

2014\_02  
ROJA140226

Analysis Information

Report Type	Protein-Peptide Summary by Spot	Analysis Type	Combined (MS+MS/MS)
Sample Set Name	ROJA140226	Database	SwissProt
Analysis Name	Plant	Creation Date	
Reported By		Last Modified	

MS Acq. : Proc. Methods (Unspecified) : (Unspecified)  
Interpretation Method (Unspecified)

Gel Idx/Pos	102/E1	Instr./Gel Origin		BA2060/140227A				Process Status		Analysis Succeeded	
Plate [#] Name	[1] 31564	Instrument Sample Name						Spectra		11	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %		
1	Putative heat shock protein HSP90 (Fragments) OS=Populus euphratica PE=1 SV=1	HSP90_POPEU	5121.5	3.79	2	65	98.984	49	99.824		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1485.7544	1485.6727	-0.0817	-55	34	47	GVVDSDDLPLNVSR					Mascot
1656.7904	1656.7083	-0.0821	-50	20	33	VFISDDFGELFPR	49	99.824			Mascot
1656.7904	1656.7083	-0.0821	-50	20	33	VFISDDFGELFPR					Mascot

2	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Vigna radiata var. radiata G	RCA_VIGRR	47871.3	7.57	7	62	97.725	41	98.83
---	--	-----------	---------	------	---	----	--------	----	-------

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
829.489	829.4861	-0.0029	-3	411	417	RVQLADK					Mascot
940.4675	940.4274	-0.0401	-43	305	311	FYWAPTR					Mascot
1656.8591	1656.7083	-0.1508	-91	375	389	LVNSKEGPTTFDQPK					Mascot
1656.8591	1656.7083	-0.1508	-91	375	389	LVNSKEGPTTFDQPK					Mascot
1882.9697	1882.8694	-0.1003	-53	335	351	LVDTFPGQSIDFFGALR	12	0			Mascot
1882.9697	1882.8694	-0.1003	-53	335	351	LVDTFPGQSIDFFGALR					Mascot
2068.075	2067.9692	-0.1158	-56	125	142	QLDNKDGFIAPFLDK					Mascot
2089.1692	2089.0493	-0.1199	-57	280	298	VPIIVTGNDFSTLYAPLIR	29	81.061			Mascot
2089.1692	2089.0493	-0.1199	-57	280	298	VPIIVTGNDFSTLYAPLIR					Mascot
2211.2722	2210.9919	-0.2803	-127	150	169	NFMTLPNIKVPILGIWGGK					Mascot

3	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Malus domestica GN=RCA PE=2	RCA_MALDO	48046.2	8.2	6	55	90.297	39	98.276
---	---	-----------	---------	-----	---	----	--------	----	--------

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
829.489	829.4861	-0.0029	-3	409	415	RVQLADK					Mascot
940.4675	940.4274	-0.0401	-43	303	309	FYWAPTR					Mascot
1882.9697	1882.8694	-0.1003	-53	333	349	LVDTFPGQSIDFFGALR	12	0			Mascot
1882.9697	1882.8694	-0.1003	-53	333	349	LVDTFPGQSIDFFGALR					Mascot
2088.9939	2089.0493	0.0554	27	184	204	ISPIMMSAGELESGNAGEPAK					Mascot
2089.1692	2089.0493	-0.1199	-57	278	296	VPIIVTGNDFSTLYAPLIR	29	81.061			Mascot
2433.0161	2433.1021	0.086	35	121	140	QYNFDNMMDGYIAPAFMDK			Oxidation (M)[8]		Mascot
2433.0161	2433.1021	0.086	35	121	140	QYNFDNMMDGYIAPAFMDK			Oxidation (M)[8]		Mascot

4	Ribulose biphosphate carboxylase/oxygenase activase B, chloroplastic OS=Hordeum vulgare GN=RCAB PE	RCAB_HORVU	47197.8	7.59	6	55	89.113	41	98.83
---	--	------------	---------	------	---	----	--------	----	-------

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
829.489	829.4861	-0.0029	-3	396	402	RVQLADK					Mascot
940.4675	940.4274	-0.0401	-43	299	296	FYWAPTR					Mascot
1882.9697	1882.8694	-0.1003	-53	320	336	LVDTFPGQSIDFFGALR	12	0			Mascot
1882.9697	1882.8694	-0.1003	-53	320	336	LVDTFPGQSIDFFGALR					Mascot
2089.1692	2089.0493	-0.1199	-57	265	283	VPIIVTGNDFSTLYAPLIR	29	81.061			Mascot
2089.1692	2089.0493	-0.1199	-57	265	283	VPIIVTGNDFSTLYAPLIR					Mascot
2211.2722	2210.9919	-0.2803	-127	136	155	NFMTLPNIKVPILGIWGGK					Mascot
2233.0298	2232.937	-0.0928	-42	170	191	MGINPIMMSAGELESGNGEPAK					Mascot
2249.0247	2248.9087	-0.116	-52	170	191	MGINPIMMSAGELESGNGEPAK			Oxidation (M)[1]		Mascot

5	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Zea mays GN=RCA1 PE=2 SV=3	RCA_MAIZE	47908	6.29	8	54	86.295	29	81.061
---	--	-----------	-------	------	---	----	--------	----	--------

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
829.489	829.4861	-0.0029	-3	405	411	RVQLADK					Mascot
940.4675	940.4274	-0.0401	-43	299	305	FYWAPTR					Mascot
1051.5167	1051.6531	0.1364	130	348	355	VYDVEVR					Mascot
1872.9524	1872.8427	-0.1097	-59	389	404	LLEYGHMLVAEQENVK					Mascot
2089.1692	2089.0493	-0.1199	-57	274	292	VPIIVTGNDFSTLYAPLIR	29	81.061			Mascot
2089.1692	2089.0493	-0.1199	-57	274	292	VPIIVTGNDFSTLYAPLIR					Mascot
2211.1404	2210.9919	-0.1485	-67	2	24	AAAFSSTVGAPASTPTRS					Mascot
2422.123	2422.1899	0.0669	28	412	433	YLNEAALGEANEDAMKTSFLGK			Oxidation (M)[15]		Mascot
2426.0137	2425.946	-0.0677	-28	117	136	SYNFDNMMDGYIAKGFMDK			Oxidation (M)[7,8]		Mascot

6	Protein ycf2 OS=Draba nemorosa GN=ycf2-A PE=3 SV=1	YCF2_DRANE	266975.4	9.03	26	54	85.314		
---	--	------------	----------	------	----	----	--------	--	--

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
842.4842	842.4669	-0.0173	-21	1114	1120	SDPLVRR					Mascot
885.3705	885.4376	0.0671	76	189	194	RDFCK			Carbamidomethyl (C)[4,5]		Mascot
955.5095	955.3918	-0.1177	-123	1016	1024	SLSISSFSK					Mascot
1051.5717	1051.6531	0.0814	77	1785	1792	FNTCKIR			Carbamidomethyl (C)[4]		Mascot
1237.6034	1237.5608	-0.0426	-34	2259	2267	RWLFPEDEK			Oxidation (M)[8]		Mascot
1463.6471	1463.6399	-0.0072	-5	1913	1924	KSCNEGDSLYK			Carbamidomethyl (C)[3]		Mascot
1463.7198	1463.6399	-0.0799	-55	693	705	ISCGNYLEDPKPK					Mascot
1513.7218	1513.7054	-0.0164	-11	2260	2271	WLFPDEMIKIGFM					Mascot
1521.7018	1521.6774	-0.0244	-16	262	272	DWICYLMFAFR			Carbamidomethyl (C)[4]		Mascot

WSLPGPDEKTR

7	Ribulose biphosphate carboxylase/oxygenase activase	RCA2_TOBAC	48312.5	8.14	5	52	77.255	41	98.83
2, chloroplastic OS=Nicotiana tabacum GN=RCA P									
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
									Rank
									Result Type
940.4675	940.4274	-0.0401	-43	307	313	FYWAPTR			Mascot
1128.5507	1128.4752	-0.0755	-67	176	184	SFOCELVFR			Mascot
1256.6456	1256.6195	-0.0261	-21	176	185	SFOCELVFRK			Mascot
1882.9697	1882.8694	-0.1003	-53	337	353	IVDTFPGQSIDFFGALR	12	0	Mascot
1882.9697	1882.8694	-0.1003	-53	337	353	IVDTFPGQSIDFFGALR			Mascot
2089.1692	2089.0493	-0.1199	-57	282	300	PVIPIVGNDFSTLYAPLIR	29	81.061	Mascot
2089.1692	2089.0493	-0.1199	-57	282	300	PVIPIVGNDFSTLYAPLIR			Mascot

8	Ribulose biphosphate carboxylase/oxygenase activase	RCA1_LARTR	52108	6.38	5	52	76.183	41	98.83
1, chloroplastic OS=Larrea tridentata GN=RCA1									
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
829.489	829.4861	-0.0029	-3	409	415	RVQLADK			
940.4675	940.4274	-0.0401	-43	303	309	FWYAPTR			Mascot
1656.8591	1656.7083	-0.1508	-91	373	387	LVNSKEGPPSFEQPK			Mascot
1656.8591	1656.7083	-0.1508	-91	373	387	LVDTFPGSGIDFFGALR			Mascot
1822.9697	1822.8694	-0.1003	-53	333	349	LVDTFPGSGIDFFGALR	12	0	Mascot
1822.9697	1822.8694	-0.1003	-53	333	349	LVDTFPGSGIDFFGALR			Mascot
2089.1692	2089.0493	-0.1199	-57	278	296	VPPIVTGNDFSTLYAPLIR	29	81.061	Mascot
2089.1692	2089.0493	-0.1199	-57	278	296	VPPIVTGNDFSTLYAPLIR			Mascot

9	Probable beta-1,3-galactosyltransferase 17 OS=Arabidopsis thaliana GN=B3GALT17 PE=2 SV=2				B3GTH_ARATH		76987.4	6.84	15	51	73.276			
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type
	829.3984	829.4861	0.0877	106	408	413	HLEMR					Oxidation (M)[4]		Mascot
	856.4423	856.4769	0.0346	40	88	94	HFQDPR							Mascot
	940.5322	940.4274	-0.1048	-111	91	98	DPRVQLR							Mascot
	955.4479	955.3918	-0.0561	-59	232	240	AVDGDPPR							Mascot
	1165.5275	1165.6791	0.1516	130	664	673	LKGPQCCNMR					Oxidation (M)[9]		Mascot
	1256.6569	1256.6195	-0.0374	-30	408	416	HLEMRIRWK					Oxidation (M)[4]		Mascot
	1348.6943	1348.5905	-0.1038	-77	315	324	TWVLLNRLMGR					Oxidation (M)[8]		Mascot
	1348.6943	1348.5905	-0.1038	-77	315	324	TWVLLNRLMGR					Oxidation (M)[8]		Mascot
	1564.677	1564.7043	0.0273	17	518	529	YWMKDDDTFVR					Carbamidomethyl (C)[5], Oxidation (M)[3]		Mascot
	1595.8097	1595.7421	-0.0676	-42	503	517	TAIVCEYGVNTAAK					Carbamidomethyl (C)[5]		Mascot
	2045.824	2045.9634	0.1394	68	278	294	ESSDDEEYVDGEVKCR					Carbamidomethyl (C)[15]		Mascot
	2045.824	2045.9634	0.1394	68	278	294	ESSDDEEYVDGEVKCR					Carbamidomethyl (C)[15]		Mascot
	2088.8298	2089.0493	0.2195	105	274	291	CDGRESSDDEEYVDGEV K					Carbamidomethyl (C)[1]		Mascot
	2088.8298	2089.0493	0.2195	105	274	291	CDGRESSDDEEYVDGEV K							Mascot
	2233.1909	2232.937	-0.2539	-114	342	361	LFVLTLRAGMEGYHISVN GR							Mascot
	2249.1858	2248.9087	-0.2771	-123	342	361	LFVLTLRAGMEGYHISVN GR					Oxidation (M)[10]		Mascot
	2422.2764	2422.1899	-0.0865	-36	362	383	HITSFPYRTGFVLEDATG LAVK							Mascot
	2426.0327	2425.946	-0.0867	-36	634	652	FCOFGCIEDYFTAHYQSP R					Carbamidomethyl (C)[2,6]		Mascot
	2691.4617	2691.1416	-0.3201	-119	417	441	APSLPQPKPVLFIGILSAG NHEAFR							Mascot

10	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (Fragments) OS=Arachis hypogaea	RCA_ARAHY	15036.4	4.35	2	50	68.603	41	98.83
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1882.9697	1882.8694	-0.1003	-53	124	140	LVDTFPGQSIDFFGALR	12	0	
1882.9697	1882.8694	-0.1003	-53	124	140	LVDTFPGQSIDFFGALR			Mascot
2089.1692	2089.0493	-0.1199	-57	96	114	VPIIVTGNDFSTLYAPLIR	29	81.061	Mascot
2089.1692	2089.0493	-0.1199	-57	96	114	VPIIVTGNDFSTLYAPLIR			Mascot
	2089.0493								Mascot

Gel Idx/Pos	103/E2	Instr./Gel Origin	BA2060/140227A	Process Status	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
------	--------------	---------------	------------	------------	------------	---------------	-----------------------	-----------------	-------------------

1										Chaperone protein ClpC, chloroplastic OS=Pisum sativum PE=2 SV=1										CLPC_PEA										102647	6.55	25	312	100	182	100
Peptide Information																																				
Calc. Mass		Obsrv. Mass		± da		± ppm		Start Seq.		End Seq.		Sequence		Ion Score		C. I. %		Modification										Rank		Result Type						
870.4138		870.4983		0.0845		97		46		53		MSGFSGLR						Oxidation (M)[1]												Mascot						
1022.5339		1022.48		-0.0539		-53		806		813		LDEMIVFR																		Mascot						
1029.5146		1029.5099		-0.0047		-5		600		607		MEDTLHKR																		Mascot						
1038.5288		1038.4738		-0.055		-53		806		813		LDEMIVFR						Oxidation (M)[4]												Mascot						
1045.5095		1045.5186		0.0091		9		600		607		MEDTLHKR						Oxidation (M)[1]												Mascot						

Chaperone protein ClpC1, chloroplasic				CLPC1_ARATH		103388.2	6.36	26	298	100	163	100
OS=Arabidopsis thaliana GN=CLPC1 PE=1 SV=1												
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
856.4635	856.4855	0.022	26	421	427	DPALERR					Mascot	
1022.5339	1022.48	-0.0539	-53	808	815	LDMIVFR					Mascot	
1029.5687	1029.5099	-0.0588	-57	309	318	TAAEGLAQR					Mascot	
1038.5288	1038.4738	-0.055	-53	808	815	LDMIVFR			Oxidation (M)[4]		Mascot	
1051.4976	1051.65	0.1524	145	875	883	LLED5MAEK			Oxidation (M)[6]		Mascot	
1085.501	1085.4475	-0.0535	-49	347	354	YRGEFEER	10	0			Mascot	
1085.501	1085.4475	-0.0535	-49	347	354	YRGEFEER					Mascot	
1102.6653	1102.5157	-0.1496	-136	141	150	VLKSMGINKL					Mascot	
1157.4966	1157.4712	-0.0254	-22	672	680	LDMSEFMER					Mascot	
1158.5612	1158.564	0.0028	2	93	101	AMFERFTEK					Mascot	
1159.5593	1159.5569	-0.0384	-33	485	495	AIDLDEAGSR					Mascot	
1173.4915	1173.4427	-0.0488	-42	672	680	LDMSEFMER			Oxidation (M)[3]		Mascot	
1207.6429	1207.5828	-0.0601	-50	417	426	HIEKDPALER					Mascot	
1352.6483	1352.6135	-0.0348	-26	37	48	MCSQLQSVGLR					Mascot	
1369.7012	1369.6356	-0.0656	-48	798	807	QYRPEFLNLR	3	0			Mascot	
1369.7012	1369.6356	-0.0656	-48	798	807	QYRPEFLNLR					Mascot	
1382.7638	1382.6945	-0.0693	-50	267	279	LAEEGLDLPVGR					Mascot	
1471.8301	1471.7015	-0.1286	-87	102	114	AKIVMLAQEAR					Mascot	
1476.7845	1476.7109	-0.0736	-50	163	176	GSGFVAVEIPTFR	38	97.83			Mascot	
1476.7845	1476.7109	-0.0736	-50	163	176	GSGFVAVEIPTFR					Mascot	
1581.8734	1581.7803	-0.0931	-59	433	446	VPEPTVDETQILK					Mascot	
1608.8632	1608.78	-0.0832	-52	709	721	RPYTVLFDIEIK	5	0			Mascot	

	1608.8632	1608.7832	-0.0832	-52	709	721	RPTYTVLFDIEIK							Mascot
	1691.8097	1691.7239	-0.0858	-51	657	671	ALAAAYFGSEEMIR						Mascot	
	1691.8097	1691.7239	-0.0858	-51	657	671	ALAAAYFGSEEMIR	19	0		Oxidation (M)[13]		Mascot	
	1707.8047	1707.7291	-0.0756	-44	657	671	ALAAAYFGSEEMIR						Mascot	
	1764.9642	1764.868	-0.0962	-55	708	721	RRPYTVLFDIEIK						Mascot	
	1853.9061	1853.8102	-0.0959	-52	401	416	GELQCIGATTLDEYRK				Carbamidomethyl (C)[5]		Mascot	
	1936.856	1936.7715	-0.0845	-44	772	787	IGFDLDYDEKSSYNR						Mascot	
	1959.0446	1958.9497	-0.0949	-48	633	651	NPNRPISAFISGPTGVG K						Mascot	
	1959.0446	1958.9497	-0.0949	-48	633	651	NPNRPISAFISGPTGVG K	19	0				Mascot	
	1985.9572	1985.8607	-0.0965	-49	722	738	AHPDVFNMMLQILEDGR						Mascot	
	2001.952	2001.8546	-0.0974	-49	722	738	AHPDVFNMMLQILEDGR				Oxidation (M)[8]		Mascot	
	2033.129	2033.0286	-0.1004	-49	190	207	QLGHNYIGSEHLLGLLR						Mascot	
	2033.129	2033.0286	-0.1004	-49	190	207	QLGHNYIGSEHLLGLLR	31	89.805				Mascot	
	2264.1558	2264.0466	-0.1092	-48	686	707	LIGSPPGYGYTEGGQLT EAVR						Mascot	
	2264.1558	2264.0466	-0.1092	-48	686	707	LIGSPPGYGYTEGGQLT EAVR	37	97.343				Mascot	
	2508.3821	2508.2573	-0.1248	-50	116	140	LGHNFVGTQEILLGLIGE GTGIAAK						Mascot	
4	Chaperone protein ClpC1, chloroplastic OS=Oryza sativa subsp. japonica GN=CLPC1 PE=2 SV=2					CLPC1_ORYSJ	101738.6	6.14	22	267	100	163	100	
	<b>Peptide Information</b>													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	856.4635	856.4855	0.022	26	415	421	DPALERR						Mascot	
	1022.5339	1022.48	-0.0539	-53	802	809	LDEMIVFR						Mascot	
	1029.5687	1029.5099	-0.0588	-57	303	312	TAIEAGLAQR						Mascot	
	1038.5288	1038.4738	-0.055	-53	802	809	LDEMIVFR				Oxidation (M)[4]		Mascot	
	1085.501	1085.4475	-0.0535	-49	341	348	YRGFEFER	10	0				Mascot	
	1085.501	1085.4475	-0.0535	-49	341	348	YRGFEFER						Mascot	
	1102.6653	1102.5157	-0.1496	-136	134	143	VLSMGINKLK						Mascot	
	1157.4966	1157.4712	-0.0254	-22	666	674	LDMSEFMR						Mascot	
	1158.5612	1158.564	0.0028	2	86	94	AMFERFTEK						Mascot	
	1159.5953	1159.5569	-0.0384	-33	479	489	AIDLIDEAGSR						Mascot	
	1173.4915	1173.4427	-0.0488	-42	666	674	LDMSEFMR				Oxidation (M)[3]		Mascot	
	1207.6429	1207.5828	-0.0601	-50	411	420	HIEKDPALER						Mascot	
	1369.7012	1369.6356	-0.0656	-48	792	801	QYRFPEFLNR	3	0				Mascot	
	1369.7012	1369.6356	-0.0656	-48	792	801	QYRFPEFLNR						Mascot	
	1382.7638	1382.6945	-0.0693	-50	261	273	LAEEGKLPVVGR						Mascot	
	1471.8301	1471.7015	-0.1286	-87	95	107	AIKVIMLAQEAR						Mascot	
	1476.7845	1476.7109	-0.0736	-50	156	169	GSGFVAVEIPTPR	38	97.83				Mascot	
	1476.7845	1476.7109	-0.0736	-5										

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
856.4635	856.4855	0.022	26	421	427	DPALERR					Mascot
1029.5687	1029.5099	-0.0588	-57	309	318	TAIAEGLAQR					Mascot
1051.4976	1051.65	0.1524	145	876	884	LLEDSMAEK			Oxidation (M)[6]		Mascot
1085.501	1085.4475	-0.0535	-49	347	354	YRGEFEER	10	0			Mascot
1085.501	1085.4475	-0.0535	-49	347	354	YRGEFEER					Mascot
1102.6653	1102.5157	-0.1496	-136	140	149	VLKSMGINLK					Mascot
1157.4966	1157.4712	-0.0254	-22	673	681	LDMSEFMER					Mascot
1158.5612	1158.564	0.0028	2	92	100	AMFERFTEK					Mascot
1159.5953	1159.5569	-0.0384	-33	485	495	AIDLDEAGSR					Mascot
1173.4915	1173.4427	-0.0488	-42	673	681	LDMSEFMER			Oxidation (M)[3]		Mascot
1207.6429	1207.5828	-0.0601	-50	417	426	HIEKDPALER					Mascot
1369.7012	1369.6356	-0.0656	-48	799	808	QYFRPEFLNR	3	0			Mascot
1369.7012	1369.6356	-0.0656	-48	799	808	QYFRPEFLNR					Mascot
1382.7638	1382.6945	-0.0693	-50	267	279	LAEEGKLDPVVGR					Mascot
1411.7539	1411.6821	-0.0718	-51	215	227	VLENLGADPTNIR					Mascot
1411.7539	1411.6821	-0.0718	-51	215	227	VLENLGADPTNIR	19	0			Mascot
1440.6835	1440.6044	-0.0791	-55	42	54	CCSSRLNMFAGLR					Mascot
1440.6835	1440.6044	-0.0791	-55	42	54	CCSSRLNMFAGLR	4	0			Mascot
1471.8301	1471.7015	-0.1286	-87	101	113	AIKVMLAQEAR					Mascot
1608.8632	1608.78	-0.0832	-52	710	722	RPYTVVLFDEIEK	5	0			Mascot
1608.8632	1608.78	-0.0832	-52	710	722	RPYTVVLFDEIEK					Mascot
1764.9642	1764.868	-0.0962	-55	709	722	RRPYTVVLFDEIEK			Carbamidomethyl (C)[5]		Mascot
1853.9061	1853.8102	-0.0959	-52	401	416	GELQCIGATTLDEYRK					Mascot
1959.0446	1958.9497	-0.0949	-48	634	652	NPNRPIASFISGPTGVG					Mascot
						K					
1959.0446	1958.9497	-0.0949	-48	634	652	NPNRPIASFISGPTGVG	19	0			Mascot
						K					
1985.9572	1985.8607	-0.0965	-49	723	739	AHPDVFNMMLQILEDGR			Oxidation (M)[8]		Mascot
2001.952	2001.8546	-0.0974	-49	723	739	AHPDVFNMMLQILEDGR					Mascot
2033.129	2033.0286	-0.1004	-49	189	206	QLGHNYIGSEHLLGLLR					Mascot
2033.129	2033.0286	-0.1004	-49	189	206	QLGHNYIGSEHLLGLLR	31	89.805			Mascot
2264.1558	2264.0466	-0.1092	-48	687	708	LIGSPPGYVGYTEGGQLT					Mascot
						EAVR					
2264.1558	2264.0466	-0.1092	-48	687	708	LIGSPPGYVGYTEGGQLT	37	97.343			Mascot
						EAVR					
2508.3821	2508.2573	-0.1248	-50	115	139	LGHNFVGTQILLGLIGE					Mascot
						GTGIAAK					

7   Chaperone protein ClpC2, chloroplastic OS=Oryza sativa subsp. japonica GN=CLPC2 PE=2 SV=2

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
856.4635	856.4855	0.022	26	416	422	DPALERR					Mascot
1022.5339	1022.48	-0.0539	-53	803	810	LDEMIVFR					Mascot
1029.5687	1029.5099	-0.0588	-57	304	313	TAIAEGLAQR			Oxidation (M)[4]		Mascot
1038.5288	1038.4738	-0.055	-53	803	810	LDEMIVFR					Mascot
1085.501	1085.4475	-0.0535	-49	342	349	YRGEFEER	10	0			Mascot
1085.501	1085.4475	-0.0535	-49	342	349	YRGEFEER					Mascot
1102.6653	1102.5157	-0.1496	-136	135	144	VLKSMGINLK					Mascot
1157.4966	1157.4712	-0.0254	-22	667	675	LDMSEFMER					Mascot
1158.6365	1158.564	-0.0725	-63	174	183	VLESLSEEAR					Mascot
1159.5953	1159.5569	-0.0384	-33	480	490	AIDLDEAGSR			Oxidation (M)[3]		Mascot
1173.4915	1173.4427	-0.0488	-42	667	675	LDMSEFMER					Mascot
1207.6429	1207.5828	-0.0601	-50	412	421	HIEKDPALER					Mascot
1369.7012	1369.6356	-0.0656	-48	793	802	QYFRPEFLNR	3	0			Mascot
1369.7012	1369.6356	-0.0656	-48	793	802	QYFRPEFLNR					Mascot
1382.7638	1382.6945	-0.0693	-50	262	274	LAEEGKLDPVVGR					Mascot
1471.8301	1471.7015	-0.1286	-87	96	108	AIKVMLAQEAR			Oxidation (M)[6]		Mascot
1608.8302	1608.78	-0.0502	-31	819	831	EIAEIMLKVEFDR					Mascot
1608.8632	1608.78	-0.0832	-52	704	716	RPYTVVLFDEIEK	5	0			Mascot
1691.8097	1691.7239	-0.0858	-51	652	666	ALAAYYFGSEEMIR					Mascot
1691.8097	1691.7239	-0.0858	-51	652	666	ALAAYYFGSEEMIR	19	0			Mascot
1707.8047	1707.7291	-0.0756	-44	652	666	ALAAYYFGSEEMIR			Oxidation (M)[13]		Mascot
1764.9642	1764.868	-0.0962	-55	703	716	RRPYTVVLFDEIEK					Mascot
1853.9061	1853.8102	-0.0959	-52	396	411	GELQCIGATTLDEYRK			Carbamidomethyl (C)[5]		Mascot
1985.9572	1985.8607	-0.0965	-49	717	733	AHPDVFNMMLQILEDGR					Mascot
2001.952	2001.8546	-0.0974	-49	717	733	AHPDVFNMMLQILEDGR			Oxidation (M)[8]		Mascot
2033.129	2033.0286	-0.1004	-49	184	201	QLGHNYIGSEHLLGLLR					Mascot
2033.129	2033.0286	-0.1004	-49	184	201	QLGHNYIGSEHLLGLLR	31	89.805			Mascot
2264.1558	2264.0466	-0.1092	-48	681	702	LIGSPPGYVGYTEGGQLT					Mascot
						EAVR					
2264.1558	2264.0466	-0.1092	-48	681	702	LIGSPPGYVGYTEGGQLT	37	97.343			Mascot
						EAVR					
2508.3821	2508.2573	-0.1248	-50	110	134	LGHNFVGTQILLGLIGE					Mascot
						GTGIAAK					

8   ATP-dependent Clp protease ATP-binding subunit clpA homolog, chloroplastic (Fragment) OS=Brassica n

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
856.4635	856.4855	0.022	26	368	374	DPALERR					Mascot
1029.5687	1029.5099	-0.0588	-57	256	265	TAIAEGLAQR					Mascot
1085.501	1085.4475	-0.0535	-49	294	301	YRGEFEER	10	0			Mascot
1085.501	1085.4475	-0.0535	-49	294	301	YRGEFEER					Mascot
1102.5739	1102.5157	-0.0582	-53	786	794	EVELOVTER					Mascot
1157.4966	1157.4712	-0.0254	-22	618	626	LDMSEFMER					Mascot
1158.5612	1158.564	0.0028	2	40	48	AMFERFTEK					Mascot
1159.614	1159.5569	-0.0571	-49	52	61	VIMLAQEEAR			Oxidation (M)[3]		Mascot
1173.4915	1173.4427	-0.0488	-42	618	626	LDMSEFMER					Mascot
1207.6429	1207.5828	-0.0601	-50	364	373	HIEKDPALER					Mascot
1369.7012	1369.6356	-0.0656	-48	743	752	QYFRPEFLNR					Mascot
1369.7012	1369.6356	-0.0656	-48	743	752	QYFRPEFLNR	3	0			Mascot
1382.7638	1382.6945	-0.0693	-50	214	226	LAEEGKLDPVVGR					Mascot
1471.8301	1471.7015	-0.1286	-87	49	61	AIKVMLAQEEAR					Mascot
1476.7845	1476.7109	-0.0736	-50	110	123	GSGFVAVEIPTPTR					Mascot
1476.7845	1476.7109	-0.0736	-50	110	123	GSGFVAVEIPTPTR	38	97.83			Mascot
1581.8734	1581.7803	-0.0931	-59	380	393	VPEPTVDETIQILK					Mascot
1608.8632	1608.78	-0.0832	-52	655	667	RPYTVVLFDEIEK	5	0			Mascot
1608.8632	1608.78	-0.0832	-52	655	667	RPYTVVLFDEIEK					Mascot
1707.7869	1707.7291	-0.0578	-34	603	617	ALAAYYFGCEAMIR			Carbamidomethyl (C)[9]		Mascot
1764.8063	1764.868	0.0597	34	603	617	ALAAYYFGCEAMIR			Carbamidomethyl (C)[5]		Mascot
1853.9061	1853.8102	-0.0959	-52	348	363	GELQCIGATTLDEYRK					Mascot
1985.9572	1985.8607	-0.0965	-49	668	684	AHPDVFNMMLQILEDGR					Mascot
2001.952	2001.8546	-0.0974	-49	668	684	AHPDVFNMMLQILEDGR			Oxidation (M)[8]		Mascot
2033.129	2033.0286	-0.1004	-49	137	154	QLGHNYIGSEHLLGLLR					Mascot
2033.129	2033.0286	-0.1004	-49	137	154	QLGHNYIGSEHLLGLLR	31	89.805			Mascot
2508.3821	2508.2573	-0.1248	-50	63	87	LGHNFVGTQILLGLIGE					Mascot
						GTGIAAK					

9   ATP-dependent Clp protease ATP-binding subunit clpA homolog (Fragments) OS=Populus euphratica PE=1

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
1158.6365	1158.564	-0.0725	-63	15	24	VLELSLEEAR	38	97.83				
1159.5953	1159.5569	-0.0384	-33	62	72	AIDLIDEAGSR						
1476.7845	1476.7109	-0.0736	-50	1	14	GSGFVAVEIPTPR						
1476.7845	1476.7109	-0.0736	-50	1	14	GSGFVAVEIPTPR						

10

Putative disease resistance protein At5g05400  
OS=Arabidopsis thaliana GN=At5g05400 PE=2 SV=1

DRL31\_ARATH99693.86.091645

0

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
1085.5837	1085.4475	-0.1362	-125	497	505	DIPKIEDQK	49	99.717	Oxidation (M)[8]		Mascot	
1085.5837	1085.4475	-0.1362	-125	497	505	DIPKIEDQK					Mascot	
1102.6401	1102.5157	-0.1244	-113	638	646	LVRQIQAMK					Mascot	
1156.4979	1156.5535	0.0556	48	109	117	CKYSVDYSK					Mascot	
1158.6365	1158.564	-0.0725	-63	123	132	LQDVENLLSK					Mascot	
1207.7157	1207.5828	-0.1329	-110	31	41	NLVDHVAALKK					Mascot	
1261.6747	1261.6548	-0.0199	-16	242	252	TENEIASTIKR					Mascot	
1382.7903	1382.6945	-0.0958	-69	29	40	FRNLVDHVAALK					Mascot	
1411.6998	1411.6821	-0.0177	-13	287	299	IAFTSRSENEVCVK				Mascot		
1411.6998	1411.6821	-0.0177	-13	287	299	IAFTSRSENEVCVK				Mascot		
1581.7036	1581.7803	0.0767	48	469	482	EMALWISSGCGDQK				Carbamidomethyl (C)[10]	Mascot	
1764.9353	1764.868	-0.0673	-38	598	611	NLLYLNLHTYMLK					Mascot	
1779.0123	1778.9105	-0.1018	-57	485	500	NVLVVEANAQLRDIPK					Mascot	
1853.8521	1853.8102	-0.0419	-23	469	484	EMALWISSGCGDQKQK				Carbamidomethyl (C)[10], Oxidation (M)[2]	Mascot	
1937.0314	1936.7715	-0.2599	-134	598	612	NLLYLNLHTYMLKR				Oxidation (M)[12]	Mascot	
2211.1477	2210.9971	-0.1506	-68	578	597	FLNLSCTGTSPLDGLYALR				Carbamidomethyl (C)[6]	Mascot	
2264.2107	2264.0466	-0.1641	-72	786	804	TCELAGVIPFRELEFLTLR	786	804	Carbamidomethyl (C)[2]	Mascot		
2264.2107	2264.0466	-0.1641	-72	786	804	TCELAGVIPFRELEFLTLR			Carbamidomethyl (C)[2]	Mascot		
2281.0298	2281.0325	0.0027	1	510	528	MSLIYNQIEACESLHCPK			Carbamidomethyl (C)[12], Oxidation (M)[1]	Mascot		

Gel Idx/Pos	104/E3	Instr./Gel Origin	BA2060/140227A	Process Statu	Analysis Succeeded
Plate [W] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	Ribulose biphosphate carboxylase large chain OS=Carica papaya GN=rbcl PE=3 SV=2	RBL_CARPA	52456.6	6.19	22	448	100	280	100

Ribulose biphosphate carboxylase large chain				RBL_CARPA		52456.6		6.19		22		448		100		280		100	
OS=Carica papaya GN=rbcl PE=3 SV=2																			
Peptide Information																			
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type					
830.4366	830.3968	-0.0398	-48	440	446	EGNEIIR	49	99.717						Mascot					
898.41	898.3635	-0.0465	-52	306	312	NHGMHFR								Mascot					
910.4451	910.3972	-0.0479	-53	188	194	AVYECLR			Carbamidomethyl (C)[5]					Mascot					
912.4719	912.415	-0.0569	-62	296	303	AMHAVIDR								Mascot					
914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]					Mascot					
914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]					Mascot					
928.4669	928.4146	-0.0523	-56	296	303	AMHAVIDR			Oxidation (M)[2]					Mascot					
1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR								Mascot					
1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR								Mascot					
1037.4899	1037.4475	-0.0424	-41	351	358	DEFVEKDR								Mascot					
1038.5143	1038.5524	0.0381	37	467	475	FEFPAVDTI								Mascot					
1059.5615	1059.5039	-0.0576	-54	422	431	VALEACVQAR								Mascot					
1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR			Carbamidomethyl (C)[6]					Mascot					
1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR			Carbamidomethyl (C)[6]					Mascot					
1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR			Oxidation (M)[6]					Mascot					
1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR			Oxidation (M)[6]					Mascot					
1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR	51	99.814						Mascot					
1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR								Mascot					
1245.6433	1245.5686	-0.0747	-60	440	450	EGNEIIR EASK								Mascot					
1261.6285	1261.6472	0.0187	15	218	227	FLFCAEAIYK	55	99.933	Carbamidomethyl (C)[4]					Mascot					
1261.7151	1261.6472	-0.0679	-54	340	350	DTLGFVDLLR								Mascot					
1392.6682	1392.6152	-0.053	-38	22	32	LTYYTPDYQTK								Mascot					
1447.7651	1447.6831	-0.082	-57	320	334	LSGGDHIHAGTVVGK	70	99.998						Mascot					
1451.6219	1451.5728	-0.0491	-34	202	213	DDENVNSQPFMR								Mascot					
1465.7546	1465.6771	-0.0775	-53	147	159	TFQGPPIHGIQVER								Mascot					
1465.7546	1465.6771	-0.0775	-53	147	159	TFQGPPIHGIQVER								Mascot					
1502.8512	1502.762	-0.0892	-59	165	177	YGRPLLCTKPK			Carbamidomethyl (C)[8]					Mascot					
1794.8149	1794.7466	-0.0683	-38	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]					Mascot					
2009.059	2008.9557	-0.1033	-51	340	356	DTLGFVDLLRDEFVEK								Mascot					
2169.9868	2169.8723	-0.1145	-53	195	213	GGLDFTKDDENVNSQPFMR								Mascot					
2169.9868	2169.8723	-0.1145	-53	195	213	GGLDFTKDDENVNSQPFMR								Mascot					
2185.9819	2185.8694	-0.1125	-51	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]					Mascot					
3854.8718	3854.688	-0.1838	-48	42	79	VTPOGPVPPEEAGAAVA								Mascot					

2

Ribulose biphosphate carboxylase large chain  
(Fragment) OS=Humiria balsamifera GN=rbcl PE=3 SV=1

RBL\_HUMBA51530.16.2321443100280100

Ribulose bispophosphate carboxylase large chain				RBL_HUMBA		51530.1	6.23	21	443	100	280	100
(Fragment) OS=Humiria balsamifera GN=rbcL PE=3 SV=1												
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
830.4366	830.3968	-0.0398	-48	430	436	EGNEIIR					Mascot	
898.41	898.3635	-0.0465	-52	296	302	NHGMHFR					Mascot	
910.4451	910.3972	-0.0479	-53	178	184	AVYECLR			Carbamidomethyl (C)[5]		Mascot	
912.4719	912.415	-0.0569	-62	286	293	AMHAVIDR					Mascot	
914.4049	914.3581	-0.0468	-51	296	302	NHGMHFR			Oxidation (M)[4]		Mascot	
914.4049	914.3581	-0.0468	-51	296	302	NHGMHFR			Oxidation (M)[4]		Mascot	
928.4669	928.4146	-0.0523	-56	286	293	AMHAVIDR			Oxidation (M)[2]		Mascot	
1021.5312	1021.4777	-0.0535	-52	23	31	DTDILAAFR					Mascot	
1021.5312	1021.4777	-0.0535	-52	23	31	DTDILAAFR					Mascot	
1037.4899	1037.4475	-0.0424	-41	341	348	DDFIEKDR	49	99.717			Mascot	
1059.5979	1059.5039	-0.094	-89	412	421	VALEACVKAR					Mascot	
1116.6194	1116.5209	-0.0985	-88	412	421	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot	
1116.6194	1116.5209	-0.0985	-88	412	421	VALEACVKAR	10	0	Carbamidomethyl (C)[6]		Mascot	
1170.5585	1170.5731	0.0146	12	294	302	QKNHGMHFR			Oxidation (M)[6]		Mascot	
1170.5585	1170.5731	0.0146	12	294	302	QKNHGMHFR			Oxidation (M)[6]		Mascot	
1187.6643	1187.6014	-0.0629	-53	276	285	DNGLLLHIHR	51	99.814			Mascot	
1187.6643	1187.6014	-0.0629	-53	276	285	DNGLLLHIHR					Mascot	
1245.6433	1245.5686	-0.0747	-60	430	440	EGNEIIREASK					Mascot	
1261.6285	1261.6472	0.0187	15	208	217	FLFCAEALYK			Carbamidomethyl (C)[4]		Mascot	
1261.7151	1261.6472	-0.0679	-54	330	340	DTLGFVDLLR	55	99.933			Mascot	
1447.7651	1447.6831	-0.082	-57	310	324	LSGGDHIHAGTVVGK					Mascot	
1451.6219	1451.5728	-0.0491	-34	192	203	DDENVNSQPFMR					Mascot	

	1465.7546	1465.6771	-0.0775	-53	137	149	TFQGGPPHGIQVER		70	99.998						Mascot
	1465.7546	1465.6771	-0.0775	-53	137	149	TFQGGPPHGIQVER									Mascot
	1502.8512	1502.762	-0.0892	-59	165	167	YGRPLLGGCTKPK									Mascot
	1794.8149	1794.7466	-0.0683	-38	227	242	GHYLNATAGTCEEIMK						Carbamidomethyl (C)[8]			Mascot
	2009.059	2008.9557	-0.1033	-51	330	346	DITLGFVDLLRDDFIEK						Carbamidomethyl (C)[11]			Mascot
	2169.9868	2169.8723	-0.1145	-53	185	203	GGLDFTKDDENVNSQPF MR									Mascot
	2169.9868	2169.8723	-0.1145	-53	185	203	GGLDFTKDDENVNSQPF MR		47	99.593						Mascot
	2185.9819	2185.8694	-0.1125	-51	185	203	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]			Mascot
	3022.4548	3022.2837	-0.1711	-57	249	275	ELGVPIVMHDYLTGGFTA NTLAHCYCR						Carbamidomethyl (C)[26]			Mascot
	3038.45	3038.2849	-0.1651	-54	249	275	ELGVPIVMHDYLTGGFTA NTLAHCYCR						Carbamidomethyl (C)[26], Oxidation (M)[8]			Mascot
	3854.8718	3854.688	-0.1838	-48	32	69	VTPQGPVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot
3	Ribulose biphosphate carboxylase large chain OS=Manihot esculenta GN=rbcl PE=3 SV=1						RBL_MANES	52648.5	6.18	21	438		100	280	100	
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification		Rank	Result Type	
	898.41	898.3635	-0.0465	-52	306	312	NHGMHFR									Mascot
	910.4451	910.3972	-0.0479	-53	188	194	AVYECLR					Carbamidomethyl (C)[5]				Mascot
	912.4719	912.415	-0.0569	-62	296	303	AMHAVIDR									Mascot
	914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR					Oxidation (M)[4]				Mascot
	914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR					Oxidation (M)[4]				Mascot
	928.4669	928.4146	-0.0523	-56	296	303	AMHAVIDR					Oxidation (M)[2]				Mascot
	1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR									Mascot
	1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR		49	99.717						Mascot
	1037.4899	1037.4475	-0.0424	-41	351	358	DDFIEKDR									Mascot
	1059.5615	1059.5039	-0.0576	-54	422	431	VALEACVQAR									Mascot
	1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR					Carbamidomethyl (C)[6]				Mascot
	1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR		10	0		Carbamidomethyl (C)[6]				Mascot
	1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR					Oxidation (M)[6]				Mascot
	1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR					Oxidation (M)[6]				Mascot
	1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR		51	99.814						Mascot
	1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR									Mascot
	1231.6277	1231.5437	-0.084	-68	440	450	EGNDIIREASK									Mascot
	1261.6285	1261.6472	0.0187	15	218	227	FLFCAEAIK					Carbamidomethyl (C)[4]				Mascot

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
830.4366	830.3968	-0.0398	-48	431	437	EGNEIIR					Mascot
898.41	898.3635	-0.0465	-52	297	303	NHGMHFR					Mascot
910.4451	910.3972	-0.0479	-53	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
912.4719	912.415	-0.0569	-62	287	294	AMHAVIDR					Mascot
914.4049	914.3581	-0.0468	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
914.4049	914.3581	-0.0468	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.4146	-0.0523	-56	287	294	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4777	-0.0535	-52	24	32	DTDILAAFR					Mascot
1021.5312	1021.4777	-0.0535	-52	24	32	DTDILAAFR	49	99.717			Mascot
1037.4899	1037.4475	-0.0424	-41	342	349	DDFIEKDR					Mascot
1059.5615	1059.5039	-0.0576	-54	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5209	-0.0621	-56	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5209	-0.0621	-56	413	422	VALEACVQAR	10	0			Mascot
1170.5585	1170.5731	0.0146	12	295	303	QKNHGMHFR			Oxidation (M)[6]		Mascot
1170.5585	1170.5731	0.0146	12	295	303	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6014	-0.0629	-53	277	286	DNGLLLIHR	51	99.814			Mascot
1187.6643	1187.6014	-0.0629	-53	277	286	DNGLLLIHR					Mascot
1245.6337	1245.5686	-0.0651	-52	209	218	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6472	-0.0679	-54	331	341	DITLGFVDLLR	55	99.933			Mascot
1261.7151	1261.6472	-0.0679	-54	331	341	DITLGFVDLLR					Mascot
1451.6219	1451.5728	-0.0491	-34	193	204	DDENVNSQPFMR					Mascot
1465.7216	1465.6771	-0.0445	-30	311	325	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6771	-0.0775	-53	138	150	TFQGPPIHGIQVER	70	99.998			Mascot
1502.8512	1502.762	-0.0892	-59	156	168	YGRPLLCTIKPK			Carbamidomethyl (C)[8]		Mascot
1794.8149	1794.7466	-0.0683	-38	228	243	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot
2009.059	2008.9557	-0.1033	-51	331	347	DITLGFVDLLRDDFIEK					Mascot
2169.9868	2169.8723	-0.1145	-53	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2169.9868	2169.8723	-0.1145	-53	186	204	GGLDFTKDDENVNSQPFMR	47	99.593			Mascot
2185.9819	2185.8694	-0.1125	-51	186	204	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3022.4548	3022.2837	-0.1711	-57	250	276	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26]		Mascot
						NTSLAHYCR					
3038.45	3038.2849	-0.1651	-54	250	276	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26], Oxidation (M)[8]		Mascot
						NTSLAHYCR					
3854.8718	3854.688	-0.1838	-48	33	70	VTQPQGVPEEAGAAVA					Mascot
						AESSTGTWTTVWTDGLTSLDR					

6 Ribulose biphosphate carboxylase large chain RBL\_PACAAQ 52040.3 6.24 19 422 100 282 100  
(Fragment) OS=Pachira aquatica GN=rbcl PE=3 SV=1

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
830.4366	830.3968	-0.0398	-48	433	439	EGNEIIR					Mascot
898.41	898.3635	-0.0465	-52	299	305	NHGMHFR					Mascot
910.4451	910.3972	-0.0479	-53	181	187	AVYECLR			Carbamidomethyl (C)[5]		Mascot
912.4719	912.415	-0.0569	-62	289	296	AMHAVIDR					Mascot
914.4049	914.3581	-0.0468	-51	299	305	NHGMHFR			Oxidation (M)[4]		Mascot
914.4049	914.3581	-0.0468	-51	299	305	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.4146	-0.0523	-56	289	296	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4777	-0.0535	-52	26	34	DTDILAAFR					Mascot
1021.5312	1021.4777	-0.0535	-52	26	34	DTDILAAFR	49	99.717			Mascot
1037.4899	1037.4475	-0.0424	-41	344	351	DDFIEKDR					Mascot
1059.5979	1059.5039	-0.094	-89	415	424	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1116.6194	1116.5209	-0.0985	-88	415	424	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1116.6194	1116.5209	-0.0985	-88	415	424	VALEACVKAR	10	0			Mascot
1170.5585	1170.5731	0.0146	12	297	305	QKNHGMHFR			Oxidation (M)[6]		Mascot
1170.5585	1170.5731	0.0146	12	297	305	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6014	-0.0629	-53	279	288	DNGLLLIHR	51	99.814			Mascot
1187.6643	1187.6014	-0.0629	-53	279	288	DNGLLLIHR					Mascot
1245.6433	1245.5686	-0.0747	-60	433	443	EGNEIREASK					Mascot
1261.7151	1261.6472	-0.0679	-54	333	343	DITLGFVDLLR	55	99.933			Mascot
1261.7151	1261.6472	-0.0679	-54	333	343	DITLGFVDLLR					Mascot
1447.7651	1447.6831	-0.082	-57	313	327	LSGGDHIHAGTVVGK					Mascot
1451.6219	1451.5728	-0.0491	-34	195	206	DDENVNSQPFMR					Mascot
1465.7546	1465.6771	-0.0775	-53	140	152	TFQGPPIHGIQVER	70	99.998			Mascot
1465.7546	1465.6771	-0.0775	-53	140	152	TFQGPPIHGIQVER					Mascot
1502.8512	1502.762	-0.0892	-59	158	170	YGRPLLCTIKPK			Carbamidomethyl (C)[8]		Mascot
2009.059	2008.9557	-0.1033	-51	333	349	DITLGFVDLLRDDFIEK					Mascot
2169.9868	2169.8723	-0.1145	-53	188	206	GGLDFTKDDENVNSQPFMR					Mascot
2169.9868	2169.8723	-0.1145	-53	188	206	GGLDFTKDDENVNSQPFMR	47	99.593			Mascot
2185.9819	2185.8694	-0.1125	-51	188	206	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3022.4548	3022.2837	-0.1711	-57	252	278	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26]		Mascot
						NTSLAHYCR					
3038.45	3038.2849	-0.1651	-54	252	278	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26], Oxidation (M)[8]		Mascot
						NTSLAHYCR					
3854.8718	3854.688	-0.1838	-48	35	72	VTQPQGVPEEAGAAVA					Mascot
						AESSTGTWTTVWTDGLTSLDR					

7 Ribulose biphosphate carboxylase large chain RBL\_GOSHI 52667.3 5.91 20 416 100 280 100  
OS=Gossypium hirsutum GN=rbcl PE=3 SV=2

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
830.4366	830.3968	-0.0398	-48	440	446	EGNEIIR					Mascot
898.41	898.3635	-0.0465	-52	306	312	NHGMHFR					Mascot
910.4451	910.3972	-0.0479	-53	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot
912.4719	912.415	-0.0569	-62	296	303	AMHAVIDR					Mascot
914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.4146	-0.0523	-56	296	303	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR					Mascot
1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR	49	99.717			Mascot
1037.4899	1037.4475	-0.0424	-41	351	358	DDFIEKDR					Mascot
1059.5615	1059.5039	-0.0576	-54	422	431	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR	10	0			Mascot
1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR			Oxidation (M)[6]		Mascot
1170.5585	1170.5731	0.0146	12	304	312	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLIHR	51	99.814			Mascot
1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLIHR					Mascot
1245.6337	1245.5686	-0.0651	-52	218	227	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6472	-0.0679	-54	340	350	DITLGFVDLLR	55	99.933			Mascot
1261.7151	1261.6472	-0.0679	-54	340	350	DITLGFVDLLR					Mascot
1451.6219	1451.5728	-0.0491	-34	202	213	DDENVNSQPFMR					Mascot
1465.7216	1465.6771	-0.0445	-30	320	334	MSGGDHIHAGTVVGK					Mascot



	1465.7546	1465.6771	-0.0775	-53	147	159	TFQGPPHGIOVER	70	99.998				Mascot
	1502.8512	1502.762	-0.0892	-59	165	177	YGRPLLGGCTKPK			Carbamidomethyl (C)[8]		Mascot	
	1794.8149	1794.7466	-0.0683	-38	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot	
	2009.059	2008.9557	-0.1033	-51	340	356	DITLGFVLLRRDDFIEK					Mascot	
	2169.9868	2169.8723	-0.1145	-53	195	213	GGDLFTKDDENVNSQPFFMR					Mascot	
	2169.9868	2169.8723	-0.1145	-53	195	213	GGDLFTKDDENVNSQPFFMR	47	99.593			Mascot	
	2185.9819	2185.8694	-0.1125	-51	195	213	GGDLFTKDDENVNSQPFFMR			Oxidation (M)[18]		Mascot	
	3022.4548	3022.2837	-0.1711	-57	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]		Mascot	
	3038.45	3038.2849	-0.1651	-54	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26], Oxidation (M)[8]		Mascot	
	3854.8718	3854.688	-0.1838	-48	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTGLTSLDR					Mascot	
8	Ribulose biphosphate carboxylase large chain OS=Viscum album GN=rbcL PE=3 SV=1	RBL_VISAL	52356.5	6.44	19	414		100	280	100			
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	830.4366	830.3968	-0.0398	-48	440	446	EGNEIIR					Mascot	
	898.41	898.3635	-0.0465	-52	306	312	NHGMHFR					Mascot	
	910.4451	910.3972	-0.0479	-53	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot	
	912.4719	912.415	-0.0569	-62	296	303	AMHAVIDR					Mascot	
	914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot	
	914.4049	914.3581	-0.0468	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot	
	928.4669	928.4146	-0.0523	-56	296	303	AMHAVIDR			Oxidation (M)[2]		Mascot	
	1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR					Mascot	
	1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR	49	99.717			Mascot	
	1037.4899	1037.4475	-0.0424	-41	351	358	DOFIEKDR					Mascot	
	1059.5615	1059.5039	-0.0576	-54	422	431	VALEACVQAR					Mascot	
	1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot	
	1116.583	1116.5209	-0.0621	-56	422	431	VALEACVQAR	10	0	Carbamidomethyl (C)[6]		Mascot	
	1170.5585	1170.5731	0.0146	12	304	312	QKNHGMMHFR			Oxidation (M)[6]		Mascot	
	1170.5585	1170.5731	0.0146	12	304	312	QKNHGMMHFR			Oxidation (M)[6]		Mascot	
	1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR	51	99.814			Mascot	
	1187.6643	1187.6014	-0.0629	-53	286	295	DNGLLLHIHR					Mascot	
	1245.6433	1245.5686	-0.0747	-60	440	450	EGNEIIREASK					Mascot	
	1261.7151	1261.6472	-0.0679	-54	340	350	DITLGFVDLLR	55	99.933			Mascot	
	1261.7151	1261.6472	-0.0679	-54	340	350	DITLGFVDLLR					Mascot	
	1451.6219	1451.5728	-0.0491	-34	202	213	DDENVNSQPFMR					Mascot	
	1465.7216	1465.6771	-0.0445	-30	320	334	MSGGDHHIACTVVGK					Mascot	
	1465.7546	1465.6771	-0.0775	-53	147	159	TFQGPPHGIOVER	70	99.998			Mascot	
	1502.8512	1502.762	-0.0892	-59	165	177	YGRPLLGGCTKPK			Carbamidomethyl (C)[8]		Mascot	
	2009.059	2008.9557	-0.1033	-51	340	356	DITLGFVLLRRDDFIEK					Mascot	

Peptide Information				Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm								
898.41	898.3658	-0.0442	-49	297	303	NHGMHFR	36	96.292	Carbamidomethyl (C)[5] Oxidation (M)[4]		Mascot
910.4451	910.3988	-0.0463	-51	179	185	AVYECLR					Mascot
914.4049	914.3587	-0.0462	-51	297	303	NHGMHFR					Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDLIAFR					Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDLIAFR			Carbamidomethyl (C)[6] Oxidation (M)[6]		Mascot
1116.6194	1116.5275	-0.0919	-82	413	422	VALEACVKAR					Mascot
1170.5585	1170.5809	0.0224	19	295	303	QKNHGMHFR					Mascot
1187.6643	1187.6013	-0.063	-53	277	286	DNGLLHIHR					Mascot

	1261.6285	1261.6495	0.021	-17	209	218	FLFCAEALYK											Carbamidomethyl (C)[4]	Mascot
	1261.7151	1261.6495	-0.0656	-52	331	341	DITLGFVDLLR		48	99.741									Mascot
	1451.6219	1451.5642	-0.0577	-40	193	204	DDENVNSQPFMR											Mascot	
	1465.7216	1465.6801	-0.0415	-28	311	325	MSGGDHIHAGTVVGK											Mascot	
	1465.7546	1465.6801	-0.0745	-51	138	150	TFQGGPHGIOVER		14		0							Mascot	
	1502.8512	1502.7705	-0.0807	-54	156	168	YGRPLLGGCTKPK						Carbamidomethyl (C)[8]					Mascot	
	1557.8231	1557.6057	-0.2174	-140	427	441	DLLAAEGNAIREASK											Mascot	
	1557.8231	1557.6057	-0.2174	-140	427	441	DLLAAEGNAIREASK											Mascot	
	2009.059	2008.9675	-0.0915	-46	331	347	DITLGFVDLLRDDFIEK											Mascot	
	2169.9868	2169.8877	-0.0991	-46	186	204	GGLDFTKDDENVNSQPFMR											Mascot	
2185.9819	2185.8796	-0.1023	-47	186	204	GGLDFTKDDENVNSQPFMR							Oxidation (M)[18]				Mascot		
3022.4548	3022.3562	-0.0986	-33	250	276	ELGVPIVMHDYLTGGFTA							Carbamidomethyl (C)[26]				Mascot		
3854.8718	3854.6746	-0.1972	-51	33	70	VTPOQGVPPPEAGAAVA												Mascot	
4	Ribulose biphosphate carboxylase large chain (Fragment) OS=Humiria balsamifera GN=rbcl PE=3 SV=1				RBL_HUMBA	51503.1	6.23	16	193			100	96	100					
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification		Rank	Result Type				
	898.41	898.3658	-0.0442	-49	296	302	NHGMHFR									Mascot			
	910.4451	910.3988	-0.0463	-51	178	184	AVYECLR					Carbamidomethyl (C)[5]				Mascot			
	914.4049	914.3587	-0.0462	-51	296	302	NHGMHFR					Oxidation (M)[4]				Mascot			
	1021.5312	1021.4841	-0.0471	-46	23	31	DTDILAAFR									Mascot			
	1021.5312	1021.4841	-0.0471	-46	23	31	DTDILAAFR		36							Mascot			
	1116.6194	1116.5275	-0.0919	-82	412	421	VALEACVKAR					Carbamidomethyl (C)[6]				Mascot			
	1170.5585	1170.5809	0.0224	19	294	302	QKNHGMHFR					Oxidation (M)[6]				Mascot			
	1187.6643	1187.6013	-0.063	-53	276	285	DNGLLLHIHR									Mascot			
	1245.6433	1245.5652	-0.0781	-63	430	440	EGNEIIREASK									Mascot			
	1261.6285	1261.6495	0.021	17	208	217	FLFCAEALYK					Carbamidomethyl (C)[4]				Mascot			
	1261.7151	1261.6495	-0.0656	-52	330	340	DITLGFVDLLR		48	99.741						Mascot			
	1451.6219	1451.5642	-0.0577	-40	192	203	DDENVNSQPFMR									Mascot			
	1465.7546	1465.6801	-0.0745	-51	137	149	TFQGGPHGIOVER		14	0						Mascot			
	1465.7546	1465.6801	-0.0745	-51	137	149	TFQGGPHGIOVER									Mascot			
	1502.8512	1502.7705	-0.0807	-54	155	167	YGRPLLGGCTKPK					Carbamidomethyl (C)[8]				Mascot			
	2009.059	2008.9675	-0.0915	-46	330	346	DITLGFVDLLRDDFIEK									Mascot			
	2169.9868	2169.8877	-0.0991																

Peptide Information									Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
898.41	898.3658	-0.0442	-49	297	303	NHGMHFR					Mascot
910.4451	910.3988	-0.0463	-51	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3587	-0.0462	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDILAAFR					Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDILAAFR	36	96.292			Mascot
1116.583	1116.5275	-0.0555	-50	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5809	0.0224	19	295	303	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6013	-0.063	-53	277	286	DNGLLLHIHR					Mascot
1245.6337	1245.5652	-0.0685	-55	209	218	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6495	-0.0656	-52	331	341	DITLGFVDLLR	48	99.741			Mascot
1261.7151	1261.6495	-0.0656	-52	331	341	DITLGFVDLLR					Mascot
1451.6219	1451.5642	-0.0577	-40	193	204	DDENVNSQPFMR					Mascot
1465.7216	1465.6801	-0.0415	-28	311	325	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6801	-0.0745	-51	138	150	TFQGPPIHGIQVER	14	0			Mascot
1502.8512	1502.7705	-0.0807	-54	156	168	YGRPLLGCCTIKPK			Carbamidomethyl (C)[8]		Mascot
2009.059	2008.9675	-0.0915	-46	331	347	DITLGFVDLLRDDFIEK					Mascot
2169.9868	2169.8877	-0.0991	-46	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8796	-0.1023	-47	186	204	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3022.4548	3022.3562	-0.0986	-33	250	276	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6746	-0.1972	-51	33	70	VTPQPGVPPEEAGAAVA					Mascot
						AESSTGTWTTVWDGLTSLDR					

8 Ribulose biphosphate carboxylase large chain RBL\_MANES 52648.5 6.18 16 189 100 96 100  
OS=Manihot esculenta GN=rbcl PE=3 SV=1

Peptide Information									Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
898.41	898.3658	-0.0442	-49	306	312	NHGMHFR					Mascot
910.4451	910.3988	-0.0463	-51	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3587	-0.0462	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4841	-0.0471	-46	33	41	DTDILAAFR					Mascot
1021.5312	1021.4841	-0.0471	-46	33	41	DTDILAAFR	36	96.292			Mascot
1116.583	1116.5275	-0.0555	-50	422	431	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5809	0.0224	19	304	312	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6013	-0.063	-53	286	295	DNGLLLHIHR					Mascot
1261.6285	1261.6495	0.021	17	218	227	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6495	-0.0656	-52	340	350	DITLGFVDLLR	48	99.741			Mascot
1392.6682	1392.6155	-0.0527	-38	22	32	LTYYTPDYQTK					Mascot
1451.6219	1451.5642	-0.0577	-40	202	213	DDENVNSQPFMR					Mascot
1465.7546	1465.6801	-0.0745	-51	147	159	TFQGPPIHGIQVER	14	0			Mascot
1465.7546	1465.6801	-0.0745	-51	147	159	TFQGPPIHGIQVER					Mascot
1502.8512	1502.7705	-0.0807	-54	165	177	YGRPLLGCCTIKPK			Carbamidomethyl (C)[8]		Mascot
2009.059	2008.9675	-0.0915	-46	340	356	DITLGFVDLLRDDFIEK					Mascot
2169.9868	2169.8877	-0.0991	-46	195	213	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8796	-0.1023	-47	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3022.4548	3022.3562	-0.0986	-33	259	285	ELGVPIMVHDYLTGGFTA			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6746	-0.1972	-51	42	79	VTPQPGVPPEEAGAAVA					Mascot
						AESSTGTWTTVWDGLTSLDR					

9 Ribulose biphosphate carboxylase large chain RBL\_DAPSP 51574 6.04 16 189 100 94 100  
(Fragment) OS=Daphniphyllum sp. GN=rbcl PE=3 SV=1

Peptide Information									Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
898.41	898.3658	-0.0442	-49	296	302	NHGMHFR					Mascot
910.4451	910.3988	-0.0463	-51	178	184	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3587	-0.0462	-51	296	302	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4841	-0.0471	-46	23	31	DTDILAAFR					Mascot
1021.5312	1021.4841	-0.0471	-46	23	31	DTDILAAFR	36	96.292			Mascot
1116.583	1116.5275	-0.0555	-50	412	421	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5809	0.0224	19	294	302	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6013	-0.063	-53	278	285	DNGLLLHIHR					Mascot
1245.6433	1245.5652	-0.0781	-63	430	440	EGNEIREASK					Mascot
1261.6285	1261.6495	0.021	17	208	217	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6495	-0.0656	-52	330	340	DITLGFVDLLR	48	99.741			Mascot
1451.6219	1451.5642	-0.0577	-40	192	203	DDENVNSQPFMR					Mascot
1465.7216	1465.6801	-0.0415	-28	310	324	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6801	-0.0745	-51	137	149	TFQGPPIHGIQVER	14	0			Mascot
1502.8512	1502.7705	-0.0807	-54	155	167	YGRPLLGCCTIKPK			Carbamidomethyl (C)[8]		Mascot
2169.9868	2169.8877	-0.0991	-46	185	203	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8796	-0.1023	-47	185	203	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
2726.2219	2726.0967	-0.1252	-46	218	242	AQAETGEIKGHYLNATAGTCEDMMK			Carbamidomethyl (C)[20]		Mascot
3854.8718	3854.6746	-0.1972	-51	32	69	VTPQPGVPPEEAGAAVA					Mascot
						AESSTGTWTTVWDGLTSLDR					

10 Ribulose biphosphate carboxylase large chain RBL\_TABHE 52026.2 6.04 16 188 100 94 100  
(Fragment) OS=Tabebuia heterophylla GN=rbcl PE=3 SV=1

Peptide Information									Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
898.41	898.3658	-0.0442	-49	297	303	NHGMHFR					Mascot
910.4451	910.3988	-0.0463	-51	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3587	-0.0462	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDILAAFR					Mascot
1021.5312	1021.4841	-0.0471	-46	24	32	DTDILAAFR	36	96.292			Mascot
1116.583	1116.5275	-0.0555	-50	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5809	0.0224	19	295	303	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.6013	-0.063	-53	277	286	DNGLLLHIHR					Mascot
1261.6285	1261.6495	0.021	17	209	218	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6495	-0.0656	-52	331	341	DITLGFVDLLR	48	99.741			Mascot
1451.6219	1451.5642	-0.0577	-40	193	204	DDENVNSQPFMR					Mascot
1465.7216	1465.6801	-0.0415	-28	311	325	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6801	-0.0745	-51	138	150	TFQGPPIHGIQVER	14	0			Mascot
1502.8512	1502.7705	-0.0807	-54	156	168	YGRPLLGCCTIKPK			Carbamidomethyl (C)[8]		Mascot
1557.8231	1557.6057	-0.2174	-140	427	441	DLAAGDNIAIREASK					Mascot
1557.8231	1557.6057	-0.2174	-140	427	441	DLAAGDNIAIREASK					Mascot

	2009.059	2008.9675	-0.0915	-46	331	347	DITLGFVDLLRDFIEK											Mascot							
	2169.9868	2169.8877	-0.0991	-46	186	204	GGLDFTKDDENVNSQPF											Mascot							
							MR																		
	2185.9819	2185.8796	-0.1023	-47	186	204	GGLDFTKDDENVNSQPF							Oxidation (M)[18]				Mascot							
							MR																		
	3022.4548	3022.3562	-0.0986	-33	250	276	ELGVPVIMHDYLTGGFTA							Carbamidomethyl (C)[26]				Mascot							
							NTSLAHYCR																		
Gel Idx/Pos	106/E5					Instr./Gel Origin		BA2060/140227A					Process Status		Analysis Succeeded										
Plate [#]	[1] 31564					Instrument Sample Name							Spectra		11										
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Total Ion Score	C. I. %	Total Ion Score	C. I. %										
1	Stromal 70 kDa heat shock-related protein, chloroplastic					HSP7S_PEA	75469.3	5.22	14	604		100	546	100											
	OS=Pisum sativum GN=HSP70 PE=2 SV=1																								
	Peptide Information																								
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type												
	870.5406	870.4902	-0.0504	-58	226	233	IAGLEVLR						Mascot												
	870.5406	870.4902	-0.0504	-58	226	233	IAGLEVLR	15	0				Mascot												
	915.4894	915.4286	-0.0608	-66	379	386	TPVENSLR						Mascot												
	970.5316	970.4725	-0.0591	-61	356	363	HIETTLTR						Mascot												
	996.6088	996.5428	-0.066	-66	407	415	IPAVQELVK						Mascot												
	1172.5807	1172.601	0.0203	17	37	46	LNSNHSPTFR						Mascot												
	1373.7271	1373.6538	-0.0733	-53	394	406	DIDEVLVGGSTR	113	100				Mascot												
	1373.7271	1373.6538	-0.0733	-53	394	406	DIDEVLVGGSTR						Mascot												
	1381.6594	1381.5758	-0.0836	-61	598	609	NQADSVVYOTEK						Mascot												
	1566.791	1566.7058	-0.0852	-54	204	217	AVVTVPAYFNDSSQR	95	100				Mascot												
	1566.791	1566.7058	-0.0852	-54	204	217	AVVTVPAYFNDSSQR						Mascot												
	1579.8114	1579.7166	-0.0948	-60	123	136	QAVVNPENTFFSVK						Mascot												
	1595.7733	1595.683	-0.0903	-57	364	376	AKFEELCSDLLDR			Carbamidomethyl (C)[7]			Mascot												
	1735.9126	1735.8131	-0.0995	-57	123	137	QAVVNPENTFFSVKR						Mascot												
	1815.0222	1814.9181	-0.1041	-57	390	406	LSIKDIDEVLVGGSTR	122	100				Mascot												
	1815.0222	1814.9181	-0.1041	-57	390	406	LSIKDIDEVLVGGSTR						Mascot												
	2437.1841	2437.0422	-0.1419	-58	484	506	SEVFSTAADGQTSVEINV	201	100				Mascot												
							LQGER																		
	2437.1841	2437.0422	-0.1419	-58	484	506	SEVFSTAADGQTSVEINV						Mascot												
							LQGER																		
	3070.5837	3070.4153	-0.1684	-55	70	100	VVGIDLGTNTNSAAMEG						Mascot												
							GKPTIITNAEGQR																		
	3086.5786	3086.3955	-0.1831	-59	70	100	VVGIDLGTNTNSAAMEG			Oxidation (M)[16]			Mascot												
							GKPTIITNAEGQR																		
2	Stromal 70 kDa heat shock-related protein, chloroplastic					HSP7S_SPIOL	64860.7	4.87	10	527		100	492	100											
	(Fragment) OS=Spinacia oleracea GN=CHSP70																								
	Peptide Information																								
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type												
	870.5406	870.4902	-0.0504	-58	106	113	IAGLEVLR						Mascot												
	870.5406	870.4902	-0.0504	-58	106	113	IAGLEVLR	15	0				Mascot												
	915.4894	915.4286	-0.0608	-66	259	266	TPVENSLR						Mascot												
	970.5316	970.4725	-0.0591	-61	236	243	HIETTLTR						Mascot												
	1165.6252	1165.6652	0.04	34	177	186	IVDWLASSFK						Mascot												
	1194.7092	1194.5487	-0.1605	-134	493	503	ELGEKVPVPVK						Mascot												
	1381.6594	1381.5758	-0.0836	-61	478	489	NQADSVVYOTEK						Mascot												
	1461.7695	1461.6884	-0.0811	-55	55	67	QFAAEEISAOVLR						Mascot												
	1461.7695	1461.6884	-0.0811	-55	55	67	QFAAEEISAOVLR	96	100				Mascot												
	1566.791	1566.7058	-0.0852	-54	84	97	AVVTVPAYFNDSSQR	95	100				Mascot												
	1566.791	1566.7058	-0.0852	-54	84	97	AVVTVPAYFNDSSQR						Mascot												
	1723.8901	1723.7848	-0.1053	-61	114	129	INEPTAASLAYGFEK	85	100				Mascot												
	1723.8901	1723.7848	-0.1053	-61	114	129	INEPTAASLAYGFEK						Mascot												
	2437.1841	2437.0422	-0.1419	-58	364	386	SEVFSTAADGQTSVEINV	201	100				Mascot												
							LQGER																		
	2437.1841	2437.0422	-0.1419	-58	364	386	SEVFSTAADGQTSVEINV						Mascot												
							LQGER																		
3	Heat shock 70 kDa protein 6, chloroplastic					HSP7F_ARATH	76461.4	5.07	13	472		100	424	100											
	OS=Arabidopsis thaliana GN=HSP70-6 PE=1 SV=1																								
	Peptide Information																								
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type												
	870.5406	870.4902	-0.0504	-58	236	243	IAGLEVLR						Mascot												
	870.5406	870.4902	-0.0504	-58	236	243	IAGLEVLR	15	0				Mascot												
	915.4894	915.4286	-0.0608	-66	389	396	TPVENSLR						Mascot												
	970.5316	970.4725	-0.0591	-61	366	373	HIETTLTR						Mascot												
	1198.6677	1198.6826	0.0149	12	623	633	ELGEKIPGEVK						Mascot												
	1373.7271	1373.6538	-0.0733	-53	404	416	DIDEVLVGGSTR	113	100				Mascot												
	1373.7271	1373.6538	-0.0733	-53	404	416	DIDEVLVGGSTR						Mascot												
	1381.6594	1381.5758	-0.0836	-61	608	619	NQADSVVYOTEK						Mascot												
	1461.7695	1461.6884	-0.0811	-55	185	197	QFAAEEISAOVLR						Mascot												
	1461.7695	1461.6884	-0.0811	-55	185	197	QFAAEEISAOVLR	96	100				Mascot												
	1579.8114	1579.7166	-0.0948	-60	133	146	QAVVNPENTFFSVK						Mascot												
	1595.7733	1595.683	-0.0903	-57	374	386	AKFEELCSDLLDR			Carbamidomethyl (C)[7]			Mascot												
	1735.9126	1735.8131	-0.0995	-57	133	147	QAVVNPENTFFSVKR						Mascot												
	2209.0918	2209.0393	-0.0525	-24	1	23	MASSAAQIHVLGGIGFAS			Oxidation (M)[1]			Mascot												

