LYK	rep2
650.9792	1299.9427	1300.47	405.47	2	2.93	1.34	WYNHIDALLR	LYT	rep3
651.0832	1300.1507	1300.47	245.52	2	2.78	1.16	WYNHIDALLR	LYK	rep2

Matching Genes:

NP_001077627.1 (elongation factor 1-beta / EF-1-beta [Arabidopsis thaliana])

Protein Group 121

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	39.64	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
784.8012	1567.5867	1567.749	103.53	2	2.05	0.88	IIGATNPAASEPGTIR	LYT	rep1
996.3474	2986.0188	2986.3066	96.4	3	2.23	0.97	KEIALWFPDGPVNWQSSVHPWVYET	LYT	rep1
996.3864	2986.1356	2986.3066	57.28	3	1.79	0.87	KEIALWFPDGPVNWQSSVHPWVYET	LYK	rep1

687.1248	1372.2339	1370.4307	1315.84	2	3.25	1.25	NVIHGSDSVESAR	LYK	rep3
685.9221	1369.8286	1370.4307	439.28	2	1.26	0.06	NVIHGSDSVESAR	LYT	rep1
750.2617	1498.5078	1498.6036	63.91	2	2.38	0.86	NVIHGSDSVESARK	LYK	rep3
514.411	1540.2096	1540.6357	276.62	3	1.66	0.25	SFAEKHYEDLSSK	LYT	rep1

Matching Genes:

NP_567346.1 (NDPK1 (nucleoside diphosphate kinase 1); ATP binding / nucl eoside diphosphate kinase [Arabidopsis thaliana])

Protein Group 122

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	24.27	28.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
638.8079	1275.6001	1276.4086	633.36	2	2.32	0.73	HNNVIPNGHFK	LYT	rep3
639.0198	1276.024	1276.4086	301.31	2	2.15	0.75	HNNVIPNGHFK	LYK	rep2
368.547	1102.6175	1102.25	333.43	3	2. 09	0.52	KHWQNYVK	LYT	rep2
368.5277	1102.5597	1102.25	280.94	3	1.92	0.41	KHWQNYVK	LYK	rep1
464.8792	1391.6142	1390.6361	703.32	3	2.6	1.22	KLAPTIGIAVDHR	LYK	rep1
464.6423	1390.9035	1390.6361	192.31	3	2.09	0.46	KLAPTIGIAVDHR	LYT	rep1
768.4508	1534.886	1535.7786	581.16	2	2.73	1.02	MKHNNVIPNGHFK	LYK	rep3
768.7005	1535.3853	1535.7786	256.07	2	2.6	1.11	MKHNNVIPNGHFK	LYT	rep2
844.1621	1686.3086	1686.9598	386.02	2	1.77	0.69	PTSGPLRPVVHGQTLK	LYT	rep3

Matching Genes:

NP_001030831.1 (ATBBC1 (brea st basic conserved 1); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 123

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	23.02	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
780.5397	1559.0638	1559.7505	440.27	2	3.28	1.86	HCVNSVSISFNPAK : +57.05000 (C2)	LYT	rep1
780.4484	1558.8811	1559.7505	557.35	2	2.02	0.89	HCVNSVSISFNPAK : +57.05000 (C2)	LYK	rep2
691.6179	2071.8303	2072.3347	243.39	3	4.471.62	RTEITCAACDGHLGHVFK : +57.05000 (C6); +57.05000 (C9)	LYK	rep3	
691.6473	2071.9185	2072.3347	200.8	3	4.2	1.87	RTEITCAACDGHLGHVFK : +57.05000 (C6); +57.05000 (C9)	LYT	rep2
958.5619	1915.1082	1916.1483	542.82	2	3.65	1.83	TEITCAACDGHLGHVFK : +57.05000 (C5); +57.05000 (C8)	LYK	rep2

Matching Genes:

NP_192392.1 (methionine sulfoxide reductase domain-cont aining protein / SeIR domain-containing protein [Arabidopsis thaliana])

Protein Group 124

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	16.26	22.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
786.6078	2356.7999	2357.6104	343.78	3	3.61	1.58	DLVLLSGAHTIGVSHCSSFSNR : +57.05000 (C16)LYT	rep3	
786.9022	2357.6832	2357.6104	30.88	3	3.57	1.29	DLVLLSGAHTIGVSHCSSFSNR : +57.05000 (C16)	LYK	rep2
781.7723	2342.2935	2342.6633	157.85	3	4.93	1.96	IVQDVVNQHINNAPSLAAGLIR	LYT	rep1
417.3369	1248.9873	1248.4405	437.92	3	2.77	1.15	MHFHDCFVR : +57.05000 (C6)	LYT	rep3
626.0274	1250.0391	1248.4405	1280.44	2	2.36	0.83	MHFHDCFVR : +57.05000 (C6)	LYK	rep3

Matching Genes:

NP_192868.1 (peroxidase, putative [Arabidopsis thaliana])

Protein Group 125

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.39	21.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
634.2124	1899.6137	1900.1116	262	3	4.4	2.72	HNIGLPSQFAAAFSFHR	LYT	rep3
634.4927	1900.4546	1900.1116	180.51	3	3.73	2.06	HNIGLPSQFAAAFSFHR	LYK	rep3
676.9723	2027.8934	2028.2845	192.84	3	4.92	2 .77	HNIGLPSQFAAAFSFHRK	LYK	rep3
677.0029	2027.9853	2028.2845	147.52	3	2.65	1.16	HNIGLPSQFAAAFSFHRK	LYT	rep2
750.068	1498.1204	1498.7502	420.21	2	1.98	0.67	VASVKPFGACFSTK : +57.05000 (C10)	LYK	rep2
750.0711	1498.1265	1498.7502	416.13	2	1.61	0.26	VASVKPFGACFSTK : +57.05000 (C10)	LYT	rep2

Matching Genes:

NP_171821.1 (extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana])

Protein Group 126

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	16.6	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
897.8472	2690.518	2690.926	151.62	3	3.49	2	GPPGAPAPPPAPLFSAESSKPSSSSNQK	LYK	rep3
897.6111	2689.8098	2690.926	414.82	3	1.7	0.35	GPPGAPAPPPAPLFSAESSKPSSSSNQK	LYT	rep3
718.7598	2153.2558	2152.4409	378.6	3	1.79	0.34	QGMSAVFQQLSSGAVTSGLRK	LYT	rep1
388.8813	1163.6204	1163.2901	283.88	3	2.13	0.69	RSDFFNHLK	LYT	rep3
1068.3372	2134.6587	2135.3901	342.51	2	3.88	2.36	SHYPLGPVWNASGKPASAPAK	LYT	rep3
1068.0701	2134.1245	2135.3901	592.67	2	3.63	2.01	SHYPLGPVWNASGKPASAPAK	LYK	rep3

Matching Genes:

NP_195175.1 (ATCAP1 (CYCLASE ASSOCIATED PROTEIN 1) [Arabidopsis thaliana])

Protein Group 127

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	27.27	15.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
608.0753	1821.2025	1821.0068	107.44	3	3.64	1.21	AMKDAIEGMNGQDLDGR	LYT	rep2
451.9636	901.9115	902.0508	154.35	2	2.62	1.1	GFGFVTFK	LYT	rep1
452.123	902.2304	902.0508	199.12	2	2.4	1.04	GFGFVTFK	LYK	rep2
638.3841	1274.7525	1274.4261	256.07	2	3.23	1.19	GFGFVTFKDEK	LYK	rep1
638.2784	1274.5411	1274.4261	90.17	2	3.05	1.26	GFGFVTFKDEK	LYT	rep3

521.3903	1561.1473	1560.504	412.23	3	1.78	0.24	SGGGGGYSGGGGSYGGGGGR	LYT	rep1

Matching Genes :

NP_179760.1 (ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding [Arabidopsis thaliana])

Protein Group 128

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	10.65	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
963.2933	2886.8565	2888.2483	481.87	3	4.07	1.39	HETLLHQVPNTGMWECVDFYPVSK : +57.05000 (C16)	LYK	rep2
1445.1465	2888.2774	2888.2483	10.08	2	2.68	0.98	HETLLHQVPNTGMWECVDFYPVSK : +57.05000 (C16)	LYT	rep3
567.0446	1698.1102	1697.8963	125.94	3	3.1	1.13	ILVDHSIVEGFAQGGR	LYK	rep2
716.5233	2146.5465	2147.5222	454.35	3	2.28	0.45	STLANDVVKPIYGSFVPVLK	LYT	rep3
1075.2681	2148.5205	2147.5222	464.88	2	1.91	0.88	STLANDVVKPIYGSFVPVLK	LYK	rep2
553.0752	1104.1348	1104.2195	76.68	2	1.83	0.18	TAFHFQPEK	LYK	rep1

Matching Genes:

NP_564798.1 (beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar [Arabidopsis thaliana])

Protein Group 129

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	29.41	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1099.4496	3295.3253	3295.6704	104.72	3	3.04	0.56	KLAGDQNLHFVETPALAPPEVHIDIADQQK	LYK	rep3
1226.7364	2451.4571	2451.7605	123.78	2	4.21	2.69	KYEPTIGVEVHPLDFFTNCGK : +57.05000 (C19)	LYK	rep1
818.2007	2451.5786	2451.7605	74.22	3	1.06	0.11	KYEPTIGVEVHPLDFFTNCGK : +57.05000 (C19)	LYT	rep2
588.3351	1761.9818	1761.9805	0.75	3	3.95	1.9	SNYNFEKPFLYLAR	LYK	rep1
588.4591	1762.3538	1761.9805	211.91	3	3.6	1.81	SNYNFEKPFLYLAR	LYT	rep1

Matching Genes:

NP_197501.1 (RAN-1 (Ras-related GTP-binding nuclear protein 1); GTP binding [Arabidopsis thaliana])

Protein Group 130

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	22.46	26.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
711.4905	1420.9654	1421.6674	493.82	2	2.84	1.25	CHFVAIDIFTAK : +57.05000 (C1)	LYT	rep2
711.7522	1421.4888	1421.6674	125.63	2	2.23	0.98	CHFVAIDIFTAK : +57.05000 (C1)	LYK	rep1
739.6539	2215.9383	2216.4419	227.21	3	5.38	3.19	KLEDIVPSSHNCDVPHVNR : +57.05000 (C12)	LYK	rep3

739.8055	2216.3931	2216.4419	22	3	4.53	2.68	KLEDIVPSSHNCDVPHVNR : +57.05000 (C12)	LYT	rep3
696.9406	2087.7982	2088.269	225.46	3	2.97	1.07	LEDIVPSSHNCDVPHVNR : +57.05000 (C11)	LYT	rep1
696.8711	2087.5898	2088.269	325.25	3	2.92	1.06	LEDIVPSSHNCDVPHVNR : +57.05000 (C11)	LYK	rep2

Matching Genes:

NP_001077597.1 (eukaryotic translation initiation factor 5A, putative / eIF-5A, putative [Arabidopsis thaliana])

Protein Group 131

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	23.87	15.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
526.3402	1575.9972	1574.8318	740.01	3	2.11	0.23	LLACISSRPGQCGR : +57.05000 (C4); +57.05000 (C12)	LYT	rep1
788.3274	1574.6392	1574.8318	122.28	2	1.84	0.34	LLACISSRPGQCGR : +57.05000 (C4); +57.05000 (C12)	LYK	rep2
804.6426	1607.2696	1607.7733	313.31	2	2.51	1.18	QWYLSHYGVELGR	LYT	rep3
537.4897	1609.4458	1607.7733	1040.23	3	2.47	0.74	QWYLSHYGVELGR	LYK	rep2
946.0133	2835.0164	2835.188	60.5	3	2.73	1.37	SAIVQVDAAPFKQWYLSHYGVELGR	LYT	rep1
945.7278	2834.1599	2835.188	362.62	3	2.05	0.46	SAIVQVDAAPFKQWYLSHYGVELGR	LYK	rep1
78 1.657	1561.2984	1561.615	202.74	2	3.79	2.24	SLDSHIEDQFASGR	LYT	rep1
781.4084	1560.8011	1561.615	521.2	2	1.92	0.69	SLDSHIEDQFASGR	LYK	rep2

Matching Genes:

NP_197529.1 (40S ribosomal protein S8 (RPS8A) [Arabidopsis thaliana])

Protein Group 132

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	15.23	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
723.0352	1444.0547	1444.4713	288.4	2	2.34	0.7	AGHQTSAESWGTGR	LYT	rep1
1239.9358	2477.856	2478.7842	374.45	2	3.64	1.89	GHKIENVPEMPLVVSDSAEAVEK	LYK	rep1
826.9038	2477.6879	2478.7842	442.24	3	1.85	0.62	GHKIENVPEMPLVVSDSAEAVEK	LYT	rep1
652.0564	1302.0972	1302.5242	327.79	2	3.16	1.65	KGPLVVFGTEGAK	LYT	rep1
652.2022	1302.3887	1302.5242	103.99	2	1.82	0.64	KGPLVVFGTEGAK	LYK	rep2
712.6692	1423.3228	1422.6138	498.37	2	2	1.06	NLPGVELCHVER : +57.05000 (C8)	LYK	rep1
711.9207	1421.8257	1422.6138	553.97	2	1.76	0.6	NLPGVELCHVER : +57.05000 (C8)	LYT	rep3

Matching Genes:

NP_195907.1 (60S ribosomal protein L4/L1 (RPL4D) [Arabidop sis thaliana])

Protein Group 133

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	19.62	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
719.9763	1437.937	1437.6668	187.95	2	2.71	1.26	CHFVAIDIFTSK : +57.05000 (C1)	LYT	rep3
719.5635	1437.1114	1437.6668	386.37	2	2.71	1.16	CHFVAIDIFTSK : +57.05000 (C1)	LYK	rep1
739.6539	2215.9383	2216.4419	227.21	3	5.38	3.19	KLEDIVPSSHNCDVPHVNR : +57.05000 (C12)	LYK	rep3
739.8055	2216.3931	2216.4419	22	3	4.53	2.68	KLEDIVPSSHNCDVPHVNR : +57.05000 (C12)	LYT	rep3
696.9406	2087.7982	2088.269	225.46	3	2.97	1.07	LEDIVPSSHNCDVPHVNR : +57.05000 (C11)	LYT	rep1

696.8711	2087.5898	2088.269	325.25	3	2.92	1.06	LEDIVPSSHNCDVPHVNR : +57.05000 (C11)	LYK	rep2

Matching Genes:

NP_172848.1 (EIF-5A (eukaryotic translation initiation factor 5A-1); translation initiation factor [Arabidopsis thaliana])

Protein Group 134

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.78	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
786.5817	2356.7215	2354.862	789.63	3	5.35	2.65	LLEMGYKNPILLLHPLGGFTK	LYK	rep3
785.9683	2354.8813	2354.862	8.18	3	3.11	1.41	LLEMGYKNPILLLHPLGGFTK	LYT	rep1
760.7489	1519.4822	1519.8354	232.41	2	2.56	1.2	NPILLLHPLGGFTK	LYK	rep2
760.9801	1519.9446	1519.8354	71.84	2	1.41	0.48	NPILLLHPLGGFTK	LYT	rep3
559.5433	1675.6065	1675.8743	159.75	3	3.04	1.42	NPVHNGHALLMTDTR	LYT	rep1
559.33	1674.9664	1675.8743	541.73	3	1.9	0.64	NPVHNGHALLMTDTR	LYK	rep2

Matching Genes:

NP_188929.1 (APS1 (ATP sulfurylase 3) [Arabidopsis thaliana])

Protein Group 135

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	15.31	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
723.0352	1444.0547	1444.4713	288.4	2	2.34	0.7	AGHQTSAESWGTGR	LYT	rep1
1239.9358	2477.856	2478.7842	374.45	2	3.64	1.89	GHKIENVPEMPLVVSDSAEAVEK	LYK	rep1
826.9038	2477.6879	2478.7842	442.24	3	1.85	0.62	GHKIENVPEMPLVVSDSAEAVEK	LYT	rep1
668.0772	1334.1387	1334.5229	287.92	2	2.9	1.51	KGPLVVYGTEGSK	LYT	rep2
712.6692	1423.3228	1422.6138	498.37	2	2	1.06	NLPGVELCHVER : +57.05000 (C8)	LYK	rep1
711.9207	1421.8257	1422.6138	553.97	2	1.76	0.6	NLPGVELCHVER : +57.05000 (C8)	LYT	rep3

Matching Genes:

NP_001030663.1 (structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 136

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	19.39	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
690.4606	2068.3582	2066.2202	1034.76	3	4.28	1.81	HTPGTFTNQMQTSFSEPR	LYK	rep2
689.5636	2065.6673	2066.2202	267.58	3	2.81	1.3	HTPGTFTNQMQTSFSEPR	LYT	rep2
705.9536	1409.8916	1409.5947	210.64	2	2.42	1.1	RNDGIYIFNLGK	LYK	rep1
1000.0645	2997.1699	2997.3746	68.29	3	4.14	2.17	TDHQPIKEGALGNIPIIAFCDTDSPMR : +57.05000 (C20)	LYT	rep1
999.9286	2996.7623	2997.3746	204.28	3	3.65	1.46	TDHQPIKEGALGNIPIIAFCDTDSPMR : +57.05000 (C20)	LYK	rep1

Matching Genes:

NP_001031267.1 (P40 (40S ribosomal protein SA); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 137

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	27.31	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
630.9508	1889.8289	1889.2084	328.49	3	2.63	0.58	ATPLIVHLVDTSSLPLGR	LYK	rep3
824.5843	1647.1529	1647.8373	415.33	2	2.51	0.88	AVSVEENPHAIPTRK	LYT	rep1
824.6433	1647.271	1647.8373	343.62	2	2.16	0.73	AVSVEENPHAIPTRK	LYK	rep2
1094.1229	3279.3453	3278.8066	164.29	3	5.42	3.27	SMYELLKPDGELITLMYPITDHVGGPPYK	LYK	rep1
1093.7479	3278.2203	3278.8066	178.82	3	4.32	2.43	SMYELLKPDGELITLMYPITDHVGGPPYK	LYT	rep3

Matching Genes:

NP_181919.1 (thiol methyltransferase, putative [Arabidopsis thaliana])

Protein Group 138

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	12.06	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1312.7782	3935.3111	3936.3664	268.09	3	5.72	3.76	FGLKEDTIDFIGHAVALHCNDNHLHQPAYDTVMR : +57.05000 (C19)	LYK	rep1
1312.7313	3935.1705	3936.3664	303.82	3	5.29	3.4	FGLKEDTIDFIGHAVALHCNDNHLHQPAYDTVMR : +57.05000 (C19)	LYT	rep3
732.1591	2193.4537	2193.4889	16.07	3	4.78	2.62	KSDMYVFCCSYSHNVAPK : +57.05000 (C8); +57.05000 (C9)	LYK	rep2
732.0355	2193.0831	2193.4889	185.03	3	3.38	1.35	KSDMYVFCCSYSHNVAPK : +57.05000 (C8); +57.05000 (C9)	LYT	rep3

&nb sp; **Matching Genes:**

NP_001078054.1 (ATGDI1 (Arabidopsis thaliana guanosine diphosphate dissociation inhibitor 1))

Protein Group 139

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	9.78	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1609.525	4825.5516	4825.2642	59.56	3	3.95	2.3	HGIVVSCSAGNSGPNPETATNIAPWILTVGASTVDREFAANAITGDGK : +57.0 5000 (C7)	LYK	rep1
441.1014	1320.2807	1320.5012	167.02	3	3.21	1.32	KAHPDWSPAAIK	LYT	rep3
440.9629	1319.8652	1320.5012	481.65	3	1.98	0.46	KAHPDWSPAAIK	LYK	rep2
834.5279	1667.0401	1666.7561	170.38	2	3.28	1.59	SSNSFIHGAGHVDPNK	LYT	rep3
833.9851	1665.9546	1666.7561	480.85	2	2.73	1.18	SSNSFIHGAGHVDPNK	LYK	rep2

Matching Genes:

NP_566473.2 (subtilase family protein [Arabidopsis thaliana])

Protein Group 140

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	18.77	21.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
837.8735	2510.5971	2509.8284	306.31	3	6.52	4.77	HGLSQTDMIALSGAHTIGFAHCGK : +57.05000 (C22)	LYK	rep1
837.3846	2509.1305	2509.8284	278.07	3	6.19	4.01	HGLSQTDMIALSGAHTIGFAHCGK : +57.05000 (C22)	LYT	rep2
414.6971	1241.0678	1240.4365	508.9	3	1.49	0.32	LFFHDCFVR : +57.05000 (C6)	LYT	rep2
414.5786	1240.7124	1240.4365	222.38	3	1.43	0.31	LFFHDCFVR : +57.05000 (C6)	LYK	rep2
1084.162	3249.4625	3248.7837	208.94	3	2.31	0.41	MEKNTSQTIFSNFFLLLLLSSCVSAQLR : +57.05000 (C22)	LYT	rep2

Matching Genes:

NP_194746.1 (peroxidase, putative [Arabidopsis thaliana])

Protein Group 141

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	22.31	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
807.41	2419.2066	2419.4953	119.33	3	3.82	2.01	HSHHHHSSSTPSSAATPTPTAGAR	LYK	rep2

807.3099	2418.9063	2419.4953	243.45	3	3.66	2.03	HSHHHHSSSTPSSAATPTPTAGAR	LYT	rep1
422.1154	1263.3228	1263.4747	120.26	3	1.67	0.34	IHIVKDHDMR	LYK	rep1
422.3662	1264.0752	1263.4747	475.23	3	1.18	0.07	IHIVKDHDMR	LYT	rep2
1171.8738	2341.732	2342.7259	424.26	2	4.82	2.99	LGSVSDYCVHHCVCPVVVVR : +57.05000 (C8); +57.05000 (C12); +57.05000 (C14)	LYK	rep3
782.1909	2343.5493	2342.7259	351.47	3	2.92	1.32	LGSVSDYCVHHCVCPVVVVR : +57.05000 (C8); +57.05000 (C12); +57.05000 (C14)	LYT	rep3

Matching Genes:

NP_568808.1 (universal stress protein (USP) family protein [Arabidopsis thaliana])

Protein Group 142

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	26.97	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
538.9132	1075.8108	1076.3174	470.63	2	2.19	0.39	ITMIWEKR	LYT	rep2
538.8972	1075.7788	1076.3174	500.34	2	1.81	0.02	ITMIWEKR	LYK	rep1
1145.1268	3432.357	3433.6306	370.92	3	2.13	0.83	NENHLFPDAVGHHIQGVSVHDGEWDTHGSIK	LYK	rep2
1259.2948	3774.8609	3776.0278	309.03	3	5.97	3.45	WRNENHLFPDAVGHHIQGVSVHDGEWDTHGSIK	LYK	rep3
1259.2089	3774.6031	3776.0278	377.3	3	4.43	2.82	WRNENHLFPDAVGHHIQGVSVHDGEWDTHGSIK	LYT	rep2

Matching Genes:

NP_189277.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 143

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	18.73	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
656.3063	1310.597	1309.4768	855.43	2	2.69	0.86	DIVALSGAHTLGR	LYT	rep1
657.1174	1968.3288	1969.2323	458.79	3	2.83	0.68	MGLDDKDIVALSGAHTLGR	LYK	rep1
657.473	1969.3956	1969.2323	82.93	3	2.56	1.14	MGLDDKDIVALSGAHTLGR	LYT	rep1
976.8142	2927.4192	2928.1194	239.16	3	3.23	1.55	VDASGPEDCPEEGRLPDAGPPSPATHLR : +57.05000 (C9)	LYT	rep1
677.9064	2030.6956	2031.1924	244.55	3	1.5	0.27	YAADQDAFFKDYAVAHAK	LYT	rep1

Matching Genes:

NP_001078356.1 (SAPX [Arabidopsis thaliana])

Protein Group 144

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.83	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
706.0161	1410.0166	1410.7324	507.38	2	3.45	1.56	IGIMPGYIHKPGK	LYK	rep3
706.1754	1410.3352	1410.7324	281.53	2	2.35	0.98	IGIMPGYIHKPGK	LYT	rep1
652.382	1954.1224	1954.1958	37.56	3	4.29	2.07	KGGTEHLGLPVFNSVAEAK	LYK	rep3
652.2623	1953.7635	1954.1958	221.2	3	3.04	1.18	KGGTEHLGLPVFNSVAEAK	LYT	rep2
877.2835	1752.5513	1753.1004	313.2	2	2.44	1.16	LIGPNCPGIIKPGECK : +57.05000 (C6); +57.05000 (C15)	LYK	rep3

Matching Genes:

NP_196447.1 (succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative [A rabidopsis thaliana])

Protein Group 145

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	16.98	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
720.2106	1438.4056	1438.6996	204.36	2	1.52	0.3	FGFEVNTLRPMK	LYT	rep3
455.9143	909.8129	910.0563	267.48	2	1.65	0.33	GRYDIMR	LYT	rep1
1033.8436	3098.5074	3098.4556	16.73	3	3.97	1.54	LPCLPGELPSYNDWENHLTTIFPEVR : +57.05000 (C3)	LYT	rep3
1033.9603	3098.8575	3098.4556	129.72	3	1.35	0.24	LPCLPGELPSYNDWENHLTTIFPEVR : +57.05000 (C3)	LYK	rep1
1323.9989	3968.9732	3969.3648	98.64	3	3.03	1.45	QSISLEPGGQFELSGAPLETLHQTCAEVNSHLYQVK : +57.05000 (C25)	LYT	rep1

Matching Genes:

NP_001031701.1 (RML1 (PHYTOALEXIN DEFICIENT 2, ROOT MERISTEMLESS 1) [Arabidopsis thaliana])

Protein Group 146

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	12.08	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
441.2336	1320.6773	1320.4581	165.97	3	2.19	0.59	FIDTASIFGHGR	LYK	rep1
661.0767	1320.1377	1320.4581	242.63	2	1.51	0.14	FIDTASIFGHGR	LYT	rep3
492.6749	983.3341	983.1286	209.02	2	2.15	0.6	HGSLGFLPR	LYK	rep2
492.5608	983.1059	983.1286	23.17	2	1.79	0.31	HGSLGFLPR	LYT	rep3
456.2028	1365.5848	1365.6103	18.68	3	3.44	1.76	KVACIGAWHPAR : +57.05000 (C4)	LYK	rep1
456.1543	1365.4394	1365.6103	125.14	3	3.06	1.45	KVACIGAWHPAR : +57.05000 (C4)	LYT	rep1
791.0612	1580.1067	1580.6818	363.78	2	2.36	1.12	VGTEAHTAMTEYDR	LYT	rep1

Matching Genes:

NP_001031146.1 (ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosom e [Arabidopsis thaliana])

Protein Group 147

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	5	10.47	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
455.2307	1362.6685	1362.4982	125.01	3	1.56	0.38	GNVHAVQFHPEK	LYT	rep3
403.4922	1207.4533	1207.3447	89.91	3	2.98	1.01	HVYFVHSYR	LYK	rep3
403.6151	1207.8217	1207.3447	395.05	3	2.55	0.4	HVYFVHSYR	LYT	rep2

519.0272	1554.0582	1553.7425	203.15	3	1.84	0.35	MEATAAPFSSIVSSR	LYT	rep1
759.8893	1517.763	1518.6846	606.83	2	1.63	0.35	RGNVHAVQFHPEK	LYK	rep1
918.7535	2753.2371	2754.0105	280.81	3	2.07	0.6	VIRVTNPGPNGEEYAWYQCTVSGGR	LYK	rep1
918.54 53	2752.6124	2754.0105	507.66	3	1.7	0.21	VIRVTNPGPNGEEYAWYQCTVSGGR	LYT	rep3

Matching Genes:

NP_194420.1 (AT-HF (Arabidopsis thaliana HisF protein))

Protein Group 148

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	16.11	23.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
785.8658	2354.5741	2355.6594	460.75	3	3.7	1.93	DLVLLSGAHTIGVSHCSSMNTR : +57.05000 (C16)	LYT	rep1
807.0321	2418.0728	2416.7471	548.58	3	3.6	0.97	IISDHIQNHIHNGPSLAAPLIR	LYK	rep3
806.5416	2416.6014	2416.7471	60.27	3	3.59	1.77	IISDHIQNHIHNGPSLAAPLIR	LYT	rep3
417.3369	1248.9873	1248.4405	437.92	3	2.77	1.15	MHFHDCFVR : +57.05000 (C6)	LYT	rep3
626.0274	1250.0391	1248.44 05	1280.44	2	2.36	0.83	MHFHDCFVR : +57.05000 (C6)	LYK	rep3

Matching Genes:

NP_188814.1 (peroxidase 30 (PER30) (P30) (PRXR9) [Arabidopsis thaliana])

Protein Group 149

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	17.39	22.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
682.9755	1363.9353	1364.5524	452.18	2	2.67	1.33	AKVHAPEVAVDTK	LYT	rep1
565.357	1128.6983	1129.3771	601.02	2	2.07	0.26	DLIVQCLLR : +57.05000 (C6)	LYK	rep3
621.8944	1862.6598	1863.0268	197.01	3	3.81	2.11	SNDPHGLHCSGGVVLASR : +57.05000 (C9)	LYT	rep1
621.951	1862.8297	1863.0268	105.8	3	3.17	1.36	SNDPHGLHCSGGVVLASR : +57.05000 (C9)	LYK	rep2
583.555	1165.0943	1165.3 011	177.52	2	1.48	0.32	VHAPEVAVDTK	LYT	rep1
583.4989	1164.9822	1165.3011	273.68	2	1.31	0.27	VHAPEVAVDTK	LYK	rep2

Matching Genes:

NP_192853.1 (TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1) [Arabidopsis thaliana])

Protein Group 150

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	22.65	19.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
998.3765	2992.1059	2991.4541	217.9	3	5.12	2.09	IHSENTGNTAILNLLPLLQGNVGLIFTK	LYK	rep3
998.0385	2991.0919	2991.4541	121.08	3	4.22	2.29	IHSENTGNTAILNLLPLLQGNVGLIFTK	LYT	rep2
1372.4247	4114.2506	4114.5815	80.44	3	4.9	2.78	LGIRPFSYGLVVQSVYDNGSVFSPEVLDLTEDQLVEK	LYT	rep3
1372.837	4115.4876	4114.5815	220.22	3	4.79	2.33	LGIRPFSYGLVVQSVYDNGSVFSPEVLDLTEDQLVEK	LYK	rep2

Matching Genes:

NP_001078125.1 (60S acidic ribosomal protein P0 (RPP0B) [Arabidopsis thaliana])

Protein Group 151

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.51	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
503.9957	1508.9637	1508.8102	101.77	3	3.45	1.99	CYFSLACLLHPK : +57.05000 (C1); +57.05000 (C7)	LYK	rep1
755.709	1509.4024	1508.8102	392.51	2	2.91	1.67	CYFSLACLLHPK : +57.05000 (C1); +57.05000 (C7)	LYT	rep3
629.5574	1257.0992	1257.4435	273.82	2	2.59	1.06	GKHTYVPVTQK	LYK	rep3
612.4531	1834.3359	1834.1329	110.67	3	3.93	2.22	QGLIKEPVFSFWLNR	LYK	rep1

Matching Genes:

NP_172655.1 (aspartyl protease family protein [Arabidopsis thaliana])

Protein Group 152

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.54	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
686.0316	2055.0714	2055.2651	94.27	3	3.98	1.57	HPNRPTFLDHIHNITDK	LYK	rep2
686.2155	2055.6229	2055.2651	174.07	3	3.24	1.34	HPNRPTFLDHIHNITDK	LYT	rep2

592.9625	1775.8641	1775.9673	58.1	3	3.28	1.54	KFEHPWPANPDPNVK	LYT	rep1
992.2478	2973.7199	2974.3811	222.28	3	2.69	1.01	MMYYADHHGFPIVTFIDTPGAYADLK	LYK	rep3

Matching Genes:

NP_565880.1 (CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit); acetyl-CoA carboxylase [Arabidopsis thaliana])

Protein Group 153

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	18.46	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
690.9884	2069.9417	2070.3618	202.9	3	3.66	1.64	FNKVFNNGMSNHSTITMK	LYT	rep1
1137.91	3410.7066	3411.8113	323.77	3	4.57	2.32	GINFDLPHVIEDAPSHPGIEHVGGDMFVSVPK	LYK	rep3
1138.1439	3411.4083	3411.8113	118.11	3	4.22	2.37	GINFDLPHVIEDAPSHPGIEHVGGDMFVSVPK	LYT	rep2
626.202	1875.5826	1875.1872	210.83	3	1.67	0.66	QVVHVDCIMLAHNPGGK : +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_200227.1 (ATOMT1 (O-METHYLTRANSFERASE 1) [Arabidopsis thaliana])

Protein Group 154

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	36.31	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

594.8757	1781.6037	1781.9686	204.77	3	2.29	1.06	EGSTNPTFLYFAHGLK	LYK	rep2
594.9049	1781.6912	1781.9686	155.65	3	1.58	0.34	EGSTNPTFLYFAHGLK	LYT	rep3
647.6184	1293.2212	1293.4277	159.65	2	2.03	0.59	LSEEDQAVFKK	LYT	rep3
1315.8153	3944.4224	3945.4199	252.82	3	5.52	3.66	MLVYQDLLTGDELLSDSFPYKEIENGILWEVEGK	LYT	rep2
1316.0243	3945.0494	3945.4199	93.91	3	4.33	2.42	MLVYQDLLTGDELLSDSFPYKEIENGILWEVEGK	LYK	rep1

Matching Genes:

NP_188286.1 (TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) [Arabidopsis thaliana])

Protein Group 155

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.52	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
740.6383	1479.261	1479.6035	231.47	2	2.69	1.27	DVAGGKVNQAHLDR	LYT	rep1
1341.3558	4021.044	4022.4261	343.6	3	5.05	3.13	IASETTPNPAASIGLYVDCGSIYEAPYFHGATHLLER : +57.05000 (C19)	LYK	rep2
1341.5316	4021.5714	4022.4261	212.5	3	4.39	2.51	IASETTPNPAASIGLYVDCGSIYEAPYFHGATHLLER : +57.05000 (C19)	LYT	rep1
692.5973	2074.7684	2076.4077	789.49	3	2.03	0.42	SAVLMNLESRMIAAEDIGR	LYK	rep3

Matching G enes:

NP_001077701.1 (mitochondrial processing peptidase alpha subunit, putative [Arabidopsis thaliana])

Protein Group 156

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	31.17	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
878.9191	2633.7337	2634.8916	439.44	3	4.64	2.82	FKGPCVSTHNCANVCHNEGFGGGK : +57.05000 (C5); +57.05000 (C11); +57.05000 (C15)	LYK	rep3
878.8857	2633.6337	2634.8916	477.38	3	3.64	1.92	FKGPCVSTHNCANVCHNEGFGGGK : +57.05000 (C5); +57.05000 (C11); +57.05000 (C15)	LYT	rep1
787.3121	2358.9129	2359.544	267.45	3	5.09	3.1	GPCVSTHNCANVCHNEGFGGGK : +57.05000 (C3); +57.05000 (C9); +57.05000 (C13)	LYT	rep3
787.1401	2358.3969	2359.544	486.13	3	4.01	1.99	GPCVSTHNCANVCHNEGFGGGK : +57.05000 (C3); +57.05000 (C9); +57.05000 (C13)	LYK	rep2

Matching Genes:

NP_178321.1 (LCR68/PDF2.3 (Low-molecular-weight cysteine-rich 68); protease inhibitor [Arabidopsis thaliana])

Protein Group 157

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	22.89	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
743.9935	2228.9571	2228.574	171.93	3	2.73	1.16	EYQIIDHLVGPTLKDEVMK	LYT	rep2
634.3297	1899.9657	1900.193	119.63	3	1.72	0.5	FKAFVVVGDGNGHVGLGVK	LYT	rep1
892.0562	1782.0967	1782.998	505.51	2	2.76	1.36	KVLQFAGIDDVFTSSR	LYT	rep1

695.0447	1388.0738	1388.5708	357.94	2	2.5	1.15	TYGFLTPEFWK	LYT	rep1

Matching Genes:

NP_176134.1 (XW6; structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 158

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	10.65	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
769.7198	1537.4239	1537.6799	166.52	2	1.57	0.43	EAFPGDVFYLHSR	LYK	rep3
480.4534	1438.3366	1438.6808	239.21	3	3.03	1.17	GIRPAINVGLSVSR	LYT	rep2
480.6814	1439.0207	1438.6808	236.29	3	2.7	0. 88	GIRPAINVGLSVSR	LYK	rep2
615.125	1842.3515	1842.0272	176.06	3	2.18	0.51	IRNFYANFQVDEIGR	LYT	rep1
615.3879	1843.1403	1842.0272	604.3	3	1.93	0.66	IRNFYANFQVDEIGR	LYK	rep1
678.0459	1354.0762	1354.5809	372.6	2	2.91	0.97	KSVHEPMQTGLK	LYK	rep3
678.1092	1354.2027	1354.5809	279.24	2	2.57	0.72	KSVHEPMQTGLK	LYT	rep1

Matching Genes:

NP_085571.2 (ATPase subunit 1 [Arabidopsis thaliana])

Protein Group 159

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	22.69	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1090.4681	3268.3809	3269.72	409.53	3	4.69	2.14	ERPFFNGLCDFLSSGPVIAMVWEGDGVIR : +57.05000 (C9)	LYK	rep3
1090.5765	3268.7061	3269.72	310.07	3	3.53	1.34	ERPFFNGLCDFLSSGPVIAMVWEGDGVIR : +57.05000 (C9)	LYT	rep1
669.7987	1337.5818	1338.4286	632.65	2	2.55	1.07	NIIHGSDGPETAK	LYK	rep3
669.9038	1337.792	1338.4286	475.59	2	1.34	0.09	NIIHGSDGPETAK	LYT	rep1
673.1265	1344.2373	1344.5 642	243.09	2	2.45	0.98	TFIAIKPDGVQR	LYT	rep1
673.107	1344.1983	1344.5642	272.15	2	2.19	0.7	TFIAIKPDGVQR	LYK	rep2

& nbsp; **Matching Genes:**

NP_192839.1 (NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3); ATP binding / nucleoside diphosphate kinase [Arabidopsis thaliana])

Protein Group 160

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.24	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
694.8043	2081.3895	2082.4336	501.38	3	1.12	0.36	AALQAGIDKLADCVGLTLGPR	LYT	rep1
694.9755	2081.9029	2082.4336	254.83	3	1	0.23	AALQAGIDKLADCVGLTLGPR	LYK	rep2
1127.0633	2252.1109	2250.6406	653.26	2	3.89	2.45	APLLIIAEDVTGEALATLVVNK	LYK	rep3
868.8744	1735.7332	1735.9892	147.5	2	4.59	2.99	HGLLSVTSGANPVSLKR	LYK	rep1
868.5734	1735.1311	1735.9892	494.3	2	4.55	2.87	HGLLSVTSGANPVSLKR	LYT	rep3

Matching Genes:

NP_180367.1 (CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded protein binding [Arabidopsis thaliana])

Protein Group 161

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.88	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
674.4392	1346.8628	1347.608	552.97	2	3.14	0.93	KLFGVTTLDVVR	LYT	rep1
951.8999	1901.7842	1901.2394	286.57	2	3.16	1.67	MSPLVSTLHLYDIANVK	LYT	rep1
1254.0865	3759.2362	3760.3344	292.06	3	3.27	1.01	TLVEAVAENCPNAFIHIISNPVNSTVPIAAEVLKK : +57.05000 (C10)	LYT	rep1
1254.5956	3760.7633	3760.3344	114.04	3	3.21	1.24	TLVEAVAENCPNAFIHIISNPVNSTVPIAAEVLKK : +57.05000 (C10)	LYK	rep2

Matching Genes:

NP_190336.1 (MDH (malate dehydrogenase); malate dehydrogenase [Arabidopsis thaliana])

Protein Group 162

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	18.51	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1187.2308	3558.669	3559.799	317.43	3	2.9	0.84	HHGVVTEECDPYFDNTGCSHPGCEPAYPTPK : +57.05000 (C9); +57.05000 (C18); +57.05000 (C23)	LYK	rep2

435.7463	1304.2154	1304.4602	187.69	3	2.69	1.05	HITGTNIGGHAVK	LYT	rep1
435.9339	1304.7782	1304.4602	243.8	3	2.66	0.73	HITGTNIGGHAVK	LYK	rep3
708.9362	2123.785	2124.3029	243.79	3	2.47	0.93	RGTNECGIEHGVVAGLPSDR : +57.05000 (C6)	LYK	rep3
1333.5294	3997.5648	3998.3207	189.07	3	1.5	0.44	YFKHHGVVTEECDPYFDNTGCSHPGCEPAYPTPK : +57.05000 (C12); +57.05000 (C21); +57.05000 (C26)	LYT	rep1

Matching Genes:

NP_563648.1 (cathepsin B-like cysteine protease, putative [Arabidopsis thaliana])

Protein Group 163

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	13.49	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
961.9763	1921.937	1922.2353	155.18	2	1.28	0.35	GFKDQIYDIFQLLPPK	LYK	rep2
914.607	1827.1983	1828.0405	460.73	2	2.92	1.49	GIYAYGFEKPSAIQQR	LYT	rep1
914.593	1827.1704	1828.0405	475.96	2	2.52	1.16	GIYAYGFEKPSAIQQR	LYK	rep2
701.4593	1400.9029	1401.5278	445.91	2	2.97	1.68	GLDVIQQAQSGTGK	LYT	rep1
553.196	1104.3763	1104.3074	62.39	2	2.39	1.18	KGVAINFVTR	LYT	rep1

Matching Genes:

NP_001030693.1 (EIF4A1 (eukaryotic translation initiation factor 4A-1); ATP-dependent helicase [Arabidopsis thaliana])

Protein Group 164

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.88	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
764.8339	2291.4781	2291.552	32.24	3	3.86	1.34	IMALDLPHGGHLSHGYQTDTK	LYK	rep3
764.5375	2290.5889	2291.552	420.26	3	2.89	1.27	IMALDLPHGGHLSHGYQTDTK	LYT	rep2
885.4236	2653.2473	2654.0432	299.89	3	2.3	0.45	INQAVFPGLQGGPHNHTITGLAVALK	LYK	rep3
1000.759	2999.2536	2999.3516	32.65	3	3.39	1.96	WGVNVQSLSGSPANFQVYTALLKPHER	LYK	rep2
1000.3622	2998.0631	2999.3516	429.59	3	3.29	0.75	WGVNVQSLSGSPANFQVYTALLKPHER	LYT	rep3

Matching Genes:

NP_568488.2 (SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2); glycine hydroxymethyltransferase [Arabidopsis thaliana])

Protein Group 165

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	26.97	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
538.9132	1075.8108	1076.3174	470.63	2	2.19	0.39	ITMIWEKR	LYT	rep2
538.8972	1075.7788	1076.3174	500.34	2	1.81	0.02	ITMIWEKR	LYK	rep1
1277.0897	3828.2457	3828.0947	39.44	3	7.29	4.55	YRNENYLFPDTIGHHIQSVTVHDGEWDTQGGIK	LYK	rep3
1276.5924	3826.7537	3828.0947	350.3	3	5.43	2.93	YRNENYLFPDTIGHHIQSVTVHDGEWDTQGGIK	LYT	rep3

Matching Genes:

NP_189276.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 166

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	20	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
732.6791	2195.0138	2195.2778	120.29	3	2.99	1.07	HSHHHSSSTPSAATPTPTAGAR	LYT	rep2
732.7008	2195.0789	2195.2778	90.59	3	2.7	0.84	HSHHHSSSTPSAATPTPTAGAR	LYK	rep2
422.1154	1263.3228	1263.4747	120.26	3	1.67	0.34	IHIVKDHDMR	LYK	rep1
422.3662	1264.0752	1263.4747	475.23	3	1.18	0.07	IHIVKDHDMR	LYT	rep2
1171.873	2341.732	2342.7259	424.26	2	4.82	2.99	LGSVSDYCVHHCVCPVVVVR : +57.05000 (C8); +57.05000 (C12); +57.05000 (C14)	LYK	rep3
782.1909	2343.5493	2342.7259	351.47	3	2.92	1.32	LGSVSDYCVHHCVCPVVVVR : +57.05000 (C8); +57.05000 (C12); +57.05000 (C14)	LYT	rep3

Matching Genes:

NP_567770.1 (universal stress protein (USP) family protein [Arabidopsis thaliana])

Protein Group 167

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.99	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
617.9381	1850.7909	1850.264	284.73	3	4.43	2.49	LKTNPPPHMMPPPPPAK	LYK	rep3
617.3242	1848.9492	1850.264	710.63	3	1.58	0.06	LKTNPPPHMMPPPPPAK	LYT	rep1
418.5895	1252.745	1252.4252	255.34	3	2.73	0.61	RLNTIHLEEK	LYT	rep1
627.1021	1252.1885	1252.4252	188.95	2	1.89	0.25	RLNTIHLEEK	LYK	rep1
805.6038	1609.1919	1608.9328	161.03	2	2.17	0.6	TNPPPHMMPPPPPAK	LYK	rep3

Matching Genes:

NP_565484.1 (unknown protein [Arabidopsis thaliana])

Protein Group 168

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	18.42	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
668.6739	1335.3321	1335.4679	101.7	2	1.71	0.61	AVVVHADPDDLGK	LYK	rep2
668.7542	1335.4927	1335.4679	18.59	2	1.33	0.22	AVVVHADPDDLGK	LYT	rep1
905.375	2713.1015	2713.9243	303.17	3	3.68	2.07	AVVVHADPDDLGKGGHELSLATGNAGGR	LYT	rep1
905.5585	2713.6519	2713.9243	100.36	3	3.03	1.86	AVVVHADPDDLGKGGHELSLATGNAGGR	LYK	rep1
698.9782	1395.9407	1396.4713	379.95	2	3.93	2.34	GGHELSLATGNAGGR	LYT	rep1
699.0398	1396.064	1396.4713	291.66	2	3.46	1.71	GGHELSLATGNAGGR	LYK	rep2

Matching Genes:

NP_001077494.1 (CSD1 (copper/zinc superoxide dismutase 1) [Arabidopsis thaliana])

Protein Group 169

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	17.66	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
883.6141	2647.8189	2648.011	72.54	3	4.25	2.18	LGVFSHGFTYSGHPVSCAVAIEALK : +57.05000 (C17	LYT	rep3
883.5452	2647.612	2648.011	150.68	3	3.38	1.31	LGVFSHGFTYSGHPVSCAVAIEALK : +57.05000 (C17)	LYK	rep3
1478.1603	4431.4574	4432.9458	335.77	3	3.32	1.52	SYHGSTLISASLSGLPPLHQNFDLPAPFVLHTDCPHYWR : +57.05000 (C34)	LYT	rep3
1478.4374	4432.2887	4432.9458	148.24	3	1.33	0.16	SYHGSTLISASLSGLPPLHQNFDLPAPFVLHTDCPHYWR : +57.05000 (C34)	LYK	rep1
963.5469	2887.6171	2887.3231	101.83	3	1.7	0.34	YDILFIADEVICAFGRLGTMFGCDK : +57.05000 (C12); +32.00000 (M20)	LYT	rep3

Matching Genes:

NP_566700.1 (POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transami nase [Arabidopsis thaliana])

Protein Group 170

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	16.67	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
823.5658	2467.6739	2467.728	21.92	3	4.26	2.4	HGLGVEEIVNHVMHSWEHATGK	LYK	rep3
918.6566	2752.9464	2753.9473	363.44	3	5.01	3.12	VYHSHDGLAPHSHEPIYSPGYFSR	LYK	rep3
918.7648	2753.2708	2753.9473	245.62	3	3.94	2.23	VYHSHDGLAPHSHEPIYSPGYFSR	LYT	rep3

Matching Genes:

NP_001031481.1 (UREG (urease accessory protein G); metal ion binding / nucleotide binding [Arabidopsis thaliana])

Protein Group 171

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	29.73	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
372.0898	1113.2461	1113.2743	25.35	3	2.21	0.79	AGVAHKIDFR	LYT	rep1
1223.9065	2445.7974	2446.8105	414.06	2	2.9	1.02	HPWNIMTTSADEGQFLNMLIK	LYK	rep3
1223.8499	2445.6841	2446.8105	460.36	2	1.73	0.33	HPWNIMTTSADEGQFLNMLIK	LYT	rep2
910.6576	2728.9493	2728.0991	311.64	3	2.47	0.9	IGGVIGYDNTLWNGSVVAPPDAPMRK	LYT	rep2
910.5591	2728.6538	2728.0991	203.31	3	2.3	0.85	IGGVIGYDNTLWNGSVVAPPDAPMRK	LYK	rep3
777.9459	2330.8143	2330.7095	44.98	3	1.66	0.41	ILAMDVNRENYELGLPIIEK	LYT	rep2

Matching Genes:

NP_195131.1 (caffeoyl-CoA 3-O-methyltransferase, putative [Arabidopsis thaliana])

Protein Group 172

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.66	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass	Char	Score	Score	Peptide	Grou	Replicat

			Error (ppm)	ge		Delta		p	e
1224.0287	3669.0626	3668.993	18.96	3	4.44	2.35	GHGFEILAFPCNQFGNQEPGTNEEIVQFACTR : +57.05000 (C11); +57.05000 (C30)	LYK	rep2
1223.7596	3668.2555	3668.993	201.03	3	4.27	2.28	GHGFEILAFPCNQFGNQEPGTNEEIVQFACTR : +57.05000 (C11); +57.05000 (C30)	LYT	rep1
1321.1271	3960.3577	3960.3401	4.47	3	4.75	2.94	YKGHGFEILAFPCNQFGNQEPGTNEEIVQFACTR : +57.05000 (C13); +57.05000 (C32)	LYT	rep1

Matching Genes:

NP_192897.2 (ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase [Arabidopsis thaliana])