		2535.301	2535.1528	-0.1482	-58	342	365	LQGER IELSSLTQTNMSLPFITAT ADGPK									Mascot
5	Heat shock 70 kDa protein OS=Chlamydomonas reinhardtii GN=HSP70 PE=2 SV=2							HSP70_CHLRE	70953.2	5.2	6	102	100	95	100		
	Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type						
949.4481	949.4913	0.0432	46	318	325	KOMDPVEK					Mascot						
949.4481	949.4913	0.0432	46	318	325	KOMDPVEK					Mascot						
1118.5437	1118.5537	9	0.01	9	131	141	ETAQASLGADR				Mascot						
1133.5078	1133.5553	0.0475	42	326	334	CLHDAKMDK			Carbamidomethyl (C)[1], Oxidation (M)[7]		Mascot						
1318.5806	1318.649	0.0684	52	308	317	FEELCDMLFR			Oxidation (M)[6]		Mascot						
1566.791	1566.7058	-0.0852	-54	146	159	AVVTVPAYFNDSQR	95	100			Mascot						
1566.791	1566.7058	-0.0852	-54	146	159	AVVTVPAYFNDSQR					Mascot						
2658.2681	2658.1128	-0.1553	-58	431	453	EQVFSTYSDNQPGLVQV YEGER					Mascot						
6	Lupeol synthase OS=Glycyrrhiza glabra GN=LUS1 PE=1 SV=1							LUPS_GLYGL	86631.9	6.61	10	46	13.524	22	0		
	Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type						
940.5111	940.4182	-0.0929	-99	574	580	KQFPQHR					Mascot						
949.4771	949.4913	0.0142	15	56	63	QSADLLMR			Oxidation (M)[7]		Mascot						
949.4771	949.4913	0.0142	15	56	63	QSADLLMR			Oxidation (M)[7]		Mascot						
1133.552	1133.5553	0.0033	3	750	758	RQVLCAHSY			Carbamidomethyl (C)[5]		Mascot						
1337.6008	1337.6373	0.0365	27	378	388	WVEDPNSAYK					Mascot						
1373.7094	1373.6538	-0.0556	-40	188	200	ILGEGPQDKAMAK			Oxidation (M)[11]		Mascot						
1373.7094	1373.6538	-0.0556	-40	188	200	ILGEGPQDKAMAK			Oxidation (M)[11]		Mascot						
1461.7665	1461.6884	-0.0781	-53	56	67	QSADLLMRMQLR					Mascot						
1461.7665	1461.6884	-0.0781	-53	56	67	QSADLLMRMQLR	22	0			Mascot						
1566.7838	1566.7058	-0.078	-50	394	406	IPDYFWLAEDGLK					Mascot						
1566.7838	1566.7058	-0.078	-50	394	406	IPDYFWLAEDGLK					Mascot						
1642.7981	1642.653	-0.1451	-88	332	343	FLNCVWPFMSLR			Carbamidomethyl (C)[4], Oxidation (M)[9]		Mascot						
1779.861	1779.845	-0.141	-79	362	377	YLIGSGEVLCLIR					Mascot						
1799.986	1799.932	0.1141	63	246	259	FAPFHPGKMLCYCR			Carbamidomethyl (C)[11,13], Oxidation (M)[9]	11.51	Mascot						
7	3-ketoacyl-CoA synthase 12 OS=Arabidopsis thaliana GN=KCS12 PE=2 SV=1							KCS12_ARATH	53938.8	8.99	12	46					
	Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type						
842.4842	842.4573	-0.0269	-32	315	321	IRONPSK					Mascot						
870.5155	870.4902	-0.0253	-29	275	282	NLPKAATR					Mascot						
870.5155	870.4902	-0.0253	-29	275	282	NLPKAATR					Mascot						
1133.5983	1133.5553	-0.043	-38	219	229	SGGCAILLTNK			Carbamidomethyl (C)[4]		Mascot						
1194.5394	1194.5487	0.0093	8	417	426	CNSCVWEVVR					Mascot						
1657.7428	1657.6915	-0.0513	-31	435	448	GNVWNHCIDDYPPK					Mascot						
1735.9337	1735.8131	-0.1206	-69	317	333	GNPSKSGTNLPPGTPLK					Mascot						
2050.1331	2049.9736	-0.1595	-78	69	87	FLKAVISGSGEQTYAPR					Mascot						
2087.0491	2086.9426	-0.1065	-51	334	352	AGINFKTGIEHFCIHTGGK			Carbamidomethyl (C)[13]		Mascot						
2225.1602	2224.988	-0.1722	-77	209	229	SMILANCLFRSGGCAILLT NK					Mascot						
2658.2239	2658.1128	-0.1111	-42	94	116	EERPSLQDGISEMEEFYV DSIGK					Mascot						
2691.3447	2691.1147	-0.23	-85	46	68	MVSTQFSGEIIYRNQNLG LTEYK					Mascot						
3327.6611	3327.5303	-0.1308	-39	189	218	LALVATSESLSPNWYSG NNRSMILANCLFR					Mascot						
8	Structural maintenance of chromosomes protein 2-1 OS=Arabidopsis thaliana GN=SMC21-1 PE=2 SV=2							SMC21_ARATH	132518	6.3	17	45	0				
	Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type						
856.5073	856.4714	-0.0359	-42	875	881	LIHAKMK			Oxidation (M)[6]		Mascot						
940.4193	940.4182	-0.0011	-1	766	773	NCFDAVSK			Carbamidomethyl (C)[2]		Mascot						
949.5464	949.4913	-0.0551	-58	113	120	NKYLINGK					Mascot						
949.5464	949.4913	-0.0551	-58	113	120	NKYLINGK					Mascot						
970.5792	970.4725	-0.1067	-110	106	114	QIVVGRNK			Oxidation (M)[8]		Mascot						
1165.5518	1165.6652	0.1134	97	303	312	VDSLAEQEMTR					Mascot						
1176.6405	1176.5779	-0.0626	-53	798	808	TKAQMOAASK					Mascot						
1198.6062	1198.6826	0.0764	64	774	783	LENSIKDHDK					Mascot						
1373.7245	1373.6538	-0.0707	-51	2	12	HIKEICLEGFK			Carbamidomethyl (C)[6]		Mascot						
1373.7245	1373.6538	-0.0707	-51	2	12	HIKEICLEGFK			Carbamidomethyl (C)[6]		Mascot						
1595.7233	1595.683	-0.0403	-25	616	629	NAMEYVFGSTFVCK					Mascot						
1716.8777	1716.7751	-0.1026	-60	233	246	FCIAFEYVQAEKIR					Mascot						
1723.853	1723.7848	-0.0682	-40	298	312	TLSEKVDSLAQEMTR			Oxidation (M)[13]		Mascot						
1723.853	1723.7848	-0.0682	-40	298	312	TLSEKVDSLAQEMTR			Oxidation (M)[13]		Mascot						
1799.881	1799.932	0.051	28	1054	1069	LEPPEDGNFLDGLVLR					Mascot						
2050.0161	2049.9736	-0.0425	-21	461	478	KALESIPYNQOMEALEK					Mascot						
2088.998	2089.0022	0.0042	2	985	1002	VMAMFEKAEDYNALISK					Mascot						
2209.0442	2209.0393	-0.0049	-2	462	480	ALESIPIYNQOMEALEKDR			Oxidation (M)[12]		Mascot						
2211.0459	2211.0161	-0.0298	-13	616	635	NAMEYVFGSTFVCKTTD VAK					Mascot						
2437.2834	2437.0422	-0.2412	-99	91	112	SPLGYEEHPEITVTRQIVV GGR					Mascot						
2437.2834	2437.0422	-0.2412	-99	91	112	SPLGYEEHPEITVTRQIVV GGR					Mascot						
9	Phenylalanine ammonia-lyase 2 OS=Arabidopsis thaliana GN=PAL2 PE=1 SV=2							PAL2_ARATH	77810.8	6.03	11	44	0	11	0		
	Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type						
842.3712	842.4573	0.0861	102	48	53	MVEEYR			Oxidation (M)[1]		Mascot						
970.4662	970.4725	0.0063	6	47	53	KMVEEYR			Oxidation (M)[2]		Mascot						
1156.5455	1156.5952	0.0497	43	708	717	EWNGAPIPIC			Carbamidomethyl (C)[10]		Mascot						
1176.6003	1176.5779	-0.0224	-19	698	707	LIDPLMDCLK			Oxidation (M)[6]		Mascot						
1337.6882	1337.6373	-0.0509	-38	338	348	VHEMDPLQKPK			Oxidation (M)[4]		Mascot						
1444.8118	1444.6562	-0.1556	-108	123	135	TKNGTALQTELIR					Mascot						
1444.8118	1444.6562	-0.1556	-108	123	135	TKNGTALQTELIR					Mascot						
1579.7455	1579.7166	-0.0289	-18	2	16	DOIEAMLCGGGEKTK	11	0			Mascot						
1595.7404	1595.683	-0.0574	-36	2	16	DOIEAMLCGGGEKTK					Mascot						

OS=Liriodendron tulipifera GN=rpoc2 PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
856.5614	856.4714	-0.09	-105	1263	1270	AILLGITR		
970.5026	970.4725	-0.0301	-31	965	972	EDPMPIR		
1118.6569	1118.5537	-0.1032	-92	868	876	DFIRDLVK		
1176.499	1176.5779	0.0789	67	1019	1027	YYLMDENGR		
1198.6538	1198.6826	0.0288	24	267	277	NQDIGILVNR		
1381.7546	1381.5758	-0.1788	-129	913	924	IQSLTQHQGTIR		
1443.7512	1443.696	-0.0552	-38	961	972	ESIKEDPMPIR		
1444.6824	1444.6562	-0.0262	-18	296	307	STSWICRLCYGR		
1444.6824	1444.6562	-0.0262	-18	296	307	STSWICRLCYGR		
1461.7478	1461.6884	-0.0594	-41	222	235	TDCGTIRGISVSPR		
1461.7478	1461.6884	-0.0594	-41	222	235	TDCGTIRGISVSPR		
1562.7485	1562.7115	-0.037	-24	721	734	IFSGDIHFPGETDK		
1644.8016	1644.6636	-0.138	-84	611	623	DTILAVFDDPRYR		
1657.7599	1657.6915	-0.0684	-41	497	510	QDDQMNVHSLSVRR		
1799.9545	1799.932	-0.0225	-13	262	277	CIATRNQDIGILVNR		
1813.861	1813.8801	0.0191	11	497	511	QDDQMNVHSLSVRR		
1882.9513	1882.8564	-0.0949	-50	251	266	VLADDIYMLRCLAIATR		
2046.0542	2045.9343	-0.1199	-59	717	734	IELKIFSGDIHFPGETDK		
2050.1001	2049.9736	-0.1265	-62	965	983	EDPMPIRNSLGLGTVPK		
2087.0039	2086.9426	-0.0613	-29	1271	1289	ASLNTQSFISEASFOETAR		

Modification	Rank	Result Type
		Mascot
		Mascot
		Mascot
Oxidation (M)[4]		Mascot
		Mascot
Oxidation (M)[8]		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[1]		Mascot
		Mascot
Carbamidomethyl (C)[12], Oxidation (M)[8]		Mascot
		Mascot
Oxidation (M)[4]		Mascot

Gel Idx/Pos	107/E6	Instr./Gel Origin	BA2060/140227A	Process Status	Analysis Succeeded
Plate [#]	Name	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Total Ion Score	Total Ion C. I. %
1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Magnolia kobus]	gi 54306650	52265.4	6.23	16	131	100	42	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
914.4049	914.3502	-0.0547	-60	303	309	NHGMHFR		
1021.5312	1021.4667	-0.0645	-63	30	38	DTDILAAFR		
1116.583	1116.5192	-0.0638	-57	419	428	VALEACVQAR		
1165.6211	1165.6703	0.0492	42	1	11	QTEAKASVGFK		
1165.6211	1165.6703	0.0492	42	1	11	QTEAKASVGFK		
1170.5585	1170.5696	0.0111	9	301	309	QKNHGMHFR		
1187.6643	1187.5897	-0.0746	-63	283	292	DNGLLLHIHR		
1261.6285	1261.6353	0.0068	5	215	224	FLFCAEAIYK	6	0
1261.7151	1261.6353	-0.0798	-63	337	347	DTLGFVDLLR		
1465.7216	1465.6664	-0.0552	-38	317	331	MSGGDHIIHAGTVVVGK		
1465.7546	1465.6664	-0.0882	-60	144	156	TFQGPPIHGIQVER	45	3.837
1671.8408	1671.6693	-0.1715	-103	429	443	NEGRDLASQGNELIR		
1812.7714	1812.7028	-0.0686	-38	234	249	GHYLNATAGTCEEMMK		
1968.8724	1968.9186	0.0462	23	234	250	GHYLNATAGTCEEMMKR		
2169.9868	2169.8831	-0.1037	-48	192	210	GGLDFTKDDENVNSQPFMR		
2715.2058	2715.0857	-0.1201	-44	225	249	AQAETGEIKGHYLNATAGTCEEMMK		
2715.2058	2715.0857	-0.1201	-44	225	249	AQAETGEIKGHYLNATAGTCEEMMK		
3854.8718	3854.6357	-0.2361	-61	39	76	VTPOPGVPPEEAGAAVAESSTGTWTTVWTDGLTSLDR		

Modification	Rank	Result Type
Oxidation (M)[4]		Mascot
Carbamidomethyl (C)[6]		Mascot
		Mascot
Oxidation (M)[6]		Mascot
		Mascot
Carbamidomethyl (C)[4]		Mascot
		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[11]		Mascot
Carbamidomethyl (C)[11]		Mascot
		Mascot
Oxidation (M)[23,24]		Mascot
Oxidation (M)[23,24]		Mascot
		Mascot

2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Salvia argentea]	gi 1419213	52387.4	6.33	16	130	100	45	3.837
---	---	------------	---------	------	----	-----	-----	----	-------

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
856.3546	856.4723	0.1177	137	467	473	FEFPAMD		
914.4049	914.3502	-0.0547	-60	306	312	NHGMHFR		
1021.5312	1021.4667	-0.0645	-63	33	41	DTDILAAFR		
1045.5823	1045.5103	-0.072	-69	422	431	VAVEACVKAR		
1170.5585	1170.5696	0.0111	9	304	312	QKNHGMHFR		
1187.6643	1187.5897	-0.0746	-63	286	295	DNGLLLHIHR		
1261.6285	1261.6353	0.0068	5	218	227	FLFCAEAIYK	6	0
1261.7151	1261.6353	-0.0798	-63	340	350	DTLGFVDLLR		
1332.6252	1332.6522	0.027	20	84	94	CYHIEPVTGEK		
1465.7546	1465.6664	-0.0882	-60	147	159	TFQGPPIHGIQVER	45	3.837
1465.7546	1465.6664	-0.0882	-60	147	159	TFQGPPIHGIQVER		
1812.7714	1812.7028	-0.0686	-38	237	252	GHYLNATAGTCEEMMK		
1920.8962	1920.9165	0.0163	10	447	463	EACKWSPELAAACEVWK		
1968.8724	1968.9186	0.0462	23	237	253	GHYLNATAGTCEEMMKR		
2169.9868	2169.8831	-0.1037	-48	195	213	GGLDFTKDDENVNSQPFMR		
2715.2058	2715.0857	-0.1201	-44	228	252	AQAETGEIKGHYLNATAGTCEEMMK		
2715.2058	2715.0857	-0.1201	-44	228	252	AQAETGEIKGHYLNATAGTCEEMMK		
3854.8718	3854.6357	-0.2361	-61	42	79	VTPOPGVPPEEAGAAVAESSTGTWTTVWTDGLTSLDR		

Modification	Rank	Result Type
Oxidation (M)[4]		Mascot
		Mascot
		Mascot
Oxidation (M)[6]		Mascot
		Mascot
Carbamidomethyl (C)[4]		Mascot
Carbamidomethyl (C)[1]		Mascot
		Mascot
Carbamidomethyl (C)[11]		Mascot
		Mascot
Carbamidomethyl (C)[11]		Mascot
		Mascot
Oxidation (M)[23,24]		Mascot
Oxidation (M)[23,24]		Mascot
		Mascot

3	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Coptosperma supra-axillare]	gi 11230505	52186.5	6.33	16	130	100	42	0
---	--	-------------	---------	------	----	-----	-----	----	---

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
914.4049	914.3502	-0.0547	-60	297	303	NHGMHFR		
1021.5312	1021.4667	-0.0645	-63	24	32	DTDILAAFR		
1116.6194	1116.5192	-0.1002	-90	413	422	VALEACVKAR		
1170.5585	1170.5696	0.0111	9	295	303	QKNHGMHFR		
1187.6643	1187.5897	-0.0746	-63	277	286	DNGLLLHIHR		
1261.6285	1261.6353	0.0068	5	209	218	FLFCAEALYK	6	0
1261.7151	1261.6353	-0.0798	-63	331	341	DTLGFVDLLR		
1465.7216	1465.6664	-0.0552	-38	311	325	MSGGDHIIHAGTVVVGK		
1465.7546	1465.6664	-0.0882	-60	138	150	TFQGPPIHGIQVER	45	3.837
1473.7372	1473.7277	-0.0095	-6	442	454	WSPELAAACEVWK		
1684.8612	1684.6848	-0.1764	-105	423	437	NEGRDLAVEGNEIIR		
1812.7714	1812.7028	-0.0686	-38	228	243	GHYLNATAGTCEEMMK		
1968.8724	1968.9186	0.0462	23	228	244	GHYLNATAGTCEEMMKR		
2169.9868	2169.8831	-0.1037	-48	186	204	GGLDFTKDDENVNSQPFMR		
2715.2058	2715.0857	-0.1201	-44	219	243	AQAETGEIKGHYLNATAGTCEEMMK		

Modification	Rank	Result Type
Oxidation (M)[4]		Mascot
		Mascot
Carbamidomethyl (C)[6]		Mascot
Oxidation (M)[6]		Mascot
		Mascot
Carbamidomethyl (C)[4]		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[11]		Mascot
Carbamidomethyl (C)[11]		Mascot
		Mascot
Oxidation (M)[23,24]		Mascot

	2715.2058	2715.0857	-0.1201	-44	219	243	TCEEMMK AQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	3854.8718	3854.6357	-0.2361	-61	33	70	VTPOQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot
4	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Argyrobolium marginatum]					gil3114727	52312.3	6.13	16	128	100	42	0			
Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %				Modification	Rank	Result Type
	856.3546	856.4723	0.1177	137	467	473	FEFPAMD									Mascot
	914.4049	914.3502	-0.0547	-60	306	312	NHGMHFR							Oxidation (M)[4]		Mascot
	1021.5312	1021.4667	-0.0645	-63	33	41	DTDILAAFR									Mascot
	1116.583	1116.5192	-0.0638	-57	422	431	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
	1170.5585	1170.5696	0.0111	9	304	312	QKNHGMHFR							Oxidation (M)[6]		Mascot
	1187.6643	1187.5897	-0.0746	-63	286	295	DNGLLLHIHR									Mascot
	1261.6285	1261.6353	0.0068	5	218	227	FLFCAEALYK							Carbamidomethyl (C)[4]		Mascot
	1261.6285	1261.6353	0.0068	5	218	227	FLFCAEALYK							Carbamidomethyl (C)[4]		Mascot
	1465.7216	1465.6664	-0.0552	-38	320	334	MSGDDHIHAGTVVGK									Mascot
	1465.7546	1465.6664	-0.0882	-60	147	159	TFQGPPHGIQVER		45	3.837						Mascot
	1473.7372	1473.7277	-0.0095	-6	451	463	WSPELAAASEVWK									Mascot
	1671.8408	1671.6693	-0.1715	-103	432	446	NEGRDLASEGNQIIR									Mascot
	1812.7714	1812.7028	-0.0686	-38	237	252	GHYLNATAGTCEEMMK							Carbamidomethyl (C)[11]		Mascot
	1968.8724	1968.9186	0.0462	23	237	253	GHYLNATAGTCEEMMKR							Carbamidomethyl (C)[11]		Mascot
	2169.9868	2169.8831	-0.1037	-48	195	213	GGLDFTKDDENVNSQPF MR									Mascot
	2715.2058	2715.0857	-0.1201	-44	228	252	AQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	2715.2058	2715.0857	-0.1201	-44	228	252	AQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	3854.8718	3854.6357	-0.2361	-61	42	79	VTPOQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot
5	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Jarilla heterophylla]					gil16445368	49373.9	6.3	15	127	100	45	3.837			
Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %				Modification	Rank	Result Type
	914.4049	914.3502	-0.0547	-60	292	298	NHGMHFR							Oxidation (M)[4]		Mascot
	1021.5312	1021.4667	-0.0645	-63	19	27	DTDILAAFR									Mascot
	1116.583	1116.5192	-0.0638	-57	408	417	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
	1170.5585	1170.5696	0.0111	9	290	298	QKNHGMHFR							Oxidation (M)[6]		Mascot
	1187.6643	1187.5897	-0.0746	-63	272	281	DNGLLLHIHR									Mascot
	1261.6285	1261.6353	0.0068	5	204	213	FLFCAEAIYK							Carbamidomethyl (C)[4]		Mascot
	1261.7151	1261.6353	-0.0798	-63	326	336	DITLGFVDLLR		6	0						Mascot
	1392.6692	1392.6217	-0.0465	-33	8	18	LTYYTPDYKTK									Mascot
	1465.7546	1465.6664	-0.0882	-60	133	145	TFQGPPHGIQVER		45	3.837						Mascot
	1465.7546	1465.6664	-0.0882	-60	133	145	TFQGPPHGIQVER									Mascot
	1684.8911	1684.6848	-0.2063	-122	402	417	GAVANRVVALEACVQAR							Carbamidomethyl (C)[12]		Mascot
	1812.7714	1812.7028	-0.0686	-38	223	238	GHYLNATAGTCEEMMK							Carbamidomethyl (C)[11]		Mascot
	1968.8724	1968.9186	0.0462	23	223	239	GHYLNATAGTCEEMMKR							Carbamidomethyl (C)[11]		Mascot
	2169.9868	2169.8831	-0.1037	-48	181	199	GGLDFTKDDENVNSQPF MR									Mascot
	2715.2058	2715.0857	-0.1201	-44	214	238	SQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23]		Mascot
	2715.2058	2715.0857	-0.1201	-44	214	238	SQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23]		Mascot
	2731.2007	2731.0718	-0.1289	-47	214	238	SQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	3854.8718	3854.6357	-0.2361	-61	28	65	VTPOQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot
6	ribulose 1,5-biphosphate carboxylase large subunit [Genista januensis]					gil1223734	50243.4	6.44	15	127	100	45	3.837			
Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %				Modification	Rank	Result Type
	914.4049	914.3502	-0.0547	-60	297	303	NHGMHFR							Oxidation (M)[4]		Mascot
	1021.5312	1021.4667	-0.0645	-63	24	32	DTDILAAFR									Mascot
	1116.583	1116.5192	-0.0638	-57	413	422	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
	1170.5585	1170.5696	0.0111	9	295	303	QKNHGMHFR							Oxidation (M)[6]		Mascot
	1187.6643	1187.5897	-0.0746	-63	277	286	DNGLLLHIHR									Mascot
	1261.6285	1261.6353	0.0068	5	209	218	FLFCAEALYK							Carbamidomethyl (C)[4]		Mascot
	1261.7151	1261.6353	-0.0798	-63	331	341	DITLGFVDLLR		6	0						Mascot
	1392.7046	1392.6217	-0.0829	-60	13	23	LTYYTPDYKTK									Mascot
	1465.7546	1465.6664	-0.0882	-60	138	150	TFQGPPHGIQVER		45	3.837						Mascot
	1465.7546	1465.6664	-0.0882	-60	138	150	TFQGPPHGIQVER									Mascot
	1671.8408	1671.6693	-0.1715	-103	423	437	NEGRDLASEGNQIIR									Mascot
	1812.7714	1812.7028	-0.0686	-38	228	243	GHYLNATAGTCEEMMK							Carbamidomethyl (C)[11]		Mascot
	1968.8724	1968.9186	0.0462	23	228	244	GHYLNATAGTCEEMMKR							Carbamidomethyl (C)[11]		Mascot
	2169.9868	2169.8831	-0.1037	-48	186	204	GGLDFTKDDENVNSQPF MR									Mascot
	2715.2058	2715.0857	-0.1201	-44	219	243	AQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	2715.2058	2715.0857	-0.1201	-44	219	243	AQAETGEIKGHYLNATAG TCEEMMK							Oxidation (M)[23,24]		Mascot
	3854.8718	3854.6357	-0.2361	-61	33	70	VTPOQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot
7	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Salvia officinalis]					gil617651	52409.4	6.23	16	127	100	45	3.837			
Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %				Modification	Rank	Result Type
	856.3546	856.4723	0.1177	137	467	473	FEFPAMD									Mascot
	914.4049	914.3502	-0.0547	-60	306	312	NHGMHFR							Oxidation (M)[4]		Mascot
	1021.5312	1021.4667	-0.0645	-63	33	41	DTDILAAFR									Mascot
	1045.5823	1045.5103	-0.072	-69	422	431	VAVEACVKAR									Mascot
	1051.5055	1051.6464	0.1409	134	351	358	DDFIEKER									Mascot
	1170.5585	1170.5696	0.0111	9	304	312	QKNHGMHFR							Oxidation (M)[6]		Mascot
	1187.6643	1187.5897	-0.0746	-63	286	295	DNGLLLHIHR									Mascot
	1261.6285	1261.6353	0.0068	5	218	227	FLFCAEAIYK							Carbamidomethyl (C)[4]		Mascot
	1261.7151	1261.6353	-0.0798	-63	340	350	DITLGFVDLLR		6	0						Mascot
	1465.7546	1465.6664	-0.0882	-60	147	159	TFQGPPHGIQVER		45	3.837						Mascot
	1465.7546	1465.6664	-0.0882	-60	147	159	TFQGPPHGIQVER									Mascot
	1700.8312	1700.686	-0.1452	-85	188	201	AVVECLRGELDFTK							Carbamidomethyl (C)[5]		Mascot
	1812.7714	1812.7028	-0.0686	-38	237	252	GHYLNATAGTCEEMMK							Carbamidomethyl (C)[11]		Mascot



8	PREDICTED: ATP-dependent zinc metalloprotease FTSH, chloroplastic [Vitis vinifera]	gi 225459844	75584.4	6.36	16	127	100	38	0
---	--	--------------	---------	------	----	-----	-----	----	---

9	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Argyrolobium	gi 182411637	47780	6.12	15	126	100	42	0
---	--	--------------	-------	------	----	-----	-----	----	---

		AESSTGTWTTVWTDGLT							
		SLDR							
10	ribulose 1,5-bisphosphate carboxylase/oxygenase large	gil200967543	51843.1	5.00	15	135	100	42	0

<b>Gel Idx/Pos</b>	108/E7	<b>Instr./Gel Origin</b>	BA2060/140227A	<b>Process Status</b>	Analysis Succeeded
--------------------	--------	--------------------------	----------------	-----------------------	--------------------

1	Ribulose biphosphate carboxylase large chain (Fragment) OS=Humiria balsamifera GN=rbcl PE=3	RBL_HUMBA	51530.1	6.23	21	421	100	266	100
---	--	-----------	---------	------	----	-----	-----	-----	-----



	2169.9868	2169.8643	-0.1225	-56	185	203	GGLDFTKDDENVNSQPF MR	24	29.312				Mascot
	2185.9819	2185.8586	-0.1233	-56	185	203	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]			Mascot
	3022.4548	3022.2974	-0.1574	-52	249	275	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]			Mascot
	3854.8718	3854.6531	-0.2187	-57	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	103	100				Mascot
	3854.8718	3854.6531	-0.2187	-57	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot

4 Ribulose biphosphate carboxylase large chain RBL\_AESPA 51619 6.18 20 409 100 266 100  
(Fragment) OS=Aesculus pavia GN=rbcl PE=3 SV=2

Peptide Information													Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %							
830.4366	830.3878	-0.0488	-59	431	437	EGNEIIR									Mascot
898.441	898.3544	-0.0556	-62	297	303	NHGMHFR									Mascot
910.4451	910.4066	-0.0385	-42	179	185	AVVECLR							Carbamidomethyl (C)[5]		Mascot
914.4049	914.3523	-0.0526	-58	297	303	NHGMHFR							Oxidation (M)[4]		Mascot
1021.5312	1021.4698	-0.0614	-60	24	32	DTDILAAFR	29	73.001							Mascot
1021.5312	1021.4698	-0.0614	-60	24	32	DTDILAAFR									Mascot
1059.5615	1059.4915	-0.07	-66	413	422	VALEACVQAR									Mascot
1116.583	1116.5172	-0.0658	-59	413	422	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5172	-0.0658	-59	413	422	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5669	0.0084	7	295	303	QKNHGMHFR							Oxidation (M)[6]		Mascot
1187.6643	1187.5924	-0.0719	-61	277	286	DNGLLLHIHR									Mascot
1245.6337	1245.564	-0.0697	-56	209	218	FLFCAEAIK							Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6405	-0.0746	-59	331	341	DITLGFVDLLR	57	99.962							Mascot
1261.7151	1261.6405	-0.0746	-59	331	341	DITLGFVDLLR									Mascot
1451.6219	1451.5601	-0.0618	-43	193	204	DDENVNSQPFMR									Mascot
1465.7216	1465.6687	-0.0529	-36	311	325	MSGGDHIHAGTVVGK									Mascot
1465.7546	1465.6687	-0.0859	-59	138	150	TFQGPPIHGIQVER	54	99.929							Mascot
1481.7166	1481.6239	-0.0927	-63	311	325	MSGGDHIHAGTVVGK							Oxidation (M)[1]		Mascot
1481.7166	1481.6239	-0.0927	-63	311	325	MSGGDHIHAGTVVGK							Oxidation (M)[1]		Mascot
1502.8512	1502.7521	-0.0991	-66	156	168	YGRPLLGCTIKPK							Carbamidomethyl (C)[8]		Mascot
1546.7358	1546.6464	-0.0894	-58	442	454	WSPELAAACEVWK							Carbamidomethyl (C)[9]		Mascot
1794.8149	1794.7172	-0.0977	-54	228	243	GHYLNATAGTCEEMIK							Carbamidomethyl (C)[11]		Mascot
1846.0068	1845.8844	-0.1224	-66	326	341	LEGERDITLGFVDLLR									Mascot
2009.059	2008.9437	-0.1153	-57	331	347	DITLGFVDLLRDFIEK									Mascot
2169.9868	2169.8643	-0.1225	-56	186	204	GGLDFTKDDENVNSQPF MR									Mascot
2169.9868	2169.8643	-0.1225	-56	186	204	GGLDFTKDDENVNSQPF MR	24	29.312							Mascot
2185.9819	2185.8586	-0.1233	-56	186	204	GGLDFTKDDENVNSQPF MR							Oxidation (M)[18]		Mascot
3022.4548	3022.2974	-0.1574	-52	250	276	ELGVPIVMHDYLTGGFTA NTSLAHYCR							Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6531	-0.2187	-57	33	70	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	103	100							Mascot
3854.8718	3854.6531	-0.2187	-57	33	70	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot

5 Ribulose biphosphate carboxylase large chain RBL\_POLSI 51642 5.99 20 409 100 266 100  
(Fragment) OS=Poliothyrsis sinensis GN=rbcl PE=3 SV=1

Peptide Information													Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %							
830.4366	830.3878	-0.0488	-59	431	437	EGNEIIR									Mascot
910.4451	910.4066	-0.0385	-42	179	185	AVVECLR							Carbamidomethyl (C)[5]		Mascot
1021.5312	1021.4698	-0.0614	-60	24	32	DTDILAAFR	29	73.001							Mascot
1021.5312	1021.4698	-0.0614	-60	24	32	DTDILAAFR									Mascot
1059.5615	1059.4915	-0.07	-66	413	422	VALEACVQAR									Mascot
1116.583	1116.5172	-0.0658	-59	413	422	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5172	-0.0658	-59	413	422	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.5924	-0.0719	-61	277	286	DNGLLLHIHR									Mascot
1245.6433	1245.564	-0.0793	-64	431	441	EGNEIREASK									Mascot
1261.6285	1261.6405	0.012	10	209	218	FLFCAEALYK							Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6405	-0.0746	-59	331	341	DITLGFVDLLR	57	99.962							Mascot
1451.6219	1451.5601	-0.0618	-43	193	204	DDENVNSQPFMR									Mascot
1465.7546	1465.6687	-0.0859	-59	138	150	TFQGPPIHGIQVER	54	99.929							Mascot
1465.7546	1465.6687	-0.0859	-59	138	150	TFQGPPIHGIQVER									Mascot
1475.7351	1475.6644	-0.0707	-48	207	218	DRFLFCAEALYK									Mascot
1481.7166	1481.6239	-0.0927	-63	311	325	MSGGDHIHSGTVVGK									Mascot
1481.7166	1481.6239	-0.0927	-63	311	325	MSGGDHIHSGTVVGK									Mascot
1502.8512	1502.7521	-0.0991	-66	156	168	YGRPLLGCTIKPK							Carbamidomethyl (C)[8]		Mascot
1546.7358	1546.6464	-0.0894	-58	442	454	WSPELAAACEVWK							Carbamidomethyl (C)[9]		Mascot
1794.8149	1794.7172	-0.0977	-54	228	243	GHYLNATAGTCEEMIK							Carbamidomethyl (C)[11]		Mascot
1846.0068	1845.8844	-0.1224	-66	326	341	LEGERDITLGFVDLLR									Mascot
2009.059	2008.9437	-0.1153	-57	331	347	DITLGFVDLLRDFIEK									Mascot
2169.9868	2169.8643	-0.1225	-56	186	204	GGLDFTKDDENVNSQPF MR									Mascot
2169.9868	2169.8643	-0.1225	-56	186	204	GGLDFTKDDENVNSQPF MR	24	29.312							Mascot
2185.9819	2185.8586	-0.1233	-56	186	204	GGLDFTKDDENVNSQPF MR							Oxidation (M)[18]		Mascot
3022.4548	3022.2974	-0.1574	-52	250	276	ELGVPIVMHDYLTGGFTA NTSLAHYCR							Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6531	-0.2187	-57	33	70	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	103	100							Mascot
3854.8718	3854.6531	-0.2187	-57	33	70	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR									Mascot

6 Ribulose biphosphate carboxylase large chain RBL\_COLPU 51962.3 6.57 20 406 100 266 100  
(Fragment) OS=Coleonema pulchellum GN=rbcl PE=3 SV=1

Peptide Information													Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %							
830.4366	830.3878	-0.0488	-59	434	440	EGNEIIR									Mascot
910.4451	910.4066	-0.0385	-42	182	188	AVVECLR							Carbamidomethyl (C)[5]		Mascot
1021.5312	1021.4698	-0.0614	-60	27	35	DTDILAAFR	29	73.001							Mascot
1021.5312	1021.4698	-0.0614	-60	27	35	DTDILAAFR									Mascot
1059.5615	1059.4915	-0.07	-66	416	425	VALEACVQAR									Mascot
1116.583	1116.5172	-0.0658	-59	416	425	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5172	-0.0658	-59	416	425	VALEACVQAR							Carbamidomethyl (C)[6]		Mascot

	1156.5568	1156.5441	-0.0127	-11	210	218	DRFLFCAER						Mascot
	1187.6643	1187.5924	-0.0719	-61	280	289	DNGLLLHHHR						Mascot
	1245.6433	1245.564	-0.0793	-64	434	444	EGNEIIR						Mascot
	1261.7151	1261.6405	-0.0746	-59	334	344	DITLGFVDLLR		57	99.962			Mascot
	1261.7151	1261.6405	-0.0746	-59	334	344	DITLGFVDLLR						Mascot
	1346.6925	1346.5979	-0.0946	-70	212	221	FLFCAERYK				Carbamidomethyl (C)[4]		Mascot
	1451.6219	1451.5601	-0.0618	-43	196	207	DDENVNSQPFMR						Mascot
	1465.7216	1465.6687	-0.0529	-36	314	328	MSGGDHIHAGTVVGK						Mascot
	1465.7546	1465.6687	-0.0859	-59	141	153	TFQGPPHGQIVR		54	99.929			Mascot
	1481.7166	1481.6239	-0.0927	-63	314	328	MSGGDHIHAGTVVGK				Oxidation (M)[1]		Mascot
	1481.7166	1481.6239	-0.0927	-63	314	328	MSGGDHIHAGTVVGK				Oxidation (M)[1]		Mascot
	1502.8512	1502.7521	-0.0991	-66	159	171	YGRPLLGCTKPK				Carbamidomethyl (C)[8]		Mascot
	1546.7358	1546.6464	-0.0894	-58	445	457	WSPLEAAACEVWK				Carbamidomethyl (C)[9]		Mascot
	1794.8149	1794.7172	-0.0977	-54	231	246	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot
	1846.0068	1845.8844	-0.1224	-66	329	344	LEGEDITLGFVDLLR						Mascot
	2009.059	2008.9437	-0.1153	-57	334	350	DITLGFVDLLRDDFIK						Mascot
	2169.9868	2169.8643	-0.1225	-56	189	207	GGLDFTKDDEVNSQPF MR						Mascot
	2169.9868	2169.8643	-0.1225	-56	189	207	GGLDFTKDDEVNSQPF MR		24	29.312			Mascot
	2185.9819	2185.8586	-0.1233	-56	189	207	GGLDFTKDDEVNSQPF MR				Oxidation (M)[18]		Mascot
	3022.4548	3022.2974	-0.1574	-52	253	279	ELGVPIVMHDYLTGGFTA NTLAHYCR				Carbamidomethyl (C)[26]		Mascot
	3854.8718	3854.6531	-0.2187	-57	36	73	VTPQPGVPPEEAGAAVA AESSTGTWTTVTDGLT SLDR		103	100			Mascot
	3854.8718	3854.6531	-0.2187	-57	36	73	VTPQPGVPPEEAGAAVA AESSTGTWTTVTDGLT SLDR						Mascot
7	Ribulose biphosphate carboxylase large chain OS=Populus trichocarpa GN=rbcL PE=3 SV=1					RBL_POPTR	52567.5	6	20	405	100	266	100
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	830.4366	830.3878	-0.0488	-59	440	446	EGNEIIR						Mascot
	910.4451	910.4066	-0.0385	-42	188	194	AVYECLR				Carbamidomethyl (C)[5]		Mascot
	933.5515	933.4611	-0.0904	-97	9	18	AGVGFKAGVK						Mascot
	1021.5312	1021.4698	-0.0614	-60	33	41	DTDIAAFR		29	73.001			Mascot
	1021.5312	1021.4698	-0.0614	-60	33	41	DTDIAAFR						Mascot
	1059.5615	1059.4915	-0.07	-66	422	431	VALEACVQAR						Mascot
	1116.583	1116.5172	-0.0658	-59	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot
	1116.583	1116.5172	-0.0658	-59	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot
	1187.6643	1187.5924	-0.0719	-61	286	295	DNGLLLHHHR						Mascot
	1245.6433	1245.564	-0.0793	-64	440	450	EGNEIIR						Mascot
	1261.6285	1261.6405	0.012	10	218	227	FLFCAEALYK				Carbamidomethyl (C)[4]		Mascot
	1261												





[illegible]

9	Ribulose biphosphate carboxylase large chain OS=Carica papaya GN=rbcl PE=3 SV=2	RBL_CARPA	52456.6	6.19	15	145	100	60	99.982				
Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	898.41	898.3478	-0.0622	-69	308	312	NHGMHFR						Mascot
	910.4451	910.3814	-0.0637	-70	188	194	AVVECLR				Carbamidomethyl (C)[5]		Mascot
	914.4049	914.3411	-0.0638	-70	306	312	NHGMHFR				Oxidation (M)[4]		Mascot
	1021.5312	1021.4651	-0.0661	-65	33	41	DTDILAAFR						Mascot
	1116.583	1116.5088	-0.0742	-66	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot
	1170.5585	1170.5627	0.0042	4	304	312	QKNHGMHFR				Oxidation (M)[6]		Mascot
	1187.6643	1187.5728	-0.0915	-77	286	295	DNGLLLHIHR	15		0			Mascot
	1187.6643	1187.5728	-0.0915	-77	286	295	DNGLLLHIHR						Mascot
	1245.6433	1245.5524	-0.0909	-73	440	450	EGNEIIR						Mascot
	1261.6285	1261.632	0.0035	3	218	227	FLFCAEAIYK				Carbamidomethyl (C)[4]		Mascot
	1261.7151	1261.632	-0.0831	-66	340	350	DTLGFVDLLR	33		89.743			Mascot
	1392.6682	1392.6061	-0.0621	-45	22	32	LYTYTPDYQTK						Mascot
	1465.7546	1465.6554	-0.0992	-68	147	159	TFQGPPIHGQVER						Mascot
	1465.7546	1465.6554	-0.0992	-68	147	159	TFQGPPIHGQVER	14		0			Mascot
	1502.8512	1502.723	-0.1282	-85	165	177	YGRPLLCTIKPK				Carbamidomethyl (C)[8]		Mascot
	2009.059	2008.9154	-0.1436	-71	340	356	DTLGFVDLLRDEFVEK						Mascot
	2169.9868	2169.8503	-0.1365	-63	195	213	GGLDFTKDDENVNSQPF MR						Mascot
	2185.9819	2185.8425	-0.1394	-64	195	213	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot
	3854.8718	3854.5942	-0.2776	-72	42	79	YTPQPGVPPEEAGAAVA AESSTGTWTVWTDGLT SLDLR						Mascot

10	Ribulose biphosphate carboxylase large chain (Fragment) OS=Tabebuia heterophylla GN=rbcl PE=3 SV=1	RBL_TABHE	52026.2	6.04	15	143	100	58	99.973		
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	898.41	898.3478	-0.0622	-69	297	303	NHGMHFR				Mascot
	910.4451	910.3814	-0.0637	-70	179	185	AVVECLR			Carbamidomethyl (C)[5]	Mascot
	914.4049	914.3411	-0.0638	-70	297	303	NHGMHFR			Oxidation (M)[4]	Mascot
	1021.5312	1021.4651	-0.0661	-65	24	32	DTDILAAFR				Mascot
	1116.583	1116.5088	-0.0742	-66	413	422	VALEACVQAR			Carbamidomethyl (C)[6]	Mascot
	1170.5585	1170.5627	0.0042	4	295	303	QKNHGMHFR			Oxidation (M)[6]	Mascot
	1187.6643	1187.5728	-0.0915	-77	277	286	DNGLLLHIHR	15	0		Mascot
	1187.6643	1187.5728	-0.0915	-77	277	286	DNGLLLHIHR				Mascot
	1261.6285	1261.632	0.0035	3	209	218	FLFCAEAIYK			Carbamidomethyl (C)[4]	Mascot
	1261.7151	1261.632	-0.0831	-66	331	341	DTLGFVDLLR	33	90.171		Mascot
	1465.7216	1465.6554	-0.0662	-45	311	325	MSGGDHIHAGTVVGK				Mascot
	1465.7546	1465.6554	-0.0992	-68	138	150	TFQGPPIHGQVER	14	0		Mascot
	1502.8512	1502.723	-0.1282	-85	156	168	YGRPLLCTIKPK			Carbamidomethyl (C)[8]	Mascot
	2009.059	2008.9154	-0.1436	-71	331	347	DTLGFVDLLRDDFIEK				Mascot
	2169.9868	2169.8503	-0.1365	-63	186	204	GGLDFTKDDENVNSQPF MR				Mascot
	2185.9819	2185.8425	-0.1394	-64	186	204	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]	Mascot
	2748.3298	2748.0859	-0.2439	-89	219	243	AQAETGEIKGHYLNATAG TWEEMIK				Mascot
	3022.4548	3022.2563	-0.1985	-66	250	276	ELGVPIVMHDYLTGFTA			Carbamidomethyl (C)[26]	Mascot

Gel Idx/Pos		110/E9		Instr./Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate (#) Name		[1] 31564		Instrument Sample Name							
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	Spectra	11

1	ATP synthase subunit alpha, chloroplastic OS=Manihot esculenta GN=atpA PE=3 SV=1	ATPA_MANES	55564.2	5.22	14	637	100	559	100
---	--	------------	---------	------	----	-----	-----	-----	-----

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0	Oxidation (M)[2]		Mascot	
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot	
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot	
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR					Mascot	
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR					Mascot	
901.485	901.4265	-0.0585	-65	406	413	ATONQLAR					Mascot	
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot	
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot	
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993			Mascot	
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR					Mascot	
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR				Mascot		
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691		Mascot		
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK				Mascot		
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100		Mascot		
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR				Mascot		
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVTTLOER	83	100		Mascot		
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVTTLOER				Mascot		
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSHR				Mascot		
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSHR	128	100		Mascot		
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK				Mascot		
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFOEISSTK				Mascot		
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR				Mascot		
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR	114	100		Mascot		
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLAIDSMIPI GR			Oxidation (M)[16]	Mascot		
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLAIDSMIPI GR				Mascot		
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLAIDSMIPI GR			Oxidation (M)[17]	Mascot		

2	ATP synthase subunit alpha, chloroplastic OS=Carica papaya GN=atpA PE=3 SV=1		GR		ATPA_CARPA		55136.9	5.1	12	620	100	559	100
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR		17	0			Mascot
	815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR						Mascot
	860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR		16	0			Mascot
	860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR						Mascot
	876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR				Oxidation (M)[2]		Mascot
	901.485	901.4265	-0.0585	-65	406	413	ATONQLAR						Mascot
	904.5614	904.5014	-0.06	-66	456	462	KFLVELR						Mascot



	904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0								Mascot
	1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993								Mascot
	1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR										Mascot
	1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR										Mascot
	1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691								Mascot
	1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100								Mascot
	1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR										Mascot
	1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER	83	100								Mascot
	1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER										Mascot
	1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR										Mascot
	1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR	128	100								Mascot
	1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFQEIHSSTK										Mascot
	2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR										Mascot
	2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100								Mascot
	2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR										Mascot
	2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR										Mascot
	2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR										Mascot

3

ATP synthase subunit alpha, chloroplastic OS=Glycine max GN=atpA PE=3 SV=1

ATPA\_SOYBN

55719.3

5.15

19

609

100

476

100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR					Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR					Mascot
901.485	901.4265	-0.0585	-65	406	413	ATONQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot
1123.563	1123.4845	-0.0785	-70	17	25	IEQYNTVEVK					Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691			Mascot
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK					Mascot
1408.7067	1408.6079	-0.0988	-70	15	25	ERIEQYNTVEVK	15				Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100			Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR	128	100			Mascot
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK					Mascot
2205.1108	2204.9502	-0.1606	-73	492	509	EAIQEQMELFLLOEQVEK					Mascot
2221.1057	2220.9746	-0.1311	-59	492	509	EAIQEQMELFLLOEQVEK					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2319.1536	2318.9807	-0.1729	-75	492	510	EAIQEQMELFLLOEQVEK N					Mascot
2335.1484	2334.9729	-0.1755	-75	492	510	EAIQEQMELFLLOEQVEK N					Mascot
2372.1655	2371.9922	-0.1733	-73	385	405	LELAQFAELEFAQFSSD LDK					Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot
2613.3445	2613.1482	-0.1963	-75	383	405	LKLELAQFAELEFAQFS SLDLK					Mascot
3623.8438	3623.6072	-0.2366	-65	423	455	QSQSAPLTVEEQIITYTG TNGYLDLSLEIGQVR					Mascot

4

ATP synthase subunit alpha, chloroplastic OS=Morus indica GN=atpA PE=3 SV=1

ATPA\_MORIN

55407.1

5.15

13

575

100

506

100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR					Mascot
876.4825	876.4377	-0.0448	-51	501	507	FLLOEQV					Mascot
901.485	901.4265	-0.0585	-65	406	413	ATONQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691			Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER	83	100			Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFLHSR	128	100			Mascot
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFQEIHSSTK					Mascot
1626.9174	1626.8071	-0.1103	-68	26	41	ILNTGTVLQVGDGIAR					Mascot
1626.9174	1626.8071	-0.1103	-68	26	41	ILNTGTVLQVGDGIAR	45	99.385			Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot

5

ATP synthase subunit alpha, chloroplastic OS=Gossypium hirsutum GN=atpA PE=3 SV=1

ATPA\_GOSHI

55379.9

5.25

14

554

100

476

100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot

860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0		Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR				Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR				Mascot
901.485	901.4265	-0.0585	-65	406	413	ATQNQLAR			Oxidation (M)[2]	Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR				Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0		Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGISR	64	99.993		Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGISR				Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR				Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691		Mascot
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK				Mascot
1408.6638	1408.6079	-0.0559	-40	492	502	DAIQDQMERFR				Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100		Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR				Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR				Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR	128	100		Mascot
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK				Mascot
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFQEIISSTK				Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR				Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR	114	100		Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLAIDSMIPI GR			Oxidation (M)[16]	Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLAIDSMIPI GR				Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLAIDSMIPI GR			Oxidation (M)[17]	Mascot

6    ATP synthase subunit alpha, chloroplastic    ATPA\_PHAVU    55676.3    5.21    15    548    100    461    100

OS=Phaseolus vulgaris GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR					Mascot
901.485	901.4265	-0.0585	-65	406	413	ATQNQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
1123.563	1123.4845	-0.0785	-70	17	25	IEQYNTVEVK					Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGISR	64	99.993			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGISR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691			Mascot
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK					Mascot
1408.7067	1408.6079	-0.0988	-70	15	25	ERIEQYNTVEK					Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTTLQER	83	100			Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTTLQER					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR	128	100			Mascot
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK					Mascot
2225.1157	2224.9956	-0.1201	-54	492	509	DAIKEQMEFLFPEQVEK					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLAIDSMIPI GR			Oxidation (M)[16]		Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLAIDSMIPI GR			Oxidation (M)[17]		Mascot

7    ATP synthase subunit alpha, chloroplastic OS=Atropa    ATPA\_ATRBE    55419.1    5.26    14    547    100    466    100

belladonna GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR					Mascot
901.485	901.4265	-0.0585	-65	406	413	ATQNQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	3	0			Mascot
1252.7372	1252.6412	-0.096	-77	108	119	VVNALAKPIDGR					Mascot
1252.7372	1252.6412	-0.096	-77	108	119	VVNALAKPIDGR					Mascot
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK					Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100			Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR					Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTTLQER	83	100			Mascot
1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTTLQER					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLSR	128	100			Mascot
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK					Mascot
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFQEIISSTK					Mascot
2225.1006	2224.9956	-0.105	-47	491	499	TFTTEAEALKKEAIOEQM K			Oxidation (M)[18]		Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLAIDSMIPI GR			Oxidation (M)[16]		Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLAIDSMIPI GR			Oxidation (M)[17]		Mascot

8    ATP synthase subunit alpha, chloroplastic    ATPA\_NICTO    55344    5.14    11    547    100    494    100

OS=Nicotiana tomentosiformis GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR					Mascot
901.485	901.4265	-0.0585	-65	406	413	ATQNQLAR					Mascot

	904.5614	904.5014	-0.06	-66	456	462	KFLVELR												Mascot
	904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0										Mascot
	1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR												Mascot
	1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691										Mascot
	1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100										Mascot
	1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR												Mascot
	1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER	83	100										Mascot
	1488.8016	1488.7006	-0.101	-68	203	216	ASSVAQVVTLOER												Mascot
	1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR												Mascot
	1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR	128	100										Mascot
	1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFOEIIISTK												Mascot
	2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR												Mascot
	2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100										Mascot
	2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR												Mascot
	2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR												Mascot
	2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR												Mascot

9 ATP synthase subunit alpha, chloroplastic  
OS=Helianthus annuus GN=atpA PE=3 SV=1

ATPA\_HELAN

55482.2

5.2

13

545

100

476

100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR					Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
901.485	901.4265	-0.0585	-65	406	413	ATONQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691			Mascot
1317.705	1317.6143	-0.0907	-69	256	266	HTLIYDDLK					Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100			Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR	128	100			Mascot
1602.8486	1602.7313	-0.1173	-73	254	266	ERHTLIYDDLK					Mascot
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFOEIIISTK					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR			Oxidation (M)[16]		Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR			Oxidation (M)[17]		Mascot

10 ATP synthase subunit alpha, chloroplastic OS=Lactuca  
sativa GN=atpA PE=3 SV=1

ATPA\_LACSA

55484.2

5.27

13

545

100

476

100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR	17	0			Mascot
815.4621	815.4097	-0.0524	-64	166	172	ELIIGDR					Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR	16	0			Mascot
860.5022	860.4446	-0.0576	-67	273	279	QMSLLLR					Mascot
876.4971	876.4377	-0.0594	-68	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
901.485	901.4265	-0.0585	-65	406	413	ATONQLAR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR					Mascot
904.5614	904.5014	-0.06	-66	456	462	KFLVELR	11	0			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR	64	99.993			Mascot
1252.726	1252.6412	-0.0848	-68	129	140	LIESPAPGIISR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR					Mascot
1266.7528	1266.6654	-0.0874	-69	108	119	VINALAKPIDGR	29	76.691			Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR	97	100			Mascot
1416.7845	1416.6931	-0.0914	-65	95	107	IAQIPVSEAYLGR					Mascot
1535.7812	1535.6375	-0.1437	-94	203	216	ASSVAQVVTNFGQER					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR					Mascot
1553.7383	1553.6332	-0.1051	-68	285	297	EAYPGDVFYLHSR	128	100			Mascot
1602.8519	1602.7313	-0.1206	-75	1	14	MVTIQADEISNIIR					Mascot
1620.8591	1620.7418	-0.1173	-72	467	480	TNKPQFOEIIISTK					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR					Mascot
2273.2209	2273.0591	-0.1618	-71	142	162	SVYEPLQTGLIAIDSMIPI GR	114	100			Mascot
2289.2158	2289.0505	-0.1653	-72	142	162	SVYEPLQTGLIAIDSMIPI GR			Oxidation (M)[16]		Mascot
2429.322	2429.1331	-0.1889	-78	141	162	RSVYEPLQTGLIAIDSMIPI GR					Mascot
2445.3169	2445.1235	-0.1934	-79	141	162	RSVYEPLQTGLIAIDSMIPI GR			Oxidation (M)[17]		Mascot

Gel Idx/Pos	111/E10	Instr./Gel Origin	BA2060/140227A	Process Statu	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
------	--------------	---------------	------------	------------	------------	---------------	-----------------------	-----------------	-------------------

1 ATP synthase subunit beta, chloroplastic OS=Morus

ATPB\_MORIN

53758.1

5.46

30

1,010

100

716

100

indica GN=atpB PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR					Mascot
975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK					Mascot
1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK					Mascot
1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR					Mascot
1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR					Mascot
1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK					Mascot
1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR					Mascot
1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR					Mascot
1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK					Mascot
1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR			Oxidation (M)[4]		Mascot
1261.6973	1261.6252	-0.0721	-67	40	50	MPNIYNALVVK					Mascot

1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER							Mascot
1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER	32	91.025					Mascot
1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR							Mascot
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR	41	98.709					Mascot
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR							Mascot
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR							Mascot
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR	25	55.124					Mascot
1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK							Mascot
1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR							Mascot
1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK							Mascot
1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQNIAESK							Mascot
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR							Mascot
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR	70	99.998					Mascot
1617.8053	1617.6876	-0.1177	-73	232	246	VALVYGQMNPPGAR							Mascot
1735.0153	1734.8885	-0.1268	-73	23	39	IAQIGPVLDAFPFGK							Mascot
1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDNIFR							Mascot
1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR	138	100					Mascot
1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR							Mascot
2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQPR							Mascot
2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQPR	94	100					Mascot
2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLQPR							Mascot
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGGATLGR	126	100					Mascot
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGGATLGR							Mascot
2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGGATLGR							Mascot
2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEEDR							Mascot
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGSLQER	105	100					Mascot
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGSLQER							Mascot
2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGSLQER							Mascot
2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGSLQER							Mascot
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQLGNRR							Mascot
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQLGNRR	86	100					Mascot
2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEEDR							Mascot
2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQLGNRR							Mascot
2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEEDRLTVAR							Mascot
2876.4927	2876.2725	-0.2202	-77	460	486	LILSGELDQLPEQAFYLVGNIDEATAK							Mascot
3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIAQAVYVPADDLTPAPATTFAPHLDAITTVLSR							Mascot

2    ATP synthase subunit beta, chloroplastic    ATPB\_GALBE    53610.9    5.44    28    835    100    579    100  
OS=Galbulimima belgraveana GN=atpB PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR					Mascot
975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK					Mascot
1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK					Mascot
1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR					Mascot
1045.604	1045.5298	-0.0742	-71	155	163	VDLLAPYR					Mascot
1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK					Mascot
1201.7052	1201.6226	-0.0826	-69	155	164	VDLLAPYRR					Mascot
1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR					Mascot
1228.5177	1229.4319	-0.0858	-70	208	217	EQNDLYMEMK					Mascot
1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR					Mascot
1261.6973	1261.6252	-0.0721	-57	40	50	MPNIYNALVVK					Mascot
1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER					Mascot
1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER	32	91.025			Mascot
1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR					Mascot
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR	41	98.709			Mascot
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR					Mascot
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR					Mascot
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR	25	55.124			Mascot
1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK					Mascot
1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR					Mascot
1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK					Mascot
1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQNIAESK					Mascot
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR					Mascot
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR	70	99.998			Mascot
1617.8053	1617.6876	-0.1177	-73	232	246	VALVYGQMNPPGAR					Mascot
1735.0153	1734.8885	-0.1268	-73	23	39	IAQIGPVLDAFPFGK					Mascot
1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDNIFR					Mascot
2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQPR					Mascot
2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQPR	94	100			Mascot
2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLQPR					Mascot
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGGATLGR	126	100			Mascot
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGGATLGR					Mascot
2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGGATLGR					Mascot
2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEEDR					Mascot
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGSLQER	105	100			Mascot
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGSLQER					Mascot
2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGSLQER					Mascot
2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGSLQER					Mascot
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQLGNRR					Mascot
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQLGNRR	86	100			Mascot

	2462.2861	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEE DR								Mascot	
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR				Carbamidomethyl (C)[13]				Mascot	
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEEDR LTVAR								Mascot	
	3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIAQVVPADDLT DPAPATTF AHLDTTVLS R								Mascot	
3	ATP synthase subunit beta, chloroplastic OS=Balaka seemannii GN=atpB PE=3 SV=1						ATPB_BALSE	53764.1	5.29	27	821		100	579	100	
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
	811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR								Mascot	
	975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK								Mascot	
	1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK								Mascot	
	1021.5676	1021.4685	-0.0991	-97	448	456	VYGLAETR								Mascot	
	1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR								Mascot	
	1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK								Mascot	
	1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR								Mascot	
	1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR								Mascot	
	1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK								Mascot	
	1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR					Oxidation (M)[4]			Mascot	
	1261.682	1261.6252	-0.0568	-45	487	497	AMNLEVESKLK								Mascot	
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGSVFVGGVGER								Mascot	
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGSVFVGGVGER		32	91.025					Mascot	
	1431.6863	1431.5853	-0.101	-71	379	390	IIGEHEYETAQR								Mascot	
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709					Mascot	
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR								Mascot	
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR								Mascot	
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124					Mascot	
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK								Mascot	
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR								Mascot	
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK					Oxidation (M)[8] Oxidation (M)[9]			Mascot	
	1517.7805	1517.6533	-0.1272	-84	218	231	ESGVINEKNIAESK								Mascot	
	1601.8104	1601.6953	-0.1151	-72	232	246	VALYVGQMNEPPGAR								Mascot	
	1601.8104	1601.6953	-0.1151	-72	232	246	VALYVGQMNEPPGAR		70	99.998					Mascot	
	1617.8053	1617.6876	-0.1177	-73	232	246	VALYVGQMNEPPGAR					Oxidation (M)[8]			Mascot	
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLFLDINIFR								Mascot	
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLOP R		94	100					Mascot	
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLOP R								Mascot	
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLOP R					Oxidation (M)[15]			Mascot	
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR		126	100					Mascot	
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR								Mascot	
	2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGG ATLGR					Oxidation (M)[2]			Mascot	
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEEDR								Mascot	
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER		105	100					Mascot	
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER								Mascot	
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LOER					Oxidation (M)[1]			Mascot	
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LOER					Oxidation (M)[1,15]			Mascot	
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR					Carbamidomethyl (C)[11]			Mascot	
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR		86	100		Carbamidomethyl (C)[11]			Mascot	
	2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEE DR								Mascot	
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR					Carbamidomethyl (C)[13]			Mascot	
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEEDR LTVAR								Mascot	
	3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIAQVVPADDLT DPAPATTF AHLDTTVLS R								Mascot	
4	ATP synthase subunit beta, chloroplastic OS=Hyophorbe lagenicaulis GN=atpB PE=3 SV=1						ATPB_HYOLA	53750	5.22	27	821		100	579	100	
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
	811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR								Mascot	
	975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK								Mascot	
	1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK								Mascot	
	1021.5676	1021.4685	-0.0991	-97	448	456	VYGLAETR								Mascot	
	1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR								Mascot	
	1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK								Mascot	
	1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR								Mascot	
	1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR								Mascot	
	1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK								Mascot	
	1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR					Oxidation (M)[4]			Mascot	
	1261.6973	1261.6252	-0.0721	-57	40	50	MPNINVALIVK								Mascot	
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGSVFVGGVGER								Mascot	
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGSVFVGGVGER		32	91.025					Mascot	
	1431.6863	1431.5853	-0.101	-71	379	390	IIGEHEYETAQR								Mascot	
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709					Mascot	
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR								Mascot	
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR								Mascot	
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124					Mascot	
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK								Mascot	
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR					Oxidation (M)[8] Oxidation (M)[9]			Mascot	
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK								Mascot	
	1517.7805	1517.6533	-0.1272	-84	218	231	ESGVINEKNIAESK								Mascot	
	1601.8104	1601.6953	-0.1151	-72	232	246	VALYVGQMNEPPGAR								Mascot	
	1601.8104	1601.6953	-0.1151	-72	232	246	VALYVGQMNEPPGAR		70	99.998					Mascot	
	1617.8053	1617.6876	-0.1177	-73	232	246	VALYVGQMNEPPGAR					Oxidation (M)[8]			Mascot	
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLFLDINIFR								Mascot	
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLOP R		94	100					Mascot	
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLOP R								Mascot	
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLOP R					Oxidation (M)[15]			Mascot	

5	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR	126	100						Mascot
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR								Mascot
	2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGG ATLGR			Oxidation (M)[2]					Mascot
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEEDR								Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER	105	100						Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER								Mascot
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LOER			Oxidation (M)[1]					Mascot
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LOER			Oxidation (M)[1,15]					Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR			Carbamidomethyl (C)[11]					Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR	86	100	Carbamidomethyl (C)[11]					Mascot
	2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEE DR								Mascot
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR			Carbamidomethyl (C)[13]					Mascot
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEEDR LTVAR								Mascot
	3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIAQVYVPADDLT DPAPATTFAHLDATTVLS R								Mascot
	ATP synthase subunit beta, chloroplastic OS=Liriodendron tulipifera GN=atpB PE=3 SV=2														
Peptide Information															
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type		
811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR							Mascot		
975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK							Mascot		
1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK							Mascot		
1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR							Mascot		
1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR							Mascot		
1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK							Mascot		
1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR							Mascot		
1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR							Mascot		
1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK							Mascot		
1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR			Oxidation (M)[4]				Mascot		
1261.682	1261.6252	-0.0568	-45	487	497	AMNLEVESKLK							Mascot		
1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER							Mascot		
1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER	32	91.025					Mascot		
1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYTAQR							Mascot		
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR	41	98.709					Mascot		
1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR							Mascot		
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALMAEYFR							Mascot		
1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALMAEYFR	25	55.124					Mascot		
1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK							Mascot		
1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALMAEYFR			Oxidation (M)[8]				Mascot		
1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK			Oxidation (M)[9]				Mascot		
1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQIAESK							Mascot		
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYQMNPEPPGAR							Mascot		
1601.8104	1601.6953	-0.1151	-72	232	246	VALVYQMNPEPPGAR	70	99.998					Mascot		
1617.8053	1617.6876	-0.1177	-73	232	246	VALVYQMNPEPPGAR			Oxidation (M)[8]				Mascot		
1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLIFIDNIFR							Mascot		
2061.0322	2060.877	-0.1552	-75	360	378	GIYPADVPLDSTSTMLOP R							Mascot		
2061.0322	2060.877	-0.1552	-75	360	378	GIYPADVPLDSTSTMLOP R	94	100					Mascot		
2077.0271	2076.8816	-0.1455	-70	360	378	GIYPADVPLDSTSTMLOP R			Oxidation (M)[15]				Mascot		
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR	126	100					Mascot		
2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR							Mascot		
2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGG ATLGR			Oxidation (M)[2]				Mascot		
2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEEDR							Mascot		
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER	105	100					Mascot		
2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LOER							Mascot		
2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LOER			Oxidation (M)[1]				Mascot		
2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LOER			Oxidation (M)[1,15]				Mascot		
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR			Carbamidomethyl (C)[11]				Mascot		
2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNRR	86	100	Carbamidomethyl (C)[11]				Mascot		
2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEE DR							Mascot		
2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR			Carbamidomethyl (C)[13]				Mascot		
2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEEDR LTVAR							Mascot		
3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIAQVYVPADDLT DPAPATTFAHLDATTVLS R							Mascot		
ATP synthase subunit beta, chloroplastic OS=Myristica fragrans GN=atpB PE=3 SV=1															
Peptide Information															
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type		
811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR							Mascot		
975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK							Mascot		
1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK							Mascot		
1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR							Mascot		
1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR							Mascot		
1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK							Mascot		
1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR							Mascot		
1222.5919	1222.5135	-0.0784	-64	76	87	AVAMSATDGLMR							Mascot		
1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK							Mascot		
1238.5868	1238.5	-0.0868	-70	76	87	AVAMSATDGLMR			Oxidation (M)[4]				Mascot		

	1261.6973	1261.6252	-0.0721	-57	40	50	MPNIYNALVVK										Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFVGGVGER										Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFVGGVGER		32	91.025							Mascot
	1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR										Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709							Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR										Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR										Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124							Mascot
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK										Mascot
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR										Mascot
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK										Mascot
	1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQNAIESK										Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVVGQMNPPGAR										Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVVGQMNPPGAR		70	99.998							Mascot
	1617.8053	1617.6876	-0.1177	-73	232	246	VALVVGQMNPPGAR										Mascot
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDINFR										Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQP R										Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQP R		94	100							Mascot
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLQP R										Mascot
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR		126	100							Mascot
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR										Mascot
	2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGG ATLGR										Mascot
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIHAILGLDELSEEDR										Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER		105	100							Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER										Mascot
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LQER										Mascot
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LQER										Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGQQINVTCEVQQL GNRR										Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGQQINVTCEVQQL GNRR		86	100							Mascot
	2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIHAILGLDELSEE DR										Mascot
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR										Mascot
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIHAILGLDELSEEDR LTVAR										Mascot
	3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIQAVVYPADDLT DPAPATTFAPLDATTVLS R										Mascot
7	ATP synthase subunit beta, chloroplastic OS=Platanus occidentalis GN=atpB PE=3 SV=1					ATPB_PLAOC		53587.9	5.22	27	818	100	579	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type				
	811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR						Mascot				
	975.5621	975.4914	-0.0707	-72	168	178	IGLFGGAGVGK						Mascot				
	1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK						Mascot				
	1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR						Mascot				
	1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR						Mascot				
	1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFIQLDTK						Mascot				
	1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR						Mascot				
	1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK						Mascot				
	1261.682	1261.6252	-0.0568	-45	487	497	AMNLEVESKLK						Mascot				
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFVGGVGER						Mascot				
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFVGGVGER		32	91.025			Mascot				
	1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR						Mascot				
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709			Mascot				
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR						Mascot				
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR						Mascot				
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124			Mascot				
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK						Mascot				
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR						Mascot				
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK						Mascot				
	1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQNAIESK						Mascot				
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVVGQMNPPGAR						Mascot				
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVVGQMNPPGAR		70	99.998			Mascot				
	1617.8053	1617.6876	-0.1177	-73	232	246	VALVVGQMNPPGAR						Mascot				
	1735.0153	1734.8885	-0.1268	-73	23	39	IAQIGPVLDFAPPGK						Mascot				
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDINFR						Mascot				
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQP R						Mascot				
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPAVDPLDSTSTMLQP R		94	100			Mascot				
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPAVDPLDSTSTMLQP R							Oxidation (M)[15]	Mascot		
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR		126	100			Mascot				
	2097.1008	2096.9463	-0.1545	-74	88	109	GMEVIDTGAPLSVPVGG ATLGR						Mascot				
	2113.0957	2112.9412	-0.1545	-73	88	109	GMEVIDTGAPLSVPVGG ATLGR							Oxidation (M)[2]	Mascot		
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIHAILGLDELSEEDR						Mascot				
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER		105	100			Mascot				
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER						Mascot				
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LQER							Oxidation (M)[1]	Mascot		
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LQER							Oxidation (M)[1,15]	Mascot		
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGQQINVTCEVQQL GNRR							Carbamidomethyl (C)[11]	Mascot		
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGQQINVTCEVQQL GNRR		86	100				Carbamidomethyl (C)[11]	Mascot		
	2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIHAILGLDELSEE DR							Mascot			
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR							Carbamidomethyl (C)[13]	Mascot		
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIHAILGLDELSEEDR							Mascot			

		3843.9287	3843.6343	-0.2944	-77	318	354	LTVAR EGSITSIQAVVYPADDLT DPAPATTF AHLDTATTVLS R										Mascot
8	ATP synthase subunit beta, chloroplastic OS=Glycine max GN=atpB PE=3 SV=1							ATPB_SOYBN	53721.1	5.29	26	817	100	590	100			
Peptide Information																		
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type				
	811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR											Mascot
	975.5621	975.4914	-0.0707	-72	168	178	IGLFGAGVGK											Mascot
	1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR											Mascot
	1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFQLDTK											Mascot
	1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR											Mascot
	1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK											Mascot
	1261.5074	1261.6252	0.1178	93	208	217	EGNDLYMEMK					Oxidation (M)[7,9]						Mascot
	1275.7129	1275.6212	-0.0917	-72	40	50	MPNIYNALIVK											Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER											Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER		32	91.025								Mascot
	1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR											Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709								Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR											Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR											Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124								Mascot
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK											Mascot
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR					Oxidation (M)[8]						Mascot
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK					Oxidation (M)[9]						Mascot
	1517.7441	1517.6533	-0.0908	-60	218	231	ESGVINEQNAESK											Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR											Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR		70	99.998								Mascot
	1617.8053	1617.6876	-0.1177	-73	232	246	VALVYGQMNPPGAR					Oxidation (M)[8]						Mascot
	1735.0153	1734.8885	-0.1268	-73	23	39	IAQIGPVLDFAPPGK											Mascot
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDNIFR											Mascot
	1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR		138	100								Mascot
	1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR											Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPVDPLDSTSTMLQP R		94	100								Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPVDPLDSTSTMLQP R					Oxidation (M)[15]						Mascot
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPVDPLDSTSTMLQP R											Mascot
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEDR											Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER		105	100								Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER											Mascot
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LQER					Oxidation (M)[1]						Mascot
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LQER					Oxidation (M)[1,15]						Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNNR					Carbamidomethyl (C)[11]						Mascot
	2386.178	2385.9895	-0.1885	-79	53	73	DTVGGQINVTCEVQQL GNNR		86	100		Carbamidomethyl (C)[11]						Mascot
	2462.2661	2462.0779	-0.1882	-76	398	418	YKELQDIIAILGLDELSEE DR											Mascot
	2599.3005	2599.1033	-0.1972	-76	51	73	GRDTVGGQINVTCEVQQ LLGNRR					Carbamidomethyl (C)[13]						Mascot
	2711.446	2711.2385	-0.2075	-77	400	423	ELQDIIAILGLDELSEDR LTVAR											Mascot
	2876.4927	2876.2725	-0.2202	-77	460	486	LILSGELDQLPEQAFYLV GNIDEATAK											Mascot
	3843.9287	3843.6343	-0.2944	-77	318	354	EGSITSIQAVVYPADDLT DPAPATTF AHLDTATTVLS R											Mascot
9	ATP synthase subunit beta, chloroplastic OS=Lotus japonicus GN=atpB PE=3 SV=1							ATPB_LOTJA	53779.2	5.37	26	816	100	590	100			
Peptide Information																		
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type				
	811.4421	811.3855	-0.0566	-70	128	134	TTSPIHR											Mascot
	975.5621	975.4914	-0.0707	-72	168	178	IGLFGAGVGK											Mascot
	1007.5771	1007.5035	-0.0736	-73	146	154	LSIFETGIK											Mascot
	1021.5676	1021.4685	-0.0991	-97	448	456	YVGLAETIR											Mascot
	1045.604	1045.5298	-0.0742	-71	155	163	VVDLLAPYR											Mascot
	1190.6416	1190.5585	-0.0831	-70	135	145	SAPAFQLDTK											Mascot
	1201.7052	1201.6226	-0.0826	-69	155	164	VVDLLAPYRR											Mascot
	1229.5177	1229.4319	-0.0858	-70	208	217	EGNDLYMEMK											Mascot
	1261.5074	1261.6252	0.1178	93	208	217	EGNDLYMEMK					Oxidation (M)[7,9]						Mascot
	1275.7129	1275.6212	-0.0917	-72	40	50	MPNIYNALIVK											Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER											Mascot
	1328.6705	1328.5762	-0.0943	-71	192	205	AHGGVSVFGGVGER		32	91.025								Mascot
	1431.6863	1431.5853	-0.101	-71	379	390	IVGEEHYETAQR											Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR		41	98.709								Mascot
	1433.7747	1433.6652	-0.1095	-76	278	291	FVQAGSEVSALLGR											Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR											Mascot
	1471.7614	1471.6675	-0.0939	-64	249	261	VGLTALTMAEYFR		25	55.124								Mascot
	1486.6665	1486.5659	-0.1006	-68	206	217	TREGNDLYMEMK											Mascot
	1487.7562	1487.6439	-0.1123	-75	249	261	VGLTALTMAEYFR					Oxidation (M)[8]						Mascot
	1502.6614	1502.6141	-0.0473	-31	206	217	TREGNDLYMEMK					Oxidation (M)[9]						Mascot
	1517.7805	1517.6533	-0.1272	-84	218	231	ESGVINEKNAESK											Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR											Mascot
	1601.8104	1601.6953	-0.1151	-72	232	246	VALVYGQMNPPGAR		70	99.998								Mascot
	1617.8053	1617.6876	-0.1177	-73	232	246	VALVYGQMNPPGAR					Oxidation (M)[8]						Mascot
	1949.9967	1949.8513	-0.1454	-75	262	277	DVNEQDVLLFDNIFR											Mascot
	1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR		138	100								Mascot
	1969.0388	1968.8937	-0.1451	-74	110	127	IFNVLGEPIDNLGPVDTR											Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPVDPLDSTSTMLQP R		94	100								Mascot
	2061.0322	2060.877	-0.1552	-75	360	378	GIYPVDPLDSTSTMLQP R					Oxidation (M)[15]						Mascot
	2077.0271	2076.8816	-0.1455	-70	360	378	GIYPVDPLDSTSTMLQP R											Mascot
	2171.1077	2170.9141	-0.1936	-89	400	418	ELQDIIAILGLDELSEDR											Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER		105	100								Mascot
	2282.0791	2281.9097	-0.1694	-74	292	312	MPSAVGYQPTLSTEMGS LQER											Mascot
	2298.074	2297.9077	-0.1663	-72	292	312	MPSAVGYQPTLSTEMGS LQER					Oxidation (M)[1]						Mascot
	2314.0688	2313.9358	-0.133	-57	292	312	MPSAVGYQPTLSTEMGS LQER					Oxidation (M)[1,15]						Mascot