Protein Group 173

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	45.71	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
519.006	1553.9945	1553.7858	134.33	3	2.43	0.3	KVEDVMPIATGHEK	LYT	rep1
518.9203	1553.7374	1553.7858	31.13	3	2.18	0.48	KVEDVMPIATGHEK	LYK	rep2
854.777	1707.5384	1706.8568	399.31	2	1.83	0.52	RLDDIDFPEGPFGTK	LYT	rep1
1284.225	3849.6514	3850.9947	348.8	3	3.33	1.5	SFECPVCTQYFELEVVGPGGPPDGHGDEDDEHHH : +57.05000 (C4); +57.05000 (C7)	LYK	rep2
602.9694	1805.8846	1808.0539	1199.82	3	1.6	0.36	SIAATTRPVGFYLAANR	LYK	rep1

Matching Genes:

NP_001078161.1 (cytochrome c oxidase family protein [Arabidopsis thaliana])

Protein Group 174

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	16.23	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1432.8104	4295.4078	4296.6596	291.33	3	4.33	2.67	AFQLYDSGIFDGSCGTQLDHGVVAVGYGTENGKDYWIVR : +57.05000 (C14)	LYK	rep1
1432.6788	4295.013	4296.6596	383.21	3	3.66	1.98	AFQLYDSGIFDGSCGTQLDHGVVAVGYGTENGKDYWIVR : +57.05000 (C14)	LYT	rep3
795.5935	1589.1714	1589.801	396.02	2	3.09	0.32	AVAHQPISIAIEAGGR	LYK	rep3
795.5578	1589.0999	1589.801	441.01	2	2.2	0.33	AVAHQPISIAIEAGGR	LYT	rep3
768.4185	2302.2319	2302.4968	115.06	3	1.75	0.6	VVTIDSYEDVPTYSEESLKK	LYT	rep1

Matching Genes:

NP_564497.1 (cysteine proteinase (RD21A) / thiol protease [Arabidopsis thaliana])

Protein Group 175

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	11.89	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

409.5635	1225.667	1225.4047	214.05	3	2.64	1.24	GHERPLTFLR	LYK	rep3
409.4731	1225.3958	1225.4047	7.24	3	2.23	0.84	GHERPLTFLR	LYT	rep3
552.6825	1655.024	1654.8299	117.27	3	1.87	0.38	GHFGPINALAFNPDGK	LYT	rep3
551.0208	1650.0388	1648.8223	737.82	3	4.62	0.39	LHHFDSDYFNIKI	LYK	rep3

Matching Genes:

NP_182151.1 (TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding [Arabidopsis thaliana])

Protein Group 176

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	11.38	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
711.0934	2130.2567	2130.4353	83.85	3	1.85	0.3	TKVCIVGSGPAAHTAAIYASR : +57.05000 (C4)	LYT	rep1
634.9664	1901.8758	1901.1581	377.53	3	2.46	0.37	VCIVGSGPAAHTAAIYASR : +57.05000 (C2)	LYK	rep3
634.5699	1900.6864	1901.1581	248.11	3	1.97	0.37	VCIVGSGPAAHTAAIYASR : +57.05000 (C2)	LYT	rep3
787.7505	1573.4854	1573.7967	197.84	2	2.8	1.29	VSGLFFAIGHEPATK	LYK	rep2
787.7491	1573.4825	1573.7967	199.7	2	1.77	0.62	VSGLFFAIGHEPATK	LYT	rep1
479.0685	956.1213	956.1496	29.63	2	2	0.37	VYIIHRR	LYK	rep3

Matching Genes:

NP_179334.4 (NTRA (NADPH-dependent thioredoxin reductase 2) [Arabidopsis thaliana])

Protein Group 177

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	18.08	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1096.8954	3287.6627	3287.8395	53.79	3	4.38	2.41	EVEVPVVGGHAGVTILPLLSQVKPPCSFTQK : +57.05000 (C26)	LYK	rep3
1096.5902	3286.7472	3287.8395	332.25	3	1.46	0.25	EVEVPVVGGHAGVTILPLLSQVKPPCSFTQK : +57.05000 (C26)	LYT	rep2
1165.4828	3493.4249	3493.9787	158.52	3	4.71	2.85	MNPLVSVLHLYDVANAPGVTADISHMDTSAVVR	LYT	rep1
1165.0858	3492.234	3493.9787	499.37	3	2.52	0.98	MNPLVSVLHLYDVANAPGVTADISHMDTSAVVR	LYK	rep2

Matching Genes:

NP_179863.1 (PMDH1 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 1); malate dehydrogenase [Arabidopsis thaliana])

Protein Group 178

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	21.34	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1156.9706	3467.8883	3467.9377	14.26	3	6.03	3.7	HKVETEFLPLYTNHGIGLTTWSPLASGVLTGK	LYK	rep3
1156.9496	3467.8253	3467.9377	32.43	3	5.04	3.24	HKVETEFLPLYTNHGIGLTTWSPLASGVLTGK	LYT	rep1
1294.9181	3881.7308	3881.4301	77.48	3	3.01	0.99	VSGLKPIADELGVTLAQLAIAWCASNPNVSSVITGATR : +57.05000 (C23)	LYT	rep3

Matching Genes:

NP_171963.1 (KAB1 (POTASSIUM CHANNEL BETA SUBUNIT); potassium channel [Arabidopsis thaliana])

Protein Group 179

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	15.14	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
712.5929	1423.1702	1423.6279	321.51	2	3.89	2.46	HSVGATHPVHLIR	LYK	rep3
1312.4677	3934.3795	3936.1518	450.28	3	5.09	2.66	SEPYFETPAPPPSFGHVSHVGHQSPNESYPPEHHR	LYK	rep3
1312.8234	3935.4466	3936.1518	179.17	3	4.08	1.96	SEPYFETPAPPPSFGHVSHVGHQSPNESYPPEHHR	LYT	rep3

Matching Genes:

NP_565899.1 (hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana])

Protein Group 180

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	21.82	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
814.3348	2439.981	2440.7459	313.37	3	2.32	1.02	FLSCHGPLANRQPGSAFLPAHY : +57.05000 (C4)	LYT	rep1

975.257	1948.4983	1949.1964	358.14	2	2.08	0.63	GVDEFPFCVHLVSWEK : +57.05000 (C8)	LYT	rep1
637.7879	1273.5601	1273.5373	17.87	2	2.98	1.23	IRVHPFHVLR	LYK	rep3
637.5288	1273.042	1273.5373	388.93	2	2.52	0.95	IRVHPFHVLR	LYT	rep1
335.8229	1004.4453	1004.1927	251.6	3	1.55	0.6	VHPFHVLR	LYT	rep3
503.2246	1004.4336	1004.1927	239.95	2	1.47	0.43	VHPFHVLR	LYK	rep2

Matching Genes:

NP_563945.2 (60S ribosomal protein L10 (RPL10A) / Wilm's tumor suppressor protein-related [Arabidopsis thaliana])

Protein Group 181

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	23.84	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
791.2784	2370.8119	2370.4531	151.34	3	3.83	2.24	AGHDYDGGRDLDDFVSFINEK	LYK	rep1
790.9562	2369.8451	2370.4531	256.52	3	2.49	1.14	AGHDYDGGRDLDDFVSFINEK	LYT	rep2
962.0225	1922.0293	1923.2273	622.88	2	2.85	1.54	GALVEFYAPWCGHCKK : +57.05000 (C11); +57.05000 (C14)	LYT	rep1
1539.282	4614.8411	4615.2216	82.44	3	2.23	0.84	LAAVPQNVVVLTPDNFDEIVLDQNKDVLVEFYAPWCGHCK : +57.05000 (C36); +57.05000 (C39)	LYT	rep3

Matching Genes:

NP_001031555.1 (ATPDIL2-1/MEE30/UNE5 (PDI-LIKE 2-1, maternal effect embryo arrest 30, unfertilized embryo sac 5); thiol-disulfide exchange intermediate [Arabidopsis thaliana])

Protein Group 182

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	11.03	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
764.8339	2291.4781	2291.552	32.24	3	3.86	1.34	IMALDLPHGGHLSHGYQTDTK	LYK	rep3
764.5375	2290.5889	2291.552	420.26	3	2.89	1.27	IMALDLPHGGHLSHGYQTDTK	LYT	rep2
885.4236	2653.2473	2654.0432	299.89	3	2.3	0.45	INQAVFPGLQGGPHNHTITGLAVALK	LYK	rep3
420.311	1257.9094	1257.4003	404.95	3	2.73	0.67	LRHEVEEFAK	LYT	rep3

Matching Genes:

NP_195506.1 (SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase [Arabidopsis thaliana])

Protein Group 183

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	20.97	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
550.9344	1099.8531	1100.2739	382.5	2	2.42	1.03	AKANSLAQLGK	LYT	rep1
551.2044	1100.3931	1100.2739	108.33	2	2.08	0.87	AKANSLAQLGK	LYK	rep1
1548.3395	4641.995	4643.2016	259.88	3	2.86	1.27	RVPPAVPGIMFLSGGQSEAEATLNLNAMNQSPNPWHVSFSYAR	LYT	rep3
1025.7872	3074.3382	3074.4104	23.47	3	3.62	1.29	YAAISQDNGLVPIVEPEILLDGDHPIER	LYT	rep1
1025.5087	3073.5025	3074.4104	295.3	3	2.87	0.97	YAAISQDNGLVPIVEPEILLDGDHPIER	LYK	rep2

Matching Genes:

NP_178224.1 (fructose-bisphosphate aldolase, putative [Arabidopsis thaliana])

Protein Group 184

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	11.97	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
848.8454	1695.6751	1696.774	647.67	2	3.85	2.17	HEEEEENKPSLLDK	LYT	rep1
849.1082	1696.2007	1696.774	337.89	2	3.7	2.07	HEEEEENKPSLLDK	LYK	rep2
709.3568	2125.047	2125.3074	122.52	3	5.05	2.38	HEEEEHKPTLLEQLHQK	LYK	rep3
709.26	2124.7566	2125.3074	259.17	3	4.75	2.15	HEEEEHKPTLLEQLHQK	LYT	rep1

Matching Genes:

NP_564114.2 (ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10) [Arabidopsis thaliana])

Protein Group 185

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	14.76	24.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
837.3992	2509.174	2509.865	275.31	3	1.66	0.32	GFCHLYDGQEALAVGMEAAITKK : +57.05000 (C3)	LYK	rep1
837.5813	2509.7204	2509.865	57.62	3	1.49	0.42	GFCHLYDGQEALAVGMEAAITKK : +57.05000 (C3)	LYT	rep1

461.696	1382.0645	1381.6228	319.69	3	1.46	0.38	KLLLTHDIATEK	LYT	rep1
503.1177	1004.2198	1004.1446	74.81	2	2.13	0.59	RGDYVPGLK	LYK	rep2
502.9271	1003.8385	1004.1446	304.84	2	2.06	0.37	RGDYVPGLK	LYT	rep3
532.4115	1594.211	1594.6702	287.92	3	3.62	1.16	YHGHSMSDPGSTYR	LYK	rep3
797.8582	1593.7007	1594.6702	607.92	2	2.84	1.5	YHGHSMSDPGSTYR	LYT	rep1

Matching Genes:

NP_173828.1 (IAR4 (IAA-conjugate-resistant 4); pyruvate dehydroge nase (acetyl-transferring) [Arabidopsis thaliana])

Protein Group 186

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.61	15.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
776.71	1551.4043	1550.6785	468.1	2	2.7	1.08	GALDGGLDIPHSDKR	LYT	rep1
776.1321	1550.2486	1550.6785	277.22	2	2.66	1.03	GALDGGLDIPHSDKR	LYK	rep2
740.3439	2218.0081	2218.4709	208.61	3	2.55	1.29	LLGEDEPEKLQTHFSAYIK	LYK	rep2
740.4532	2218.3363	2218.4709	60.7	3	1.71	0.44	LLGEDEPEKLQTHFSAYIK	LYT	rep2
773.5076	1544.9995	1545.7239	468.59	2	3.53	1.46	NYIYGGHVSNYMK	LYK	rep2
773.5862	1545.1568	1545.7239	366.88	2	3.3	1.14	NYIYGGHVSNYMK	LYT	rep1

Mat ching Genes:

NP_198790.1 (60S ribosomal protein L5 (RPL5B) [Arabidopsis thaliana])

Protein Group 187

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.98	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
737.5877	1473.1597	1473.6341	321.95	2	3.01	1.27	IHYETTGPEIWK	LYT	rep1
737.7383	1473.461	1473.6341	117.51	2	2.06	0.77	IHYETTGPEIWK	LYK	rep2
692.3284	1382.6411	1382.6109	21.84	2	1.98	0.36	LFVAIFPSFGER	LYT	rep1
1068.2805	2134.5454	2135.4285	413.5	2	3.77	2.12	LYGVEPVESAILSGGKPGPHK	LYK	rep3

Matching Genes:

NP_193224.1 (OASA1 (O-ACETYLSERINE (THIOL) LYASE (OAS-TL) ISOFORM A1) [Arabidopsis thaliana])

Protein Group 188

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.96	3	14.13	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
787.7505	1573.4854	1573.7967	197.84	2	2.8	1.29	VSGLFFAIGHEPATK	LYK	rep2
787.7491	1573.4825	1573.7967	199.7	2	1.77	0.62	VSGLFFAIGHEPATK	LYT	rep1
479.0685	956.1213	956.1496	29.63	2	2	0.37	VYIIHRR	LYK	rep3
1114.1307	3339.3687	3339.6839	94.37	3	3.91	0.42	YRQAITAAGTGCMAALDAEHYLQEIGSQQGK : +57.05000 (C12)	LYT	rep1

Matching Genes:

NP_195271.2 (NTR1 (NADPH-dependent thioredoxin reductase 1) [Arabidopsis thaliana])

Protein Group 189

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	17.3	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
861.4751	2581.4018	2581.8906	189.32	3	2.36	0.56	FSLNGVNYTLPINKPPNSLHGGNK	LYT	rep3
861.2465	2580.7159	2581.8906	454.98	3	2.04	0.02	FSLNGVNYTLPINKPPNSLHGGNK	LYK	rep3
938.764	2813.2686	2814.1474	312.28	3	4.14	1.84	HAGVCLETQGFPNAINQSNFPSVVVK : +57.05000 (C5)	LYT	rep1
548.5279	1095.0401	1095.259	199.9	2	2.18	0.45	IWEVAGHKR	LYT	rep1
366.1683	1095.4815	1095.259	203.15	3	1.62	0.01	IWEVAGHKR	LYK	rep1

Matching Genes:

NP_566594.2 (aldose 1-epimerase family protein [Arabidopsis thaliana])

Protein Group 190

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	9.62	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
749.5613	2245.6604	2246.4526	352.67	3	5.08	1.96	ASGVAHEVHIYPGNGHAFLNR	LYK	rep2
749.7396	2246.1954	2246.4526	114.5	3	4.37	2.08	ASGVAHEVHIYPGNGHAFLNR	LYT	rep3
830.1189	2487.3332	2487.7839	181.17	3	3.54	1.24	LKASGVAHEVHIYPGNGHAFLNR	LYT	rep1

Matching Genes:

NP_180811.1 (dienelactone hydrolase family protein [Arabidopsis thaliana])

Protein Group 191

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.96	3	14.13	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
720.8445	1439.6734	1439.704	21.25	2	3.34	0	IEQIYLHSLPVK	LYT	rep1
892.0562	1782.0967	1782.998	505.51	2	2.76	1.36	KVLQFAGIDDVFTSSR	LYT	rep1
695.0447	1388.0738	1388.5708	357.94	2	2.5	1.15	TYGFLTPEFWK	LYT	rep1

Matching Genes:

NP_191308.1 (40S ribosomal protein S2 (RPS2D) [Arabidopsis thaliana])

Protein Group 192

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.31	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1234.3926	2466.7696	2466.8459	30.96	2	2.79	1.47	HFSLIPPGGGGILAHSLAHVASSLK	LYK	rep1
1233.9505	2465.8853	2466.8459	389.42	2	1.86	0.71	HFSLIPPGGGGILAHSLAHVASSLK	LYT	rep2
801.3383	2400.9913	2401.6843	288.56	3	3.9	1.98	LEAVPKPGDSPIIVNAQSSSVHR	LYT	rep1

801.3475	2401.0191	2401.6843	276.97	3	3.19	1.65	LEAVPKPGDSPIIVNAQSSSVHR	LYK	rep2
697.9269	2090.7572	2091.2014	212.43	3	1.89	0.36	LEEAHHLNVPSGVEDSTEK	LYT	rep1

Matching Genes:

NP_568066.1 (unknown protein [Arabidopsis thaliana])

Protein Group 193

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	28.77	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
683.1925	1364.3694	1364.5972	166.89	2	2.65	1.41	GHLPENKPFVVK	LYK	rep3
455.7637	1364.2677	1364.5972	241.41	3	2.4	0.83	GHLPENKPFVVK	LYT	rep2
748.1313	1494.2469	1494.7615	344.31	2	2.63	1	NKFFCPIVNLDK : +57.05000 (C5)	LYT	rep1
678.3732	2032.096	2032.265	83.14	3	3.25	1.14	SSKDNVPLIDVTQHGFFK	LYK	rep1
678.4303	2032.2674	2032.265	1.19	3	2.65	1.07	SSKDNVPLIDVTQHGFFK	LYT	rep1

Matching Genes:

NP_173743.1 (RPL27A (RIBOSOMAL PROTEIN L27A); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 194

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	4	19.01	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1428.08	4281.2164	4281.688	110.15	3	1.45	0.56	AFQLYSSGVFDGLCGTELDHGVVAVGYGTENGKDYWIVR : +57.05000 (C14)	LYK	rep1
1427.7389	4280.1932	4281.688	349.12	3	1.41	0.16	AFQLYSSGVFDGLCGTELDHGVVAVGYGTENGKDYWIVR : +57.05000 (C14)	LYT	rep3
796.0284	1590.0411	1589.801	150.99	2	2.49	0.93	ALAHQPISVAIEAGGR	LYT	rep2
795.6377	1589.2598	1589.801	340.43	2	2.44	0.75	ALAHQPISVAIEAGGR	LYK	rep1
490.3954	1468.1629	1467.7579	275.91	3	2.29	0.62	CGIAMEASYPIKK : +57.05000 (C1)	LYT	rep2
742.7008	2225.0789	2223.3996	755.28	3	2.26	0.64	VVTIDSYEDVPENSEASLKK	LYT	rep2
741.9401	2222.7967	2223.3996	271.18	3	2.04	0.76	VVTIDSYEDVPENSEASLKK	LYK	rep1

Matching Genes:

NP_568620.1 (cysteine proteinase, putative / thiol protease, putative [Arabidopsis thaliana])

Protein Group 195

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	3	13.61	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
451.9636	901.9115	902.0508	154.35	2	2.62	1.1	GFGFVTFK	LYT	rep1
452.123	902.2304	902.0508	199.12	2	2.4	1.04	GFGFVTFK	LYK	rep2
638.3841	1274.7525	1274.4261	256.07	2	3.23	1.19	GFGFVTFKDEK	LYK	rep1
638.2784	1274.5411	1274.4261	90.17	2	3.05	1.26	GFGFVTFKDEK	LYT	rep3
673.1538	1344.292	1343.4436	631.54	2	2.58	0.63	TFSQFGDVIDSK	LYT	rep2

Matching Genes:

NP_195637.1 (ATGRP8/GR-RBP8 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 1, GLYCINE-RICH PROTEIN 8); RNA binding [Arabidopsis thaliana])

Protein Group 196

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	4.26	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
840.3729	2518.0953	2518.7336	253.43	3	3.97	2.11	HGTGHGVGSYLCVHEGPHQVSFR : +57.05000 (C12)	LYK	rep3
977.3862	2929.1352	2930.1915	360.49	3	4.41	2.38	HGTGHGVGSYLCVHEGPHQVSFRPSAR : +57.05000 (C12)	LYK	rep3

Matching Genes:

NP_195394.1 (ATAPP1 (aminopeptidase P1) [Arabidopsis thaliana])

Protein Group 197

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	9.92	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
714.901	2141.6795	2140.3652	614.06	3	5.35	2.3	NVGLDRPSDLVALSGGHTFGK	LYK	rep3
714.2773	2139.8086	2140.3652	260.08	3	4.48	2.2	NVGLDRPSDLVALSGGHTFGK	LYT	rep1
568.3727	1702.0946	1701.9233	100.61	3	2.79	1.3	TPTVFDNKYYVNLK	LYK	rep1
568.4823	1702.4234	1701.9233	293.84	3	2.55	1.17	TPTVFDNKYYVNLK	LYT	rep2

Matching Genes:

NP_190481.1 (ATPCB/ATPERX34/PERX34/PRXCB (PEROXIDASE 34); peroxidase [Arabidopsis thaliana])

Protein Group 198

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	23.22	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1611.7679	4832.2804	4833.5197	256.4	3	3.87	1.99	KVIISAPSADAPMFVVGVNEHTYQPNMDIVSNASCTTNCLAPLAK : +57.05000 (C35); +57.05000 (C39)	LYT	rep1
1130.9218	3389.7418	3389.7641	6.6	3	2.34	0.35	LVSWYDNEWGYSNRVLDLIEHMALVAASH	LYT	rep1
871.7848	2612.3309	2612.9634	242.05	3	1.94	0.57	VVHEEFGILEGLMTTVHATTATQK	LYT	rep3
871.7614	2612.2606	2612.9634	268.96	3	1.85	0.65	VVHEEFGILEGLMTTVHATTATQK	LYK	rep1

Matching Genes:

NP_178071.1 (GAPCP-1; glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana])

Protein Group 199

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.25	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
544.8058	1631.3939	1631.8379	272.08	3	2.63	0.99	DTLKVPHTSVGGGHVK	LYT	rep3

1286.0673	3855.1783	3856.2993	290.69	3	5.48	3.29	NALPEWETTGFVEYIAGGPQPGGMYFPVAHGVHAVR	LYK	rep3
1285.7416	3854.2013	3856.2993	544.06	3	2.41	0.93	NALPEWETTGFVEYIAGGPQPGGMYFPVAHGVHAVR	LYT	rep3

Matching Genes:

NP_566328.1 (unknown protein [Arabidopsis thaliana])

Protein Group 200

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	29.27	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
668.6739	1335.3321	1335.4679	101.7	2	1.71	0.61	AVVVHADPDDLGK	LYK	rep2
668.7542	1335.4927	1335.4679	18.59	2	1.33	0.22	AVVVHADPDDLGK	LYT	rep1
1260.535	3778.5816	3780.1216	407.38	3	6.33	4	ISGLSPGFHGFHIHSFGDTTNGCISTGPHFNPLNR : +57.05000 (C23)	LYK	rep3

Matching Genes:

NP_197311.1 (CSD3 (COPPER/ZINC SUPEROXIDE DISMUTASE 3); copper, zinc superoxide dismutase [Arabidopsis thaliana])

Protein Group 201

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.91	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

1039.2216	3114.6412	3115.5583	294.37	3	5.7	3.47	GGHAALPQHTIDPILAASNVIVSLQHLVSR	LYK	rep1
1039.5458	3115.6139	3115.5583	17.82	3	4.58	2.11	GGHAALPQHTIDPILAASNVIVSLQHLVSR	LYT	rep1
641.7377	1922.1895	1922.2243	18.07	3	2.32	0.68	MHACGHDAHTTMLLGAAK : +57.05000 (C4)	LYK	rep1

Matching Genes:

NP_175587.1 (IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase [Arabidopsis thaliana])

Protein Group 202

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.8	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1010.8724	3029.5938	3030.4526	283.39	3	2.28	0.83	IDMGCHIDGFIALVGHTHVLQEGPLSGR : +57.05000 (C5)	LYT	rep3
1011.1215	3030.3409	3030.4526	36.87	3	1.89	0.57	IDMGCHIDGFIALVGHTHVLQEGPLSGR : +57.05000 (C5)	LYK	rep2
1141.3663	3421.0755	3421.9341	250.91	3	5.73	3.4	LGLVECVNHGHLQPYPVLYEKPGDFVAQIK : +57.05000 (C6)	LYT	rep3
1141.2648	3420.7708	3421.9341	339.95	3	5.61	3	LGLVECVNHGHLQPYPVLYEKPGDFVAQIK : +57.05000 (C6)	LYK	rep3

Matching Genes:

NP_190748.1 (ATG2 (G2p-related protein); metalloexopeptidase [Arabidopsis thaliana])

Protein Group 203

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	14.61	20.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
414.9313	827.847	827.9734	152.76	2	2.03	0.52	GLVHFQK	LYK	rep1
414.9557	827.8958	827.9734	93.78	2	2.02	0.57	GLVHFQK	LYT	rep1
872.0307	1742.0457	1741.9109	77.39	2	3.37	1.34	IDYAPGGLNPPHTHPR	LYK	rep3
871.5226	1741.0296	1741.9109	505.94	2	2.61	0.93	IDYAPGGLNPPHTHPR	LYT	rep2
504.9884	1007.9612	1008.1749	211.96	2	2.56	0.93	KGDVFAFPK	LYT	rep1
504.9739	1007.9322	1008.1749	240.78	2	2.02	0.66	KGDVFAFPK	LYK	rep1

Matching Genes:

NP_172427.1 (GLP5 (GERMIN-LIKE PROTEIN 5); manganese ion binding / metal ion binding / nutrient reservoir [Arabidopsis thaliana])

Protein Group 204

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	11.4	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
543.1937	1626.5577	1626.6919	82.49	3	3.41	1.35	HKEHISAYGEGNER	LYK	rep3
1282.088	3843.2406	3844.3633	292.04	3	4.4	2.14	RPASNMDPYIVTSLLAETTLLWEPTLEAEALAAQK	LYK	rep3
1283.0302	3846.067	3844.3633	443.17	3	4.14	1.83	RPASNMDPYIVTSLLAETTLLWEPTLEAEALAAQK	LYT	rep3

Matching Genes:

NP_001031969.1 (GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase [Arabidopsis thaliana])

Protein Group 205

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.88	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
585.0009	1751.9791	1751.8976	46.53	3	3.57	1.45	IRPSLFDAFGDDSSPK	LYT	rep1
678.4232	2032.2462	2032.2436	1.25	3	2.36	0.59	LNDEDYVKPAMQTHVGSK	LYT	rep1
678.2899	2031.8463	2032.2436	195.53	3	2.33	0.88	LNDEDYVKPAMQTHVGSK	LYK	rep2
868.1354	2601.3827	2600.9548	164.49	3	1.88	0.41	VPPGCRMTIISDSCHSGGLIDEAK : +57.05000 (C5); +57.05000 (C14)	LYK	rep3

Matching Genes:

NP_178052.1 (latex-abundant protein, putative (AMC7) / caspase family protein [Arabidopsis thaliana])

Protein Group 206

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	34.32	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
641.9573	1922.8483	1923.1653	164.79	3	4.51	2.29	GRLHACISPSENGLINGK : +57.05000 (C6)	LYK	rep1
642.0327	1923.0747	1923.1653	47.11	3	3.79	1.62	GRLHACISPSENGLINGK : +57.05000 (C6)	LYT	rep2
1525.8795	4574.6151	4576.1919	344.56	3	3.28	1.3	SLSHDVFVYGSFQEPSVVNLILECSPVMVPAQLHGYHVYR : +57.05000 (C24)	LYT	rep3
1526.2177	4575.6295	4576.1919	122.89	3	2.68	1.26	SLSHDVFVYGSFQEPSVVNLILECSPVMVPAQLHGYHVYR : +57.05000 (C24)	LYK	rep2

Matching Genes:

NP_566840.1 (avirulence-responsive protein, putative / avirulence induced gene (AIG) protein, putative [Arabidopsis thaliana])

Protein Group 207

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	4	17.96	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
437.0707	1308.1887	1307.4226	586	3	1.88	0.12	HNNVIPSSHFR	LYK	rep2
654.8135	1307.6114	1307.4226	144.38	2	1.66	0.26	HNNVIPSSHFR	LYT	rep3
368.547	1102.6175	1102.25	333.43	3	2.09	0.52	KHWQNYVK	LYT	rep2
368.5277	1102.5597	1102.25	280.94	3	1.92	0.41	KHWQNYVK	LYK	rep1
784.0343	1566.053	1566.7926	472.03	2	2.04	0.48	MKHNNVIPSSHFR	LYT	rep1
844.1621	1686.3086	1686.9598	386.02	2	1.77	0.69	PTSGPLRPVVHGQTLK	LYT	rep3

Matching Genes :

NP_197778.1 (60S ribosomal protein L13 (RPL13D) [Arabidopsis thaliana])

Protein Group 208

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	3.83	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
569.9742	1706.8993	1706.8683	18.15	3	4.47	2.37	AHAHNLQVHPYTYR	LYK	rep3

854.5102	1707.0047	1706.8683	79.91	2	3.02	1.48	AHAHNLQVHPYTYR	LYT	rep2
621.8411	1862.4997	1863.0546	297.81	3	3.26	1.46	RAHAHNLQVHPYTYR	LYK	rep3
622.176	1863.5046	1863.0546	241.56	3	1.6	0.25	RAHAHNLQVHPYTYR	LYT	rep2

Matching Genes:

NP_177561.1 (glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis thaliana])

Protein Group 209

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.28	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
968.5377	1935.0598	1935.093	17.13	2	2.87	0.98	DSEIAMGGYQPHHLSHR	LYK	rep2
646.0631	1935.1659	1935.093	37.65	3	2.44	0.64	DSEIAMGGYQPHHLSHR	LYT	rep2
772.6026	1543.1895	1543.651	298.97	2	3.38	1. 17	GGPREPWHDIHSR	LYT	rep2
515.3732	1543.096	1543.651	359.51	3	2.55	0.57	GGPREPWHDIHSR	LYK	rep1
1152.6642	3454.9691	3456.9341	568.42	3	1.45	0.38	MSLWYEHLGMLDETFLDPSSLECIEKVNR	LYT	rep3

Matching Genes:

NP_188194.1 (PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D [Arabidopsis thaliana])

Protein Group 210

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	9.52	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1067.9376	3200.7894	3201.5359	233.17	3	3.97	1.43	EAPEGSFILLHGCAHNPTGIDPTPEQWVK : +57.05000 (C13)	LYT	rep1
1067.8353	3200.4825	3201.5359	329.02	3	2.96	1.3	EAPEGSFILLHGCAHNPTGIDPTPEQWVK : +57.05000 (C13)	LYK	rep2
556.7748	1667.3009	1665.9242	826.38	3	3.68	1.62	IARPMYSNPPVHGAR	LYK	rep3
833.7619	1665.5081	1665.9242	249.77	2	3.44	1.79	IARPMYSNPPVHGAR	LYT	rep2

Matching Genes:

NP_001031767.1 (ASP5 (ASPARTATE AMINOTRANSFERASE 5) [Arabidopsis thaliana])

Protein Group 211

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.89	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
724.9813	2171.9205	2172.4868	260.67	3	5	1.64	DGLTFLDLIVIQIENLNNK	LYK	rep3
703.7284	2108.1617	2108.3599	93.98	3	2.65	0.84	VQLLEIAQVPDEHVNEFK	LYK	rep2

Matching Genes:

NP_186975.1 (UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase [Arabidopsis thaliana])

Protein Group 212

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	21.86	20.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
386.4553	1156.3423	1156.2977	38.56	3	2.74	0.89	KHVSAWWDK	LYT	rep1
386.4109	1156.2092	1156.2977	76.56	3	2.6	0.8	KHVSAWWDK	LYK	rep1
1050.8998	3149.6759	3150.5483	276.92	3	2.59	1.12	NEYLAGDFVSLADLAHLPFTEYLVGPIGK	LYK	rep3
508.2614	1014.5072	1014.2241	279.16	2	2.32	0.17	RAVVTLVEK	LYT	rep2

Matching Genes:

NP_180644.1 (ATGSTF10 (EARLY DEHYDRATION-INDUCED 13); glutathione transferase [Arabidopsis thaliana])

Protein Group 213

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	11.81	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
565.357	1128.6983	1129.3771	601.02	2	2.07	0.26	DLIVQCLLR : +57.05000 (C6)	LYK	rep3
635.3752	1903.1023	1903.0342	35.78	3	2.05	0.31	VSQHGFFNHHHHQYK	LYT	rep1
799.0758	2394.2039	2394.6633	191.83	3	3.47	1.29	VSQHGFFNHHHHQYKHLLK	LYK	rep3

Matching Genes:

NP_176602.1 (VHA-E3 (VACUOLAR H+-ATPASE SUBUNIT E ISOFORM 3); hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism [Arabidopsis thaliana])

Protein Group 214

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	0.98	2	9.84	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
599.9724	1796.8938	1797.2192	181.06	3	5.24	1.63	FVIQTLAPLGCLPIVR : +57.05000 (C11)	LYK	rep2
600.1675	1797.479	1797.2192	144.56	3	3.48	1.25	FVIQTLAPLGCLPIVR : +57.05000 (C11)	LYT	rep2
1239.177	2476.3384	2477.7778	580.93	2	2.32	0.66	TAPASAPFQFTVFDFYNAILTR	LYK	rep3

Matching Genes:

NP_564647.1 (myrosinase-associated protein, putative [Arabidopsis thaliana])

Protein Group 215

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.81	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
617.3229	1848.9452	1848.0138	503.98	3	3.1	1.03	FNYMHYDNTHGAIHK	LYT	rep3
553.2799	1656.8162	1656.9307	69.05	3	2.09	0.48	IFLLGPSHHFYTPK	LYT	rep2
553.3424	1657.0037	1656.9307	44.11	3	1.87	0. 22	IFLLGPSHHFYTPK	LYK	rep2
658.002	1970.9824	1972.1297	581.79	3	2.32	0.91	IRQPTHAGSWYTDNPTK	LYT	rep3

Matching Genes:

NP_565590.1 (unknown protein [Arabidopsis thaliana])

Protein Group 216

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	16.19	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
542.635	1083.2544	1083.3099	51.23	2	2.45	1.14	HAMVAAGSLVK	LYK	rep2
542.4247	1082.8338	1083.3099	439.53	2	2.44	1.09	HAMVAAGSLVK	LYT	rep1
421.1401	1260.3969	1260.4708	58.61	3	2.61	0.23	HRTLMNVFDK	LYT	rep1
941.0779	2820.2102	2820.0437	59.03	3	2.43	0.32	NYINLAQIHASENSKSFEQIEVER	LYK	rep3

Matching Genes:

NP_175159.1 (APFI; carbonate dehydratase [Arabidopsis thaliana])

Protein Group 217

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	6.17	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
903.7321	1805.4485	1806.0829	351.23	2	2.64	1	FPDKIGGHLPGVHYIR	LYT	rep2
440.516	1318.5245	1318.5317	5.48	3	2.96	0.58	IGGHLPGVHYIR	LYK	rep3
660.1939	1318.3721	1318.5317	121.06	2	2.58	1.1	IGGHLPGVHYIR	LYT	rep2
482.3655	1444.073	1443.5916	333.47	3	1.86	0.25	LPGFHTCVGGGGER : +57.05000 (C7)	LYK	rep2
722.5818	1443.148	1443.5916	307.28	2	1.47	0.71	LPGFHTCVGGGGER : +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_564818.1 (monodehydroascorbate reductase, putative [Arabidopsis thaliana])

Protein Group 218

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	19.55	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
691.2849	2070.8313	2070.405	205.87	3	4.37	1.74	FVVHNTSELELLMMHNR	LYK	rep3
691.2682	2070.7811	2070.405	181.64	3	1.59	0.34	FVVHNTSELELLMMHNR	LYT	rep3
369.0834	1104.2268	1103.2779	860.06	3	2.89	0.77	HYLPNGFKK	LYK	rep3
368.7832	1103.3261	1103.2779	43.68	3	1.76	0.05	HYLPNGFKK	LYT	rep2

Matching Genes:

NP_193544.1 (60S ribosomal protein L32 (RPL32A) [Arabidopsis thaliana])

Protein Group 219

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.82	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1116.5055	3346.493	3347.7673	380.65	3	5.53	3.66	FSVNGKPIYHFMGTSTFSQYTVVHDVSVAK	LYK	rep1
1117.0072	3347.9981	3347.7673	68.94	3	4.23	2.49	FSVNGKPIYHFMGTSTFSQYTVVHDVSVAK	LYT	rep3
640.1175	1278.2193	1278.461	189.11	2	1.73	0.52	KFGVNEFVNPK	LYK	rep2
639.7356	1277.4556	1278.461	786.45	2	1.11	0.01	KFGVNEFVNPK	LYT	rep1

Matching Genes:

NP_199207.1 (ADH2 (ALCOHOL DEHYDROGENASE 2); formaldehyde dehydrogenase (glutathione) [Arabidopsis thaliana])

Protein Group 220

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.86	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
431.299	1290.8736	1290.4335	341.05	3	3.87	1.55	HITGSNIGGHAVK	LYK	rep3
431.3528	1291.0351	1290.4335	466.2	3	2.77	0.95	HITGSNIGGHAVK	LYT	rep3
593.1453	1184.2749	1184.303	23.67	2	1.71	0.25	HYSVSTYTVK	LYT	rep3
592.8736	1183.7315	1184.303	482.55	2	1.55	0.25	HYSVSTYTVK	LYK	rep2
592.3463	1774.0155	1774.0791	35.86	3	1.65	0.53	KHFLGVPIVSHDPSLK	LYT	rep3

Matching Genes:

NP_567215.1 (cathepsin B-like cysteine protease, putative [Arabidopsis thaliana])

Protein Group 221

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.23	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
718.0066	2150.9963	2151.3928	184.3	3	2.95	0.78	AGSVEPAHHHTFGHDLVVIK	LYT	rep3
717.9933	2150.9564	2151.3928	202.86	3	2.65	0.96	AGSVEPAHHHTFGHDLVVIK	LYK	rep2

809.6989	2426.0731	2426.7405	275.01	3	2.67	0.81	FKAGSVEPAHHHTFGHDLVVIK	LYK	rep3
662.3551	1984.0418	1983.2142	417.31	3	1.58	0.3	FPGVYAATCLSVEDAVNAR	LYK	rep1

Matching Genes:

NP_566241.1 (DRT102 (DNA-DAMAGE-REPAIR/TOLERATION 2) [Arabidopsis thaliana])

Protein Group 222

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	20.88	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
905.8519	2714.5323	2715.963	526.78	3	4.94	2.79	HACPSSFTFAHDSPSLMHDCASPR : +57.05000 (C3); +57.05000 (C 20)	LYK	rep3
905.9386	2714.7923	2715.963	431.05	3	4.75	2.57	HACPSSFTFAHDSPSLMHDCASPR : +57.05000 (C3); +57.05000 (C20)	LYT	rep3
1055.14	3162.3966	3162.6739	87.69	3	2.24	0.68	LFLTVVNNCPFTVWPAIQPNAGHPVLEK : +57.05000 (C9)	LYT	rep1

Matching Genes:

NP_180445.1 (osmotin-like protein, putative [Arabidopsis thaliana])

Protein Group 223

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	11.29	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

915.4551	1828.8946	1829.0716	96.81	2	3.39	1.85	EHVEAWKPIVDAVHAK	LYT	rep3
610.714	1829.1185	1829.0716	25.61	3	2.88	1.47	EHVEAWKPIVDAVHAK	LYK	rep2
576.9706	1727.8883	1727.9656	44.73	3	2.36	0.7 4	RLGIEEIPGIVNDFR	LYT	rep1
453.1508	1356.4288	1356.5766	108.99	3	1.41	0.26	WFLANPDLPKR	LYT	rep1

Matching Genes:

NP_177794.1 (OPR1 (12-oxophytodienoate reductase 1); 12-oxophytodienoate reductase [Arabidopsis thaliana])

Protein Group 224

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	26.85	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
736.0918	1470.168	1470.6749	344.68	2	3.6	1.72	AFVVHELKDDLGK	LYT	rep3
736.0313	1470.0469	1470.6749	427.02	2	2.32	0.51	AFVVHELKDDLGK	LYK	rep2
1643.8427	4928.5045	4929.2951	160.39	3	3.53	1.51	ITGLTPGPHGFHLHEFGDTTNGCISTGPHFNPNNMTHGAPEDECR : +57.05000 (C23); +57.05000 (C44)	LYK	rep2

Matching Genes:

NP_565666.1 (CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); copper, zinc superoxide dismutase [Arabidopsis thaliana])

Protein Group 225

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	2	21.57	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1121.2169	3360.6273	3362.6338	596.7	3	3.56	1.62	SENHLVPEAIGHLIQGVTVHDGDWDSHGTIK	LYK	rep3
1121.7782	3362.3111	3362.6338	95.95	3	2.91	1	SENHLVPEAIGHLIQGVTVHDGDWDSHGTIK	LYT	rep3
1235.827	3704.4576	3705.031	154.76	3	3.55	1.52	WRSENHLVPEAIGHLIQGVTVHDGDWDSHGTIK	LYT	rep2
1235.4891	3703.4439	3705.031	428.35	3	1.94	0.25	WRSENHLVPEAIGHLIQGVTVHDGDWDSHGTIK	LYK	rep1

Matching Genes:

NP_172949.1 (major latex protein-related / MLP-related [Arabidopsis thaliana])

Protein Group 226

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	12.89	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
709.1082	1416.2007	1416.536	236.69	2	3.52	1.44	KGETPETAVVEEK	LYK	rep3
709.0804	1416.1451	1416.536	275.99	2	3.24	1.18	KGETPETAVVEEK	LYT	rep3
883.6183	1765.221	1765.8314	345.69	2	3.5	1.54	TEGTSGEKEEIVEETK	LYT	rep3

Matching Genes:

NP_001031676.1 (DREPP plasma membrane polypeptide family protein [Arabidopsis thaliana])

Protein Group 227

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.42	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
946.7947	2837.3606	2839.1538	631.61	3	6.95	4.02	ASHMAHVYDFYKPNLASEYPVVDGK	LYK	rep3
947.2057	2838.5936	2839.1538	197.31	3	5.86	3.62	ASHMAHVYDFYKPNLASEYPVVDGK	LYT	rep3

Matching Genes:

NP_192919.1 (BAP1 (hydroxymethylglutaryl-CoA synthase) [Arabidopsis thaliana])

Protein Group 228

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	19.87	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
639.6732	1915.9962	1916.1892	100.73	3	3.47	1.48	AHGLAPEIPEDLYHLIK	LYK	rep2
639.5927	1915.7545	1916.1892	226.87	3	1.89	0.49	AHGLAPEIPEDLYHLIK	LYT	rep1
461.4479	1381.3202	1381.6692	252.61	3	3.44	0.57	KGLTPSQIGVILR	LYT	rep1
691.5262	1381.0367	1381.6692	457.79	2	1.95	0.91	KGLTPSQIGVILR	LYK	rep1

Matching Genes:

NP_567104.1 (40S ribosomal protein S13 (RPS13A) [Arabidopsis thaliana])

Protein Group 229

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.46	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
505.5201	1513.5369	1513.7429	136.06	3	2.83	1.13	FSLEETVAILHVR	LYT	rep3
505.6613	1513.9603	1513.7429	143.6	3	2.33	0.74	FSLEETVAILHVR	LYK	rep2
718.4138	2152.218	2151.4709	347.22	3	4.05	2.05	LEGTIGFGKPTADVSAIHIPK	LYK	rep2
1076.0777	2150.1397	2151.4709	618.76	2	2.53	1.08	LEGTIGFGKPTADVSAIHIPK	LYT	rep1

Matching Genes:

NP_181934.1 (late embryogenesis abundant family protein / LEA family protein [Arabidopsis thaliana])

Protein Group 230

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	31.61	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
742.256	1482.4964	1482.5115	10.18	2	1.99	0.53	KDDEESGGGLGGYAK	LYK	rep3
1147.3578	3439.0499	3439.5808	154.35	3	4.78	2.93	YLNDYESSHSTGAGGPPPPTSQAEPASQPEPAAK	LYT	rep1
1147.3246	3438.9503	3439.5808	183.31	3	2.85	1.36	YLNDYESSHSTGAGGPPPPTSQAEPASQPEPAAK	LYK	rep2

Matching Genes:

NP_563934.1 (unknown protein [Arabidopsis thaliana])

Protein Group 231

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	9.96	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
545.0392	1088.0628	1088.3015	219.35	2	2.09	0.3	FKDEIIPVK	LYT	rep1
546.166	1090.3164	1088.3015	1851.45	2	1.51	0.19	FKDEIIPVK	LYK	rep2
537.1084	1072.2012	1072.2604	55.17	2	2.28	0.7	KVEAQGLLSK	LYT	rep1
877.3345	2628.9799	2630.0002	387.94	3	2.36	0.68	LGLDPEKINVNGGAMAIGHPLGATGAR	LYK	rep1
877.6478	2629.92	2630.0002	30.5	3	1.49	0.44	LGLDPEKINVNGGAMAIGHPLGATGAR	LYT	rep2

Matching Genes:

NP_180873.1 (PED1 (PEROXISOME DEFECTIVE 1); acetyl-CoA C-acyltransferase [Arabidopsis thaliana])

Protein Group 232

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.46	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1215.8313	2429.647	2429.8012	63.48	2	4.45	2.21	HGIICTEDLIHEILTVGPHFK : +57.05000 (C5)	LYT	rep1
810.7758	2429.3038	2429.8012	204.73	3	4.39	2.33	HGIICTEDLIHEILTVGPHFK : +57.05000 (C5)	LYK	rep1
842.0565	1682.0974	1682.9232	490.67	2	2.28	0.92	RVEPYVTYGFPNLK	LYT	rep1

Matching Genes:

NP_178234.1 (60S ribosomal protein L7 (RPL7B) [Arabidopsis thaliana])

Protein Group 233

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.98	2	6.3	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
635.8989	1904.6733	1904.1654	266.74	3	1.52	0.57	HSPFFAGYRPQFYMR	LYT	rep3
635.7235	1904.1471	1904.1654	9.63	3	1.44	0.19	HSPFFAGYRPQFYMR	LYK	rep2
590.6725	1768.994	1768.9119	46.39	3	5.2	2.95	HYAHVDCPGHADYVK : +57.05000 (C7)	LYT	rep3
590.6534	1768.9369	1768.9119	14.1	3	5.2	2.86	HYAHVDCPGHADYVK : +57.05000 (C7)	LYK	rep1

Matching Genes:

NP_193769.1 (AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor [Arabidopsis thaliana])

Protein Group 234

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.43	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1060.7843	3179.3294	3180.3735	328.29	3	2.1	0.54	GGWPTWSGDSTVFFHHQADDGWWSIFR	LYK	rep3
1627.411	4879.2096	4879.2471	7.69	3	4.58	3	HIEIYDLENTTFQPVTESLNPSFHHYNPFVSPDSEFLGYHR	LYT	rep3
1627.514	4879.5186	4879.2471	55.66	3	4.38	2.76	HIEIYDLENTTFQPVTESLNPSFHHYNPFVSPDSEFLGYHR	LYK	rep2

Matching Genes:

NP_192096.1 (tolB protein-related [Arabidopsis thaliana])

Protein Group 235

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	13.86	29.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
941.6618	1881.3079	1882.1336	438.68	2	3.78	2.33	TVGINYFICSTPGHCR : +57.05000 (C9); +57.05000 (C15)	LYT	rep1
941.7246	1881.4336	1882.1336	371.88	2	2.96	1.64	TVGINYFICSTPGHCR : +57.05000 (C9); +57.05000 (C15)	LYK	rep1
654.0279	1306.0401	1306.3834	262.81	2	2.87	1.11	YGSSHTVDVVDK	LYT	rep2
653.9441	1305.8726	1306.3834	391.02	2	2.39	0.88	YGSSHTVDVVDK	LYK	rep2

Matching Genes:

NP_182006.1 (UCC2 (UCLACYANIN 2); copper ion binding [Arabidopsis thaliana])

Protein Group 236

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.09	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
817.8196	2450.4353	2450.5779	58.19	3	3.41	1.97	HVVDEPANEEKPSESSAALSPEK	LYT	rep1
694.3258	2079.9539	2080.2185	127.18	3	3.24	1.73	HVVEEPLKDEQENVSEAK	LYT	rep1
694.2919	2079.8521	2080.2185	176.12	3	2.82	1.25	HVVEEPLKDEQENVSEAK	LYK	rep2

Matching Genes:

NP_187241.2 (neurofilament protein-related [Arabidopsis thaliana])

Protein Group 237

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	12.14	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1020.043	3057.1054	3058.4613	443.32	3	4.26	2.3	KGCTPAQLALAWVHHQGDDVCPIPGTTK : +57.05000 (C3); +57.0500 0 (C21)	LYT	rep1
612.8365	1835.4862	1836.0861	326.73	3	2.35	0.88	RLDIACIDLYYQHR : +57.05000 (C6)	LYT	rep3
612.7855	1835.3331	1836.0861	410.1	3	1.74	0.41	RLDIACIDLYYQHR : +57.05000 (C6)	LYK	rep1

Matching Genes:

NP_176267.3 (AGD2 (ARF-GAP DOMAIN 2); aldo-keto reductase [Arabidopsis thaliana])

Protein Group 238

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	17.35	22.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
576.5093	1151.003	1151.2777	238.63	2	3.26	1.43	IGDALHIGGGNK	LYT	rep3
576.6607	1151.3057	1151.2777	24.32	2	2.94	1.21	IGDALHIGGGNK	LYK	rep3

578.2056	1731.5932	1731.8712	160.51	3	3.31	1.66	IGDALHIGGGNKEGEHK	LYT	rep3

Matching Genes:

NP_175843.1 (dehydrin family protein [Arabidopsis thaliana])

Protein Group 239

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	13.59	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
983.2428	2946.7049	2947.383	230.08	3	6.56	3.33	SMTQHNVGALVVVKPGEQQALAGIITER	LYK	rep3
983.545	2947.6117	2947.383	77.56	3	5.49	2.03	SMTQHNVGALVVVKPGEQQALAGIITER	LYT	rep3

Matching Genes:

NP_196647.1 (CBS domain-containing protein [Arabidopsis thaliana])