2	Ribulose biphosphate carboxylase large chain OS=Manihot esculenta GN=rbcl PE=3 SV=1	RBL_MANES	52648.5	6.18	22	793	100	628	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
898.41	898.3482	-0.0618	-69	306	312	NHGMHFR				Mascot
910.4451	910.3833	-0.0618	-68	188	194	AVYECLR			Carbamidomethyl (C)[5]	Mascot
912.4719	912.4003	-0.0716	-78	296	303	AMHAVIDR				Mascot
914.4049	914.3571	-0.0478	-52	306	312	NHGMHFR			Oxidation (M)[4]	Mascot
928.4669	928.4019	-0.065	-70	296	303	AMHAVIDR			Oxidation (M)[2]	Mascot
1021.5312	1021.4615	-0.0697	-68	33	41	DTDLAAFR				Mascot
1037.4899	1037.4182	-0.0717	-69	351	358	DDFIEKDR				Mascot
1116.583	1116.5592	-0.0738	-66	422	431	VALGAGVQAR			Carbamidomethyl (C)[6]	Mascot
1170.5595	1170.5565	-0.002	-2	304	312	QKNHGMHFR			Oxidation (M)[6]	Mascot
1187.6643	1187.5881	-0.0762	-64	286	295	DNGLLLHIHR				Mascot
1261.6285	1261.6326	0.0041	3	218	227	FLFCAEAYK			Carbamidomethyl (C)[4]	Mascot
1261.7151	1261.6326	-0.0825	-65	340	350	DITLGFVDLLR	95	100		Mascot
1392.6682	1392.687	0.0188	13	22	32	LTYYTPDYQTK	18	0		Mascot
1392.6682	1392.687	0.0188	13	22	32	LTYYTPDYQTK				Mascot
1447.7651	1447.6692	-0.0959	-66	320	334	LSGGDHIHAGTVVGK				Mascot
1451.6219	1451.5536	-0.0683	-47	202	213	DDENVNSQPFMR				Mascot
1465.7546	1465.6565	-0.0981	-67	147	159	TFQGPPIHGIQVER	82	100		Mascot
1465.7546	1465.6565	-0.0981	-67	147	159	TFQGPPIHGIQVER				Mascot
1502.8512	1502.7451	-0.1061	-71	165	177	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]	Mascot
1546.7358	1546.6331	-0.1027	-66	451	463	WSEPLAAACEVWK			Carbamidomethyl (C)[9]	Mascot
1846.0068	1845.8658	-0.141	-76	335	350	LEGERDITLGFVDLLR				Mascot
2009.059	2008.9305	-0.1285	-64	340	356	DITLGFVDLLRDFIEK				Mascot
2097.1135	2096.9497	-0.1638	-78	286	303	DNGLLLHIHRAMHAVIDR			Oxidation (M)[12]	Mascot
2169.9868	2169.8359	-0.1509	-70	195	213	GGDLFTKDDENVNSQPFMR				Mascot
2169.9868	2169.8359	-0.1509	-70	195	213	GGDLFTKDDENVNSQPFMR	116	100		Mascot
2185.9819	2185.8372	-0.1447	-66	195	213	GGDLFTKDDENVNSQPFMR			Oxidation (M)[18]	Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100	Carbamidomethyl (C)[26]	Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]	Mascot
3038.45	3038.2468	-0.2032	-67	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26], Oxidation (M)[8]	Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTWTDGLT SLDR	175	100		Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTWTDGLT SLDR				Mascot

	Ribulose biphosphate carboxylase large chain (Fragment) OS=Pachira aquatica GN=rbcl PE=3 SV=1	RBL_PACAQ	52040.3	6.24	23	793	100	612	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
830.4366	830.3836	-0.053	-64	433	439	EGNEIIR				Mascot
898.41	898.3482	-0.0618	-69	299	305	NHGMHFR				Mascot
910.4451	910.3833	-0.0618	-68	181	187	AVYECLR			Carbamidomethyl [C][5]	Mascot
912.4719	912.4003	-0.0716	-78	289	296	AMHAVIDR				Mascot
914.4049	914.3571	-0.0478	-52	299	305	NHGMHFR			Oxidation [M][4]	Mascot
928.4669	928.4019	-0.065	-70	289	296	AMHAVIDR			Oxidation [M][2]	Mascot
1021.5312	1021.4615	-0.0697	-68	26	34	DTDLAAR				Mascot
1037.4899	1037.4182	-0.0717	-69	344	351	DDFIEKR				Mascot
1116.6194	1116.5992	-0.1102	-99	415	424	VALEACVKAR			Carbamidomethyl [C][6]	Mascot
1170.5585	1170.5565	-0.002	-2	297	305	QKNHGMR			Oxidation [M][6]	Mascot
1187.6643	1187.5881	-0.0762	-64	279	288	DNGLLLHIHR				Mascot
1245.6433	1245.5452	-0.0981	-79	433	443	EGNEIREASK				Mascot
1261.7151	1261.6326	-0.0825	-65	333	343	DTLGFVDLLR	95	100		Mascot
1261.7151	1261.6326	-0.0825	-65	333	343	DTLGFVDLLR				Mascot
1447.7651	1447.6692	-0.0959	-66	313	327	LSGGDHHAGTVVGK				Mascot
1451.6219	1451.5536	-0.0683	-47	195	206	DDENVNSQPFMR				Mascot
1465.7546	1465.6565	-0.0981	-67	140	152	TFQGPPHQIQVER	82	100		Mascot
1465.7546	1465.6565	-0.0981	-67	140	152	TFQGPPHQIQVER				Mascot
1502.8512	1502.7451	-0.1061	-71	158	170	YGRPLLGCTKPK			Carbamidomethyl [C][8]	Mascot
1546.7358	1546.6331	-0.1027	-66	444	456	WSPELAACEVWK			Carbamidomethyl [C][9]	Mascot
1845.0068	1845.8658	-0.141	-76	328	343	LEGEDRLGFDVLLR				Mascot
1968.8724	1968.8931	0.0207	11	230	246	GHYLNATAGTCSEMMKR			Carbamidomethyl [C][11]	Mascot
2009.059	2008.9305	-0.1285	-64	333	349	DTLGFVDLLRDDFIK				Mascot
2097.1135	2096.9497	-0.1638	-78	279	296	DNGLLLHIRHAMHAVIDR			Oxidation [M][12]	Mascot
2169.9868	2169.8359	-0.1509	-70	188	206	GGLDFTKDDENVNSQPF MR				Mascot
2169.9868	2169.8359	-0.1509	-70	188	206	GGLDFTKDDENVNSQPF MR	116	100		Mascot
2185.9819	2185.8372	-0.1447	-66	188	206	GGLDFTKDDENVNSQPF MR			Oxidation [M][18]	Mascot
3022.4548	3022.2417	-0.2131	-71	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100	Carbamidomethyl [C][26]	Mascot
3022.4548	3022.2417	-0.2131	-71	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl [C][26]	Mascot
3038.45	3038.2468	-0.2032	-67	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl [C][26], Oxidation [M][8]	Mascot
3854.8718	3854.6001	-0.2717	-70	35	72	VTPQGPVPPEEAGAAVA AESSTGTWTVTVDGLT SLDR	175	100		Mascot



	1170.5585	1170.5565	-0.002	-2	304	312	OKNHGMHFR				Oxidation [M][6]	Mascot	
	1187.6643	1187.5881	-0.0762	-4	298	295	DNGLLLHIHR					Mascot	
	1245.6433	1245.5452	-0.0981	-79	440	450	EGNEIIREASK					Mascot	
	1261.7151	1261.6326	-0.0825	-65	340	350	DITLGFVDLLR	95	100			Mascot	
	1261.7151	1261.6326	-0.0825	-65	340	350	DITLGFVDLLR					Mascot	
	1451.6219	1451.5536	-0.0683	-47	202	213	DDENVNSQPFMR					Mascot	
	1465.7216	1465.6565	-0.0651	-44	320	334	MSGGDHHAGTVVGK					Mascot	
	1465.7546	1465.6565	-0.0981	-67	147	159	TFQGPPHGIOVER	82	100			Mascot	
	1502.8512	1502.7451	-0.1061	-71	165	177	YGRPLLGCTIKPK			Carbamidomethyl [C][8]		Mascot	
	1546.7358	1546.6331	-0.1027	-66	451	463	WSPELAAACEVWK			Carbamidomethyl [C][9]		Mascot	
	1846.0068	1846.8658	-0.141	-76	335	350	LEGERDITLGFVDLLR					Mascot	
	1968.8724	1968.8931	0.0207	11	237	253	GHYLNATAGTCEEMMKR			Carbamidomethyl [C][11]		Mascot	
	2009.059	2008.9305	-0.1285	-64	340	356	DITLGFVDLLRDDFIEK					Mascot	
	2097.1135	2096.9497	-0.1638	-78	286	303	DNGLLLHHRAMHAVIDR			Oxidation [M][12]		Mascot	
	2169.9868	2169.8359	-0.1509	-70	195	213	GGLDFTKDDENVNSQPF MR					Mascot	
	2169.9868	2169.8359	-0.1509	-70	195	213	GGLDFTKDDENVNSQPF MR	116	100			Mascot	
	2185.9819	2185.8372	-0.1447	-66	195	213	GGLDFTKDDENVNSQPF MR			Oxidation [M][18]		Mascot	
	3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100	Carbamidomethyl [C][26]		Mascot	
	3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl [C][26]		Mascot	
	3038.45	3038.2468	-0.2032	-67	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR			Carbamidomethyl [C][26], Oxidation [M][8]		Mascot	
	3854.8718	3854.6001	-0.2717	-70	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTGDLT SLDR	175	100			Mascot	
	3854.8718	3854.6001	-0.2717	-70	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTGDLT SLDR					Mascot	
7	Ribulose biphosphate carboxylase large chain (Fragment) OS=Brexia madagascariensis GN=rbcl PE=3 SV					RBL_BREMA	52023.1	6.22	23	781	100	611	100
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	830.4366	830.3836	-0.053	-64	440	446	EGNEIIR						Mascot
	898.41	898.3482	-0.0618	-69	306	312	NHGMHFR						Mascot
	910.4451	910.3833	-0.0618	-68	188	194	AYVECLR				Carbamidomethyl [C][5]		Mascot
	912.4719	912.4003	-0.0716	-78	296	303	AMHAVIDR						Mascot
	914.4049	914.3571	-0.0478	-52	306	312	NHGMHFR				Oxidation [M][4]		Mascot
	928.4669	928.4019	-0.065	-70	296	303	AMHAVIDR				Oxidation [M][2]		Mascot
	1021.5312	1021.4615	-0.0697	-68	33	41	DTDIAAFR						Mascot
	1037.4899	1037.4182	-0.0717	-69	351	358	DDFIEKDR						Mascot
	1116.583	1116.5092	-0.0738	-66	422	431	VALEACVQAR				Carbamidomethyl [C][6]		Mascot
	1170.5585	1170.5565	-0.002	-2	304	312	OKNHGMHFR				Oxidation [M][6]		Mascot
	1187.6643	1187.5881	-0.0762	-4	298	295	DNGLLLHIHR						Mascot
	1245.6433	1245.5452	-0.09										

2185.9819	2185.8372	-0.1447	-66	195	213	MR GGLDFTKDDENVNSQPF				Oxidation (M)[18]	Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100		Carbamidomethyl (C)[26]	Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26]	Mascot
3038.45	3038.2468	-0.2032	-67	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26], Oxidation (M)[8]	Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	175	100			Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot

9 Ribulose biphosphate carboxylase large chain (Fragment) OS=Corvus alternifolia GN=rbcl PE=3 SV=3 RBL\_CORAT 51811.1 6.14 22 775 100 611 100

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
910.4451	910.3833	-0.0618	-68	181	187	AVYECLR				Carbamidomethyl (C)[5]		Mascot
912.4719	912.4003	-0.0716	-78	289	296	AMHAVIDR						Mascot
928.4669	928.4019	-0.065	-70	289	296	AMHAVIDR				Oxidation (M)[2]		Mascot
1021.5312	1021.4615	-0.0697	-68	26	34	DTDILAAFR						Mascot
1037.4899	1037.4182	-0.0717	-69	344	351	DDFIEKDR						Mascot
1116.583	1116.5092	-0.0738	-66	415	424	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.5881	-0.0762	-64	279	288	DNGLLLHIHR						Mascot
1245.6337	1245.5452	-0.0885	-71	211	220	FLFCAEAIK				Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6326	-0.0825	-65	333	343	DITLGFVDLLR	95	100				Mascot
1261.7151	1261.6326	-0.0825	-65	333	343	DITLGFVDLLR						Mascot
1451.6219	1451.5536	-0.0683	-47	195	206	DDENVNSQPFMR						Mascot
1465.7216	1465.6565	-0.0651	-44	313	327	MSGGDHIHAGTVVGK						Mascot
1465.7546	1465.6565	-0.0981	-67	140	152	TFQGPPIHGIQVER	82	100				Mascot
1472.6978	1472.6294	-0.0684	-46	457	468	EIKFEFEAMDTL						Mascot
1488.6926	1488.6122	-0.0804	-54	457	468	EIKFEFEAMDTL				Oxidation (M)[9]		Mascot
1502.8512	1502.7451	-0.1061	-71	158	170	YGRPLLCTIKPK				Carbamidomethyl (C)[8]		Mascot
1516.7616	1516.6934	-0.0682	-45	209	220	DRFLFCAEAIK				Carbamidomethyl (C)[6]		Mascot
1546.7358	1546.6331	-0.1027	-66	444	456	WSPELAAACEVWK				Carbamidomethyl (C)[9]		Mascot
1846.0068	1845.8658	-0.141	-76	328	343	LEGERDITLGFVDLLR						Mascot
1968.8724	1968.8931	0.0207	11	230	246	GHYLNATAGTCEEMMKR				Carbamidomethyl (C)[11]		Mascot
2009.059	2008.9305	-0.1285	-64	333	349	DITLGFVDLLRDDFIEK						Mascot
2097.1135	2096.9497	-0.1638	-78	279	296	DNGLLLHIHRAMHAVIDR				Oxidation (M)[12]		Mascot
2169.9868	2169.8359	-0.1509	-70	188	206	GGLDFTKDDENVNSQPF MR						Mascot
2169.9868	2169.8359	-0.1509	-70	188	206	GGLDFTKDDENVNSQPF MR	116	100				Mascot
2185.9819	2185.8372	-0.1447	-66	188	206	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot
3022.4548	3022.2417	-0.2131	-71	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100		Carbamidomethyl (C)[26]		Mascot
3022.4548	3022.2417	-0.2131	-71	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26]		Mascot
3038.45	3038.2468	-0.2032	-67	252	278	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26], Oxidation (M)[8]		Mascot
3854.8718	3854.6001	-0.2717	-70	35	72	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	175	100				Mascot
3854.8718	3854.6001	-0.2717	-70	35	72	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot

10 Ribulose biphosphate carboxylase large chain OS=Gossypium hirsutum GN=rbcl PE=3 SV=2 RBL\_GOSHI 52667.3 5.91 23 774 100 611 100

Peptide Information										Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				
830.4366	830.3836	-0.053	-64	440	446	EGNEIIR						Mascot
898.41	898.3482	-0.0618	-69	306	312	NHGMHFR						Mascot
910.4451	910.3833	-0.0618	-68	188	194	AVYECLR				Carbamidomethyl (C)[5]		Mascot
912.4719	912.4003	-0.0716	-78	296	303	AMHAVIDR						Mascot
914.4049	914.3571	-0.0478	-52	306	312	NHGMHFR				Oxidation (M)[4]		Mascot
928.4669	928.4019	-0.065	-70	296	303	AMHAVIDR				Oxidation (M)[2]		Mascot
1021.5312	1021.4615	-0.0697	-68	33	41	DTDILAAFR						Mascot
1037.4899	1037.4182	-0.0717	-69	351	358	DDFIEKDR						Mascot
1116.583	1116.5092	-0.0738	-66	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5565	-0.002	-2	304	312	QKNHGMHFR				Oxidation (M)[6]		Mascot
1187.6643	1187.5881	-0.0762	-64	286	295	DNGLLLHIHR						Mascot
1245.6337	1245.5452	-0.0885	-71	218	227	FLFCAEAIK				Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6326	-0.0825	-65	340	350	DITLGFVDLLR	95	100				Mascot
1261.7151	1261.6326	-0.0825	-65	340	350	DITLGFVDLLR						Mascot
1451.6219	1451.5536	-0.0683	-47	202	213	DDENVNSQPFMR						Mascot
1465.7216	1465.6565	-0.0651	-44	320	334	MSGGDHIHAGTVVGK						Mascot
1465.7546	1465.6565	-0.0981	-67	147	159	TFQGPPIHGIQVER	82	100				Mascot
1502.8512	1502.7451	-0.1061	-71	165	177	YGRPLLCTIKPK				Carbamidomethyl (C)[8]		Mascot
1516.7616	1516.6934	-0.0682	-45	216	227	DRFLFCAEAIK				Carbamidomethyl (C)[6]		Mascot
1546.7358	1546.6331	-0.1027	-66	451	463	WSPELAAACEVWK				Carbamidomethyl (C)[9]		Mascot
1846.0068	1845.8658	-0.141	-76	335	350	LEGERDITLGFVDLLR						Mascot
2009.059	2008.9305	-0.1285	-64	340	356	DITLGFVDLLRDDFIEK						Mascot
2097.1135	2096.9497	-0.1638	-78	286	303	DNGLLLHIHRAMHAVIDR				Oxidation (M)[12]		Mascot
2169.9868	2169.8359	-0.1509	-70	195	213	GGLDFTKDDENVNSQPF MR						Mascot
2169.9868	2169.8359	-0.1509	-70	195	213	GGLDFTKDDENVNSQPF MR	116	100				Mascot
2185.9819	2185.8372	-0.1447	-66	195	213	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR	145	100		Carbamidomethyl (C)[26]		Mascot
3022.4548	3022.2417	-0.2131	-71	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26]		Mascot
3038.45	3038.2468	-0.2032	-67	259	285	ELGVPIVMHDYLTGGFTA NTSLAHYCR				Carbamidomethyl (C)[26], Oxidation (M)[8]		Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR	175	100				Mascot
3854.8718	3854.6001	-0.2717	-70	42	79	VTQPQGVPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot

Gel Idx/Pos	113/E12	Instr./Gel Origin	BA2060/140227A	Process Statu	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	Enolase 2 OS=Hevea brasiliensis GN=ENO2 PE=1 SV=1	ENO2_HEVBR	47883.7	5.92	9	167	100	130	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
806.4518	806.4028	-0.049	-61	417	422	YNQLLR			
1005.576	1005.5445	-0.0315	-31	1	9	MAITIVSVR			
1200.583	1200.4604	-0.1226	-102	190	199	MGAEVYHHLK			
1227.6163	1227.641	0.0247	20	372	382	RAGWGMASHR			
1838.8918	1838.7765	-0.1153	-63	423	439	IEEELGAEAVYAGANFR	130	100	
1838.8918	1838.7765	-0.1153	-63	423	439	IEEELGAEAVYAGANFR			
1868.9648	1868.8278	-0.137	-73	169	185	LAHQEFMILPVGASSFK			
1936.0055	1935.821	-0.1845	-95	354	371	VNQIGSVTESIEAVKMSK			
2252.1292	2251.9929	-0.1363	-61	383	404	SGETEDTFIADLSVGLAT			
						GQIK			
3030.3679	3030.1938	-0.1741	-57	290	314	SFVTEYPVSIEDPFDQD			
						DWEHYAK			
2	Ribulose biphosphate carboxylase large chain OS=Manihot esculenta GN=rbcl PE=3 SV=1	RBL_MANES	52648.5	6.18	13	119	100	58	99.979
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1021.5312	1021.4695	-0.0617	-60	33	41	DTDILAAFR			
1116.583	1116.5131	-0.0699	-63	422	431	VALEACVQAR			
1170.5585	1170.5673	0.0088	8	304	312	QKNHGMHFR			
1187.6643	1187.5951	-0.0692	-58	286	295	DNGLLLHIHR			
1231.6277	1231.5387	-0.089	-72	440	450	EGNDIREASK			
1261.6285	1261.635	0.0065	5	218	227	FLFCAEAYK			
1271.6703	1271.6697	-0.0006	0	436	446	DLAREGNDIIR			
1271.6703	1271.6697	-0.0006	0	436	446	DLAREGNDIIR			
1343.6525	1343.6355	-0.017	-13	184	194	NYGRAVVECLR	4	0	
1387.7579	1387.6653	-0.0926	-67	135	146	LEDLRVPPAYSK			
1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER			
1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER	54	99.947	
1909.8894	1909.907	0.0176	9	237	253	GHYLNATAGTCEEMIKR			
2009.059	2008.877	-0.182	-91	340	356	DITLGFVDLLRDDFIK			
2169.9868	2169.8464	-0.1404	-65	195	213	GGLDFTKDDENVNSQPF			
						MR			
3	Enolase OS=Ricinus communis PE=2 SV=1	ENO_RICCO	47882.5	5.56	8	116	100	86	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
806.4518	806.4028	-0.049	-61	417	422	YNQLLR			
1005.576	1005.5445	-0.0315	-31	1	9	MAITIVSVR			
1200.583	1200.4604	-0.1226	-102	190	199	MGAEVYHHLK			
1227.6163	1227.641	0.0247	20	372	382	RAGWGMASHR			
1601.8492	1601.7461	-0.1031	-64	354	368	VNQIGSVTESIEAVR			
1601.8492	1601.7461	-0.1031	-64	354	368	VNQIGSVTESIEAVR	37	97.322	
1804.9438	1804.8314	-0.1124	-62	36	53	AAVPSGASTGIYEALRLR			
1804.9438	1804.8314	-0.1124	-62	36	53	AAVPSGASTGIYEALRLR	49	99.796	
1868.9648	1868.8278	-0.137	-73	169	185	LAHQEFMILPVGASSFK			
2252.1292	2251.9929	-0.1363	-61	383	404	SGETEDTFIADLSVGLAT			
						GQIK			
4	Ribulose biphosphate carboxylase large chain OS=Coffea arabica GN=rbcl PE=3 SV=2	RBL_COFAR	53319.8	6.13	13	112	100	53	99.922
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1021.5312	1021.4695	-0.0617	-60	33	41	DTDILAAFR			
1116.6194	1116.5131	-0.1063	-95	422	431	VALEACVKAR			
1170.5585	1170.5673	0.0088	8	304	312	QKNHGMHFR			
1187.6643	1187.5951	-0.0692	-58	286	295	DNGLLLHIHR			
1200.6218	1200.4604	-0.1614	-134	436	446	DLAEGNEIIR			
1261.7151	1261.635	-0.0801	-63	340	350	DITLGFVDLLR			
1343.6525	1343.6355	-0.017	-13	184	194	NYGRAVVECLR			
1465.7216	1465.6687	-0.0529	-36	320	334	MSGDDHIAGTVVGK			
1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER	54	99.947	
1887.9421	1887.7008	-0.2413	-128	451	466	WSPELAAACEVWKEIR			
1909.8894	1909.907	0.0176	9	237	253	GHYLNATAGTCEEMIKR			
2009.059	2008.877	-0.182	-91	340	356	DITLGFVDLLRDDFIK			
2169.9868	2169.8464	-0.1404	-65	195	213	GGLDFTKDDENVNSQPF			
						MR			
5	Ribulose biphosphate carboxylase large chain OS=Picea pungens GN=rbcl PE=3 SV=1	RBL_PICPU	52558.4	6.09	12	110	100	54	99.947
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1021.5312	1021.4695	-0.0617	-60	33	41	DTDILAAFR			
1067.5731	1067.5304	-0.0427	-40	5	14	TETKASVGFK			
1116.583	1116.5131	-0.0699	-63	422	431	VALEACVQAR			
1170.5585	1170.5673	0.0088	8	304	312	QKNHGMHFR			
1187.6643	1187.5951	-0.0692	-58	286	295	DNGLLLHIHR			
1231.6277	1231.5387	-0.089	-72	440	450	EGNEVIREASK			
1261.7151	1261.635	-0.0801	-63	340	350	DITLGFVDLLR			
1271.6702	1271.6697	-0.0005	0	436	446	DLAREGNEVIR			
1271.6702	1271.6697	-0.0005	0	436	446	DLAREGNEVIR			
1343.6525	1343.6355	-0.017	-13	184	194	NYGRAVVECLR			
1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER			
1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER	54	99.947	
2009.059	2008.877	-0.182	-91	340	356	DITLGFVDLLRDDFIK			
2169.9868	2169.8464	-0.1404	-65	195	213	GGLDFTKDDENVNSQPF			
						MR			
6	Ribulose biphosphate carboxylase large chain OS=Cycas taitungensis GN=rbcl PE=3 SV=1	RBL_CYCTA	52689.4	6.09	13	110	100	52	99.902
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1021.5312	1021.4695	-0.0617	-60	33	41	DTDILAAFR			
1067.5731	1067.5304	-0.0427	-40	5	14	TETKASVGFK			
1116.4918	1116.5131	0.0213	19	467	475	FEFEAMDLV			
1187.6643	1187.5951	-0.0692	-58	286	295	DNGLLLHIHR			
1231.6277	1231.5387	-0.089	-72	440	450	EGNEVIREASK			
1271.6702	1271.6697	-0.0005	0	436	446	DLAREGNEVIR			
1271.6702	1271.6697	-0.0005	0	436	446	DLAREGNEVIR			
1343.6525	1343.6355	-0.017	-13	184	194	NYGRAVVECLR			
1387.7579	1387.6653	-0.0926	-67	135	146	LEDLRVPPAYSK			

	1465.6603	1465.6687	-0.0084	6	216	227	DRFCFCAEAIVK								Mascot
	1465.7546	1465.6987	-0.0559	-59	147	159	TFQGPPIGQVER		54	99.947					Mascot
	1909.8894	1909.907	0.0176	9	237	253	GHYLNATAGTCEEMIKR				Oxidation [M][14]				Mascot
	2023.0494	2022.7963	-0.2531	-125	340	356	DVTLGFVDLLRDDFIER								Mascot
	2169.9868	2169.8464	-0.1404	-65	195	213	GGLDFTKDDENVNSQPFFMR								Mascot
7	Ribulose biphosphate carboxylase large chain OS=Phalaenopsis aphrodite subsp. formosana GN=rbcL PE					RBL_PHAAO	53228.7	5.95	12	109		100	57	99.97	
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type	
	1021.5312	1021.4695	-0.0617	-60	33	41	DTDILAAFR							Mascot	
	1116.583	1116.5131	-0.0699	-63	422	431	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
	1170.5585	1170.5673	0.0088	8	304	312	QKNHGMHFR				Oxidation [M][6]			Mascot	
	1187.6643	1187.5951	-0.0692	-58	286	295	DNGLLLIHR							Mascot	
	1231.6277	1231.5387	-0.089	-72	440	450	EGNDIREASK				Carbamidomethyl (C)[4]			Mascot	
	1261.6285	1261.635	0.0065	5	218	227	FLFCAEAIK							Mascot	
	1271.6703	1271.6697	-0.0006	0	436	446	DLAREGNDIR							Mascot	
	1271.6703	1271.6697	-0.0006	0	436	446	DLAREGNDIR		4	0				Mascot	
	1343.6525	1343.6355	-0.017	-13	184	194	NYGRAVVECLR							Mascot	
	1465.7216	1465.6687	-0.0529	-36	320	334	MSGGDHIHAGTVVGK							Mascot	
	1465.7546	1465.6687	-0.0859	-59	147	159	TFQGPPIGQVER		54	99.947				Mascot	
	1909.8894	1909.907	0.0176	9	237	253	GHYLNATAGTCEEMIKR				Oxidation [M][14]			Mascot	
	2169.9868	2169.8464	-0.1404	-65	195	213	GGLDFTKDDENVNSQPFFMR							Mascot	
8	Ribulose biphosphate carboxylase large chain (Fragment) OS=Acer saccharum GN=rbcL PE=3 SV=1					RBL_ACESA	51546	6.19	12	108		100	53	99.922	
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type	
	1021.5312	1021.4695	-0.0617	-60	23	31	DTDILAAFR							Mascot	
	1116.583	1116.5131	-0.0699	-63	412	421	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
	1170.5585	1170.5673	0.0088	8	294	302	QKNHGMHFR				Oxidation [M][6]			Mascot	
	1187.6643	1187.5951	-0.0692	-58	276	285	DNGLLLIHR							Mascot	
	1261.7151	1261.635	-0.0801	-63	330	340	DITLGFDVLLR							Mascot	
	1343.6525	1343.6355	-0.017	-13	174	184	NYGRAVVECLR							Mascot	
	1465.7216	1465.6687	-0.0529	-36	310	324	MSGGDHIHAGTVVGK							Mascot	
	1465.7546	1465.6687	-0.0859	-59	137	149	TFQGPPIGQVER		54	99.947				Mascot	
	1909.8894	1909.907	0.0176	9	227	243	GHYLNATAGTCEEMIKR				Oxidation [M][14]			Mascot	
	1935.9269	1935.821	-0.1059	-55	437	453	EASKWSAELAAACEVVVK				Carbamidomethyl (C)[13]			Mascot	
	2009.059	2008.877	-0.182	-91	330	346	DITLGFDVLL								







	Peptide Information										Modification			Rank	Result Type		
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence										
3	895.4155	895.3658	-0.0497	-56	354	360	VYDDEVVR									Mascot	
	940.4675	940.416	-0.0515	-55	305	311	FYWAPTR	34	94.978							Mascot	
	940.4675	940.416	-0.0515	-55	305	311	FYWAPTR									Mascot	
	1023.5105	1023.4514	-0.0591	-58	354	361	VYDDEVRK									Mascot	
	1152.7139	1152.6451	-0.0688	-60	159	169	VPLILGIWGGK									Mascot	
	1228.603	1228.5377	-0.0653	-53	174	183	SFQCELVFAK									Mascot	
	1326.6226	1326.5453	-0.0773	-58	305	314	FYWAPTRDDR	21	0				Carbamidomethyl (C)[4]			Mascot	
	1326.6226	1326.5453	-0.0773	-58	305	314	FYWAPTRDDR									Mascot	
	1363.7579	1363.6891	-0.0688	-50	50	62	VTNGSFKIVAAEK									Mascot	
	1566.7402	1566.6748	-0.0654	-42	224	238	MCALFINDLDAGAGR									Mascot	
	1623.7617	1623.6646	-0.0971	-60	224	238	MCALFINDLDAGAGR	81	100				Carbamidomethyl (C)[2]			Mascot	
	1623.7617	1623.6646	-0.0971	-60	224	238	MCALFINDLDAGAGR						Carbamidomethyl (C)[2]			Mascot	
	1639.7567	1639.6636	-0.093	-57	224	238	MCALFINDLDAGAGR						Carbamidomethyl (C)[2], Oxidation (M)[1]			Mascot	
	1709.7977	1709.6957	-0.102	-60	77	91	GLAYDISDDQQDITR	120	100							Mascot	
	1709.7977	1709.6957	-0.102	-60	77	91	GLAYDISDDQQDITR									Mascot	
	1882.9697	1882.859	-0.1107	-59	335	351	LVDFTFGQSIDFFGALR	168	100							Mascot	
	1882.9697	1882.859	-0.1107	-59	335	351	LVDFTFGQSIDFFGALR									Mascot	
	2089.1692	2089.043	-0.1262	-60	280	298	VPIVITGNDFSTLYAPLIR									Mascot	
	2211.2722	2210.9839	-0.2883	-130	150	169	NFMTLPNIKVPLILGIWGGK									Mascot	
		2304.0669	2303.9297	-0.1372	-60	184	206	MGINPIMMSAGELESGNAGEPAK									Mascot
		2320.0618	2319.9187	-0.1431	-62	184	206	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1]			Mascot
		2336.0566	2335.916	-0.1406	-60	184	206	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1,7]			Mascot
	Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic OS=Larrea tridentata GN=RCA1																
	Peptide Information																
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				Modification		Rank	Result Type
		940.4675	940.416	-0.0515	-55	303	309	FYWAPTR	34	94.978							Mascot
	940.4675	940.416	-0.0515	-55	303	309	FYWAPTR									Mascot	
	1078.5891	1078.5233	-0.0658	-61	210	218	YREAADIHK									Mascot	
	1228.603	1228.5377	-0.0653	-53	172	181	SFQCELVFAK									Mascot	
	1326.647	1326.5453	-0.1017	-77	1	13	MAAAYSTVGAVNR	12	0				Carbamidomethyl (C)[4]			Mascot	
	1326.647	1326.5453	-0.1017	-77	1	13	MAAAYSTVGAVNR						Oxidation (M)[1]			Mascot	
	1639.9054	1639.6636	-0.2418	-147	25	40	ASLVPSIAFFGSLLKK									Mascot	
	1709.7977	1709.6957	-0.102	-60	73	87	GLAYDISDDQQDITR	120	100							Mascot	
	1709.7977	1709.6957	-0.102	-60	73	87	GLAYDISDDQQDITR									Mascot	
	1882.9697	1882.859	-0.1107	-59	333	349	LVDFTFGQSIDFFGALR	168	100							Mascot	
	1882.9697	1882.859	-0.1107	-59	333	349	LVDFTFGQSIDFFGALR									Mascot	
	2089.1692	2089.043	-0.1262	-60	278	296	VPIVITGNDFSTLYAPLIR									Mascot	
	2304.0669	2303.9297	-0.1372	-60	182	204	MGINPIMMSAGELESGNAGEPAK									Mascot	
	2320.0618	2319.9187	-0.1431	-62	182	204	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1]			Mascot	
	2336.0566	2335.916	-0.1406	-60	182	204	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1,7]			Mascot	
	2367.042	2366.8931	-0.1489	-63	121	140	QYNLDNNMDGFYIAPAFMDK									Mascot	
	2383.0369	2382.9089	-0.128	-54	121	140	QYNLDNNMDGFYIAPAFMDK						Oxidation (M)[8]			Mascot	
Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic OS=Hordeum vulgare GN=RCA1																	
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				Modification		Rank	Result Type	
	895.4155	895.3658	-0.0497	-56	339	345	VYDDEVVR									Mascot	
	940.4675	940.416	-0.0515	-55	290	296	FYWAPTR	34	94.978							Mascot	
	940.4675	940.416	-0.0515	-55	290	296	FYWAPTR									Mascot	
	1023.5105	1023.4514	-0.0591	-58	339	346	VYDDEVRK									Mascot	
	1152.7139	1152.6451	-0.0688	-60	145	155	VPLILGIWGGK									Mascot	
	1228.603	1228.5377	-0.0653	-53	160	169	SFQCELVFAK	120	100				Carbamidomethyl (C)[4]			Mascot	
	1709.7977	1709.6957	-0.102	-60	61	75	GLAYDISDDQQDITR									Mascot	
	1709.7977	1709.6957	-0.102	-60	61	75	GLAYDISDDQQDITR									Mascot	
	1882.9697	1882.859	-0.1107	-59	320	336	LVDFTFGQSIDFFGALR	168	100							Mascot	
	1882.9697	1882.859	-0.1107	-59	320	336	LVDFTFGQSIDFFGALR									Mascot	
	2089.1692	2089.043	-0.1262	-60	265	283	VPIVITGNDFSTLYAPLIR									Mascot	
	2211.2722	2210.9839	-0.2883	-130	136	155	NFMTLPNIKVPLILGIWGGK									Mascot	
	2367.1497	2366.8931	-0.2566	-108	397	418	VQLADKYLEAALGQANDDAIK						Oxidation (M)[21]			Mascot	
Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic (Fragments) OS=Arachis hypogaea																	
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				Modification		Rank	Result Type	
	1152.7139	1152.6451	-0.0688	-60	47	57	VPLILGIWGGK									Mascot	
	1709.7977	1709.6957	-0.102	-60	1	15	GLAYDISDDQQDITR	120	100							Mascot	
	1709.7977	1709.6957	-0.102	-60	1	15	GLAYDISDDQQDITR									Mascot	
	1882.9697	1882.859	-0.1107	-59	124	140	LVDFTFGQSIDFFGALR	168	100							Mascot	
	1882.9697	1882.859	-0.1107	-59	124	140	LVDFTFGQSIDFFGALR									Mascot	
	2089.1692	2089.043	-0.1262	-60	96	114	VPIVITGNDFSTLYAPLIR									Mascot	
	2304.0669	2303.9297	-0.1372	-60	58	80	MGINPIMMSAGELESGNAGEPAK									Mascot	
	2320.0618	2319.9187	-0.1431	-62	58	80	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1]			Mascot	
	2336.0566	2335.916	-0.1406	-60	58	80	MGINPIMMSAGELESGNAGEPAK						Oxidation (M)[1,7]			Mascot	
Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic OS=Malus domestica GN=RCA1																	
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %				Modification		Rank	Result Type	
	895.4155	895.3658	-0.0497	-56	352	358	VYDDEVVR									Mascot	
	940.4675	940.416	-0.0515	-55	303	309	FYWAPTR	34	94.978							Mascot	
	940.4675	940.416	-0.0515	-55	303	309	FYWAPTR									Mascot	
	1023.5105	1023.4514	-0.0591	-58	352	359	VYDDEVRK									Mascot	
	1152.7139	1152.6451	-0.0688	-60	157	167	VPLILGIWGGK									Mascot	
	1228.603	1228.5377	-0.0653	-53	172	181	SFQCELVFAK						Carbamidomethyl (C)[4]			Mascot	
	1566.7402	1566.6748	-0.0654	-42	222	236	MCALFINDLDAGAGR									Mascot	
	1623.7617	1623.6646	-0.0971	-60	222	236	MCALFINDLDAGAGR	81	100				Carbamidomethyl (C)[2]			Mascot	

1623.7617	1623.6646	-0.0971	-60	222	236	MCALFINDLDAGAGR				Carbamidomethyl (C)[2]	Mascot
1639.7567	1639.6636	-0.0931	-57	222	236	MCALFINDLDAGAGR				Carbamidomethyl (C)[2], Oxidation (M)[1]	Mascot
1882.9697	1882.859	-0.1107	-59	333	349	LVDTFPGQSIDFFGALR	168	100			Mascot
1882.9697	1882.859	-0.1107	-59	333	349	LVDTFPGQSIDFFGALR					Mascot
2088.9939	2089.043	0.0491	24	184	204	ISPIMMSAGELESGNAGEPAK					Mascot

Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Cucumis sativus PE=2 SV=1				RCA_CUCSA	45681.2	7.57	9	233	100	203	100
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
895.4155	895.3658	-0.0497	-56	349	355	VYDDEV					Mascot
940.4675	940.416	-0.0515	-55	300	306	FYWAPTR	34	94.978			Mascot
940.4675	940.416	-0.0515	-55	300	306	FYWAPTR					Mascot
972.5261	972.4052	-0.1209	-124	357	365	WAVGVGVER					Mascot
1023.5105	1023.4514	-0.0591	-58	349	356	VYDDEV					Mascot
1078.5891	1078.5233	-0.0658	-61	207	215	YREAAIIK					Mascot
1228.603	1228.5377	-0.0653	-53	169	178	SFQCELVFAK			Carbamidomethyl (C)[4]		Mascot
1882.9697	1882.859	-0.1107	-59	330	346	LVDTFPGQSIDFFGALR	168	100			Mascot
1882.9697	1882.859	-0.1107	-59	330	346	LVDTFPGQSIDFFGALR					Mascot
2089.1692	2089.043	-0.1262	-60	275	293	VPIIVTGNDFSTLYAPLIR					Mascot
2304.0669	2303.9297	-0.1372	-60	179	201	MGINPIMMSAGELESGNAGEPAK					Mascot
2320.0618	2319.9187	-0.1431	-62	179	201	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1]		Mascot
2336.0566	2335.916	-0.1406	-60	179	201	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1,7]		Mascot

8	Ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic OS=Nicotiana tabacum GN=RCA P	RCA2_TOBAC	48312.5	8.14	7	224	100	203	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
895.4155	895.3658	-0.0497	-56	356	362	VYDDEV					Mascot
940.4675	940.416	-0.0515	-55	307	313	FYWAPTR	34	94.978			Mascot
940.4675	940.416	-0.0515	-55	307	313	FYWAPTR					Mascot
1023.5105	1023.4514	-0.0591	-58	356	363	VYDDEV					Mascot
1256.6456	1256.6012	-0.0444	-35	176	185	SFQCELVFRK					Mascot
1256.6456	1256.6012	-0.0444	-35	176	185	SFQCELVFRK					Mascot
1882.9697	1882.859	-0.1107	-59	337	353	IVDTFPGQSIDFFGALR	168	100			Mascot
1882.9697	1882.859	-0.1107	-59	337	353	IVDTFPGQSIDFFGALR					Mascot
2089.1692	2089.043	-0.1262	-60	282	300	VPIIVTGNDFSTLYAPLIR					Mascot
2304.0669	2303.9297	-0.1372	-60	186	208	MGINPIMMSAGELESGNAGEPAK					Mascot
2320.0618	2319.9187	-0.1431	-62	186	208	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1]		Mascot
2336.0566	2335.916	-0.1406	-60	186	208	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1,7]		Mascot

Ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic OS=Larrea tridentata GN=RCA2				RCA2_LARTR		48023.1	6.78	12	221	100	166	100
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
895.4155	895.3658	-0.0497	-56	352	358	VYDDEV					Mascot	
940.4675	940.416	-0.0515	-55	303	309	FYWAPTR	34	94.978			Mascot	
940.4675	940.416	-0.0515	-55	303	309	FYWAPTR					Mascot	
1023.5105	1023.4514	-0.0591	-58	352	359	VYDDEV					Mascot	
1078.5891	1078.5233	-0.0658	-61	210	218	YREADIIK					Mascot	
1129.5524	1129.4855	-0.0669	-59	378	387	EGPIITFEQPK					Mascot	
1228.603	1228.5377	-0.0653	-53	172	181	SFQCELVFAK			Carbamidomethyl (C)[4]		Mascot	
1326.647	1326.5453	-0.1017	-77	1	13	MAAAYSTVGAVNR	12	0	Oxidation (M)[1]		Mascot	
1326.647	1326.5453	-0.1017	-77	1	13	MAAAYSTVGAVNR			Oxidation (M)[1]		Mascot	
1639.9054	1639.6636	-0.2418	-147	25	40	ASLVPTSAFFGSSLKK					Mascot	
1709.7977	1709.6957	-0.102	-60	73	87	GLAYDISDDQQDITR	120	100			Mascot	
1709.7977	1709.6957	-0.102	-60	73	87	GLAYDISDDQQDITR					Mascot	
2089.1692	2089.043	-0.1262	-60	278	296	VPIIVTGNDFSTLYAPLIR					Mascot	
2304.0669	2303.9297	-0.1372	-60	182	204	MGINPIMMSAGELESGNAGEPAK					Mascot	
2320.0618	2319.9187	-0.1431	-62	182	204	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1]		Mascot	
2336.0566	2335.916	-0.1406	-60	182	204	MGINPIMMSAGELESGNAGEPAK			Oxidation (M)[1,7]		Mascot	
2367.042	2366.8931	-0.1489	-63	121	140	QYNLDNNMDGFIAPAFMDK					Mascot	
2383.0369	2382.9089	-0.128	-54	121	140	QYNLDNNMDGFIAPAFMDK			Oxidation (M)[8]		Mascot	

10	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Oryza sativa subsp. japonica	RCA_ORYSJ	51421.4	5.43	12	220	100	175	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
895.4155	895.3658	-0.0497	-56	343	349	VYDDEV					Mascot
902.4689	902.4163	-0.0526	-58	394	400	EQENVKR					Mascot
940.4675	940.416	-0.0515	-55	294	300	FYWAPTR	34	94.978			Mascot
940.4675	940.416	-0.0515	-55	294	300	FYWAPTR					Mascot
1023.5105	1023.4514	-0.0591	-58	343	350	VYDDEV					Mascot
1078.5891	1078.5233	-0.0658	-61	201	209	YREAAIIK					Mascot
1152.7139	1152.6451	-0.0688	-60	148	158	VLPLGIWGGK					Mascot
1228.603	1228.5377	-0.0653	-53	163	172	SFQCELVFAK			Carbamidomethyl (C)[4]		Mascot
1326.6226	1326.5453	-0.0773	-58	294	303	FYWAPTRDDR	21	0			Mascot
1326.6226	1326.5453	-0.0773	-58	294	303	FYWAPTRDDR					Mascot
1709.7977	1709.6957	-0.102	-60	64	78	GLAYDISDDQQDITR	120	100			Mascot
1709.7977	1709.6957	-0.102	-60	64	78	GLAYDISDDQQDITR					Mascot
2089.1692	2089.043	-0.1262	-60	269	287	VPIIVTGNDFSTLYAPLIR					Mascot
2211.2722	2210.9839	-0.2883	-130	139	158	NFMTLPNIKVPILGIWGGK					Mascot
2303.9988	2303.9297	-0.0691	-30	112	131	TYDFDNTMGGFYIAPAFMDK					Mascot
2319.9937	2319.9187	-0.075	-32	112	131	TYDFDNTMGGFYIAPAFMDK			Oxidation (M)[8]		Mascot
2335.9885	2335.916	-0.0725	-31	112	131	TYDFDNTMGGFYIAPAFMDK			Oxidation (M)[8,18]		Mascot

Gel Idx/Pos		116/E15		Instr./Gel Origin			BA2060/140227A			Process Status		Analysis Succeeded	
Plate [#] Name		[1] 31564		Instrument Sample Name						Spectra		11	
Rank	Protein Name			Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %		
1	Phosphoglycerate kinase, chloroplastic OS=Nicotiana			PGKH_TOBAC	50145.9	8.48	12	505	100	446	100		







Plate [#]	Pos	118/E17	Instr./Gel Origin		BA2060/140227A		Process Statu		Analysis Succeeded	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	11
1	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Spinacia oleracea PE=2 SV=1	S17P_SPIOL	42054.4	5.87	10	146	100	96	100	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
809.4515	809.4076	-0.0439	-54	278	283	EKYTLR				Mascot
908.5451	908.4984	-0.0467	-51	216	223	TTYVLALK				Mascot
940.5502	940.481	-0.0692	-74	271	277	LIQYIK				Mascot
940.5502	940.481	-0.0692	-74	271	277	LIQYIK				Mascot
1175.4313	1175.5688	0.1375	117	1	10	METSMACCSR			Carbamidomethyl (C)[7]	Mascot
1348.6677	1348.601	-0.0667	-49	203	215	DQVAAAMGIYGR				Mascot
1348.6677	1348.601	-0.0667	-49	203	215	DQVAAAMGIYGR	5	0		Mascot
1625.7994	1625.7329	-0.0665	-41	85	98	GLRLMMCMGEALR			Oxidation (M)[6,7]	Mascot
1625.7994	1625.7329	-0.0665	-41	85	98	GLRLMMCMGEALR			Oxidation (M)[6,7]	Mascot
1633.8618	1633.7743	-0.0875	-54	284	298	YTGGMVPDVNQIIVK				Mascot
1649.8567	1649.7662	-0.0905	-55	284	298	YTGGMVPDVNQIIVK			Oxidation (M)[5]	Mascot
1716.8303	1716.776	-0.0543	-32	89	103	LMMCGMEALRTIGFK			Oxidation (M)[2]	Mascot
1733.8381	1733.7485	-0.0896	-52	224	238	DYPGTHEFLLDDEGK				Mascot
1733.8381	1733.7485	-0.0896	-52	224	238	DYPGTHEFLLDDEGK	91	100		Mascot
2412.1982	2412.0767	-0.1215	-50	224	243	DYPGTHEFLLDDEGKWQ HVK				Mascot
2	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Triticum aestivum PE=2 SV=1	S17P_WHEAT	42034.1	6.04	7	64	98.691	47	99.672	
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
809.4515	809.4076	-0.0439	-54	284	289	EKYTLR				Mascot
853.4413	853.3422	-0.0991	-116	360	367	TQVAVGSK				Mascot
1188.5531	1188.4982	-0.0549	-46	373	382	FEETLYGSSR	47	99.672		Mascot
1188.5531	1188.4982	-0.0549	-46	373	382	FEETLYGSSR				Mascot
1193.584	1193.556	-0.028	-23	95	104	LLICMGEAMR			Carbamidomethyl (C)[4]	Mascot
1434.795	1434.6998	-0.0952	-66	307	320	GIFTNVTSPATAK				Mascot
1592.7485	1592.8191	0.0706	44	1	16	METVAAAGYAHAQATR			Oxidation (M)[1]	Mascot
1633.8618	1633.7743	-0.0875	-54	290	304	YTGGMVPDVNQIIVK				Mascot
1649.8567	1649.7662	-0.0905	-55	290	304	YTGGMVPDVNQIIVK			Oxidation (M)[5]	Mascot
3	Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana GN=PUMP1 PE=1 SV=1	PUMP1_ARATH	32641.4	9.62	10	53	83.897			
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
882.4389	882.5236	0.0847	96	251	258	GTIDCFVK				Mascot
959.3961	959.4704	0.0743	77	242	250	MMGDSGAYK				Mascot
959.3961	959.4704	0.0743	77	242	250	MMGDSGAYK				Mascot
1234.519	1234.6187	0.0997	81	240	250	SRMMGDSGAYK			Oxidation (M)[3,4]	Mascot
1316.7242	1316.5361	-0.1881	-143	1	13	MVAAGKSDLPLK				Mascot
1332.7191	1332.6105	-0.1086	-81	1	13	MVAAGKSDLPLK			Oxidation (M)[1]	Mascot
1332.7191	1332.6105	-0.1086	-81	1	13	MVAAGKSDLPLK			Oxidation (M)[1]	Mascot
1348.7848	1348.601	-0.1838	-136	73	84	SLWKGVVPLHR				Mascot
1348.7848	1348.601	-0.1838	-136	73	84	SLWKGVVPLHR				Mascot
1357.682	1357.6504	-0.0316	-23	259	270	TLKSDGPMAFYK				Mascot
1376.8008	1376.6515	-0.1493	-108	55	67	YRGLLGTVTGIAR				Mascot
1390.7699	1390.6161	-0.1528	-110	44	56	SALAGDVTLPKYR				Mascot
1838.8121	1838.826	0.0139	8	242	258	MMGDSGAYKGTIDCFVK			Oxidation (M)[1]	Mascot
1994.0779	1993.8777	-0.2002	-100	279	295	LGSWNVIMFLTLEQAKK			Oxidation (M)[8]	Mascot
1994.0779	1993.8777	-0.2002	-100	279	295	LGSWNVIMFLTLEQAKK			Oxidation (M)[8]	Mascot
4	Kinesin-5 OS=Arabidopsis thaliana GN=ATK5 PE=2 SV=1	ATK5_ARATH	89138.7	7.25	16	49	57.646			
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
809.4073	809.4076	0.0003	0	147	153	ATITEMK			Oxidation (M)[6]	Mascot
1090.5813	1090.4843	-0.097	-89	89	97	IEQMTDIK				Mascot
1123.5967	1123.5806	-0.0161	-14	171	179	LDAIENHRR				Mascot
1175.4933	1175.5688	0.0755	64	392	400	QCMHELDQR			Oxidation (M)[3]	Mascot
1179.6078	1179.5494	-0.0584	-50	361	370	MLEQELAFAK				Mascot
1234.6677	1234.6187	-0.049	-40	18	28	KEALSSIPFDK				Mascot
1284.6841	1284.6898	0.0057	4	766	776	VNAECIGIPRR			Carbamidomethyl (C)[4]	Mascot
1329.7372	1329.6046	-0.1326	-100	190	200	LQVSLREELDK				Mascot
1357.6667	1357.6504	-0.0163	-12	210	220	QKVTSLDMYK			Oxidation (M)[9]	Mascot
1434.7811	1434.6998	-0.0813	-57	5	17	NONRAPLPSPNVK				Mascot
1460.691	1460.7129	0.0219	15	635	647	SVGKTHMNEQSSR				Mascot
1553.8243	1553.6577	-0.1666	-107	320	333	LAGEILMYKESVGK			Oxidation (M)[7]	Mascot
1649.8453	1649.7662	-0.0791	-48	580	595	TAIESVRADSSSTGR				Mascot
2370.1316	2369.9829	-0.1487	-63	740	761	TLMFVNISPDSPSTGESL CSLR			Oxidation (M)[3]	Mascot
2755.3896	2755.1189	-0.2707	-98	222	244	LOEYNTSLQQYNTKLQT DLEVAR				Mascot
2872.3967	2872.2646	-0.1321	-46	740	765	TLMFVNISPDSPSTGESL CSLRFAAR			Carbamidomethyl (C)[19], Oxidation (M)[3]	Mascot
5	Proteinase inhibitor B OS=Sagittaria sagittifolia PE=1 SV=2	IPRB_SAGSA	19161.6	5.76	7	46	19.296			
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
1109.5812	1109.4469	-0.1343	-121	103	111	FSFLMPVPR			Oxidation (M)[5]	Mascot
1188.4846	1188.4982	0.0136	11	131	140	LAACSCFECK			Carbamidomethyl (C)[4,6]	Mascot
1188.4846	1188.4982	0.0136	11	131	140	LAACSCFECK			Carbamidomethyl (C)[4,6]	Mascot
1329.5957	1329.6046	0.0089	7	69	79	SYVYEAPETDR				Mascot
1434.7046	1434.6998	-0.0048	-3	141	154	IACPEVGSFNVNGK				Mascot
2211.1089	2210.9817	-0.1272	-58	103	121	FSFLMPVPRICDTAWSVG K			Carbamidomethyl (C)[11]	Mascot
2412.2227	2412.0767	-0.146	-61	80	102	GLPVSFASATSEPVMQ LGSRYK				Mascot
2872.4773	2872.2646	-0.2127	-74	141	167	IACPEVGSFNVNGKLTLLG IGGEHFTVR			Carbamidomethyl (C)[3]	Mascot
6	Long chain acyl-CoA synthetase 8 OS=Arabidopsis thaliana GN=LACS8 PE=2 SV=1	LACS8_ARATH	78293.5	7.51	13	44	0			
Peptide Information										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
908.4836	908.4984	0.0148	16	157	164	VAIFSDDR				Mascot
959.4978	959.4704	-0.0274	-29	519	526	ISDKPMPR			Oxidation (M)[6]	Mascot
959.4978	959.4704	-0.0274	-29	519	526	ISDKPMPR			Oxidation (M)[6]	Mascot







Peptide Information													
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
842.5709	842.47	-0.1009	-120	332	338	EILKIVK						Mascot	
873.5151	873.4187	-0.0964	-110	292	300	SIVASGLAR						Mascot	
873.5151	873.4187	-0.0964	-110	292	300	SIVASGLAR	18	0				Mascot	
1271.743	1271.6736	-0.0694	-55	288	300	QAAKSIVASGLAR						Mascot	
1466.7924	1466.6372	-0.1552	-106	48	60	TNLVMIFGEITTK						Mascot	
2316.1792	2316.0669	-0.1123	-48	48	67	TNLVMIFGEITTKANLDYE K				Oxidation (M)[5]		Mascot	
2416.1921	2416.0356	-0.1565	-65	40	60	VACETCTKTNLVMIFGEIT TK				Carbamidomethyl (C)[3,6]		Mascot	
10	Protein RF1, mitochondrial OS=Oryza sativa subsp. indica GN=RF1 PE=2 SV=1				RF1_ORYSI	87557.1	6.1	13	38	0			
Peptide Information													
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
873.4424	873.4187	-0.0237	-27	63	71	DSPAAAVSR						Mascot	
873.4424	873.4187	-0.0237	-27	63	71	DSPAAAVSR	7	0				Mascot	
985.5023	985.497	-0.0053	-5	322	329	KIFDSMTK				Oxidation (M)[6]		Mascot	
985.5023	985.497	-0.0053	-5	322	329	KIFDSMTK				Oxidation (M)[6]		Mascot	
1121.6313	1121.5204	-0.1109	-99	597	606	TAAAKELYVR						Mascot	
1233.582	1233.6136	0.0316	26	782	791	YKSFIELSC				Carbamidomethyl (C)[10]		Mascot	
1466.7672	1466.6372	-0.13	-89	384	396	GQKVDQAMLVFSK				Oxidation (M)[8]		Mascot	
1592.8716	1592.8168	-0.0548	-34	492	504	VIESEKLFELMVR						Mascot	
1592.8716	1592.8168	-0.0548	-34	492	504	VIESEKLFELMVR						Mascot	
2139.0361	2139.1331	0.097	45	471	488	GICLNTIFFNSIIDSHCK				Carbamidomethyl (C)[3,17]		Mascot	
2211.1665	2210.99	-0.1765	-80	148	166	RMTELGCPNVFSYNILLK						Mascot	
2386.145	2386.1357	-0.0093	-4	629	648	NKLTDDALQMFQNLCLM DLK				Oxidation (M)[10,17]		Mascot	
2416.2764	2416.0356	-0.2408	-100	399	421	QQGLNPNAVTYGAVIGIL CKSGR				Carbamidomethyl (C)[19]		Mascot	
2424.1797	2424.168	-0.0117	-5	471	491	GICLNTIFFNSIIDSHCKEG R				Carbamidomethyl (C)[3]		Mascot	
2748.1521	2748.166	0.0139	5	260	283	NGVMPDCMTYNSILHG YCSSGQPK				Carbamidomethyl (C)[7,18], Oxidation (M)[4,8]		Mascot	
3337.6628	3337.5601	-0.1027	-31	460	488	AEEILEMLDRGICLNTIF FNSIIDSHCK						Mascot	
Gel Idx/Pos Plate [ # ] Name		120/E19 [1] 31564		Instr./Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded Spectra 11			
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Protein Total Ion Score	Protein Total Ion C. I. %				
1	glutamine synthase [Gossypium hirsutum]	gil211906462	39188.6	0	5	138	100	123	100				
Peptide Information										C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score						
1303.6787	1303.463	-0.2157	-165	256	267	SMRNDGGINVIK							Mascot
1793.9255	1793.8506	-0.0749	-42	19	34	IIAEYIWIGSGMDLR							Mascot
1793.9255	1793.8506	-0.0749	-42	19	34	IIAEYIWIGSGMDLR	40						Mascot
1809.9204	1809.8501	-0.0703	-39	19	34	IIAEYIWIGSGMDLR				Oxidation (M)[13]		Mascot	
2531.238	2531.1252	-0.1128	-45	85	107	GNNILVMCDAYTPAGEPI PTNKR				Carbamidomethyl (C)[8]		Mascot	
2662.2549	2662.1467	-0.1082	-41	141	165	WPLGWVPGFPGPQGP YYCGVGADK				Carbamidomethyl (C)[19]		Mascot	
2662.2549	2662.1467	-0.1082	-41	141	165	WPLGWVPGFPGPQGP YYCGVGADK	83			Carbamidomethyl (C)[19]		Mascot	
2720.3787	2720.2363	-0.1424	-52	333	356	RPASNMDPYVVTSMIAET TIWKP						Mascot	
2	glutamine synthetase isoform Gse1 [Triticum aestivum]	gil40317420	39458.6	0	1	112	100	112	100				
Peptide Information										C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score						
2990.4934	2990.3599	-0.1335	-45	113	137	IFGHPDVKAEEPWYGIEQ EYTLQK							Mascot
2990.4934	2990.3599	-0.1335	-45	113	137	IFGHPDVKAEEPWYGIEQ EYTLQK	112						Mascot
3	predicted protein [Populus trichocarpa]	gil224079530	39231.7	0	4	105	99.996	93	100				
Peptide Information										C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score						
2720.3787	2720.2363	-0.1424	-52	333	356	RPASNMDPYVVTSMIAET TIWKP							Mascot
2990.5298	2990.3599	-0.1699	-57	113	137	IFSHPDVVAEKPWYGLE QEYTLQK							Mascot
2990.5298	2990.3599	-0.1699	-57	113	137	IFSHPDVVAEKPWYGLE QEYTLQK	93						Mascot
3076.5027	3076.4312	-0.0715	-23	138	165	DVKWPLGWPIGGYPGQ GPYYCGIGVDK				Carbamidomethyl (C)[22]		Mascot	
3076.5027	3076.4312	-0.0715	-23	138	165	DVKWPLGWPIGGYPGQ GPYYCGIGVDK				Carbamidomethyl (C)[22]		Mascot	
3337.6489	3337.5789	-0.07	-21	50	79	LPKWNYDGSSTGQAPG QDSEVILYQAIKR						Mascot	
4	glutamine synthetase 1 [Datisca glomerata]	gil39636489	39052.7	0	5	98	99.978	83	99.997				
Peptide Information										C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score						
1805.8817	1805.8289	-0.0528	-29	50	66	LPKWNYDGSSTGQAPGK							Mascot
2211.1265	2211.0161	-0.1104	-50	292	311	LTGRHETADINTSLWGVA NR							Mascot
2531.238	2531.1252	-0.1128	-45	85	107	GNNILVMCDAYTPAGEPI PTNKR				Carbamidomethyl (C)[8]		Mascot	
2662.2549	2662.1467	-0.1082	-41	141	165	WPIGWVPGFPGPQGP YYCGVGADK				Carbamidomethyl (C)[19]		Mascot	
2662.2549	2662.1467	-0.1082	-41	141	165	WPIGWVPGFPGPQGP YYCGVGADK	83			Carbamidomethyl (C)[19]		Mascot	
2720.3787	2720.2363	-0.1424	-52	333	356	RPASNMDPYVVTSMIAET TIWKP						Mascot	
5	ATGSKB6 [Arabidopsis lyrata subsp. lyrata]	gil297830414	38483.2	0	6	61	11.442	40	44.571				
Peptide Information										C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score						
870.5771	870.5079	-0.0692	-79	269	276	AIGKLQLK							Mascot
1759.9436	1759.7303	-0.2133	-121	2	18	SLLSDLVNLNLSGATDK							Mascot
1759.9436	1759.7303	-0.2133	-121	2	18	SLLSDLVNLNLSGATDK							Mascot
1793.9255	1793.8506	-0.0749	-42	19	34	IIAEYIWIGSGMDIR							Mascot
1793.9255	1793.8506	-0.0749	-42	19	34	IIAEYIWIGSGMDIR	40						Mascot



10	cytosolic glutamine synthetase [Cucumis melo]				gi 113171384		39166.7	0	4	50	0	40	44.571	
Peptide Information														
Calc. Mass		Obsrv. Mass		± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score		C. I. %	Modification	Rank	Result Type
1793.9255		1793.8506		-0.0749	-42	19	34	IIAEYIWIGSGMDLR						Mascot
1793.9255		1793.8506		-0.0749	-42	19	34	IIAEYIWIGSGMDLR	40					Mascot
1809.9204		1809.8501		-0.0703	-39	19	34	IIAEYIWIGSGMDLR				Oxidation (M)[13]		Mascot
1817.8566		1817.8231		-0.0335	-18	296	311	HETADINTFSWGVANR						Mascot
2647.2803		2647.2537		-0.0266	-10	141	165	WPIGWPIGGFPGPQGPY						Mascot
								YCGVGVDK						
3000.4011		3000.2524		-0.1487	-50	53	79	WNYDGSSTGQAPGEDS						Mascot
								EVILYPQAIIR						

Gel Idx/Pos	121/E20	Instr./Gel Origin	BA2060/140227A	Process Statu	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %		
1	predicted protein [Populus trichocarpa]	gi 224079530	39231.7	0	3	100	99.987	91	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
2990.5298	2990.3752	-0.1546	-52	113	137	IFSHPDVVAEKPWYGLE					Mascot
						QEYTLQK					
2990.5298	2990.3752	-0.1546	-52	113	137	IFSHPDVVAEKPWYGLE	91				Mascot
						QEYTLQK					
3076.5027	3076.4375	-0.0652	-21	138	165	DKVSWPLGWPIGGYPGPO			Carbamidomethyl (C)[22]		Mascot
						GPYYCGIGVDK					
3337.6489	3337.5857	-0.0632	-19	50	79	LPKWNYDGSSTGQAPG					Mascot
						QDSEVILYPQAIIR					
2	glutamine synthetase isoform GSe1 [Triticum aestivum]	gi 40317420	39458.6	0	1	79	98.564	79	99.993		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
2990.4934	2990.3752	-0.1182	-40	113	137	IFGHPDVKAEEPWYGIEQ					Mascot
						EYTLQK					
2990.4934	2990.3752	-0.1182	-40	113	137	IFGHPDVKAEEPWYGIEQ	79				Mascot
						EYTLQK					
3	glutamine synthetase [Elaeagnus umbellata]	gi 47933888	39166.7	0	3	69	83.126	61	99.491		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1817.8566	1817.8373	-0.0193	-11	295	310	HETADINTFSWGVANR					Mascot
2531.238	2531.1118	-0.1262	-50	84	106	GNNILVMCDAYTPAGEPI			Carbamidomethyl (C)[8]		Mascot
						PTNKR					
2547.2332	2547.114	-0.1192	-47	84	106	GNNILVMCDAYTPAGEPI			Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot
						PTNKR					
3043.4067	3043.2717	-0.135	-44	52	78	WNYDGSSTNQAPGDDS					Mascot
						EVILYPQAIIR					
3043.4067	3043.2717	-0.135	-44	52	78	WNYDGSSTNQAPGDDS	61				Mascot
						EVILYPQAIIR					
4	calcium-dependent protein kinase 30 [Arabidopsis lyrata subsp. lyrata]	gi 297842215	61454.4	0	14	53	0				
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1049.4761	1049.5066	0.0305	29	439	446	QAFMFFDK			Oxidation (M)[4]		Mascot
1049.5659	1049.5066	-0.0593	-56	83	92	EALACKSISK					Mascot
1196.6708	1196.4982	-0.1726	-144	515	524	FKSLSLNLMK			Oxidation (M)[9]		Mascot
1196.6708	1196.4982	-0.1726	-144	515	524	FKSLSLNLMK			Oxidation (M)[9]		Mascot
1254.5653	1254.5525	-0.0128	-10	173	182	MCHINGVMHR			Carbamidomethyl (C)[2]		Mascot
1303.6277	1303.4482	-0.1795	-138	10	20	FDPENSKPNQK					Mascot
1402.7186	1402.6527	-0.0659	-47	153	165	GHYTERAAATVAR					Mascot
1485.7367	1485.6958	-0.0409	-28	46	58	VIPMSHQSQSDK			Oxidation (M)[4]		Mascot
1485.7367	1485.6958	-0.0409	-28	46	58	VIPMSHQSQSDK			Oxidation (M)[4]		Mascot
1748.7982	1748.7909	-0.0073	-4	485	498	GRINRYDEFVMMK			Oxidation (M)[12,13]		Mascot
1793.9467	1793.8346	-0.1121	-62	107	122	EVTIMSTLPEHPNVVK					Mascot
1793.9467	1793.8346	-0.1121	-62	107	122	EVTIMSTLPEHPNVVK	5				Mascot
1809.9415	1809.8363	-0.1052	-58	107	122	EVTIMSTLPEHPNVVK			Oxidation (M)[5]		Mascot
1817.8488	1817.8373	-0.0115	-6	68	82	GEFGITYLCTDRETR			Carbamidomethyl (C)[9]		Mascot
1943.9823	1943.9558	-0.0265	-14	217	233	FTEIVGSPYYMAPEVLK					Mascot
1965.9933	1965.9062	-0.0871	-44	166	182	TIAEVVRMCHINGVMHR					Mascot
2145.1233	2144.9204	-0.2029	-95	40	58	THAPLRVIPMSHQSQSDK					Mascot
						K					
3076.5483	3076.4375	-0.1108	-36	403	430	LLMEVADVNGNGCLDYG			Oxidation (M)[3]		Mascot
						EFVAVIHLQK					
5	hypothetical protein SELMODRAFT_424273 [Selaginella moellendorffii]	gi 302807074	50192.9	0	11	52	0	19	0		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
842.5094	842.4732	-0.0362	-43	352	360	KPAVAATGK					Mascot
1049.5521	1049.5066	-0.0455	-43	132	140	LTTSGRVCR			Carbamidomethyl (C)[8]		Mascot
1049.683	1049.5066	-0.1764	-168	43	52	VIGVAKPLPR	22				Mascot
1121.5334	1121.5184	-0.015	-13	275	284	GSSHFRSEK					Mascot
1553.7748	1553.6388	-0.136	-88	248	260	SIPPEEWLPGSWPR					Mascot
1553.7748	1553.6388	-0.136	-88	248	260	SIPPEEWLPGSWPR					Mascot
1709.8759	1709.7258	-0.1501	-88	247	260	RSIPEEWLPGSWPR					Mascot
1791.876	1791.6476	-0.2284	-127	282	297	SEKTSLDFVSESTPHK					Mascot
1805.8413	1805.8295	-0.0118	-7	15	31	GEAAARTPEETAGQFDR					Mascot
1817.8456	1817.8373	-0.0083	-5	74	90	ACCLSSVAACFSSSIRR			Carbamidomethyl (C)[2]		Mascot
2145.0071	2144.9204	-0.0867	-40	248	265	SIPPEEWLPGSWPRCDTS			Carbamidomethyl (C)[14]		Mascot
						K					
3386.6719	3386.5596	-0.1123	-33	155	186	AVVPPMVPGVRRWQEIET			Oxidation (M)[6]		Mascot
						GSTVLACSSDDGTR					
6	hypothetical protein MTR_3g060270 [Medicago truncatula]	gi 357460143	8928.2	0	7	52	0				
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
933.4709	933.4736	0.0027	3	53	61	MIEGGAEVK					Mascot
1010.4757	1010.4287	-0.047	-47	38	45	GKNMIEMR			Oxidation (M)[4,7]		Mascot
1010.4757	1010.4287	-0.047	-47	38	45	GKNMIEMR	3		Oxidation (M)[4,7]		Mascot
1206.6035	1206.5569	-0.0466	-39	53	63	MIEGGAEVKEK			Oxidation (M)[1]		Mascot

1796.7976	1796.8386	0.041	23	2	19	LVVDGGCCGESEAMVVG R	Oxidation (M)[14]	Mascot
1943.833	1943.9558	0.1228	63	1	19	MLVVDGGCCGESEAMV VGR	Oxidation (M)[1,15]	Mascot
2384.0461	2383.8406	-0.2055	-86	2	23	LVVDGGCCGESEAMVVG RSDMR	Carbamidomethyl (C)[7,8]	Mascot
2531.0815	2531.1118	0.0303	12	1	23	MLVVDGGCCGESEAMV VGRSDMR	Carbamidomethyl (C)[8,9], Oxidation (M)[1]	Mascot
2547.0767	2547.114	0.0373	15	1	23	MLVVDGGCCGESEAMV VGRSDMR	Carbamidomethyl (C)[8,9], Oxidation (M)[1,15]	Mascot

7 PREDICTED: vacuolar protein sorting-associated protein 4B-like [Glycine max] gi|356542738 48588.8 0 10 50 0

Peptide Information								C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score				
862.3661	862.5283	0.1622	184	204	210	WMGESEK	12	Oxidation (M)[2]			Mascot
933.4723	933.4736	0.0013	1	302	308	ARCHMFK		Oxidation (M)[5]			Mascot
1064.5735	1064.4895	-0.084	-79	402	410	TDFDKVLAR					Mascot
1064.5735	1064.4895	-0.084	-79	402	410	TDFDKVLAR					Mascot
1254.7642	1254.5525	-0.2117	-169	407	417	VLARORPTVSK					Mascot
1402.613	1402.6527	0.0397	28	362	373	NPEDMWIPCGPK		Oxidation (M)[5]			Mascot
1485.6891	1485.6958	0.0067	5	330	343	TEGFSGSDISVCVK		Carbamidomethyl (C)[12]			Mascot
1485.6891	1485.6958	0.0067	5	330	343	TEGFSGSDISVCVK		Carbamidomethyl (C)[12]			Mascot
1498.79	1498.7689	-0.0211	-14	53	64	EAITQKFTYLR					Mascot
1796.896	1796.8386	-0.0574	-32	253	268	TELLVQMGGVGHNDQK					Mascot
2384.1804	2383.8406	-0.3398	-143	330	351	TEGFSGSDISVCVKD/LF EPVR					Mascot
3076.4172	3076.4375	0.0203	7	362	388	NPEDMWIPCGPKQSAV QTTMQDLAAK		Carbamidomethyl (C)[9], Oxidation (M)[5,21]			Mascot