Protein Group 240

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	7.07	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
779.741	1557.4663	1557.5815	73.95	2	1.63	0.41	SGEDADTLGLTGHER	LYK	rep1
1057.7643	3170.2694	3170.6128	108.31	3	2.39	0.42	WGSTAFQNMLVVPPGSGIVHQVNLEYLGR	LYT	rep2
957.9995	2870.9751	2871.1289	53.58	3	2.53	1.06	YTIHLPTDISEIRPGQDVTVTTDNGK	LYK	rep2

957.7878	2870.34	2871.1289	274.75	3	1.85	0.66	YTIHLPTDISEIRPGQDVTVTTDNGK	LYT	rep2

Matching Genes:

NP_178634.2 (aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative [Arabidopsis thaliana])

Protein Group 241

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	4	15.35	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
634.8925	1901.6539	1902.098	233.48	3	1.37	0.47	DIVNIVACEGEERIER : +57.05000 (C8)	LYT	rep2
903.7233	2708.1463	2708.0436	37.93	3	1.93	0.28	EEMGELHFCWEEKSLIVASAWR : +57.05000 (C9)	LYT	rep1
921.1199	1840.2242	1842.155	1048.16	2	1.26	0.37	IAAYMVEGLAARMAASGK : +32.00000 (M5)	LYK	rep3
1276.4738	3826.3978	3826.0691	85.91	3	1.92	0.47	YFLDSPTDEFVQHPIGSGASVSSFGSLDSFPYQSR	LYT	rep2

Matching Genes:

NP_173566.1 (SCL1 (SCARECROW-LIKE 1); transcription factor [Arabidopsis thaliana])

Protein Group 242

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.62	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
485.569	1453.6836	1453.6044	54.52	3	3.48	1.64	KIEFPHPTEEAR	LYK	rep3

485.3573	1453.0484	1453.6044	382.45	3	2.57	1.05	KIEFPHPTEEAR	LYT	rep2
617.3102	1848.9071	1849.2076	162.54	3	2.98	1.2	QIQELVEAIVLPMTHK	LYT	rep1

Matching Genes:

NP_172384.1 (RPT5B (26S PROTEASOME AAA-ATPASE SUBUNIT RPT5B); ATPase/ calmodulin binding [Arabidopsis thaliana])

Protein Group 243

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.13	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1088.7579	3263.2503	3263.5405	88.92	3	3.3	1.96	ADGPAGILAIGTANPENHVLQAEYPDYYFR	LYK	rep2
644.2632	1286.5108	1284.4891	1573.9	2	3.12	1.32	HMHLTEEFLK	LYK	rep2
429.1258	1284.3539	1284.4891	105.27	3	2.97	0.36	HMHLTEEFLK	LYT	rep1

Matching Genes:

NP_196897.1 (CHS (CHALCONE SYNTHASE); naringenin-chalcone synthase [Arabidopsis thaliana])

Protein Group 244

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	5.1	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

1042.2806	3123.8184	3124.6125	254.13	3	2.96	1.14	IAVGGHSYGAFMTANLLAHAPHLFACGIAR : +57.05000 (C26)	LYK	rep1
1042.1454	3123.4127	3124.6125	383.99	3	2.63	0.88	IAVGGHSYGAFMTANLLAHAPHLFACGIAR : +57.05000 (C26)	LYT	rep2
755.8568	2264.547	2264.6561	48.17	3	3.43	1.92	YLLVSSLHRPYSFIVPCGR : +57.05000 (C17)	LYK	rep2
756.3772	2266.1081	2264.6561	641.18	3	2.29	0.9	YLLVSSLHRPYSFIVPCGR : +57.05000 (C17)	LYT	rep3

Matching Genes:

NP_850473.1 (serine-type peptidase [Arabidopsis thaliana])

Protein Group 245

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	39.02	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1175.2308	3522.669	3523.9002	349.39	3	6.38	3.96	DHASVQLNIGHLDANGLYTGQFTTFALCGFVR : +57.05000 (C28)	LYT	rep1
1175.2721	3522.7928	3523.9002	314.26	3	2	0.65	DHASVQLNIGHLDANGLYTGQFTTFALCGFVR : +57.05000 (C28)	LYK	rep2

Matching Genes:

NP_001078280.1 (40S ribosomal protein S21 (RPS21B) [Arabidopsis thaliana])

Protein Group 246

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.57	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
636.0994	1905.2746	1905.1664	56.82	3	2.81	0.66	EFFNQGVKPGELAIISR	LYT	rep3
953.1446	1904.2735	1905.1664	468.67	2	1.78	0.32	EFFNQGVKPGELAIISR	LYK	rep3
487.4276	972.8396	973.0874	254.61	2	1.55	0.35	GYIHLENK	LYK	rep2
487.4468	972.878	973.0874	215.22	2	1.52	0.3	GYIHLENK	LYT	rep2
1099.1121	2196.2085	2197.626	644.98	2	2	0.83	TLEADIVIVGVGGRPIISLFK	LYT	rep3
733.2118	2196.6119	2197.626	461.44	3	1.81	0.68	TLEADIVIVGVGGRPIISLFK	LYK	rep1

Matching Genes:

NP_568125.1 (monodehydroascorbate reductase, putative [Arabidopsis thaliana])

Protein Group 247

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	5.88	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
838.8376	1675.6595	1675.9355	164.73	2	2.34	0.44	AVSQSKPPYVPPHLR	LYK	rep3
566.9967	1131.9778	1132.3607	338.13	2	1.59	0.59	HAIPILLAER	LYT	rep1
441.3605	1321.0579	1320.5262	402.65	3	2.43	1.19	SHLMDLLHAQR	LYT	rep3
441.3964	1321.1656	1320.5262	484.18	3	1.43	0.43	SHLMDLLHAQR	LYK	rep2

Matching Genes:

NP_001030884.1 (ATP-dependent helicase [Arabidopsis thaliana])

Protein Group 248

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	17.69	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
992.2421	2973.7027	2973.2449	153.99	3	2.77	0.8	FGDAANEEAGSHLTMVSTEEILLERPR	LYT	rep1
959.2986	2874.8723	2875.186	109.12	3	3.58	1.83	VTNLSEDTREPDLMELFHPFGAVTR	LYT	rep3
959.5211	2875.5399	2875.186	123.07	3	2.43	0.91	VTNLSEDTREPDLMELFHPFGAVTR	LYK	rep2

Matching Genes:

NP_187747.1 (EIF3G1 (eukaryotic translation initiation factor 3G1); RNA binding / translation initiation factor [Arabidopsis thaliana])

Protein Group 249

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.18	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1094.8597	3281.5557	3282.5439	301.04	3	3.65	2.13	AINTGWLHPSINQFNPEQAVDFDTVPNEK	LYT	rep3
1094.9061	3281.6949	3282.5439	258.65	3	1.8	0.23	AINTGWLHPSINQFNPEQAVDFDTVPNEK	LYK	rep2
1137.993	3410.9556	3410.7168	70.03	3	2.69	1.33	AINTGWLHPSINQFNPEQAVDFDTVPNEKK	LYK	rep1

Matching Genes:

NP_001032018.1 (KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); fatty-acid synthase [Arabidopsis thaliana])

Protein Group 250

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
608.6321	1822.8728	1823.1719	164.07	3	2.94	1.01	KIVSLDNHIALACAGLK : +57.05000 (C13)	LYT	rep1
911.9577	1821.8997	1823.1719	697.79	2	2.51	0.66	KIVSLDNHIALACAGLK : +57.05000 (C13)	LYK	rep3
701.6312	2101.8702	2100.2864	754.1	3	3.4	0.89	QLEEEEIDIIVAEIEAEK	LYK	rep3

Matching Genes:

NP_190694.1 (PAD1 (20S proteasome alpha subunit D1); peptidase [Arabidopsis thaliana])

Protein Group 251

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	5.41	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
851.2936	1700.5716	1700.9402	216.71	2	2.86	0.95	IVHHIVQELLGADEK	LYT	rep1
444.3831	1330.1257	1330.5409	312.04	3	1.24	0.29	PGAGGLMPGMPGTR : +32.00000 (M7)	LYK	rep2
476.7794	1427.3148	1427.4822	117.26	3	2.21	0.25	SRSTQPPPSGEER	LYK	rep3

Matching Genes:

NP_200595.2 (eukaryotic translation initiation factor 4F, putative / eIF-4F, putative [Arabidopsis thaliana])

Protein Group 252

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	10.74	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1447.2726	4338.7943	4339.8456	242.25	3	6.3	3.08	AAIRDPDPVVFLENELLYGESFPISEEALDSSFCLPIGK : +57.05000 (C 34)	LYK	rep3
1447.5355	4339.5831	4339.8456	60.49	3	3.69	1.86	AAIRDPDPVVFLENELLYGESFPISEEALDSSFCLPIGK : +57.05000 (C34)	LYT	rep1

Matching Genes:

NP_199898.1 (pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2) [Arabidopsis thaliana])

Protein Group 253

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.4	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
958.4034	2872.1869	2873.1719	342.83	3	1.88	0.51	MFNTEFNHIAGNPDLDLYPSHLQAK	LYK	rep2
1139.6205	3415.838	3417.6728	536.88	3	4.34	2.48	QHYYGSHPSINPFGIIPHGPNIDYTSPHDR	LYK	rep3
1139.7919	3416.3521	3417.6728	386.43	3	3.75	1.89	QHYYGSHPSINPFGIIPHGPNIDYTSPHDR	LYT	rep1

Matching Genes:

NP_001031671.1 (unknown protein [Arabidopsis thaliana])

Protein Group 254

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.64	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
817.5437	2449.6076	2449.9634	145.2	3	3.01	0.9	LVVRPMYSSPPIHGASIVATILK	LYK	rep2
743.5828	1485.1499	1485.6913	364.37	2	3.2	1.79	THYHQSVIYIPK	LYT	rep3
743.9848	1485.9539	1485.6913	176.77	2	2.86	1.07	THYHQSVIYIPK	LYK	rep2

Matching Genes:

NP_197456.1 (ASP2 (ASPARTATE AMINOTRANSFERASE 2) [Arabidopsis thaliana])

Protein Group 255

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	20.51	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1131.4762	3391.4051	3392.6567	368.92	3	6.21	3.61	ATFGITDHAQDHLGDVVYVELPDVGHSVSQGK	LYK	rep1
1131.5629	3391.6651	3392.6567	292.28	3	5.78	3.09	ATFGITDHAQDHLGDVVYVELPDVGHSVSQGK	LYT	rep3

Matching Genes:

NP_181057.1 (glycine cleavage system H protein, mitochondrial, putative [Arabidopsis thaliana])

Protein Group 256

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.98	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
948.2584	2841.7518	2842.1577	142.82	3	3.95	1.99	MVFAHGVDKEGHVVIYSSYGEFQNK	LYT	rep2
948.4161	2842.2249	2842.1577	23.66	3	2.55	0.32	MVFAHGVDKEGHVVIYSSYGEFQNK	LYK	rep1
552.7008	1655.0789	1654.777	182.49	3	2.24	0.47	VEEEKPAVPAAEEEK	LYT	rep1

Matching Genes:

NP_177360.1 (PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana])

Protein Group 257

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.14	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1145.1805	3432.5181	3433.8569	389.87	3	6.17	3.82	KGEDLFVEHTLSLTEALCGFQFVLTHLDGR : +57.05000 (C18)	LYK	rep3
1145.5131	3433.5157	3433.8569	99.37	3	3.17	1.49	KGEDLFVEHTLSLTEALCGFQFVLTHLDGR : +57.05000 (C18)	LYT	rep3

Matching Genes:

NP_189997.1 (ATJ3 (Arabidopsis thaliana DnaJ homologue 3))

Protein Group 258

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	13.95	19.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1305.45	2608.8843	2608.9162	12.24	2	1.96	0.43	FSPGSQIYIPVPTWSNHHNIWK	LYT	rep1
870.5988	2608.7728	2608.9162	54.99	3	1.57	0.55	FSPGSQIYIPVPTWSNHHNIWK	LYK	rep2
1061.2023	3180.5833	3181.4216	263.49	3	1.44	0.13	NAPEGSFFLLHACAHNPTGVDPTEEQWR : +57.05000 (C13)	LYK	rep2
669.9562	1337.8968	1338.4287	397.43	2	2.78	1.24	TYHYYHPETK	LYK	rep3
670.3858	1338.7559	1338.4287	244.46	2	2.32	0.78	TYHYYHPETK	LYT	rep3

Matching Genes:

NP_180654.1 (ASP1 (ASPARTATE AMINOTRANSFERASE 1) [Arabidopsis thaliana])

Protein Group 259

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.88	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
411.1826	1230.5242	1230.4017	99.54	3	2.86	1.07	LHFHDCFVR : +57.05000 (C6)	LYK	rep2
411.1906	1230.5482	1230.4017	119.03	3	2.63	1.1	LHFHDCFVR : +57.05000 (C6)	LYT	rep1
549.3276	1644.9594	1642.8857	1262.23	3	3.29	1.73	MGNLRPLTGTQGEIR	LYK	rep2
548.7224	1643.1438	1642.8857	157.06	3	2.83	1.24	MGNLRPLTGTQGEIR	LYT	rep1

Matching Genes:

NP_181372.1 (peroxidase 22 (PER22) (P22) (PRXEA) / basic peroxidase E [Arabidopsis thaliana])

Protein Group 260

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.08	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1047.3456	3139.0133	3138.5408	150.55	3	3.72	1.75	IPSSWVQYYTPLLAIQPPSGHDAADIVAK	LYK	rep1
1047.1942	3138.5592	3138.5408	5.86	3	1.19	0.14	IPSSWVQYYTPLLAIQPPSGHDAADIVAK	LYT	rep3
784.0262	2349.0553	2348.7461	131.64	3	2.4	0.5	KVPSFENVQIYNVISSILGLK	LYK	rep2
1175.3382	2348.6607	2348.7461	36.36	2	2.16	0.03	KVPSFENVQIYNVISSILGLK	LYT	rep1

Matching Genes:

NP_194697.1 (type I phosphodiesterase/nucleotide pyrophosphatase family protein [Arabidopsis thaliana])

Protein Group 261

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	39.39	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
800.8478	2399.5199	2399.8613	142.28	3	3.24	1.59	LLGDVTIANGGVMPNIHNLLLPK	LYT	rep1
801.0792	2400.2142	2399.8613	147.04	3	1.29	0.11	LLGDVTIANGGVMPNIHNLLLPK	LYK	rep1
958.7777	2873.3097	2872.2881	355.67	3	2.88	1.1	VGAGAPVYLAAVLEYLAAEVLELAGNAAR	LYK	rep3
958.25	2871.7265	2872.2881	195.51	3	1.26	0.28	VGAGAPVYLAAVLEYLAAEVLELAGNAAR	LYT	rep1

Matching Genes:

NP_175517.1 (histone H2A, putative [Arabidopsis thaliana])

Protein Group 262

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	16.57	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
514.0861	1539.2347	1539.7208	315.7	3	3.07	0.14	KDEHLIVACNAGGR : +57.05000 (C9)	LYT	rep1
839.891	1677.7664	1677.9253	94.69	2	3.05	1.25	SHVEEALNIPYMFK	LYT	rep1

Matching Genes:

NP_565497.3 (unknown protein [Arabidopsis thaliana])

Protein Group 263

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.96	3	0.71	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
724.3379	2169.9902	2169.4012	271.5	3	2.18	0.4	AQFLPLLDPDLMDGASDMR : +32.00000 (M12); +32.00000 (M18)	LYT	rep3
808.4923	2422.4535	2422.7021	102.63	3	2.53	0.33	ERAQFLPLLDPDLMDGASDMR : +32.00000 (M20)	LYT	rep2
809.1095	2424.305	2422.7021	661.62	3	2.35	0.23	ERAQFLPLLDPDLMDGASDMR : +32.00000 (M20)	LYK	rep1
613.6029	1837.7852	1839.0615	693.98	3	1.4	0.41	LLWAIDAHASELGVDTK	LYT	rep1

Matchi ng Genes:

NP_176883.3 (midasin-related [Arabidopsis thaliana])

Protein Group 264

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.94	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
349.784	1046.3285	1048.1974	1782.93	3	1.87	0.23	KLQQEQFK	LYK	rep3
773.5438	2317.608	2317.5627	19.53	3	1.77	0.31	LQQEQFKPAEQVTLEPFER	LYT	rep1
837.1767	1672.3377	1672.978	382.75	2	2.44	0.88	VIVEPHRHAGVFIAK	LYT	rep1

Matching Genes:

NP_567724.1 (FIB2 (FIBRILLARIN 2) [Arabidopsis thaliana])

Protein Group 265

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	3.07	16.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
876.6863	2627.0354	2627.9382	343.56	3	3.62	2.1	ESPYLTHPIFNMYHTEHELLR	LYK	rep2
876.8605	2627.5579	2627.9382	144.71	3	2.68	1.27	ESPYLTHPIFNMYHTEHELLR	LYT	rep3
709.0828	1416.1499	1416.6322	340.42	2	2.46	0.87	RLESHYPVLFR	LYT	rep2

709.105	1416.1944	1416.6322	309.06	2	2.15	0.68	RLESHYPVLFR	LYK	rep1

Matching Genes:

NP_180178.1 (glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative [Arabidopsis thaliana])

Protein Group 266

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	11.82	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
387.2678	1158.7798	1158.4199	310.68	3	2.5	0.84	LGMKPITGVSR	LYT	rep1
760.7918	1519.5679	1519.8321	173.86	2	3.57	1.48	NILFVISKPDVFK	LYT	rep3
760.9405	1519.8653	1519.8321	21.8	2	2.84	0.65	NILFVISKPDVFK	LYK	rep3

Matching Genes:

NP_187845.1 (nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative [Arabidopsis thaliana])

Protein Group 267

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	17.2	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1235.1532	3702.4361	3704.1645	466.62	3	6.01	4.07	TPNAVNPLVLGSFPLLTIDVWEHAYYLDFQNR	LYK	rep3
1235.9542	3704.8392	3704.1645	182.13	3	3.52	1.81	TPNAVNPLVLGSFPLLTIDVWEHAYYLDFQNR	LYT	rep3

Matching Genes:

NP_001031710.1 (FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase [Arabidopsis thaliana])

Protein Group 268

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.63	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
962.3597	2884.0557	2885.1596	382.61	3	2.37	0.82	CTGCELGGDSGVEPYTVAHNQLLAHAK : +57.05000 (C1); +57.0500 0 (C4)	LYT	rep2
962.4561	2884.3447	2885.1596	282.46	3	1.49	0.07	CTGCELGGDSGVEPYTVAHNQLLAHAK : +57.05000 (C1); +57.05000 (C4)	LYK	rep1
748.8181	1495.6206	1496.7179	733.09	2	3.56	1.81	IQNHCSHLSCLK : +57.05000 (C5); +57.05000 (C10)	LYK	rep2
749.3433	1496.6709	1496.7179	31.36	2	3.24	1.89	IQNHCSHLSCLK : +57.05000 (C5); +57.05000 (C10)	LYT	rep2

Matching Genes:

NP_175191.2 (glycosyl hydrolase family 1 protein [Arabidopsis thaliana])

Protein Group 269

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	9.8	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
801.6455	2401.913	2402.6775	318.16	3	2.64	0.86	KVYYAGLPDHPGHHLHFSQAK	LYK	rep3

842.1453	2523.4123	2522.7932	245.39	3	1.5	0.47	SVDAMNIKEEASVSTLLVNLDNK : +32.00000 (M5)	LYK	rep2
758.8932	2273.6561	2274.5044	372.96	3	1.78	0.55	VYYAGLPDHPGHHLHFSQAK	LYT	rep3
759.1058	2274.294	2274.5044	92.48	3	1.72	0.31	VYYAGLPDHPGHHLHFSQAK	LYK	rep3

Matching Genes:

NP_850712.1 (CBL (CYSTATHIONINE BETA-LYASE) [Arabidopsis thaliana])

Protein Group 270

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.23	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
362.2026	1083.5843	1083.2051	350.06	3	2.41	0.34	HFRPELER	LYK	rep1
362.2725	1083.7941	1083.2051	543.78	3	2.32	0.68	HFRPELER	LYT	rep3
1128.9161	3383.7249	3384.9121	350.72	3	3.51	1.78	LKPPFPANAGLYGCPTTVTNVETVAVSPTILR : +57.05000 (C14)	LYT	rep1
1128.963	3383.8656	3384.9121	309.17	3	2.28	0.58	LKPPFPANAGLYGCPTTVTNVETVAVSPTILR : +57.05000 (C14)	LYK	rep2

Matching Genes:

NP_196470.1 (NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial, putative [Arabidopsis thaliana])

Protein Group 271

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	23.53	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1177.5587	3529.6527	3530.9726	373.81	3	5.88	3.73	FQSHAVLALQEAAEAYLVGLFEDTNLCAIHAK : +57.05000 (C27)	LYT	rep3
1177.4254	3529.2528	3530.9726	487.07	3	5.61	3.37	FQSHAVLALQEAAEAYLVGLFEDTNLCAIHAK : +57.05000 (C27)	LYK	rep3

Matching Genes:

NP_001031816.1 (DNA binding [Arabidopsis thaliana])

Protein Group 272

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.42	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
736.9536	1471.8916	1472.5663	458.14	2	2.64	0.8	DAFVVYQGHHGDK	LYT	rep1
737.3644	1472.7132	1472.5663	99.76	2	2.29	0.38	DAFVVYQGHHGDK	LYK	rep2
1217.5831	3649.7259	3649.2121	140.79	3	3.21	1.17	DALAVVGDIIHQVKPDEIVGVAGQLSDAESMMVLK	LYK	rep3

Matching Genes:

NP_568550.1 (EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase [Arabidopsis thaliana])

Protein Group 273

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	10.16	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
478.2046	954.3936	954.0858	322.6	2	2.01	0.27	FFVGGNWK	LYT	rep1
541.0664	1620.1757	1618.7992	850.36	3	1.71	0.61	VASPQQAQEVHVAVR	LYK	rep1
540.6742	1618.9991	1618.7992	123.5	3	1.65	0.54	VASPQQAQEVHVAVR	LYT	rep3
549.2117	1096.4077	1096.2438	149.59	2	2.12	0.64	WVILGHSER	LYT	rep2

Matching Genes:

NP_179713.1 (TIM (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase [Arabidopsis thaliana])

Protein Group 274

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	16.04	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1005.696	2009.3763	2010.1366	378.25	2	3.98	1.62	ATYHFYNPAQNNWDLR	LYK	rep2
1005.825	2009.6343	2010.1366	249.87	2	3.7	1.2	ATYHFYNPAQNNWDLR	LYT	rep3
716.6957	2147.0636	2147.3334	125.65	3	1.85	0.59	AVSAYCSTWDADKPYAWR : +57.05000 (C6)	LYT	rep3
716.6066	2146.7962	2147.3334	250.15	3	1.25	0.14	AVSAYCSTWDADKPYAWR : +57.05000 (C6)	LYK	rep2

Matching Genes:

NP_187123.1 (PR4 (PATHOGENESIS-RELATED 4) [Arabidopsis thaliana])

Protein Group 275

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	0.96	3	14.02	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
689.377	2065.1074	2066.3871	619.28	3	1.97	0.39	CLADLCGALHCDFVLSSK : +57.05000 (C1); +57.05000 (C6); +57.05000 (C11)	LYK	rep3
651.0643	1950.1695	1952.2871	1084.65	3	1.59	0.42	CLADLCGALHCDFVLSSK : +57.05000 (C1)	LYK	rep1
771.1488	2310.4229	2310.5105	37.89	3	2.22	0.34	LVNEEVEVSNAPEIHCSRER	LYK	rep3
771.1617	2310.4618	2310.5105	21.09	3	1.97	0.16	LVNEEVEVSNAPEIHCSRER	LYT	rep2

Matching G enes:

NP_568969.1 (zinc finger (C2H2 type) family protein [Arabidopsis thaliana])

Protein Group 276

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.64	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
517.9293	1550.7645	1550.7234	26.51	3	3.55	1.17	HFHSLGAGVIEEVR	LYT	rep3
517.9103	1550.7074	1550.7234	10.33	3	2.48	0.68	HFHSLGAGVIEEVR	LYK	rep2
684.6554	2050.9427	2050.4238	253.07	3	2.21	0.67	MAGMNPMMHHPQGQHAFK	LYT	rep3

Matching Genes:

NP_564018.1 (UBP1B (OLIGOURIDYLATE BINDING PROTEIN 1B); mRNA 3'-UTR binding [Arabidopsis thaliana])

Protein Group 277

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	9.62	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
441.9328	1322.7749	1324.4636	1275	3	1.98	0.54	ATDNTLSLCSTAK	LYK	rep3
566.6642	1696.9691	1695.8406	665.46	3	3.75	1.75	KGDGTTHVFLHDVNR	LYT	rep3
566.6134	1696.8167	1695.8406	575.63	3	2.94	1. 06	KGDGTTHVFLHDVNR	LYK	rep2

Matching Genes:

NP_176901.1 (unknown protein [Arabidopsis thaliana])

Protein Group 278

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	15.29	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
756.6346	1511.2535	1511.6472	260.48	2	3.23	1.63	AVSLQGQHGPFQSR	LYT	rep1
795.3275	1588.6394	1588.7519	70.79	2	2.48	0.62	CQKEFQQSQHLR : +57.05000 (C1)	LYT	rep1

Matching Genes:

NP_194445.1 (2S seed storage protein 2 / 2S albumin storage protein / NWMU2-2S albumin 2 [Arabidopsis thaliana])

Protein Group 279

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	18.67	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1042.6127	3124.8145	3122.4153	768.4	3	5.71	3.85	EGEQVFGVVHIFASFNDTFIHVTDLSGR	LYK	rep3
1042.0841	3123.2288	3122.4153	260.56	3	2.47	0.99	EGEQVFGVVHIFASFNDTFIHVTDLSGR	LYT	rep3

Matching Genes:

NP_181158.1 (40S ribosomal protein S14 (RPS14A) [Arabidopsis thaliana])

Protein Group 280

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	9.83	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
483.5424	1447.6036	1447.7692	114.35	3	1.5	0.19	FLKPSVAGFLLQK	LYK	rep1
483.7423	1448.2035	1447.7692	299.98	3	1.22	0.36	FLKPSVAGFLLQK	LYT	rep3
791.3812	2371.1202	2370.707	174.29	3	1.89	0.28	GVSLLLPTDVVIADKFAPDANSK	LYK	rep1
611.0755	1220.1353	1220.4695	273.81	2	2.3	0.77	VILSTHLGRPK	LYK	rep2
611.0091	1220.0025	1220.4695	382.63	2	1.9	0.57	VILSTHLGRPK	LYT	rep2

Matching Genes:

NP_176015.1 (phosphoglycerate kinase, putative [Arabidopsis thaliana])

Protein Group 281

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	26.15	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1439.0555	4314.1431	4315.6841	357.05	3	2.24	0.56	LHSHDVPYGSGSGQQSVTGFPGVVDSNSYWIVKPVPGTTEK	LYK	rep3
940.5288	1879.042	1879.0459	2.05	2	3.43	1.84	LQHIDTSGYLHSHDKK	LYK	rep2
940.5677	1879.1197	1879.0459	39.26	2	3.36	1.56	LQHIDTSGYLHSHDKK	LYT	rep3

Matching Genes:

NP_565585.1 (MIR domain-containing protein [Arabidopsis thaliana])

Protein Group 282

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	15.31	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
824.3174	2469.9287	2470.6392	287.59	3	1.31	0.48	ATPGHTAGCVTYVTGEGADQPQPR : +57.05000 (C9)	LYT	rep1
764.63	2290.8665	2291.6382	336.72	3	4.35	2.34	LIYAMNTHVHADHVTGTGLLK	LYK	rep2
764.5751	2290.7017	2291.6382	408.63	3	3.57	2	LIYAMNTHVHADHVTGTGLLK	LYT	rep3

Matching Genes:

NP_564636.2 (ETHE1/GLX2-3 (GLYOXALASE 2-3); hydroxyacylglutathione hydrolase [Arabidopsis thaliana])

Protein Group 283

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.11	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
830.4761	2488.4047	2487.8987	203.42	3	3.69	1.83	EVIELPIKHPELFESLGIAQPK	YT	rep3
1244.4417	2486.8677	2487.8987	414.39	2	2.23	0.6	EVIELPIKHPELFESLGIAQPK	LYK	rep2
814.5302	1627.0447	1627.8077	468.74	2	1.96	0.59	QYYLQHIHELQR	LYT	rep1
543.5741	1627.6988	1627.8077	66.91	3	1.43	0.12	QYYLQHIHELQR	LYK	rep1

Matching Genes:

NP_568389.1 (ATSUG1; ATPase [Arabidopsis thaliana])

Protein Group 284

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.98	3	23.38	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1311.2103	3930.6075	3931.4197	206.58	3	2.01	0.32	DMGDSISGKGMIQGVSAVGAFYQLLSQSSLSILPSEEK	LYT	rep1
990.8812	2969.6202	2971.3628	586.48	3	2.04	0.43	FLRQPHFIVWDNSDLVTHEVMGGLK : +32.00000 (M21)	LYK	rep3
1626.629	4876.8636	4878.4933	334.06	3	1.55	0.52	NVYAIGAGMVAALTNESATSKSVYFAHCTSEMIFITHLLAEEPEK : +32.00000 (M9)	LYT	rep2

Matching Genes:

NP_001031525.1 (GPDHC1; glycerol-3-phosphate dehydrogenase (NAD+) [Arabidopsis thaliana])

Protein Group 285

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	11.3	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
481.132	960.2483	960.0455	211.31	2	1.48	0.32	DIVDAHYK	LYK	rep1
480.881	959.7463	960.0455	311.66	2	1.44	0.19	DIVDAHYK	LYT	rep3
1139.8427	3416.5045	3417.7712	370.63	3	4.11	2.22	ITEISGVIVSFDPKPVPGDWNGAGAHCNYSTK : +57.05000 (C27)	LYT	rep3

Matching Genes:

NP_188409.1 (ATGSKB6 (Arabidopsis thaliana glutamine synthase clone KB6); glutamate-ammonia ligase)

Protein Group 286

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	15.29	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
705.8667	1409.7178	1409.5898	90.79	2	1.68	0.29	DIESALLDHLGVK	LYT	rep1
692.1209	1382.2261	1382.6124	279.4	2	1.56	0.47	TLLGEPKPPQFR	LYT	rep1
692.4445	1382.8733	1382.6124	188.71	2	1.36	0.01	TLLGEPKPPQFR	LYK	rep2

861.1658	1720.316	1721.0819	445.02	2	2.34	0.84	YHLLVCGTTPCMIR : +57.05000 (C6); +57.05000 (C11)	LYT	rep1

Matching Genes:

NP_567244.1 (NADH-ubiquinone oxidoreductase 24 kDa subunit, putative [Arabidopsis thaliana])

Protein Group 287

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	4.93	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1220.6049	3658.7911	3660.045	342.59	3	1.99	0.51	LVGRLSQEELMDQLSSFLPAVFEAFGSQSADVR : +32.00000 (M11)	LYT	rep3
572.0276	1713.0593	1714.922	1086.17	3	2.14	0.67	NGGLGLSDIITQIQASK	LYK	rep3
807.8771	2420.6077	2419.72	366.87	3	1.45	0.29	SVDLYEDLIRCCVADAMSEVR : +32.00000 (M17)	LYK	rep3

Matching Genes:

NP_849997.2 (CLIP-associating protein (CLASP) -related [Arabidopsis thaliana])

Protein Group 288

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	16.39	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1045.8128	2089.6099	2090.2834	322.22	2	2.72	1.35	NLEAWGGLMGPGYNYYER	LYT	rep2

731.6193	1461.2229	1461.6233	273.9	2	2.83	1.06	VYDKYGDYIGIR	LYT	rep2
488.6037	1462.7876	1461.6233	796.61	3	2.5	0.49	VYDKYGDYIGIR	LYK	rep1

Matching Genes:

NP_565527.1 (lipid-associated family protein [Arabidopsis thaliana])

Protein Group 289

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.23	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1069.704	3206.0885	3206.6484	174.63	3	5.55	3.39	WGSNAFHNMLVVPPGSGIVHQVNLEYLAR	LYK	rep1
1069.9293	3206.7645	3206.6484	36.19	3	4.39	1.77	WGSNAFHNMLVVPPGSGIVHQVNLEYLAR	LYT	rep3

Matching Genes:

NP_195308.1 (aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) [Arabidopsis thaliana])

Protein Group 290

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.11	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
647.3627	1939.0645	1939.2947	118.71	3	2.45	1.04	GQIHVEHMCSNALAMIK : +57.05000 (C9)	LYT	rep1

1227.6268	3679.857	3680.0272	46.23	3	3.06	1.5	TALHDCLETIDETLDELHETVEDLHLYPTKK : +57.05000 (C6)	LYT	rep1

Matching Genes:

NP_188048.1 (ATPME3 (Arabidopsis thaliana pectin methylesterase 3))

Protein Group 291

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	14.21	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
559.5935	1117.1714	1117.2865	102.99	2	1.67	0.49	FMQLTNAHR	LYK	rep2
759.0315	1516.0474	1516.7303	450.27	2	2.5	1.21	FMQLTNAHRGDVK	LYT	rep1
714.2483	1426.481	1426.5342	37.28	2	1.34	0. 35	TYATASAQTTANVK	LYT	rep2

Matching Genes:

NP_001031875.1 (ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative [Arabidopsis thaliana])

Protein Group 292

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.14	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
701.3434	2101.0067	2101.3257	151.81	3	2.93	1.35	GHYTEGAELIDSVLDVVRK	LYK	rep1
701.4745	2101.4	2101.3257	35.37	3	1.15	0.08	GHYTEGAELIDSVLDVVRK	LYT	rep1

934.0017	2798.9817	2799.0312	17.72	3	2.54	0.85	SGPFGQIFRPDNFVFGQSGAGNNWAK	LYT	rep3

Matching Genes:

NP_193821.1 (TUB9 (tubulin beta-9 chain); structural molecule [Arabidopsis thaliana])

Protein Group 293

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.16	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1234.8187	3701.4327	3702.3249	240.99	3	5.46	3.25	HGLIPVFPTMTFPNHYSIATGLYPAYHGIIMNK	LYK	rep3
1235.2714	3702.7906	3702.3249	125.78	3	3.72	1.94	HGLIPVFPTMTFPNHYSIATGLYPAYHGIIMNK	LYT	rep2

Matching Genes:

NP_194699.1 (type I phosphodiesterase/nucleotide pyrophosphatase family protein [Arabidopsis thaliana])

Protein Group 294

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.8	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
752.9806	2255.9183	2256.4827	250.11	3	2.44	0.79	GFTQTFEINHLNGEHVVSVK	LYK	rep2
752.8191	2255.4338	2256.4827	464.82	3	1.66	0.3	GFTQTFEINHLNGEHVVSVK	LYT	rep3
569.3887	1705.1425	1705.0135	75.66	3	2.98	1.15	KVYYVTFSPVSISHIK	LYT	rep1

569.5001	1705.4769	1705.0135	271.76	3	2.6	0.97	KVYVTFSPVSISHIK	LYK	rep1

Matching Genes:

NP_180168.1 (jacalin lectin family protein [Arabidopsis thaliana])

Protein Group 295

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	15.62	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
666.4397	1996.2956	1996.2284	33.68	3	1.92	0.46	SSVLMDVKPWDDETDMK	LYT	rep3
931.1346	1860.2535	1861.1103	460.42	2	3.49	1.67	VYAAVPVKPSDAFPNASK	LYK	rep3
931.3763	1860.7369	1861.1103	200.68	2	2.5	1.22	VYAAVPVKPSDAFPNASK	LYT	rep1

Matching Genes:

NP_568375.2 (elongation factor 1B alpha-subunit 2 (eEF1Balpha2) [Arabidopsis thaliana])

Protein Group 296

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.95	3	12.43	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
947.1343	2838.3794	2838.2104	59.52	3	1.69	0.45	DSLRGFMDLANDNLPAPFFTLNQLK	LYK	rep1
517.5482	1033.0808	1032.223	831.06	2	1.17	0.35	LNCRVVNSK	LYT	rep2

607.0564	1212.0972	1211.3754	595.87	2	2.52	1.01	NQCQFIMDR : +57.05000 (C3)	LYT	rep2
606.3299	1210.6441	1211.3754	603.7	2	1.6	0.58	NQCQFIMDR : +57.05000 (C3)	LYK	rep2

Matching Genes:

NP_192617.1 (peroxidase, putative [Arabidopsis thaliana])

Protein Group 297

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	5.62	21.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
437.051	1308.1296	1307.4625	510.22	3	2.84	1.16	KGYVGIHSSGFR	LYK	rep2
654.6848	1307.354	1307.4625	82.96	2	2.42	0.91	KGYVGIHSSGFR	LYT	rep1
711.6817	1421.3477	1421.6919	242.1	2	2.53	1.17	LTLHGLVQHYIK	LYT	rep1
475.0193	1422.0344	1421.6919	240.91	3	2.52	0.95	LTLHGLVQHYIK	LYK	rep2

Matching Genes:

NP_568244.1 (DEAD/DEAH box helicase, putative (RH15) [Arabidopsis thaliana])

Protein Group 298

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.73	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

777.9296	2330.7652	2331.425	283.01	3	5.35	3.21	FNFSHGSHEYHQETLDNLR	LYT	rep1
778.2279	2331.6602	2331.425	100.88	3	5.25	2.72	FNFSHGSHEYHQETLDNLR	LYK	rep3

Matching Genes:

NP_196474.1 (pyruvate kinase, putative [Arabidopsis thaliana])

Protein Group 299

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	9.11	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
777.7306	2330.1683	2330.4971	141.07	3	3.2	1.06	AFVHWYVGEGMEEGEFSEAR	LYT	rep3
795.9659	2384.8744	2385.6003	304.32	3	2.12	0.73	QLFHPEQLISGKEDAANNFAR	LYK	rep1
796.0156	2385.0234	2385.6003	241.84	3	1.81	0.6	QLFHPEQLISGKEDAANNFAR	LYT	rep2

Matching Genes:

NP_171974.1 (TUA4 (tubulin alpha-4 chain) [Arabidopsis thaliana])

Protein Group 300

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	16.88	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1010.85	3029.5264	3028.3418	391.19	3	5.2	2.8	WAIENLADKGDTIYIIHTLPLSGDESR	LYT	rep1

1010.3279	3027.9602	3028.3418	126.02	3	4.7	2.8	WAIENLADKGDTIYIIHTLPLSGDESR	LYK	rep2

Matching Genes:

NP_566991.2 (universal stress protein (USP) family protein [Arabidopsis thaliana])

Protein Group 301

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	32.9	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1080.7748	3239.3009	3240.4164	344.27	3	1.86	0.25	AGACSTCAGQIVSGNVDQSDGSFLEDSHLEK : +57.05000 (C4); +57 .05000 (C7)	LYT	rep1
1080.8876	3239.6392	3240.4164	239.84	3	1.82	0.61	AGACSTCAGQIVSGNVDQSDGSFLEDSHLEK : +57.05000 (C4); +57.05000 (C7)	LYK	rep2
1175.4651	2348.9146	2348.6638	106.78	2	3.32	1.54	GYVLTCVAYPQSDCVIHTHK : +57.05000 (C6); +57.05000 (C14)	LYK	rep3
783.7561	2348.2448	2348.6638	178.39	3	3.08	1.29	GYVLTCVAYPQSDCVIHTHK : +57.05000 (C6); +57.05000 (C14)	LYT	rep1

Matching Genes:

NP_180320.1 (ATFD3 (FERREDOXIN 3); electron carrier [Arabidopsis thaliana])

Protein Group 302

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.63	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
480.7554	1439.2426	1438.5718	466.33	3	1.7	0.52	HYNKDFGIECR : +57.05000 (C10)	LYT	rep2
775.7342	1549.4527	1549.8248	240.12	2	3.35	1.76	KLPIHHIPGPEGVR	LYK	rep3
775.9152	1549.8147	1549.8248	6.51	2	2.52	1.08	KLPIHHIPGPEGVR	LYT	rep3

Matching Genes:

NP_198236.1 (GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD binding / catalytic [Arabidopsis thaliana])

Protein Group 303

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.43	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1152.9747	3455.9007	3457.9216	584.43	3	3.34	1.39	KGDALLFFNLHPDAIPDPLSLHGGCPVIEGEK : +57.05000 (C25)	LYK	rep3
487.0735	1458.197	1457.5069	473.44	3	1.67	0.62	YDAHFDYFHDK	LYK	rep2
729.4446	1456.8736	1457.5069	434.56	2	1.08	0.17	YDAHFDYFHDK	LYT	rep3

Matching Genes:

NP_197391.1 (oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana])

Protein Group 304

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	15.27	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
774.7839	2321.3283	2321.6612	143.39	3	4.99	2.75	KPWQITGPCAHPEYLEAVPK : +57.05000 (C9)	LYK	rep3
774.8029	2321.3851	2321.6612	118.94	3	4.31	2.5	KPWQITGPCAHPEYLEAVPK : +57.05000 (C9)	LYT	rep3

Matching Genes:

NP_196423.1 (unknown protein [Arabidopsis thaliana])

Protein Group 305

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	13.41	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
615.4823	1228.949	1229.4186	381.93	2	1.9	0.88	GMPHKFYHGR	LYT	rep1
410.9266	1229.7562	1229.4186	274.67	3	1.3	0.28	GMPHKFYHGR	LYK	rep1
744.6833	1487.3509	1487.672	215.85	2	3.02	1.65	IHVRVEHVQQSR	LYT	rep1
497.1914	1488.5507	1487.672	590.69	3	2.26	0.79	IHVRVEHVQQSR	LYK	rep2

Matching Genes:

NP_563847.1 (60S ribosomal protein L21 (RPL21A) [Arabidopsis thaliana])

Protein Group 306

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	16.96	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1006.7776	2011.5396	2012.1742	315.4	2	4.85	2.67	VGVHHYNGNNVDLGTACGK : +57.05000 (C17)	LYK	rep3
671.9629	2012.8652	2012.1742	343.39	3	3.24	1.67	VGVHHYNGNNVDLGTACGK : +57.05000 (C17)	LYT	rep3

Matching Genes:

NP_565164.1 (60S ribosomal protein L30 (RPL30B) [Arabidopsis thaliana])

Protein Group 307

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.88	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1458.1923	4371.5533	4373.0563	343.69	3	1.76	0.51	INYYPPCPRPDLALGVPAHTDLSGITLLVPNEVPGLQVFK : +57.05000 (C7)	LYK	rep2
437.4095	1309.205	1308.4953	542.32	3	3.07	0.65	KAWVDHLFHR	LYK	rep2
437.2184	1308.6317	1308.4953	104.19	3	3.06	0.68	KAWVDHLFHR	LYT	rep1

Matching Genes:

NP_196481.1 (FLS (FLAVONOL SYNTHASE) [Arabidopsis thaliana])

Protein Group 308

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	5.51	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
439.4747	1315.4007	1315.5261	95.32	3	2.17	1.02	APIETAVKPPHR	LYT	rep1
658.6872	1315.3587	1315.5261	127.27	2	1.81	0.52	APIETAVKPPHR	LYK	rep1
655.6823	1964.0233	1964.2793	130.32	3	2.63	0.74	MVCAQAANANPLYLHYK : +57.05000 (C3)	LYT	rep1

Matching Genes:

NP_194713.1 (MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase [Arabidopsis thaliana])

Protein Group 309

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	10.14	22.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
398.9938	1193.9578	1193.3196	534.88	3	2.37	1.18	HATFVPHTAGR	LYK	rep1
399.1562	1194.4451	1193.3196	943.19	3	2.25	1.09	HATFVPHTAGR	LYT	rep2
387.6208	1159.8391	1159.3883	388.81	3	2.42	0.61	LTNSLMMHGR	LYT	rep1

Matching Genes:

NP_001031502.1 (ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 310

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.7	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1032.2652	2062.5147	2063.3303	395.3	2	4.77	3.06	GSGGGRPHALPIFLYAQGHK	LYT	rep2
1032.2232	2062.4307	2063.3303	436	2	4.14	2.4	GSGGGRPHALPIFLYAQGHK	LYK	rep3

Matching Genes:

NP_568483.1 (meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana])

Protein Group 311

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.37	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
678.1438	2031.4079	2031.3284	39.17	3	2.77	1.31	HNIGLPLQFAAAFSFNRK	LYK	rep1
678.1957	2031.5636	2031.3284	115.79	3	1.77	0.69	HNIGLPLQFAAAFSFNRK	LYT	rep3
750.068	1498.1204	1498.7502	420.21	2	1.98	0.67	VASVKPFGACFSTK : +57.05000 (C10)	LYK	rep2
750.0711	1498.1265	1498.7502	416.13	2	1.61	0.26	VASVKPFGACFSTK : +57.05000 (C10)	LYT	rep2

Matching Genes:

NP_563679.1 (extracellular dermal glycoprotein, putative / EDGP, putative [Arabidopsis thaliana])

Protein Group 312

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.98	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1211.9781	3632.911	3635.1418	613.69	3	4.73	2.41	IVGFHGSSSDLIHSVGVYIIPSTTPLTPPVSGGLTK	LYK	rep3
1212.2604	3633.7577	3635.1418	380.78	3	3.79	2.02	IVGFHGSSSDLIHSVGVYIIPSTTPLTPPVSGGLTK	LYT	rep3

Matching Genes:

NP_001030712.1 (JR1 (Jacalin lectin family protein) [Arabidopsis thaliana])

Protein Group 313

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.13	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
545.4691	1088.9226	1089.2976	344.21	2	2.98	1.03	RFLHVVYR	LYT	rep3
545.5594	1089.1031	1089.2976	178.59	2	2.5	0.59	RFLHVVYR	LYK	rep1
786.8283	1571.6409	1570.7927	539.98	2	1.74	0.36	SGEVIKIVNQELGGK	LYT	rep1
786.8592	1571.7027	1570.7927	579.3	2	1.64	0.61	SGEVIKIVNQELGGK	LYK	rep2

Matching Genes:

NP_001031025.1 (ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase [Arabidopsis thaliana])

Protein Group 314

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.26	19.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1003.0231	2004.0306	2005.2477	606.97	2	4.68	2.82	YFLHQHTIQHGQPATVK	LYK	rep3
669.434	2005.2784	2005.2477	15.33	3	4.06	2.42	YFLHQHTIQHGQPATVK	LYT	rep2

Matching Genes:

NP_001031759.1 (PBA1 (20S proteasome beta subunit A 1); peptidase [Arabidopsis thaliana])

Protein Group 315

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	14.44	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1031.5214	3091.5406	3090.5708	313.8	3	2.84	1.4	GVMDQTVGEGTHFLIPILQRPHIFDIR	LYK	rep2
1031.1693	3090.4845	3090.5708	27.93	3	2.38	0.67	GVMDQTVGEGTHFLIPILQRPHIFDIR	LYT	rep2
464.556	1390.6446	1390.5466	70.47	3	1.83	0.58	TKPHTFSSISGTK	LYT	rep1
696.1021	1390.1885	1390.5466	257.53	2	1.76	0.5	TKPHTFSSISGTK	LYK	rep2

Matching Genes:

NP_198893.1 (ATPHB3 (PROHIBITIN 3) [Arabidopsis thaliana])

Protein Group 316

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.55	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
691.6854	2072.0328	2072.1599	61.34	3	4.66	2.65	HFQNEPDGDGTSAVHVYAK	LYT	rep3
691.4933	2071.4564	2072.1599	339.51	3	3.54	1.97	HFQNEPDGDGTSAVHVYAK	LYK	rep2

Matching Genes:

NP_191872.1 (RANGAP1 (RAN GTPASE ACTIVATING PROTEIN 1); RAN GTPase activator [Arabidopsis thaliana])

Protein Group 317

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	23.53	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1147.2169	3438.6273	3438.8303	59.05	3	4.56	2.51	FQSSAVAALQEAAEAYLVGLFEDTNLCAIHAK : +57.05000 (C27)	LYT	rep1
1147.1732	3438.4962	3438.8303	97.17	3	4.24	2.08	FQSSAVAALQEAAEAYLVGLFEDTNLCAIHAK : +57.05000 (C27)	LYK	rep3

Matching Genes:

NP_189372.1 (histone H3 [Arabidopsis thaliana])

Protein Group 318

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.97	2	20.16	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

455.6441	1363.9088	1363.5212	284.27	3	2.48	0.5	AGLEEPLEQIHK	LYT	rep1
455.7327	1364.1747	1363.5212	479.26	3	1.99	0.29	AGLEEPLEQIHK	LYK	rep2
498.1592	1491.4541	1491.5899	91.04	3	2.07	0.47	KAPCGEGTNTWDR : +57.05000 (C4)	LYT	rep1
746.4355	1490.8553	1491.5899	492.49	2	1.98	0.63	KAPCGEGTNTWDR : +57.05000 (C4)	LYK	rep3

Matching Genes:

NP_001078781.1 (40S ribosomal protein S20 (RPS20C) [Arabidopsis thaliana])

Protein Group 319

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.98	3	9.38	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
731.6004	1461.1851	1460.5358	444.59	2	1.5	0.48	PPGSGSTMNGQSANR	LYK	rep3
731.6336	1461.2515	1460.5358	490.06	2	1.23	0.3	PPGSGSTMNGQSANR	LYT	rep1
403.4691	1207.3839	1208.266	730.04	3	1.68	0.3	QMSSSNGVGPGR : +32.00000 (M2)	LYT	rep2
1318.8934	3953.6568	3955.2715	408.23	3	1.35	0.44	SFLSSLRSILSSPSQSFVLSSPSDSSDIFDFSSFHR	LYT	rep3

Matching Genes:

NP_973512.1 (unknown protein [Arabidopsis thaliana])