8 Os12g0209700 [Oryza sativa Japonica Group] gi|297612845 133496.7 0 17 50 0

Peptide Information								C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score				
873.5152	873.4229	-0.0923	-106	550	556	IRENLTK	10				Mascot
933.5615	933.4736	-0.0879	-94	680	688	VLSSSIISK					Mascot
1049.6215	1049.5066	-0.1149	-109	768	776	HNKVPLSVR					Mascot
1049.6215	1049.5066	-0.1149	-109	768	776	HNKVPLSVR					Mascot
1105.5848	1105.5266	-0.0582	-53	955	964	LQSTDSDIVR					Mascot
1196.6132	1196.4982	-0.115	-96	883	893	TGHSDLRASPR					Mascot
1196.6132	1196.4982	-0.115	-96	883	893	TGHSDLRASPR					Mascot
1303.6376	1303.4482	-0.1894	-145	224	235	DLLNETVADAK					Mascot
1485.5945	1485.6958	0.1013	68	2	15	SMQMDVDGESSGAR		Oxidation (M)[2]			Mascot
1485.5945	1485.6958	0.1013	68	2	15	SMQMDVDGESSGAR		Oxidation (M)[2]			Mascot
1488.754	1488.7437	-0.0103	-7	1090	1102	OSKIPLDSTEDR					Mascot
1553.7959	1553.6388	-0.1571	-101	507	519	ENAFDEKLLTAFR					Mascot
1553.7959	1553.6388	-0.1571	-101	507	519	ENAFDEKLLTAFR					Mascot
1786.8752	1786.748	-0.1272	-71	820	835	SSSKSVYVNLCSQATR		Carbamidomethyl (C)[11]			Mascot
1796.8372	1796.8386	0.0014	1	432	447	SVPDIMSIVGEDYSR					Mascot
1817.9062	1817.8373	-0.0689	-38	798	814	RCADTELAIAVNVKEK					Mascot
1965.8971	1965.9062	0.0091	5	1045	1064	EIPADTNMPDEGAGHV GAK					Mascot
2144.9336	2144.9204	-0.0132	-6	1068	1088	VPASDLNHSQANSSP TEGK					Mascot
2159.9985	2160.0371	0.0386	18	392	410	ARSEVPEQINMIGNSDD R					Mascot
2175.9934	2176.0381	0.0447	21	392	410	ARSEVPEQINMIGNSDD R		Oxidation (M)[12]			Mascot
2501.1396	2501.1318	-0.0078	-3	1065	1088	EVKVPASDLNHSQAN SSPTEGK					Mascot
3076.2959	3076.4375	0.1416	46	44	67	GVLDCCQHWFCYTCIDN WSAITNR		Carbamidomethyl (C)[5,6,11,14]			Mascot

9 hypothetical protein VOLCADRAFT\_97847 [Volvox carteri f. nagariensis] gi|302850637 40331.9 0 8 50 0 17 0

Peptide Information								C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score				
1010.5781	1010.4287	-0.1494	-148	256	263	QKYGFLVR	17				Mascot
1010.5781	1010.4287	-0.1494	-148	256	263	QKYGFLVR					Mascot
1064.5922	1064.4895	-0.1027	-96	209	216	RPKLFMEK		Oxidation (M)[6]			Mascot
1064.5922	1064.4895	-0.1027	-96	209	216	RPKLFMEK		Oxidation (M)[6]			Mascot
1196.6422	1196.4982	-0.144	-120	240	249	YINVPAASKVR					Mascot
1196.6422	1196.4982	-0.144	-120	240	249	YINVPAASKVR					Mascot
1485.6864	1485.6958	0.0094	6	47	59	HQGDPMTRDTVGR		Oxidation (M)[6]			Mascot
1485.6864	1485.6958	0.0094	6	47	59	HQGDPMTRDTVGR		Oxidation (M)[6]			Mascot
1852.0076	1851.8457	-0.1619	-87	139	153	ERLDVLQLQWAEVPR					Mascot
1943.86	1943.9558	0.0958	49	39	55	GCWQLSGRHQGDPMTR					Mascot
2384.2861	2383.8406	-0.4455	-187	225	247	LLAYGTVAGLLADKYIN VPASK					Mascot
2990.4663	2990.3752	-0.0911	-30	95	122	LYPGDAATATATKLSYLS EEDMSTVSR					Mascot
2990.4663	2990.3752	-0.0911	-30	95	122	LYPGDAATATATKLSYLS EEDMSTVSR					Mascot

10 hypothetical protein VITISV\_030456 [Vitis vinifera] gi|147807312 51726.5 0 12 49 0

Peptide Information								C. I. %	Modification	Rank	Result Type
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score				
842.5458	842.4732	-0.0726	-86	271	278	LLSAALVR	17				Mascot
873.4061	873.4229	0.0168	19	433	440	EVGPSNDR					Mascot
882.4138	882.5283	0.1145	130	426	432	QCYEIAR					Mascot
1553.7668	1553.6388	-0.128	-82	145	158	NICPSTPFFFESLAK					Mascot
1553.7668	1553.6388	-0.128	-82	145	158	NICPSTPFFFESLAK					Mascot
1638.8096	1638.7802	-0.0294	-18	412	425	DRHDIHYSQLAAR					Mascot
1709.868	1709.7258	-0.1422	-83	144	158	RNICPSTPFFFESLAK					Mascot
1793.8235	1793.8346	0.0111	6	426	440	QCYEIAREVGPSNDR		Carbamidomethyl (C)[2]			Mascot
1793.8235	1793.8346	0.0111	6	426	440	QCYEIAREVGPSNDR		Carbamidomethyl (C)[2]			Mascot
1796.9033	1796.8386	-0.0647	-36	42	56	QLMTFDIRNDALLCK		Oxidation (M)[3]			Mascot
2211.0161	2211.0151	-0.001	0	433	452	EVGPSNDRRESPLEQVNT PDQ					Mascot
2647.3813	2647.2649	-0.1164	-44	50	72	NDALLCKVFLTSLQGQAL SWFHR					Mascot
2662.4829	2662.1658	-0.3171	-119	292	315	SAHLINGVILFPLVDPTQI PQPHR					Mascot
2663.3901	2663.2263	-0.1638	-62	123	144	FGQILQVESYSMDVVFQI FKR		Oxidation (M)[13]			Mascot

Gel Idx/Pos	122/E21	Instr./Gel Origin	BA2060/140227A	Process Statu	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	Fructose-bisphosphate aldolase 1, chloroplastic (Fragment) OS=Pisum sativum PE=1 SV=1	ALFC1_PEA	38633	5.83	7	272	100	243	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4576	873.4279	-0.0297	-34	161	168	EAAWGLAR	32	90.225	
873.4576	873.4279	-0.0297	-34	161	168	EAAWGLAR			
1105.5564	1105.5405	-0.0159	-14	348	356	ELFKVGYSY			
1114.5276	1114.4906	-0.037	-33	131	140	SAAYYQQGAR	61	99.987	
1114.5276	1114.4906	-0.037	-33	131	140	SAAYYQQGAR			
1452.842	1452.7859	-0.0561	-39	146	160	TVVSIPNGPSALAVK			
1466.6614	1466.6488	-0.0126	-9	26	39	GLAMDESATCGK			Carbamidomethyl (C)[12]
1592.8643	1592.8478	-0.0165	-10	1	15	GLTRAGSYADELVK			
2402.1404	2402.0586	-0.0818	-34	108	130	GLVPLAGSNDESWCQGLDGLASR			Carbamidomethyl (C)[14]
2402.1404	2402.0586	-0.0818	-34	108	130	GLVPLAGSNDESWCQGLDGLASR	150	100	Carbamidomethyl (C)[14]
2	Fructose-bisphosphate aldolase, chloroplastic OS=Spinacia oleracea PE=1 SV=3	ALFC_SPIOL	42441.7	6.85	7	157	100	131	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4576	873.4279	-0.0297	-34	201	208	EAAWGLAR	32	90.225	
873.4576	873.4279	-0.0297	-34	201	208	EAAWGLAR			
1114.5276	1114.4906	-0.037	-33	171	180	SAAYYQQGAR	61	99.987	
1114.5276	1114.4906	-0.037	-33	171	180	SAAYYQQGAR			
1387.7175	1387.6674	-0.0501	-36	81	93	LASIGLENTEANR			
1387.7175	1387.6674	-0.0501	-36	81	93	LASIGLENTEANR	38	97.393	
1452.842	1452.7859	-0.0561	-39	186	200	TVVSIPNGPSALAVK			
1466.6614	1466.6488	-0.0126	-9	66	79	GLAMDESATCGK			Carbamidomethyl (C)[12]
1543.8186	1543.7583	-0.0603	-39	80	93	RLASIGLENTEANR			
1626.9135	1626.827	-0.0865	-53	130	144	MVDVLIEQGIVPGIK			Oxidation (M)[1]
3	Fructose-bisphosphate aldolase 2, chloroplastic OS=Pisum sativum PE=1 SV=2	ALFC2_PEA	37803.4	5.48	6	116	100	93	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4576	873.4279	-0.0297	-34	155	162	EAAWGLAR	32	90.225	
873.4576	873.4279	-0.0297	-34	155	162	EAAWGLAR			
1114.5276	1114.4906	-0.037	-33	125	134	SAAYYQQGAR	61	99.987	
1114.5276	1114.4906	-0.037	-33	125	134	SAAYYQQGAR			
1325.6219	1325.641	0.0191	14	330	341	YIGDGESEAKK			
1452.842	1452.7859	-0.0561	-39	140	154	TVVSIPNGPSALAVK			
1466.6614	1466.6488	-0.0126	-9	20	33	GLAMDESATCGK			Carbamidomethyl (C)[12]
2401.1565	2401.0964	-0.0601	-25	102	124	GLVPLAGSNDESWCQGLDGLASR			Carbamidomethyl (C)[14]
4	Fructose-bisphosphate aldolase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os11g0171300 PE=1	ALFC_ORYSJ	41979.5	6.38	6	91	99.997	70	99.998
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4576	873.4279	-0.0297	-34	193	200	EAAWGLAR	32	90.225	
873.4576	873.4279	-0.0297	-34	193	200	EAAWGLAR			
1249.5922	1249.6233	0.0311	25	379	388	EGMFVKNNVYY			
1249.5922	1249.6233	0.0311	25	379	388	EGMFVKNNVYY			
1387.7175	1387.6674	-0.0501	-36	73	85	LASIGLENTEANR			
1387.7175	1387.6674	-0.0501	-36	73	85	LASIGLENTEANR	38	97.393	
1466.6614	1466.6488	-0.0126	-9	58	71	GLAMDESATCGK			Carbamidomethyl (C)[12]
1543.8186	1543.7583	-0.0603	-39	72	85	RLASIGLENTEANR			
2401.1565	2401.0964	-0.0601	-25	140	162	GLVPLAGSNDESWCQGLDGLASR			Carbamidomethyl (C)[14]
5	Probable fructose-bisphosphate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=FBA1 PE=1 SV=2	ALFC1_ARATH	42903.9	6.18	5	85	99.989	70	99.998
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4576	873.4279	-0.0297	-34	204	211	EAAWGLAR	32	90.225	
873.4576	873.4279	-0.0297	-34	204	211	EAAWGLAR			
1147.5742	1147.5488	-0.0254	-22	349	358	TWGGKEENVK			
1387.7175	1387.6674	-0.0501	-36	84	96	LASIGLENTEANR			
1387.7175	1387.6674	-0.0501	-36	84	96	LASIGLENTEANR	38	97.393	
1452.842	1452.7859	-0.0561	-39	189	203	TVVSIPNGPSALAVK			
1543.8186	1543.7583	-0.0603	-39	83	96	RLASIGLENTEANR			
6	S-adenosylmethionine synthase 1 (Fragment) OS=Pisum sativum GN=SAMS1 PE=2 SV=2	METK1_PEA	39914.5	6.45	7	49	61.373	21	0
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
842.5709	842.4794	-0.0915	-109	307	313	EILKIVK			
873.5151	873.4279	-0.0872	-100	267	275	SIVASGLAR	21	0	
873.5151	873.4279	-0.0872	-100	267	275	SIVASGLAR			
1097.552	1097.5293	-0.0227	-21	203	212	TICHLNPSGR			
1271.743	1271.6921	-0.0509	-40	263	275	QAAKSIVASGLAR			
1452.7766	1452.7859	0.0093	6	23	35	TNLVMVFGEITTK			
1453.7546	1453.7816	0.027	19	213	227	FVIGPHGDAGLTGR			
2402.1763	2402.0586	-0.1177	-49	15	35	VACETCTKTNLMVFGEITTK			Carbamidomethyl (C)[3,6]
2402.1763	2402.0586	-0.1177	-49	15	35	VACETCTKTNLMVFGEITTK			Carbamidomethyl (C)[3,6]
7	S-adenosylmethionine synthase 1 OS=Solanium tuberosum GN=METK1 PE=2 SV=1	METK1_SOLTU	43188.8	5.52	7	48	44.167	21	0
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
842.5709	842.4794	-0.0915	-109	332	338	EILKIVK			
873.5151	873.4279	-0.0872	-100	292	300	SIVASGLAR	21	0	
873.5151	873.4279	-0.0872	-100	292	300	SIVASGLAR			
1271.743	1271.6921	-0.0509	-40	288	300	QAAKSIVASGLAR			
1452.7766	1452.7859	0.0093	6	48	60	TNLVMVFGEITTK			
1453.7546	1453.7816	0.027	19	238	252	FVIGPHGDAGLTGR			
1936.8923	1936.8892	-0.0031	-2	2	18	ETPLTSESVEIGHPOK			
2402.1763	2402.0586	-0.1177	-49	40	60	VACETCTKTNLMVFGEI			Carbamidomethyl (C)[3,6]







2211.0024	2211.0144	0.012	5	1101	1118	GMPVAMERLNINEMECR		Carbamidomethyl (C)[17], Oxidation (M)[2,6,15]	Mascot
2262.0088	2261.9561	-0.0527	-23	411	430	CEDDRYEMDMLLGVSVS AIK			Mascot
2691.2429	2691.2041	-0.0388	-14	217	240	GHEDDLMEFVNFLPNCP ESAPSTK		Oxidation (M)[7]	Mascot
2748.2644	2748.2041	-0.0603	-22	217	240	GHEDDLMEFVNFLPNCP ESAPSTK		Carbamidomethyl (C)[16], Oxidation (M)[7]	Mascot
2807.4084	2807.2068	-0.2016	-72	1011	1033	FFDLVYHENACALLHEAN IYRIR			Mascot

Gel Idx/Pos		124/E23				Instr./Gel Origin				BA2060/140227A				Process Statu		Analysis Succeeded	
Plate [#] Name		[1] 31564				Instrument Sample Name								Spectra		11	
Rank	Protein Name					Accession No.		Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %			
1	isoflavone reductase, putative [Ricinus communis]					gi 255543713		31307.3	6.54	5	180	100	162	100			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	850.4451	850.5084	0.0633	74	212	218	MGKTLER					Oxidation (M)[1]				Mascot	
	1429.6382	1429.5945	-0.0437	-31	86	97	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	86	97	FFPSEFGNDVDR									Mascot	
	1755.8547	1755.8403	-0.0144	-8	164	178	AIFNEENDIGTYTIR									Mascot	
	1755.8547	1755.8403	-0.0144	-8	164	178	AIFNEENDIGTYTIR			89	99.996					Mascot	
	2084.179	2084.0083	-0.1707	-82	7	26	ILFIGGTGYIGKFIVEASAK									Mascot	
	2705.4548	2705.0857	-0.3691	-136	189	211	TLYISPPQNIISFNDLVSL WEKK									Mascot	
2	isoflavone reductase related protein [Pyrus communis]					gi 3243234		33801.8	6.02	3	178	100	170	100			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	1182.5637	1182.5389	-0.0248	-21	191	200	EDDIGTYTIR									Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR									Mascot	
	1755.8911	1755.8403	-0.0508	-29	186	200	AIFNKEDDIGTYTIR									Mascot	
3	RecName: Full=isoflavone reductase homolog; AltName: Full=CP100					gi 1708422		33830.8	6.16	4	85	97.149	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	850.4781	850.5084	0.0303	36	120	127	VHAVPEAK									Mascot	
	1114.6003	1114.512	-0.0883	-79	27	36	AGHDTFVLVR									Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR									Mascot	
	2084.179	2084.0083	-0.1707	-82	7	26	ILFIGGTGYIGKFIVEASAK									Mascot	
4	phenylcoumaran benzylic ether reductase 3 [Populus trichocarpa]					gi 224105373		33730.8	6.02	4	85	97.014	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	946.4839	946.4948	0.0109	12	35	43	ESTLSNPAK									Mascot	
	1429.6382	1429.5945	-0.0437	-31	106	117	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	106	117	FFPSEFGNDVDR									Mascot	
	2084.179	2084.0083	-0.1707	-82	5	24	ILFIGGTGYIGKFIVEASAK									Mascot	
	2093.0986	2093.0322	-0.0664	-32	74	92	QVDVIVISTVGHQAQLVEQ DR									Mascot	
	2093.0986	2093.0322	-0.0664	-32	74	92	QVDVIVISTVGHQAQLVEQ DR									Mascot	
5	isoflavone reductase homolog Bet v 6.0101 [Betula pendula]					gi 4731376		33132.7	7.82	4	83	96.064	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	850.4781	850.5084	0.0303	36	120	127	VHAVPEAK									Mascot	
	1182.5637	1182.5389	-0.0248	-21	191	200	EDDIGTYTIR									Mascot	
	1204.73	1204.6831	-0.0469	-39	7	18	ILIIIGGTGYIGK									Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR									Mascot	
6	pterocarpin reductase-like protein [Linum catharticum]					gi 169639232		33863.6	7.03	4	83	95.972	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	842.4617	842.4854	0.0237	28	123	130	VEAVEPAK									Mascot	
	999.5833	999.6033	0.02	20	179	188	VILGDGNAK									Mascot	
	999.5833	999.6033	0.02	20	179	188	VILGDGNAK									Mascot	
	1429.6382	1429.5945	-0.0437	-31	111	122	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	111	122	FFPSEFGNDVDR									Mascot	
	2084.179	2084.0083	-0.1707	-82	10	29	ILFIGGTGYIGKFIVEASAK									Mascot	
7	allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula pendula]					gi 10764491		34169.2	6.73	4	83	95.684	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	850.4781	850.5084	0.0303	36	120	127	VHAVPEAK									Mascot	
	1182.5637	1182.5389	-0.0248	-21	191	200	EDDIGTYTIR									Mascot	
	1204.73	1204.6831	-0.0469	-39	7	18	ILIIIGGTGYIGK									Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	108	119	FFPSEFGNDVDR									Mascot	
8	PREDICTED: isoflavone reductase homolog [Vitis vinifera]					gi 225428436		33862.8	6.11	3	81	93.316	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification			Rank	Result Type	
	850.4781	850.5084	0.0303	36	118	125	VHAVPEAK									Mascot	
	1204.73	1204.6831	-0.0469	-39	7	18	ILIIIGGTGYIGK									Mascot	
	1429.6382	1429.5945	-0.0437	-31	106	117	FFPSEFGNDVDR			73	99.833					Mascot	
	1429.6382	1429.5945	-0.0437	-31	106	117	FFPSEFGNDVDR									Mascot	
9	phenylcoumaran benzylic ether reductase-like protein F1 [Striga asiatica]					gi 90811671		34346.9	5.44	3	81	93.001	73	99.833			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence			Ion	C. I. %	Modification			Rank	Result Type	

																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

	2015.0967	2014.7542	-0.3425	-170	97	116	GDIVLGRPAGAGCPVQH VIR							Mascot
	2015.0967	2014.7542	-0.3425	-170	97	116	GDIVLGRPAGAGCPVQH VIR							Mascot
	2143.1917	2142.8579	-0.3338	-156	96	116	KGDIVLGRPAGAGCPVQ HVIR							Mascot
	2184.1594	2184.0542	-0.1052	-48	183	201	THTGIVNMILEKSYGLHV R				Oxidation (M)[8]			Mascot
	2224.8687	2225.0432	0.1745	78	9	30	DCGACGAESCDAFMILA ESGMK				Oxidation (M)[14]			Mascot
	2663.3696	2663.2649	-0.1047	-39	148	170	MYHMIGFEGVARVVARP PQFGIR				Oxidation (M)[1,4]			Mascot
	3063.3025	3063.1978	-0.1047	-34	2	30	VWTPPGKDCGACGAES CDAFMILAESGMK	1		0	Carbamidomethyl (C)[12], Oxidation (M)[21,28]			Mascot
	3063.3025	3063.1978	-0.1047	-34	2	30	VWTPPGKDCGACGAES CDAFMILAESGMK				Carbamidomethyl (C)[9], Oxidation (M)[21,28]			Mascot
	3105.3318	3105.2629	-0.0689	-22	1	30	MVWTPPGKDCGACGAE SCDAFMILAESGMK							Mascot
5	isopropylmalate isomerase small subunit [Nitrobacter sp. Nb-311A]					gi 85714465	22448.4	5.35	9	58		0		
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	875.4468	875.435	-0.0118	-13	121	128	VSQADLDK						Mascot	
	1051.5571	1051.6838	0.1267	120	160	167	FEIDPRFK						Mascot	
	1177.6099	1177.5582	-0.0517	-44	184	193	KPAIEAYEEK						Mascot	
	1177.6099	1177.5582	-0.0517	-44	184	193	KPAIEAYEEK						Mascot	
	1371.7552	1371.6327	-0.1225	-89	16	27	IINVDTMIIPK						Mascot	
	1956.9882	1956.9248	-0.0634	-32	167	183	KHCLLGLDDIGLTMEK				Carbamidomethyl (C)[3]		Mascot	
	2014.9037	2014.7542	-0.1495	-74	97	113	CVISTSFGDIFYNNCFK				Carbamidomethyl (C)[1]		Mascot	
	2014.9037	2014.7542	-0.1495	-74	97	113	CVISTSFGDIFYNNCFK				Carbamidomethyl (C)[1]		Mascot	
	2615.4365	2615.0151	-0.4214	-161	4	27	FTTLEGVAAPLKINVDTD MIIPK				Oxidation (M)[20]		Mascot	
	2615.4365	2615.0151	-0.4214	-161	4	27	FTTLEGVAAPLKINVDTD MIIPK				Oxidation (M)[20]		Mascot	
	2721.3528	2721.1125	-0.2403	-88	97	120	CVISTSFGDIFYNNCFKN GILPIR						Mascot	
	3577.7031	3577.4575	-0.2456	-69	84	113	EHAPWALLDFGIRCVIST SFGDIFYNNCFK				Carbamidomethyl (C)[14,28]		Mascot	
	3577.7031	3577.4575	-0.2456	-69	84	113	EHAPWALLDFGIRCVIST SFGDIFYNNCFK				Carbamidomethyl (C)[14,28]		Mascot	
6	PREDICTED: metalloendopeptidase OMA1, mitochondrial [Canis lupus familiaris]					gi 73956390	60229.5	9.03	13	55		0		
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	842.3977	842.4876	0.0899	107	13	18	NCVFFR				Carbamidomethyl (C)[2]		Mascot	
	850.3975	850.5129	0.1154	136	250	256	NDMLTEK						Mascot	
	1051.6986	1051.6838	-0.0148	-14	452	460	LIPQALKIR						Mascot	
	1239.615	1239.5023	-0.1127	-91	2	12	SFICGLQSATR				Carbamidomethyl (C)[4]		Mascot	
	1458.7952	1458.7529	-0.0423	-29	365	377	DSLALLGQWIQSK						Mascot	
	1932.8936	1932.8906	-0.003	-2	235	249	LLSELEYEAWMEEFK				Oxidation (M)[11]		Mascot	
	2184.2322	2184.0542	-0.178	-81	112	131	EVAGVPALSLHLPLNCLP KR				Carbamidomethyl (C)[16]		Mascot	
	2194.0354	2194.0293	-0.0061	-3	1	18	MSFICGLQSATRNCVFFR				Carbamidomethyl (C)[5,14]		Mascot	
	2210.0303	2210.0273	-0.003	-1	1	18	MSFICGLQSATRNCVFFR				Carbamidomethyl (C)[5,14], Oxidation (M)[1]		Mascot	
	2211.0691	2211.0366	-0.0325	-15	61	77	LTLFPENFYFCRTFNKK				Carbamidomethyl (C)[11]		Mascot	
	2615.2744	2615.0151	-0.2593	-99	89	111	EFGMVTPNCTAWNGSFS RQLLIK				Oxidation (M)[4]		Mascot	
	2615.2744	2615.0151	-0.2593	-99	89	111	EFGMVTPNCTAWNGSFS RQLLIK				Oxidation (M)[4]		Mascot	
	2742.5237	2742.2615	-0.2622	-96	341	364	ASLVHLLDFLGLIFLTMIW AICPR						Mascot	
	2742.5237	2742.2615	-0.2622	-96	341	364	ASLVHLLDFLGLIFLTMIW AICPR						Mascot	
	2764.2732	2764.1951	-0.0781	-28	235	256	LLSELEYEAWMEEFKND MLTEK				Oxidation (M)[11]		Mascot	
	3191.7002	3191.2891	-0.4111	-129	195	222	LLLCFSSFGLLFVVFYFTH LEVSPVTGR						Mascot	
7	hypothetical protein Msed_1555 [Metallosphaera sedula DSM 5348]					gi 146304318	46369.9	4.86	11	54		0		
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	850.4338	850.5129	0.0791	93	36	42	LSEMDKK						Mascot	
	875.5196	875.435	-0.0846	-97	123	130	LTSDKAIK						Mascot	
	1165.5769	1165.702	0.1251	107	32	41	VAEKLEMDK				Oxidation (M)[8]		Mascot	
	1281.5823	1281.5775	-0.0048	-4	265	275	AMNSLMPMMQK						Mascot	
	1328.7784	1328.7014	-0.077	-58	116	127	LTPVLNKLTS DK						Mascot	
	2172.1216	2172.0566	-0.065	-30	1	18	MSQQDPLEILLKEENLQK	19		0	Oxidation (M)[1]		Mascot	
	2172.1216	2172.0566	-0.065	-30	1	18	MSQQDPLEILLKEENLQK				Oxidation (M)[1]		Mascot	
	2234.2656	2234.0042	-0.2614	-117	372	393	IWASDLPNVKPVGIGGLA GLTR						Mascot	
	2328.1133	2327.8521	-0.2612	-112	245	264	MTSEDINMIQKMDIDGL LK				Oxidation (M)[1,9]		Mascot	
	2588.3462	2588.269	-0.0772	-30	235	256	VQALWPLLEKMTSEDIN MIQK						Mascot	
	2611.3179	2611.1187	-0.1992	-76	284	306	LIQLQDVESMLGAFAEASM PMLKK				Oxidation (M)[10,18]		Mascot	
	2807.478	2807.2144	-0.2636	-94	159	184	TLKIQSLMDALLSAAET MTPTLAK				Oxidation (M)[10,20]		Mascot	
8	protein RhsH [Escherichia coli O157:H7 str. Sakai]					gi 15834118	157751	6.29	20	53		0		
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	842.4413	842.4876	0.0463	55	344	350	GRMV AHR				Oxidation (M)[3]		Mascot	
	875.3781	875.435	0.0569	65	335	341	SFTYDDK						Mascot	
	882.4389	882.5398	0.1009	114	1276	1283	EYGLICK						Mascot	
	996.5148	996.5705	0.0557	56	992	999	YLYDPLGR						Mascot	
	1110.4963	1110.4871	-0.0092	-8	487	494	REYDEWGR						Mascot	
	1165.567	1165.702	0.135	116	1011	1020	DLTGWMSLSR						Mascot	
	1177.5994	1177.5582	-0.0412	-35	623	633	AICTQGG LTR				Carbamidomethyl (C)[3]		Mascot	
	1177.5994	1177.5582	-0.0412	-35	623	633	AICTQGG LTR				Carbamidomethyl (C)[3]		Mascot	
	1371.644	1371.6327	-0.0113	-8	932	941	DAHLYRYDR	2		0			Mascot	
	1458.6716	1458.7529	0.0813	56	1349	1361	DLTNSVMYMGGKK						Mascot	
	2143.1594	2142.8579	-0.3015	-141	1143	1160	IHLHYCDHRGLPLALISK				Carbamidomethyl (C)[6]		Mascot	
	2211.1055	2211.0366	-0.0689	-31	755	772	QTVHHPQTEALLWQHET R						Mascot	

	2225.0369	2225.0432	0.0063	3	1191	1208	LPGQQYDEESGLYYNRH R										Mascot
	2233.9778	2234.0042	0.0264	12	510	529	YDNPHSDLPCATEDATG SRK	Carbamidomethyl (C)[10]									Mascot
	2328.1506	2327.8521	-0.2985	-128	981	999	TQYEEPLVESRYLYDPLG R										Mascot
	2588.1909	2588.269	0.0781	30	530	551	TMTWSRYGQLLSFTDCS GYVTR	Oxidation (M)[2]									Mascot
	2596.238	2596.1021	-0.1359	-52	1252	1275	SKNIDDIGIFALAMCNGES INENK										Mascot
	2637.3743	2637.0056	-0.3687	-140	885	909	LTGVHTTAANLDIRIPYAT DPAGNR										Mascot
	2710.2786	2710.1523	-0.1263	-47	1118	1141	WLASCGLTV AQMQSQM DPVYTPAR	Carbamidomethyl (C)[5]									Mascot
	2726.2734	2726.2109	-0.0625	-23	1118	1141	WLASCGLTV AQMQSQM DPVYTPAR	Carbamidomethyl (C)[5], Oxidation (M)[12]									Mascot
	2742.2683	2742.2615	-0.0068	-2	1118	1141	WLASCGLTV AQMQSQM DPVYTPAR	Carbamidomethyl (C)[5], Oxidation (M)[12,16]									Mascot
	2742.2683	2742.2615	-0.0068	-2	1118	1141	WLASCGLTV AQMQSQM DPVYTPAR	Carbamidomethyl (C)[5], Oxidation (M)[12,16]									Mascot
	2831.3748	2831.1399	-0.2349	-83	1227	1251	GGWNLTYPLSPVNGMD PLGLYEFK										Mascot
	2870.3633	2870.3459	-0.0174	-6	1118	1142	WLASCGLTV AQMQSQM DPVYTPARK	Carbamidomethyl (C)[5], Oxidation (M)[12,16]									Mascot
	2870.3633	2870.3459	-0.0174	-6	1118	1142	WLASCGLTV AQMQSQM DPVYTPARK	Carbamidomethyl (C)[5], Oxidation (M)[12,16]									Mascot

9	hypothetical protein XCV2641 [Xanthomonas campestris pv. vesicatoria str. 85-10]				gi 78048197		17841	6.28	5	53	0		
Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	1110.4884	1110.4871	-0.0013	-1	93	102	FGCAVAQDDK				Carbamidomethyl (C)[3]		Mascot
	1794.7687	1794.7474	-0.0213	-12	139	154	VDPHCQNGPMGSAFYR				Oxidation (M)[10]		Mascot
	2172.144	2172.0566	-0.0874	-40	27	47	OQLAASCVSVAAGQATIL LDR	27		0	Carbamidomethyl (C)[7]		Mascot
	2172.144	2172.0566	-0.0874	-40	27	47	OQLAASCVSVAAGQATIL LDR				Carbamidomethyl (C)[7]		Mascot
	2210.1353	2210.0273	-0.108	-49	118	138	GQAAIWQTQSPPGFAPAL EVNR						Mascot
	2721.447	2721.1125	-0.3345	-123	114	138	LLERGQAAIWQTQSPPGF APALEVNR						Mascot
10	RecName: Full=Glutathione amide reductase; Short=GAR				gi 387942491		49128.3	5.25	4	52	0 42 0		
Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
	1676.8577	1676.7694	-0.0883	-53	51	64	KVMWYASHLAEAVR				Oxidation (M)[3]		Mascot
	2172.1118	2172.0566	-0.0552	-25	1	22	MTQHFDLIAIGGSGGLA VAEK	45		25.262			Mascot
	2172.1118	2172.0566	-0.0552	-25	1	22	MTQHFDLIAIGGSGGLA VAEK						Mascot
	2831.4429	2831.1399	-0.303	-107	400	427	VVGVHIVGDGADEMLQG FAVAVKMGATK				Oxidation (M)[14,24]		Mascot
	3337.7031	3337.6665	-0.0366	-11	391	422	LVCAGPEQRVVGVHIVG DGADEMLQGFVAVK				Carbamidomethyl (C)[3], Oxidation (M)[23]		Mascot

Gel Idx/Pos		126/F1	Instr./Gel Origin		BA2060/140227A				Process Statu		Analysis Succeeded	
Plate [#]	Name	[1] 31564	Instrument Sample Name						Spectra		11	
Rank	Protein Name		Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %		

1	Ferredoxin--NADP reductase, leaf isozyme, chloroplastic OS=Pisum sativum GN=PETH PE=1 SV=1		FENR1_PEA	40168.6	8.56	10	335	100	291	100		
---	--	--	-----------	---------	------	----	-----	-----	-----	-----	--	--

Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type
	811.413	811.3679	-0.0451	-56	291	298	MYIQTR	7	0			Mascot	
	811.413	811.3679	-0.0451	-56	291	298	MYIQTR					Mascot	
	827.408	827.3622	-0.0458	-55	291	298	MYIQTR			Oxidation (M)[1]		Mascot	
	990.5002	990.4451	-0.0551	-56	267	274	EKAPENFR					Mascot	
	1363.6021	1363.5186	-0.0835	-61	311	321	DNTFVYMCGLK			Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot	
	1363.6021	1363.5186	-0.0835	-61	311	321	DNTFVYMCGLK	12	0	Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot	
	1378.6864	1378.6415	-0.0449	-33	225	234	SFLWKMFFEK			Oxidation (M)[6]		Mascot	
	1491.697	1491.61	-0.087	-58	310	321	KDNTFVYMCGLK			Carbamidomethyl (C)[9], Oxidation (M)[8]		Mascot	
	1623.8087	1623.7192	-0.0895	-55	297	309	MAQYAEELWELLK					Mascot	
	1630.7959	1630.7007	-0.0952	-58	140	155	LYSIASSAIGDFGDSK					Mascot	
	1630.7959	1630.7007	-0.0952	-58	140	155	LYSIASSAIGDFGDSK	88	100			Mascot	
	1639.8036	1639.7109	-0.0927	-57	297	309	MAQYAEELWELLK			Oxidation (M)[1]		Mascot	
	1751.7802	1751.7998	0.0196	11	311	325	DNTFVYMCGLKGMEK			Oxidation (M)[7]		Mascot	
	1751.9037	1751.7998	-0.1039	-59	297	310	MAQYAEELWELLK	60	99.989			Mascot	
	1787.775	1787.7998	0.0248	14	311	325	DNTFVYMCGLKGMEK			Oxidation (M)[7,13]		Mascot	
	2694.2141	2694.0713	-0.1428	-53	94	117	ITGDDAPGETWHMVFAST EGEVPYR	125	100			Mascot	
	2694.2141	2694.0713	-0.1428	-53	94	117	ITGDDAPGETWHMVFAST EGEVPYR					Mascot	
	2710.209	2710.0798	-0.1292	-48	94	117	ITGDDAPGETWHMVFAST EGEVPYR			Oxidation (M)[13]		Mascot	

2	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic OS=Nicotiana tabacum GN=PETH PE=2 SV=1		FENR1_TOBAC	40419.5	8.37	5	256	100	241	100		
---	---	--	-------------	---------	------	---	-----	-----	-----	-----	--	--

Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification		Rank	Result Type
	811.413	811.3679	-0.0451	-56	293	298	MYIQTR	7	0			Mascot	
	811.413	811.3679	-0.0451	-56	293	298	MYIQTR					Mascot	
	827.408	827.3622	-0.0458	-55	293	298	MYIQTR			Oxidation (M)[1]		Mascot	
	990.5002	990.4451	-0.0551	-56	269	276	EKAPENFR					Mascot	
	1378.6864	1378.6415	-0.0449	-33	227	236	SFLWKMFFEK			Oxidation (M)[8]		Mascot	
	2546.3105	2546.1331	-0.1774	-70	178	201	GVCSNFLCDLKPGA EVKI TGPVGK			Carbamidomethyl (C)[3,8]		Mascot	
	2546.3105	2546.1331	-0.1774	-70	178	201	GVCSNFLCDLKPGA EVKI TGPVGK	109	100	Carbamidomethyl (C)[3,8]		Mascot	
	2694.2141	2694.0713	-0.1428	-53	96	119	ITGDDAPGETWHMVFAST EGEVPYR	125	100			Mascot	

	2694.2141	2694.0713	-0.1428	-53	96	119	ITGDDAPGETWHMVFS EGEVPYR										Mascot
	2710.209	2710.0798	-0.1292	-48	96	119	ITGDDAPGETWHMVFS EGEVPYR						Oxidation (M)[13]				Mascot
3	Ferredoxin--NADP reductase, chloroplastic OS=Mesembryanthemum crystallinum GN=PETH PE=2 SV=1					FENR_MESCR	41036.9	8.54	10	241		100	196	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	811.413	811.3679	-0.0451	-56	296	301	MYIQTR			7	0			Mascot			
	811.413	811.3679	-0.0451	-56	296	301	MYIQTR							Mascot			
	827.408	827.3622	-0.0458	-55	296	301	MYIQTR					Oxidation (M)[1]		Mascot			
	990.5002	990.4451	-0.0551	-56	272	279	EKAPENFR							Mascot			
	1363.6021	1363.5186	-0.0835	-61	316	326	DNTFVVMCGLK					Carbamidomethyl (C)[8]		Mascot			
	1363.6021	1363.5186	-0.0835	-61	316	326	DNTFVVMCGLK	49	99.837			Carbamidomethyl (C)[8]		Mascot			
	1378.6864	1378.6415	-0.0449	-33	230	239	SFLWKMFEEK					Oxidation (M)[6]		Mascot			
	1379.597	1379.6017	0.0047	3	316	326	DNTFVVMCGLK					Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot			
	1491.697	1491.61	-0.087	-58	315	326	KDNTFVVMCGLK					Carbamidomethyl (C)[9]		Mascot			
	1534.8224	1534.7355	-0.0869	-57	168	180	RLYTNDNGEIVK							Mascot			
	1534.8297	1534.7355	-0.0942	-61	74	86	MEEGVIVNKYPK							Mascot			
	1751.7802	1751.7998	0.0196	11	316	330	DNTFVVMCGLKGMKEK							Mascot			
	1751.7802	1751.7998	0.0196	11	316	330	DNTFVVMCGLKGMKEK							Mascot			
	1767.775	1767.7998	0.0248	14	316	330	DNTFVVMCGLKGMKEK					Oxidation (M)[7]		Mascot			
	1959.0369	1958.9315	-0.1054	-54	211	229	DPNATIIMLATGTGIAFPR							Mascot			
	1959.0369	1958.9315	-0.1054	-54	211	229	DPNATIIMLATGTGIAFPR	140	100					Mascot			
	1975.0317	1974.9222	-0.1095	-55	211	229	DPNATIIMLATGTGIAFPR					Oxidation (M)[8]		Mascot			
	2720.3821	2720.1094	-0.2727	-100	205	229	EMLMPKDPNATIIMLATG TGIAFPR					Oxidation (M)[2,4]		Mascot			
4	Ferredoxin--NADP reductase, chloroplastic OS=Vicia faba GN=PETH PE=2 SV=1					FENR_VICFA	40552.9	8.7	9	196		100	166	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	811.413	811.3679	-0.0451	-56	294	299	MYIQTR			7	0			Mascot			
	811.413	811.3679	-0.0451	-56	294	299	MYIQTR							Mascot			
	827.408	827.3622	-0.0458	-55	294	299	MYIQTR					Oxidation (M)[1]		Mascot			
	990.5002	990.4451	-0.0551	-56	270	277	EKAPENFR							Mascot			
	1363.6021	1363.5186	-0.0835	-61	314	324	DNTFVVMCGLK					Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot			
	1363.6021	1363.5186	-0.0835	-61	314	324	DNTFVVMCGLK	12	0			Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot			
	1378.6864	1378.6415	-0.0449	-33	228	237	SFLWKMFEEK					Oxidation (M)[6]		Mascot			
	1491.697	1491.61	-0.087	-58	313	324	KDNTFVVMCGLK					Carbamidomethyl (C)[9], Oxidation (M)[8]		Mascot			
	1623.8087	1623.7192	-0.0895	-55	300	312	MAQYAEELWELLK							Mascot			
	1630.7959	1630.7007	-0.0952	-58	143	158	LYSIASSAIGDFGDSK							Mascot			
	1630.7959	1630.7007	-0.0952	-58	143	158	LYSIASSAIGDFGDSK	88	100					Mascot			
	1639.8036	1639.7109	-0.0927	-57	300	312	MAQYAEELWELLK					Oxidation (M)[1]		Mascot			
	1751.7802	1751.7998	0.0196	11	314	328	DNTFVVMCGLKGMKEK					Oxidation (M)[7]		Mascot			
	1751.9037	1751.7998	-0.1039	-59	300	313	MAQYAEELWELLKK			60	99.989			Mascot			
	1767.775	1767.7998	0.0248	14	314	328	DNTFVVMCGLKGMKEK					Oxidation (M)[7,13]		Mascot			
5	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=LFNR1 PE=1 SV=					FNRL1_ARATH	40300.6	8.32	8	135		100	107	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	811.413	811.3679	-0.0451	-56	291	296	MYIQTR			7	0			Mascot			
	811.413	811.3679	-0.0451	-56	291	296	MYIQTR							Mascot			
	827.408	827.3622	-0.0458	-55	291	296	MYIQTR					Oxidation (M)[1]		Mascot			
	856.4345	856.474	0.0395	46	35	41	KSTVCYR							Mascot			
	1363.6021	1363.5186	-0.0835	-61	311	321	DNTFVVMCGLK					Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot			
	1363.6021	1363.5186	-0.0835	-61	311	321	DNTFVVMCGLK	12	0			Carbamidomethyl (C)[8], Oxidation (M)[7]		Mascot			
	1379.71	1379.6017	-0.1083	-78	82	93	NPYTCRLLNTK							Mascot			
	1491.697	1491.61	-0.087	-58	310	321	KDNTFVVMCGLK					Carbamidomethyl (C)[9], Oxidation (M)[8]		Mascot			
	1630.7959	1630.7007	-0.0952	-58	140	155	LYSIASSAIGDFGDSK							Mascot			
	1630.7959	1630.7007	-0.0952	-58	140	155	LYSIASSAIGDFGDSK	88	100					Mascot			
	1751.7802	1751.7998	0.0196	11	311	325	DNTFVVMCGLKGMKEK					Oxidation (M)[7]		Mascot			
	1751.7802	1751.7998	0.0196	11	311	325	DNTFVVMCGLKGMKEK					Oxidation (M)[7]		Mascot			
	1767.775	1767.7998	0.0248	14	311	325	DNTFVVMCGLKGMKEK					Oxidation (M)[7,13]		Mascot			
	2417.188	2417.01	-0.178	-74	291	309	MYQTRMAEYAEELWELL K							Mascot			
6	Ferredoxin--NADP reductase, chloroplastic OS=Spinacia oleracea GN=PETH PE=1 SV=1					FENR_SPIOL	41161.9	8.67	3	124		100	116	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	811.413	811.3679	-0.0451	-56	300	305	MYIQTR			7	0			Mascot			
	811.413	811.3679	-0.0451	-56	300	305	MYIQTR							Mascot			
	827.408	827.3622	-0.0458	-55	300	305	MYIQTR					Oxidation (M)[1]		Mascot			
	1378.6864	1378.6415	-0.0449	-33	234	243	SFLWKMFEEK					Oxidation (M)[6]		Mascot			
	2546.3105	2546.1331	-0.1774	-70	185	208	GVCSNFLCDLKPGAEVK LTGPVGK					Carbamidomethyl (C)[3,8]		Mascot			
	2546.3105	2546.1331	-0.1774	-70	185	208	GVCSNFLCDLKPGAEVK LTGPVGK	109	100			Carbamidomethyl (C)[3,8]		Mascot			
7	Ferredoxin--NADP reductase, leaf isozyme, chloroplastic OS=Oryza sativa subsp. japonica GN=Os06g010					FENR1_ORYSJ	39982.3	8.72	5	106		100	95	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	811.413	811.3679	-0.0451	-56	293	298	MYIQTR			7	0			Mascot			
	811.413	811.3679	-0.0451	-56	293	298	MYIQTR							Mascot			
	827.408	827.3622	-0.0458	-55	293	298	MYIQTR					Oxidation (M)[1]		Mascot			
	1378.6864	1378.6415	-0.0449	-33	227	236	SFLWKMFEEK					Oxidation (M)[6]		Mascot			
	1465.6814	1465.6666	-0.0148	-10	293	303	MYQTRMAEYK					Oxidation (M)[1,7]		Mascot			
	1534.8224	1534.7355	-0.0869	-57	165	177	RLVYTNDQGGEVVK							Mascot			
	1534.8224	1534.7355	-0.0869	-57	165	177	RLVYTNDQGGEVVK							Mascot			
	1630.7959	1630.7007	-0.0952	-58	142	157	LYSIASSALGDFGDSK							Mascot			
	1630.7959	1630.7007	-0.0952	-58	142	157	LYSIASSALGDFGDSK	88	100					Mascot			
8	Ribulose biphosphate carboxylase large chain (Fragment) OS=Asclepias exaltata GN=rbcl PE=3 SV=2					RBL_ASCEX	48791.5	6.09	10	43		0					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification	Rank	Result Type			
	910.4451	910.3873	-0.0578	-63	154	160	AVYECLR					Carbamidomethyl (C)[5]		Mascot			
	1116.583	1116.5203	-0.0627	-56	388	397	VALEACVQAR					Carbamidomethyl (C)[6]		Mascot			
	1170.5585	1170.5649	0.0064	5	270	278	QKNHGMHFR					Oxidation (M)[6]		Mascot			
	1245.6337	1245.5575	-0.0762	-61	184	193	FLFCAEAIK					Carbamidomethyl (C)[4]		Mascot			

		1261.7151	1261.6465	-0.0686	-54	306	316	DITLGFVDLLR										Mascot
		1413.8101	1413.6416	-0.1685	-119	101	112	LEDLRIPPAYVK										Mascot
		1465.7546	1465.6666	-0.088	-60	113	125	TFQGGPHGIQVER										Mascot
		1491.7261	1491.61	-0.1161	-78	286	300	MSGGDHIYAGTVVGK										Mascot
		2076.0178	2075.9661	-0.0517	-25	286	305	MSGGDHIYAGTVVGKLE GER										Mascot
		2169.9868	2169.8572	-0.1296	-60	161	179	GGLDFTKDDENVNSQPF MR										Mascot
		2185.9819	2185.8843	-0.0976	-45	161	179	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]							Mascot
9	Ribulose biphosphate carboxylase large chain (Fragment) OS=Daphniphyllum sp. GN=rbcl PE=3 SV=1										RBL_DAPSP	51574	6.04	10	42	0		
	Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type					
	910.4451	910.3873	-0.0578	-63	178	184	AVYECLR				Carbamidomethyl (C)[5]		Mascot					
	1116.583	1116.5203	-0.0627	-56	412	421	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot					
	1170.5585	1170.5649	0.0064	5	294	302	QKNHGMHFR				Oxidation (M)[6]		Mascot					
	1245.6433	1245.5575	-0.0858	-69	430	440	EGNEIIR EASK						Mascot					
	1261.6285	1261.6465	0.018	14	208	217	FLFCAEALYK				Carbamidomethyl (C)[4]		Mascot					
	1379.6366	1379.6017	-0.0349	-25	12	22	LTYTPDPYDTK						Mascot					
	1465.7216	1465.6666	-0.055	-38	310	324	MSGGDHIHAGTVVGK						Mascot					
	1975.0746	1974.9222	-0.1524	-77	330	346	DITLGFVDLLRDDLEK						Mascot					
	2169.9868	2169.8572	-0.1296	-60	185	203	GGLDFTKDDENVNSQPF MR						Mascot					
	2185.9819	2185.8843	-0.0976	-45	185	203	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot					
	2726.2219	2726.0977	-0.1242	-46	218	242	AQAEETGEIKGHYLNATAG TCEDMMK				Carbamidomethyl (C)[20]		Mascot					
	2742.2168	2742.0601	-0.1567	-57	218	242	AQAEETGEIKGHYLNATAG TCEDMMK				Carbamidomethyl (C)[20], Oxidation (M)[23]		Mascot					
10	Subtilisin-chymotrypsin inhibitor CI-1B OS=Hordeum vulgare PE=1 SV=1										ICIB_HORVU	8957.7	5.33	5	40	0		
	Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type					
	842.5458	842.4641	-0.0817	-97	39	45	AKEILRL						Mascot					
	850.3974	850.49	0.0926	109	3	10	SMEGSVPK				Oxidation (M)[2]		Mascot					
	990.5036	990.4451	-0.0585	-59	2	10	RSMEGSVPK						Mascot					
	1491.7261	1491.61	-0.1161	-78	26	38	RSWPEVVGMSAEK				Oxidation (M)[9]		Mascot					
	1534.757	1534.7355	-0.0215	-14	27	40	SWPEVVGMSAEKAK				Oxidation (M)[8]		Mascot					
	1534.757	1534.7355	-0.0215	-14	27	40	SWPEVVGMSAEKAK				Oxidation (M)[8]		Mascot					
Gel Idx/Pos		127/F2								BA2060/140227A						Process Status		
Plate [#] Name		[1] 31564						Instr./Gel Origin		Instrument Sample Name						Analysis Succeeded		
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %					
1	Isoflavone reductase homolog OS=Solanum tuberosum PE=2 SV=1					IFRH_SOLTU	33830.8	6.16	5	161	100	142	100					
	Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type					
	850.4781	850.4382	-0.0399	-47	120	127	VHAEPAK						Mascot					
	864.4825	864.4444	-0.0381	-44	19	26	FIVEASAK						Mascot					
	1238.7142	1238.6439	-0.0703	-57	7	18	ILFIGGTGYIGK		62	99.989			Mascot					
	1238.7142	1238.6439	-0.0703	-57	7	18	ILFIGGTGYIGK						Mascot					
	1429.6382	1429.5648	-0.0734	-51	108	119	FFPSEFGNDVDR		80	100			Mascot					
	1429.6382	1429.5648	-0.0734	-51	108	119	FFPSEFGNDVDR						Mascot					
	1585.7394	1585.6883	-0.0711	-45	107	119	RFFPSEFGNDVDR						Mascot					
2	Ribulose biphosphate carboxylase large chain (Fragment) OS=Illex crenata GN=rbcl PE=3 SV=1										RBL_ILECR	51518	6.1	13	142	100	76	100
	Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type					
	832.4596	832.4293	-0.0303	-36	412	419	VALEACVK						Mascot					
	910.4451	910.4	-0.0451	-50	178	184	AVYECLR				Carbamidomethyl (C)[5]		Mascot					
	914.4049	914.3586	-0.0463	-51	296	302	NHGMHFR				Oxidation (M)[4]		Mascot					
	928.4669	928.416	-0.0509	-55	286	293	AMHAVIDR				Oxidation (M)[2]		Mascot					
	1021.5312	1021.4799	-0.0513	-50	23	31	DTDILAAFR		46	99.583			Mascot					
	1021.5312	1021.4799	-0.0513	-50	23	31	DTDILAAFR						Mascot					
	1116.6194	1116.5205	-0.0989	-89	412	421	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot					
	1187.6643	1187.6108	-0.0535	-45	276	285	DNLGLLIHHR						Mascot					
	1392.6318	1392.6185	-0.0133	-10	12	22	LNYTPDPYDTK						Mascot					
	1451.6219	1451.5433	-0.0786	-54	192	203	DDENVNSQPFMR						Mascot					
	1465.7216	1465.6748	-0.0468	-32	310	324	MSGGDHIHAGTVVGK						Mascot					
	1465.7546	1465.6748	-0.0798	-54	137	149	TFQGGPHGIQVER		31	86.928			Mascot					
	1502.8512	1502.757	-0.0942	-63	155	167	YGRPLLGTCTKPK				Carbamidomethyl (C)[8]		Mascot					
	2169.9868	2169.8657	-0.1211	-56	185	203	GGLDFTKDDENVNSQPF MR						Mascot					
	2185.9819	2185.8572	-0.1247	-57	185	203	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot					
3	Ribulose biphosphate carboxylase large chain OS=Anthoceros formosae GN=rbcl PE=2 SV=2										RBL_ANTFO	52783.5	6.09	13	138	100	78	100
	Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type					
	910.4451	910.4	-0.0451	-50	188	194	AVYECLR				Carbamidomethyl (C)[5]		Mascot					
	928.4669	928.416	-0.0509	-55	296	303	AMHAVIDR				Oxidation (M)[2]		Mascot					
	933.5515	933.4649	-0.0866	-93	9	18	AGVGFKAGVK						Mascot					
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR		46	99.583			Mascot					
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR						Mascot					
	1084.5562	1084.5367	-0.0195	-18	467	475	VFETIDTL						Mascot					
	1084.5562	1084.5367	-0.0195	-18	467	475	VFETIDTL						Mascot					
	1116.583	1116.5205	-0.0625	-56	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot					
	1164.6133	1164.5062	-0.1071	-92	304	312	QRNHGHIFR						Mascot					
	1187.6643	1187.6108	-0.0535	-45	286	295	DNLGLLIHHR						Mascot					
	1212.6266	1212.6171	-0.0095	-8	296	305	AMHAVIDRGR				Oxidation (M)[2]		Mascot					
	1451.6219	1451.5433	-0.0786	-54	202	213	DDENVNSQPFMR						Mascot					
	1465.7546	1465.6748	-0.0798	-54	147	159	TFQGGPHGIQVER						Mascot					
	1465.7546	1465.6748	-0.0798	-54	147	159	TFQGGPHGIQVER		31	86.928			Mascot					
	1502.8512	1502.757	-0.0942	-63	165	177	YGRPLLGTCTKPK				Carbamidomethyl (C)[8]		Mascot					
	2169.9868	2169.8657	-0.1211	-56	195	213	GGLDFTKDDENVNSQPF MR						Mascot					
	2185.9819	2185.8572	-0.1247	-57	195	213	GGLDFTKDDENVNSQPF MR				Oxidation (M)[18]		Mascot					
4	Ribulose biphosphate carboxylase large chain (Fragment) OS=Bertiera breviflora GN=rbcl PE=3										RBL_BERBR	51952.1	6.04	13	137	100	76	100

SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
832.4596	832.4293	-0.0303	-36	413	420	VALEACVK					Mascot
910.4451	910.4	-0.0451	-50	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3586	-0.0463	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.416	-0.0509	-55	287	294	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4799	-0.0513	-50	24	32	DTDILAAFR	46	99.583			Mascot
1021.5312	1021.4799	-0.0513	-50	24	32	DTDILAAFR					Mascot
1116.6194	1116.5205	-0.0989	-89	413	422	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.6108	-0.0535	-45	277	286	DNGLLLHIHR					Mascot
1381.6635	1381.692	0.0285	21	458	470	FNFAAVDTLDPTA					Mascot
1451.6219	1451.5433	-0.0786	-54	193	204	DDENVNSQPFMR					Mascot
1465.6603	1465.6748	0.0145	10	207	218	DRFCFCAEALYK					Mascot
1465.7546	1465.6748	-0.0798	-54	138	150	TFQGPPHGIQVER	31	86.928	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.757	-0.0942	-63	156	168	YGRPLLGTCTIKPK					Mascot
2169.9868	2169.8657	-0.1211	-56	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8572	-0.1247	-57	186	204	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot

5 Ribulose biphosphate carboxylase large chain (Fragment) OS=Galium scabrum GN=rbcl PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
832.4596	832.4293	-0.0303	-36	422	429	VALEACVK					Mascot
910.4451	910.4	-0.0451	-50	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3586	-0.0463	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.416	-0.0509	-55	296	303	AMHAVIDR			Oxidation (M)[2]		Mascot
933.5515	933.4649	-0.0866	-93	9	18	AGVGFKAGVK					Mascot
1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR	46	99.583			Mascot
1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR					Mascot
1116.6194	1116.5205	-0.0989	-89	422	431	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.6108	-0.0535	-45	286	295	DNGLLLHIHR					Mascot
1451.6219	1451.5433	-0.0786	-54	202	213	DDENVNSQPFMR					Mascot
1465.7216	1465.6748	-0.0468	-32	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6748	-0.0798	-54	147	159	TFQGPPHGIQVER	31	86.928	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.757	-0.0942	-63	165	177	YGRPLLGTCTIKPK					Mascot
2169.9868	2169.8657	-0.1211	-56	195	213	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8572	-0.1247	-57	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot

6 Ribulose biphosphate carboxylase large chain (Fragment) OS=Hydnophytum formicarum GN=rbcl PE=3 SV=

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
832.4596	832.4293	-0.0303	-36	422	429	VALEACVK					Mascot
910.4451	910.4	-0.0451	-50	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3586	-0.0463	-51	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.416	-0.0509	-55	296	303	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR	46	99.583			Mascot
1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR					Mascot
1116.6194	1116.5205	-0.0989	-89	422	431	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.6108	-0.0535	-45	286	295	DNGLLLHIHR					Mascot
1451.6219	1451.5433	-0.0786	-54	202	213	DDENVNSQPFMR					Mascot
1465.7216	1465.6748	-0.0468	-32	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6748	-0.0798	-54	147	159	TFQGPPHGIQVER	31	86.928	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.757	-0.0942	-63	165	177	YGRPLLGTCTIKPK					Mascot
2169.9868	2169.8657	-0.1211	-56	195	213	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8572	-0.1247	-57	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
2250.2393	2250.1055	-0.1338	-59	140	159	IPIAYVKTQGGPPHGIQVER					Mascot

7 Ribulose biphosphate carboxylase large chain (Fragment) OS=Isophysis tasmanica GN=rbcl PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
864.4937	864.4444	-0.0493	-57	1	9	SAGFKAGVK					Mascot
910.4451	910.4	-0.0451	-50	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3586	-0.0463	-51	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.416	-0.0509	-55	287	294	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4799	-0.0513	-50	24	32	DTDILAAFR	46	99.583			Mascot
1021.5312	1021.4799	-0.0513	-50	24	32	DTDILAAFR					Mascot
1116.583	1116.5205	-0.0625	-56	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.6108	-0.0535	-45	277	286	DNGLLLHIHR					Mascot
1451.6219	1451.5433	-0.0786	-54	193	204	DDENVNSQPFMR					Mascot
1465.7546	1465.6748	-0.0798	-54	138	150	TFQGPPHGIQVER					Mascot
1465.7546	1465.6748	-0.0798	-54	138	150	TFQGPPHGIQVER	31	86.928	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.757	-0.0942	-63	156	168	YGRPLLGTCTIKPK			Oxidation (M)[1]		Mascot
2066.9558	2066.9636	0.0078	4	311	330	MSGGDHIHAGTVVGELEGER					Mascot
2169.9868	2169.8657	-0.1211	-56	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2185.9819	2185.8572	-0.1247	-57	186	204	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot

8 Ribulose biphosphate carboxylase large chain (Fragment) OS=Ulmus alata GN=rbcl PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
832.4596	832.4293	-0.0303	-36	412	419	VALEACVK					Mascot
910.4451	910.4	-0.0451	-50	178	184	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3586	-0.0463	-51	296	302	NHGMHFR			Oxidation (M)[4]		Mascot
928.4669	928.416	-0.0509	-55	286	293	AMHAVIDR			Oxidation (M)[2]		Mascot
1021.5312	1021.4799	-0.0513	-50	23	31	DTDILAAFR	46	99.583			Mascot
1021.5312	1021.4799	-0.0513	-50	23	31	DTDILAAFR					Mascot
1084.4867	1084.5367	0.05	46	457	465	LEFEAMDTL			Oxidation (M)[6]		Mascot
1084.4867	1084.5367	0.05	46	457	465	LEFEAMDTL			Oxidation (M)[6]		Mascot
1116.6194	1116.5205	-0.0989	-89	412	421	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1187.6643	1187.6108	-0.0535	-45	276	285	DNGLLLHIHR					Mascot
1451.6219	1451.5433	-0.0786	-54	192	203	DDENVNSQPFMR					Mascot
1465.7546	1465.6748	-0.0798	-54	137	149	TFQGPPHGIQVER					Mascot
1465.7546	1465.6748	-0.0798	-54	137	149	TFQGPPHGIQVER	31	86.928			Mascot
1502.8512	1502.757	-0.0942	-63	155	167	YGRPLLGTCTIKPK			Carbamidomethyl (C)[8]		Mascot

	2169.9868	2169.8657	-0.1211	-56	185	203	GGLDFTKDDENVNSQPF MR										Mascot
	2185.9819	2185.8572	-0.1247	-57	185	203	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]				Mascot
9	Ribulose biphosphate carboxylase large chain OS=Coffea arabica GN=rbcl PE=3 SV=2					RBL_COFAR	53319.8	6.13	13	134	100	76	100				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %			Modification	Rank	Result Type		
	832.4596	832.4293	-0.0303	-36	422	429	VALEACVK								Mascot		
	910.4451	910.4	-0.0451	-50	188	194	AVYECLR						Carbamidomethyl (C)[5]		Mascot		
	914.4049	914.3586	-0.0463	-51	306	312	NHGMHFR						Oxidation (M)[4]		Mascot		
	928.4669	928.416	-0.0509	-55	296	303	AMHAVDR						Oxidation (M)[2]		Mascot		
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR	46	99.583						Mascot		
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR								Mascot		
	1116.6194	1116.5205	-0.0989	-89	422	431	VALEACVKAR						Carbamidomethyl (C)[6]		Mascot		
	1187.6643	1187.6108	-0.0535	-45	286	295	DNGLLLHIHR								Mascot		
	1373.6406	1373.7242	0.0836	61	467	477	FNFEAMDKLDK						Oxidation (M)[6]		Mascot		
	1451.6219	1451.5433	-0.0786	-54	202	213	DDENVNSQPFMR								Mascot		
	1465.7216	1465.6748	-0.0468	-32	320	334	MSGGDHIHAGTVVGK								Mascot		
	1465.7546	1465.6748	-0.0798	-54	147	159	TFQGPPHGIOVER	31	86.928						Mascot		
	1502.8512	1502.757	-0.0942	-63	165	177	YGRPLLGCTIKPK						Carbamidomethyl (C)[8]		Mascot		
	2169.9868	2169.8657	-0.1211	-56	195	213	GGLDFTKDDENVNSQPF MR								Mascot		
	2185.9819	2185.8572	-0.1247	-57	195	213	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]		Mascot		
10	Ribulose biphosphate carboxylase large chain OS=Physcomitrella patens subsp. patens GN=rbcl PE=1 S					RBL_PHYPA	52671.5	6.29	12	134	100	78	100				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %			Modification	Rank	Result Type		
	910.4451	910.4	-0.0451	-50	188	194	AVYECLR						Carbamidomethyl (C)[5]		Mascot		
	914.4049	914.3586	-0.0463	-51	306	312	NHGMHFR						Oxidation (M)[4]		Mascot		
	928.4669	928.416	-0.0509	-55	296	303	AMHAVLDR						Oxidation (M)[2]		Mascot		
	933.5515	933.4649	-0.0866	-93	9	18	AGVGFKAGVK								Mascot		
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR	46	99.583						Mascot		
	1021.5312	1021.4799	-0.0513	-50	33	41	DTDILAAFR								Mascot		
	1116.583	1116.5205	-0.0625	-56	422	431	VALEACVQAR						Carbamidomethyl (C)[6]		Mascot		
	1187.6643	1187.6108	-0.0535	-45	286	295	DNGLLLHIHR								Mascot		
	1392.6682	1392.6185	-0.0497	-36	22	32	LTYYTPDYQTK								Mascot		
	1451.6219	1451.5433	-0.0786	-54	202	213	DDENVNSQPFMR								Mascot		
	1465.7546	1465.6748	-0.0798	-54	147	159	TFQGPPHGIOVER								Mascot		
	1465.7546	1465.6748	-0.0798	-54	147	159	TFQGPPHGIOVER	31	86.928						Mascot		
	1502.8512	1502.757	-0.0942	-63	165	177	YGRPLLGCTIKPK						Carbamidomethyl (C)[8]		Mascot		
	2169.9868	2169.8657	-0.1211	-56	195	213	GGLDFTKDDENVNSQPF MR								Mascot		
	2185.9819	2185.8572	-0.1247	-57	195	213	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]		Mascot		
Gel Idx/Pos		128/F3				Instr./Gel Origin		BA2060/140227A				Process Statu		Analysis Succeeded			
Plate [#] Name		[1] 31564				Instrument Sample Name						Spectra		11			
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %				
1	Ribulose biphosphate carboxylase large chain (Fragment) OS=Sinapis alba GN=rbcl PE=3 SV=1					RBL_SINAL	52405.4	6.23	13	144	100	75	100				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %			Modification	Rank	Result Type		
	856.3546	856.4814	0.1268	148	467	473	FEFPAMD								Mascot		
	910.4451	910.3968	-0.0483	-53	188	194	AVYECLR						Carbamidomethyl (C)[5]		Mascot		
	914.4049	914.3513	-0.0536	-59	306	312	NHGMHFR						Oxidation (M)[4]		Mascot		
	1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR	22	0						Mascot		
	1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR								Mascot		
	1245.6433	1245.5615	-0.0818	-66	440	450	EGNEIIREASK						Carbamidomethyl (C)[4]		Mascot		
	1261.6285	1261.6399	0.0114	9	218	227	FLFCAEAIYK								Mascot		
	1392.6682	1392.6154	-0.0528	-38	22	32	LTYYTPDYQTK								Mascot		
	1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPHGIOVER	27	69.089						Mascot		
	1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPHGIOVER								Mascot		
	1515.7695	1515.7415	-0.028	-18	422	435	VALEACVQARNEGR								Mascot		
	1753.7883	1753.8031	0.0148	8	237	252	GHYLNATAGTCEEMIK						Oxidation (M)[14]		Mascot		
	2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR								Mascot		
	2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR	26	61.442						Mascot		
	2185.9819	2185.8633	-0.1186	-54	195	213	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]		Mascot		
	3022.4548	3022.3066	-0.1482	-49	259	285	ELGVPVIMHDYLTGGFTA NTSLAHYCR						Carbamidomethyl (C)[26]		Mascot		
	3854.8718	3854.6362	-0.2356	-61	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR								Mascot		
2	Ribulose biphosphate carboxylase large chain (Fragment) OS=Quisqualis indica GN=rbcl PE=3 SV=1					RBL_QUIN	51658	6.13	13	142	100	74	100				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %			Modification	Rank	Result Type		
	910.4451	910.3968	-0.0483	-53	178	184	AVYECLR						Carbamidomethyl (C)[5]		Mascot		
	914.4049	914.3513	-0.0536	-59	296	302	NHGMHFR						Oxidation (M)[4]		Mascot		
	1021.5312	1021.4767	-0.0545	-53	23	31	DTDILAAFR	22	0						Mascot		
	1021.5312	1021.4767	-0.0545	-53	23	31	DTDILAAFR								Mascot		
	1245.6433	1245.5615	-0.0818	-66	430	440	EGNEIIREASK								Mascot		
	1392.6682	1392.6154	-0.0528	-38	12	22	LTYYTPDYQTK								Mascot		
	1465.7216	1465.6776	-0.044	-30	310	324	MSGGDHIHAGTVVGK								Mascot		
	1465.7546	1465.6776	-0.077	-53	137	149	TFQGPPHGIOVER	27	69.089						Mascot		
	1515.7695	1515.7415	-0.028	-18	412	425	VALEACVQARNEGR								Mascot		
	1753.7883	1753.8031	0.0148	8	227	242	GHYLNATAGTCEEMIK						Oxidation (M)[14]		Mascot		
	2039.0696	2038.7991	-0.2705	-133	330	346	EITLGFVDLLRDDYIEK								Mascot		
	2118.0576	2117.948	-0.1096	-52	208	226	FLFCAEGYKAAQETGEIK								Mascot		
	2169.9868	2169.8733	-0.1135	-52	185	203	GGLDFTKDDENVNSQPF MR								Mascot		
	2169.9868	2169.8733	-0.1135	-52	185	203	GGLDFTKDDENVNSQPF MR	26	61.442						Mascot		
	2185.9819	2185.8633	-0.1186	-54	185	203	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]		Mascot		
	3854.8718	3854.6362	-0.2356	-61	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT								Mascot		



SLDR											
3	Ribulose biphosphate carboxylase large chain OS=Viscum album GN=rbcl PE=3 SV=1	RBL_VISAL	52356.5	6.44	13	141	100	74	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
910.4451	910.3968	-0.0483	-53	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
914.4049	914.3513	-0.0536	-59	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1245.6433	1245.5615	-0.0818	-66	440	450	EGNEIREASK	27	69.089			Mascot
1261.7151	1261.6399	-0.0752	-60	340	350	DTLGFVDLLR					Mascot
1465.7216	1465.6776	-0.044	-30	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPIHGIQVER					Mascot
1515.7695	1515.7415	-0.028	-18	422	435	VALEACVQARNEGR	27	69.089			Mascot
1755.7499	1755.792	0.0421	24	237	252	GHYLNATAGTCEEMMK					Mascot
2118.0576	2117.948	-0.1096	-52	218	236	FVFCAEAIYKAAETGEIK					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR	26	61.442			Mascot
2185.9819	2185.8633	-0.1186	-54	195	213	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]		Mascot
3022.4548	3022.3066	-0.1482	-49	259	285	ELGVPIMVMDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6362	-0.2356	-61	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot
4	Ribulose biphosphate carboxylase large chain OS=Pseudotsuga menziesii GN=rbcl PE=1 SV=1	RBL_PSEMZ	52694.5	6.09	13	140	100	74	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
910.4451	910.3968	-0.0483	-53	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
914.4049	914.3513	-0.0536	-59	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1245.6433	1245.5615	-0.0818	-66	440	450	EGNEVIREATK	27	69.089			Mascot
1465.7216	1465.6776	-0.044	-30	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPIHGIQVER					Mascot
1515.7695	1515.7415	-0.028	-18	422	435	VALEACVQARNEGR					Mascot
1755.7499	1755.792	0.0421	24	237	252	GHYLNATAGTCEEMMK	27	69.089			Mascot
1918.9368	1918.8544	-0.0824	-43	447	463	EATKWSPELAAACEVWK					Mascot
2118.0576	2117.948	-0.1096	-52	218	236	FVFCAEAIYKAAETGEI K					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR	26	61.442			Mascot
2185.9819	2185.8633	-0.1186	-54	195	213	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]		Mascot
3022.4548	3022.3066	-0.1482	-49	259	285	ELGVPIMVMDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6362	-0.2356	-61	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot
5	Ribulose biphosphate carboxylase large chain (Fragment) OS=Serenoa repens GN=rbcl PE=3 SV=1	RBL_SERRE	51794	6.33	13	137	100	74	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
910.4451	910.3968	-0.0483	-53	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
914.4049	914.3513	-0.0536	-59	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1245.6433	1245.5615	-0.0818	-66	440	450	EGNEIREASK	27	69.089			Mascot
1261.6285	1261.6399	0.0114	9	218	227	FLFCAEAIYK			Carbamidomethyl (C)[4]		Mascot
1465.7216	1465.6776	-0.044	-30	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPIHGIQVER					Mascot
1515.7695	1515.7415	-0.028	-18	422	435	VALEACVQARNEGR	27	69.089			Mascot
1753.7883	1753.8031	0.0148	8	237	252	GHYLNATAGTCEEMIK			Oxidation (M)[14]		Mascot
2057.0259	2056.9373	-0.0886	-43	340	356	EMTLGFVDLLRDDFIEK			Oxidation (M)[2]		Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR	26	61.442			Mascot
2185.9819	2185.8633	-0.1186	-54	195	213	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]		Mascot
3022.4548	3022.3066	-0.1482	-49	259	285	ELGVPIMVMDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6362	-0.2356	-61	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot
6	Ribulose biphosphate carboxylase large chain OS=Hyophorbe lagenicaulis GN=rbcl PE=3 SV=1	RBL_HYOLA	52928.5	6.13	13	136	100	74	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
910.4451	910.3968	-0.0483	-53	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
914.4049	914.3513	-0.0536	-59	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1021.5312	1021.4767	-0.0545	-53	33	41	DTDILAAFR					Mascot
1245.6433	1245.5615	-0.0818	-66	440	450	EGNEIREASK	27	69.089			Mascot
1261.6285	1261.6399	0.0114	9	218	227	FLFCAEAIYK			Carbamidomethyl (C)[4]		Mascot
1465.7216	1465.6776	-0.044	-30	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6776	-0.077	-53	147	159	TFQGPPIHGIQVER					Mascot
1515.7695	1515.7415	-0.028	-18	422	435	VALEACVQARNEGR	27	69.089			Mascot
1753.7883	1753.8031	0.0148	8	237	252	GHYLNATAGTCEEMIK			Oxidation (M)[14]		Mascot
2057.0259	2056.9373	-0.0886	-43	340	356	EMTLGFVDLLRDDFIEK			Oxidation (M)[2]		Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR					Mascot
2169.9868	2169.8733	-0.1135	-52	195	213	GGLDFTKDDENVNSQPF MR	26	61.442			Mascot
2185.9819	2185.8633	-0.1186	-54	195	213	GGLDFTKDDENVNSQPF MR			Oxidation (M)[18]		Mascot
3022.4548	3022.3066	-0.1482	-49	259	285	ELGVPIMVMDYLTGGFTA NTSLAHYCR			Carbamidomethyl (C)[26]		Mascot
3854.8718	3854.6362	-0.2356	-61	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot





	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	914.4002	914.3472	-0.053	-58	116	123	SPGYDGR	30	84.664			Mascot
	914.4002	914.3472	-0.053	-58	116	123	SPGYDGR					Mascot
	933.5151	933.4581	-0.057	-61	159	166	IIGFDNVR					Mascot
	933.5151	933.4581	-0.057	-61	159	166	IIGFDNVR	20	0	Carbamidomethyl (C)[6], Oxidation (M)[3]		Mascot
	2384.1294	2383.9363	-0.1931	-81	130	150	LPMFGCTDATQVLAIEVQ ECKK					Mascot
	2691.2407	2691.1245	-0.1162	-43	94	115	NGWVPCLEFETEHGFVY RENHK					Mascot
	2748.2622	2748.1501	-0.1121	-41	94	115	NGWVPCLEFETEHGFVY RENHK			Carbamidomethyl (C)[6]		Mascot
8	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Capsicum annuum GN=RBCS PE=2 SV=1				RBS_CAPAN		21185.5	6.82	4	66	99.247	49 99.796
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	914.4002	914.3472	-0.053	-58	115	122	SPGYDGR	30	84.664			Mascot
	914.4002	914.3472	-0.053	-58	115	122	SPGYDGR					Mascot
	933.5151	933.4581	-0.057	-61	158	165	IIGFDNVR					Mascot
	933.5151	933.4581	-0.057	-61	158	165	IIGFDNVR	20	0			Mascot
	1556.8328	1556.7281	-0.1047	-67	55	67	VECMVLVWPPINKK					Mascot
	2125.98	2125.9556	-0.0244	-11	94	110	GWVPCLEFETEHGFVYR			Carbamidomethyl (C)[5]		Mascot
9	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Hevea brasiliensis GN=RBCS PE=2 SV=				RBS_HEVBR		20707.3	8.7	4	66	99.135	49 99.796
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	914.4002	914.3472	-0.053	-58	117	124	SPGYDGR	30	84.664			Mascot
	914.4002	914.3472	-0.053	-58	117	124	SPGYDGR					Mascot
	933.5151	933.4581	-0.057	-61	160	167	IIGFDNVR					Mascot
	933.5151	933.4581	-0.057	-61	160	167	IIGFDNVR	20	0	Carbamidomethyl (C)[7], Oxidation (M)[18]		Mascot
	2691.2976	2691.1245	-0.1731	-64	43	66	TTTDTISIASNGRRVQCM QVWPPR					Mascot
	3337.5247	3337.5742	0.0495	15	131	159	LPMFGCTDAVQVLQELD EMIKAYPCDCYGR			Oxidation (M)[3,19]		Mascot
10	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Oryza sativa subsp. japonica GN=RBC				RBS1_ORYSJ		19633.9	9.04	4	65	98.96	49 99.796
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	914.4002	914.3472	-0.053	-58	104	111	SPGYDGR	30	84.664			Mascot
	914.4002	914.3472	-0.053	-58	104	111	SPGYDGR					Mascot
	933.5151	933.4581	-0.057	-61	147	154	IIGFDNVR					Mascot
	933.5151	933.4581	-0.057	-61	147	154	IIGFDNVR	20	0			Mascot
	1045.5571	1045.512	-0.0451	-43	21	30	STAGMPVARR					Mascot
	1165.571	1165.671	0.1	86	85	93	VVPCLEFSK			Carbamidomethyl (C)[4]		Mascot
Gel Idx/Pos	130/F5				Instr./Gel Origin			BA2060/140227A		Process Status Analysis Succeeded		
Plate [ # ] Name	[1] 31564				Instrument Sample Name					Spectra 11		
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %			
1	Oxygen-evolving enhancer protein 1, chloroplastic OS=Spinacia oleracea GN=PSBO PE=1 SV=1	PSBO_SPIOL	35148.9	5.58	9	349	100	301	100			
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	964.5865	964.5229	-0.0636	-66	207	214	VPFLFTIK					Mascot
	964.5865	964.5229	-0.0636	-66	207	214	VPFLFTIK	51	99.902			Mascot
	1096.5521	1096.4832	-0.0689	-63	90	98	LTIDEIQSK					Mascot
	1252.6532	1252.5736	-0.0796	-64	89	98	RLTYDEIQSK	24	49.871			Mascot
	1252.6532	1252.5736	-0.0796	-64	89	98	RLTYDEIQSK					Mascot
	1760.8813	1760.7664	-0.1149	-65	190	206	DGIDYAAVTQLPGGER	134	100			Mascot
	1760.8813	1760.7664	-0.1149	-65	190	206	DGIDYAAVTQLPGGER					Mascot
	1977.0764	1976.887	-0.1894	-96	2	20	AASLQASTTFLQPTKVAS R					Mascot
	2284.1606	2284.0127	-0.1479	-65	215	235	QLVASGKPEFSFGDFLV PSYR					Mascot
	2294.1299	2293.9822	-0.1477	-64	186	206	FEKKGIDYAAVTQLPG GER	91	100			Mascot
	2294.1299	2293.9822	-0.1477	-64	186	206	FEKKGIDYAAVTQLPG GER					Mascot
	2300.1179	2300.0061	-0.1118	-49	165	185	LTYTLEIEGPFVSSDG TVK					Mascot
	3229.7295	3229.4216	-0.3079	-95	207	235	VPFLFTIKQLVASGKPE FSGDFLVPSYR					Mascot
2	Oxygen-evolving enhancer protein 1, chloroplastic OS=Solanum lycopersicum GN=PSBO PE=2 SV=2	PSBO_SOLL	34925.9	5.91	8	340	100	301	100			
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	964.5865	964.5229	-0.0636	-66	206	213	VPFLFTIK					Mascot
	964.5865	964.5229	-0.0636	-66	206	213	VPFLFTIK	51	99.902			Mascot
	1096.5521	1096.4832	-0.0689	-63	89	97	LTIDEIQSK					Mascot
	1252.6532	1252.5736	-0.0796	-64	88	97	RLTYDEIQSK	24	49.871			Mascot
	1252.6532	1252.5736	-0.0796	-64	88	97	RLTYDEIQSK					Mascot
	1328.6556	1328.5901	-0.0954	-72	133	143	FQLEPTSTFTVK			Carbamidomethyl (C)[2]		Mascot
	1456.7505	1456.6499	-0.1006	-69	132	143	KFQLEPTSTFTVK			Carbamidomethyl (C)[3]		Mascot
	1760.8813	1760.7664	-0.1149	-65	189	205	DGIDYAAVTQLPGGER	134	100			Mascot
	1760.8813	1760.7664	-0.1149	-65	189	205	DGIDYAAVTQLPGGER					Mascot
	2294.1299	2293.9822	-0.1477	-64	185	205	FEKKGIDYAAVTQLPG GER	91	100			Mascot
	2294.1299	2293.9822	-0.1477	-64	185	205	FEKKGIDYAAVTQLPG GER					Mascot
	2310.1387	2309.9917	-0.147	-64	164	184	LTYTLEIEGPFVSPDG TVK					Mascot
3	Oxygen-evolving enhancer protein 1, chloroplastic OS=Helianthus annuus GN=PSBO PE=1 SV=1	PSBO_HELAN	34202.3	5.4	7	332	100	301	100			
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	964.5865	964.5229	-0.0636	-66	201	208	VPFLFTIK					Mascot
	964.5865	964.5229	-0.0636	-66	201	208	VPFLFTIK	51	99.902			Mascot

		1096.5521	1096.4832	-0.0689	-63	84	92	LTIDEIQSK										Mascot
		1189.6609	1189.5824	-0.0785	-66	18	28	VQLKSSPSICK										Mascot
		1252.6532	1252.5736	-0.0796	-64	83	92	RLTYDEIQSK	24	49.871							Mascot	
		1252.6532	1252.5736	-0.0796	-64	83	92	RLTYDEIQSK									Mascot	
		1328.6555	1328.5601	-0.0954	-72	128	138	FCLEPTSFTVK									Mascot	
		1760.8813	1760.7664	-0.1149	-65	184	200	DGIDYAAVTQLPGGER	134	100							Mascot	
		1760.8813	1760.7664	-0.1149	-65	184	200	DGIDYAAVTQLPGGER									Mascot	
		2294.1299	2293.9822	-0.1477	-64	180	200	FEKKGIDYAAVTQLPG GER	91	100							Mascot	
		2294.1299	2293.9822	-0.1477	-64	180	200	FEKKGIDYAAVTQLPG GER									Mascot	
4	Oxygen-evolving enhancer protein 1, chloroplastic OS=Nicotiana tabacum GN=PSBO PE=2 SV=1	PSBO_TOBAC 35206 5.89 7 307 100 277 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
		964.5865	964.5229	-0.0636	-66	209	216	VPFLFTIK					Mascot					
		964.5865	964.5229	-0.0636	-66	209	216	VPFLFTIK	51	99.902			Mascot					
		1145.595	1145.4816	-0.1134	-99	153	162	NAPPDFQKTK					Mascot					
		1328.6555	1328.5601	-0.0954	-72	136	146	FCLEPTSFTVK			Carbamidomethyl (C)[2]		Mascot					
		1456.7505	1456.6499	-0.1006	-69	135	146	KFCLEPTSFTVK			Carbamidomethyl (C)[3]		Mascot					
		1760.8813	1760.7664	-0.1149	-65	192	208	DGIDYAAVTQLPGGER	134	100			Mascot					
		1760.8813	1760.7664	-0.1149	-65	192	208	DGIDYAAVTQLPGGER					Mascot					
		2294.1299	2293.9822	-0.1477	-64	188	208	FEKKGIDYAAVTQLPG GER	91	100			Mascot					
		2294.1299	2293.9822	-0.1477	-64	188	208	FEKKGIDYAAVTQLPG GER					Mascot					
		2300.1179	2300.0061	-0.1118	-49	167	187	LTYLDEIEGPFVSSDG TVK					Mascot					
5	Oxygen-evolving enhancer protein 1, chloroplastic OS=Solanum tuberosum GN=PSBO PE=2 SV=1	PSBO_SOLTU 35367 5.84 7 307 100 277 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
		964.5865	964.5229	-0.0636	-66	209	216	VPFLFTIK					Mascot					
		964.5865	964.5229	-0.0636	-66	209	216	VPFLFTIK	51	99.902			Mascot					
		1307.6631	1307.5745	-0.0886	-68	323	333	IQGIWYAQLES					Mascot					
		1328.6555	1328.5601	-0.0954	-72	136	146	FCLEPTSFTVK			Carbamidomethyl (C)[2]		Mascot					
		1456.7505	1456.6499	-0.1006	-69	135	146	KFCLEPTSFTVK			Carbamidomethyl (C)[3]		Mascot					
		1760.8813	1760.7664	-0.1149	-65	192	208	DGIDYAAVTQLPGGER	134	100			Mascot					
		1760.8813	1760.7664	-0.1149	-65	192	208	DGIDYAAVTQLPGGER					Mascot					
		2294.1299	2293.9822	-0.1477	-64	188	208	FEKKGIDYAAVTQLPG GER	91	100			Mascot					
		2294.1299	2293.9822	-0.1477	-64	188	208	FEKKGIDYAAVTQLPG GER					Mascot					
		2310.1387	2309.9917	-0.147	-64	167	187	LTYLDEIEGPFVSPDG TVK					Mascot					
6	Oxygen-evolving enhancer protein 1, chloroplastic OS=Pisum sativum GN=PSBO PE=2 SV=1	PSBO_PEA 34871.8 6.25 5 296 100 277 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
		964.5865	964.5229	-0.0636	-66	205	212	VPFLFTIK					Mascot					
		964.5865	964.5229	-0.0636	-66	205	212	VPFLFTIK	51	99.902			Mascot					
		1760.8813	1760.7664	-0.1149	-65	188	204	DGIDYAAVTQLPGGER	134	100			Mascot					
		1760.8813	1760.7664	-0.1149	-65	188	204	DGIDYAAVTQLPGGER					Mascot					
		2284.1606	2284.0127	-0.1479	-65	213	233	QLVASGKPDSPFSGEFLV PSYR					Mascot					
		2294.1299	2293.9822	-0.1477	-64	184	204	FEKKGIDYAAVTQLPG GER	91	100			Mascot					
		2294.1299	2293.9822	-0.1477	-64	184	204	FEKKGIDYAAVTQLPG GER					Mascot					
		3229.7295	3229.4216	-0.3079	-95	205	233	VPFLFTIKQLVASGKPDSPFSGEFLVPSYR					Mascot					
7	Oxygen-evolving enhancer protein 1, chloroplastic OS=Triticum aestivum GN=PSBO PE=2 SV=1	PSBO_WHEAT 34718.7 8.73 9 271 100 225 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
		842.4076	842.4568	0.0492	58	122	128	AGKYEMK			Oxidation (M)[6]		Mascot					
		1328.6555	1328.5601	-0.0954	-72	130	140	FCLEPTSFTVK			Carbamidomethyl (C)[2]		Mascot					
		1456.7505	1456.6499	-0.1006	-69	129	140	KFCLEPTSFTVK			Carbamidomethyl (C)[3]		Mascot					
		1760.8813	1760.7664	-0.1149	-65	186	202	DGIDYAAVTQLPGGER	134	100			Mascot					
		1760.8813	1760.7664	-0.1149	-65	186	202	DGIDYAAVTQLPGGER					Mascot					
		1950.0138	1949.8661	-0.1477	-76	266	284	ENVKNASSSTGNITLSVT K					Mascot					
		2267.1411	2266.9939	-0.1472	-65	157	175	LMTRLTYTLDEMEGPLEV R					Mascot					
		2267.1411	2266.9939	-0.1472	-65	157	175	LMTRLTYTLDEMEGPLEV R					Mascot					
		2292.2498	2292.0015	-0.2483	-108	211	230	QLVATGKPESFRPFLVPS YR					Mascot					
		2294.1299	2293.9822	-0.1477	-64	182	202	FEKKGIDYAAVTQLPG GER	91	100			Mascot					
		2294.1299	2293.9822	-0.1477	-64	182	202	FEKKGIDYAAVTQLPG GER					Mascot					
		2306.2173	2305.9917	-0.2256	-98	62	85	MAGFALATSALLVSGATA EGAPKR			Oxidation (M)[1]		Mascot					
8	Oxygen-evolving enhancer protein 1, chloroplastic (Fragments) OS=Populus euphratica GN=PSBO PE=1 SV	PSBO_POPEU 10664.5 5.36 4 238 100 210 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
		964.5865	964.5229	-0.0636	-66	48	55	VPFLFTIK					Mascot					
		964.5865	964.5229	-0.0636	-66	48	55	VPFLFTIK	51	99.902			Mascot					
		1096.5521	1096.4832	-0.0689	-63	2	10	LTIDEIQSK					Mascot					
		1252.6532	1252.5736	-0.0796	-64	1	10	RLTYDEIQSK	24	49.871			Mascot					
		1252.6532	1252.5736	-0.0796	-64	1	10	RLTYDEIQSK					Mascot					
		1760.8813	1760.7664	-0.1149	-65	31	47	DGIDYAAVTQLPGGER	134	100			Mascot					
		1760.8813	1760.7664	-0.1149	-65	31	47	DGIDYAAVTQLPGGER					Mascot					
9	Oxygen-evolving enhancer protein 1, chloroplastic OS=Fritillaria agrestis GN=PSBO PE=2 SV=1	PSBO_FRIAG 34847.8 6.26 2 229 100 224 100																
Peptide Information		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					

	1760.8813	1760.7664	-0.1149	-65	189	205	DGIDYAAVTVQLPGER	134	100				Mascot		
	1760.8813	1760.7664	-0.1149	-65	189	205	DGIDYAAVTVQLPGER						Mascot		
	2294.1299	2293.9822	-0.1477	-64	185	205	FEEDKGIDYAAVTVQLPGER	91	100				Mascot		
	2294.1299	2293.9822	-0.1477	-64	185	205	FEEDKGIDYAAVTVQLPGER						Mascot		
10	Oxygen-evolving enhancer protein 1-2, chloroplastic OS=Arabidopsis thaliana GN=PSBO2 PE=1 SV=1					PSBO2_ARATH	34997.7	5.92	6	220	100	196	100		
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	1096.5521	1096.4832	-0.0689	-63	91	99	LTIDEIQSK						Mascot		
	1252.6532	1252.5736	-0.0796	-64	90	99	RLTYDEIQSK	24	49.871				Mascot		
	1252.6532	1252.5736	-0.0796	-64	90	99	RLTYDEIQSK						Mascot		
	1433.7134	1433.667	-0.0464	-32	134	145	KCFEPTSFTVK						Mascot		
	1949.9313	1949.8661	-0.0652	-33	135	151	FCFEPTSFTVKADSVSK				Carbamidomethyl (C)[2]		Mascot		
	2294.1299	2293.9822	-0.1477	-64	187	207	FKEEDGIDYAAVTVQLPGER	67	99.997				Mascot		
	2294.1299	2293.9822	-0.1477	-64	187	207	FKEEDGIDYAAVTVQLPGER						Mascot		
	2604.304	2604.1416	-0.1624	-62	291	315	SKPETGEVIGVFESLQPSDTDLGAK						Mascot		
	2604.304	2604.1416	-0.1624	-62	291	315	SKPETGEVIGVFESLQPSDTDLGAK	104	100				Mascot		
Gel Idx/Pos	131/F6					Instr./Gel Origin					BA2060/140227A			Process Status	
Plate [#] Name	[1] 31564					Instrument Sample Name								Analysis Succeeded	
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	11	
1	Ribulose biphosphate carboxylase small chain clone 512 (Fragment) OS=Triticum aestivum PE=3 SV=1					RBS3_WHEAT	13046.5	5.84	6	41	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	1165.571	1165.6602	0.0892	77	23	31	WVPCLEFSK				Carbamidomethyl (C)[4]		Mascot		
	1974.9377	1974.8884	-0.0493	-25	77	92	EYPDAYVRIIGFDNMR				Oxidation (M)[15]		Mascot		
	2211.0571	2210.9431	-0.114	-52	93	112	QVQCVSFIAPKPPGCEESGK				Carbamidomethyl (C)[4]		Mascot		
	2225.073	2224.9575	-0.1155	-52	93	113	QVQCVSFIAPKPPGCEESGKA						Mascot		
	2239.062	2238.9648	-0.0972	-43	56	75	LPMFGCTDATQVINEVEEVK				Oxidation (M)[3]		Mascot		
	3191.4885	3191.1492	-0.3393	-106	50	75	YWTMWKLPMPGCTDATQVINEVEEVK				Carbamidomethyl (C)[12], Oxidation (M)[4]		Mascot		
2	Coproporphyrinogen-III oxidase, chloroplastic OS=Oryza sativa subsp. japonica GN=CPX PE=2 SV=2					HEM6_ORYSJ	43843.9	6.23	9	40	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	875.4879	875.4048	-0.0831	-95	45	52	GALGMRVR				Oxidation (M)[5]		Mascot		
	882.458	882.506	0.048	54	240	246	HFHSVOK						Mascot		
	1051.5353	1051.6376	0.1023	97	85	92	ERFEAMIR						Mascot		
	1499.7377	1499.6962	-0.0415	-28	60	72	ETPESEPPPTFLR						Mascot		
	1573.7104	1573.7446	0.0342	22	247	259	QACDKFDPSPFYPR						Mascot		
	1634.7809	1634.827	0.0461	28	204	218	YFETDAPKDAPGAPR						Mascot		
	1974.9297	1974.8884	-0.0413	-21	93	111	RVQGEVCAALEEADGSGAR				Carbamidomethyl (C)[7]		Mascot		
	2211.1802	2210.9431	-0.2371	-107	1	23	MAPSLTTPSQALALAPGAAASR				Oxidation (M)[1]		Mascot		
	3105.4951	3105.0762	-0.4189	-135	212	239	DAPGAPRQWVFGGTDLTSPVIIIEDVK						Mascot		
3	Aliphatic (R)-hydroxynitrile lyase OS=Linum usitatissimum PE=1 SV=1					AHNL_LINUS	45753.2	5.6	9	37	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	842.5094	842.4526	-0.0568	-67	243	249	QIIVVDR						Mascot		
	882.3994	882.506	0.1066	121	57	64	MLCASVCR				Carbamidomethyl (C)[3,7]		Mascot		
	996.4423	996.5294	0.0871	87	57	64	MLCASVCR				Carbamidomethyl (C)[5,9], Oxidation (M)[3]		Mascot		
	1239.6006	1239.4431	-0.1575	-127	55	64	VKMLCASVCR						Mascot		
	1381.7798	1381.6967	-0.0831	-60	271	283	LPEGVTPSOAVRK						Mascot		
	1634.7335	1634.827	0.0935	57	256	270	MAMELGATHCINSEK						Mascot		
	1932.934	1932.7814	-0.1526	-79	254	270	LKMAMELGATHCINSEK				Carbamidomethyl (C)[12]		Mascot		
	1948.929	1948.7931	-0.1359	-70	254	270	LKMAMELGATHCINSEK				Carbamidomethyl (C)[12], Oxidation (M)[3]		Mascot		
	1964.9238	1964.7953	-0.1285	-65	254	270	LKMAMELGATHCINSEK				Carbamidomethyl (C)[12], Oxidation (M)[3,5]		Mascot		
	1975.0681	1974.8884	-0.1797	-91	2	20	ASLPVSFAKPKNGVITCK						Mascot		
	2804.3489	2804.0745	-0.2744	-98	57	81	MLCASVCRTDILTIEGFMAPTQFPK				Oxidation (M)[1,18]		Mascot		
	2849.3218	2849.094	-0.2278	-80	284	309	LTPKEVGVDASIESGGYDVFMNEAMK				Oxidation (M)[21,25]		Mascot		
	2849.3218	2849.094	-0.2278	-80	284	309	LTPKEVGVDASIESGGYDVFMNEAMK				Oxidation (M)[21,25]		Mascot		
4	Peptide methionine sulfoxide reductase B5 OS=Arabidopsis thaliana GN=MSRB5 PE=2 SV=1					MSRB5_ARATH	15241.4	5.62	5	32	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	1281.5957	1281.5389	-0.0568	-44	31	42	GTEKPGTGEYDK						Mascot		
	1493.6439	1493.6384	-0.0055	-4	43	55	FFEEGIDFCVGCK						Mascot		
	2014.9585	2014.6736	-0.2849	-141	92	109	RTEITCAACDGHLGHVFK				Carbamidomethyl (C)[6]		Mascot		
	2014.9585	2014.6736	-0.2849	-141	92	109	RTEITCAACDGHLGHVFK				Carbamidomethyl (C)[6]		Mascot		
	2615.2346	2614.8987	-0.3359	-128	61	84	STTKFDSGCGWPAFFEGLPGAIR				Carbamidomethyl (C)[9]		Mascot		
	2615.2346	2614.8987	-0.3359	-128	61	84	STTKFDSGCGWPAFFEGLPGAIR				Carbamidomethyl (C)[9]		Mascot		
	2870.2646	2870.2261	-0.0385	-13	31	55	GTEKPGTGEYDKFFEEGIFDCVGCK				Carbamidomethyl (C)[21,24]		Mascot		
5	(3S,6E)-nerolidol synthase 1, chloroplastic OS=Fraxia vesca PE=1 SV=1					NES1_FRAVE	66489.8	6.31	10	32	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	882.4501	882.506	0.0559	63	235	242	SLASFMAR						Mascot		
	996.5359	996.5294	-0.0065	-7	120	127	EIDEILHK						Mascot		
	1045.5902	1045.4922	-0.098	-94	37	44	QLPTFQRR						Mascot		

	1177.5347	1177.5103	-0.0244	-21	1	10	MASSSWAFFK							Oxidation (M)[1]		Mascot
	1177.5347	1177.5103	-0.0244	-21	1	10	MASSSWAFFK							Oxidation (M)[1]		Mascot
	1493.7305	1493.6384	-0.0921	-62	513	524	EKTINMISDEWK									Mascot
	1794.9167	1794.6931	-0.2236	-125	20	35	SISHIGSDLMQLTHK									Mascot
	2057.0083	2056.8726	-0.1357	-66	550	567	MIPLMYSYDGNQSLPSLK									Mascot
	2172.0947	2171.9631	-0.1316	-61	1	19	MASSSWAFFKVFNQIA PK							Oxidation (M)[1]		Mascot
	2172.0947	2171.9631	-0.1316	-61	1	19	MASSSWAFFKVFNQIA PK							Oxidation (M)[1]		Mascot
	2230.2112	2230.032	-0.1792	-80	455	475	KSVELLNETPAMISSAAI LR									Mascot
	2239.0925	2238.9648	-0.1277	-57	356	373	WEITAIHLPDYMKICFK							Oxidation (M)[13] 0		Mascot
6	Proteinase inhibitor IIA (Fragment) OS=Solanum tuberosum PE=1 SV=1										IP2A_SOLTU	4952.1	5.05	4	31	
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	875.3853	875.4048	0.0195	22	1	8	SEGSPENR									Mascot
	1622.6573	1622.7638	0.1065	66	19	32	GCNYNCDTNIASYK							Carbamidomethyl (C)[2]		Mascot
	2056.8811	2056.8726	-0.0085	-4	1	18	SEGSPENRICTNNCAGY K							Carbamidomethyl (C)[10,14]		Mascot
	2804.1531	2804.0745	-0.0786	-28	9	32	ICTNNCAGYKGCYNCD TNIASYK							Carbamidomethyl (C)[2,6,12]		Mascot
7	Beta-glucosidase 10 OS=Oryza sativa subsp. japonica GN=BGLU10 PE=2 SV=1										BGL10_ORYSJ	60814	8.42	9	31	0
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	850.4417	850.4809	0.0392	46	190	196	EFGDRVK									Mascot
	882.4468	882.506	0.0592	67	112	118	FSISWSR									Mascot
	1045.4659	1045.4922	0.0263	25	182	189	DYAEICFK							Carbamidomethyl (C)[6]		Mascot
	1622.7955	1622.7638	-0.0317	-20	332	345	GDYPLSMRELVGNR							Oxidation (M)[7]		Mascot
	1675.7897	1675.6772	-0.1125	-67	505	518	FGINFVDYDNGMKR									Mascot
	1965.048	1964.7953	-0.2527	-129	292	308	IGILNSEWVFVPSQSK									Mascot
	2225.062	2224.9575	-0.1045	-47	42	63	GFIFGTSSSYQFEGAAA KGGK									Mascot
	2804.3608	2804.0745	-0.2863	-102	317	339	VLDFMLGWFMPLIRGD YPLSMR							Oxidation (M)[5,10]		Mascot
	3794.9463	3794.5417	-0.4046	-107	1	37	MAVAGAMVMSSGVLILL LAFTCAAYNDAGELPPIS RR							Oxidation (M)[1]		Mascot
8	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase 2, chloroplastic OS=Chlamydomonas										CTH1_CHLRE	47451	8.7	9	31	0
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	996.4965	996.5294	0.0329	33	1	8	MATMLNKR							Oxidation (M)[1,4]		Mascot
	1177.6112	1177.5103	-0.1009	-86	108	116	HFVRNETFK									Mascot
	1177.6112	1177.5103	-0.1009	-86	108	116	HFVRNETFK									Mascot
	1381.7039	1381.6967	-0.0072	-5	209	219	FIFYATYLYSEK									Mascot
	1465.7031	1465.6461	-0.057	-39	137	149	SCTAEFSGFLLYK									Mascot
	1932.9966	1932.7814	-0.2152	-111	328	343	IFPAVPDVENPEFFRR									Mascot
	1975.0317	1974.8884	-0.1433	-73	350	367	YNAQLVNIGSMNLPSPK							Oxidation (M)[11]		Mascot
	2057.053	2056.8726	-0.1804	-88	209	224	FIFYATYLYSEKGYWR									Mascot
	2749.3376	2749.1079	-0.2297	-84	279	299	LWSRFFCLSVYITMYLND HOR							Carbamidomethyl (C)[7]		Mascot
	2870.2932	2870.2261	-0.0671	-23	79	101	LFSLELNKNMDMEEFEA MLNEFK							Oxidation (M)[10,12,18]		Mascot
9	Ras-related protein RABA5d OS=Arabidopsis thaliana GN=RABA5D PE=2 SV=1										RAA5D_ARATH	24346	5.26	6	30	0
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	882.4315	882.506	0.0745	84	98	105	STFESVGR									Mascot
	1493.745	1493.6384	-0.1066	-71	121	133	MLVGNKCDLESIR							Oxidation (M)[1]		Mascot
	1622.6526	1622.7638	0.1112	69	1	14	MSSDDEGGEEYLFK							Oxidation (M)[1]		Mascot
	1634.8054	1634.827	0.0216	13	127	141	CDLESIRAVSVEEGK									Mascot
	2267.1223	2266.9502	-0.1721	-76	43	62	ATIGVEFQTNMEIEGKE VK							Oxidation (M)[12]		Mascot
	3337.6331	3337.541	-0.0921	-28	142	171	ALAEETGLFFMETSALDS TNVKTAFEMVR							Oxidation (M)[11]		Mascot
10	Flap endonuclease 1-A OS=Physcomitrella patens subsp. patens GN=FEN1-A PE=3 SV=1										FEN11_PHYPA	43623.7	9	8	29	0
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	856.525	856.4659	-0.0591	-69	372	380	TAAAVKPAK									Mascot
	1189.5695	1189.5149	-0.0546	-46	357	368	KEAPDSEASAGK									Mascot
	1493.807	1493.6384	-0.1686	-113	9	22	LIADNAHGAVKEQK									Mascot
	1593.8595	1593.6838	-0.1757	-110	253	266	QHSLEIVLENLNK									Mascot
	1948.8956	1948.7931	-0.1025	-53	173	190	VFAVASEDMDSLTYGST R									Mascot
	1964.8906	1964.7953	-0.0953	-49	173	190	VFAVASEDMDSLTYGST R							Oxidation (M)[9]		Mascot
	1974.9515	1974.8884	-0.0631	-32	337	355	ASQGRLESFFGVSSSSS NK									Mascot
	2691.2673	2691.1086	-0.1587	-59	148	172	LMGVPPVEAPSEAEAEK ASLCKAEK							Carbamidomethyl (C)[17,21], Oxidation (M)[2]		Mascot
	2849.3845	2849.094	-0.2905	-102	49	74	SGSELLTNDAGEVTSHL QGMFNRRTIR							Oxidation (M)[20]		Mascot
	2849.3845	2849.094	-0.2905	-102	49	74	SGSELLTNDAGEVTSHL QGMFNRRTIR							Oxidation (M)[20]		Mascot
Gel Idx/Pos		132/F7		Instr./Gel Origin		BA2060/140227A		Process Statu		Analysis Succeeded						
Plate [#] Name		[1] 31564		Instrument Sample Name				Spectra		11						
Rank	Protein Name		Accession No.		Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Total Ion Score	Total Ion C. I. %					
1	Ribulose biphosphate carboxylase large chain (Fragment) OS=Sinapis alba GN=rbcl PE=3 SV=1		RBL_SINAL		52405.4	6.23	14	76	99.925	7	0					
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence					Ion Score	C. I. %	Modification	Rank	Result Type
	856.3546	856.4741	0.1195	140	467	473	FEFPAMD									Mascot
	910.4451	910.3906	-0.0545	-60	188	194	AVYECLR							Carbamidomethyl (C)[5]		Mascot
	914.4049	914.3532	-0.0517	-57	306	312	NHGMHFR							Oxidation (M)[4]		Mascot

	1021.5312	1021.4725	-0.0587	-57	33	41	DTDILAFR										Mascot
	1116.583	1116.5402	-0.0428	-38	422	431	VALEACVQAR										Mascot
	1170.5585	1170.5723	0.0138	12	304	312	QKNHGMHFR							Carbamidomethyl (C)[6]			Mascot
	1187.6643	1187.5925	-0.0718	-60	286	295	DNGLLLHIHR							Oxidation (M)[6]			Mascot
	1245.6433	1245.5608	-0.0825	-66	440	450	EGNEIIREASK										Mascot
	1261.6285	1261.6349	0.0064	5	218	227	FLFCAEAIYK							Carbamidomethyl (C)[4]			Mascot
	1392.6682	1392.6106	-0.0576	-41	22	32	LTYYTPDYQTK										Mascot
	1465.7546	1465.6689	-0.0857	-58	147	159	TFQGGPHGIOVER			7		0					Mascot
	1465.7546	1465.6689	-0.0857	-58	147	159	TFQGGPHGIOVER										Mascot
	1502.8512	1502.7402	-0.111	-74	165	177	YGRPLLGGTIKPK							Carbamidomethyl (C)[8]			Mascot
	1794.8149	1794.7175	-0.0974	-54	237	252	GHYLNATAGTCEEMIK							Carbamidomethyl (C)[11]			Mascot
	2169.9868	2169.8538	-0.133	-61	195	213	GGLDFTKDDENVNSQPF										Mascot
							MR										
	2185.9819	2185.8555	-0.1264	-58	195	213	GGLDFTKDDENVNSQPF							Oxidation (M)[18]			Mascot
							MR										
2	Ribulose biphosphate carboxylase large chain (Fragment) OS=Cornus obliqua GN=rbcl PE=3 SV=2			RBL_COROB			51536.8			6	13	72	99.767	7	0		
Peptide Information																	
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification	Rank	Result Type			
910.4451	910.3906	-0.0545	-60	178	184	AVYECLR						Carbamidomethyl (C)[5]		Mascot			
914.4049	914.3532	-0.0517	-57	296	302	NHGMHFR						Oxidation (M)[4]		Mascot			
1021.5312	1021.4725	-0.0587	-57	23	31	DTDILAFR								Mascot			
1116.583	1116.5402	-0.0428	-38	412	421	VALEACVQAR						Carbamidomethyl (C)[6]		Mascot			
1170.5585	1170.5723	0.0138	12	294	302	QKNHGMHFR						Oxidation (M)[6]		Mascot			
1187.6643	1187.5925	-0.0718	-60	276	285	DNGLLLHIHR								Mascot			
1245.6433	1245.5608	-0.0825	-66	430	440	EGNEIIREASK								Mascot			
1261.6285	1261.6349	0.0064	5	208	217	FLFCAEAIYK						Carbamidomethyl (C)[4]		Mascot			
1381.6635	1381.7002	0.0367	27	12	22	LYTHTPEYETK								Mascot			
1465.7546	1465.6689	-0.0857	-58	137	149	TFQGGPHGIOVER			7		0			Mascot			
1465.7546	1465.6689	-0.0857	-58	137	149	TFQGGPHGIOVER								Mascot			
1502.8512	1502.7402	-0.111	-74	155	167	YGRPLLGGTIKPK						Carbamidomethyl (C)[8]		Mascot			
1794.8149	1794.7175	-0.0974	-54	227	242	GHYLNATAGTCEEMIK						Carbamidomethyl (C)[11]		Mascot			
2169.9868	2169.8538	-0.133	-61	185	203	GGLDFTKDDENVNSQPF											



Gel Idx/Pos		133/F8		Instr/Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate # Name		[1] 31564		Instrument Sample Name				Spectra		11	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %		
1	BTB/POZ domain-containing protein At5g48130 OS=Arabidopsis thaliana GN=At5g48130 PE=2 SV=1	Y5813_ARATH	71317.4	8.04	11	38	0				
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence	Ion	C. I. %	Modification	Rank Result Type

				Seq.	Seq.		Score
1130.6205	1130.5032	-0.1173	-104	213	221	IINQDTWIK	
1165.6323	1165.6589	0.0266	23	36	46	ETGLPASVHVR	
1215.5497	1215.4994	-0.0503	-41	429	439	GSICSYLNCQK	
1265.6493	1265.6077	-0.0416	-33	516	525	NRPLCFLMQK	
1329.5925	1329.6136	0.0211	16	429	439	GSICSYLNCQK	
1333.7627	1333.5857	-0.177	-133	369	379	VGKLWDIFLSR	
1882.9672	1882.814	-0.1532	-81	287	302	FVPVGFYFACLAHNLK	
2040.9438	2040.9061	-0.0377	-18	171	188	CIESLAFTACMEILDPER	
2040.9438	2040.9061	-0.0377	-18	171	188	CIESLAFTACMEILDPER	
2056.9387	2056.9055	-0.0332	-16	171	188	CIESLAFTACMEILDPER	
2273.1687	2272.8799	-0.2888	-127	284	302	AYRFPVPGFYFACLAHNLK	
2273.1687	2272.8799	-0.2888	-127	284	302	AYRFPVPGFYFACLAHNLK	
2289.1292	2288.8789	-0.2503	-109	575	595	NTFGQVTTACIGSVSFTSQRK	
2663.4443	2663.0972	-0.3471	-130	133	154	FDLYLNQVVLQNWDDTLVVLKK	
2748.312	2748.0842	-0.2278	-83	516	538	NRPLCFLMQKDATLDEFESTSR	

2 Valine-tRNA ligase OS=Arabidopsis thaliana GN=VALRS PE=1 SV=2 SYV\_ARATH 125846.4 6.69 15 38 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
856.525	856.4589	-0.0661	-77	769	775	INLDLR		
882.4944	882.5027	0.0083	9	387	393	YKHLHGK		
1051.608	1051.6333	0.0253	24	1	8	MSLLFLRR		
1215.4769	1215.4994	0.0225	19	276	284	ECFTMDEQR		
1252.6255	1252.5889	-0.0366	-29	776	785	VVGYSRQWCNK		
1329.6695	1329.6112	-0.0549	-41	757	768	FALVSITACSDK		
1382.7072	1382.6636	-0.0436	-32	786	796	LWNAVRFAMMK		
1515.8101	1515.7649	-0.0462	-30	304	315	DIRLVNWDILR		
1708.8071	1708.792	-0.0151	-9	424	438	TPAHDPNDCVEGKR		
1858.8925	1858.8341	-0.0584	-31	1059	1074	MMSVSTYEEKVPANIK		
1993.0364	1992.9081	-0.1283	-64	673	689	LGGEVFPKSVYFPMIR		
2159.9485	2159.8982	-0.0503	-23	267	284	LGASLDWSRECFMTDEQR		
2225.2136	2224.9634	-0.2502	-112	986	1005	SHELEIRTLANLSSLEVVS		
2402.0742	2401.8831	-0.1911	-80	109	129	RDASEENPEDFVDPETPLGER		
2663.4436	2663.0972	-0.3464	-130	696	720	MSKSLGNVIDPLEVINGVTLEGLHK		

3 Bowman-Birk type proteinase inhibitor I-2B (Fragment) OS=Triticum aestivum PE=1 SV=1 IBB1\_WHEAT 6218.9 8.67 6 37 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
842.4553	842.452	-0.0033	-4	18	24	SIPPICR		
854.3712	854.3812	0.01	12	50	56	VCCDQYV		
1045.4731	1045.4873	0.0142	14	38	48	ACGPSVGDPSR		
1201.5742	1201.4822	-0.092	-77	38	49	ACGPSVGDPSRR		
1201.5742	1201.4822	-0.092	-77	38	49	ACGPSVGDPSRR		
1992.8871	1992.9081	0.021	11	9	24	CDDQAVCTRSIPPICR		
2272.9893	2272.8799	-0.1094	-48	18	37	SIPPICRCMDQVFECPSTCK		
2272.9893	2272.8799	-0.1094	-48	18	37	SIPPICRCMDQVFECPSTCK		

4 Protein FRIGIDA OS=Arabidopsis thaliana GN=FRIGIDA PE=2 SV=1 FRIGI\_ARATH 68400 9.15 12 36 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
940.4556	940.4042	-0.0514	-55	447	453	MYNQIK		
1045.5889	1045.4873	-0.1016	-97	288	296	STDLLDLR		
1130.6125	1130.5032	-0.1093	-97	171	180	LMEIEPSALK		
1333.6892	1333.5857	-0.1035	-78	297	309	MSGSEIAGALKR		
1384.6204	1384.731	0.1106	80	148	158	MCELMCSKGLR		
1625.8104	1625.7628	-0.0476	-29	511	525	SPEYMVPLPHGGLGR		
1882.9908	1882.814	-0.1768	-94	58	74	SIDELAAFSVAVETFKR		
1993.0786	1992.9081	-0.1705	-86	310	327	SQFLVPMVSGIVESSIKR		
2230.0986	2230.0024	-0.0962	-43	75	93	QFDDLQKHIESIENAIKSK		
2273.0398	2272.8799	-0.1599	-70	327	345	RGMHIEALEMYYTFGME		
2273.0398	2272.8799	-0.1599	-70	327	345	RGMHIEALEMYYTFGME		
2289.0349	2288.8789	-0.156	-68	327	345	RGMHIEALEMYYTFGME		
2321.1299	2320.9124	-0.2175	-94	378	398	EAATKQLAVLSSVMQCM		
2402.1877	2401.8831	-0.3046	-127	383	403	QLAVLSSVMQCMETHKL		

5 F-box protein SKP2B OS=Arabidopsis thaliana GN=SKP2B PE=1 SV=1 SKP2B\_ARATH 39882.9 7.45 10 36 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
842.5458	842.452	-0.0938	-111	92	98	LQTLVLR		
850.4087	850.4736	0.0649	76	1	8	MVSEGATR		
1256.5649	1256.6405	0.0756	60	10	19	ELNLQFENMK		
1384.6599	1384.731	0.0711	51	9	19	KELNLQFENMK		
1465.729	1465.6582	-0.0708	-48	47	59	TVIIASCICSGWR		
1710.8567	1710.7552	-0.1015	-59	247	259	CIHLRSLGLYCR		
1710.8567	1710.7552	-0.1015	-59	247	259	CIHLRSLGLYCR		
1993.0171	1992.9081	-0.109	-55	130	147	ITDHSLSYLARGCTNLTK		
2230.186	2230.0024	-0.1836	-82	20	38	MEGVLISEWKDIPVELLMK		
2321.2104	2320.9124	-0.298	-128	47	68	TVIIASCICSGWRDAVSL		
2807.332	2807.1184	-0.2136	-76	327	350	HSLVMGSLNLQSVHCA		

6 ABC transporter I family member 1 OS=Arabidopsis thaliana GN=ABC1 PE=2 SV=1 AB11\_ARATH 25959.1 9.82 7 35 0

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %

	Mascot
	Mascot
	Mascot
Oxidation (M)[8]	Mascot
Carbamidomethyl (C)[4,9]	Mascot
	Mascot
Carbamidomethyl (C)[10]	Mascot
	Mascot
Oxidation (M)[11]	Mascot
Carbamidomethyl (C)[13]	Mascot
Carbamidomethyl (C)[13]	Mascot
Carbamidomethyl (C)[10]	Mascot
	Mascot
	Mascot

Modification	Rank	Result Type
		Mascot
		Mascot
Oxidation (M)[1]		Mascot
Carbamidomethyl (C)[2]		Mascot
		Mascot
		Mascot
Oxidation (M)[9]		Mascot
Carbamidomethyl (C)[10]		Mascot
Oxidation (M)[1,2]		Mascot
Oxidation (M)[15]		Mascot
Oxidation (M)[14]		Mascot
		Mascot
		Mascot

Modification	Rank	Result Type
		Mascot
Carbamidomethyl (C)[6]		Mascot
Carbamidomethyl (C)[1,2,7,15]		Mascot
Oxidation (M)[9]		Mascot
Oxidation (M)[9]		Mascot

Modification	Rank	Result Type
		Mascot
Oxidation (M)[1]		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[2,6]		Mascot
Oxidation (M)[5]		Mascot
		Mascot
Oxidation (M)[7]		Mascot
		Mascot
Oxidation (M)[3]		Mascot
Oxidation (M)[3]		Mascot
Oxidation (M)[3,10]		Mascot
Oxidation (M)[14]		Mascot
Carbamidomethyl (C)[11], Oxidation (M)[9]		Mascot

Modification	Rank	Result Type
		Mascot
		Mascot
		Mascot
Oxidation (M)[9]		Mascot
Oxidation (M)[10]		Mascot
Carbamidomethyl (C)[7]		Mascot
Carbamidomethyl (C)[1,12]		Mascot
Carbamidomethyl (C)[1,12]		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[8,16,18], Oxidation (M)[5]		Mascot

		842.4842	842.452	-0.0322	-38	21	27	NAOQILR						Oxidation (M)[1,4]	Mascot
		854.3859	854.3812	-0.0047	-6	138	144	MLSMGQR							Mascot
		882.5308	882.5027	-0.0281	-32	209	215	LPPRFRR							Mascot
		1256.6997	1256.6405	-0.0592	-47	176	185	LLEYIAEHR							Mascot
		1384.7947	1384.731	-0.0637	-46	176	186	LLEYIAEHRK							Mascot
		1924.0731	1923.8792	-0.1939	-101	5	20	RPOIPLRLLLQNVSCMR							Mascot
		2057.1106	2056.9055	-0.2051	-100	11	27	LLQNVSCMRNAQOILR							Mascot
7	Small RNA degrading nuclease 3 OS=Arabidopsis thaliana GN=SDN3 PE=1 SV=1	SDN3_ARATH	87410.2	6.72	10	35	0	14	0						
	Peptide Information	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type		
		842.5345	842.452	-0.0825	-98	295	302	LVLAAVEK					Mascot		
		856.5039	856.4589	-0.045	-53	331	337	AQLFLHK					Mascot		
		1045.5889	1045.4873	-0.1016	-97	204	213	ATLSVADIQK					Mascot		
		1051.4976	1051.6333	0.1357	129	721	728	EEMELKEK			Oxidation (M)[2]		Mascot		
		1130.6165	1130.5032	-0.1133	-100	42	52	KLGSLSLDPAR					Mascot		
		1165.6398	1165.6589	0.0191	16	674	684	GGLAQKMVAFK			Oxidation (M)[7]		Mascot		
		1457.6866	1457.6975	0.0109	7	92	103	QETPDKETPEQR					Mascot		
		1457.6866	1457.6975	0.0109	7	92	103	QETPDKETPEQR					Mascot		
		1923.8535	1923.8792	0.0257	13	420	436	MVGDDSPCEISTSERAR					Mascot		
		2272.9917	2272.8799	-0.1118	-49	145	164	MLSIDCEMVTCEDGSQA LVR			Carbamidomethyl (C)[6], Oxidation (M)[1]		Mascot		
		2272.9917	2272.8799	-0.1118	-49	145	164	MLSIDCEMVTCEDGSQA LVR	14	0	Carbamidomethyl (C)[6], Oxidation (M)[8]		Mascot		
		2288.9866	2288.8789	-0.1077	-47	145	164	MLSIDCEMVTCEDGSQA LVR			Carbamidomethyl (C)[6], Oxidation (M)[1,8]		Mascot		
		2321.1084	2320.9124	-0.196	-84	645	664	YYNAVTFNSPEEANKAF EK					Mascot		
8	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic OS=Draba nemorosa GN	ACCD_DRANE	55809.3	6.98	10	35	0								
	Peptide Information	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type		
		1265.6484	1265.6077	-0.0407	-32	13	23	GELEYRSGLNK					Mascot		
		1329.6355	1329.6136	-0.0219	-16	380	391	ISSVLCDYQSSK					Mascot		
		1457.7305	1457.6975	-0.033	-23	380	392	ISSVLCDYQSSKK					Mascot		
		1457.7305	1457.6975	-0.033	-23	380	392	ISSVLCDYQSSKK					Mascot		
		1465.6584	1465.6582	-0.0012	-1	129	140	SNDLHDYPYVK					Mascot		
		1469.6797	1469.6532	-0.0265	-18	367	379	MQEGSLSLMQMAK			Oxidation (M)[1]		Mascot		
		1485.6746	1485.6444	-0.0302	-20	367	379	MQEGSLSLMQMAK			Oxidation (M)[1,9]		Mascot		
		1485.6746	1485.6444	-0.0302	-20	367	379	MQEGSLSLMQMAK			Oxidation (M)[1,9]		Mascot		
		1710.7284	1710.7552	0.0268	16	240	253	VMENVCEECHGYLK			Carbamidomethyl (C)[6]		Mascot		
		1710.7284	1710.7552	0.0268	16	240	253	VMENVCEECHGYLK			Carbamidomethyl (C)[6]		Mascot		
		2229.9763	2230.0024	0.0261	12	141	159	NTKSNCCNNHNSCIDSYF R					Mascot		
		2321.1992	2320.9124	-0.2868	-124	345	366	LIEYATNQCLPLILVCSSG GAR					Mascot		
		2402.0244	2401.8831	-0.1413	-59	240	259	VMENVCEECHGYLKMTS SER			Carbamidomethyl (C)[6]		Mascot		
		2691.4321	2691.095	-0.3371	-125	342	366	ITRLIEYATNQCLPLILVCS SGGAR					Mascot		
		2748.4534	2748.0842	-0.3692	-134	342	366	ITRLIEYATNQCLPLILVCS SGGAR			Carbamidomethyl (C)[12]		Mascot		
9	Soybean toxin 17 kDa chain (Fragment) OS=Glycine max PE=1 SV=1	SBTXB_SOYBN	2756.3	4.68	3	34	0								
	Peptide Information	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type		
		854.3964	854.3812	-0.0152	-18	19	25	IVMEEYA					Mascot		
		870.3913	870.4827	0.0914	105	19	25	IVMEEYA			Oxidation (M)[3]		Mascot		
		1485.7155	1485.6444	-0.0711	-48	5	18	VFFDMTIGGQSAGR					Mascot		
		1485.7155	1485.6444	-0.0711	-48	5	18	VFFDMTIGGQSAGR					Mascot		
		2321.094	2320.9124	-0.1816	-78	5	25	VFFDMTIGGQSAGRIVME EYA					Mascot		
10	Cytochrome P450 83B1 OS=Arabidopsis thaliana GN=CYP83B1 PE=1 SV=1	C83B1_ARATH	56809.6	8.52	10	33	0								
	Peptide Information	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type		
		882.4389	882.5027	0.0638	72	318	324	YPEAMKK					Mascot		
		1265.5687	1265.6077	0.039	31	477	487	MDVMTGLAMHK			Oxidation (M)[5]		Mascot		
		1384.6171	1384.731	0.1139	82	128	138	MCMVNLVSPNR			Oxidation (M)[1,4]		Mascot		
		1465.7832	1465.6582	-0.125	-85	35	47	GLPIIGNLHMQEK			Carbamidomethyl (C)[2], Oxidation (M)[1]		Mascot		
		1578.8022	1578.6332	-0.169	-107	426	439	GQDFELLPGSGRR			Oxidation (M)[11]		Mascot		
		2148.1587	2147.9045	-0.2542	-118	337	355	GYVSEEDINLPYLKAVIK					Mascot		
		2297.1462	2297.0061	-0.1401	-61	128	146	MCMVNLVSPNRVASFRP VR			Carbamidomethyl (C)[2], Oxidation (M)[1]		Mascot		
		2402.2085	2401.8831	-0.3254	-135	242	261	ELDTYLQELLDETDPNR PK					Mascot		
		2691.3643	2691.095	-0.2693	-100	439	461	RMCPAMHLGIAMVEIPFA NLLYK			Carbamidomethyl (C)[3], Oxidation (M)[2]		Mascot		
		2748.4089	2748.0842	-0.3247	-118	239	261	AFKELDTYLQELLDETLD PNRPK					Mascot		
Gel Idx/Pos	134/F9	Instr./Gel Origin								BA2060/140227A		Process Statu		Analysis Succeeded	
Plate [#] Name	[1] 31564	Instrument Sample Name										Spectra		11	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %	Rank	Result Type				
1	Ribulose biphosphate carboxylase large chain OS=Carica papaya GN=rbcl PE=3 SV=2	RBL_CARPA	52456.6	6.19	18	569	100	449	100						
	Peptide Information	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type		
		898.41	898.3533	-0.0567	-63	306	312	NHGMHFR					Mascot		
		910.4451	910.3836	-0.0615	-68	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot		
		910.4451	910.3836	-0.0615	-68	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot		
		914.4049	914.3448	-0.0601	-66	306	312	NHGMHFR			Oxidation (M)[4]		Mascot		
		1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAR					Mascot		
		1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAR	57	99.963			Mascot		
		1116.583	1116.5095	-0.0735	-66	422	431	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot		
		1170.5585	1170.5521	-0.0064	-5	304	312	QKNHGMHFR			Oxidation (M)[6]		Mascot		
		1187.6643	1187.5826	-0.0817	-69	286	295	DNGLLLIHR					Mascot		
		1245.6433	1245.5469	-0.0974	-78	440	450	EGNEIREASK					Mascot		
		1245.6433	1245.5469	-0.0974	-78	440	450	EGNEIREASK					Mascot		
		1261.6285	1261.6268	-0.0017	-1	218	227	FLFCAEAIYK			Carbamidomethyl (C)[4]		Mascot		
		1261.7151	1261.6268	-0.0883	-70	340	350	DTLFGVDLLR	39	97.581			Mascot		
		1285.6859	1285.6572	-0.0287	-22	436	446	DLAREGNEIIR					Mascot		

1392.6682	1392.5826	-0.0856	-61	22	32	LYTYTPDYQTK	50	99.806		Mascot
1392.6682	1392.5826	-0.0856	-61	22	32	LYTYTPDYQTK				Mascot
1451.6219	1451.5211	-0.1008	-69	202	213	DDENVNSQPFMR				Mascot
1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER	81	100		Mascot
1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER				Mascot
1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK	7	0	Carbamidomethyl (C)[8]	Mascot
1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]	Mascot
1546.7358	1546.6255	-0.1103	-71	451	463	WSPELAAACEVWK			Carbamidomethyl (C)[9]	Mascot
1794.8149	1794.6927	-0.1222	-68	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]	Mascot
2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR				Mascot
2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR	77	100		Mascot
2185.9819	2185.8284	-0.1535	-70	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]	Mascot
3854.8718	3854.6101	-0.2617	-68	42	79	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR				Mascot
3854.8718	3854.6101	-0.2617	-68	42	79	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR	118	100		Mascot

2 Ribulose biphosphate carboxylase large chain (Fragment) OS=Aesculus pavia GN=rbcl PE=3 SV=2 RBL\_AESPA 51619 6.18 18 560 100 443 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
898.41	898.3533	-0.0567	-63	297	303	NHGMHFR					Mascot
910.4451	910.3836	-0.0615	-68	179	185	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
910.4451	910.3836	-0.0615	-68	179	185	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3448	-0.0601	-66	297	303	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4636	-0.0676	-66	24	32	DTDLAAFR	57	99.963			Mascot
1021.5312	1021.4636	-0.0676	-66	24	32	DTDLAAFR					Mascot
1116.583	1116.5095	-0.0735	-66	413	422	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5521	-0.0064	-5	295	303	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.5826	-0.0817	-69	277	286	DNGLLLHIHR					Mascot
1245.6337	1245.5459	-0.0878	-70	209	218	FLFCAEAIK	45	99.395	Carbamidomethyl (C)[4]		Mascot
1245.6337	1245.5459	-0.0878	-70	209	218	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6268	-0.0883	-70	331	341	DTLGFVDLLR	39	97.581			Mascot
1261.7151	1261.6268	-0.0883	-70	331	341	DTLGFVDLLR					Mascot
1285.6859	1285.6572	-0.0287	-22	427	437	DLAREGNEIR					Mascot
1451.6219	1451.5211	-0.1008	-69	193	204	DDENVNSQPFMR					Mascot
1465.7216	1465.6512	-0.0704	-48	311	325	MSGGDHIHAGTVVGK	81	100			Mascot
1465.7546	1465.6512	-0.1034	-71	138	150	TFQGPPIHGIQVER					Mascot
1471.7137	1471.684	-0.0297	-20	455	466	EIKFEFQAMDTL					Mascot
1502.8512	1502.7397	-0.1115	-74	156	168	YGRPLLGCTIKPK	7	0	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.7397	-0.1115	-74	156	168	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]		Mascot
1546.7358	1546.6255	-0.1103	-71	442	454	WSPELAAACEVWK			Carbamidomethyl (C)[9]		Mascot
1794.8149	1794.6927	-0.1222	-68	228	243	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot
2169.9868	2169.8325	-0.1543	-71	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2169.9868	2169.8325	-0.1543	-71	186	204	GGLDFTKDDENVNSQPFMR	77	100			Mascot
2185.9819	2185.8284	-0.1535	-70	186	204	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3854.8718	3854.6101	-0.2617	-68	33	70	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot
3854.8718	3854.6101	-0.2617	-68	33	70	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR	118	100			Mascot

3 Ribulose biphosphate carboxylase large chain (Fragment) OS=Actinidia chinensis GN=rbcl PE=3 SV=1 RBL\_ACTCH 51553 6.23 17 554 100 445 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
898.41	898.3533	-0.0567	-63	296	302	NHGMHFR					Mascot
910.4451	910.3836	-0.0615	-68	178	184	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
910.4451	910.3836	-0.0615	-68	178	184	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3448	-0.0601	-66	296	302	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4636	-0.0676	-66	23	31	DTDLAAFR	57	99.963			Mascot
1021.5312	1021.4636	-0.0676	-66	23	31	DTDLAAFR					Mascot
1116.583	1116.5095	-0.0735	-66	412	421	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1170.5585	1170.5521	-0.0064	-5	294	302	QKNHGMHFR			Oxidation (M)[6]		Mascot
1187.6643	1187.5826	-0.0817	-69	276	285	DNGLLLHIHR					Mascot
1245.6337	1245.5459	-0.0878	-70	208	217	FLFCAEAIK	45	99.395	Carbamidomethyl (C)[4]		Mascot
1245.6337	1245.5459	-0.0878	-70	208	217	FLFCAEAIK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.6268	-0.0883	-70	330	340	DTLGFVDLLR	39	97.581			Mascot
1261.7151	1261.6268	-0.0883	-70	330	340	DTLGFVDLLR					Mascot
1285.6859	1285.6572	-0.0287	-22	426	436	DLAREGNEIR					Mascot
1451.6219	1451.5211	-0.1008	-69	192	203	DDENVNSQPFMR					Mascot
1465.7216	1465.6512	-0.0704	-48	310	324	MSGGDHIHAGTVVGK	81	100			Mascot
1465.7546	1465.6512	-0.1034	-71	137	149	TFQGPPIHGIQVER					Mascot
1471.7137	1471.684	-0.0297	-20	454	465	EIKFEFQAMDTL					Mascot
1502.8512	1502.7397	-0.1115	-74	155	167	YGRPLLGCTIKPK	7	0	Carbamidomethyl (C)[8]		Mascot
1502.8512	1502.7397	-0.1115	-74	155	167	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]		Mascot
1546.7358	1546.6255	-0.1103	-71	441	453	WSPELAAACEVWK			Carbamidomethyl (C)[9]		Mascot
2169.9868	2169.8325	-0.1543	-71	185	203	GGLDFTKDDENVNSQPFMR					Mascot
2169.9868	2169.8325	-0.1543	-71	185	203	GGLDFTKDDENVNSQPFMR	77	100			Mascot
2185.9819	2185.8284	-0.1535	-70	185	203	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot
3854.8718	3854.6101	-0.2617	-68	32	69	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR					Mascot
3854.8718	3854.6101	-0.2617	-68	32	69	VTQPQGVPPPEAGAAVA AESSTGTWTTVWTDGLT SLDR	118	100			Mascot

4 Ribulose biphosphate carboxylase large chain (Fragment) OS=Acer saccharum GN=rbcl PE=3 SV=1 RBL\_ACESA 51546 6.19 17 551 100 443 100

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
898.41	898.3533	-0.0567	-63	296	302	NHGMHFR					Mascot
910.4451	910.3836	-0.0615	-68	178	184	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot
910.4451	910.3836	-0.0615	-68	178	184	AVYECLR			Carbamidomethyl (C)[5]		Mascot
914.4049	914.3448	-0.0601	-66	296	302	NHGMHFR			Oxidation (M)[4]		Mascot
1021.5312	1021.4636	-0.0676	-66	23	31	DTDLAAFR	57	99.963			Mascot
1021.5312	1021.4636	-0.0676	-66	23	31	DTDLAAFR					Mascot

	1116.583	1116.5095	-0.0735	-66	412	421	VALEACVQAR						Carbamidomethyl (C)[6]	Mascot
	1170.5585	1170.5521	-0.0064	-5	294	302	QKNHGMHFR						Oxidation (M)[6]	Mascot
	1187.6643	1187.5826	-0.0817	-69	276	285	DNGLLLHIHR							Mascot
	1245.6337	1245.5459	-0.0878	-70	208	217	FLFCAEAIFK	45	99.395				Carbamidomethyl (C)[4]	Mascot
	1245.6337	1245.5459	-0.0878	-70	208	217	FLFCAEAIFK						Carbamidomethyl (C)[4]	Mascot
	1261.7151	1261.6268	-0.0883	-70	330	340	DITLGFVDLLR	39	97.581					Mascot
	1261.7151	1261.6268	-0.0883	-70	330	340	DITLGFVDLLR							Mascot
	1285.6859	1285.6572	-0.0287	-22	426	436	DLAREGNEIR							Mascot
	1451.6219	1451.5211	-0.1008	-69	192	203	DDENVNSQPFMR							Mascot
	1465.7216	1465.6512	-0.0704	-48	310	324	MSGGDHIIAGTVVGK							Mascot
	1465.7546	1465.6512	-0.1034	-71	137	149	TFQGPPIHGIQVER	81	100					Mascot
	1471.7137	1471.684	-0.0297	-20	454	465	EIKFQFEAMDTL							Mascot
	1502.8512	1502.7397	-0.1115	-74	155	167	YGRPLLGCTIKPK						Carbamidomethyl (C)[8]	Mascot
	1502.8512	1502.7397	-0.1115	-74	155	167	YGRPLLGCTIKPK	7	0				Carbamidomethyl (C)[8]	Mascot
	1794.8149	1794.6927	-0.1222	-68	227	242	GHYLNATAGTCEEMIK						Carbamidomethyl (C)[11]	Mascot
	2169.9868	2169.8325	-0.1543	-71	185	203	GGLDFTKDDENVNSQPFMR							Mascot
	2169.9868	2169.8325	-0.1543	-71	185	203	GGLDFTKDDENVNSQPFMR	77	100					Mascot
	2185.9819	2185.8284	-0.1535	-70	185	203	GGLDFTKDDENVNSQPFMR						Oxidation (M)[18]	Mascot
	3854.8718	3854.6101	-0.2617	-68	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR							Mascot
	3854.8718	3854.6101	-0.2617	-68	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR	118	100					Mascot
5	Ribulose biphosphate carboxylase large chain OS=Manihot esculenta GN=rbcl PE=3 SV=1					RBL_MANES	52648.5	6.18	16	546	100	449	100	
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	898.41	898.3533	-0.0567	-63	306	312	NHGMHFR							Mascot
	910.4451	910.3836	-0.0615	-68	188	194	AVYECLR	22	0		Carbamidomethyl (C)[5]		Mascot	
	910.4451	910.3836	-0.0615	-68	188	194	AVYECLR				Carbamidomethyl (C)[5]		Mascot	
	914.4049	914.3448	-0.0601	-66	306	312	NHGMHFR				Oxidation (M)[4]		Mascot	
	1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR						Mascot	
	1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR	57	99.963				Mascot	
	1116.583	1116.5095	-0.0735	-66	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot	
	1170.5585	1170.5521	-0.0064	-5	304	312	QKNHGMHFR				Oxidation (M)[6]		Mascot	
	1187.6643	1187.5826	-0.0817	-69	286	295	DNGLLLHIHR						Mascot	
	1261.6285	1261.6268	-0.0017	-1	218	227	FLFCAEAIFK				Carbamidomethyl (C)[4]		Mascot	
	1261.7151	1261.6268	-0.0883	-70	340	350	DITLGFVDLLR	39	97.581				Mascot	
	1392.6682	1392.5826	-0.0856	-61	22	32	LTYYTPDYQTK	50	99.806				Mascot	
	1392.6682	1392.5826	-0.0856	-61	22	32	LTYYTPDYQTK						Mascot	
	1451.6219	1451.5211	-0.1008	-69	202	213	DDENVNSQPFMR						Mascot	
	1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER	81	100				Mascot	
	1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER						Mascot	
	1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot	
	1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK	7	0		Carbamidomethyl (C)[8]		Mascot	
	1546.7358	1546.6255	-0.1103	-71	451	463	WSPELAAACEVWK				Carbamidomethyl (C)[9]		Mascot	
	1794.8149	1794.6927	-0.1222	-68	237	252	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot	
	2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR						Mascot	
	2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR	77	100				Mascot	
	2185.9819	2185.8284	-0.1535	-70	195	213	GGLDFTKDDENVNSQPFMR				Oxidation (M)[18]		Mascot	
	3854.8718	3854.6101	-0.2617	-68	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR						Mascot	
	3854.8718	3854.6101	-0.2617	-68	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR	118	100				Mascot	
6	Ribulose biphosphate carboxylase large chain OS=Gossypium hirsutum GN=rbcl PE=3 SV=2					RBL_GOSHI	52667.3	5.91	17	542	100	443	100	
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	898.41	898.3533	-0.0567	-63	306	312	NHGMHFR							Mascot
	910.4451	910.3836	-0.0615	-68	188	194	AVYECLR	22	0		Carbamidomethyl (C)[5]		Mascot	
	910.4451	910.3836	-0.0615	-68	188	194	AVYECLR				Carbamidomethyl (C)[5]		Mascot	
	914.4049	914.3448	-0.0601	-66	306	312	NHGMHFR				Oxidation (M)[4]		Mascot	
	1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR						Mascot	
	1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR	57	99.963				Mascot	
	1116.583	1116.5095	-0.0735	-66	422	431	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot	
	1170.5585	1170.5521	-0.0064	-5	304	312	QKNHGMHFR				Oxidation (M)[6]		Mascot	
	1187.6643	1187.5826	-0.0817	-69	286	295	DNGLLLHIHR						Mascot	
	1245.6337	1245.5459	-0.0878	-70	218	227	FLFCAEAIFK	45	99.395		Carbamidomethyl (C)[4]		Mascot	
	1245.6337	1245.5459	-0.0878	-70	218	227	FLFCAEAIFK				Carbamidomethyl (C)[4]		Mascot	
	1261.7151	1261.6268	-0.0883	-70	340	350	DITLGFVDLLR	39	97.581				Mascot	
	1261.7151	1261.6268	-0.0883	-70	340	350	DITLGFVDLLR						Mascot	
	1285.6859	1285.6572	-0.0287	-22	436	446	DLAREGNEIR						Mascot	
	1451.6219	1451.5211	-0.1008	-69	202	213	DDENVNSQPFMR						Mascot	
	1465.7216	1465.6512	-0.0704	-48	320	334	MSGGDHIIAGTVVGK						Mascot	
	1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER	81	100				Mascot	
	1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot	
	1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK	7	0		Carbamidomethyl (C)[8]		Mascot	
	1546.7358	1546.6255	-0.1103	-71	451	463	WSPELAAACEVWK				Carbamidomethyl (C)[9]		Mascot	
	1794.8149	1794.6927	-0.1222	-68	237	252	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot	
	2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR						Mascot	
	2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR	77	100				Mascot	
	2185.9819	2185.8284	-0.1535	-70	195	213	GGLDFTKDDENVNSQPFMR				Oxidation (M)[18]		Mascot	
	3854.8718	3854.6101	-0.2617	-68	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR						Mascot	
	3854.8718	3854.6101	-0.2617	-68	42	79	VTPQPGVPPEEAGAAVA AESSTGTWTTVWDGLT SLDR	118	100				Mascot	
7	Ribulose biphosphate carboxylase large chain (Fragment) OS=Capsicum baccatum GN=rbcl PE=3 SV=1					RBL_CAPBA	51997.3	6.54	16	542	100	443	100	
	Peptide Information													
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type	
	898.41	898.3533	-0.0567	-63	297	303	NHGMHFR							Mascot
	910.4451	910.3836	-0.0615	-68	179	185	AVYECLR	22	0		Carbamidomethyl (C)[5]		Mascot	

910.4451	910.3836	-0.0615	-68	179	185	AVYECLR				Carbamidomethyl (C)[5]	Mascot
914.4049	914.3448	-0.0601	-66	297	303	NHGMHFR				Oxidation (M)[4]	Mascot
1021.5312	1021.4636	-0.0676	-66	24	32	DTDILAAFR					Mascot
1021.5312	1021.4636	-0.0676	-66	24	32	DTDILAAFR	57	99.963			Mascot
1170.5585	1170.5521	-0.0064	-5	295	303	QKNHGMHFR				Oxidation (M)[6]	Mascot
1187.6643	1187.5826	-0.0817	-69	277	286	DNGLLLHIHR					Mascot
1245.6337	1245.5459	-0.0878	-70	209	218	FLFCAEALFK	45	99.395		Carbamidomethyl (C)[4]	Mascot
1245.6337	1245.5459	-0.0878	-70	209	218	FLFCAEALFK				Carbamidomethyl (C)[4]	Mascot
1261.6205	1261.6268	0.0063	5	431	441	EGNEIREACK					Mascot
1261.7151	1261.6268	-0.0883	-70	331	341	DITLGFVDLLR	39	97.581			Mascot
1285.6859	1285.6572	-0.0287	-22	427	437	DLAREGNEIIR					Mascot
1451.6219	1451.5211	-0.1008	-69	193	204	DDENVNSQPFMR					Mascot
1465.7216	1465.6512	-0.0704	-48	311	325	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6512	-0.1034	-71	138	150	TFQGPPIHGIQVER	81	100			Mascot
1502.8512	1502.7397	-0.1115	-74	156	168	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]	Mascot
1502.8512	1502.7397	-0.1115	-74	156	168	YGRPLLGCTIKPK	7	0		Carbamidomethyl (C)[8]	Mascot
1546.7358	1546.6255	-0.1103	-71	442	454	WSPELAAACEVWK				Carbamidomethyl (C)[9]	Mascot
2169.9868	2169.8325	-0.1543	-71	186	204	GGLDFTKDDENVNSQPFMR					Mascot
2169.9868	2169.8325	-0.1543	-71	186	204	GGLDFTKDDENVNSQPFMR	77	100			Mascot
2185.9819	2185.8284	-0.1535	-70	186	204	GGLDFTKDDENVNSQPFMR				Oxidation (M)[18]	Mascot
3854.8718	3854.6101	-0.2617	-68	33	70	VTPQGPVPPEEAGAAVA					Mascot
						AESSTGTWTTVWTDGLTSLDR					
3854.8718	3854.6101	-0.2617	-68	33	70	VTPQGPVPPEEAGAAVA	118	100			Mascot
						AESSTGTWTTVWTDGLTSLDR					

8 Ribulose biphosphate carboxylase large chain RBL\_SOLTU 52910.8 6.55 16 541 100 446 100  
OS=Solanum tuberosum GN=rbcl PE=1 SV=2

Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
898.41	898.3533	-0.0567	-63	306	312	NHGMHFR					Mascot	
910.4451	910.3836	-0.0615	-68	188	194	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot	
910.4451	910.3836	-0.0615	-68	188	194	AVYECLR			Carbamidomethyl (C)[5]		Mascot	
914.4049	914.3448	-0.0601	-66	306	312	NHGMHFR			Oxidation (M)[4]		Mascot	
1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR					Mascot	
1021.5312	1021.4636	-0.0676	-66	33	41	DTDILAAFR	57	99.963			Mascot	
1116.6194	1116.5095	-0.1099	-98	422	431	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot	
1170.5585	1170.5521	-0.0064	-5	304	312	QKNHGMHFR			Oxidation (M)[6]		Mascot	
1187.6643	1187.5826	-0.0817	-69	286	295	DNGLLLHIHR					Mascot	
1245.6337	1245.5459	-0.0878	-70	218	227	FLFCAEALFK	45	99.395	Carbamidomethyl (C)[4]		Mascot	
1245.6337	1245.5459	-0.0878	-70	218	227	FLFCAEALFK			Carbamidomethyl (C)[4]		Mascot	
1261.7151	1261.6268	-0.0883	-70	340	350	DITLGFVDLLR	39	97.581			Mascot	
1261.7151	1261.6268	-0.0883	-70	340	350	DITLGFVDLLR					Mascot	
1285.6859	1285.6572	-0.0287	-22	436	446	DLAREGNEIIR					Mascot	
1451.6219	1451.5211	-0.1008	-69	202	213	DDENVNSQPFMR					Mascot	
1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER	81	100			Mascot	
1465.7546	1465.6512	-0.1034	-71	147	159	TFQGPPIHGIQVER					Mascot	
1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]		Mascot	
1502.8512	1502.7397	-0.1115	-74	165	177	YGRPLLGCTIKPK	7	0	Carbamidomethyl (C)[8]		Mascot	
1546.7358	1546.6255	-0.1103	-71	451	463	WSPELAAACEVWK			Carbamidomethyl (C)[9]		Mascot	
2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR					Mascot	
2169.9868	2169.8325	-0.1543	-71	195	213	GGLDFTKDDENVNSQPFMR	77	100			Mascot	
2185.9819	2185.8284	-0.1535	-70	195	213	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot	
2280.1506	2280.0181	-0.1325	-58	340	358	DITLGFVDLLRDFIEQDR					Mascot	
3854.8718	3854.6101	-0.2617	-68	42	79	VTPQGPVPPEEAGAAVA					Mascot	
						AESSTGTWTTVWTDGLTSLDR						
3854.8718	3854.6101	-0.2617	-68	42	79	VTPQGPVPPEEAGAAVA	118	100			Mascot	
						AESSTGTWTTVWTDGLTSLDR						

9 Ribulose biphosphate carboxylase large chain RBL\_DENCL 52418.5 6.47 15 541 100 449 100  
(Fragment) OS=Dendrophthora clavata GN=rbcl PE=3 SV=1

Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
910.4451	910.3836	-0.0615	-68	187	193	AVYECLR	22	0	Carbamidomethyl (C)[5]		Mascot	
910.4451	910.3836	-0.0615	-68	187	193	AVYECLR			Carbamidomethyl (C)[5]		Mascot	
1021.5312	1021.4636	-0.0676	-66	32	40	DTDILAAFR					Mascot	
1021.5312	1021.4636	-0.0676	-66	32	40	DTDILAAFR	57	99.963			Mascot	
1116.583	1116.5095	-0.0735	-66	421	430	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot	
1187.6643	1187.5826	-0.0817	-69	285	294	DNGLLLHIHR					Mascot	
1245.6433	1245.5459	-0.0974	-78	439	449	EGNEIIRASK					Mascot	
1245.6433	1245.5459	-0.0974	-78	439	449	EGNEIIRASK					Mascot	
1261.7151	1261.6268	-0.0883	-70	339	349	DITLGFVDLLR	39	97.581			Mascot	
1261.7151	1261.6268	-0.0883	-70	339	349	DITLGFVDLLR					Mascot	
1285.6859	1285.6572	-0.0287	-22	435	445	DLAREGNEIIR					Mascot	
1392.7046	1392.5826	-0.122	-88	21	31	LTYYTPDYKTK	50	99.806			Mascot	
1392.7046	1392.5826	-0.122	-88	21	31	LTYYTPDYKTK					Mascot	
1451.6219	1451.5211	-0.1008	-69	201	212	DDENVNSQPFMR					Mascot	
1465.7546	1465.6512	-0.1034	-71	146	158	TFQGPPIHGIQVER	81	100			Mascot	
1465.7546	1465.6512	-0.1034	-71	146	158	TFQGPPIHGIQVER					Mascot	
1502.8512	1502.7397	-0.1115	-74	164	176	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]		Mascot	
1502.8512	1502.7397	-0.1115	-74	164	176	YGRPLLGCTIKPK	7	0	Carbamidomethyl (C)[8]		Mascot	
1546.7358	1546.6255	-0.1103	-71	450	462	WSPELAAACEVWK			Carbamidomethyl (C)[9]		Mascot	
1794.8149	1794.6927	-0.1222	-68	236	251	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot	
2169.9868	2169.8325	-0.1543	-71	194	212	GGLDFTKDDENVNSQPFMR					Mascot	
2169.9868	2169.8325	-0.1543	-71	194	212	GGLDFTKDDENVNSQPFMR	77	100			Mascot	
2185.9819	2185.8284	-0.1535	-70	194	212	GGLDFTKDDENVNSQPFMR			Oxidation (M)[18]		Mascot	
3854.8718	3854.6101	-0.2617	-68	41	78	VTPQGPVPPEEAGAAVA					Mascot	
						AESSTGTWTTVWTDGLTSLDR						
3854.8718	3854.6101	-0.2617	-68	41	78	VTPQGPVPPEEAGAAVA	118	100			Mascot	
						AESSTGTWTTVWTDGLTSLDR						

10 Ribulose biphosphate carboxylase large chain RBL\_SOLLC 52920.9 6.55 16 537 100 445 100  
OS=Solanum lycopersicum GN=rbcl PE=1 SV=4

Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	

Gel Idx/Pos		135/F10		Instr./Gel Origin				BA2060/140227A		Process Status		Analysis Succeeded	
Plate [#] Name		[1] 31564		Instrument Sample Name						Spectra		11	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %				

1	Endochitinase A2 OS=Pisum sativum GN=CHI2 PE=1 SV=2					CHI2_PEA	34655.4	7.33	3	207	100	198	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
1912.8759		1912.7391	-0.1368	-72	180	195	GPIQISWYNYNYGQCGR		106	100	Carbamidomethyl (C)[14]			Mascot
1912.8759		1912.7391	-0.1368	-72	180	195	GPIQISWYNYNYGQCGR				Carbamidomethyl (C)[14]			Mascot
2311.2544		2311.0791	-0.1753	-76	196	217	AIGVDLLNNPDLVATDPV SFK							Mascot
2311.2544		2311.0791	-0.1753	-76	196	217	AIGVDLLNNPDLVATDPV SFK		92	100				Mascot
2534.2415		2534.1965	-0.045	-18	253	276	LPGYGTVTNIINGGLECG RGQDSR				Carbamidomethyl (C)[17]			Mascot
2	Endochitinase OS=Phaseolus vulgaris PE=1 SV=1					CHIT_PHAVU	35420.7	8.43	2	112	100	106	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
1912.8759		1912.7391	-0.1368	-72	188	203	GPIQISWYNYNYGQCGR		106	100	Carbamidomethyl (C)[14]			Mascot
1912.8759		1912.7391	-0.1368	-72	188	203	GPIQISWYNYNYGQCGR				Carbamidomethyl (C)[14]			Mascot
2534.2415		2534.1965	-0.045	-18	261	284	LPGYGTVTNIINGGLECG RGQDSR				Carbamidomethyl (C)[17]			Mascot
3	Endochitinase 4 (Fragment) OS=Solanum tuberosum GN=CHTB4 PE=2 SV=1					CHI4_SOLTU	32296.3	8.58	3	102	100	92	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
2249.9338		2249.7795	-0.1543	-69	166	186	EQGSPGDYCTPSGQWP CAPGR				Carbamidomethyl (C)[9]			Mascot
2311.2544		2311.0791	-0.1753	-76	208	229	AIGVDLLNNPDLVATDPV SFK							Mascot
2311.2544		2311.0791	-0.1753	-76	208	229	AIGVDLLNNPDLVATDPV SFK		92	100				Mascot
2497.9451		2497.9478	0.0027	1	30	53	CAAGLCCSNFGWCNGT NDYCGPGK				Carbamidomethyl (C)[1]			Mascot
2669.0093		2668.9851	-0.0242	-9	30	53	CAAGLCCSNFGWCNGT NDYCGPGK				Carbamidomethyl (C)[1,6,7,13]			Mascot
2669.0093		2668.9851	-0.0242	-9	30	53	CAAGLCCSNFGWCNGT NDYCGPGK				Carbamidomethyl (C)[1,6,7,13]			Mascot
4	Endochitinase B OS=Nicotiana tabacum GN=CHN50 PE=1 SV=1					CHI2_TOBAC	34698.4	8.28	2	98	100	92	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
2249.9338		2249.7795	-0.1543	-69	162	182	EQGSPGDYCTPSGQWP CAPGR				Carbamidomethyl (C)[9]			Mascot
2311.2544		2311.0791	-0.1753	-76	204	225	AIGVDLLNNPDLVATDPV SFK							Mascot
2311.2544		2311.0791	-0.1753	-76	204	225	AIGVDLLNNPDLVATDPV SFK		92	100				Mascot
5	Endochitinase A OS=Nicotiana tabacum GN=CHN48 PE=1 SV=2					CHI1_TOBAC	35133.6	8.4	2	98	100	92	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
2249.9338		2249.7795	-0.1543	-69	167	187	EQGSPGDYCTPSGQWP CAPGR				Carbamidomethyl (C)[9]			Mascot
2311.2544		2311.0791	-0.1753	-76	209	230	AIGVDLLNNPDLVATDPV SFK							Mascot
2311.2544		2311.0791	-0.1753	-76	209	230	AIGVDLLNNPDLVATDPV SFK		92	100				Mascot
6	Endochitinase CH25 OS=Brassica napus PE=2 SV=1					CHI2_BRANA	34793.3	6.29	2	97	100	91	100	
Peptide Information														
Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification		Rank	Result Type
1414.6598		1414.5604	-0.0994	-70	109	122	SFPGFGTTGDTATR		91	100				Mascot
1414.6598		1414.5604	-0.0994	-70	109	122	SFPGFGTTGDTATR							Mascot
2169.9805		2169.8472	-0.1333	-61	291	309	YCNILGVNPGGNLDCYN QR				Carbamidomethyl (C)[2]			Mascot

7	Endochitinase OS=Solanan tuberosum PE=2 SV=1	CHIT_SOLTU	35383.8	8.64	1	92	99.998	92	100
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	2311.2544	2311.0791	-0.1753	-76	208	229	AIGVDLLNPNDLVATDPVI SFK		
	2311.2544	2311.0791	-0.1753	-76	208	229	AIGVDLLNPNDLVATDPVI SFK	92	100
8	Basic endochitinase B OS=Arabidopsis thaliana GN=CHI-B PE=1 SV=3	CHIB_ARATH	36160.1	7.81	1	91	99.998	91	100
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	1414.6598	1414.5604	-0.0994	-70	124	137	SFPGFGTTGDTATR	91	100
	1414.6598	1414.5604	-0.0994	-70	124	137	SFPGFGTTGDTATR		
9	Ribulose biphosphate carboxylase large chain (Fragment) OS=Prunus domestica GN=rbcL PE=3 SV=1	RBL_PRUDO	50914.6	6.23	13	64	98.661		
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	910.4451	910.3803	-0.0648	-71	178	184	AVVECLR		
	914.4049	914.3407	-0.0642	-70	296	302	NHGMHFR		
	1116.583	1116.4993	-0.0837	-75	412	421	VALEACVQAR		
	1170.5585	1170.5527	-0.0058	-5	294	302	QKNHGMHFR		
	1187.6643	1187.5702	-0.0941	-79	276	285	DNGLLLHIHR		
	1245.6433	1245.5392	-0.1041	-84	430	440	EGNEIIREASK		
	1261.6285	1261.6205	-0.008	-6	208	217	FLFCAEAIYK		
	1465.7216	1465.6577	-0.0639	-44	310	324	MSGGDHIHAGTVVGK		
	1821.9388	1821.7279	-0.2109	-116	307	324	ALRMSGGDHIHAGTVVG K		
	2009.059	2008.9247	-0.1343	-67	330	346	EITLGFVDLLRDDFVEK		
	2169.9868	2169.8472	-0.1396	-64	185	203	GGLDFTKDDENVNSQPF MR		
	2185.9819	2185.8259	-0.156	-71	185	203	GGLDFTKDDENVNSQPF MR		
	2669.2004	2668.9851	-0.2153	-81	218	242	AQAETGEIKGHYLNATAG TCEDMMK		
	2669.2004	2668.9851	-0.2153	-81	218	242	AQAETGEIKGHYLNATAG TCEDMMK		
	3022.4548	3022.2539	-0.2009	-66	249	275	ELGVPIVMHDYLTGGFTA NTSLAHYCR		
10	Ribulose biphosphate carboxylase large chain (Fragment) OS=Acer saccharum GN=rbcL PE=3 SV=1	RBL_ACESA	51546	6.19	13	63	98.426		
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	910.4451	910.3803	-0.0648	-71	178	184	AVVECLR		
	914.4049	914.3407	-0.0642	-70	296	302	NHGMHFR		
	1116.583	1116.4993	-0.0837	-75	412	421	VALEACVQAR		
	1170.5585	1170.5527	-0.0058	-5	294	302	QKNHGMHFR		
	1187.6643	1187.5702	-0.0941	-79	276	285	DNGLLLHIHR		
	1245.6337	1245.5392	-0.0945	-76	208	217	FLFCAEAIK		
	1261.7151	1261.6205	-0.0946	-75	330	340	DITLGFVDLLR		
	1465.7216	1465.6577	-0.0639	-44	310	324	MSGGDHIHAGTVVGK		
	1471.7137	1471.6824	-0.0313	-21	454	465	EIKFQFEAMDTL		
	1821.9388	1821.7279	-0.2109	-116	307	324	ALRMSGGDHIHAGTVVG K		
	2009.059	2008.9247	-0.1343	-67	330	346	DITLGFVDLLRDDFIEK		
	2169.9868	2169.8472	-0.1396	-64	185	203	GGLDFTKDDENVNSQPF MR		
	2185.9819	2185.8259	-0.156	-71	185	203	GGLDFTKDDENVNSQPF MR		
	3022.4548	3022.2539	-0.2009	-66	249	275	ELGVPIVMHDYLTGGFTA NTSLAHYCR		
Gel Idx/Pos									
136/F11		Instr./Gel Origin				BA2060/140227A		Process Statu	
Plate [#] Name		Instrument Sample Name						Analysis Succeeded	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion	Total Ion C. I. %
1	Oxygen-evolving enhancer protein 1-2, chloroplastic OS=Arabidopsis thaliana GN=PSBO2 PE=1 SV=1	PSBO2_ARATH	34997.7	5.92	10	52	76.725		
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	850.4304	850.4393	0.0089	10	237	244	GSSFLDPK		
	1096.5521	1096.4497	-0.1024	-93	91	99	LYDEIQSK		
	1112.504	1112.4429	-0.0611	-55	56	66	DVAGKMSDAAK		
	1116.5718	1116.4375	-0.1343	-120	46	55	LTCSLHSCLK		
	1252.6532	1252.6292	-0.024	-19	90	99	RLTYDEIQSK		
	1433.7134	1433.6637	-0.0497	-35	134	145	KFCFCEPTSFTVK		
	1648.8112	1648.7285	-0.0827	-50	152	165	NAPPDFONTKLMTR		
	1648.8727	1648.7285	-0.1442	-87	1	16	MATSLQAAATFLQPAK	0	0
	1949.9313	1949.8521	-0.0792	-41	135	151	FCFEPTSFTVKADSVSK		
	2165.0654	2164.9434	-0.122	-56	36	55	SFGLDSSQARLTCSLHS DLK		
	2165.0654	2164.9434	-0.122	-56	36	55	SFGLDSSQARLTCSLHS DLK		
2	ATP synthase subunit beta, chloroplastic OS=Phalaenopsis aphrodite subsp. formosana GN=atpB PE=3 SV	ATPB_PHAAO	53941.1	5.44	11	51	71.365		
Peptide Information									
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
	1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR		
	1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR		
	1493.7562	1493.6613	-0.0949	-64	74	87	VRVAVMSATDGLMR		
	1493.7562	1493.6613	-0.0949	-64	74	87	VRVAVMSATDGLMR		
	1509.7512	1509.7067	-0.0445	-29	74	87	VRVAVMSATDGLMR		
	1601.8104	1601.6904	-0.12	-75	232	246	VALVYGGMNEPPGAR		
	1767.0415	1766.8337	-0.2078	-118	23	39	IAQIGPVLDFVPSGK		
	1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLFDINFR		
	2061.0322	2060.8933	-0.1389	-67	360	378	GIYPVDPLDSTSTMLOP R		
	2077.0271	2076.8867	-0.1404	-68	360	378	GIYPVDPLDSTSTMLOP		



		2244.144	2243.9758	-0.1682	-75	226	246	R NIAESKVALVYGQMNPEP GAR								Mascot
		2282.0791	2281.9001	-0.179	-78	292	312	MPSAVGYQPTLSTEMGS LQER								Mascot
		2298.074	2297.9446	-0.1294	-56	292	312	MPSAVGYQPTLSTEMGS LQER	Oxidation (M)[1]							Mascot
		2807.4839	2807.1533	-0.3306	-118	110	134	IFNVLGEPVDNLGPVDTR TTFPIHR								Mascot
		3843.9287	3843.7002	-0.2285	-59	318	354	EGSITSIQAVVYPADDLT DPAPATTFAHLDTTVLS R								Mascot
3	ATP synthase subunit beta, chloroplastic OS=Salacca zalacca GN=atpB PE=3 SV=1	ATPB_SALZA	53753	5.16	11	50	66.357									
Peptide Information																
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type			
		1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR					Mascot			
		1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR					Mascot			
		1475.7675	1475.6389	-0.1286	-67	40	52	MPNINVALVVEGR					Mascot			
		1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot			
		1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot			
		1509.7512	1509.7067	-0.0445	-29	74	87	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot			
		1601.8104	1601.6904	-0.12	-75	232	246	VALVYGQMNPPGAR					Mascot			
		1689.8541	1689.7067	-0.1474	-67	3	18	TNPTTSSPVVSTLEEK					Mascot			
		1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLFDINIFR					Mascot			
		2061.0322	2060.8933	-0.1389	-67	360	378	GIYPAVDPLDSTSTMLQP R					Mascot			
		2077.0271	2076.8867	-0.1404	-68	360	378	GIYPAVDPLDSTSTMLQP R			Oxidation (M)[15]		Mascot			
		2244.144	2243.9758	-0.1682	-75	226	246	NIAESKVALVYGQMNPEP GAR					Mascot			
		2282.0791	2281.9001	-0.179	-78	292	312	MPSAVGYQPTLSTEMGS LQER					Mascot			
		2298.074	2297.9446	-0.1294	-56	292	312	MPSAVGYQPTLSTEMGS LQER			Oxidation (M)[1]		Mascot			
		3843.9287	3843.7002	-0.2285	-59	318	354	EGSITSIQAVVYPADDLT DPAPATTFAHLDTTVLS R					Mascot			
4	Lycopene beta cyclase, chloroplastic OS=Nicotiana tabacum GN=LCY1 PE=1 SV=1	LCYB_TOBAC	56030.9	6.9	11	45	0									
Peptide Information																
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type			
		941.5527	941.455	-0.0977	-104	428	435	LDLPATRR					Mascot			
		941.5527	941.455	-0.0977	-104	428	435	LDLPATRR					Mascot			
		1509.8213	1509.7067	-0.1146	-76	11	23	LEFLHPVHGFSVK					Mascot			
		1601.8032	1601.6904	-0.1128	-70	280	293	VPTFLYAMPFSSNK					Mascot			
		1648.8553	1648.7285	-0.1268	-77	24	38	ASSFNSVKPHKFGSR					Mascot			
		1648.8553	1648.7285	-0.1268	-77	24	38	ASSFNSVKPHKFGSR					Mascot			
		1713.7676	1713.7671	-0.0005	0	67	80	ENLDFELPMYDPSK			Oxidation (M)[9]		Mascot			
		1713.7676	1713.7671	-0.0005	0	67	80	ENLDFELPMYDPSK			Oxidation (M)[9]		Mascot			
		1803.8921	1803.7861	-0.106	-59	414	427	QREFFCFGMDILLK			Carbamidomethyl (C)[6]		Mascot			
		1803.8921	1803.7861	-0.106	-59	414	427	QREFFCFGMDILLK			Carbamidomethyl (C)[6]		Mascot			
		1950.0596	1949.8521	-0.2075	-106	7	23	TPNKLEFLHPVHGFSVK					Mascot			
		2537.2036	2537.0625	-0.1411	-56	436	455	FFDAFFDLEPRYWHGFL SSR					Mascot			
		2588.3501	2588.0159	-0.3342	-129	294	315	IFLEETSLVARPGLRMDDI QER					Mascot			
		2632.3572	2631.978	-0.3792	-144	478	500	IEIMTKGTLPVNMNNLL QDTE			Oxidation (M)[4,14]		Mascot			
		3390.7031	3390.3269	-0.3762	-111	194	224	VIHEEAKSLMICNDGVTIQ ATVVLDTGFSR			Carbamidomethyl (C)[12], Oxidation (M)[9]		Mascot			
5	ATP synthase subunit beta, chloroplastic OS=Aristolochia macrophylla GN=atpB PE=3 SV=1	ATPB_ARIMA	53617.8	5.27	10	44	0									
Peptide Information																
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type			
		1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR					Mascot			
		1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR					Mascot			
		1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot			
		1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot			
		1509.7512	1509.7067	-0.0445	-29	74	87	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot			
		1601.8104	1601.6904	-0.12	-75	232	246	VALVYGQMNPPGAR					Mascot			
		1803.9269	1803.7861	-0.1408	-78	1	17	MRINPTTSGPGVSTLEK			Oxidation (M)[1]		Mascot			
		1803.9269	1803.7861	-0.1408	-78	1	17	MRINPTTSGPGVSTLEK			Oxidation (M)[1]		Mascot			
		1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLFDINIFR					Mascot			
		2061.0322	2060.8933	-0.1389	-67	360	378	GIYPAVDPLDSTSTMLQP R					Mascot			
		2077.0271	2076.8867	-0.1404	-68	360	378	GIYPAVDPLDSTSTMLQP R			Oxidation (M)[15]		Mascot			
		2282.0791	2281.9001	-0.179	-78	292	312	MPSAVGYQPTLSTEMGS LQER					Mascot			
		2298.074	2297.9446	-0.1294	-56	292	312	MPSAVGYQPTLSTEMGS LQER			Oxidation (M)[1]		Mascot			
		2807.4839	2807.1533	-0.3306	-118	110	134	IFNVLGEPVDNLGPVDTR TTFPIHR					Mascot			
		3843.9287	3843.7002	-0.2285	-59	318	354	EGSITSIQAVVYPADDLT DPAPATTFAHLDTTVLS R					Mascot			
6	Histone-lysine N-methyltransferase EZ2 OS=Zea mays GN=EZ2 PE=2 SV=1	EZ2_MAIZE	99915.8	8.47	17	44	0									
Peptide Information																
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type			
		973.4849	973.4419	-0.043	-44	437	444	YREHSPGK					Mascot			
		993.3764	993.4303	0.0539	54	705	712	ECDPDVCR			Carbamidomethyl (C)[2]		Mascot			
		1096.4662	1096.4497	-0.0165	-15	696	704	QCPCFAASR			Carbamidomethyl (C)[2,4]		Mascot			
		1189.5969	1189.5588	-0.0381	-32	320	329	KPGHLCYLRL					Mascot			
		1429.5215	1429.6074	0.0859	60	658	670	DQPCADKGTCCCK			Carbamidomethyl (C)[2]		Mascot			
		1475.7019	1475.6389	-0.063	-43	162	174	NORMADDSGVVGR					Mascot			
		1493.804	1493.6613	-0.1427	-96	150	161	IPPYTTWIFLDK					Mascot			
		1493.804	1493.6613	-0.1427	-96	150	161	IPPYTTWIFLDK					Mascot			
		1509.6539	1509.7067	0.0528	35	820	832	FANHSSNPNCYAK			Carbamidomethyl (C)[10]		Mascot			
		1672.7119	1672.6753	-0.0366	-22	362	375	VDVNVMEYSEDSNR			Oxidation (M)[6]		Mascot			
		1713.6877	1713.7671	0.0794	46	497	512	DMCGESPATTMENVGR			Oxidation (M)[2]		Mascot			
		1713.6877	1713.7671	0.0794	46	497	512	DMCGESPATTMENVGR			Oxidation (M)[2]		Mascot			
		1803.8041	1803.7861	-0.018	-10	272	286	TMDAVLDSFDNLFGR			Carbamidomethyl (C)[14]		Mascot			
		1803.8402	1803.7861	-0.0541	-30	94	110	AAERCCGSDLANGIGR			Carbamidomethyl (C)[6]		Mascot			

	2243.9326	2243.9758	0.0432	19	497	516	DMCGESPATTMENVGR QSNK					Carbamidomethyl (C)[3], Oxidation (M)[2,11]	Mascot
	2289.1404	2289.0552	-0.0852	-37	62	82	TLQRHSCSLFDVAAAAEV ASR					Carbamidomethyl (C)[7]	Mascot
	2587.9978	2588.0159	0.0181	7	636	657	TDDGKQCQYQYSPCACQ QMC GK					Carbamidomethyl (C)[7,14], Oxidation (M)[19]	Mascot
	2902.085	2902.1423	0.0573	20	641	664	QCYTQYSPCACQCMCG KDCPCADK					Carbamidomethyl (C)[2,9,11,15]	Mascot
	2988.249	2988.3833	0.1343	45	713	739	NCWVSCGDGSLGEPLAR GDGYQCGNMK					Carbamidomethyl (C)[2,6,23]	Mascot
7	ATP synthase subunit beta, chloroplastic OS=Trachycarpus fortunei GN=atpB PE=3 SV=1					ATPB_TRAFO	53586.9	5.29	10	43	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	1431.6863	1431.5916	-0.0947	-66	377	388	IVGEEHYETAQR					Mascot	
	1433.7747	1433.6637	-0.111	-77	276	289	FVQAGSEVSALLGR					Mascot	
	1493.7562	1493.6613	-0.0949	-64	72	85	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1493.7562	1493.6613	-0.0949	-64	72	85	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1509.7512	1509.7067	-0.0445	-29	72	85	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot	
	1601.8104	1601.6904	-0.12	-75	230	244	VALVYGQMNPPGAR					Mascot	
	1689.8541	1689.7067	-0.1474	-87	3	18	TNPTTSSPVVSTLEEK					Mascot	
	1949.9967	1949.8521	-0.1446	-74	260	275	DVNEQDVLLFDNIFR					Mascot	
	2061.0322	2060.8933	-0.1389	-67	358	376	GIYPAVDPLDSTSTMLOP R					Mascot	
	2077.0271	2076.8867	-0.1404	-68	358	376	GIYPAVDPLDSTSTMLOP R			Oxidation (M)[15]		Mascot	
	2244.144	2243.9758	-0.1682	-75	224	244	NIAESKVALVYGQMNPP GAR					Mascot	
	2282.0791	2281.9001	-0.179	-78	290	310	MPSAVGYQPTLSTEMGS LQER					Mascot	
	2298.074	2297.9446	-0.1294	-56	290	310	MPSAVGYQPTLSTEMGS LQER			Oxidation (M)[1]		Mascot	
	3843.9287	3843.7002	-0.2285	-59	316	352	EGSITSIAQVYVPADDLT DPAPATTFAHLDATTVLS R					Mascot	
8	ATP synthase subunit beta, chloroplastic OS=Elaeis oleifera GN=atpB PE=3 SV=1					ATPB_ELAOL	53762.1	5.29	10	43	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR					Mascot	
	1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR					Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1509.7512	1509.7067	-0.0445	-29	74	87	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot	
	1601.8104	1601.6904	-0.12	-75	232	246	VALVYGQMNPPGAR					Mascot	
	1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLLFDNIFR					Mascot	
	1987.0165	1986.866	-0.1505	-76	1	18	MRTNPTTSSPVVPTLEEK					Mascot	
	2061.0322	2060.8933	-0.1389	-67	360	378	GIYPAVDPLDSTSTMLOP R					Mascot	
	2077.0271	2076.8867	-0.1404	-68	360	378	GIYPAVDPLDSTSTMLOP R			Oxidation (M)[15]		Mascot	
	2244.144	2243.9758	-0.1682	-75	226	246	NIAESKVALVYGQMNPP GAR					Mascot	
	2282.0791	2281.9001	-0.179	-78	292	312	MPSAVGYQPTLSTEMGS LQER					Mascot	
	2298.074	2297.9446	-0.1294	-56	292	312	MPSAVGYQPTLSTEMGS LQER			Oxidation (M)[1]		Mascot	
	3843.9287	3843.7002	-0.2285	-59	318	354	EGSITSIAQVYVPADDLT DPAPATTFAHLDATTVLS R					Mascot	
9	ATP synthase subunit beta, chloroplastic OS=Caryota mitis GN=atpB PE=3 SV=1					ATPB_CARMI	53735.9	5.29	10	43	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR					Mascot	
	1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR					Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1509.7512	1509.7067	-0.0445	-29	74	87	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot	
	1601.8104	1601.6904	-0.12	-75	232	246	VALVYGQMNPPGAR					Mascot	
	1689.8541	1689.7067	-0.1474	-87	3	18	TNPTTSSPVVSTLEEK					Mascot	
	1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLLFDNIFR					Mascot	
	2061.0322	2060.8933	-0.1389	-67	360	378	GIYPAVDPLDSTSTMLOP R					Mascot	
	2077.0271	2076.8867	-0.1404	-68	360	378	GIYPAVDPLDSTSTMLOP R			Oxidation (M)[15]		Mascot	
	2244.144	2243.9758	-0.1682	-75	226	246	NIAESKVALVYGQMNPP GAR					Mascot	
	2282.0791	2281.9001	-0.179	-78	292	312	MPSAVGYQPTLSTEMGS LQER					Mascot	
	2298.074	2297.9446	-0.1294	-56	292	312	MPSAVGYQPTLSTEMGS LQER			Oxidation (M)[1]		Mascot	
	3843.9287	3843.7002	-0.2285	-59	318	354	EGSITSIAQVYVPADDLT DPAPATTFAHLDATTVLS R					Mascot	
10	ATP synthase subunit beta, chloroplastic OS=Calamus usitatus GN=atpB PE=3 SV=1					ATPB_CALUS	53743	5.16	10	43	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	1431.6863	1431.5916	-0.0947	-66	379	390	IVGEEHYETAQR					Mascot	
	1433.7747	1433.6637	-0.111	-77	278	291	FVQAGSEVSALLGR					Mascot	
	1475.7675	1475.6389	-0.1286	-87	40	52	MPNINVALVVEGR					Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1493.7562	1493.6613	-0.0949	-64	74	87	VRAVAMSATDGLMR			Oxidation (M)[6]		Mascot	
	1509.7512	1509.7067	-0.0445	-29	74	87	VRAVAMSATDGLMR			Oxidation (M)[6,13]		Mascot	
	1601.8104	1601.6904	-0.12	-75	232	246	VALVYGQMNPPGAR					Mascot	
	1949.9967	1949.8521	-0.1446	-74	262	277	DVNEQDVLLFDNIFR					Mascot	
	2061.0322	2060.8933	-0.1389	-67	360	378	GIYPAVDPLDSTSTMLOP R					Mascot	
	2077.0271	2076.8867	-0.1404	-68	360	378	GIYPAVDPLDSTSTMLOP R			Oxidation (M)[15]		Mascot	
	2244.144	2243.9758	-0.1682	-75	226	246	NIAESKVALVYGQMNPP GAR					Mascot	

		Seq.		Seq.		Score	
842.473	842.4448	-0.0282	-33	26	33	DIPGKGQK	Mascot
1261.6859	1261.6178	-0.0681	-54	14	25	DVSSGSVVISRR	Mascot
1333.5907	1333.5681	-0.0226	-17	92	103	GPWASDSEDELK	Mascot

Gel Idx/Pos		138/F13		Instr./Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate #/ Name		[1] 31564		Instrument Sample Name				Spectra		11	
Rank	Protein Name	Accession No.		Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	
1	Triosephosphate isomerase, cytosolic OS=Zea mays PE=3 SV=3	TPIS_MAIZE		27008	5.52	5	104	100	82	100	
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK				Mascot
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953		Mascot
	1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK				Mascot
	1261.6019	1261.6355	0.0336	27	195	206	TNASPEVAESTR				Mascot
	1407.6785	1407.6179	-0.0606	-43	136	149	EAGSTMDVVAAGTK				Mascot
	2332.2336	2332.0579	-0.1757	-75	155	175	IKDWSNVVAYEPVWAIGTK				Mascot
	2332.2336	2332.0579	-0.1757	-75	155	175	IKDWSNVVAYEPVWAIGTK	28	76.466		Mascot
2	Triosephosphate isomerase, cytosolic OS=Petunia hybrida GN=TPIP1 PE=2 SV=1	TPIS_PETHY		27115.1	5.54	3	95	99.999	84	100	
Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank Result Type
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK				Mascot

		954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953							Mascot
		1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK									Mascot
		2332.2336	2332.0579	-0.1757	-75	155	175	VKDWTNVVVAYEPVWAI									Mascot
								GTGK									
		2332.2336	2332.0579	-0.1757	-75	155	175	VKDWTNVVVAYEPVWAI	30	85.151							Mascot
								GTGK									
3	Triosephosphate isomerase, chloroplastic OS=Spinacia oleracea GN=TPIP1 PE=1 SV=1	TPIC_SPIOL	34387.5	6.45	7	86					99.991	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	73	80	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	73	80	FFVGGNWK	55	99.953				Mascot				
	1498.8011	1498.6523	-0.1488	-99	167	179	HVIGEQNEFIGKK						Mascot				
	1548.7904	1548.6812	-0.1092	-71	290	304	QEDIDGFLVGGASLK						Mascot				
	1612.79	1612.6863	-0.1037	-64	152	165	DLGCQWVILGHSER						Mascot				
	1629.7941	1629.7321	-0.062	-38	202	215	EAGKTFDVCYQQLK						Mascot				
	1629.7941	1629.7321	-0.062	-38	202	215	EAGKTFDVCYQQLK						Mascot				
	2148.1196	2147.9331	-0.1865	-87	242	260	VASPDQAEVHVAVRD						Mascot				
							WLK										
	2346.2122	2346.0359	-0.1763	-75	180	201	AAYALNQGVGIACIGEL				Carbamidomethyl (C)[14]		Mascot				
							LEER										
4	Triosephosphate isomerase, chloroplastic OS=Fragaria ananassa GN=TPI PE=2 SV=1	TPIC_FRAAN	33505.4	7.64	4	77					99.933	63	99.994				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	65	72	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	65	72	FFVGGNWK	55	99.953				Mascot				
	1096.5898	1096.5227	-0.0671	-61	149	157	WVILGHSER	9	0				Mascot				
	1096.5898	1096.5227	-0.0671	-61	149	157	WVILGHSER						Mascot				
	1331.6953	1331.6105	-0.0848	-64	118	129	IEISGQNSWVAK						Mascot				
	2748.4202	2748.137	-0.2832	-103	118	143	IEISGQNSWVAKGGAFTG						Mascot				
							EISVEQLK										
5	Triosephosphate isomerase, cytosolic OS=Oryza sativa subsp. japonica GN=TPI PE=1 SV=3	TPIS_ORYSJ	27046	5.38	5	76					99.915	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953				Mascot				
	1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK						Mascot				
	1339.6674	1339.5536	-0.1138	-85	207	219	IYGGSVTGANCK						Mascot				
	1603.8075	1603.6484	-0.1591	-99	192	206	WLAANVSAEVAESTR				Carbamidomethyl (C)[12]		Mascot				
	2346.2493	2346.0359	-0.2134	-91	155	175	IKDWTNVVVAYEPVWAI						Mascot				
							TKG										
6	Triosephosphate isomerase, chloroplastic OS=Arabidopsis thaliana GN=TIM PE=1 SV=1	TPIC_ARATH	33325.1	7.67	3	72					99.783	63	99.994				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	66	73	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	66	73	FFVGGNWK	55	99.953				Mascot				
	1096.5898	1096.5227	-0.0671	-61	150	158	WVILGHSER	9	0				Mascot				
	1096.5898	1096.5227	-0.0671	-61	150	158	WVILGHSER						Mascot				
	1612.8264	1612.6863	-0.1401	-87	145	158	DLGCQWVILGHSER						Mascot				
7	Triosephosphate isomerase, cytosolic OS=Secale cereale PE=2 SV=3	TPIS_SECCE	26910	5.24	4	71					99.707	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953				Mascot				
	1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK						Mascot				
	2332.2693	2332.0579	-0.2114	-91	114	135	VAYALAQGLKVIACVGET						Mascot				
							LEQR										
	2332.2693	2332.0579	-0.2114	-91	114	135	VAYALAQGLKVIACVGET						Mascot				
							LEQR										
	2346.2493	2346.0359	-0.2134	-91	155	175	IKDWTNVVVAYEPVWAI						Mascot				
							TKG										
8	Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	TPIS_ARATH	27152.1	5.39	4	70					99.631	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953				Mascot				
	1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK						Mascot				
	1338.647	1338.5575	-0.0895	-67	207	219	IYGGSVNNGGNCK				Carbamidomethyl (C)[12]		Mascot				
	1407.6785	1407.6179	-0.0606	-43	136	149	EAGSTMDEVAAQTK						Mascot				
9	Triosephosphate isomerase, chloroplastic OS=Secale cereale PE=1 SV=1	TPIC_SECCE	31613.1	6	4	68					99.442	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	49	56	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	49	56	FFVGGNWK	55	99.953				Mascot				
	1486.7537	1486.6674	-0.0863	-58	143	155	HVIGEDDEFIQQK						Mascot				
	1548.8268	1548.6812	-0.1456	-94	266	280	KEDIDGFLVGGASLK						Mascot				
	1747.8717	1747.8152	-0.0565	-32	166	181	VMACIGELLEEREAGK						Mascot				
10	Triosephosphate isomerase, cytosolic OS=Hordeum vulgare PE=1 SV=3	TPIS_HORVU	26719.9	5.39	3	65					98.984	55	99.953				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK						Mascot				
	954.4832	954.4254	-0.0578	-61	5	12	FFVGGNWK	55	99.953				Mascot				
	1082.5781	1082.5115	-0.0666	-62	4	12	KFFVGGNWK						Mascot				
	2332.2693	2332.0579	-0.2114	-91	114	135	VAYALAQGLKVIACVGET						Mascot				
							LEQR										
	2332.2693	2332.0579	-0.2114	-91	114	135	VAYALAQGLKVIACVGET						Mascot				
							LEQR										

Gel Idx/Pos		140/F15		Instr./Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate [#] Name		[1] 31564		Instrument Sample Name				Spectra		11	
Rank	Protein Name	Accession No.	Protein MW	Protein	Pep.	Protein	Protein	Total Ion	Total Ion		

					PI	Count	Score	Score C. I. %	Score	Score	C. I. %
1	Triosephosphate isomerase, chloroplastic OS=Spinacia oleracea GN=TPIP1 PE=1 SV=1	TPIC_SPIOL	34387.5	6.45	5	191	100	172	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	73	80	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	73	80	FFVGGNWK					Mascot
1548.7904	1548.6958	-0.0946	-61	290	304	QEDIDGFLVGGASLK	66	99.996			Mascot
1548.7904	1548.6958	-0.0946	-61	290	304	QEDIDGFLVGGASLK					Mascot
1669.8115	1669.8245	0.013	8	152	165	DLSCQWVILGHSE			Carbamidomethyl (C)[4]		Mascot
2346.2122	2346.071	-0.1412	-60	180	201	AAYALNQGVGIACIGEL	64	99.993	Carbamidomethyl (C)[14]		Mascot
						LEER					
2346.2122	2346.071	-0.1412	-60	180	201	AAYALNQGVGIACIGEL			Carbamidomethyl (C)[14]		Mascot
						LEER					
2474.3071	2474.1594	-0.1477	-60	179	201	KAAYALNQGVGIACIGEL			Carbamidomethyl (C)[15]		Mascot
						LEER					
2	Triosephosphate isomerase, chloroplastic OS=Secale cereale PE=1 SV=1	TPIC_SECCE	31613.1	6	3	117	100	108	100		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	49	56	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	49	56	FFVGGNWK					Mascot
1548.8268	1548.6958	-0.131	-85	266	280	KEDIDGFLVGGASLK	66	99.996			Mascot
1548.8268	1548.6958	-0.131	-85	266	280	KEDIDGFLVGGASLK					Mascot
1747.8717	1747.834	-0.0377	-22	166	181	VMACIGELLEEREAGK					Mascot
3	Triosephosphate isomerase, chloroplastic OS=Frugaria ananassa GN=TPI PE=2 SV=1	TPIC_FRAAN	33505.4	7.64	6	93	99.998	67	99.997		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	65	72	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	65	72	FFVGGNWK					Mascot
1096.5898	1096.5265	-0.0633	-58	149	157	WVILGHSE	25	50.76			Mascot
1096.5898	1096.5265	-0.0633	-58	149	157	WVILGHSE					Mascot
1331.6953	1331.6072	-0.0881	-66	118	129	IEISGQNSWVAK					Mascot
1513.7758	1513.7512	-0.0246	-16	158	170	RHVIGEDDDQFIGK					Mascot
1991.0193	1990.9041	-0.1152	-58	112	129	SSLTDRIEISGQNSWVAK					Mascot
2748.4202	2748.1541	-0.2661	-97	118	143	IEISGQNSWVAKGGAGFTG					Mascot
						EISVEQLK					
4	Triosephosphate isomerase, chloroplastic OS=Arabidopsis thaliana GN=TIM PE=1 SV=1	TPIC_ARATH	33325.1	7.67	3	76	99.917	67	99.997		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	66	73	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	66	73	FFVGGNWK					Mascot
1096.5898	1096.5265	-0.0633	-58	150	158	WVILGHSE	25	50.76			Mascot
1096.5898	1096.5265	-0.0633	-58	150	158	WVILGHSE					Mascot
1669.8479	1669.8245	-0.0234	-14	145	158	DLGCKWVILGHSE			Carbamidomethyl (C)[4]		Mascot
5	Triosephosphate isomerase, cytosolic OS=Zea mays PE=3 SV=3	TPIS_MAIZE	27008	5.52	3	52	79.256	42	98.905		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK					Mascot
1261.6019	1261.6454	0.0435	34	195	206	TNASPEVAESTR					Mascot
1261.6019	1261.6454	0.0435	34	195	206	TNASPEVAESTR					Mascot
1407.6785	1407.6217	-0.0568	-40	136	149	EAGSTMDEVVAAQTK					Mascot
1407.6785	1407.6217	-0.0568	-40	136	149	EAGSTMDEVVAAQTK					Mascot
6	Triosephosphate isomerase, cytosolic OS=Secale cereale PE=2 SV=3	TPIS_SECCE	26910	5.24	2	49	53.56	42	98.905		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK					Mascot
2346.2493	2346.071	-0.1783	-76	155	175	IKDWTNVVVAEPVWAIG					Mascot
						TGK					
2346.2493	2346.071	-0.1783	-76	155	175	IKDWTNVVVAEPVWAIG					Mascot
						TGK					
7	Triosephosphate isomerase, cytosolic OS=Coptis japonica PE=2 SV=1	TPIS_COPJA	27073.1	5.54	2	48	49.079	42	98.905		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK					Mascot
1051.5782	1051.6462	0.068	65	114	123	TAYALSQGLK					Mascot
8	Triosephosphate isomerase, cytosolic OS=Arabidopsis thaliana GN=CTIMC PE=1 SV=2	TPIS_ARATH	27152.1	5.39	2	48	49.079	42	98.905		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK					Mascot
1407.6785	1407.6217	-0.0568	-40	136	149	EAGSTMDEVVAAQTK					Mascot
1407.6785	1407.6217	-0.0568	-40	136	149	EAGSTMDEVVAAQTK					Mascot
9	Triosephosphate isomerase, cytosolic OS=Stellaria longipes GN=TPI PE=2 SV=1	TPIS_STELP	27482.1	5.54	2	48	47.893	42	98.905		
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK	42	98.905			Mascot
954.4832	954.4278	-0.0554	-58	5	12	FFVGGNWK					Mascot
1619.85	1619.7405	-0.1095	-68	177	191	VASPEQAQEVHVAVR					Mascot
10	Oxygen-evolving enhancer protein 1-1, chloroplastic OS=Arabidopsis thaliana GN=PSBO1 PE=1 SV=2	PSBO1_ARATH	35120.6	5.55	9	46	13.524				
Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1096.5521	1096.5265	-0.0256	-23	92	100	LYTDEIQSK					Mascot

	1096.5521	1096.5265	-0.0256	-23	92	100	LTVEIQSK								Mascot				
	1170.6450	1170.5675	0.0216	18	57	67	DFTKGSSDAVK								Mascot				
	1388.6903	1388.6387	-0.0516	-37	265	276	GDEELVKENVK								Mascot				
	1531.869	1531.665	-0.204	-133	277	291	NTAASVGTEILKVTK								Mascot				
	1654.8469	1654.7548	-0.0921	-56	1	16	MAASLQSTATFLQSAK								Mascot				
	1712.9006	1712.7627	-0.1379	-81	231	245	FLVPSYRGSSFLDPK								Mascot				
	1775.8783	1775.8048	-0.0735	-41	246	264	GRGGSTGYDNAVALPAG GR								Mascot				
	2211.0386	2210.9644	-0.0742	-34	37	56	SFGLTSSARLTCSFQSD FK								Mascot				
	2748.4236	2748.1541	-0.2695	-98	62	90	CSDAVKIAGFALATSALV VSGASAEAPK				Carbamidomethyl (C)[1]				Mascot				
Gel Idx/Pos	141/F16					Instr./Gel Origin					BA2060/140227A					Process Status		Analysis Succeeded	
Plate [#] Name	[1] 31564					Instrument Sample Name										Spectra		11	
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %						
1	Carbonic anhydrase OS=Flaveria bidentis PE=2 SV=2					CAHX_FLABI	35522.9	5.85	4	294	100	280	100						
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type						
	1219.5234	1219.4606	-0.0628	-51	156	165	FMVFACSDSR		36	96.649	Carbamidomethyl (C)[6]	Mascot							
	1219.5234	1219.4606	-0.0628	-51	156	165	FMVFACSDSR				Carbamidomethyl (C)[6]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	156	165	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	156	165	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1892.0276	1891.9335	-0.0941	-50	277	293	EAVNVSLGNLLTYPFVR					Mascot							
	1892.0276	1891.9335	-0.0941	-50	277	293	EAVNVSLGNLLTYPFVR	123	100			Mascot							
	2000.0057	1999.8959	-0.1098	-55	166	183	VCPSHVLDQPGEAFVV R					Mascot							
	2057.0273	2056.9241	-0.1032	-50	166	183	VCPSHVLDQPGEAFVV R				Carbamidomethyl (C)[2]	Mascot							
	2057.0273	2056.9241	-0.1032	-50	166	183	VCPSHVLDQPGEAFVV R	121	100		Carbamidomethyl (C)[2]	Mascot							
	2230.0994	2230.0127	-0.0867	-39	1	22	MSAASAFAMNAPSFVNA SSLKK					Mascot							
2	Carbonic anhydrase OS=Flaveria brownii PE=2 SV=1					CAHX_FLABR	35524.8	5.7	4	293	100	280	100						
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type						
	1219.5234	1219.4606	-0.0628	-51	156	165	FMVFACSDSR		36	96.649	Carbamidomethyl (C)[6]	Mascot							
	1219.5234	1219.4606	-0.0628	-51	156	165	FMVFACSDSR				Carbamidomethyl (C)[6]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	156	165	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	156	165	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1892.0276	1891.9335	-0.0941	-50	277	293	EAVNVSLGNLLTYPFVR					Mascot							
	1892.0276	1891.9335	-0.0941	-50	277	293	EAVNVSLGNLLTYPFVR	123	100			Mascot							
	1928.9019	1928.7439	-0.158	-82	37	55	FTCNSSSSSSSATPPSLI R					Mascot							
	1928.9019	1928.7439	-0.158	-82	37	55	FTCNSSSSSSSATPPSLI R					Mascot							
	2000.0057	1999.8959	-0.1098	-55	166	183	VCPSHVLDQPGEAFVV R					Mascot							
	2057.0273	2056.9241	-0.1032	-50	166	183	VCPSHVLDQPGEAFVV R				Carbamidomethyl (C)[2]	Mascot							
	2057.0273	2056.9241	-0.1032	-50	166	183	VCPSHVLDQPGEAFVV R	121	100		Carbamidomethyl (C)[2]	Mascot							
3	Carbonic anhydrase, chloroplastic OS=Pisum sativum PE=1 SV=1					CAHC_SPEA	35355.1	7.01	5	219	100	201	100						
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type						
	849.4617	849.4159	-0.0458	-54	126	132	TGFLHFK					Mascot							
	948.446	948.3942	-0.0518	-55	303	310	GGYDFVK					Mascot							
	1481.7634	1481.6888	-0.0746	-50	136	148	YDKNPALYGELAK					Mascot							
	1610.8683	1610.7814	-0.0869	-54	211	226	VSNIVIGHSACGGIK				Carbamidomethyl (C)[12]	Mascot							
	1610.8683	1610.7814	-0.0869	-54	211	226	VSNIVIGHSACGGIK	79	100		Carbamidomethyl (C)[12]	Mascot							
	2000.0057	1999.8959	-0.1098	-55	164	181	VCPSHVLDQPGEAFVV R					Mascot							
	2057.0273	2056.9241	-0.1032	-50	164	181	VCPSHVLDQPGEAFVV R				Carbamidomethyl (C)[2]	Mascot							
	2057.0273	2056.9241	-0.1032	-50	164	181	VCPSHVLDQPGEAFVV R	121	100		Carbamidomethyl (C)[2]	Mascot							
4	Carbonic anhydrase, chloroplastic OS=Spinacia oleracea PE=1 SV=2					CAHC_SPIOL	34547.6	6.61	5	179	100	159	100						
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type						
	1219.5234	1219.4606	-0.0628	-51	145	154	FMVFACSDSR		36	96.649	Carbamidomethyl (C)[6]	Mascot							
	1219.5234	1219.4606	-0.0628	-51	145	154	FMVFACSDSR				Carbamidomethyl (C)[6]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	145	154	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	145	154	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1566.7615	1566.677	-0.0845	-54	1	15	MSTINGCLTSISPSR					Mascot							
	1566.7615	1566.677	-0.0845	-54	1	15	MSTINGCLTSISPSR					Mascot							
	1892.0276	1891.9335	-0.0941	-50	266	282	EAVNVSLGNLLTYPFVR					Mascot							
	1892.0276	1891.9335	-0.0941	-50	266	282	EAVNVSLGNLLTYPFVR	123	100			Mascot							
	2327.0901	2326.9526	-0.1375	-59	218	238	GLMSFPDAGPTTDDFIED VWK					Mascot							
	2343.085	2342.9548	-0.1302	-56	218	238	GLMSFPDAGPTTDDFIED VWK				Oxidation (M)[3]	Mascot							
	3349.6165	3349.4871	-0.1294	-39	155	183	VCPSHVLDQPGEAFMV RNIANMVPVFDK				Carbamidomethyl (C)[2], Oxidation (M)[16,23]	Mascot							
5	Carbonic anhydrase, chloroplastic OS=Nicotiana tabacum PE=2 SV=1					CAHC_TOBAC	34488.6	6.41	5	176	100	157	100						
Peptide Information																			
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type						
	1219.5234	1219.4606	-0.0628	-51	147	156	FMVFACSDSR		36	96.649	Carbamidomethyl (C)[6]	Mascot							
	1219.5234	1219.4606	-0.0628	-51	147	156	FMVFACSDSR				Carbamidomethyl (C)[6]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	147	156	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1235.5183	1235.4514	-0.0669	-54	147	156	FMVFACSDSR				Carbamidomethyl (C)[6], Oxidation (M)[2]	Mascot							
	1891.9794	1891.9335	-0.0469	-24	2	20	STAINSLTLTSPDAQSLK					Mascot							
	1892.0276	1891.9335	-0.0941	-50	268	284	EAVNVSLGNLLTYPFVR	123	100			Mascot							
	2224.9419	2225.0139	0.072	32	249	267	VQGEHVDKCFADQCTAC EK				Carbamidomethyl (C)[8],14]	Mascot							
	2418.3391	2418.0908	-0.2483	-103	268	289	EAVNVSLGNLLTYPFVRE GLVK					Mascot							
	2418.3391	2418.0908	-0.2483	-103	268	289	EAVNVSLGNLLTYPFVRE GLVK					Mascot							

6	Carbonic anhydrase 2 (Fragment) OS=Flaveria linearis PE=2 SV=1	CAH2_FLALI	20571.5	6.21	3	137	100	123	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
1684.8508	1684.7822	-0.0686	-41	73	88	VENIVVIGHSCCGGIK			
1892.0276	1891.9335	-0.0941	-50	137	153	EAVNVSLGNLLTYPFVR			
1892.0276	1891.9335	-0.0941	-50	137	153	EAVNVSLGNLLTYPFVR	123	100	
3337.6892	3337.6145	-0.0747	-22	161	190	LSLKGAHYDFVNGAFDL WNLDFGISPSLLQ			
7	Cytochrome P450 83B1 OS=Arabidopsis thaliana GN=CYP83B1 PE=1 SV=1	C83B1_ARATH	56809.6	8.52	12	45	2.973		
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
882.4389	882.5175	0.0786	89	318	324	YPEAMKK			
933.504	933.4648	-0.0392	-42	378	386	IGGYDIPAK			
1384.6171	1384.7518	0.1347	97	128	138	MCMVNLFSNPR			
1409.6586	1409.6217	-0.0369	-26	477	488	MDVMTGLAMHKK			
1465.7832	1465.6819	-0.1013	-69	35	47	GLPIIGNLHOMEK			
1471.6854	1471.7162	0.0308	21	127	138	KMCMVNLFSNPR			
1471.6854	1471.7162	0.0308	21	127	138	KMCMVNLFSNPR			
1873.9252	1873.8872	-0.038	-20	262	276	QETESFIOLLMQIYK			
1968.9813	1968.929	-0.0523	-27	421	438	GVDFKGQDFELLPFSGS R			
2000.1538	1999.8959	-0.2579	-129	85	101	ELLKTQDLNFTARPLLK			
2297.1462	2297.0791	-0.0671	-29	128	146	MCMVNLFSNPRVASFRP VR			
2691.3643	2691.1758	-0.1885	-70	439	461	RMCPAMHLGIAMVEIPFA NLLYK			
2748.4089	2748.1941	-0.2148	-78	239	261	AFKELDTYLQELLDETLD PNRPK			
8	Carbonic anhydrase 2, chloroplastic OS=Arabidopsis thaliana GN=CA2 PE=1 SV=2	CAH2_ARATH	28326.4	5.36	7	45	0	12	0
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
849.41	849.4159	0.0059	7	48	54	SFDPVER			
1045.5524	1045.5227	-0.0297	-28	21	30	DDLKDVAAAK			
1235.5183	1235.4514	-0.0669	-54	85	94	YMFVACSDSR			
1235.5183	1235.4514	-0.0669	-54	85	94	YMFVACSDSR			
1566.7645	1566.677	-0.0875	-56	2	15	GNESYDEAIEALKK			
1566.7645	1566.677	-0.0875	-56	2	15	GNESYDEAIEALKK	12	0	
1999.9025	1999.8959	-0.0066	-3	185	202	SKVLAESSESAFEDQCGR			
2229.95	2230.0127	0.0627	28	187	205	VLAESSESAFEDQCGR ER			
2418.3391	2418.0908	-0.2483	-103	206	227	EAVNVSLANLLTYPFVRE GVVK			
2418.3391	2418.0908	-0.2483	-103	206	227	EAVNVSLANLLTYPFVRE GVVK			
9	Protein argonaute 1D OS=Oryza sativa subsp. japonica GN=AGO1D PE=2 SV=1	AGO1D_ORYSJ	115850.8	9.19	15	44	0		
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
842.5206	842.4655	-0.0551	-65	720	727	INVKVGGR			
849.3269	849.4159	0.089	105	1033	1038	NVMFYC			
910.4814	910.4054	-0.076	-83	704	710	QVFKMNK			
933.5151	933.4648	-0.0503	-54	294	301	LEQFLAGR			
1005.6091	1005.5576	-0.0515	-51	818	825	ELLISPKR			
1219.5411	1219.4606	-0.0805	-66	8	18	LPGFGEDECPER			
1219.5411	1219.4606	-0.0805	-66	8	18	LPGFGEDECPER			
1235.6024	1235.4514	-0.151	-122	578	587	VGQWNMMNKK			
1235.6024	1235.4514	-0.151	-122	578	587	VGQWNMMNKK			
1256.7321	1256.6686	-0.0635	-51	546	556	ISERLALVEAR			
1662.7928	1662.7927	-0.0001	0	261	275	ISLEEEDDGS GSERR			
1662.7928	1662.7927	-0.0001	0	261	275	ISLEEEDDGS GSERR			
1719.9285	1719.6744	-0.2541	-148	809	824	GPICGGMVRELLISFK			
1873.9291	1873.8872	-0.0419	-22	199	214	DLHQYDV SITPELTSR			
2056.8335	2056.9241	0.0906	44	985	1003	ARFYMESDSDSGSMAS GR			
2056.8335	2056.9241	0.0906	44	985	1003	ARFYMESDSDSGSMAS GR			
2230.0737	2230.0127	-0.061	-27	688	707	ICEIDLGLVSQCCTKQV FK			
2748.3086	2748.1941	-0.1145	-42	523	545	DIQMNVNHSYHEDPYAK EFGIK			
2807.5413	2807.187	-0.3543	-126	294	318	LEQFLAGRAEAPQEAL QVLDIVLR			
10	Ribulose biphosphate carboxylase large chain OS=Populus trichocarpa GN=rbcL PE=3 SV=1	RBL_POPTR	52567.5	6	10	42	0		
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	
910.4451	910.4054	-0.0397	-44	188	194	AVVECLR			
933.5515	933.4648	-0.0867	-93	9	18	AGVGFKAGVK			
1021.5312	1021.4777	-0.0535	-52	33	41	DTDILAAFR			
1465.7546	1465.6819	-0.0727	-50	147	159	TFQGGPPHQIQUER			
1471.7137	1471.7162	0.0025	2	464	475	EIKFEFQAMDTL			
1471.7137	1471.7162	0.0025	2	464	475	EIKFEFQAMDTL			
1481.7166	1481.6888	-0.0278	-19	320	334	MSGGDHHS GTVVGK			
1502.8512	1502.7661	-0.0851	-57	165	177	YGRPLLGTCTKPK			
1794.8149	1794.7247	-0.0902	-50	237	252	GHYLNATAGTCEEMIK			
2185.9819	2185.8806	-0.1013	-46	195	213	GGLDFTKDDENVNSQPF MR			
3854.8718	3854.7161	-0.1557	-40	42	79	VTPQGPVPEEAGAAYA AESSTGTWTTWTDGLT SLDR			

Gel Idx/Pos	142/F17	Instr./Gel Origin	BA2060/140227A					Process Statu	Analysis Succeeded	
Plate [#] Name	[1] 31564	Instrument Sample Name						Spectra	11	
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	
1	2-Cys peroxidoxin BAS1-like, chloroplastic OS=Arabidopsis thaliana GN=At5g06290 PE=2 SV=3	BAS1B_ARATH	29761.2	5.55	5	163	100	141	100	



## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
805.4818	805.4461	-0.0357	-44	203	209	GLFIIDK	21	0
805.4818	805.4461	-0.0357	-44	203	209	GLFIIDK		
809.4403	809.4078	-0.0325	-40	104	110	LSEYIGK		
2272.3064	2272.0881	-0.2183	-96	189	209	SFGVLIPDQGIARGLFIIDK		
2426.2808	2426.0273	-0.2535	-104	2	25	SMASIASSSSTLLSSSRVLLPSK		
2426.2808	2426.0273	-0.2535	-104	2	25	SMASIASSSSTLLSSSRVLLPSK		
2857.3826	2857.2473	-0.1353	-47	233	257	TLQALQVQENPDEVCPAGWKPGEK		
2857.3826	2857.2473	-0.1353	-47	233	257	TLQALQVQENPDEVCPAGWKPGEK	119	100

2 2-Cys peroxiredoxin BAS1, chloroplastic OS=Oryza sativa subsp. japonica GN=BAS1 PE=1 SV=1

## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
805.4818	805.4461	-0.0357	-44	191	197	GLFIIDK	21	0
805.4818	805.4461	-0.0357	-44	191	197	GLFIIDK		
1035.5721	1035.5234	-0.0467	-47	164	172	YPLISDVTK		
1035.5721	1035.5234	-0.0467	-47	164	172	YPLISDVTK	38	98.045
1051.5643	1051.6591	0.0948	90	51	60	SARASSFVAR		
1539.8713	1539.7032	-0.1681	-109	36	50	APAAERPLRLSASSSR		
1762.9585	1762.8585	-0.1	-57	156	172	SGGLGDLKYPILSDVTK		
2272.3064	2272.0881	-0.2183	-96	177	197	SFGVLIPDQGIARGLFIIDK		

3 Ubiquinol oxidase 1, mitochondrial OS=Glycine max GN=AOX1 PE=1 SV=1

## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
834.2977	834.3918	0.0941	113	2	7	MMMMSR		
882.4542	882.5265	0.0723	82	122	128	MAFWTVK		
1051.5604	1051.6591	0.0987	94	13	22	VANTAMPVAK		
1173.5746	1173.578	0.0034	3	181	190	ALLEEAENER		
1717.9343	1717.8577	-0.0766	-45	23	40	GLSGEVGLRALYGGGVRR		
1718.984	1718.866	-0.118	-69	70	84	VIVSYWGIQPSKITK		
1762.9374	1762.8585	-0.0789	-45	67	81	EEKVIVSYWGIQPSK		
2273.1348	2273.0955	-0.0393	-17	146	167	AMMLETVAAPGMVAGMLLHCK		
2560.4214	2560.2454	-0.176	-69	208	230	ALVITVGQVFFNAYFLGYLLSPK		
2857.3359	2857.2473	-0.0886	-31	142	167	YGCRRMMLETVAAPGMVAGMLLHCK		
2857.3359	2857.2473	-0.0886	-31	142	167	YGCRRMMLETVAAPGMVAGMLLHCK		
2873.3308	2873.2332	-0.0976	-34	142	167	YGCRRMMLETVAAPGMVAGMLLHCK		

4 Pentatricopeptide repeat-containing protein At5g14080 OS=Arabidopsis thaliana GN=At5g14080 PE=2 SV=

## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
809.4702	809.4078	-0.0624	-77	174	179	LFVKMR		
842.4341	842.4674	0.0333	40	592	597	HMQWIK		
856.4635	856.4855	0.0222	26	532	538	DHKTVTR		
1051.5605	1051.6591	0.0986	94	489	496	LFDKMLER		
1173.5609	1173.578	0.0171	15	97	106	QFSAMDALFK		
1193.6346	1193.5914	-0.0432	-36	518	527	IEAAMEVFRK		
1215.5562	1215.6008	0.0446	37	415	424	ESYTAQEMK		
1465.8196	1465.6821	-0.1375	-94	465	476	MNLTYYNLIRK		
1717.8102	1717.8577	0.0475	28	158	173	LLAGLTSDGCDYIAQK		
1868.0137	1867.8976	-0.1161	-62	563	578	EREHLEHTGAHVLLK		
2116.0129	2115.7903	-0.2226	-105	392	409	GYFSELQSYSLMISFLCK		
2426.1829	2426.0273	-0.1556	-64	497	517	GIEPDETIYMSLIEGLCKE TK		
2426.1829	2426.0273	-0.1556	-64	497	517	GIEPDETIYMSLIEGLCKE TK		
2691.2979	2691.1335	-0.1644	-61	454	475	LWDEMFVEGCKMNLTTY NVLIR		
2748.3193	2748.1858	-0.1335	-49	454	475	LWDEMFVEGCKMNLTTY NVLIR		

5 Probable monogalactosyldiacylglycerol synthase, chloroplastic OS=Glycine max GN=MGD A PE=2 SV=1

## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1499.7998	1499.7419	-0.0579	-39	140	153	KVLILMSDTGGGHR		
1561.8525	1561.6957	-0.1568	-100	193	205	SYSFLVKHSPILWK		
1717.6722	1717.8577	0.1855	108	414	427	MEECMGACDCIITK		
1718.8972	1718.866	-0.0312	-18	215	230	VVHQSNTFAATGTFIAR		
1725.8411	1725.9036	0.0625	36	288	302	LVTRCYPTTDVAQR		
1773.7382	1773.8177	0.0795	45	97	116	VGDGGDGADGNGNGEGNGVR		
2224.9414	2225.0005	0.0591	27	409	427	GFVTKMEECMGACDCIITK		
2272.2271	2272.0881	-0.139	-61	239	257	YQPDIIISVHPLMQHVPLR		
2857.2656	2857.2473	-0.0183	-6	414	439	MEECMGACDCITKAGPGTIAEAQIR		
2857.2656	2857.2473	-0.0183	-6	414	439	MEECMGACDCITKAGPGTIAEAQIR		
2903.4607	2903.2317	-0.229	-79	440	467	GLPIILNDYAGQEAQGNVPYVVENGCCK		
2903.4607	2903.2317	-0.229	-79	440	467	GLPIILNDYAGQEAQGNVPYVVENGCCK		

6 Pentatricopeptide repeat-containing protein At3g13150 OS=Arabidopsis thaliana GN=At3g13150 PE=2 SV=

## Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
805.4277	805.4461	0.0184	23	250	255	IWDLMK		

Modification	Rank	Result Type
		Mascot
		Mascot
		Mascot
		Mascot
Oxidation (M)[2]		Mascot
Oxidation (M)[2]		Mascot
Carbamidomethyl (C)[16]		Mascot
Carbamidomethyl (C)[16]		Mascot
99.994	60	99.986

Modification	Rank	Result Type
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot

Modification	Rank	Result Type
		0
Oxidation (M)[1,2,3]		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[3], Oxidation (M)[6,7,17]		Mascot
Carbamidomethyl (C)[3], Oxidation (M)[6,7,17]		Mascot
Carbamidomethyl (C)[3], Oxidation (M)[6,7,17,21]		Mascot
0		

Modification	Rank	Result Type
Oxidation (M)[5]		Mascot
		Mascot
		Mascot
		Mascot
Oxidation (M)[5]		Mascot
		Mascot
Oxidation (M)[9]		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[17]		Mascot
		Mascot
Carbamidomethyl (C)[17]		Mascot
		Mascot
Oxidation (M)[5]		Mascot
Carbamidomethyl (C)[10], Oxidation (M)[5]		Mascot

Modification	Rank	Result Type
		0
Oxidation (M)[6]		Mascot
		Mascot
Carbamidomethyl (C)[4,8,10]		Mascot
		Mascot
		Mascot
Carbamidomethyl (C)[9,13], Oxidation (M)[6,10]		Mascot
Oxidation (M)[13]		Mascot
Carbamidomethyl (C)[4,8], Oxidation (M)[1,5]		Mascot
Carbamidomethyl (C)[4,8], Oxidation (M)[1,5]		Mascot
		Mascot
		Mascot

Gen Idx/Pos	143F18	Instr/Gel Origin	BA2060/140227A					Process Status	Analysis Succeeded
Plate #	[1] 31564	Instrument Sample Name						Spectra	11
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	Oxygen-evolving enhancer protein 2, chloroplastic OS=Solarium tuberosum GN=PSBP PE=2 SV=1	PSBP_SOLTU	27987.1	8.27	6	111	100	83	100

1	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type	
	807.461	807.4203	-0.0407	-50	158	164	VDYLLGK	83	100	100	83	100	Mascot			
	1501.8049	1501.7609	-0.044	-29	158	170	VDYLLGKQAYFGK						Mascot			
	1572.7428	1572.6649	-0.0779	-50	144	157	SITDYGSPPEELSK						Mascot			
	1572.7428	1572.6649	-0.0779	-50	144	157	SITDYGSPPEELSK						Mascot			
	1597.9999	1597.8152	-0.1847	-116	53	68	RLALTLTGTAIGSK						Mascot			
	1626.8632	1626.8236	-0.0396	-24	22	36	TSSPSTSPKPNQLICR						Mascot			
2125.1182	2125.0105	-0.1077	-51	17	36	TSSPSTSPKPNQLICR	Mascot									
2	Oxygen-evolving enhancer protein 2, chloroplastic OS=Solarium lycopersicum GN=PSBP PE=2 SV=1					PSBP_SOLLC	27775	8.26	4	98	100	83	100			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
807.461	807.4203	-0.0407	-50	156	162	VDYLLGK	83	100	100	83	100	Mascot				
1501.8049	1501.7609	-0.044	-29	156	168	VDYLLGKQAYFGK						Mascot				
1572.7428	1572.6649	-0.0779	-50	142	155	SITDYGSPPEELSK						Mascot				
1572.7428	1572.6649	-0.0779	-50	142	155	SITDYGSPPEELSK						Mascot				
1597.9999	1597.8152	-0.1847	-116	51	66	RLALTLTGTAIGSK						Mascot				
1572.7428	1572.6649	-0.0779	-50	143	156	SITDYGSPPEELSK						Mascot				
3	Oxygen-evolving enhancer protein 2, chloroplastic OS=Pisum sativum GN=PSBP PE=1 SV=1					PSBP_PEA	28030.3	8.29	4	98	100	83	100			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
807.461	807.4203	-0.0407	-50	157	163	VDYLLGK	83	100	100	83	100	Mascot				
1010.5992	1010.4995	-0.0997	-99	217	225	HQLITATVK						Mascot				
1310.7427	1310.6458	-0.0969	-74	217	228	HQLITATVKDGGK						Mascot				
1572.7428	1572.6649	-0.0779	-50	143	156	SITDYGSPPEELSK						Mascot				
1572.7428	1572.6649	-0.0779	-50	143	156	SITDYGSPPEELSK						Mascot				
1572.7428	1572.6649	-0.0779	-50	143	156	SITDYGSPPEELSK						Mascot				
4	Oxygen-evolving enhancer protein 2, chloroplastic OS=Fritillaria agrestis GN=PSBP PE=2 SV=1					PSBP_FRIAG	28094.2	8.31	2	88	99.994	79	100			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
1173.6262	1173.5758	-0.0504	-43	117	126	EVEFPGQVLR	79	100	100	79	100	Mascot				
1173.6262	1173.5758	-0.0504	-43	117	126	EVEFPGQVLR						Mascot				
3955.9922	3955.8237	-0.1685	-43	175	212	TASEGGFDPDSVATANIL						Mascot				
						EVSTPVVGKQYYNISVL										
						TR										
3955.9922	3955.8237	-0.1685	-43	175	212	TASEGGFDPDSVATANIL						Mascot				
						EVSTPVVGKQYYNISVL										
						TR										
5	Oxygen-evolving enhancer protein 2, chloroplastic OS=Narcissus pseudonarcissus GN=PSBP PE=2 SV=1					PSBP_NARPS	28503.3	6.6	2	83	99.982	77	100			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
1173.5422	1173.5758	0.0336	29	254	265	FVESAASSFSA	79	100	100	77	100	Mascot				
1173.6262	1173.5758	-0.0504	-43	118	127	EVEFPGQVLR						Mascot				
6	Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Nicotiana tabacum GN=PSBP1 PE=3 SV=2					PSBP1_TOBAC	28634.4	6.84	1	78	99.952	79	100			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
1173.6262	1173.5758	-0.0504	-43	121	130	EVEFPGQVLR	79	100	100	79	100	Mascot				
1173.6262	1173.5758	-0.0504	-43	121	130	EVEFPGQVLR						Mascot				
7	Bowman-Birk type proteinase inhibitor I-2B (Fragment) OS=Triticum aestivum PE=1 SV=1					IBB1_WHEAT	6218.9	8.67	7	45	0					
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
842.4553	842.4736	0.0183	22	18	24	SIPPICR	37	45	45	0	0	Carbamidomethyl (C)[6]	Mascot			
998.3852	998.5199	0.1347	135	9	17	CCDQAVCTR						Mascot				
1010.4724	1010.4995	0.0271	27	49	RVCCDQYV	Mascot										
1258.5957	1258.6252	0.0295	23	38	49	ACGPSVGDPSRR						Carbamidomethyl (C)[2]	Mascot			
1258.5957	1258.6252	0.0295	23	38	49	ACGPSVGDPSRR						Carbamidomethyl (C)[2]	Mascot			
1620.6161	1620.7795	0.1634	101	25	37	CMDDQVFCPSCK						Carbamidomethyl (C)[1,8], Oxidation (M)[2]	Mascot			
1736.7777	1736.8563	0.0786	45	5	17	RPWKCDDQAVCTR						Carbamidomethyl (C)[5,6,11]	Mascot			
2272.9893	2273.0874	0.0981	43	18	37	SIPPICRMDQVFCPSTCK						Oxidation (M)[9]	Mascot			
8	50S ribosomal protein L20, plastid OS=Aneura mirabilis GN=rpL20 PE=3 SV=1					RK20_ANEMR	13920.9	12.01	7	42	0					
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
842.5359	842.4736	-0.0623	-74	59	64	RLWIVR	30	42	42	0	0	Mascot				
870.5155	870.5006	-0.0149	-17	86	92	NOILLNR						Mascot				
998.6105	998.5199	-0.0906	-91	86	93	NOILLNRK						Mascot				
1155.6157	1155.5593	-0.0564	-49	16	25	NLFTLTSGFR						Mascot				
1310.8055	1310.6458	-0.1597	-122	60	70	LWIVRNAAVR						Mascot				
1665.849	1665.808	-0.041	-25	34	48	TANQGMRALVASYR						Mascot				
1665.8707	1665.808	-0.0627	-38	16	30	NLFTLTSGFRGTHSK						Mascot				
9	Photosystem I iron-sulfur center OS=Chlamydomonas reinhardtii GN=psaC PE=1 SV=2					PSAC_CHLRE	8854.1	5.65	7	41	0					
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
1010.4393	1010.4995	0.0602	60	45	53	TEDCVGCKR	19	41	41	0	0	Carbamidomethyl (C)[5,8]	Mascot			
1588.6917	1588.653	-0.0387	-24	7	19	YDTCIGCTQCVR						Carbamidomethyl (C)[5,8]	Mascot			
1588.6917	1588.653	-0.0387	-24	7	19	YDTCIGCTQCVR						Carbamidomethyl (C)[5,8]	Mascot			
1597.7461	1597.8152	0.0691	43	53	66	RCETACPTDLSVR						Mascot				
1665.7788	1665.808	0.0292	18	67	81	VYLGSESTRSMGLSY						Oxidation (M)[11]	Mascot			
1665.7788	1665.808	0.0292	18	67	81	VYLGSESTRSMGLSY						Oxidation (M)[11]	Mascot			
1810.7881	1810.84	0.0519	29	36	52	ASQMASAPRTEDCVGCK						Carbamidomethyl (C)[13]	Mascot			
2211.0542	2210.9902	-0.064	-29	1	19	MAHIVKIYDTCIGCTQCV						Carbamidomethyl (C)[11]	Mascot			
2691.2397	2691.1631	-0.0766	-28	20	44	ACPLDVLEMVPWDGCKA						Oxidation (M)[9]	Mascot			
						SQMASAPR										
2748.2612	2748.1672	-0.094	-34	20	44	ACPLDVLEMVPWDGCKA	Carbamidomethyl (C)[2], Oxidation (M)[9]	Mascot								
						SQMASAPR										
10	Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Arabidopsis thaliana GN=PSBP1 PE=1 SV=2					PSBP1_ARATH	28077.9	6.9	2	40	0	34	93.644			
Peptide Information																
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		

				Seq.	Seq.	Score
1588.7278	1588.653	-0.0748	-47	91	104	TNTDFLPYNGDGFK
1588.7278	1588.653	-0.0748	-47	91	104	TNTDFLPYNGDGFK
2211.1079	2210.9902	-0.1177	-53	91	110	TNTDFLPYNGDGFKVQV PAK

Mascot
Mascot
Mascot

Gel Idx/Pos	144/F19	Instr./Gel Origin	BA2060/140227A	Process Status	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN21 PE=1 SV=2	CH10C_ARATH	26785.5	8.86	5	110	100	89	100
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
922.455	922.4202	-0.0348	-38	245	253	ASDVMAILS			
970.5316	970.4867	-0.0449	-46	159	166	DLKPLNDR	58	99.976	Oxidation (M)[5]
970.5316	970.4867	-0.0449	-46	159	166	DLKPLNDR			
1149.6262	1149.5675	-0.0587	-51	59	68	YTSIKPLGDR	30	85.535	
1149.6262	1149.5675	-0.0587	-51	59	68	YTSIKPLGDR			
1403.7853	1403.6495	-0.1358	-97	17	30	SLASLDGLRASSVK			
1403.7853	1403.6495	-0.1358	-97	17	30	SLASLDGLRASSVK			
1457.8474	1457.6346	-0.2128	-146	159	170	DLKPLNDRVFIK			
2	Chlorophyll a-b binding protein 3, chloroplastic OS=Pisum sativum GN=hca3 PE=1 SV=1	CB23_PEA	29588.2	8.84	4	86	99.991	70	99.998
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
997.5352	997.4864	-0.0488	-49	185	192	QYFLGLEK			
1179.7208	1179.5626	-0.1582	-134	38	49	GLVRAAATPPVK			
1277.6637	1277.6028	-0.0609	-48	97	107	WLAYGEVINGR			
1277.6637	1277.6028	-0.0609	-48	97	107	WLAYGEVINGR	70	99.998	
3556.6753	3556.4795	-0.1958	-55	63	96	QSLSYLDGSLPGDYGFD PLGLSDPEGTGGFIEPR			
3	Chlorophyll a-b binding protein 8, chloroplastic OS=Solanum lycopersicum GN=CAB8 PE=3 SV=1	CB13_SOLLC	29344.2	8.96	3	80	99.966	70	99.998
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
997.5352	997.4864	-0.0488	-49	183	190	QYFLGLEK			
1277.6637	1277.6028	-0.0609	-48	95	105	WLAYGEVINGR			
1277.6637	1277.6028	-0.0609	-48	95	105	WLAYGEVINGR	70	99.998	
2547.2512	2547.0955	-0.1557	-61	191	216	GLGSGDPAYPGGPLFN PLGFGKDEK			
4	ATP synthase subunit alpha, chloroplastic OS=Cucumis sativus GN=atpA PE=3 SV=1	ATPA_CUCSA	55348	5.13	9	78	99.951	46	99.561
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			
901.485	901.4409	-0.0441	-49	406	413	ATQNQLAR			
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1278.778	1278.5961	-0.1819	-142	129	140	LIESPAPGILLR			
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIIRER			
1403.6802	1403.6495	-0.0307	-22	255	266	QHTSIYDDPSK			
1403.6802	1403.6495	-0.0307	-22	255	266	QHTSIYDDPSK			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR	46	99.561	
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFQEIISSTK			
5	ATP synthase subunit alpha, chloroplastic OS=Daucus carota GN=atpA PE=3 SV=1	ATPA_DAUCA	55451.2	5.34	9	78	99.948	46	99.561
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.4825	876.4386	-0.0439	-50	501	507	FILQEQV			
901.485	901.4409	-0.0441	-49	406	413	ATQNQLAR			
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1179.6005	1179.5626	-0.0379	-32	17	25	IEEYNREVK			
1278.6722	1278.5961	-0.0761	-60	1	11	MYTRADEISK			
1457.7747	1457.6346	-0.1401	-96	255	266	RHTLIYDDPSK			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR	46	99.561	
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFQEIISSTK			
6	ATP synthase subunit alpha, chloroplastic OS=Ceratophyllum demersum GN=atpA PE=3 SV=1	ATPA_CERDE	55173	5.48	7	75	99.891	46	99.561
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
870.4791	870.5017	0.0226	26	423	430	QSQAAPLR	8	0	
870.4791	870.5017	0.0226	26	423	430	QSQAAPLR			
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			
901.485	901.4409	-0.0441	-49	406	413	ATQNQLAR			
1107.5542	1107.5231	-0.0311	-28	15	22	ERIEQYNNR			
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIIRER			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR	46	99.561	
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFQEIISSTK			
7	ATP synthase subunit alpha, chloroplastic OS=Carica papaya GN=atpA PE=3 SV=1	ATPA_CARPA	55136.9	5.1	8	72	99.802	46	99.561
Peptide Information									
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			
901.485	901.4409	-0.0441	-49	406	413	ATQNQLAR			
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR			
1107.5542	1107.5231	-0.0311	-28	15	22	ERIEQYNNR			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1149.5205	1149.5675	0.0047	41	492	500	EAIQEQMER			
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIIRER			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR			
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFYLHSR	46	99.561	
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFQEIISSTK			
8	ATP synthase subunit alpha, chloroplastic OS=Atropa	ATPA_ATTRBE	55419.1	5.26	8	72	99.783	46	99.561

belladonna GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
901.485	901.4409	-0.0441	-49	406	413	ATONQLAR					Mascot
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR					Mascot
1107.5542	1107.5231	-0.0311	-28	15	22	ERIEQYNR					Mascot
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIRER					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR	46	99.561			Mascot
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFOEISSTK			Oxidation (M)[18]		Mascot
2225.1006	2224.9854	-0.1152	-52	481	499	TFTEEAELLKEAIEQMK					Mascot

9 ATP synthase subunit alpha, chloroplastic  
OS=Nicotiana tomentosiformis GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
901.485	901.4409	-0.0441	-49	406	413	ATONQLAR					Mascot
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR					Mascot
1089.5171	1089.4922	-0.0249	-23	492	500	EAIEQQTDR					Mascot
1107.5542	1107.5231	-0.0311	-28	15	22	ERIEQYNR					Mascot
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIRER					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR	46	99.561			Mascot
1620.8591	1620.7693	-0.0898	-55	467	480	TNKPQFOEISSTK					Mascot

10 ATP synthase subunit alpha, chloroplastic OS=Panax ginseng GN=atpA PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
876.4971	876.4386	-0.0585	-67	273	279	QMSLLLR			Oxidation (M)[2]		Mascot
901.485	901.4409	-0.0441	-49	406	413	ATONQLAR					Mascot
904.5614	904.5168	-0.0446	-49	456	462	KFLVELR					Mascot
1089.5171	1089.4922	-0.0249	-23	492	500	EAIEQQTDR					Mascot
1107.5542	1107.5231	-0.0311	-28	15	22	ERIEQYNR					Mascot
	1107.5231										Mascot
1315.6964	1315.5541	-0.1423	-108	6	16	ADEISNIRER					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR					Mascot
1553.7383	1553.6553	-0.083	-53	285	297	EAYPGDVFLHSR	46	99.535			Mascot
1620.8955	1620.7693	-0.1262	-78	467	480	TNKPQFOEISSTK					Mascot

Gel Idx/Pos		145/F20		Instr./Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate [#] Name		[1] 31564									
Rank	Protein Name	Accession No.	Protein MW	Protein	Pep.	Protein	Protein	Total Ion	Spectra	11	
								Total Ion			

1 Oxygen-evolving enhancer protein 2, chloroplastic  
OS=Solanum tuberosum GN=PSBP PE=2 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
807.461	807.4173	-0.0437	-54	158	164	VDYLLGK					Mascot
1187.6418	1187.5825	-0.0593	-50	113	122	IEFFPGQVLR					Mascot
1501.8049	1501.7622	-0.0427	-28	158	170	VDYLLGKQAYFGK					Mascot
1572.7428	1572.6691	-0.0737	-47	144	157	SITDYGSPPEEFLSK	85	100			Mascot
1572.7428	1572.6691	-0.0737	-47	144	157	SITDYGSPPEEFLSK					Mascot
1597.9999	1597.8198	-0.1801	-113	53	68	RLALLTLIGTAAIGSK					Mascot
2125.1182	2125.0164	-0.1018	-48	17	36	SSPARTSSVSPKPNQLICR					Mascot

2 Oxygen-evolving enhancer protein 2, chloroplastic  
OS=Pisum sativum GN=PSBP PE=1 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
807.461	807.4173	-0.0437	-54	157	163	VDYLLGK					Mascot
1010.5992	1010.4967	-0.1025	-101	217	225	HQLITATVK					Mascot
1310.7427	1310.642	-0.1007	-77	217	228	HQLITATVKDGGK					Mascot
1572.7428	1572.6691	-0.0737	-47	143	156	SITDYGSPPEEFLSK	85	100			Mascot
1572.7428	1572.6691	-0.0737	-47	143	156	SITDYGSPPEEFLSK					Mascot
2807.3716	2807.1792	-0.1924	-69	1	24	MASTOCFLHHQYAITTPTRTLSGR					Mascot
									Oxidation (M)[1]		

3 Oxygen-evolving enhancer protein 2, chloroplastic  
OS=Solanum lycopersicum GN=PSBP PE=2 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
807.461	807.4173	-0.0437	-54	156	162	VDYLLGK					Mascot
1501.8049	1501.7622	-0.0427	-28	156	168	VDYLLGKQAYFGK					Mascot
1572.7428	1572.6691	-0.0737	-47	142	155	SITDYGSPPEEFLSK	85	100			Mascot
1572.7428	1572.6691	-0.0737	-47	142	155	SITDYGSPPEEFLSK					Mascot
1597.9999	1597.8198	-0.1801	-113	51	66	RLALLTLIGTAAIGSK					Mascot

4 Oxygen-evolving enhancer protein 2-1, chloroplastic  
OS=Arabidopsis thaliana GN=PSBP1 PE=1 SV=2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1588.7278	1588.6523	-0.0755	-48	91	104	TNTDFLPYNGDGFK					Mascot
1588.7278	1588.6523	-0.0755	-48	91	104	TNTDFLPYNGDGFK	92	100			Mascot
2211.1079	2210.9929	-0.115	-52	91	110	TNTDFLPYNGDGFKVQVPAK					Mascot

5 Oxygen-evolving enhancer protein 2, chloroplastic  
OS=Fritillaria agrestis GN=PSBP PE=2 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
1173.6262	1173.5789	-0.0473	-40	117	126	EVEFFPGQVLR	78	100			Mascot
1173.6262	1173.5789	-0.0473	-40	117	126	EVEFFPGQVLR					Mascot
3955.9922	3955.8384	-0.1538	-39	175	212	TASEGGFDPDSVATANILEVSTPVVGGKQYYNISVLTR					Mascot
3955.9922	3955.8384	-0.1538	-39	175	212	TASEGGFDPDSVATANILEVSTPVVGGKQYYNISVL					Mascot

6	Oxygen-evolving enhancer protein 2, chloroplastic OS=Narcissus pseudonarcissus GN=PSBP PE=2 SV=1	PSBP_NARPS	28503.3	6.6	2	82	99.98	76	100			
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1173.5422	1173.5789	0.0367	31	254	265	FVESAASSFSA					Mascot
	1173.6262	1173.5789	-0.0473	-40	118	127	EVEFPGQVLR					Mascot
7	Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Nicotiana tabacum GN=PSBP1 PE=3 SV=2	PSBP1_TOBAC	28634.4	6.84	1	78		78	100	99.945	78	100
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1173.6262	1173.5789	-0.0473	-40	121	130	EVEFPGQVLR					Mascot
	1173.6262	1173.5789	-0.0473	-40	121	130	EVEFPGQVLR	78	100			Mascot
8	50S ribosomal protein L16, chloroplastic OS=Chloranthus spicatus GN=rpl16 PE=3 SV=1	RK16_CHLSC	15447.2	11.36	7	44				0		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	807.4246	807.4173	-0.0073	-9	130	136	TQFVIAE					Mascot
	870.4501	870.5037	0.0536	62	18	24	MKGISYR			Oxidation (M)[1]		Mascot
	1456.7113	1456.5941	-0.1172	-80	20	32	GISYRGNNICFGR					Mascot
	1554.7832	1554.7006	-0.0826	-53	103	116	ILYEMAGVSESIAR			Oxidation (M)[5]		Mascot
	2230.2012	2230.1104	-0.0908	-41	69	88	IFDPKPVITRPTETRMGS GK					Mascot
	2273.2036	2273.0762	-0.1274	-56	33	52	YALQALEPAWITSRQIEA GR					Mascot
	2424.2625	2424.2339	-0.0286	-12	103	125	ILYEMAGVSESIARAAISIA ACK			Carbamidomethyl (C)[22]		Mascot
	2424.2625	2424.2339	-0.0286	-12	103	125	ILYEMAGVSESIARAAISIA ACK			Carbamidomethyl (C)[22]		Mascot
9	Carbonic anhydrase, chloroplastic OS=Hordeum vulgare PE=2 SV=1	CAHC_HORVU	35051.8	8.93	9	43				0		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1059.5906	1059.5385	-0.0521	-49	2	10	SLQIGRTER					Mascot
	1059.5906	1059.5385	-0.0521	-49	2	10	SLQIGRTER					Mascot
	1187.6683	1187.5825	-0.0858	-72	13	22	SPVFFVFAHKK					Mascot
	1206.626	1206.5693	-0.0567	-47	1	10	MSLQIGRTER			Oxidation (M)[1]		Mascot
	1258.7054	1258.6292	-0.0762	-61	11	21	ARSPVFVFAHK					Mascot
	1258.7054	1258.6292	-0.0762	-61	11	21	ARSPVFVFAHK					Mascot
	1465.729	1465.6846	-0.0444	-30	188	200	NIANMVPAYCKNK					Mascot
	1665.9468	1665.8046	-0.1422	-85	217	232	VEVIVIGHSRCGGIK					Mascot
	1794.7717	1794.7456	-0.0261	-15	239	253	DGADDSFHFVEDWVR					Mascot
	2272.0295	2272.0859	0.0564	25	261	280	KVQTECASMPFDDQCTV LEK					Mascot
	2455.1572	2454.9763	-0.1809	-74	63	84	TTSHYSTAAANWCYATV APRAR			Carbamidomethyl (C)[13]		Mascot
10	Cyclic dof factor 2 OS=Arabidopsis thaliana GN=CDF2 PE=1 SV=2	CDF2_ARATH	49777	5.19	10	43				0		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1059.6198	1059.5385	-0.0813	-77	2	11	ADPAIKLFGK					Mascot
	1059.6198	1059.5385	-0.0813	-77	2	11	ADPAIKLFGK					Mascot
	1158.6226	1158.5629	-0.0597	-52	426	436	SSLSEGRLLPGR					Mascot
	1173.5759	1173.5789	0.003	3	190	199	NKSPASHYNR					Mascot
	1173.5759	1173.5789	0.003	3	190	199	NKSPASHYNR					Mascot
	1195.4896	1195.5499	0.0603	50	82	91	DSECOEESLR					Mascot
	1206.655	1206.5693	-0.0857	-71	1	11	MADPAIKLFGK			Oxidation (M)[1]		Mascot
	1357.6958	1357.6117	-0.0841	-62	386	397	TLRIDDPPEAAK					Mascot
	1357.6958	1357.6117	-0.0841	-62	386	397	TLRIDDPPEAAK					Mascot
	1456.7642	1456.5941	-0.1701	-117	252	264	TQTVLQEPNEGLK					Mascot
	1554.6337	1554.7006	0.0669	43	116	130	TNEESGGTACSQEGK			Carbamidomethyl (C)[10]		Mascot
	1767.7814	1767.8726	0.0912	52	113	130	AAKTNEESGGTACSQEG K					Mascot
	2230.0669	2230.1104	0.0435	20	192	211	SPASHYNRHVITSAEAM QK			Oxidation (M)[18]		Mascot
Gel Idx/Pos Plate [#] Name	146/F21 [1] 31564	Instr./Gel Origin Instrument Sample Name		BA2060/140227A				Process Statu Spectra		Analysis Succeeded 11		
Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %			
1	Carbonic anhydrase OS=Flaveria brownii PE=2 SV=1	CAHX_FLABR	35524.8	5.7	4	144	100	131	100			
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1219.5234	1219.4845	-0.0389	-32	156	165	FMVFACSDSR			Carbamidomethyl (C)[6]		Mascot
	1235.5183	1235.4778	-0.0405	-33	156	165	FMVFACSDSR			Carbamidomethyl (C)[6]		Mascot
	1892.0276	1891.9531	-0.0745	-39	277	293	EAVNVSLGNLLTYPFVR			Oxidation (M)[2]		Mascot
	1892.0276	1891.9531	-0.0745	-39	277	293	EAVNVSLGNLLTYPFVR	51	99.873			Mascot
	1928.9019	1928.783	-0.1189	-62	37	55	FTCNSSSSSSATPPSLI R					Mascot
	2057.0273	2056.9507	-0.0766	-37	166	183	VCPSHVLDFQPGAEFVV R	80	100	Carbamidomethyl (C)[2]		Mascot
	2057.0273	2056.9507	-0.0766	-37	166	183	VCPSHVLDFQPGAEFVV R			Carbamidomethyl (C)[2]		Mascot
2	Carbonic anhydrase OS=Flaveria bidentis PE=2 SV=2	CAHX_FLABI	35522.9	5.85	3	140		100	131	100		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1219.5234	1219.4845	-0.0389	-32	156	165	FMVFACSDSR			Carbamidomethyl (C)[6]		Mascot
	1235.5183	1235.4778	-0.0405	-33	156	165	FMVFACSDSR			Carbamidomethyl (C)[6]		Mascot
	1892.0276	1891.9531	-0.0745	-39	277	293	EAVNVSLGNLLTYPFVR			Oxidation (M)[2]		Mascot
	1892.0276	1891.9531	-0.0745	-39	277	293	EAVNVSLGNLLTYPFVR	51	99.873			Mascot
	2057.0273	2056.9507	-0.0766	-37	166	183	VCPSHVLDFQPGAEFVV R	80	100	Carbamidomethyl (C)[2]		Mascot
	2057.0273	2056.9507	-0.0766	-37	166	183	VCPSHVLDFQPGAEFVV R			Carbamidomethyl (C)[2]		Mascot
3	Carbonic anhydrase, chloroplastic OS=Pisum sativum PE=1 SV=1	CAHC_PEA	35355.1	7.01	4	93		99.998	80	100		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type

		948.446	948.4158	-0.0302	-32	303	310	GGYDFVK									Mascot
		1481.7634	1481.7046	-0.0588	-30	136	148	YKNPALYGELAK									Mascot
		1610.8683	1610.8073	-0.061	-38	211	226	VSNIVVGHHSACGGIK									Mascot
		2057.0273	2056.9507	-0.0766	-37	164	181	VCPSHVLDFQPGAEFVV R	80	100			Carbamidomethyl (C)[12]				Mascot
													Carbamidomethyl (C)[2]				Mascot
		2057.0273	2056.9507	-0.0766	-37	164	181	VCPSHVLDFQPGAEFVV R					Carbamidomethyl (C)[2]				Mascot
4	Carbonic anhydrase, chloroplastic OS=Nicotiana tabacum PE=2 SV=1						CAHC_TOBAC	34488.6	6.41	6	73		99.831	49	99.813		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	954.5366	954.45	-0.0866	-91	85	94	GELGPAAAR										Mascot
	1219.5234	1219.4845	-0.0389	-32	147	156	FMVFACSDSR						Carbamidomethyl (C)[6]				Mascot
	1235.5183	1235.4776	-0.0405	-33	147	156	FMMVFACSDSR						Carbamidomethyl (C)[6], Oxidation (M)[2]				Mascot
	1652.8788	1652.8159	-0.0629	-38	204	219	VENIVVGHHSACGGIK						Carbamidomethyl (C)[12]				Mascot
	1891.9794	1891.9531	-0.0263	-14	2	20	STASINSLTISPAQASLK										Mascot
	1892.0276	1891.9531	-0.0745	-39	268	284	EAVNVSLGNLLTYPFVR		51	99.873							Mascot
	2224.9419	2225.0371	0.0952	43	249	267	VGGEHVDKCFADQCCTAC EK						Carbamidomethyl (C)[9,14]				Mascot
5	Carbonic anhydrase, chloroplastic OS=Spinacia oleracea PE=1 SV=2						CAHC_SPIOL	34547.6	6.61	4	63		98.462	51	99.873		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	1219.5234	1219.4845	-0.0389	-32	145	154	FMVFACSDSR						Carbamidomethyl (C)[6]				Mascot
	1235.5183	1235.4778	-0.0405	-33	145	154	FMMVFACSDSR						Carbamidomethyl (C)[6], Oxidation (M)[2]				Mascot
	1652.8788	1652.8159	-0.0629	-38	202	217	VENIVVGHHSACGGIK						Carbamidomethyl (C)[12]				Mascot
	1892.0276	1891.9531	-0.0745	-39	266	282	EAVNVSLGNLLTYPFVR										Mascot
	1892.0276	1891.9531	-0.0745	-39	266	282	EAVNVSLGNLLTYPFVR		51	99.873							Mascot
	2327.0901	2326.9954	-0.0947	-41	218	238	GLMSFPDAGPTTTDFIED WVK										Mascot
6	Carbonic anhydrase 2 (Fragment) OS=Flaveria linearis PE=2 SV=1						CAH2_FLALI	20571.5	6.21	1	55		89.361	51	99.873		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	1892.0276	1891.9531	-0.0745	-39	137	153	EAVNVSLGNLLTYPFVR										Mascot
	1892.0276	1891.9531	-0.0745	-39	137	153	EAVNVSLGNLLTYPFVR		51	99.873							Mascot
7	Ribulose biphosphate carboxylase large chain (Fragment) OS=Amorphophallus titanum GN=rbcL PE=3 SV=						RBL_AMOTI	52548.4	6.32	11	44		0				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	837.4828	837.389	-0.0938	-112	1	8	TKASVGFK										Mascot
	914.3858	914.3723	-0.0135	-15	182	188	ACYEQLR						Carbamidomethyl (C)[2]				Mascot
	1219.5789	1219.4845	-0.0944	-77	298	306	QKYHGMHFR						Oxidation (M)[6]				Mascot
	1261.6285	1261.6704	0.0419	33	212	221	FLFCAALYK						Carbamidomethyl (C)[4]				Mascot
	1465.7216	1465.6996	-0.022	-15	314	328	MSGGDHIHAGTVVGK										Mascot
	1481.7166	1481.7046	-0.012	-8	314	328	MSGGDHIHAGTVVGK						Oxidation (M)[1]				Mascot
	1632.7509	1632.8217	0.0708	43	182	195	ACYECLRGGLDFTK						Carbamidomethyl (C)[2]				Mascot
	1794.8149	1794.7432	-0.0717	-40	231	246	GHYLNATAGTCEMIK						Carbamidomethyl (C)[11]				Mascot
	1966.9109	1966.826	-0.0849	-43	231	247	GHYLNATAGTCEMIKIR						Carbamidomethyl (C)[11], Oxidation (M)[14]				Mascot
	2057.0259	2056.9507	-0.0752	-37	334	350	EMTLGFVLLRDDYIEK										Mascot
	2057.0259	2056.9507	-0.0752	-37	334	350	EMTLGFVLLRDDYIEK										Mascot
	2169.9868	2170.0371	0.0503	23	189	207	GGLDFTKDDENVNSQPF MR										Mascot
	2185.9819	2186.0249	0.043	20	189	207	GGLDFTKDDENVNSQPF MR						Oxidation (M)[18]				Mascot
	2211.1191	2211.0229	-0.0962	-44	134	153	IPPAYSKTFEGPHGIQS ER										Mascot
8	ADP-ribosylation factor GTPase-activating protein AGD2 OS=Arabidopsis thaliana GN=AGD2 PE=2 SV=1						AGD2_ARATH	87748.1	6.21	13	44		0				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	1096.5065	1096.5542	0.0477	44	663	671	RHPDNACQR										Mascot
	1132.5593	1132.5425	-0.0168	-15	229	237	EQSKIEQDR										Mascot
	1261.7085	1261.6704	-0.0381	-30	388	397	LCFRISPOK						Carbamidomethyl (C)[2]				Mascot
	1388.7573	1388.6703	-0.087	-63	528	538	VWEPTILDLFR										Mascot
	1589.8381	1589.8923	-0.1458	-92	374	387	TSLLKLDADETDLR										Mascot
	1647.8897	1647.8289	-0.0599	-36	410	423	MDWVVKITAATIR						Oxidation (M)[1]				Mascot
	1738.9156	1738.8536	-0.082	-47	169	183	SRFNLVNSLMTIEAK						Oxidation (M)[10]				Mascot
	1759.803	1759.7826	-0.0204	-12	1	15	MAGFINLEDSPMFOK						Oxidation (M)[1,12]				Mascot
	1891.9257	1891.9531	0.0274	14	603	619	EANSTASSRIWEAVQSR										Mascot
	1891.9257	1891.9531	0.0274	14	603	619	EANSTASSRIWEAVQSR										Mascot
	2225.0901	2225.0371	-0.053	-24	359	378	SASQGLSDCNMIDLR TSLIK						Carbamidomethyl (C)[9], Oxidation (M)[11]				Mascot
	2308.1145	2308.0266	-0.0879	-38	312	330	FFVLDNHGSLYYRNTG NK										Mascot
	2760.282	2760.4453	0.1633	59	247	272	TQSELD SQASAKADPS DVGNGHYVR										Mascot
	2760.282	2760.4453	0.1633	59	247	272	TQSELD SQASAKADPS DVGNGHYVR										Mascot
	2807.4614	2807.2153	-0.2461	-88	205	228	LGYDLLSQLEPYIHQVLT YAAQSK										Mascot
9	Antiviral protein DAP-30 OS=Dianthus caryophyllus PE=1 SV=2						RIP0_DIACA	32696.9	9.07	8	41		0				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	933.5073	933.4817	-0.0256	-27	264	271	DLQMLLK						Oxidation (M)[4]				Mascot
	948.4097	948.4158	0.0061	6	251	258	YDYDFGFK										Mascot
	1647.925	1647.8289	-0.0961	-58	264	277	DLQMLKKYLGRPK						Oxidation (M)[4]				Mascot
	2057.1675	2056.9507	-0.2168	-105	161	179	KELGLGINLLTIMDGVNKK						Oxidation (M)[13]				Mascot
	2057.1675	2056.9507	-0.2168	-105	162	180	ELGLGINLLTIMDGVNKK						Oxidation (M)[12]				Mascot
	2225.113	2225.0371	-0.0759	-34	92	110	RENLYVVAYLAMDNAV NR										Mascot
	2272.2183	2272.1069	-0.1114	-49	116	136	NQITSAELTALFPEVVVA NQK										Mascot
	2314.1899	2314.1257	-0.0642	-28	225	244	VIQFQVSWSKISTAIFGDC K						Carbamidomethyl (C)[19]				Mascot
10	Ribulose biphosphate carboxylase large chain (Fragment) OS=Galium parisiense GN=rbcL PE=3 SV=1						RBL_GALPR	50275.4	6.58	10	40		0				
	Peptide Information																

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
914.4049	914.3723	-0.0326	-36	306	312	NHGMHFR			Oxidation (M)[4]		Mascot
933.5515	933.4817	-0.0698	-75	9	18	AGVGFKAGVK			Carbamidomethyl (C)[4]		Mascot
1261.6285	1261.6704	0.0419	33	218	227	FLFCAEAIYK					Mascot
1465.7546	1465.6996	-0.055	-38	147	159	TFQGPPIGQVER					Mascot
1481.7166	1481.7046	-0.012	-8	320	334	MSGGDHIHSGTVVGK					Mascot
1647.8007	1647.8289	0.0282	17	436	450	DLASEGGIIREACK			Carbamidomethyl (C)[14]		Mascot
1794.8149	1794.7432	-0.0717	-40	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot
1966.9109	1966.826	-0.0849	-43	237	253	GHYLNATAGTCEEMIKR			Carbamidomethyl (C)[11], Oxidation (M)[14]		Mascot
2169.9868	2170.0371	0.0503	23	195	213	GGDLFTKDDENVNSQPF MR					Mascot
2185.9819	2186.0249	0.043	20	195	213	GGDLFTKDDENVNSQPF MR			Oxidation (M)[18]		Mascot
2308.1931	2308.0266	-0.1665	-72	33	53	DTDILAAFRVTPQPGVPP EER					Mascot

Gel Idx/Pos		147/F22		Instr./Gel Origin			BA2060/140227A			Process Status		Analysis Succeeded			
Plate [#] Name		[1] 31564										Spectra		11	
Rank	Protein Name			Accession No.		Protein MW	Protein	Pep.	Protein	Protein	Total Ion	Total Ion			

1	ATP synthase delta chain, chloroplastic OS=Spinacia oleracea GN=ATPD PE=1 SV=2	ATPD_SPIOL	27663.7	5.8	3	142	100	132	100
---	--	------------	---------	-----	---	-----	-----	-----	-----

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
858.5155	858.455	-0.0605	-70	201	208	ITGAKNVR	32	89.253			Mascot
858.5155	858.455	-0.0605	-70	201	208	ITGAKNVR					Mascot
1488.842	1488.7886	-0.0534	-36	211	224	TVIDPSLVAGFTIR	100	100			Mascot
1488.842	1488.7886	-0.0534	-36	211	224	TVIDPSLVAGFTIR					Mascot
1526.752	1526.7103	-0.0417	-27	225	238	YQNEGSKLVDMSVK					Mascot

2	Ribulose biphosphate carboxylase large chain OS=Castanea sativa GN=rbcl PE=3 SV=1	RBL_CASSA	52662.6	6.33	12	90	99.997	36	95.787
---	---	-----------	---------	------	----	----	--------	----	--------

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
853.4236	853.5193	0.0957	112	188	194	AVYECLR					Mascot
880.4536	880.4293	-0.0243	-28	306	312	NHGHFR					Mascot
1021.5312	1021.4948	-0.0364	-36	33	41	DTDILAAFR					Mascot
1053.4847	1053.5804	0.0957	91	351	358	DDYIEKDR					Mascot
1275.7307	1275.6049	-0.1258	-99	340	350	EITLGFVDLLR					Mascot
1291.7382	1291.6158	-0.1224	-95	306	316	NHGHFRVLAK					Mascot
1392.6682	1392.6205	-0.0477	-34	22	32	LTYYTPDYOTK					Mascot
1465.7216	1465.6974	-0.0242	-17	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPIGQVER	38	97.141			Mascot
1475.7351	1475.694	-0.0411	-28	216	227	DRFLCAEAIYK					Mascot
1510.757	1510.7632	0.0062	4	1	14	MSPQETKASVGFK					Mascot
1526.752	1526.7103	-0.0417	-27	1	14	MSPQETKASVGFK			Oxidation (M)[1]		Mascot
1794.8149	1794.7539	-0.061	-34	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot

3	Ribulose biphosphate carboxylase large chain (Fragment) OS=Rhododendron hippophaeoides GN=rbcl PE=	RBL_RHOHI	51453.9	6.09	11	85	99.989	36	95.787
---	--	-----------	---------	------	----	----	--------	----	--------

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
853.4236	853.5193	0.0957	112	178	184	AVYECLR					Mascot
880.4536	880.4293	-0.0243	-28	296	302	NHGHFR					Mascot
1021.5312	1021.4948	-0.0364	-36	23	31	DTDILAAFR					Mascot
1053.4847	1053.5804	0.0957	91	341	348	DDYIEKDR					Mascot
1275.7307	1275.6049	-0.1258	-99	330	340	EITLGFVDLLR					Mascot
1291.7382	1291.6158	-0.1224	-95	296	306	NHGHFRVLAK					Mascot
1392.6682	1392.6205	-0.0477	-34	12	22	LTYYTPNYETK					Mascot
1465.7216	1465.6974	-0.0242	-17	310	324	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6974	-0.0572	-39	137	149	TFQGPPIGQVER	38	97.141			Mascot
1475.7351	1475.694	-0.0411	-28	206	217	DRFLCAEAIYK					Mascot
1863.8694	1863.8481	-0.0213	-11	437	453	EAGQWSNELSAACAIWK					Mascot
1863.8694	1863.8481	-0.0213	-11	437	453	EAGQWSNELSAACAIWK					Mascot

4	Ribulose biphosphate carboxylase large chain OS=Platanus occidentalis GN=rbcl PE=3 SV=2	RBL_PLAOC	52652.5	6.04	11	82	99.98	36	95.787
---	---	-----------	---------	------	----	----	-------	----	--------

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
853.4236	853.5193	0.0957	112	188	194	AVYECLR					Mascot
880.4536	880.4293	-0.0243	-28	306	312	NHGHFR					Mascot
1021.5312	1021.4948	-0.0364	-36	33	41	DTDILAAFR					Mascot
1275.7307	1275.6049	-0.1258	-99	340	350	EITLGFVDLLR					Mascot
1291.7382	1291.6158	-0.1224	-95	306	316	NHGHFRVLAK					Mascot
1465.7216	1465.6974	-0.0242	-17	320	334	MSGGDHIHAGTVVGK					Mascot
1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPIGQVER	38	97.141			Mascot
1475.7351	1475.694	-0.0411	-28	216	227	DRFLCAEAIYK					Mascot
1488.6926	1488.7886	0.096	64	464	475	EIKFEFEAMDTL			Oxidation (M)[9]		Mascot
1488.6926	1488.7886	0.096	64	464	475	EIKFEFEAMDTL			Oxidation (M)[9]		Mascot
1510.757	1510.7632	0.0062	4	1	14	MSPQETKASVGFK					Mascot
1526.752	1526.7103	-0.0417	-27	1	14	MSPQETKASVGFK			Oxidation (M)[1]		Mascot
1794.8149	1794.7539	-0.061	-34	237	252	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot

5	Ribulose biphosphate carboxylase large chain OS=Scenedesmus obliquus GN=rbcl PE=3 SV=1	RBL_SCEOB	52574.2	6.18	10	78	99.951	38	97.141
---	--	-----------	---------	------	----	----	--------	----	--------

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
853.4236	853.5193	0.0957	112	188	194	AVYECLR					Mascot
880.4536	880.4293	-0.0243	-28	306	312	NHGHFR					Mascot
977.472	977.5054	0.0334	34	1	8	MVPTET			Oxidation (M)[1]		Mascot
1021.5312	1021.4948	-0.0364	-36	33	41	DTDILAAFR					Mascot
1053.4847	1053.5804	0.0957	91	351	358	DDYIEKDR					Mascot
1291.7382	1291.6158	-0.1224	-95	306	316	NHGHFRVLAK					Mascot
1361.6987	1361.6012	-0.0975	-72	22	32	LTYYTPDYVVK					Mascot
1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPIGQVER	38	97.141			Mascot
1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPIGQVER					Mascot
1655.9877	1655.8798	-0.1079	-65	168	183	GLLGCTKPKLGLSAK			Carbamidomethyl (C)[5]		Mascot
1863.9633	1863.8481	-0.1152	-62	335	350	LEGEREVTLGFDLMR					Mascot
1863.9633	1863.8481	-0.1152	-62	335	350	LEGEREVTLGFDLMR					Mascot

6	Ribulose biphosphate carboxylase large chain OS=Perlaquonum hortorum GN=rbcl-A PE=3 SV=2	RBL_PELHO	52788.6	6.33	10	77	99.931	38	97.141
---	--	-----------	---------	------	----	----	--------	----	--------

Peptide Information											
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
853.4236	853.5193	0.0957	112	188	194	AVYECLR					Mascot



	880.4536	880.4293	-0.0243	-28	306	312	NHGIHFR										Mascot
	1021.5312	1021.4948	-0.0364	-36	33	41	DTDLAAFR										Mascot
	1176.5718	1176.6172	0.0454	39	454	463	ELAAACEVWK										Mascot
	1291.6392	1291.6158	-0.0234	-18	218	227	FLFCTEALYK										Mascot
	1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPHGIQVER			38		97.141					Mascot
	1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPHGIQVER										Mascot
	1488.6926	1488.7886	0.096	64	464	475	EIKFEFAMDTL										Mascot
	1488.6926	1488.7886	0.096	64	464	475	EIKFEFAMDTL										Mascot
	1510.757	1510.7632	0.0062	4	1	14	MSPQETKASVGFK										Mascot
	1526.752	1526.7103	-0.0417	-27	1	14	MSPQETKASVGFK										Mascot
	1605.7842	1605.8199	0.0357	22	451	463	WSRELAACEVWK										Mascot
	1605.7842	1605.8199	0.0357	22	451	463	WSRELAACEVWK										Mascot
	1794.8149	1794.7539	-0.061	-34	237	252	GHYLNATAGTCEEMIK										Mascot
7	Ribulose biphosphate carboxylase large chain OS=Quercus rubra GN=rbcl PE=3 SV=1 RBL_QUERU 52657.5 6.26 10 76 99.923 36 95.787																
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	853.4236	853.5193	0.0957	112	188	194	AVYECLR										Mascot
	880.4536	880.4293	-0.0243	-28	306	312	NHGIHFR										Mascot
	1021.5312	1021.4948	-0.0364	-36	33	41	DTDLAAFR										Mascot
	1053.4847	1053.5804	0.0957	91	351	358	DDYIEKDR										Mascot
	1275.7307	1275.6049	-0.1258	-99	340	350	EITLGFVDLLR										Mascot
	1291.7382	1291.6158	-0.1224	-95	306	316	NHGIHFRVLAK										Mascot
	1465.7216	1465.6974	-0.0242	-17	320	334	MSGGDHIHAGTVVGK										Mascot
	1465.7546	1465.6974	-0.0572	-39	147	159	TFQGPPHGIQVER			38		97.141					Mascot
	1510.757	1510.7632	0.0062	4	1	14	MSPQETKASVGFK										Mascot
	1526.752	1526.7103	-0.0417	-27	1	14	MSPQETKASVGFK										Mascot
	1794.8149	1794.7539	-0.061	-34	237	252	GHYLNATAGTCEEMIK						Oxidation (M)[1]				Mascot
													Carbamidomethyl (C)[11]				Mascot
8	Ribulose biphosphate carboxylase large chain (Fragment) OS=Coriaria myrtifolia GN=rbcl PE=3 SV=1 RBL_CORMY 51666.1 6 10 76 99.921 36 95.787																
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %		Modification		Rank	Result Type	
	853.4236	853.5193	0.0957	11													

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1165.571	1165.5486	-0.0224	-19	85	93	VVPCLEFSK		
1265.608	1265.6018	-0.0062	-5	31	44	SGSTGLSSVSNNGR		
1381.5768	1381.5872	0.0104	8	100	111	EHNSSPGYYDGR		
1488.7701	1488.7616	-0.0085	-6	47	58	CMQVWPVIEGIKK		
1994.0085	1993.9014	-0.1071	-54	1	20	MAPAVMASSATTVPFQ		
						GLK		
1994.0085	1993.9014	-0.1071	-54	1	20	MAPAVMASSATTVPFQ		
						GLK		
2367.157	2367.175	0.018	8	118	138	LPMFGCTDATQVLNEVE		
						EVKK		
2367.157	2367.175	0.018	8	118	138	LPMFGCTDATQVLNEVE		
						EVKK		
3052.5264	3052.5017	-0.0247	-8	1	30	MAPAVMASSATTVPFQ		
						GLKSTAGLPISCR		

3 DNA polymerase epsilon catalytic subunit B DPOE2\_ARATH 244836.2 6.49 22 36

OS=Arabidopsis thaliana GN=POL2B PE=2 SV=1

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
870.4719	870.515	0.0431	50	1314	1320	VFYNSK		
995.4614	995.4784	0.017	17	347	354	MNEELGFR		
1106.5299	1106.4879	-0.042	-38	1543	1551	ALEDFPCVR		
1109.4099	1109.4491	0.0392	35	355	363	CDQNGECER		
1141.5497	1141.4598	-0.0899	-79	1401	1409	HRNTQDGWK		
1234.5813	1234.6368	0.0555	45	1087	1095	SIIDWMYK		
1234.5813	1234.6368	0.0555	45	1087	1095	SIIDWMYK		
1265.5289	1265.6018	0.0729	58	2037	2047	EWSCADQCVK		
1308.542	1308.6073	0.0653	50	355	365	CDQNGECRAK		
1365.5634	1365.5909	0.0275	20	355	365	CDQNGECRAK		
1381.7144	1381.5872	-0.1272	-92	1022	1033	RLADFLGDTMVK		
1465.6967	1465.7006	0.0039	3	775	786	CILNSFYGYVMR		
1475.6869	1475.7057	0.0188	13	1808	1820	TYCESLLTVMGSR		
1493.7271	1493.6916	-0.0455	-30	1214	1225	NVOYQGVWLELEK		
1493.7271	1493.6916	-0.0455	-30	1214	1225	NVOYQGVWLELEK		
1716.9061	1716.7859	-0.1202	-70	2052	2065	EQIESLIQMVQR		
1716.9061	1716.7859	-0.1202	-70	2052	2065	EQIESLIQMVQR		
1796.8611	1796.9384	0.0773	43	364	377	AKFVCHLDCFSWYK		
1838.972	1838.8337	-0.1383	-75	851	866	FTISYPCVLNVDAK		
1890.9304	1890.8926	-0.0378	-20	867	882	NNSNDQYQTLVDPVRK		
2112.0471	2111.9641	-0.083	-39	1079	1095	ISSYTGIRSIIDWMYK		
2210.9739	2211.0203	0.0464	21	2079	2098	CNQVKAHLTEQCECSG		
						SFR		
2212.1067	2212.0283	-0.0784	-35	756	774	IQEAHDMVVVYDSLQLAH		
						K		
2399.1477	2398.9294	-0.2183	-91	1379	1400	MPLFSAICQIGCVCKIED		
						TAK		
3052.5125	3052.5017	-0.0108	-4	818	844	IGKPLELDTDGIWCALPG		
						SFPENFTFK		
3086.3943	3086.3557	-0.0386	-13	249	274	FPDAEYDQIMMISYMDG		
						QGFLITNR		

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
973.5312	973.4981	-0.0331	-34	115	122	VLVQEETR		
1090.48	1090.4897	0.0097	9	147	155	YEHNDGEVK		
1316.5466	1316.4955	-0.0511	-39	2	12	MDRGECLMSMK		
1332.5415	1332.4637	-0.0778	-58	2	12	MDRGECLMSMK		
1334.7063	1334.6023	-0.104	-78	172	183	KQLINGSSSSWK		
1348.5364	1348.6174	0.081	60	2	12	MDRGECLMSMK		
1357.5731	1357.662	0.0889	65	2	12	MDRGECLMSMK		
1393.6753	1393.6682	-0.0071	-5	66	78	SAQALGGHMNVHR		
1488.6136	1488.7616	0.148	99	1	12	MMDRGECLMSMK		
1838.8258	1838.8337	0.0079	4	130	145	EISDVCCNNVLESSMK		
3104.2542	3104.3225	0.0683	22	35	62	AFASAEYEGGGGCMW		
						PPRSYSCSCFGR		

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1003.5067	1003.5151	0.0084	8	282	289	RHEAAYTR		
1109.4528	1109.4491	-0.0037	-3	68	75	REDEEMR		
1155.6005	1155.5597	-0.0408	-35	294	304	LLEADPDAGVR		
1155.6005	1155.5597	-0.0408	-35	294	304	LLEADPDAGVR		
1277.5903	1277.6685	0.0782	61	17	28	CKPNTNSSPSR		
1277.5903	1277.6685	0.0782	61	17	28	CKPNTNSSPSR		
1302.6913	1302.6603	-0.031	-24	283	293	HEAAYTRIVSR		
1334.6117	1334.6023	-0.0094	-7	17	28	CKPNTNSSPSR		
1465.696	1465.7006	0.0046	3	1	14	MAATATMAMPLANR		
1475.7059	1475.7057	-0.0002	0	209	220	FDMAEYERVAHR		
1488.6757	1488.7616	0.0859	58	35	46	VTMISSRWMCRR		
1908.9344	1908.7279	-0.2065	-108	17	33	CKPNTNSSPSRRTLFR		

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
995.4879	995.4784	-0.0095	-10	151	158	GLMWHHAK		
1003.4301	1003.5151	0.085	85	549	556	GSDCYVFR		
1106.5952	1106.4879	-0.1073	-97	25	33	SVINKENFR		
1107.5615	1107.4979	-0.0636	-57	908	916	YMDKPPRGK		
1109.5143	1109.4491	-0.0652	-59	246	254	EKEMEADTK		
1308.5712	1308.6073	0.0361	28	875	884	SAQCYCTCK		
1316.6191	1316.4955	-0.1236	-94	464	473	EDLYLDCFKK		
1320.6893	1320.5337	-0.1556	-118	484	495	IEDTSESLVTVK		
1348.6281	1348.6174	-0.0107	-8	812	822	EGEFDKYAPHR		
1365.6069	1365.5909	-0.016	-12	591	601	TGNTWESWEQK		
1371.6686	1371.6101	-0.0585	-43	332	343	CSHSTLDPRIK		
1381.6958	1381.5872	-0.1086	-79	112	123	LEVGYESQTSR		
1393.7362	1393.6682	-0.068	-49	611	622	FLPLDIDYGNK		
1427.7576	1427.7241	-0.0335	-23	825	836	LGNKMLLWHGSR		
1488.7727	1488.7616	-0.0111	-7	736	748	MLEALQDIEASR		
1493.745	1493.6916	-0.0634	-42	434	447	GTSLVVCGLTDIR		
1493.745	1493.6916	-0.0634	-42	434	447	GTSLVVCGLTDIR		
2111.9883	2111.9641	-0.0242	-11	434	452	GTSLVVCGLTDIRDDEM		
						R		

Modification	Rank	Result Type
Carbamidomethyl (C)[4]		Mascot
Carbamidomethyl (C)[1]		Mascot
Oxidation (M)[1]		Mascot
Oxidation (M)[1]		Mascot
Oxidation (M)[3]		Mascot
Oxidation (M)[3]		Mascot
Carbamidomethyl (C)[29], Oxidation (M)[1,6]		Mascot

Modification	Rank	Result Type
Carbamidomethyl (C)[7]		Mascot
Carbamidomethyl (C)[1]		Mascot
Oxidation (M)[6]		Mascot
Oxidation (M)[6]		Mascot
Carbamidomethyl (C)[1]		Mascot
Carbamidomethyl (C)[1,8]		Mascot
Oxidation (M)[10]		Mascot
Oxidation (M)[10]		Mascot
Carbamidomethyl (C)[5,9]		Mascot
Carbamidomethyl (C)[7]		Mascot
Oxidation (M)[14]		Mascot
Oxidation (M)[7]		Mascot
Carbamidomethyl (C)[14]		Mascot
Oxidation (M)[10,11]		Mascot

Modification	Rank	Result Type
Oxidation (M)[1]		Mascot
Oxidation (M)[1,8]		Mascot
Oxidation (M)[1,8,10]		Mascot
Carbamidomethyl (C)[6]		Mascot
Oxidation (M)[9]		Mascot
Carbamidomethyl (C)[7]		Mascot
Carbamidomethyl (C)[6]		Mascot
Carbamidomethyl (C)[14,23,26]		Mascot

Modification	Rank	Result Type
Oxidation (M)[7]		Mascot
Carbamidomethyl (C)[1]		Mascot
Oxidation (M)[1]		Mascot
Oxidation (M)[3]		Mascot
Oxidation (M)[3,10]		Mascot
Carbamidomethyl (C)[1]		Mascot

Modification	Rank	Result Type
Oxidation (M)[3]		Mascot
Carbamidomethyl (C)[4]		Mascot
Oxidation (M)[2]		Mascot
Carbamidomethyl (C)[5,8]		Mascot
Carbamidomethyl (C)[7]		Mascot
Oxidation (M)[5]		Mascot
Carbamidomethyl (C)[4]		Mascot
Carbamidomethyl (C)[4]		Mascot
Carbamidomethyl (C)[4], Oxidation (M)[18]		Mascot

7	50S ribosomal protein L33, chloroplastic OS=Fagopyrum esculentum subsp. ancestrale GN=rp133 PE=3 SV Peptide Information	RK33_FAGEA	7736.1	10.17	5	36	0																																																																																																																																																																																																								
	<table><tr><th>Calc. Mass</th><th>Obsrv. Mass</th><th>± da</th><th>± ppm</th><th>Start Seq.</th><th>End Seq.</th><th>Sequence</th><th>Ion Score</th><th>C. I. %</th></tr><tr><td>1165.5168</td><td>1165.5486</td><td>0.0318</td><td>27</td><td>50</td><td>57</td><td>KFCPCYCYK</td><td></td><td></td></tr><tr><td>1308.665</td><td>1308.6073</td><td>-0.0577</td><td>-44</td><td>9</td><td>20</td><td>VSVILECTSCVR</td><td></td><td></td></tr><tr><td>1365.6864</td><td>1365.5909</td><td>-0.0955</td><td>-70</td><td>9</td><td>20</td><td>VSVILECTSCVR</td><td></td><td></td></tr><tr><td>1493.7814</td><td>1493.6816</td><td>-0.0998</td><td>-67</td><td>9</td><td>21</td><td>VSVILECTSCVRK</td><td></td><td></td></tr><tr><td>1493.7814</td><td>1493.6816</td><td>-0.0998</td><td>-67</td><td>9</td><td>21</td><td>VSVILECTSCVRK</td><td></td><td></td></tr><tr><td>1707.8516</td><td>1707.7059</td><td>-0.1457</td><td>-85</td><td>6</td><td>20</td><td>DARVSVILECTSCVR</td><td></td><td></td></tr><tr><td>1838.8717</td><td>1838.8337</td><td>-0.038</td><td>-21</td><td>51</td><td>65</td><td>FCPCYCKHTIHGEIK</td><td></td><td></td></tr></table>	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	1165.5168	1165.5486	0.0318	27	50	57	KFCPCYCYK			1308.665	1308.6073	-0.0577	-44	9	20	VSVILECTSCVR			1365.6864	1365.5909	-0.0955	-70	9	20	VSVILECTSCVR			1493.7814	1493.6816	-0.0998	-67	9	21	VSVILECTSCVRK			1493.7814	1493.6816	-0.0998	-67	9	21	VSVILECTSCVRK			1707.8516	1707.7059	-0.1457	-85	6	20	DARVSVILECTSCVR			1838.8717	1838.8337	-0.038	-21	51	65	FCPCYCKHTIHGEIK																																																																																																																																								
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %																																																																																																																																																																																																							
1165.5168	1165.5486	0.0318	27	50	57	KFCPCYCYK																																																																																																																																																																																																									
1308.665	1308.6073	-0.0577	-44	9	20	VSVILECTSCVR																																																																																																																																																																																																									
1365.6864	1365.5909	-0.0955	-70	9	20	VSVILECTSCVR																																																																																																																																																																																																									
1493.7814	1493.6816	-0.0998	-67	9	21	VSVILECTSCVRK																																																																																																																																																																																																									
1493.7814	1493.6816	-0.0998	-67	9	21	VSVILECTSCVRK																																																																																																																																																																																																									
1707.8516	1707.7059	-0.1457	-85	6	20	DARVSVILECTSCVR																																																																																																																																																																																																									
1838.8717	1838.8337	-0.038	-21	51	65	FCPCYCKHTIHGEIK																																																																																																																																																																																																									
8	Putative F-box/FBD/LRR-repeat protein At1g66300 OS=Arabidopsis thaliana GN=At1g66300 PE=4 SV=1 Peptide Information	FDL8_ARATH	52302.9	6.08	11	35	0																																																																																																																																																																																																								
	<table><tr><th>Calc. Mass</th><th>Obsrv. Mass</th><th>± da</th><th>± ppm</th><th>Start Seq.</th><th>End Seq.</th><th>Sequence</th><th>Ion Score</th><th>C. I. %</th></tr><tr><td>870.4791</td><td>870.515</td><td>0.0359</td><td>41</td><td>380</td><td>387</td><td>TSIISGHR</td><td></td><td></td></tr><tr><td>995.4098</td><td>995.4784</td><td>0.0686</td><td>69</td><td>1</td><td>8</td><td>MDEDGEKR</td><td></td><td></td></tr><tr><td>1033.604</td><td>1033.4862</td><td>-0.1178</td><td>-114</td><td>304</td><td>313</td><td>NFLVGISGVK</td><td></td><td></td></tr><tr><td>1106.5775</td><td>1106.4879</td><td>-0.0896</td><td>-81</td><td>54</td><td>62</td><td>NCVLSTKWR</td><td></td><td></td></tr><tr><td>1201.6245</td><td>1201.5874</td><td>-0.0371</td><td>-31</td><td>437</td><td>446</td><td>ACEILTIPT</td><td></td><td></td></tr><tr><td>1302.6583</td><td>1302.6603</td><td>0.002</td><td>2</td><td>377</td><td>387</td><td>MERTSIISGHR</td><td></td><td></td></tr><tr><td>1357.7256</td><td>1357.662</td><td>-0.0636</td><td>-47</td><td>437</td><td>447</td><td>ACEILTIPT</td><td></td><td></td></tr><tr><td>1488.8672</td><td>1488.7616</td><td>-0.1056</td><td>-71</td><td>411</td><td>423</td><td>LVSYLENSPIK</td><td></td><td></td></tr><tr><td>2112.0217</td><td>2111.9641</td><td>-0.0576</td><td>-27</td><td>272</td><td>290</td><td>SSLVGAHINIEFNCFCGEK</td><td></td><td></td></tr><tr><td>2888.4143</td><td>2888.2852</td><td>-0.1291</td><td>-45</td><td>314</td><td>338</td><td>NMAIAACTLEVIYDYSRC</td><td></td><td></td></tr><tr><td></td><td></td><td></td><td></td><td></td><td></td><td>EPLPLFR</td><td></td><td></td></tr><tr><td>3052.4138</td><td>3052.5017</td><td>0.0879</td><td>29</td><td>105</td><td>131</td><td>LGFDCLVGDDEETGNAQ</td><td></td><td></td></tr><tr><td></td><td></td><td></td><td></td><td></td><td></td><td>MARWINDVVK</td><td></td><td></td></tr></table>	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	870.4791	870.515	0.0359	41	380	387	TSIISGHR			995.4098	995.4784	0.0686	69	1	8	MDEDGEKR			1033.604	1033.4862	-0.1178	-114	304	313	NFLVGISGVK			1106.5775	1106.4879	-0.0896	-81	54	62	NCVLSTKWR			1201.6245	1201.5874	-0.0371	-31	437	446	ACEILTIPT			1302.6583	1302.6603	0.002	2	377	387	MERTSIISGHR			1357.7256	1357.662	-0.0636	-47	437	447	ACEILTIPT			1488.8672	1488.7616	-0.1056	-71	411	423	LVSYLENSPIK			2112.0217	2111.9641	-0.0576	-27	272	290	SSLVGAHINIEFNCFCGEK			2888.4143	2888.2852	-0.1291	-45	314	338	NMAIAACTLEVIYDYSRC									EPLPLFR			3052.4138	3052.5017	0.0879	29	105	131	LGFDCLVGDDEETGNAQ									MARWINDVVK																																																																																		
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %																																																																																																																																																																																																							
870.4791	870.515	0.0359	41	380	387	TSIISGHR																																																																																																																																																																																																									
995.4098	995.4784	0.0686	69	1	8	MDEDGEKR																																																																																																																																																																																																									
1033.604	1033.4862	-0.1178	-114	304	313	NFLVGISGVK																																																																																																																																																																																																									
1106.5775	1106.4879	-0.0896	-81	54	62	NCVLSTKWR																																																																																																																																																																																																									
1201.6245	1201.5874	-0.0371	-31	437	446	ACEILTIPT																																																																																																																																																																																																									
1302.6583	1302.6603	0.002	2	377	387	MERTSIISGHR																																																																																																																																																																																																									
1357.7256	1357.662	-0.0636	-47	437	447	ACEILTIPT																																																																																																																																																																																																									
1488.8672	1488.7616	-0.1056	-71	411	423	LVSYLENSPIK																																																																																																																																																																																																									
2112.0217	2111.9641	-0.0576	-27	272	290	SSLVGAHINIEFNCFCGEK																																																																																																																																																																																																									
2888.4143	2888.2852	-0.1291	-45	314	338	NMAIAACTLEVIYDYSRC																																																																																																																																																																																																									
						EPLPLFR																																																																																																																																																																																																									
3052.4138	3052.5017	0.0879	29	105	131	LGFDCLVGDDEETGNAQ																																																																																																																																																																																																									
						MARWINDVVK																																																																																																																																																																																																									
9	Disease susceptibility protein LOV1 OS=Arabidopsis thaliana GN=LOV1 PE=1 SV=1 Peptide Information	LOV1B_ARATH	104444	6.83	16	35	0																																																																																																																																																																																																								
	<table><tr><th>Calc. Mass</th><th>Obsrv. Mass</th><th>± da</th><th>± ppm</th><th>Start Seq.</th><th>End Seq.</th><th>Sequence</th><th>Ion Score</th><th>C. I. %</th></tr><tr><td>842.4518</td><td>842.4817</td><td>0.0299</td><td>35</td><td>313</td><td>319</td><td>SFGFKTR</td><td></td><td></td></tr><tr><td>1090.5164</td><td>1090.4897</td><td>-0.0267</td><td>-24</td><td>278</td><td>285</td><td>EEDWDRIK</td><td></td><td></td></tr><tr><td>1106.5323</td><td>1106.4879</td><td>-0.0444</td><td>-40</td><td>339</td><td>348</td><td>DEGTGLSEVR</td><td></td><td></td></tr><tr><td>1107.5979</td><td>1107.4979</td><td>-0.1</td><td>-90</td><td>293</td><td>301</td><td>GWKMLLT</td><td></td><td></td></tr><tr><td>1109.5812</td><td>1109.4491</td><td>-0.1321</td><td>-119</td><td>821</td><td>830</td><td>GGFPQLCFLK</td><td></td><td></td></tr><tr><td>1155.652</td><td>1155.5597</td><td>-0.0923</td><td>-80</td><td>2</td><td>12</td><td>AEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1155.652</td><td>1155.5597</td><td>-0.0923</td><td>-80</td><td>2</td><td>12</td><td>AEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1201.651</td><td>1201.5874</td><td>-0.0636</td><td>-53</td><td>329</td><td>337</td><td>LCEKIVFHR</td><td></td><td></td></tr><tr><td>1302.6874</td><td>1302.6603</td><td>-0.0271</td><td>-21</td><td>1</td><td>12</td><td>MAEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1316.548</td><td>1316.4955</td><td>-0.0525</td><td>-40</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1332.5428</td><td>1332.4637</td><td>-0.0791</td><td>-59</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1348.5377</td><td>1348.6174</td><td>0.0797</td><td>59</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1493.7161</td><td>1493.6816</td><td>-0.0345</td><td>-23</td><td>359</td><td>372</td><td>EMVTCCGGPLPAVK</td><td></td><td></td></tr><tr><td>1493.7161</td><td>1493.6816</td><td>-0.0345</td><td>-23</td><td>359</td><td>372</td><td>EMVTCCGGPLPAVK</td><td></td><td></td></tr><tr><td>1838.9442</td><td>1838.8337</td><td>-0.1105</td><td>-60</td><td>199</td><td>213</td><td>TTLARQVFHDMVQR</td><td></td><td></td></tr><tr><td>1993.8169</td><td>1993.9014</td><td>0.0845</td><td>42</td><td>496</td><td>510</td><td>HCCQMHDMMREVCLSK</td><td></td><td></td></tr><tr><td>1993.8169</td><td>1993.9014</td><td>0.0845</td><td>42</td><td>496</td><td>510</td><td>HCCQMHDMMREVCLSK</td><td></td><td></td></tr><tr><td>2211.2107</td><td>2211.0203</td><td>-0.1904</td><td>-86</td><td>1</td><td>19</td><td>MAEGVVLFGVHKLWELLNR</td><td></td><td></td></tr><tr><td>2211.9744</td><td>2212.0283</td><td>0.0539</td><td>24</td><td>339</td><td>358</td><td>DEGTGLSEVRVDEDEMEAMGK</td><td></td><td></td></tr><tr><td>2240.1558</td><td>2240.0491</td><td>-0.1067</td><td>-48</td><td>513</td><td>532</td><td>EENFLEIFKVSTATSAINAR</td><td></td><td></td></tr><tr><td>3104.5623</td><td>3104.3225</td><td>-0.2398</td><td>-77</td><td>236</td><td>261</td><td>IWQELQPQNGDISHMDEHILQGLFK</td><td></td><td></td></tr></table>	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	842.4518	842.4817	0.0299	35	313	319	SFGFKTR			1090.5164	1090.4897	-0.0267	-24	278	285	EEDWDRIK			1106.5323	1106.4879	-0.0444	-40	339	348	DEGTGLSEVR			1107.5979	1107.4979	-0.1	-90	293	301	GWKMLLT			1109.5812	1109.4491	-0.1321	-119	821	830	GGFPQLCFLK			1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK			1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK			1201.651	1201.5874	-0.0636	-53	329	337	LCEKIVFHR			1302.6874	1302.6603	-0.0271	-21	1	12	MAEGVVLFGVHK			1316.548	1316.4955	-0.0525	-40	495	504	KHCQMHDMMR			1332.5428	1332.4637	-0.0791	-59	495	504	KHCQMHDMMR			1348.5377	1348.6174	0.0797	59	495	504	KHCQMHDMMR			1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK			1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK			1838.9442	1838.8337	-0.1105	-60	199	213	TTLARQVFHDMVQR			1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK			1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK			2211.2107	2211.0203	-0.1904	-86	1	19	MAEGVVLFGVHKLWELLNR			2211.9744	2212.0283	0.0539	24	339	358	DEGTGLSEVRVDEDEMEAMGK			2240.1558	2240.0491	-0.1067	-48	513	532	EENFLEIFKVSTATSAINAR			3104.5623	3104.3225	-0.2398	-77	236	261	IWQELQPQNGDISHMDEHILQGLFK										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %																																																																																																																																																																																																							
842.4518	842.4817	0.0299	35	313	319	SFGFKTR																																																																																																																																																																																																									
1090.5164	1090.4897	-0.0267	-24	278	285	EEDWDRIK																																																																																																																																																																																																									
1106.5323	1106.4879	-0.0444	-40	339	348	DEGTGLSEVR																																																																																																																																																																																																									
1107.5979	1107.4979	-0.1	-90	293	301	GWKMLLT																																																																																																																																																																																																									
1109.5812	1109.4491	-0.1321	-119	821	830	GGFPQLCFLK																																																																																																																																																																																																									
1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK																																																																																																																																																																																																									
1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK																																																																																																																																																																																																									
1201.651	1201.5874	-0.0636	-53	329	337	LCEKIVFHR																																																																																																																																																																																																									
1302.6874	1302.6603	-0.0271	-21	1	12	MAEGVVLFGVHK																																																																																																																																																																																																									
1316.548	1316.4955	-0.0525	-40	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1332.5428	1332.4637	-0.0791	-59	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1348.5377	1348.6174	0.0797	59	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK																																																																																																																																																																																																									
1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK																																																																																																																																																																																																									
1838.9442	1838.8337	-0.1105	-60	199	213	TTLARQVFHDMVQR																																																																																																																																																																																																									
1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK																																																																																																																																																																																																									
1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK																																																																																																																																																																																																									
2211.2107	2211.0203	-0.1904	-86	1	19	MAEGVVLFGVHKLWELLNR																																																																																																																																																																																																									
2211.9744	2212.0283	0.0539	24	339	358	DEGTGLSEVRVDEDEMEAMGK																																																																																																																																																																																																									
2240.1558	2240.0491	-0.1067	-48	513	532	EENFLEIFKVSTATSAINAR																																																																																																																																																																																																									
3104.5623	3104.3225	-0.2398	-77	236	261	IWQELQPQNGDISHMDEHILQGLFK																																																																																																																																																																																																									
10	Inactive disease susceptibility protein LOV1 OS=Arabidopsis thaliana GN=LOV1 PE=3 SV=1 Peptide Information	LOV1C_ARATH	104358.9	6.66	16	35	0																																																																																																																																																																																																								
	<table><tr><th>Calc. Mass</th><th>Obsrv. Mass</th><th>± da</th><th>± ppm</th><th>Start Seq.</th><th>End Seq.</th><th>Sequence</th><th>Ion Score</th><th>C. I. %</th></tr><tr><td>842.4518</td><td>842.4817</td><td>0.0299</td><td>35</td><td>313</td><td>319</td><td>SFGFKTR</td><td></td><td></td></tr><tr><td>1090.5164</td><td>1090.4897</td><td>-0.0267</td><td>-24</td><td>278</td><td>285</td><td>EEDWDRIK</td><td></td><td></td></tr><tr><td>1106.5323</td><td>1106.4879</td><td>-0.0444</td><td>-40</td><td>339</td><td>348</td><td>DEGTGLSEVR</td><td></td><td></td></tr><tr><td>1107.5979</td><td>1107.4979</td><td>-0.1</td><td>-90</td><td>293</td><td>301</td><td>GWKMLLT</td><td></td><td></td></tr><tr><td>1109.5812</td><td>1109.4491</td><td>-0.1321</td><td>-119</td><td>821</td><td>830</td><td>GGFPQLCFLK</td><td></td><td></td></tr><tr><td>1155.652</td><td>1155.5597</td><td>-0.0923</td><td>-80</td><td>2</td><td>12</td><td>AEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1155.652</td><td>1155.5597</td><td>-0.0923</td><td>-80</td><td>2</td><td>12</td><td>AEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1201.651</td><td>1201.5874</td><td>-0.0636</td><td>-53</td><td>329</td><td>337</td><td>LCEKIVFHR</td><td></td><td></td></tr><tr><td>1302.6874</td><td>1302.6603</td><td>-0.0271</td><td>-21</td><td>1</td><td>12</td><td>MAEGVVLFGVHK</td><td></td><td></td></tr><tr><td>1316.548</td><td>1316.4955</td><td>-0.0525</td><td>-40</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1332.5428</td><td>1332.4637</td><td>-0.0791</td><td>-59</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1348.5377</td><td>1348.6174</td><td>0.0797</td><td>59</td><td>495</td><td>504</td><td>KHCQMHDMMR</td><td></td><td></td></tr><tr><td>1493.7161</td><td>1493.6816</td><td>-0.0345</td><td>-23</td><td>359</td><td>372</td><td>EMVTCCGGPLPAVK</td><td></td><td></td></tr><tr><td>1493.7161</td><td>1493.6816</td><td>-0.0345</td><td>-23</td><td>359</td><td>372</td><td>EMVTCCGGPLPAVK</td><td></td><td></td></tr><tr><td>1838.9442</td><td>1838.8337</td><td>-0.1105</td><td>-60</td><td>199</td><td>213</td><td>TTLARQVFHDMVQR</td><td></td><td></td></tr><tr><td>1993.8169</td><td>1993.9014</td><td>0.0845</td><td>42</td><td>496</td><td>510</td><td>HCCQMHDMMREVCLSK</td><td></td><td></td></tr><tr><td>1993.8169</td><td>1993.9014</td><td>0.0845</td><td>42</td><td>496</td><td>510</td><td>HCCQMHDMMREVCLSK</td><td></td><td></td></tr><tr><td>2211.2107</td><td>2211.0203</td><td>-0.1904</td><td>-86</td><td>1</td><td>19</td><td>MAEGVVLFGVHKLWELLNR</td><td></td><td></td></tr><tr><td>2211.9744</td><td>2212.0283</td><td>0.0539</td><td>24</td><td>339</td><td>358</td><td>DEGTGLSEVRVDEDEMEAMGK</td><td></td><td></td></tr><tr><td>2240.1558</td><td>2240.0491</td><td>-0.1067</td><td>-48</td><td>513</td><td>532</td><td>EENFLEIFKVSTATSAINAR</td><td></td><td></td></tr><tr><td>3104.5623</td><td>3104.3225</td><td>-0.2398</td><td>-77</td><td>236</td><td>261</td><td>IWQELQPQNGDISHMDEHILQGLFK</td><td></td><td></td></tr></table>	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	842.4518	842.4817	0.0299	35	313	319	SFGFKTR			1090.5164	1090.4897	-0.0267	-24	278	285	EEDWDRIK			1106.5323	1106.4879	-0.0444	-40	339	348	DEGTGLSEVR			1107.5979	1107.4979	-0.1	-90	293	301	GWKMLLT			1109.5812	1109.4491	-0.1321	-119	821	830	GGFPQLCFLK			1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK			1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK			1201.651	1201.5874	-0.0636	-53	329	337	LCEKIVFHR			1302.6874	1302.6603	-0.0271	-21	1	12	MAEGVVLFGVHK			1316.548	1316.4955	-0.0525	-40	495	504	KHCQMHDMMR			1332.5428	1332.4637	-0.0791	-59	495	504	KHCQMHDMMR			1348.5377	1348.6174	0.0797	59	495	504	KHCQMHDMMR			1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK			1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK			1838.9442	1838.8337	-0.1105	-60	199	213	TTLARQVFHDMVQR			1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK			1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK			2211.2107	2211.0203	-0.1904	-86	1	19	MAEGVVLFGVHKLWELLNR			2211.9744	2212.0283	0.0539	24	339	358	DEGTGLSEVRVDEDEMEAMGK			2240.1558	2240.0491	-0.1067	-48	513	532	EENFLEIFKVSTATSAINAR			3104.5623	3104.3225	-0.2398	-77	236	261	IWQELQPQNGDISHMDEHILQGLFK										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %																																																																																																																																																																																																							
842.4518	842.4817	0.0299	35	313	319	SFGFKTR																																																																																																																																																																																																									
1090.5164	1090.4897	-0.0267	-24	278	285	EEDWDRIK																																																																																																																																																																																																									
1106.5323	1106.4879	-0.0444	-40	339	348	DEGTGLSEVR																																																																																																																																																																																																									
1107.5979	1107.4979	-0.1	-90	293	301	GWKMLLT																																																																																																																																																																																																									
1109.5812	1109.4491	-0.1321	-119	821	830	GGFPQLCFLK																																																																																																																																																																																																									
1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK																																																																																																																																																																																																									
1155.652	1155.5597	-0.0923	-80	2	12	AEGVVLFGVHK																																																																																																																																																																																																									
1201.651	1201.5874	-0.0636	-53	329	337	LCEKIVFHR																																																																																																																																																																																																									
1302.6874	1302.6603	-0.0271	-21	1	12	MAEGVVLFGVHK																																																																																																																																																																																																									
1316.548	1316.4955	-0.0525	-40	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1332.5428	1332.4637	-0.0791	-59	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1348.5377	1348.6174	0.0797	59	495	504	KHCQMHDMMR																																																																																																																																																																																																									
1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK																																																																																																																																																																																																									
1493.7161	1493.6816	-0.0345	-23	359	372	EMVTCCGGPLPAVK																																																																																																																																																																																																									
1838.9442	1838.8337	-0.1105	-60	199	213	TTLARQVFHDMVQR																																																																																																																																																																																																									
1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK																																																																																																																																																																																																									
1993.8169	1993.9014	0.0845	42	496	510	HCCQMHDMMREVCLSK																																																																																																																																																																																																									
2211.2107	2211.0203	-0.1904	-86	1	19	MAEGVVLFGVHKLWELLNR																																																																																																																																																																																																									
2211.9744	2212.0283	0.0539	24	339	358	DEGTGLSEVRVDEDEMEAMGK																																																																																																																																																																																																									
2240.1558	2240.0491	-0.1067	-48	513	532	EENFLEIFKVSTATSAINAR																																																																																																																																																																																																									
3104.5623	3104.3225	-0.2398	-77	236	261	IWQELQPQNGDISHMDEHILQGLFK																																																																																																																																																																																																									

Gel Idx/Pos		149/F24		Instr/Gel Origin		BA2060/140227A		Process Status		Analysis Succeeded	
Plate # [# Name]		[1] 31564		Instrument Sample Name				Spectra		11	
Rank	Protein Name	Accession No.		Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	
1	Germin-like protein [Pisum sativum]	gi 13277342		22004.6	7.81	1	212	100	212	100	
Peptide Information											
Calc. Mass		Obsrv. Mass		± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
2272.2085		2272.1348		-0.0737	-32	69	91	AAVTPAFDAQFPGVNGLGISAR			Rank
											Result Type
											Mascot

	2272.2085	2272.1348	-0.0737	-32	69	91	AAVTPAFDAQFPGVNGL GISIAR	212	100						Mascot
2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Fevillea pedatifolia]	gil171909340	50023.1	5.81	12	104				99.966	49	59.054			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	814.5145	814.4755	-0.039	-48	291	297	VLDKALR						Mascot		
	814.5145	814.4755	-0.039	-48	291	297	VLDKALR						Mascot		
	1021.5312	1021.4936	-0.0376	-37	11	19	DTDILAAFR						Mascot		
	1116.583	1116.5642	-0.0188	-17	400	409	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot		
	1261.6285	1261.6678	0.0393	31	196	205	FLFCAEAIYK				Carbamidomethyl (C)[4]		Mascot		
	1261.7151	1261.6678	-0.0473	-37	318	328	DITLGFVDLLR	25	0				Mascot		
	1465.7546	1465.7075	-0.0471	-32	125	137	TFQGPPHGIQVER	27	0				Mascot		
	1465.7546	1465.7075	-0.0471	-32	125	137	TFQGPPHGIQVER						Mascot		
	1475.7351	1475.7103	-0.0248	-17	194	205	DRFLFCAEAIYK						Mascot		
	1502.8512	1502.7975	-0.0537	-36	143	155	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot		
	1794.8149	1794.7405	-0.0744	-41	215	230	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot		
	2009.059	2008.981	-0.078	-39	318	334	DITLGFVDLLRDDFIEK						Mascot		
	2297.0972	2297.1145	0.0173	8	1	19	TYTPEYETKDDILAAFR						Mascot		
	3854.8718	3854.7678	-0.104	-27	20	57	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot		
3	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cyathocalyx martabanicus]	gil57338598	52066.2	6.15	13	103				99.957	46	16.342			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	856.3723	856.4931	0.1208	141	464	470	FEFEAVD						Mascot		
	1021.5312	1021.4936	-0.0376	-37	30	38	DTDILAAFR						Mascot		
	1116.6194	1116.5642	-0.0552	-49	419	428	VALEACVKAR				Carbamidomethyl (C)[6]		Mascot		
	1261.6285	1261.6678	0.0393	31	215	224	FLFCAEAIYK				Carbamidomethyl (C)[4]		Mascot		
	1261.7151	1261.6678	-0.0473	-37	337	347	DITLGFVDLLR	25	0				Mascot		
	1465.7216	1465.7075	-0.0141	-10	317	331	MSGGDHIHAGTVVGK						Mascot		
	1465.7546	1465.7075	-0.0471	-32	144	156	TFQGPPHGIQVER	27	0				Mascot		
	1475.7351	1475.7103	-0.0248	-17	213	224	DRFLFCAEAIYK						Mascot		
	1502.8512	1502.7975	-0.0537	-36	162	174	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot		
	1794.8149	1794.7405	-0.0744	-41	234	249	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot		
	2009.059	2008.981	-0.078	-39	337	353	DITLGFVDLLRDDFIEK						Mascot		
	2254.1978	2254.113	-0.0848	-38	137	156	VPTSIVKTFQGPPIHGIQV ER						Mascot		
	3854.8718	3854.7678	-0.104	-27	39	76	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot		
4	ribulose 1,5-bisphosphate carboxylase [Polyalthia suberosa]	gil11066021	48794.6	6.46	12	100				99.914	46	16.342			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	868.4926	868.468	-0.0246	-28	1	8	VFFTAGVK						Mascot		
	1021.5312	1021.4936	-0.0376	-37	23	31	DTDILAAFR						Mascot		
	1045.5459	1045.5314	-0.0145	-14	412	421	VAVEACVQAR						Mascot		
	1261.6285	1261.6678	0.0393	31	208	217	FLFCAEALYK				Carbamidomethyl (C)[4]		Mascot		
	1261.7151	1261.6678	-0.0473	-37	330	340	DITLGFVDLLR	25	0				Mascot		
	1465.7216	1465.7075	-0.0141	-10	310	324	MSGGDHIHAGTVVGK						Mascot		
	1465.7546	1465.7075	-0.0471	-32	137	149	TFQGPPIHGIQVER	27	0				Mascot		
	1475.7351	1475.7103	-0.0248	-17	206	217	DRFLFCAEALYK						Mascot		
	1502.8512	1502.7975	-0.0537	-36	155	167	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot		
	2009.059	2008.981	-0.078	-39	330	346	DITLGFVDLLRDDFIEK						Mascot		
	2254.1978	2254.113	-0.0848	-38	130	149	IPTSIVKTFQGPPIHGIQV ER						Mascot		
	3854.8718	3854.7678	-0.104	-27	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot		
5	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Elateriospermum tapos]	gil155029247	48560.6	6.57	12	100				99.912	46	16.342			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	1021.5312	1021.4936	-0.0376	-37	23	31	DTDILAAFR						Mascot		
	1116.583	1116.5642	-0.0188	-17	412	421	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot		
	1261.6285	1261.6678	0.0393	31	208	217	FLFCAEAIYK				Carbamidomethyl (C)[4]		Mascot		
	1261.7151	1261.6678	-0.0473	-37	330	340	DITLGFVDLLR	25	0				Mascot		
	1392.6682	1392.6312	-0.037	-27	12	22	LTYYTPDYQTK						Mascot		
	1465.7216	1465.7075	-0.0141	-10	310	324	MSGGDHIHAGTVVGK						Mascot		
	1465.7546	1465.7075	-0.0471	-32	137	149	TFQGPPIHGIQVER	27	0				Mascot		
	1475.7351	1475.7103	-0.0248	-17	206	217	DRFLFCAEAIYK						Mascot		
	1502.8512	1502.7975	-0.0537	-36	155	167	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot		
	1794.8149	1794.7405	-0.0744	-41	227	242	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]		Mascot		
	2009.059	2008.981	-0.078	-39	330	346	DITLGFVDLLRDDFIEK						Mascot		
	3854.8718	3854.7678	-0.104	-27	32	69	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot		
6	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Apodanthera sagittifolia]	gil171909332	50064.2	5.9	12	99				99.899	46	16.342			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type		
	803.5025	803.4921	-0.0104	-13	118	124	IPIAYVK						Mascot		
	1021.5312	1021.4936	-0.0376	-37	11	19	DTDILAAFR						Mascot		
	1116.583	1116.5642	-0.0188	-17	400	409	VALEACVQAR				Carbamidomethyl (C)[6]		Mascot		
	1261.6285	1261.6678	0.0393	31	196	205	FLFCAEAIYK				Carbamidomethyl (C)[4]		Mascot		
	1261.7151	1261.6678	-0.0473	-37	318	328	DITLGFVDLLR	25	0				Mascot		
	1465.7216	1465.7075	-0.0141	-10	298	312	MSGGDHIHAGTVVGK						Mascot		
	1465.7546	1465.7075	-0.0471	-32	125	137	TFQGPPIHGIQVER	27	0				Mascot		
	1475.7351	1475.7103	-0.0248	-17	194	205	DRFLFCAEAIYK						Mascot		
	1502.8512	1502.7975	-0.0537	-36	143	155	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]		Mascot		
	2009.059	2008.981	-0.078	-39	318	334	DITLGFVDLLRDDFIEK						Mascot		
	2297.0972	2297.1145	0.0173	8	1	19	TYTPEYETKDDILAAFR						Mascot		
	3854.8718	3854.7678	-0.104	-27	20	57	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR						Mascot		
7	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Adenia sp. Tokuoka 261]	gil119368104	48844.7	6.75	12	99				99.884	46	16.342			
Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence	Ion	C. I. %		Modification	Rank	Result Type		

				Seq.		Seq.		Score																			
		1021.5312	1021.4936	-0.0376	-37	26	34	DTDILAAFR																			
		1116.583	1116.5642	-0.0188	-17	415	424	VALEACVQAR																			
		1261.6285	1261.6678	-0.0393	-31	211	220	FLFCAEALYK																			
		1261.7151	1261.6678	-0.0473	-37	333	343	DITLGFVDLLR	25		0																
		1465.7216	1465.7075	-0.0141	-10	313	327	MSGGDHIIAGTVVGK																			
		1465.7546	1465.7075	-0.0471	-32	140	152	TFQGGPHGIQVER	27		0																
		1475.7351	1475.7103	-0.0248	-17	209	220	DRFLFCAEALYK																			
		1502.8512	1502.7975	-0.0537	-36	158	170	YGRLLGCTIKPK																			
		1794.8585	1794.7405	-0.118	-66	12	25	DYKLTYYTPEYNPK																			
		2009.059	2008.981	-0.078	-39	333	349	DITLGFVDLLRDDFIEK																			
		2391.1868	2391.0442	-0.1426	-60	15	34	LTYYTPEYNPKDILAAFR																			
		3854.8718	3854.7678	-0.104	-27	35	72	VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR																			
8	ribulose biphosphate carboxylase oxygenase [Schistocarpaea johnsonii]			gij9968776			50253.2			5.87		12		98		99.878		46		16.342							
Peptide Information																											
Calc. Mass		Obsrv. Mass		± da		± ppm		Start Seq.		End Seq.		Sequence		Ion Score		C. I. %		Modification		Rank Result Type							
1021.5312		1021.4936		-0.0376		-37		11		19		DTDILAAFR								Mascot							
1116.6194		1116.5642		-0.0552		-49		400		409		VALEACVQAR						Carbamidomethyl (C)[6]		Mascot							
1261.6285		1261.6678		-0.0393		-31		196		205		FLFCAEALYK						Carbamidomethyl (C)[4]		Mascot							
1261.7151		1261.6678		-0.0473		-37		318		328		DITLGFVDLLR		25		0				Mascot							
1465.7216		1465.7075		-0.0141		-10		298		312		MSGGDHIIAGTVVGK								Mascot							
1465.7546		1465.7075		-0.0471		-32		125		137		TFQGGPHGIQVER		27		0				Mascot							
1475.7351		1475.7103		-0.0248		-17		194		205		DRFLFCAEALYK						Carbamidomethyl (C)[8]		Mascot							
1502.8512		1502.7975		-0.0537		-36		143		155		YGRLLGCTIKPK						Carbamidomethyl (C)[11]		Mascot							
1794.8149		1794.7405		-0.0744		-41		215		230		GHYLNATAGTCEEMIK								Mascot							
2009.059		2008.981		-0.078		-39		318		334		DITLGFVDLLRDDFIEK								Mascot							
2297.0972		2297.1145		0.0173		8		1		19		TYTPEYETKDDILAAFR								Mascot							
3854.8718		3854.7678		-0.104		-27		20		57		VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR								Mascot							
9	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Pentaphylax euryoides]			gij22797085			50606.2			5.95		12		98		99.85		46		16.342							
Peptide Information																											
Calc. Mass		Obsrv. Mass		± da		± ppm		Start Seq.		End Seq.		Sequence		Ion Score		C. I. %		Modification		Rank Result Type							
1021.5312		1021.4936		-0.0376		-37		14		22		DTDILAAFR								Mascot							
1116.583		1116.5642		-0.0188		-17		403		412		VALEACVQAR						Carbamidomethyl (C)[6]		Mascot							
1261.6285		1261.6678		-0.0393		-31		199		208		FLFCAEALYK						Carbamidomethyl (C)[4]		Mascot							
1261.7151		1261.6678		-0.0473		-37		321		331		DITLGFVDLLR		25		0				Mascot							
1465.7216		1465.7075		-0.0141		-10		301		315		MSGGDHIIAGTVVGK								Mascot							
1465.7546		1465.7075		-0.0471		-32		128		140		TFQGGPHGIQVER		27		0				Mascot							
1475.7351		1475.7103		-0.0248		-17		197		208		DRFLFCAEALYK						Carbamidomethyl (C)[8]		Mascot							
1502.8512		1502.7975		-0.0537		-36		146		158		YGRLLGCTIKPK								Mascot							
2009.059		2008.981		-0.078		-39		321		337		DITLGFVDLLRDDFIEK								Mascot							
2138.1189		2138.0676		-0.0513		-24		267		284		DHGLLFHIIHRAMHAVIDR								Mascot							
2138.1189		2138.0676		-0.0513		-24		267		284		DHGLLFHIIHRAMHAVIDR								Mascot							
2176.063		2176.0212		-0.0418		-19		199		217		FLFCAEALYKADDETGEIK								Mascot							
3854.8718		3854.7678		-0.104		-27		23		60		VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR								Mascot							
10	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Adenia digitata]			gij1769839			51477			6.19		12		97		99.843		46		16.342							
Peptide Information																											
Calc. Mass		Obsrv. Mass		± da		± ppm		Start Seq.		End Seq.		Sequence		Ion Score		C. I. %		Modification		Rank Result Type							
1021.5312		1021.4936		-0.0376		-37		23		31		DTDILAAFR								Mascot							
1116.583		1116.5642		-0.0188		-17		412		421		VALEACVQAR						Carbamidomethyl (C)[6]		Mascot							
1261.6285		1261.6678		-0.0393		-31		208		217		FLFCAEALYK						Carbamidomethyl (C)[4]		Mascot							
1261.7151		1261.6678		-0.0473		-37		330		340		DITLGFVDLLR		25		0				Mascot							
1465.7216		1465.7075		-0.0141		-10		310		324		MSGGDHIIAGTVVGK								Mascot							
1465.7546		1465.7075		-0.0471		-32		137		149		TFQGGPHGIQVER		27		0				Mascot							
1475.7351		1475.7103		-0.0248		-17		206		217		DRFLFCAEALYK						Carbamidomethyl (C)[8]		Mascot							
1502.8512		1502.7975		-0.0537		-36		155		167		YGRLLGCTIKPK								Mascot							
1794.8585		1794.7405		-0.118		-66		9		22		DYKLTYYTPEYNPK								Mascot							
2009.059		2008.981		-0.078		-39		330		346		DITLGFVDLLRDDFIEK								Mascot							
2391.1868		2391.0442		-0.1426		-60		12		31		LTYYTPEYNPKDILAAFR								Mascot							
3854.8718		3854.7678		-0.104		-27		32		69		VTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLT SLDR								Mascot							
Gel Idx/Pos		150/G1						Instr./Gel Origin		BA2060/140227A						Process Status		Analysis Succeeded									
Plate # Name		[1] 31564						Instrument Sample Name								Spectra		11									
Rank	Protein Name			Accession No.			Protein MW			Protein PI			Pep. Count			Protein Score			Protein Score C. I. %			Total Ion Score			Total Ion C. I. %		
1	Putative protein phosphatase 2C 22 OS=Oryza sativa subsp. japonica GN=Os02g0607500 PE=3 SV=2			P2C22_ORYSJ			63261.4			4.89			9			37			0								
Peptide Information																											
Calc. Mass		Obsrv. Mass		± da		± ppm		Start Seq.		End Seq.		Sequence		Ion Score		C. I. %		Modification		Rank Result Type							
870.4203		870.4839		0.0636		73		222		229		SSEAVSYK								Mascot							
870.4203		870.4839		0.0636		73		222		229		SSEAVSYK								Mascot							
1083.5251		1083.5325		0.0074		7		103		112		VASSAMQGLR								Mascot							
2173.0442		2172.9626		-0.0816		-38		440		459		NIAPNTTTLGEETLHTTCE K								Mascot							
2173.0442		2172.9626		-0.0816		-38		440		459		NIAPNTTTLGEETLHTTCE K								Mascot							
2230.0657		2230.0347		-0.031		-14		440		459		NIAPNTTTLGEETLHTTCE K						Carbamidomethyl (C)[18]		Mascot							
2281.136		2280.9895		-0.1465		-64		178		196		LDDELEAPNVWRASLYP HR								Mascot							
2297		2297.0139		0.0139		6		130		151		STSFFGVYDGHGGAEVA MYCAK								Mascot							
2691.3882		2691.0667		-0.3215		-119		258		281		CVLSKNGQAILDSTDHKP NVPLER						Carbamidomethyl (C)[1]		Mascot							
2691.3882		2691.0667		-0.3215		-119		258		281		CVLSKNGQAILDSTDHKP NVPLER						Carbamidomethyl (C)[1]		Mascot							
3795.1604		3794.6902		-0.4702		-124		2		38		VISVPLFSSVLLALVVAVP ADFDVGRLLGVLGCSV R						Carbamidomethyl (C)[34]		Mascot							
3913.0818		3912.5039		-0.5779		-148		358		392		VAKITGDTEFLVIASDGC						Carbamidomethyl (C)[19]		Mascot							

	3926.2009	3926.5334	0.3325	85	1	38	SIQILVLDLNTFFPFR MVISVPLFSSVLLALVVAV PADFDVGGRLLGVLCS VR					Carbamidomethyl (C)[35]	Mascot
	3926.2009	3926.5334	0.3325	85	1	38	MVISVPLFSSVLLALVVAV PADFDVGGRLLGVLCS VR					Carbamidomethyl (C)[35]	Mascot
2	Alcohol dehydrogenase 1 OS=Petunia hybrida GN=ADH1 PE=3 SV=1					ADH1_PETHY	41546.8	6.19	8	34	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	996.536	996.5368	0.0008	.1	165	173	IDPQAPLDK					Mascot	
	1083.6157	1083.5325	-0.0832	-77	224	233	IGVDLNPGR					Mascot	
	1179.5786	1179.5244	-0.0542	-46	1	11	MSNTAGQVIR			Oxidation (M)[1]		Mascot	
	1320.6688	1320.5026	-0.1662	-126	2	13	SSNTAGQVIRCK			Carbamidomethyl (C)[11]		Mascot	
	1475.7423	1475.6777	-0.0646	-44	125	137	GVMHGDQTRFSK					Mascot	
	1638.9286	1638.7797	-0.1489	-91	218	233	IAGASRIIGVDLNPGR					Mascot	
	1794.7567	1794.6936	-0.0631	-35	106	119	HCKSEESNMCDLR			Carbamidomethyl (C)[2,10], Oxidation (M)[9]		Mascot	
	3940.8884	3940.5977	-0.2907	-74	138	173	DGKPIYHFGVTSTFSEYT VCHSGCVTKIDPQAPLDK					Mascot	
3	BON1-associated protein 1 OS=Arabidopsis thaliana GN=BAP1 PE=1 SV=1					BAP1_ARATH	21978.1	9.42	6	34	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	1165.575	1165.6731	0.0981	84	61	69	RSNPTWNYK					Mascot	
	1165.575	1165.6731	0.0981	84	61	69	RSNPTWNYK					Mascot	
	1475.8005	1475.6777	-0.1228	-83	178	190	TVTGVPPWGLYOR					Mascot	
	2225.0188	2224.9612	-0.0576	-26	1	18	MIYFGRSIDNHYYTMMTK			Oxidation (M)[1]		Mascot	
	2225.0188	2224.9612	-0.0576	-26	1	18	MIYFGRSIDNHYYTMMTK			Oxidation (M)[1]		Mascot	
	2298.1104	2298.0315	-0.0789	-34	7	25	SIDNHYYTMMTKTLEIDLR			Oxidation (M)[9]		Mascot	
	2333.127	2332.9531	-0.1739	-75	70	88	SEMPINGNEQIFIEVFYR					Mascot	
	3339.5779	3339.5632	-0.0147	-4	62	88	SNPTWNYKSEMPINGNE QIFIEVFYR			Oxidation (M)[11]		Mascot	
4	Cysteine protease 1 OS=Oryza sativa subsp. japonica GN=CP1 PE=2 SV=2					CYSP1_ORYSJ	52608.4	7.74	8	33	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	850.4529	850.4891	0.0362	43	142	148	RVGEAYR					Mascot	
	1794.7607	1794.6936	-0.0671	-37	433	446	DHSTCCPKPEYVPCNAK					Mascot	
	1838.8667	1838.8113	-0.0554	-30	149	164	HDGVEALPDSVDWRDK					Mascot	
	2211.061	2210.9573	-0.1037	-47	377	397	GNPKPSPSPAPSPPPQ QCQR			Carbamidomethyl (C)[19]		Mascot	
	2230.9604	2231.0432	0.0828	37	214	234	NGQNSGCNGIMDDAFA FIAR			Carbamidomethyl (C)[7], Oxidation (M)[12]		Mascot	
	2297.0437	2297.0139	-0.0298	-13	173	194	NOGCGSCWAFSAVAA VEGINK			Carbamidomethyl (C)[5]		Mascot	
	3795.052	3794.6902	-0.3618	-95	2	41	AGGGGKSVAAALAMACF LLILAAFAPPAAAAPPDIM SIIR					Mascot	
	3926.0925	3926.5334	0.4409	112	1	41	MAGGGKSVAAALAMA CFLLILAAFAPPAAAAPPD IMSIR					Mascot	
	3926.0925	3926.5334	0.4409	112	1	41	MAGGGKSVAAALAMA CFLLILAAFAPPAAAAPPD IMSIR					Mascot	
5	Protein PsbN OS=Huperzia lucidula GN=psbN PE=3 SV=1					PSBN_HUPLU	4866.4	4.36	3	33	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	3339.7334	3339.5632	-0.1702	-51	2	32	ETATLVAIFISCLLVSTFG YALYAFGQPSR					Mascot	
	3794.9824	3794.6902	-0.2922	-77	2	35	ETATLVAIFISCLLVSTFG YALYAFGQPSRELRL			Carbamidomethyl (C)[12]		Mascot	
	3926.0229	3926.5334	0.5105	130	1	35	METATLVAIFISCLLVSTFG GYALYAFGQPSRELRL			Carbamidomethyl (C)[13]		Mascot	
	3926.0229	3926.5334	0.5105	130	1	35	METATLVAIFISCLLVSTFG GYALYAFGQPSRELRL			Carbamidomethyl (C)[13]		Mascot	
6	Protein PsbN OS=Staurastrum punctulatum GN=psbN PE=3 SV=1					PSBN_STAPU	4866.4	4.36	3	33	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	3339.7585	3339.5632	-0.1953	-58	2	32	ETATLVVIFISCLLVSTFG YALYAFGQPSK					Mascot	
	3795.0076	3794.6902	-0.3174	-84	2	35	ETATLVVIFISCLLVSTFG YALYAFGQPSKELR			Carbamidomethyl (C)[12]		Mascot	
	3926.0481	3926.5334	0.4853	124	1	35	METATLVVIFISCLLVSTFG GYALYAFGQPSKELR			Carbamidomethyl (C)[13]		Mascot	
	3926.0481	3926.5334	0.4853	124	1	35	METATLVVIFISCLLVSTFG GYALYAFGQPSKELR			Carbamidomethyl (C)[13]		Mascot	
7	Ras-related protein RAB1c OS=Arabidopsis thaliana GN=RAB1C PE=2 SV=1					RAB1C_ARATH	23149.6	6.96	6	31	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	870.4362	870.4839	0.0477	55	121	127	CDLAHRR					Mascot	
	870.4362	870.4839	0.0477	55	121	127	CDLAHRR					Mascot	
	1045.5425	1045.5024	-0.0401	-38	70	77	SITRSYYR					Mascot	
	1475.8329	1475.6777	-0.1552	-105	78	91	GAAGALLVYDITRR					Mascot	
	2284.2256	2284.0232	-0.2024	-89	9	29	YIIIGDTGVKSCLLQLFT DK					Mascot	
	2296.9668	2297.0139	0.0471	21	187	211	VGGGIPGPSGGRDGST SQGGGCCG			Carbamidomethyl (C)[23,24]		Mascot	
	2720.4077	2720.1379	-0.2698	-99	47	69	MITIDNKPILQIWDTAGQ ESFR			Oxidation (M)[1]		Mascot	
8	Putative defensin-like protein 110 OS=Arabidopsis thaliana GN=At1g15757 PE=3 SV=1					DF110_ARATH	8990.4	8.09	5	30	0		
	Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type	
	856.3803	856.4758	0.0955	112	58	65	GCIAFCSR					Mascot	

	856.3803	856.4758	0.0955	112	58	65	GCIACFSR								Mascot
	1006.4298	1006.5231	-0.1067	-106	38	45	EDEHYGFK								Mascot
	2172.9255	2172.9626	0.0371	17	66	83	MKFTTGLCLGSWCCCY T							Carbamidomethyl (C)[8,14,15,16], Oxidation (M)[1]	Mascot
	2172.9255	2172.9626	0.0371	17	66	83	MKFTTGLCLGSWCCCY T							Carbamidomethyl (C)[8,14,15,16], Oxidation (M)[1]	Mascot
	2195.0283	2194.9646	-0.0637	-29	26	45	STSDIVSGSGIKEDEHVC FK							Carbamidomethyl (C)[18]	Mascot
	2225.0146	2224.9612	-0.0534	-24	46	65	TSPCLPEVGGKEKGCIACF SR							Carbamidomethyl (C)[4,14,18]	Mascot
	2225.0146	2224.9612	-0.0534	-24	46	65	TSPCLPEVGGKEKGCIACF SR							Carbamidomethyl (C)[4,14,18]	Mascot
9	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic OS=Zea mays GN=CRS1 PE=1 SV					CRS1_MAIZE	81355.4	9.88	10	30	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type	
	882.5519	882.5101	-0.0418	-47	219	225	IVEPLRR								Mascot
	896.5359	896.5368	0.0009	1	661	669	SSFSNLLTK								Mascot
	1045.5887	1045.5024	-0.0863	-83	193	202	KAGVTDEVVK								Mascot
	1051.5895	1051.6451	0.0556	53	50	59	IDSPKPAPAR								Mascot
	1051.5895	1051.6451	0.0556	53	50	59	IDSPKPAPAR								Mascot
	1179.6844	1179.5244	-0.16	-136	50	60	IDSPKPAPARK								Mascot
	1320.6808	1320.5026	-0.1782	-135	264	274	HSHFTLTNVHK								Mascot
	1638.9286	1638.7797	-0.1489	-91	61	77	NKTAKALPTAGVPGGR								Mascot
	2664.374	2664.1196	-0.2544	-95	439	462	DFLPGGVAAQTVIQREAQ VHDEQVK								Mascot
	2921.5415	2921.1492	-0.3923	-134	402	427	IGIONTNNEQMAWNLKHL TGGTVILR								Mascot
	3794.9468	3794.6902	-0.2566	-68	306	338	LDDTLGPRFDWWWDTP LPVDADLLPFEVPGSK								Mascot
10	Phosphoenolpyruvate carboxylase 4 OS=Arabidopsis thaliana GN=PPC4 PE=2 SV=1					CAPP4_ARATH	116513.1	6.68	12	29	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type	
	856.5363	856.4758	-0.0605	-71	514	520	LADLIRR								Mascot
	856.5363	856.4758	-0.0605	-71	514	520	LADLIRR								Mascot
	870.3886	870.4839	0.0953	109	311	317	CSDRFISR								Mascot
	870.3886	870.4839	0.0953	109	311	317	CSDRFISR								Mascot
	1051.5419	1051.6451	0.1032	98	322	329	ILEKDYDR								Mascot
	1051.5419	1051.6451	0.1032	98	322	329	ILEKDYDR								Mascot
	1475.7794	1475.6777	-0.1017	-69	868	879	AIPWFVAWTQTR								Mascot
	1795.8102	1795.702	-0.1062	-60	809	823	NLMEEISGISCOHYR					Oxidation (M)[3]			Mascot
	1838.8966	1838.8113	-0.0853	-46	351	366	AHLPAIDIFGESRH TK					Carbamidomethyl (C)[6]			Mascot
	2173.1069	2172.9626	-0.1443	-66	741	762	GGGPTYLAIQSQPPGSV MGLSR								Mascot
	2173.1069	2172.9626	-0.1443	-66	741	762	GGGPTYLAIQSQPPGSV MGLSR								Mascot
	2195.012	2194.9646	-0.0474	-22	807	823	WRNLMEEISGISCOHYR					Carbamidomethyl (C)[13], Oxidation (M)[5]			Mascot
	2263.9749	2284.0232	0.0483	21	382	400	ONEQDFSESDWEKDNG SR								Mascot
	2721.5186	2721.1399	-0.3787	-139	783	806	QLEVYTTAVLATLKKPPQ PPREEK								Mascot
	2748.3662	2748.1113	-0.2549	-93	906	927	EMYKEWPFQSTLELIEM VLAK					Oxidation (M)[2]			Mascot
	2748.3662	2748.1113	-0.2549	-93	906	927	EMYKEWPFQSTLELIEM VLAK					Oxidation (M)[2]			Mascot
	3926.946	3926.5334	-0.4126	-105	824	857	STVYENPEFLSYFHEATP QAELGFLNGSRPTRR								Mascot
	3926.946	3926.5334	-0.4126	-105	824	857	STVYENPEFLSYFHEATP QAELGFLNGSRPTRR								Mascot
Gel Idx/Pos	155/G6						Instr./Gel Origin	BA2060/140227A				Process Status	Analysis Succeeded		
Plate [#] Name	[1] 31564						Instrument Sample Name					Spectra	11		
Rank	Protein Name				Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %			
1	Probable protein arginine N-methyltransferase 6.1 OS=Orzyza sativa subsp. indica GN=PRMT6.1 PE=2 SV=				ANM61_ORYSI	42193.2	5.41	9	44	0					
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type	
	1045.4908	1045.5004	0.0096	9	361	369	VSQSEENPR								Mascot
	1270.5806	1270.6647	0.0841	66	370	379	FLNIQLDCTM					Carbamidomethyl (C)[8], Oxidation (M)[10]			Mascot
	1270.5806	1270.6647	0.0841	66	370	379	FLNIQLDCTM					Carbamidomethyl (C)[8], Oxidation (M)[10]			Mascot
	1685.7622	1685.7649	0.0027	2	108	122	CYVAVAEASEMATQAR					Carbamidomethyl (C)[1]			Mascot
	1685.9016	1685.7649	-0.1367	-81	1	15	MLPSHLNGHSLPARR								Mascot
	2211.1082	2210.9558	-0.1524	-69	86	107	VVMDVGGGTGLSVFCA RAGAK					Carbamidomethyl (C)[7]			Mascot
	2297.0537	2296.9937	-0.06	-26	361	379	VSQSEENPRFLNIQLDCT M					Carbamidomethyl (C)[17], Oxidation (M)[19]			Mascot
	2677.2854	2677.1062	-0.1792	-67	203	228	YEGSVDFWSDVYGINMS ALVPLAK					Oxidation (M)[16]			Mascot
	3353.6506	3353.5449	-0.1057	-32	150	177	VDVHSEWMGYMLLYESM LPSVLFARDK					Oxidation (M)[9,12,18]			Mascot
	3498.686	3498.4368	-0.2492	-71	270	300	YKVSSMMLAPIHGFLW FEVEFNGPSNPTDK								Mascot
	3498.686	3498.4368	-0.2492	-71	270	300	YKVSSMMLAPIHGFLW FEVEFNGPSNPTDK								Mascot
2	Acyl-[acyl-carrier-protein] desaturase, chloroplastic OS=Gossypium hirsutum PE=2 SV=1					STAD_GOSHI	45204.9	5.99	9	40	0				
	Peptide Information														
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type	
	1160.5807	1160.5504	-0.0303	-26	231	241	ATFISHGNTGR								Mascot
	1179.619	1179.5565	-0.0625	-53	1	11	MALNFNAIAASK								Mascot
	1179.619	1179.5565	-0.0625	-53	1	11	MALNFNAIAASK								Mascot
	1270.6348	1270.6647	0.0299	24	31	42	FSMISTIPSGSK					Oxidation (M)[3]			Mascot
	1318.7001	1318.5907	-0.1094	-83	265	275	HETAYTKIVEK					Oxidation (M)[3]			Mascot
	1794.881	1794.741	-0.14	-78	378	393	AQGSTPVPSPFSWIFDR								Mascot
	2178.1553	2177.9526	-0.2027	-93	75	93	SLEGWAENNILTHLKPVE K								Mascot
	2178.1553	2177.9526	-0.2027	-93	75	93	SLEGWAENNILTHLKPVE K								Mascot
	2230.2053	2230.0623	-0.143	-64	56	74	EVPPQVITHSMPPHKIEFK								Mascot

	2239.0659	2238.9529	-0.113	-50	245	264	EYGDINLAQICGSIASDEK R	Carbamidomethyl (C)[11]	Mascot			
	2430.082	2430.0703	-0.0117	-5	94	114	CWQPADFLPDPNSDGFH EQVK		Mascot			
3	Alpha-barbatene synthase OS=Arabidopsis thaliana GN=BS PE=1 SV=2					BARS_ARATH	64867.6	5.25	11	38	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1375.7368	1375.5535	-0.1833	-133	431	441	EAFEWLISRPK					Mascot
	1439.823	1439.6421	-0.1809	-126	198	209	LIONALHIPQHR					Mascot
	1503.8318	1503.6823	-0.1495	-99	430	441	KEAFEWLISRPK					Mascot
	1515.7764	1515.6562	-0.1202	-79	368	379	SFVLEKMIEEFK			Oxidation (M)[7]		Mascot
	1695.8562	1695.699	-0.1572	-93	262	275	LDHTSNLPPNFRER					Mascot
	1794.8182	1794.741	-0.0772	-43	493	507	MNGDMNKIVNEECKL			Carbamidomethyl (C)[13]		Mascot
	1879.9662	1879.8452	-0.121	-64	350	363	FVMYLFKEYEILR					Mascot
	2210.9998	2210.9558	-0.044	-20	332	349	WDPDYMENLQGHMKTA FK					Mascot
	2220.1699	2219.9553	-0.2146	-97	69	87	TLSIHFLDSLGLSYHFEK					Mascot
	2297.0244	2296.9937	-0.0307	-13	218	235	EYISFYEHEDHDETLLK					Mascot
	3353.5803	3353.5449	-0.0354	-11	302	331	LYLVITFLDDACDTYGSIS EVESLADCLER					Mascot
4	V-type proton ATPase subunit E2 OS=Arabidopsis thaliana GN=VHA-E2 PE=2 SV=1					VATE2_ARATH	26836.3	9.2	7	37	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	882.5519	882.5177	-0.0342	-39	217	223	QKLQPIR					Mascot
	901.5353	901.4468	-0.0885	-98	41	48	LQLLESAK					Mascot
	1318.7412	1318.5907	-0.1505	-114	9	18	QIQQMVR FIR					Mascot
	1631.817	1631.7566	-0.0604	-37	2	15	NDADVSKIQQMVR					Mascot
	1794.8473	1794.741	-0.1063	-59	1	15	MNDADVSKIQQMVR			Oxidation (M)[1,13]		Mascot
	1953.9586	1953.9188	-0.0398	-20	81	98	YLAQDDVVTAMKDSAA K					Mascot
	3233.5312	3233.3047	-0.2265	-70	180	210	LPDSDPHPCSGGVVLAS QDGKIVCENTLDAR					Mascot
	3233.5312	3233.3047	-0.2265	-70	180	210	LPDSDPHPCSGGVVLAS QDGKIVCENTLDAR					Mascot
5	60S ribosomal protein L13a-3 OS=Arabidopsis thaliana GN=RPL13AC PE=2 SV=1					R13A3_ARATH	23613.8	10.39	9	36	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	870.5519	870.4927	-0.0592	-68	100	108	GAALARLQK					Mascot
	870.5519	870.4927	-0.0592	-68	100	108	GAALARLQK					Mascot
	901.4712	901.4468	-0.0244	-27	59	64	YMRFLR			Oxidation (M)[2]		Mascot
	1165.5817	1165.6698	0.0881	76	1	11	MVSGSGICAKR			Carbamidomethyl (C)[8]		Mascot
	1261.6462	1261.632	-0.0142	-11	109	119	VFEGIPPPYDK					Mascot
	1270.7551	1270.6647	-0.0904	-71	123	133	MVIPDALKVLR			Oxidation (M)[1]		Mascot
	1270.7551	1270.6647	-0.0904	-71	123	133	MVIPDALKVLR			Oxidation (M)[1]		Mascot
	1375.7375	1375.5535	-0.184	-134	12	23	VVVDGRHHMLGR					Mascot
	1502.8253	1502.6847	-0.1406	-94	109	121	VFEGIPPPYDKIK					Mascot
	1502.8253	1502.6847	-0.1406	-94	107	119	LKVFEGIPPPYDK					Mascot
	2040.1447	2039.9109	-0.2338	-115	24	42	LASNTAKELLNGQEVVVV R					Mascot
6	Putative AC9 transposase OS=Zea mays PE=4 SV=1					TRAC9_MAIZE	97005.7	6.86	14	34	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	842.4406	842.4583	0.0177	21	790	795	DYLLR					Mascot
	882.4059	882.5177	0.1118	127	527	534	MAMAMSEK			Oxidation (M)[1]		Mascot
	944.5352	944.4783	-0.0569	-60	473	479	WHLTLFK					Mascot
	996.507	996.5322	0.0252	25	642	649	YMSEPLLK			Oxidation (M)[2]		Mascot
	1160.6211	1160.5504	-0.0707	-61	274	283	IVGFFHVEGR					Mascot
	1270.6169	1270.6647	0.0478	38	527	537	MAMAMSEKFEK					Mascot
	1270.6169	1270.6647	0.0478	38	527	537	MAMAMSEKFEK					Mascot
	1375.7501	1375.5535	-0.1966	-143	705	717	LGSEIVEALICTK			Carbamidomethyl (C)[7,8]		Mascot
	1503.6355	1503.6823	0.0468	31	511	521	DLIDQWCHEK			Oxidation (M)[5]		Mascot
	1695.6812	1695.699	0.0178	10	241	254	FSTTMDMWTSCQNK			Carbamidomethyl (C)[8]		Mascot
	1751.7781	1751.7793	0.0012	1	106	119	VQVVGHCNFPNCK			Carbamidomethyl (C)[9]		Mascot
	1879.873	1879.8452	-0.0278	-15	105	119	KYVQVWGHCFNPNCK			Oxidation (M)[16]		Mascot
	2178.0647	2177.9526	-0.1121	-51	400	417	GISYDVSTRWNSTYML R					Mascot
	2178.0647	2177.9526	-0.1121	-51	400	417	GISYDVSTRWNSTYML R			Oxidation (M)[16]		Mascot
	2296.9631	2296.9937	0.0306	13	236	254	DVQSRFSTTMDMWTSC QNK			Oxidation (M)[10,12]		Mascot
	2313.0137	2313.0149	0.0012	1	255	272	SYMCVTIHWIDDDWCLQ K			Carbamidomethyl (C)[4]		Mascot
7	Putative AC transposase OS=Zea mays PE=2 SV=2					TRA1_MAIZE	91963	6.84	14	34	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	856.5111	856.4749	-0.0362	-42	54	60	IQNVRR					Mascot
	870.411	870.4927	0.0817	94	61	68	ARGHGCGR			Carbamidomethyl (C)[6]		Mascot
	870.411	870.4927	0.0817	94	61	68	ARGHGCGR			Carbamidomethyl (C)[6]		Mascot
	882.4059	882.5177	0.1118	127	558	565	MAMAMSEK			Oxidation (M)[1]		Mascot
	996.507	996.5322	0.0252	25	673	680	YMSEPLLK			Oxidation (M)[2]		Mascot
	1160.6211	1160.5504	-0.0707	-61	329	338	IVGFFHVEGR					Mascot
	1270.6169	1270.6647	0.0478	38	558	568	MAMAMSEKFEK					Mascot
	1270.6169	1270.6647	0.0478	38	558	568	MAMAMSEKFEK					Mascot
	1375.7501	1375.5535	-0.1966	-143	736	748	LGSEIVEALICTK					Mascot
	1695.6812	1695.699	0.0178	10	296	309	FSTTMDMWTSCQNK			Oxidation (M)[5]		Mascot
	1751.7781	1751.7793	0.0012	1	161	174	VQVVGHCNFPNCK			Carbamidomethyl (C)[8]		Mascot
	1879.873	1879.8452	-0.0278	-15	160	174	KYVQVWGHCFNPNCK			Carbamidomethyl (C)[9]		Mascot
	2177.0154	2176.9568	-0.0586	-27	536	552	GFCEIKDLIDQWCVHEK			Carbamidomethyl (C)[3,13]		Mascot
	2178.0647	2177.9526	-0.1121	-51	455	472	GISYDVSTRWNSTYML R			Oxidation (M)[16]		Mascot
	2178.0647	2177.9526	-0.1121	-51	455	472	GISYDVSTRWNSTYML R			Oxidation (M)[16]		Mascot
	2296.9631	2296.9937	0.0306	13	291	309	DVQSRFSTTMDMWTSC QNK			Oxidation (M)[10,12]		Mascot
	2313.0137	2313.0149	0.0012	1	310	327	SYMCVTIHWIDDDWCLQ K			Carbamidomethyl (C)[4]		Mascot
8	Vacuolar-sorting receptor 5 OS=Arabidopsis thaliana GN=VSR5 PE=2 SV=1					VSR5_ARATH	69211.7	5.64	12	32	0	
	Peptide Information											
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence	Ion	C. I. %	Modification	Rank	Result Type



							Score		
870.4025	870.4927	0.0902	104	257	263	YCALDTK		Carbamidomethyl (C)[2]	Mascot
870.4025	870.4927	0.0902	104	257	263	YCALDTK		Carbamidomethyl (C)[2]	Mascot
882.5771	882.5177	-0.0594	-67	147	154	IPSALILR			Mascot
1301.5402	1301.5912	0.051	39	529	539	CKNNWGGYECK		Carbamidomethyl (C)[2]	Mascot
1495.6919	1495.6555	-0.0364	-24	442	454	VCECPVVDGVQYK			Mascot
1502.5458	1502.6847	0.1389	92	469	481	CSMNNGDCWSETR			Mascot
1502.5458	1502.6847	0.1389	92	469	481	CSMNNGDCWSETR			Mascot
1630.6407	1630.7649	0.1242	76	469	482	CSMNNGDCWSETRK			Mascot
1631.9302	1631.7566	-0.1736	-106	93	106	LLIDRGVCNFK		Carbamidomethyl (C)[9]	Mascot
2177.2361	2176.9568	-0.2793	-128	7	27	GTVLALILALTMVVVNGFSSR		Oxidation (M)[12]	Mascot
2224.9275	2224.9919	0.0644	29	187	205	VEYELWANTNDECGVHC DK			Mascot
2224.9275	2224.9919	0.0644	29	187	205	VEYELWANTNDECGVHC DK			Mascot
2430.4045	2430.0703	-0.3342	-138	564	586	GLFTIVVLTAIAGISLGAYI FYK			Mascot
3338.4722	3338.4607	-0.0115	-3	401	428	TEPSICLNSDIETNECLIE NGGCWQDKR		Carbamidomethyl (C)[6,16,23]	Mascot
3353.4719	3353.5449	0.073	22	399	427	ERTEPSICLNSDIETNECL IENGCCWQDK		Carbamidomethyl (C)[8]	Mascot

9 Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1

VILI4\_ARATH

109258.9

5.83

13

32

0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
850.3975	850.4895	0.092	108	275	281	EMLDTNK		
856.4232	856.4749	0.0517	60	947	953	EKFGMTK		
1261.7515	1261.632	-0.1195	-95	190	200	AKALEVVQYIK		
1318.6896	1318.5907	-0.0989	-75	317	327	SSSRPKSQMR		
1439.7965	1439.6421	-0.1544	-107	577	588	OLDLIKPNQOSR		
1503.7584	1503.6823	-0.0761	-51	310	322	AAEEMIRSSSRPK		
1695.786	1695.699	-0.087	-51	592	606	EGSESEQFVWLLGQK		
1794.877	1794.741	-0.136	-76	787	803	SPAFNALAATFESQNAIR		
1953.9156	1953.9188	0.0032	2	1	18	MSVSMRDLDPAFGAG QK		
2199.99	2199.9231	-0.0669	-30	341	359	FESWTQETNTTVSEDGR GR		
2219.9927	2219.9553	-0.0374	-17	715	733	FFTSWDSKSKAMHGNFS QR		
2238.9324	2238.9529	0.0205	9	415	432	FYSGDCVYFQYSYPGEE K		
3498.5874	3498.4368	-0.1506	-43	415	443	FYSGDCVYFQYSYPGEE KEEVLIGTWFGK		
3498.5874	3498.4368	-0.1506	-43	415	443	FYSGDCVYFQYSYPGEE KEEVLIGTWFGK		

10 DEAD-box ATP-dependent RNA helicase 18 OS=Oryza

RH18\_ORYSJ

72172.5

9.45

10

32

0

sativa subsp. japonica GN=Os01g0164500 PE=1 SV=2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
882.5267	882.5177	-0.009	-10	224	231	AGLRNPVR		
1165.5807	1165.6698	0.0891	76	2	14	SSSSSSLA AAAAR		
1179.6844	1179.5565	-0.1279	-108	540	549	APEKPEKPKR		
1179.6844	1179.5565	-0.1279	-108	540	549	APEKPEKPKR		
1502.8101	1502.6847	-0.1254	-83	23	36	FSELSPALSPVEVK		
1502.8101	1502.6847	-0.1254	-83	23	36	FSELSPALSPVEVK		
1880.0197	1879.8452	-0.1745	-93	125	142	GVSSMLLVGGFDIKAEIK		
1953.9772	1953.9188	-0.0584	-30	255	271	TPLGLRLLEYMICEASNK		
2039.9338	2039.9109	-0.0229	-11	557	573	QAVQTKEMDLANEYR		
2177.0232	2176.9568	-0.0664	-31	453	469	EHHCYSYFVSKDLEIGR		
2297.1917	2296.9937	-0.198	-86	407	427	GVPLTERECSTNAVDIPIQR		
3353.7273	3353.5449	-0.1824	-54	470	499	LGMEYGLLQIPSMPEVKH HSLSLGEGFTPVK		

Gel Idx/Pos	156/G7	Instr./Gel Origin	BA2060/140227A	Process Status	Analysis Succeeded
Plate [#] Name	[1] 31564	Instrument Sample Name		Spectra	11

Rank	Protein Name	Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %
1	Ribulose biphosphate carboxylase large chain (Fragment) OS=Humiria balsamifera GN=rbcl PE=3 SV=1	RBL_HUMBA	51530.1	6.23	13	239	100	176	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
830.4366	830.3813	-0.0553	-67	430	436	EGNEIIR	22	0			Mascot
830.4366	830.3813	-0.0553	-67	430	436	EGNEIIR					Mascot
1037.4899	1037.4155	-0.0744	-72	341	348	DDFIEKDR					Mascot
1116.6194	1116.5057	-0.1137	-102	412	421	VALEACVKAR	15	0	Carbamidomethyl (C)[6]		Mascot
1116.6194	1116.5057	-0.1137	-102	412	421	VALEACVKAR			Carbamidomethyl (C)[6]		Mascot
1168.6255	1168.4631	-0.1624	-139	286	295	AMHAVIDROK					Mascot
1245.6433	1245.4946	-0.1487	-119	430	440	EGNEIIREASK					Mascot
1261.6285	1261.629	0.0005	0	208	217	FLFCAEALYK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.629	-0.0861	-68	330	340	DITLGFVDLLR	89	100			Mascot
1447.7651	1447.6581	-0.107	-74	310	324	LSGGDHIHAGTVVGK	52	99.896			Mascot
1502.8512	1502.6613	-0.1899	-126	155	167	YGRPLLGCTIKPK			Carbamidomethyl (C)[8]		Mascot
1546.7358	1546.6248	-0.111	-72	441	453	WSPLEAAACEVWK			Carbamidomethyl (C)[9]		Mascot
1628.8101	1628.7357	-0.0744	-46	178	191	AVVECLRGGLDFTK			Carbamidomethyl (C)[5]		Mascot
1794.8149	1794.6927	-0.1222	-68	227	242	GHYLNATAGTCEEMIK			Carbamidomethyl (C)[11]		Mascot
2009.059	2008.9146	-0.1444	-72	330	346	DITLGFVDLLRDDFIEK					Mascot

2 Ribulose biphosphate carboxylase large chain

RBL\_AILAL

51613.1

6.09

13

237

100

173

100

(Fragment) OS=Ailanthus altissima GN=rbcl PE=3 SV=1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
830.4366	830.3813	-0.0553	-67	430	436	EGNEIIR	22	0			Mascot
830.4366	830.3813	-0.0553	-67	430	436	EGNEIIR					Mascot
1037.4899	1037.4155	-0.0744	-72	341	348	DDFIEKDR					Mascot
1116.583	1116.5057	-0.0773	-69	412	421	VALEACVQAR	12	0	Carbamidomethyl (C)[6]		Mascot
1116.583	1116.5057	-0.0773	-69	412	421	VALEACVQAR			Carbamidomethyl (C)[6]		Mascot
1168.6255	1168.4631	-0.1624	-139	286	295	AMHAVIDROK					Mascot
1245.6433	1245.4946	-0.1487	-119	430	440	EGNEIIREASK					Mascot
1261.6285	1261.629	0.0005	0	208	217	FLFCAEAIYK			Carbamidomethyl (C)[4]		Mascot
1261.7151	1261.629	-0.0861	-68	330	340	DITLGFVDLLR	89	100			Mascot

1447.7651	1447.6581	-0.107	-74	310	324	LSGGDHIHAGTVVGK	52	99.896						Mascot
1447.7651	1447.6581	-0.107	-74	310	324	LSGGDHIHAGTVVGK								Mascot
1502.8512	1502.6613	-0.1899	-126	155	167	YGRPLLGCTIKPK					Carbamidomethyl (C)[8]			Mascot
1546.7358	1546.6248	-0.111	-72	441	453	WSPELAAACEVWK					Carbamidomethyl (C)[9]			Mascot
1628.8101	1628.7357	-0.0744	-46	178	191	AVYECLRGGLDFTK					Carbamidomethyl (C)[5]			Mascot
1794.8149	1794.6927	-0.1222	-68	227	242	GHYLNATAGTCEEMIK					Carbamidomethyl (C)[11]			Mascot
2009.059	2008.9146	-0.1444	-72	330	346	DITLGFVDLLRDFIEK					Carbamidomethyl (C)[11]			Mascot
Ribulose biphosphate carboxylase large chain							RBL_CARPA	52456.6	6.19	13	234	100	173	100
OS=Carica papaya GN=rbcl PE=3 SV=2														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type	
830.4366	830.3813	-0.0553	-67	440	446	EGNEIIR	22	0					Mascot	
830.4366	830.3813	-0.0553	-67	440	446	EGNEIIR							Mascot	
1037.4899	1037.4155	-0.0744	-72	351	358	DEFVEKDR							Mascot	
1116.583	1116.5057	-0.0773	-69	422	431	VALEACVQAR	12	0		Carbamidomethyl (C)[6]			Mascot	
1116.583	1116.5057	-0.0773	-69	422	431	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
1168.6255	1168.4631	-0.1624	-139	296	305	AMHAVIDROK							Mascot	
1245.6433	1245.4946	-0.1487	-119	440	450	EGNEIIREASK							Mascot	
1261.6285	1261.629	0.0005	0	218	227	FLFCAEAYK							Mascot	
1261.7151	1261.629	-0.0861	-68	340	350	DITLGFVDLLR	89	100		Carbamidomethyl (C)[4]			Mascot	
1447.7651	1447.6581	-0.107	-74	320	334	LSGGDHIHAGTVVGK	52	99.896					Mascot	
1447.7651	1447.6581	-0.107	-74	320	334	LSGGDHIHAGTVVGK							Mascot	
1502.8512	1502.6613	-0.1899	-126	165	177	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]			Mascot	
1546.7358	1546.6248	-0.111	-72	451	463	WSPELAAACEVWK				Carbamidomethyl (C)[9]			Mascot	
1628.8101	1628.7357	-0.0744	-46	188	201	AVYECLRGGLDFTK				Carbamidomethyl (C)[5]			Mascot	
1794.8149	1794.6927	-0.1222	-68	237	252	GHYLNATAGTCEEMIK				Carbamidomethyl (C)[11]			Mascot	
2009.059	2008.9146	-0.1444	-72	340	356	DITLGFVDLLRDFIEK							Mascot	
Ribulose biphosphate carboxylase large chain							RBL_BIXOR	51746.9	6.04	12	228	100	173	100
(Fragment) OS=Bixa orellana GN=rbcl PE=3 SV=2														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type	
830.4366	830.3813	-0.0553	-67	431	437	EGNEIIR	22	0					Mascot	
830.4366	830.3813	-0.0553	-67	431	437	EGNEIIR							Mascot	
1037.4899	1037.4155	-0.0744	-72	342	349	DDFIEKDR							Mascot	
1116.583	1116.5057	-0.0773	-69	413	422	VALEACVQAR	12	0		Carbamidomethyl (C)[6]			Mascot	
1116.583	1116.5057	-0.0773	-69	413	422	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
1168.6255	1168.4631	-0.1624	-139	287	298	AMHAVIDROK							Mascot	
1245.6433	1245.4946	-0.1487	-119	431	441	EGNEIIREASK							Mascot	
1261.6285	1261.629	0.0005	0	209	218	FLFCAEAYK	89	100		Carbamidomethyl (C)[4]			Mascot	
1261.7151	1261.629	-0.0861	-68	331	341	DITLGFVDLLR	52	99.896					Mascot	
1447.7651	1447.6581	-0.107	-74	311	325	LSGGDHIHAGTVVGK							Mascot	
1447.7651	1447.6581	-0.107	-74	311	325	LSGGDHIHAGTVVGK							Mascot	
1488.6926	1488.5801	-0.1125	-76	455	466	EKFEFEAMDTL				Oxidation (M)[9]			Mascot	
1502.8512	1502.6613	-0.1899	-126	156	168	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]			Mascot	
1546.7358	1546.6248	-0.111	-72	442	454	WSPELAAACEVWK				Carbamidomethyl (C)[9]			Mascot	
2009.059	2008.9146	-0.1444	-72	331	347	DITLGFVDLLRDFIEK							Mascot	
Ribulose biphosphate carboxylase large chain							RBL_PACAAQ	52040.3	6.24	11	227	100	178	100
(Fragment) OS=Pachira aquatica GN=rbcl PE=3 SV=1														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type	
830.4366	830.3813	-0.0553	-67	433	439	EGNEIIR	22	0					Mascot	
830.4366	830.3813	-0.0553	-67	433	439	EGNEIIR							Mascot	
1037.4899	1037.4155	-0.0744	-72	344	351	DDFIEKDR							Mascot	
1116.6194	1116.5057	-0.1137	-102	415	424	VALEACVQAR	15	0		Carbamidomethyl (C)[6]			Mascot	
1116.6194	1116.5057	-0.1137	-102	415	424	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
1168.6255	1168.4631	-0.1624	-139	289	298	AMHAVIDROK							Mascot	
1245.6433	1245.4946	-0.1487	-119	433	443	EGNEIIREASK							Mascot	
1261.7151	1261.629	-0.0861	-68	333	343	DITLGFVDLLR	89	100					Mascot	
1261.7151	1261.629	-0.0861	-68	333	343	DITLGFVDLLR							Mascot	
1447.7651	1447.6581	-0.107	-74	313	327	LSGGDHIHAGTVVGK	52	99.896					Mascot	
1447.7651	1447.6581	-0.107	-74	313	327	LSGGDHIHAGTVVGK							Mascot	
1502.8512	1502.6613	-0.1899	-126	158	170	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]			Mascot	
1546.7358	1546.6248	-0.111	-72	444	456	WSPELAAACEVWK				Carbamidomethyl (C)[9]			Mascot	
1628.8101	1628.7357	-0.0744	-46	181	194	AVYECLRGGLDFTK				Carbamidomethyl (C)[5]			Mascot	
2009.059	2008.9146	-0.1444	-72	333	349	DITLGFVDLLRDFIEK							Mascot	
Ribulose biphosphate carboxylase large chain							RBL_CITSI	52485.5	6.29	12	225	100	173	100
OS=Citrus sinensis GN=rbcl PE=3 SV=1														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type	
830.4366	830.3813	-0.0553	-67	440	446	EGNEIIR	22	0					Mascot	
830.4366	830.3813	-0.0553	-67	440	446	EGNEIIR							Mascot	
1116.583	1116.5057	-0.0773	-69	422	431	VALEACVQAR	12	0		Carbamidomethyl (C)[6]			Mascot	
1116.583	1116.5057	-0.0773	-69	422	431	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
1168.6255	1168.4631	-0.1624	-139	296	305	AMHAVIDROK							Mascot	
1245.6433	1245.4946	-0.1487	-119	440	450	EGNEIIREASK							Mascot	
1261.6285	1261.629	0.0005	0	218	227	FLFCAEAYK							Mascot	
1261.7151	1261.629	-0.0861	-68	340	350	DITLGFVDLLR	89	100		Carbamidomethyl (C)[4]			Mascot	
1447.7651	1447.6581	-0.107	-74	320	334	LSGGDHIHAGTVVGK	52	99.896					Mascot	
1447.7651	1447.6581	-0.107	-74	320	334	LSGGDHIHAGTVVGK							Mascot	
1502.8512	1502.6613	-0.1899	-126	165	177	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]			Mascot	
1546.7358	1546.6248	-0.111	-72	451	463	WSPELAAACEVWK				Carbamidomethyl (C)[9]			Mascot	
1628.8101	1628.7357	-0.0744	-46	188	201	AVYECLRGGLDFTK				Carbamidomethyl (C)[5]			Mascot	
1794.8149	1794.6927	-0.1222	-68	237	252	GHYLNATAGTCEEMLK				Carbamidomethyl (C)[11]			Mascot	
1995.0433	1994.7704	-0.2729	-137	340	356	DITLGFVDLLRDFVEK							Mascot	
Ribulose biphosphate carboxylase large chain							RBL_CUCPE	51555	6.09	11	220	100	173	100
(Fragment) OS=Cucurbita pepo GN=rbcl PE=3 SV=1														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification		Rank	Result Type	
830.4366	830.3813	-0.0553	-67	431	437	EGNEIIR	22	0					Mascot	
830.4366	830.3813	-0.0553	-67	431	437	EGNEIIR							Mascot	
1116.583	1116.5057	-0.0773	-69	413	422	VALEACVQAR	12	0		Carbamidomethyl (C)[6]			Mascot	
1116.583	1116.5057	-0.0773	-69	413	422	VALEACVQAR				Carbamidomethyl (C)[6]			Mascot	
1168.6255	1168.4631	-0.1624	-139	287	296	AMHAVIDROK							Mascot	
1245.6433	1245.4946	-0.1487	-119	431	441	EGNEIIREASK							Mascot	
1261.6285	1261.629	0.0005	0	209	218	FLFCAEAYK	89	100		Carbamidomethyl (C)[4]			Mascot	
1261.7151	1261.629	-0.0861	-68	340	350	DITLGFVDLLR	52	99.896					Mascot	
1447.7651	1447.6581	-0.107	-74	311	325	LSGGDHIHAGTVVGK							Mascot	
1447.7651	1447.6581	-0.107	-74	311	325	LSGGDHIHAGTVVGK							Mascot	
1502.8512	1502.6613	-0.1899	-126	156	168	YGRPLLGCTIKPK				Carbamidomethyl (C)[8]			Mascot	
1546.7358	1546.6248	-0.111	-72	445	457	WSPELAAACEVWK				Carbamidomethyl (C)[9]			Mascot	
1628.8101	1628.7357	-0.0744	-46	179	192	AVYECLRGGLDFTK				Carbamidomethyl (C)[5]			Mascot	
1794.8149	1794.6927	-0.1222	-68	230	243	GHYLNATAGTCEEMLK				Carbamidomethyl (C)[11]			Mascot	
1995.0433	1994.7704	-0.2729	-137	331	347	DITLGFVDLLRDFVEK							Mascot	
Ribulose biphosphate carboxylase large chain							RBL_ANTLU	52118.2	6.44	12	210	100	154	100
(Fragment) OS=Antirhea lucida GN=rbcl PE=3 SV=1														
Peptide Information														
Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence	Ion	C. I. %		Modification		Rank	Result Type	

	1037.4899	1037.4155	-0.0744	-72	342	349	DDFIEKDR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
--	-----------	-----------	---------	-----	-----	-----	----------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

		944.5887	944.4632	-0.1255	-133	19	27	TLATKAAR										Mascot						
		1032.5948	1032.5236	-0.0712	-69	42	50	YRPGTVALR	16	0								Mascot						
		1032.5948	1032.5236	-0.0712	-69	42	50	YRPGTVALR										Mascot						
6	Histone H3.3 OS=Capsicum annuum PE=2 SV=3																							
	H33_CAPAN																							
		15396.6	11.15	4	54	86.911	42	98.85																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	831.4934	831.4346	-0.0588	-71	58	64	STELLIR	25	49.807			Mascot												
	831.4934	831.4346	-0.0588	-71	58	64	STELLIR					Mascot												
	850.4304	850.3724	-0.058	-68	74	80	EIAQDFK					Mascot												
	860.5022	860.4453	-0.0569	-66	117	123	RVTIMPK					Mascot												
	1032.5948	1032.5236	-0.0712	-69	42	50	YRPGTVALR	16	0	Oxidation (M)[5]		Mascot												
	1032.5948	1032.5236	-0.0712	-69	42	50	YRPGTVALR					Mascot												
7	Histone H3 type 3 OS=Chlamydomonas reinhardtii																							
	GN=ch3-IV PE=1 SV=2																							
	H33_CHLRE																							
		15250.5	11.15	4	54	84.972	42	98.85																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	831.4934	831.4346	-0.0588	-71	57	63	STELLIR	25	49.807			Mascot												
	831.4934	831.4346	-0.0588	-71	57	63	STELLIR					Mascot												
	850.4304	850.3724	-0.058	-68	73	79	EIAQDFK					Mascot												
	860.5022	860.4453	-0.0569	-66	116	122	RVTIMPK			Oxidation (M)[5]		Mascot												
	1032.5948	1032.5236	-0.0712	-69	41	49	YRPGTVALR	16	0			Mascot												
	1032.5948	1032.5236	-0.0712	-69	41	49	YRPGTVALR					Mascot												
8	Histone H3.3b OS=Lilium longiflorum GN=soH3-1 PE=2																							
	SV=3																							
	H33B_LILLO																							
		15606.7	11.26	3	48	52.478	42	98.85																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	831.4934	831.4346	-0.0588	-71	59	65	STELLIR	25	49.807			Mascot												
	831.4934	831.4346	-0.0588	-71	59	65	STELLIR					Mascot												
	860.5022	860.4453	-0.0569	-66	118	124	RVTIMPK			Oxidation (M)[5]		Mascot												
	1032.5948	1032.5236	-0.0712	-69	43	51	YRPGTVALR	16	0			Mascot												
	1032.5948	1032.5236	-0.0712	-69	43	51	YRPGTVALR					Mascot												
9	Ribulose bispophosphate carboxylase small chain 1,																							
	chloroplastic OS=Mesembryanthemum crystallinum																							
	GN=																							
	RBS1_MESCR																							
		20263	7.63	4	48	52.478	29	76.898																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	914.4229	914.3417	-0.0812	-89	123	128	YWTMWK					Mascot												
	933.5151	933.4507	-0.0644	-69	158	165	IIGFDNVR	10	0			Mascot												
	933.5151	933.4507	-0.0644	-69	158	165	IIGFDNVR					Mascot												
	1318.6345	1318.5612	-0.0733	-56	42	54	NNDITSVATNGGR					Mascot												
	1318.6345	1318.5612	-0.0733	-56	42	54	NNDITSVATNGGR	19	0			Mascot												
	1446.7295	1446.6464	-0.0831	-57	41	54	KNNDITSVATNGGR					Mascot												
10	Glutamate dehydrogenase 1 OS=Arabidopsis thaliana																							
	GN=GDH1 PE=1 SV=1																							
	DHE1_ARATH																							
		44495.9	6.38	10	47	32.873																		
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	807.4219	807.4619	0.04	50	256	261	HTKEHR					Mascot												
	831.3777	831.4346	0.0569	68	383	389	THSCDLR	7	0			Mascot												
	831.4504	831.4346	-0.0158	-19	63	70	GPMKGGIR			Oxidation (M)[3]		Mascot												
	882.4059	882.4964	0.0905	103	376	382	DLKEMCK			Oxidation (M)[5]		Mascot												
	1016.537	1016.531	-0.006	-6	297	305	ENANEIKAK					Mascot												
	1016.537	1016.531	-0.006	-6	297	305	ENANEIKAK					Mascot												
	1054.6143	1054.4935	-0.1208	-115	246	255	DGIDIPALLK					Mascot												
	1156.7048	1156.535	-0.1698	-147	13	23	LAARLLGLDSK					Mascot												
	1322.5651	1322.5615	-0.0036	-3	379	389	EMCKTHSCDLR					Mascot												
	1350.6947	1350.5996	-0.0951	-70	1	12	MNALAATNRNFK					Mascot												
	1760.8846	1760.8029	-0.0817	-46	103	119	GGIGCDPSKLSISELER					Mascot												
Gel Idx/Pos	158/G9						Instr./Gel Origin				BA2060/140227A													
Plate [#] Name	[1] 31564						Instrument Sample Name				Process Statu Analysis Succeeded													
Rank	Protein Name						Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	11									
1	Histone H2B.3 OS=Arabidopsis thaliana						H2B3_ARATH	16519.2	10	8	155	100	113	100										
	GN=At2g28720 PE=1 SV=3																							
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	802.4781	802.4216	-0.0565	-70	113	119	KPTITSR					Mascot												
	816.4573	816.405	-0.0523	-64	120	126	EIQTAVR					Mascot												
	816.4573	816.405	-0.0523	-64	120	126	EIQTAVR					Mascot												
	856.441	856.4676	0.0266	31	59	65	KSTETVK					Mascot												
	939.5873	939.519	-0.0683	-73	127	135	LVLPGELAK					Mascot												
	942.5254	942.573	0.0476	51	25	33	VAEKAPAEK					Mascot												
	1180.6321	1180.5487	-0.0834	-71	74	84	QVHPDIGISSK					Mascot												
	1180.6321	1180.5487	-0.0834	-71	74	84	QVHPDIGISSK	33	90.972			Mascot												
	1392.741	1392.6274	-0.1136	-82	60	70	STETYKYIFK					Mascot												
	1729.8287	1729.7405	-0.0882	-51	85	99	AMGIMNSFINDIFEK					Mascot												
	1745.8237	1745.7058	-0.1179	-68	85	99	AMGIMNSFINDIFEK			Oxidation (M)[2]		Mascot												
	1761.8186	1761.7013	-0.1173	-67	85	99	AMGIMNSFINDIFEK	80	100	Oxidation (M)[2,5]		Mascot												
	1761.8186	1761.7013	-0.1173	-67	85	99	AMGIMNSFINDIFEK			Oxidation (M)[2,5]		Mascot												
2	Probable histone H2B.2 OS=Medicago truncatula PE=3																							
	SV=3																							
	H2B2_MEDTR																							
		16288	10.02	6	141	100	113	100																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	802.4781	802.4216	-0.0565	-70	110	116	KPTITSR					Mascot												
	816.4573	816.405	-0.0523	-64	117	123	EIQTAVR					Mascot												
	816.4573	816.405	-0.0523	-64	117	123	EIQTAVR					Mascot												
	933.4635	933.4536	-0.0099	-11	41	50	EGGSAGEKK					Mascot												
	939.5873	939.519	-0.0683	-73	124	132	LVLPGELAK					Mascot												
	1180.6321	1180.5487	-0.0834	-71	71	81	QVHPDIGISSK					Mascot												
	1180.6321	1180.5487	-0.0834	-71	71	81	QVHPDIGISSK	33	90.972			Mascot												
	1729.8287	1729.7405	-0.0882	-51	82	96	AMGIMNSFINDIFEK					Mascot												
	1745.8237	1745.7058	-0.1179	-68	82	96	AMGIMNSFINDIFEK			Oxidation (M)[2]		Mascot												
	1761.8186	1761.7013	-0.1173	-67	82	96	AMGIMNSFINDIFEK	80	100	Oxidation (M)[2,5]		Mascot												
	1761.8186	1761.7013	-0.1173	-67	82	96	AMGIMNSFINDIFEK			Oxidation (M)[2,5]		Mascot												
3	Histone H2B.7 OS=Arabidopsis thaliana																							
	GN=At3g46030 PE=1 SV=3																							
	H2B7_ARATH																							
		15901.8	10.02	6	139	100	113	100																
	Peptide Information																							
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type												
	802.4781	802.4216	-0.0565	-70	107	113	KPTITSR					Mascot												
	816.4573	816.405	-0.0523	-64	114	120	EIQTAVR					Mascot												

		816.4573	816.405	-0.0523	-64	114	120	EIQTA VR									Mascot
		939.5873	939.519	-0.0683	-73	121	129	LVLPGELAK									Mascot
		944.5411	944.47	-0.0711	-75	13	20	KPVEEKSK									Mascot
		944.5411	944.47	-0.0711	-75	13	20	KPVEEKSK									Mascot
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK									Mascot
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK		33	90.972						Mascot
		1729.8287	1729.7405	-0.0882	-51	79	93	AMGIMNSFINDIFEK									Mascot
		1745.8237	1745.7058	-0.1179	-68	79	93	AMGIMNSFINDIFEK					Oxidation (M)[2]				Mascot
		1761.8186	1761.7013	-0.1173	-67	79	93	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]				Mascot
		1761.8186	1761.7013	-0.1173	-67	79	93	AMGIMNSFINDIFEK					Oxidation (M)[2.5]				Mascot
4	Histone H2B.3 (Fragment) OS=Solanum lycopersicum GN=H2B-3 PE=2 SV=1	H2B3_SOLLC		15035.4	10.11	5	136						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	99	105	KPTITSR							Mascot		
		816.4573	816.405	-0.0523	-64	106	112	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	106	112	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	113	121	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	60	70	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	60	70	QVHPDIGISSK		33	90.972				Mascot		
		1729.8287	1729.7405	-0.0882	-51	71	85	AMGIMNSFINDIFEK							Mascot		
		1745.8237	1745.7058	-0.1179	-68	71	85	AMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	71	85	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	71	85	AMGIMNSFINDIFEK					Oxidation (M)[2.5]		Mascot		
5	Histone H2B (Fragments) OS=Pisum sativum GN=HIS2B PE=1 SV=2	H2B_PEA		13462.6	10.22	5	136						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	81	87	KSTITPR							Mascot		
		816.4573	816.405	-0.0523	-64	88	94	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	88	94	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	95	103	LLLPGEVAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	42	52	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	42	52	QVHPDIGISSK		33	90.972				Mascot		
		1729.8287	1729.7405	-0.0882	-51	53	67	AMGIMNSFINDIFEK							Mascot		
		1745.8237	1745.7058	-0.1179	-68	53	67	AMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	53	67	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	53	67	AMGIMNSFINDIFEK					Oxidation (M)[2.5]		Mascot		
6	Histone H2B.10 OS=Arabidopsis thaliana GN=At5g22880 PE=1 SV=3	H2B10_ARATH		15722.7	10.05	5	134						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	107	113	KPTITSR							Mascot		
		816.4573	816.405	-0.0523	-64	114	120	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	114	120	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	121	129	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK		33	90.972				Mascot		
		1729.8287	1729.7405	-0.0882	-51	79	93	AMGIMNSFINDIFEK							Mascot		
		1745.8237	1745.7058	-0.1179	-68	79	93	AMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	79	93	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	79	93	AMGIMNSFINDIFEK					Oxidation (M)[2.5]		Mascot		
7	Histone H2B OS=Capsicum annuum GN=HIS2B PE=2 SV=3	H2B_CAPAN		16034.9	10.11	5	134						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	107	113	KPTITSR							Mascot		
		816.4573	816.405	-0.0523	-64	114	120	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	114	120	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	121	129	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	68	78	QVHPDIGISSK		33	90.972				Mascot		
		1745.8237	1745.7058	-0.1179	-68	79	93	SMGIMNSFINDIFEK							Mascot		
		1761.8186	1761.7013	-0.1173	-67	79	93	SMGIMNSFINDIFEK		80	100		Oxidation (M)[5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	79	93	SMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
8	Histone H2B OS=Gossypium hirsutum GN=HIS2B PE=2 SV=3	H2B_GOSHI		16077	10.08	5	133						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	109	115	KPTITSR							Mascot		
		816.4573	816.405	-0.0523	-64	116	122	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	116	122	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	123	131	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	70	80	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	70	80	QVHPDIGISSK		33	90.972				Mascot		
		1729.8287	1729.7405	-0.0882	-51	81	95	AMGIMNSFINDIFEK							Mascot		
		1745.8237	1745.7058	-0.1179	-68	81	95	AMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	81	95	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	81	95	AMGIMNSFINDIFEK					Oxidation (M)[2.5]		Mascot		
9	Histone H2B.1 OS=Arabidopsis thaliana GN=At1g07790 PE=1 SV=3	H2B1_ARATH		16392.1	10.05	5	133						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.424	802.4216	-0.0024	-3	1	7	MAPRAEK							Mascot		
		816.4573	816.405	-0.0523	-64	117	123	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	117	123	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	124	132	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	71	81	QVHPDIGISSK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	71	81	QVHPDIGISSK		33	90.972				Mascot		
		1729.8287	1729.7405	-0.0882	-51	82	96	AMGIMNSFINDIFEK							Mascot		
		1745.8237	1745.7058	-0.1179	-68	82	96	AMGIMNSFINDIFEK					Oxidation (M)[2]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	82	96	AMGIMNSFINDIFEK		80	100		Oxidation (M)[2.5]		Mascot		
		1761.8186	1761.7013	-0.1173	-67	82	96	AMGIMNSFINDIFEK					Oxidation (M)[2.5]		Mascot		
10	Histone H2B.11 OS=Arabidopsis thaliana GN=At5g59910 PE=1 SV=5	H2B11_ARATH		16439.1	10	5	132						100	113	100		
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %		Modification	Rank	Result Type		
		802.4781	802.4216	-0.0565	-70	112	118	KPTITSR							Mascot		
		816.4573	816.405	-0.0523	-64	119	125	EIQTA VR							Mascot		
		816.4573	816.405	-0.0523	-64	119	125	EIQTA VR							Mascot		
		939.5873	939.519	-0.0683	-73	126	134	LVLPGELAK							Mascot		
		1180.6321	1180.5487	-0.0834	-71	73	83	QVHPDIGISSK							Mascot		

	1180.6321	1180.5487	-0.0834	-71	73	83	QVHPDIGISSK	33	90.972								Mascot
	1729.8287	1729.7405	-0.0882	-51	84	98	AMGIMNSFINDIFEK										Mascot
	1745.8237	1745.7058	-0.1179	-68	84	98	AMGIMNSFINDIFEK										Mascot
	1761.8186	1761.7013	-0.1173	-67	84	98	AMGIMNSFINDIFEK	80	100				Oxidation (M)[2]				Mascot
	1761.8186	1761.7013	-0.1173	-67	84	98	AMGIMNSFINDIFEK						Oxidation (M)[2,5]				Mascot
													Oxidation (M)[2,5]				Mascot
Gel Idx/Pos	159/G10						Instr./Gel Origin	BA2060/140227A				Process Status		Analysis Succeeded			
Plate [#] Name	[1] 31564						Instrument Sample Name										
Rank	Protein Name						Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %			
1	Peptidyl-prolyl cis-trans isomerase OS=Catharanthus roseus GN=PKCR1 PE=2 SV=1						CYPH_CATRO	18273	8.36	7	147	100	100	100			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	848.4148	848.3635	-0.0513	-60	126	132	TEWLDGK								Mascot		
	929.5203	929.4559	-0.0644	-69	49	56	SGKPLHYK	20	0						Mascot		
	929.5203	929.4559	-0.0644	-69	49	56	SGKPLHYK								Mascot		
	983.4832	983.4135	-0.0697	-71	90	97	FADENFIK								Mascot		
	1111.5782	1111.4988	-0.0794	-71	90	98	FADENFIKK								Mascot		
	1392.7191	1392.624	-0.0951	-68	20	31	IVMELFADTTTPR								Mascot		
	1392.7191	1392.624	-0.0951	-68	20	31	IVMELFADTTTPR	80	100						Mascot		
	1408.7141	1408.6184	-0.0957	-68	20	31	IVMELFADTTTPR			Oxidation (M)[3]					Mascot		
	1408.7141	1408.6184	-0.0957	-68	20	31	IVMELFADTTTPR	60	99.981	Oxidation (M)[3]					Mascot		
	2127.054	2126.9541	-0.0999	-47	20	37	IVMELFADTTTPRTAENFR			Oxidation (M)[3]					Mascot		
	2807.324	2807.0945	-0.2295	-82	99	125	HTGPGILSMANAGPNTN GSQFFICTAK			Carbamidomethyl (C)[24], Oxidation (M)[9]					Mascot		
2	Histone H2B.3 OS=Arabidopsis thaliana GN=A12g28720 PE=1 SV=3						H2B3_ARATH	16519.2	10	8	101	100	59	99.976			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	802.4781	802.4175	-0.0606	-76	113	119	KPTITSR	38	96.882						Mascot		
	802.4781	802.4175	-0.0606	-76	113	119	KPTITSR								Mascot		
	816.4573	816.4022	-0.0551	-67	120	126	EIQTAVR	21	0						Mascot		
	816.4573	816.4022	-0.