Protein Group 320

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	7.27	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
808.1221	1614.2286	1614.8536	387.08	2	2.9	1.28	GLLLVDHQLAHDKR	LYK	rep3
539.1129	1614.3153	1614.8536	333.38	3	1.93	0.76	GLLLVDHQLAHDKR	LYT	rep3
420.9929	1259.9551	1259.4211	423.98	3	1.61	0.28	HKNTAFSWLR	LYT	rep2

Matching Genes:

NP_567641.1 (PRXR1 (peroxidase 42); peroxidase [Arabidopsis thaliana])

Protein Group 321

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	2	7.81	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
556.3175	1110.6194	1111.3234	633.42	2	1.88	0.75	HAMVASGALVR	LYT	rep1
556.3272	1110.6387	1111.3234	616.06	2	1.57	0.73	HAMVASGALVR	LYK	rep2
421.1401	1260.3969	1260.4708	58.61	3	2.61	0.23	HRTLMNVFDK	LYT	rep1

Matching Genes:

NP_001078808.1 (GAMMA CA3 (GAMMA CARBONIC ANHYDRASE 3) [Arabidopsis thaliana])

Protein Group 322

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.92	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
965.7567	2894.2467	2895.2368	341.99	3	4.49	2.36	DFGSIDILVHSLANGPEVSKPLLETSR	LYK	rep1
965.8851	2894.6319	2895.2368	208.92	3	1.9	0.42	DFGSIDILVHSLANGPEVSKPLLETSR	LYT	rep1

Matching Genes:

NP_565331.1 (MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase [Arabidopsis thaliana])

Protein Group 323

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	16.67	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1206.5634	3616.6666	3615.9097	209.33	3	4.48	1.09	HTGPGFLSMANAGQDTNGSQFFITTVTTSWLDGR	LYT	rep1
1206.4965	3616.4659	3615.9097	153.83	3	1.94	0.59	HTGPGFLSMANAGQDTNGSQFFITTVTTSWLDGR	LYK	rep1

Matching Genes:

NP_200679.1 (ROC7 (rotamase CyP 7); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana])

Protein Group 324

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.6	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
750.4999	2248.4762	2248.5947	52.73	3	4.48	2.9	HAVGLVRPVSVAFEVVHEFR	LYT	rep3
750.4757	2248.4036	2248.5947	84.97	3	3.99	2.26	HAVGLVRPVSVAFEVVHEFR	LYK	rep1

Matching Genes:

NP_001030812.1 (cysteine-type peptidase [Arabidopsis thaliana])

Protein Group 325

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.88	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1262.434	3784.2784	3784.3176	10.36	3	4.43	2.06	SIGNIVTGDDLQTQCVISHGALLSLLSLLTHNHKK : +57.05000 (C15)	LYK	rep2
1261.9784	3782.9117	3784.3176	371.51	3	3.26	1.33	SIGNIVTGDDLQTQCVISHGALLSLLSLLTHNHKK : +57.05000 (C15)	LYT	rep3

Matching Genes:

NP_567485.1 (importin alpha-2, putative (IMPA-2) [Arabidopsis thaliana])

Protein Group 326

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	3.44	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

795.7162	2384.1251	2384.74	257.85	3	2.57	0.8	KIHLSLVANPSHLEAADSVVVGK	LYK	rep1
733.3634	1464.7112	1465.5753	589.59	2	1.85	0.22	YHLGTSYDRPTR	LYT	rep3
733.4788	1464.9419	1465.5753	432.17	2	1.8	0.48	YHLGTSYDRPTR	LYK	rep2

Matching Genes:

NP_191101.2 (2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative [Arabidopsis thaliana])

Protein Group 327

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	20.49	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
436.2758	1305.804	1305.4849	244.45	3	2.35	0.78	AGLEAPLEQIHK	LYT	rep1
498.1592	1491.4541	1491.5899	91.04	3	2.07	0.47	KAPCGEGTNTWDR : +57.05000 (C4)	LYT	rep1
746.4355	1490.8553	1491.5899	492.49	2	1.98	0.63	KAPCGEGTNTWDR : +57.05000 (C4)	LYK	rep3

Matching Genes:

NP_001030826.1 (structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 328

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.71	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
876.6885	2627.042	2627.918	333.35	3	4.42	2.21	SHGGLSYGQNGSHFEPKPVPPPIPK	LYK	rep3
876.9548	2627.841	2627.918	29.27	3	2.23	1.12	SHGGLSYGQNGSHFEPKPVPPPIPK	LYT	rep1

Matching Genes:

NP_172853.1 (protein kinase family protein / ankyrin repeat family protein [Arabidopsis thaliana])

Protein Group 329

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.31	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
904.6994	1807.3831	1806.943	243.57	2	4.42	2.77	GAHEGQGLGNNFLSHIR	LYK	rep1
603.4572	1807.348	1806.943	224.14	3	3.01	1.54	GAHEGQGLGNNFLSHIR	LYT	rep3

Matching Genes:

NP_174346.1 (GTP binding [Arabidopsis thaliana])

Protein Group 330

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	23.15	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
464.1771	1389.5079	1389.6449	98.58	3	2.2	0.65	FKLITPSILSDR	LYT	rep1

746.5381	1491.0606	1491.6777	413.72	2	2.2	0.9	MVAAHSSQQIYTR	LYT	rep1
498.4421	1492.3029	1491.6777	419.14	3	1.23	0.37	MVAAHSSQQIYTR	LYK	rep1

Matching Genes:

NP_195631.1 (40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana])

Protein Group 331

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	18.75	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1110.2872	3327.8382	3328.7508	274.14	3	4.4	2.36	NHPHGFVAKPETGQDGTVNLMVWHCTIPGK : +57.05000 (C25)	LYK	rep1
1110.4364	3328.2857	3328.7508	139.7	3	4.1	2.2	NHPHGFVAKPETGQDGTVNLMVWHCTIPGK : +57.05000 (C25)	LYT	rep3

Matching Genes:

NP_191346.1 (AHUS5 (EMBRYO DEFECTIVE 1637); ubiquitin-protein ligase [Arabidopsis thaliana])

Protein Group 332

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.92	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1057.2782	3168.8111	3169.6168	254.2	3	4.38	2.18	HDVTEPLLIEVDQIYHLACPASPIFYK : +57.05000 (C19)	LYT	rep3

1057.5922	3169.753	3169.6168	42.96	3	2.89	1.4	HDVTEPLLIEVDQIYHLACPASPIFYK : +57.05000 (C19)	LYK	rep1

Matching Genes:

NP_001030820.1 (UXS5 (UDP-Xyl synthase 5); catalytic [Arabidopsis thaliana])

Protein Group 333

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	14.5	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
994.939	1987.8623	1988.1659	152.67	2	4.33	2.12	DFEEAGHLAPTGLFLGGEK	LYT	rep1
994.809	1987.6023	1988.1659	283.45	2	3.78	1.84	DFEEAGHLAPTGLFLGGEK	LYK	rep2

Matching Genes:

NP_194664.1 (PFN2/PRF2/PRO2 (PROFILIN 2); actin binding / protein binding [Arabidopsis thaliana])

Protein Group 334

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	2	23.36	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
464.1771	1389.5079	1389.6449	98.58	3	2.2	0.65	FKLITPSILSDR	LYT	rep1
503.558	1507.6505	1507.6771	17.67	3	2.07	0.64	MVSAHSSQQIYTR	LYT	rep1

Matching Genes:

NP_001031390.1 (structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 335

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	3	4.21	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
661.2476	1320.4795	1320.5816	77.33	2	1.55	0.49	KIPCSSDICLK : +57.05000 (C4); +57.05000 (C9)	LYT	rep1
686.8297	1371.6438	1373.5161	1363.12	2	1.41	0.35	LLYVGPPNETDR	LYT	rep2
1074.7969	2147.5782	2149.5666	925.03	2	1.3	0.4	PPSGILMFGPPGCSKTLMAR : +32.00000 (M7); +57.05000 (C13)	LYT	rep3

Matching Genes:

NP_191228.1 (CIP111 (CAM INTERACTING PROTEIN 111); ATPase/ calmodulin binding [Arabidopsis thaliana])

Protein Group 336

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	17.69	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1433.8414	4298.5008	4299.7083	280.82	3	2.02	0.86	RPYGVGLLVGGLDESGAHLYYNCPSGNYFEYQAFAIGSR : +57.05000 (C23)	LYT	rep3
564.0415	1126.0674	1126.3333	236.03	2	2.18	0.9	SHVVLACVNK : +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_175158.1 (PAF2 (20S proteasome alpha subunit F2); peptidase [Arabidopsis thaliana])

Protein Group 337

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	10.43	18.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
608.4355	1214.8553	1213.389	1208.38	2	4.19	2.22	GKDLAELIAAGR	LYK	rep3
607.7156	1213.4156	1213.389	21.87	2	3.92	1.75	GKDLAELIAAGR	LYT	rep3

Matching Genes:

NP_180339.1 (60S acidic ribosomal protein P2 (RPP2B) [Arabidopsis thaliana])

Protein Group 338

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	6.95	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
684.7163	1367.417	1366.4469	709.97	2	1.94	0.53	FNNHHTVNDIR	LYK	rep1
398.6086	1192.8023	1192.4429	301.41	3	2.24	0.6	RAPVHVNLMR	LYK	rep1
398.4753	1192.4025	1192.4429	33.8	3	2.14	0.79	RAPVHVNLMR	LYT	rep2

Matching Genes:

NP_193946.1 (PUX3 (LANT UBX DOMAIN-CONTAINING PROTEIN 3) [Arabidopsis thaliana])

Protein Group 339

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.47	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
781.658	1561.3003	1561.811	326.99	2	4.16	2.5	MHSSHLLLEEPIR	LYT	rep1
521.6132	1561.816	1561.811	3.19	3	3.34	1.46	MHSSHLLLEEPIR	LYK	rep2

Matching Genes:

NP_565850.1 (pyruvate kinase, putative [Arabidopsis thaliana])

Protein Group 340

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.59	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
662.8531	1985.536	1986.1182	293.12	3	4.15	2.36	FVLTTHHHWDHAGGNEK	LYK	rep2
662.9208	1985.7389	1986.1182	190.98	3	3.6	1.47	FVLTTHHHWDHAGGNEK	LYT	rep3

Matching Genes:

NP_187696.1 (GLX2-2 (GLYOXALASE 2-2); hydroxyacylglutathione hydrolase [Arabidopsis thaliana])

Protein Group 341

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.32	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
616.025	1845.0516	1844.0902	521.31	3	4.11	2.29	HLNFFAVSAAPCGHCR : +57.05000 (C12); +57.05000 (C15)	LYK	rep1
616.0172	1845.0282	1844.0902	508.6	3	3.67	1.96	HLNFFAVSAAPCGHCR : +57.05000 (C12); +57.05000 (C15)	LYT	rep1

Matching Genes:

NP_179547.1 (CDA1 (CYTIDINE DEAMINASE 1) [Arabidopsis thaliana])

Protein Group 342

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.42	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
520.4636	1558.3674	1558.7691	257.7	3	4.1	1.63	HAFDWALVHFCR : +57.05000 (C11)	LYK	rep2
520.7059	1559.0943	1558.7691	208.64	3	3.78	1.47	HAFDWALVHFCR : +57.05000 (C11)	LYT	rep3

Matching Genes:

NP_850015.1 (RD2 (RESPONSIVE TO DESSICATION 2) [Arabidopsis thaliana])

Protein Group 343

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.12	13.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1038.2803	2074.545	2075.3413	383.71	2	4.06	2.62	GDGGGRPHALPIFLFAQGHK	LYK	rep1
693.0509	2076.1292	2075.3413	379.67	3	3.63	1.62	GDGGGRPHALPIFLFAQGHK	LYT	rep3

Matching Genes:

NP_001078623.1 (meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana])

Protein Group 344

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.61	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
816.1753	2445.5024	2445.8673	149.19	3	4.05	2.3	HGIICVEDLIHEIMTVGPHFK : +57.05000 (C5)	LYT	rep3
816.649	2446.9237	2445.8673	431.89	3	2.19	0.68	HGIICVEDLIHEIMTVGPHFK : +57.05000 (C5)	LYK	rep2

Matching Genes:

NP_187967.1 (60S ribosomal protein L7 (RPL7D) [Arabidopsis thaliana])

Protein Group 345

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	1	3.39	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
905.7677	1809.5198	1810.0087	270.11	2	4.02	2.46	CHISHEVNHLHEGLK : +57.05000 (C1)	LYT	rep2

Matching Genes:

NP_001077698.1 (UBP6 (UBIQUITIN-SPECIFIC PROTEASE 6) [Arabidopsis thaliana])

Protein Group 346

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	8.36	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
791.574	1581.1324	1581.6632	335.65	2	2.34	0.88	SLSENKDDLSDCAK : +57.05000 (C12)	LYT	rep1
487.0735	1458.197	1457.5069	473.44	3	1.67	0.62	YDAHFDYFHDK	LYK	rep2
729.4446	1456.8736	1457.5069	434.56	2	1.08	0.17	YDAHFDYFHDK	LYT	rep3

Matching Genes:

NP_566279.1 (AT-P4H-2 (A. THALIANA P4H ISOFORM 2); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors / procollagen-proline 4-dioxygenase [Arabidopsis thaliana])

Protein Group 347

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.28	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
508.2253	1521.6524	1521.7518	65.35	3	3.98	2.08	MNTKPSHGPIHFR	LYK	rep3
761.6465	1521.2774	1521.7518	311.77	2	2.94	1.49	MNTKPSHGPIHFR	LYT	rep1

Matching Genes:

NP_001030654.1 (structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 348

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.79	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
864.3572	2590.0481	2590.8147	295.9	3	3.94	2.03	NLTYILNTHHHYDHTGGNLELK	LYT	rep3
864.4744	2590.3996	2590.8147	160.21	3	3.57	1.33	NLTYILNTHHHYDHTGGNLELK	LYK	rep2

Matching Genes:

NP_180693.1 (GLX2-5 (GLYOXALASE 2-5); hydroxyacylglutathione hydrolase/ iron ion binding / zinc ion binding [Arabidopsis thaliana])

Protein Group 349

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	27.62	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

1125.4642	3373.3692	3372.6442	214.98	3	1.7	0.61	HWYIQSTCATSGEGLYEGLDWLSNNIASKA : +57.05000 (C8)	LYT	rep1
809.3202	2424.9371	2424.5935	141.71	3	2.22	0.79	HYFQNTQGLIFVVDSNDRDR	LYT	rep2

Matching Genes:

NP_172533.2 (ADP-ribosylation factor, putative [Arabidopsis thaliana])

Protein Group 350

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.71	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
934.2565	1866.4973	1867.163	356.48	2	3.9	2.27	DHFNHVILSVLGYKPK	LYK	rep2
934.4615	1866.9073	1867.163	136.94	2	3.89	2.03	DHFNHVILSVLGYKPK	LYT	rep3

Matching Genes:

NP_001031683.1 (translation initiation factor [Arabidopsis thaliana])

Protein Group 351

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.09	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1146.0448	3435.1109	3436.7624	480.54	3	3.9	2.13	NFAYSHLHPAGGVYDAHPKPVGIGFGGTLGNER	LYK	rep1
1146.3143	3435.9195	3436.7624	245.27	3	3.76	1.84	NFAYSHLHPAGGVYDAHPKPVGIGFGGTLGNER	LYT	rep3

Matching Genes:

NP_198775.1 (unknown protein [Arabidopsis thaliana])

Protein Group 352

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.25	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
579.724	1736.1485	1735.8883	149.91	3	3.88	2.61	HGFSGMPASHGASLSHR	LYT	rep3
580.139	1737.3936	1735.8883	867.19	3	3.62	2.27	HGFSGMPASHGASLSHR	LYK	rep2

Matching Genes:

NP_566579.1 (RPL3P (ribosomal protein large subunit 3P); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 353

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	2	4.36	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
673.8016	2018.3814	2018.3613	9.97	3	1.88	0.51	LAEPIGYVPKEDILYAVK	LYK	rep1
460.6832	1379.026	1378.6011	308.24	3	1.99	0.53	VCEPLFYHWK : +57.05000 (C2)	LYT	rep3

Matching Genes:

NP_196079.1 (SIR (sulfite reductase); sulfite reductase (ferredoxin) [Arabidopsis thaliana])

Protein Group 354

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.7	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
603.4414	1807.3007	1807.026	152.05	3	3.85	1.66	KQHSFIQPSLIEHSR	LYK	rep1
603.3116	1806.9115	1807.026	63.38	3	3.06	1.08	KQHSFIQPSLIEHSR	LYT	rep2

Matching Genes:

NP_197178.1 (inositol 1,3,4-trisphosphate 5/6-kinase [Arabidopsis thaliana])

Protein Group 355

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.58	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
757.1205	2268.338	2268.6477	136.52	3	3.84	2.05	NKPIILSHHMLPGLQQGQEK	LYT	rep3
757.5726	2269.6944	2268.6477	461.39	3	3.46	1.63	NKPIILSHHMLPGLQQGQEK	LYK	rep2

Matching Genes:

NP_174157.3 (ATP binding / aminoacyl-tRNA ligase [Arabidopsis thaliana])

Protein Group 356

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.32	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
764.1595	1526.3033	1526.7018	261.03	2	3.8	1.87	ISSATAFTHVLHSR	LYT	rep1
764.0989	1526.1822	1526.7018	340.35	2	3.56	1.8	ISSATAFTHVLHSR	LYK	rep3

Matching Genes:

NP_180725.1 (unknown protein [Arabidopsis thaliana])

Protein Group 357

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.16	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1042.6793	3125.0145	3124.6272	123.95	3	3.79	1.52	MGSYLAVAAASANPPHFIHLIYKPSSGPVK	LYT	rep3
1042.0433	3123.1065	3124.6272	486.67	3	3.47	1.32	MGSYLAVAAASANPPHFIHLIYKPSSGPVK	LYK	rep3

Matching Genes:

NP_194820.1 (cytosol aminopeptidase family protein [Arabidopsis thaliana])

Protein Group 358

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	9.63	14.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
981.2113	1960.407	1961.1949	401.75	2	3.77	2.09	HFGPAPGVPHSNTKPYVR	LYK	rep3
981.8061	1961.5965	1961.1949	204.74	2	3.17	1.6	HFGPAPGVPHSNTKPYVR	LYT	rep1

Matching Genes:

NP_198137.1 (60S ribosomal protein L18 (RPL18C) [Arabidopsis thaliana])

Protein Group 359

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.54	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
986.9436	1971.8716	1972.238	185.76	2	3.76	2.05	VSHYPPCPHPELVNGLR : +57.05000 (C7)	LYK	rep3
658.4224	1972.2436	1972.238	2.86	3	1.37	0.06	VSHYPPCPHPELVNGLR : +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_565154.1 (1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative [Arabidopsis thaliana])

Protein Group 360

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.42	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
647.8561	1940.5448	1940.1161	220.96	3	3.74	1.55	HASPMHLISPSHGGNGGGAR	LYK	rep2
647.775	1940.3016	1940.1161	95.62	3	3.36	0.87	HASPMHLISPSHGGNGGGAR	LYT	rep3

Matching Genes:

NP_001031725.1 (RNA binding [Arabidopsis thaliana])

Protein Group 361

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	17.73	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1300.7689	3899.2833	3900.3669	277.83	3	3.74	1.82	YFLSSGFAFLHANSVADIIAVEAVPLDHIDPSQVQK	LYK	rep1
1300.7216	3899.1412	3900.3669	314.26	3	3.34	1.52	YFLSSGFAFLHANSVADIIAVEAVPLDHIDPSQVQK	LYT	rep1

Matching Genes:

NP_199514.1 (ATP synthase delta' chain, mitochondrial [Arabidopsis thaliana])

Protein Group 362

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.99	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1318.3954	3952.1627	3953.5784	358.09	3	3.73	1.74	VLVLDGVIQLTERDECAYQEMITHLPLCSIPNPK : +57.05000 (C16); +57.05000 (C28)	LYK	rep1
1318.9308	3953.7689	3953.5784	48.18	3	3.58	1.96	VLVLDGVIQLTERDECAYQEMITHLPLCSIPNPK : +57.05000 (C16); +57.05000 (C28)	LYT	rep3

Matching Genes:

NP_173794.2 (SPDS1 (SPERMIDINE SYNTHASE 1) [Arabidopsis thaliana])

Protein Group 363

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.41	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
766.1737	2295.4976	2295.4822	6.74	3	3.69	1.9	FGGSGARPNLPWVSTTGSGPHGR	LYT	rep3
765.8201	2294.4367	2295.4822	455.43	3	2.16	0.37	FGGSGARPNLPWVSTTGSGPHGR	LYK	rep2

Matching Genes:

NP_001078466.1 (unknown protein [Arabidopsis thaliana])

Protein Group 364

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	1	11.94	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
879.2615	2634.7609	2636.0434	486.5	3	3.69	1.94	KVVIFGLPGAYTGVCSQQHVPSYK : +57.05000 (C15)	LYK	rep3
879.7493	2636.2243	2636.0434	68.64	3	3.49	2.14	KVVIFGLPGAYTGVCSQQHVPSYK : +57.05000 (C15)	LYT	rep3

Matching Genes:

NP_566268.1 (ATPRXIIF/PRXIIF (PEROXIREDOXIN IIF); antioxidant/ peroxidase [Arabidopsis thaliana])

Protein Group 365

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.79	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
968.6794	2903.0149	2901.1299	649.74	3	3.64	2.04	DFQLHLQQQQQEFFLHHHQQQR	LYT	rep3
967.7786	2900.3122	2901.1299	281.84	3	3.56	1.97	DFQLHLQQQQQEFFLHHHQQQR	LYK	rep1

Matching Genes:

NP_194012.1 (DNA-binding protein-related [Arabidopsis thaliana])

Protein Group 366

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.88	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
838.5886	2512.7424	2512.8332	36.15	3	3.64	1.83	QTTSNLGHLNKPSIQALIHGLNR	LYT	rep3
838.5411	2512.5999	2512.8332	92.84	3	3.48	1.57	QTTSNLGHLNKPSIQALIHGLNR	LYK	rep2

Matching Genes:

NP_001078617.1 (26S proteasome regulatory subunit, putative [Arabidopsis thaliana])

Protein Group 367

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.11	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
916.6103	1831.2049	1831.9012	380.13	2	3.6	2.28	LHSELHAEDGNEVEPR	LYK	rep2
916.5365	1831.0574	1831.9012	460.63	2	3.32	1.98	LHSELHAEDGNEVEPR	LYT	rep3

Matching Genes:

NP_196063.1 (KH domain-containing protein NOVA, putative [Arabidopsis thaliana])

Protein Group 368

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.12	17.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
508.0623	1521.1633	1521.7072	357.41	3	3.51	1.28	HSNIPAHVSPCFR : +57.05000 (C11)	LYK	rep3

761.5935	1521.1714	1521.7072	352.06	2	3.07	1.46	HSNIPAHVSPCFR : +57.05000 (C11)	LYT	rep1

Matching Genes:

NP_190462.1 (EMB1080 (EMBRYO DEFECTIVE 1080); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 369

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	11.28	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
909.0999	1816.1841	1817.0631	483.74	2	3.46	1.65	TQYCVSCAIHSHVVR : +57.05000 (C4); +57.05000 (C7)	LYK	rep1
607.1588	1818.453	1817.0631	764.89	3	2.74	1.15	TQYCVSCAIHSHVVR : +57.05000 (C4); +57.05000 (C7)	LYT	rep3

Matching Genes:

NP_181583.1 (40S ribosomal protein S26 (RPS26A) [Arabidopsis thaliana])

Protein Group 370

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	10.84	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
794.6473	2380.9185	2380.5342	161.46	3	3.44	1.39	GFGFITPDDGGDDLFVHQSSIR	LYK	rep3
795.2207	2382.6386	2380.5342	884.03	3	3.22	1.22	GFGFITPDDGGDDLFVHQSSIR	LYT	rep3

Matching Genes:

NP_195580.1 (GRP2 (COLD SHOCK DOMAIN PROTEIN 2); nucleic acid binding [Arabidopsis thaliana])

Protein Group 371

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.46	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
644.3013	1929.8803	1930.1792	154.83	3	3.44	1.54	SPRPDVAFTHHLPASGLK	LYK	rep2
644.2777	1929.8097	1930.1792	191.45	3	2.27	0.82	SPRPDVAFTHHLPASGLK	LYT	rep1

Matching Genes:

NP_001032101.1 (subtilase [Arabidopsis thaliana])

Protein Group 372

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4	11.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
516.2657	1545.7738	1545.8564	53.48	3	3.43	1.81	HLRPEMALFYLR	LYT	rep3
516.7618	1547.262	1545.8564	909.28	3	3.43	1.58	HLRPEMALFYLR	LYK	rep1

Matching Genes:

NP_001031879.1 (3-isopropylmalate dehydrogenase [Arabidopsis thaliana])

Protein Group 373

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	8.88	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
758.6908	2273.0489	2272.3892	290.32	3	3.4	0.87	EVERLLDMVDSENSDCEEK : +32.00000 (M8)	LYK	rep3
1137.7605	2273.5054	2272.3892	491.21	2	1.51	0.11	EVERLLDMVDSENSDCEEK : +32.00000 (M8)	LYT	rep1

Matching Genes:

NP_178212.2 (XH domain-containing protein [Arabidopsis thaliana])

Protein Group 374

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.75	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
997.487	1992.9583	1994.2851	665.3	2	3.36	1.8	CYTGLTSAHAALLTHHLK : +57.05000 (C1)	LYT	rep3
665.7509	1994.2291	1994.2851	28.08	3	2.08	0.38	CYTGLTSAHAALLTHHLK : +57.05000 (C1)	LYK	rep1

Matching Genes:

NP_188431.3 (HON4; DNA binding [Arabidopsis thaliana])

Protein Group 375

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	14.04	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
925.22	2772.6364	2773.2702	228.52	3	3.35	1.57	MFLGSVSNYCTNHAHCPVVIIKPK : +57.05000 (C10); +57.05000 (C 16)	LYT	rep1
924.9374	2771.7887	2773.2702	534.21	3	3.29	1.21	MFLGSVSNYCTNHAHCPVVIIKPK : +57.05000 (C10); +57.05000 (C16)	LYK	rep3

Matching Genes:

NP_172445.2 (ethylene-responsive protein, putative [Arabidopsis thaliana])

Protein Group 376

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.79	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
982.6873	2945.0383	2946.4019	462.8	3	3.35	1.81	IKPISGGIPHCFPQFGPGLIQQHGFGR : +57.05000 (C11)	LYK	rep3
983.46	2947.3564	2946.4019	323.96	3	2.56	1.16	IKPISGGIPHCFPQFGPGLIQQHGFGR : +57.05000 (C11)	LYT	rep3

Matching Genes:

NP_201454.1 (aldose 1-epimerase family protein [Arabidopsis thaliana])

Protein Group 377

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	19.5	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1197.6981	3590.0709	3590.9663	249.35	3	3.35	1.85	YNASQVPAEWHGWLHFITDHTGDELLSLKPK	LYT	rep3
1197.6088	3589.8028	3590.9663	324	3	3.33	1.54	YNASQVPAEWHGWLHFITDHTGDELLSLKPK	LYK	rep2

Matching Genes:

NP_001030628.1 (oxidoreductase [Arabidopsis thaliana])

Protein Group 378

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.02	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
401.9922	1202.9533	1202.3297	518.63	3	3.34	1.46	RPHVGFYGNR	LYT	rep2
402.0425	1203.1041	1202.3297	644.12	3	3.01	1.39	RPHVGFYGNR	LYK	rep1

Matching Genes:

NP_201215.1 (peroxidase, putative [Arabidopsis thaliana])

Protein Group 379

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.56	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
597.7726	1790.2943	1789.9986	165.16	3	3.32	1.37	ALNREPAGHAFHSAALK	LYT	rep2
598.0631	1791.1659	1789.9986	652.07	3	2.72	1.14	ALNREPAGHAFHSAALK	LYK	rep2

Matching Genes:

NP_187752.1 (DNAJ heat shock N-terminal domain-containing protein / cell division protein-related [Arabidopsis thaliana])

Protein Group 380

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.73	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
838.9633	2513.8663	2513.8579	3.34	3	3.31	1.25	HIPDLHVLISTPFHPAYVTAER	LYK	rep1
839.2948	2514.8609	2513.8579	399	3	2.86	1.34	HIPDLHVLISTPFHPAYVTAER	LYT	rep2

Matching Genes:

NP_196982.1 (FDH (FORMATE DEHYDROGENASE); NAD binding / cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor [Arabidopsis thaliana])

Protein Group 381

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	1	1.72	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
525.3734	1573.0968	1572.8168	178.03	3	3.3	1.44	KIHVHNEQVSLIR	LYT	rep3
787.1741	1572.3326	1572.8168	307.86	2	3.05	1.16	KIHVHNEQVSLIR	LYK	rep1

Matching Genes:

NP_001032163.1 (unknown protein [Arabidopsis thaliana])

Protein Group 382

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.18	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
943.6121	1885.2085	1886.1848	517.59	2	3.3	1.67	MSQHFASLKPGDVLEVK	LYK	rep3
629.4413	1885.3004	1886.1848	468.9	3	2.45	0.43	MSQHFASLKPGDVLEVK	LYT	rep1

Matching Genes:

NP_568391.1 (NADH-cytochrome b5 reductase, putative [Arabidopsis thaliana])

Protein Group 383

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	9.63	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
657.6339	1969.8783	1970.2051	165.88	3	3.29	1.75	HFGPAPGVPHSHSKPYVR	LYK	rep3
657.9666	1970.8762	1970.2051	340.63	3	3.1	1.51	HFGPAPGVPHSHSKPYVR	LYT	rep3

Matching Genes:

NP_187210.1 (RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 384

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	11.05	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
729.9854	2186.9326	2187.5308	273.46	3	3.27	0.95	TPGPHYFICGIPGHCTGGMK : +57.05000 (C9); +57.05000 (C15)	LYK	rep3
1094.097	2186.1783	2187.5308	618.28	2	2.5	1.01	TPGPHYFICGIPGHCTGGMK : +57.05000 (C9); +57.05000 (C15)	LYT	rep1

Matching Genes:

NP_177368.1 (plastocyanin-like domain-containing protein [Arabidopsis thaliana])

Protein Group 385

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	7.04	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
504.9787	1511.9126	1511.84	48.06	3	3.27	1.14	KGGMIVLPAGIYHR	LYK	rep1

504.8787	1511.6127	1511.84	150.32	3	1.62	0.11	KGGMIVLPAGIYHR	LYT	rep3

Matching Genes:

NP_001031640.2 (ATARD2; metal ion binding [Arabidopsis thaliana])

Protein Group 386

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.68	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
473.0674	1416.1787	1415.6457	376.46	3	3.26	0.85	VVHHSEIVNILR	LYK	rep2
473.1081	1416.3008	1415.6457	462.73	3	2.88	0.98	VVHHSEIVNILR	LYT	rep2

Matching Genes:

NP_197445.1 (cinnamyl-alcohol dehydrogenase, putative (CAD) [Arabidopsis thaliana])

Protein Group 387

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.71	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
532.4755	1594.4029	1593.7898	384.7	3	3.25	1.49	HLHVYSWPQGELK	LYK	rep3
532.2128	1593.6148	1593.7898	109.77	3	2.77	1	HLHVYSWPQGELK	LYT	rep3

Matching Genes:

NP_189022.1 (selenium-binding family protein [Arabidopsis thaliana])

Protein Group 388

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	6.41	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
729.9845	2186.93	2186.6479	129	3	3.25	0.97	QQLPSIAPKPLIIPPIFSAR	LYT	rep2
730.3314	2187.9708	2186.6479	604.97	3	2.7	0.49	QQLPSIAPKPLIIPPIFSAR	LYK	rep3

Matching Genes:

NP_196701.1 (protein kinase-related [Arabidopsis thaliana])

Protein Group 389

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.5	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
590.3602	1768.0572	1767.9897	38.17	3	3.19	1.79	HLSLNGNSEVAVFRPK	LYT	rep3
590.2518	1767.732	1767.9897	145.77	3	3.01	1.34	HLSLNGNSEVAVFRPK	LYK	rep2

Matching Genes:

NP_566401.1 (unknown protein [Arabidopsis thaliana])

Protein Group 390

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	11.51	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
868.1147	1734.2137	1734.9182	406.1	2	3.19	1.26	VNELRPGTNGHSLNVK	LYK	rep3
579.4113	1735.2103	1734.9182	168.36	3	2.6	1.2	VNELRPGTNGHSLNVK	LYT	rep3

Matching Genes:

NP_563874.1 (DNA-binding protein-related [Arabidopsis thaliana])

Protein Group 391

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.69	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
677.8954	2030.6627	2031.2435	285.95	3	3.18	1.04	ALSNTRPSAHLHAHLYDK	LYK	rep2

Matching Genes:

NP_565791.1 (katanin, putative [Arabidopsis thaliana])

Protein Group 392

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.81	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
739.5641	2215.6688	2216.5649	404.29	3	3.17	1.47	AHEAVKPYMPTVEEVVAFAK	LYK	rep3
739.5927	2215.7545	2216.5649	365.63	3	2.15	0.31	AHEAVKPYMPTVEEVVAFAK	LYT	rep1

Matching Genes:

NP_174033.1 (ATGSTU13 (GLUTATHIONE S-TRANSFERASE 12); glutathione transferase [Arabidopsis thaliana])

Protein Group 393

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.16	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
710.2159	1418.4161	1418.5649	104.95	2	3.14	1.47	HGLHNPFKSPER	LYT	rep1
473.9672	1418.878	1418.5649	220.7	3	2.09	0.63	HGLHNPFKSPER	LYK	rep1

Matching Genes:

NP_568955.1 (ALDH12A1 (Aldehyde dehydrogenase 12A1); 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase [Arabidopsis thaliana])

Protein Group 394

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.14	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
673.9769	2018.9073	2019.3143	201.56	3	3.09	0.76	HVSHLFGLFPGHTITVEK	LYT	rep3
673.8729	2018.5953	2019.3143	356.07	3	2.82	0.32	HVSHLFGLFPGHTITVEK	LYK	rep2

Matching Genes:

NP_195152.2 (unknown protein [Arabidopsis thaliana])

Protein Group 395

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.6	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
558.4476	1672.3194	1671.894	254.43	3	3.04	1.27	FKFPVDSVELYAEK	LYK	rep2
836.5775	1671.1394	1671.894	451.34	2	2.5	1.13	FKFPVDSVELYAEK	LYT	rep2

Matching Genes:

NP_180719.1 (40S ribosomal protein S3 (RPS3A) [Arabidopsis thaliana])

Protein Group 396

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.56	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

476.3461	1426.0149	1424.5713	1013.38	3	3.02	1.13	SPAGLFFQHAGHR	LYK	rep3
713.0777	1424.1397	1424.5713	302.96	2	2.95	1.65	SPAGLFFQHAGHR	LYT	rep3

Matching Genes:

NP_565456.2 (FVE (FVE) [Arabidopsis thaliana])

Protein Group 397

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	13.98	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1223.8685	3668.5821	3669.0754	134.45	3	2.99	1.44	VAASGFYVVVPDYFGGDPYNPSNQDRPIPVWIK	LYK	rep2
1224.2938	3669.858	3669.0754	213.29	3	2.66	1.06	VAASGFYVVVPDYFGGDPYNPSNQDRPIPVWIK	LYT	rep3

Matching Genes:

NP_001030749.1 (hydrolase [Arabidopsis thaliana])

Protein Group 398

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.46	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
894.5061	2680.4948	2680.845	130.6	3	2.94	1.58	HDETGVSNDLYDFLQAFFAEHPK	LYK	rep2
894.54	2680.5966	2680.845	92.63	3	2.77	1.43	HDETGVSNDLYDFLQAFFAEHPK	LYT	rep3

Matching Genes:

NP_187652.1 (SCPL49 (serine carboxypeptidase-like 49); serine carboxypeptidase [Arabidopsis thaliana])

Protein Group 399

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.66	7.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
440.6762	1319.0051	1318.4853	394.25	3	2.94	1.37	KFTSAFPHVER	LYT	rep2
440.3031	1317.8858	1318.4853	454.7	3	2.9	1	KFTSAFPHVER	LYK	rep2

Matching Genes:

NP_001031202.1 (translation elongation factor [Arabidopsis thaliana])

Protein Group 400

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.49	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1007.1648	2012.314	2013.2696	474.67	2	2.92	1.27	LHVHTVQQLQQELANVR	LYT	rep3
672.7556	2015.2434	2013.2696	980.36	3	1.9	0.36	LHVHTVQQLQQELANVR	LYK	rep1

Matching Genes:

NP_001078752.1 (unknown protein [Arabidopsis thaliana])

Protein Group 401

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	9.02	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
470.6429	1408.9052	1408.6532	178.89	3	2.92	1.28	KQFVIDVLHPGR	LYT	rep1

Matching Genes:

NP_187143.1 (40S ribosomal protein S24 (RPS24A) [Arabidopsis thaliana])

Protein Group 402

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.02	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
343.7741	1028.2988	1027.1831	1086.23	3	2.92	0.74	HHFAQLFK	LYK	rep1
343.389	1027.1436	1027.1831	38.41	3	2.84	0.96	HHFAQLFK	LYT	rep2

Matching Genes:

NP_001030868.1 (zinc ion binding [Arabidopsis thaliana])

Protein Group 403

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.4	9.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
649.5332	1297.0508	1297.4213	285.52	2	2.89	1.3	YHVHSPESLTK	LYT	rep1
433.532	1297.5727	1297.4213	116.69	3	2.56	0.7	YHVHSPESLTK	LYK	rep1

Matching Genes:

NP_188850.1 (PAC1 (20S proteasome alpha subunit C1); peptidase [Arabidopsis thaliana])

Protein Group 404

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.04	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
757.6809	1513.3462	1513.7687	279.09	2	2.86	1.18	ACGVCHSDLHVMK : +57.05000 (C2); +57.05000 (C5)	LYK	rep1
505.5596	1513.6552	1513.7687	74.96	3	1.4	0.19	ACGVCHSDLHVMK : +57.05000 (C2); +57.05000 (C5)	LYT	rep3

Matching Genes:

NP_568975.2 (oxidoreductase, zinc-binding dehydrogenase family protein [Arabidopsis thaliana])

Protein Group 405

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra

Total (Non-Redundant)	1	1	2.1	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
648.0777	1294.1397	1294.4637	250.33	2	2.86	1.39	FTQLSSHPLHK	LYT	rep3
648.0349	1294.0542	1294.4637	316.35	2	2.13	0.7	FTQLSSHPLHK	LYK	rep2

Matching Genes:

NP_001030958.1 (nucleotide binding [Arabidopsis thaliana])

Protein Group 406

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.78	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
580.4052	1738.192	1736.9724	702.13	3	2.84	1.28	VPALDYVDIPHTQIR	LYK	rep2
579.9332	1736.7762	1736.9724	112.95	3	2.33	0.72	VPALDYVDIPHTQIR	LYT	rep3

Matching Genes:

NP_566470.1 (dihydrolipoamide S-acetyltransferase, putative [Arabidopsis thaliana])

Protein Group 407

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.34	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
535.6073	1603.7984	1603.7862	7.59	3	2.83	1.34	YHASAIHVPGPEVAR	LYK	rep3
802.4871	1602.9585	1603.7862	516.1	2	2.66	1.5	YHASAIHVPGPEVAR	LYT	rep3

Matching Genes:

NP_001078234.1 (NIT1 (NITRILASE 1) [Arabidopsis thaliana])

Protein Group 408

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	6.93	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
947.8824	2840.6239	2840.3613	92.44	3	2.8	1.27	GALIANPNCSTIICLMAVTPLHHHAK : +57.05000 (C9); +57.05000 (C14)	LYK	rep1
947.4652	2839.3722	2840.3613	348.24	3	2.09	0.06	GALIANPNCSTIICLMAVTPLHHHAK : +57.05000 (C9); +57.05000 (C14)	LYT	rep1

Matching Genes:

NP_172934.1 (semialdehyde dehydrogenase family protein [Arabidopsis thaliana])

Protein Group 409

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.88	10.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
407.7485	1220.2221	1220.4271	167.96	3	2.77	1.24	MHFHDCFVK : +57.05000 (C6)	LYK	rep2
407.7997	1220.3756	1220.4271	42.23	3	2.47	0.96	MHFHDCFVK : +57.05000 (C6)	LYT	rep3

Matching Genes:

NP_197284.1 (peroxidase 57 (PER57) (P57) (PRXR10) [Arabidopsis thaliana])

Protein Group 410

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.45	15.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
603.5821	1205.1485	1205.3718	185.29	2	2.77	1.23	KGHAVGDIPGVR	LYT	rep1
603.5775	1205.1394	1205.3718	192.78	2	2.73	1.4	KGHAVGDIPGVR	LYK	rep1

Matching Genes:

NP_195916.1 (40S ribosomal protein S23 (RPS23B) [Arabidopsis thaliana])

Protein Group 411

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	9.15	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate

735.2112	1468.4068	1469.607	816.73	2	2.76	1.19	STHGYHIILSEGR	LYT	rep3
490.7954	1469.3628	1469.607	166.23	3	2.4	0.6	STHGYHIILSEGR	LYK	rep2

Matching Genes:

NP_564250.1 (peptidyl-prolyl cis-trans isomerase PPIC-type family protein [Arabidopsis thaliana])

Protein Group 412

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.65	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
827.0214	1652.0271	1652.8124	475.09	2	2.7	1.27	SYEHPSNELKPVPR	LYT	rep3
551.7494	1652.2247	1652.8124	355.56	3	2.59	1.18	SYEHPSNELKPVPR	LYK	rep1

Matching Genes:

NP_188925.1 (unknown protein [Arabidopsis thaliana])

Protein Group 413

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.59	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
596.0968	1785.2669	1784.9789	161.38	3	2.67	1.26	HIDFALTSPFGGGRPGR	LYT	rep1
595.8495	1784.525	1784.9789	254.28	3	2.16	0.88	HIDFALTSPFGGGRPGR	LYK	rep2

Matching Genes:

NP_197024.1 (40S ribosomal protein S9 (RPS9B) [Arabidopsis thaliana])

Protein Group 414

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	14.71	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
955.1667	2862.4768	2862.0806	138.44	3	2.62	1.28	DAFDLYDQDKNGLISASELHQVLNR	LYT	rep3
954.9895	2861.945	2862.0806	47.35	3	1.61	0.31	DAFDLYDQDKNGLISASELHQVLNR	LYK	rep1

Matching Genes:

NP_173259.1 (calcium-binding protein, putative [Arabidopsis thaliana])

Protein Group 415

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	11.81	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
931.6239	1861.2322	1862.0185	422.3	2	2.6	1.16	SWTGTIIGPHNTVHEGR	LYT	rep1
621.61	1861.8065	1862.0185	113.89	3	2.57	0.68	SWTGTIIGPHNTVHEGR	LYK	rep3

Matching Genes:

NP_001078011.1 (MMZ3 (MMS ZWEI HOMOLOGE 3) [Arabidopsis thaliana])

Protein Group 416

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.21	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
428.8571	1283.5477	1283.5083	30.7	3	2.59	1.15	HMYHDMYMR	LYT	rep2
429.1337	1284.3777	1283.5083	677.38	3	2.39	0.83	HMYHDMYMR	LYK	rep2

Matching Genes:

NP_171777.1 (EMB2386 (EMBRYO DEFECTIVE 2386); structural constituent of ribosome [Arabidopsis thaliana])

Protein Group 417

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.19	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
474.5856	1420.7332	1420.6622	49.99	3	2.58	1.01	ELLKPSASVALHR	LYT	rep3
474.7122	1421.1132	1420.6622	317.43	3	2.26	0.54	ELLKPSASVALHR	LYK	rep1

Matching Genes:

NP_200637.1 (RPT3 (root phototropism 3); ATPase [Arabidopsis thaliana])

Protein Group 418

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.27	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
722.6172	1443.2188	1443.6395	291.44	2	2.58	1.07	EVQIMHHLSGHR	LYT	rep1
722.7373	1443.459	1443.6395	125.03	2	1.98	0.38	EVQIMHHLSGHR	LYK	rep2

Matching Genes:

NP_194096.1 (CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); anion channel/ calcium- and calmodulin-dependent protein kinase/ kinase [Arabidopsis thaliana])

Protein Group 419

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.63	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
763.2416	2286.7013	2286.5535	64.64	3	2.55	1	ELVDRNPELGHVLNDPSILR	LYK	rep2
763.1749	2286.5013	2286.5535	22.81	3	2	0.56	ELVDRNPELGHVLNDPSILR	LYT	rep1

Matching Genes:

NP_179311.1 (ubiquitin family protein [Arabidopsis thaliana])

Protein Group 420

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	4.83	8.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
699.1507	1396.2857	1396.6024	226.78	2	2.52	1.13	GSVLRPGFIHGTR	LYK	rep3
466.4772	1396.408	1396.6024	139.17	3	1.96	0.57	GSVLRPGFIHGTR	LYT	rep1

Matching Genes:

NP_568323.1 (dehydrogenase-related [Arabidopsis thaliana])

Protein Group 421

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	5.42	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
500.2148	1497.6209	1497.8124	127.88	3	2.46	0.68	GHLLTAGMCHLCK : +57.05000 (C9); +57.05000 (C12)	LYK	rep1
500.152	1497.4326	1497.8124	253.55	3	2.11	0.86	GHLLTAGMCHLCK : +57.05000 (C9); +57.05000 (C12)	LYT	rep1

Matching Genes:

NP_001030872.1 (ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN); soluble NSF attachment protein [Arabidopsis thaliana])

Protein Group 422

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.89	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
747.6303	1493.2449	1493.7352	328.21	2	2.43	1.08	LVGAHCHLGSTITK : +57.05000 (C6)	LYT	rep3

Matching Genes:

NP_188056.1 (diaminopimelate decarboxylase, putative / DAP carboxylase, putative [Arabidopsis thaliana])

Protein Group 423

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	1.85	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
976.6507	1951.2857	1952.1848	460.57	2	2.42	1.04	LNVHVVPHSHDDVGWLK	LYK	rep2
651.6649	1951.9713	1952.1848	109.38	3	2.3	1.1	LNVHVVPHSHDDVGWLK	LYT	rep3

Matching Genes:

NP_001031878.1 (alpha-mannosidase [Arabidopsis thaliana])

Protein Group 424

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	2.76	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
555.743	1664.2056	1663.8833	193.74	3	2.41	0.87	HFKGEHTFVPVTHK	LYT	rep2

555.9792	1664.9143	1663.8833	619.62	3	2.1	0.83	HFKGEHTFVPVTHK	LYK	rep1

Matching Genes:

NP_192355.1 (aspartyl protease family protein [Arabidopsis thaliana])

Protein Group 425

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.02	5.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
672.0326	2013.0743	2011.2906	886.83	3	2.4	1.16	ILYSSVVYPHNYGFVPR	LYT	rep2
1006.4026	2010.7896	2011.2906	249.12	2	2.37	1.14	ILYSSVVYPHNYGFVPR	LYK	rep2

Matching Genes:

NP_171613.1 (inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative [Arabidopsis thaliana])

Protein Group 426

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	3.38	4.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
670.1166	2007.3263	2007.4313	52.31	3	2.27	0.57	LVELLLHHSPSVLIPALR	LYK	rep2
670.2384	2007.6917	2007.4313	129.75	3	1.83	0.43	LVELLLHHSPSVLIPALR	LYT	rep3

Matching Genes:

NP_187328.1 (AT-IMP (Arabidopsis thaliana importin alpha); protein transporter)

Protein Group 427

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	2.65	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
522.9019	1565.6821	1565.7347	33.62	3	2.16	0.55	TGHYTPISAGHSPLK	LYT	rep3
523.2244	1566.6496	1565.7347	584.32	3	2.03	0.75	TGHYTPISAGHSPLK	LYK	rep2

Matching Genes:

NP_191274.1 (NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57) [Arabidopsis thaliana])

Protein Group 428

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	1	1	8.4	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
686.5862	1371.1568	1371.6131	332.73	2	2.14	1.01	LVNYQHLMPTR	LYT	rep1
687.1632	1372.3108	1371.6131	508.66	2	1.57	0.25	LVNYQHLMPTR	LYK	rep2

Matching Genes:

NP_001078392.1 (60S ribosomal protein L27 (RPL27C) [Arabidopsis thaliana])

Protein Group 429

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	16.36	6.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
1207.201	3618.5797	3619.2768	192.63	3	2.13	0.81	DSHVPILAPLPIGFAVFLVHLATIPITGTGINPAR	LYT	rep1
1207.1327	3618.3746	3619.2768	249.29	3	1.64	0.51	DSHVPILAPLPIGFAVFLVHLATIPITGTGINPAR	LYK	rep1

Matching Genes:

NP_001077441.1 (PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3) [Arabidopsis thaliana])

Protein Group 430

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	4.15	3.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
686.8221	2057.443	2058.3685	449.67	3	2.11	0.8	EVLPWNGKGEAIMVVIDR : +32.00000 (M13)	LYK	rep2
686.8824	2057.6239	2058.3685	361.78	3	1.95	0.28	EVLPWNGKGEAIMVVIDR : +32.00000 (M13)	LYT	rep2

Matching Genes:

NP_198202.1 (unknown protein [Arabidopsis thaliana])

Protein Group 431

Expression Quality:

Group	Group Probability	Num Peptides	% Seq Coverage	Num Spectra
Total (Non-Redundant)	0.99	1	9.47	12.0

Peptides:

Observed	Mr(expt)	Mr(calc)	Mass Error (ppm)	Charge	Score	Score Delta	Peptide	Group	Replicate
965.6377	1929.2598	1930.1809	477.21	2	1.95	0.84	HVPQHRPGPLPEQFYK	LYT	rep3
965.6324	1929.2491	1930.1809	482.77	2	1.86	0.7	HVPQHRPGPLPEQFYK	LYK	rep2

Matching Genes:

NP_568778.1 (NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana])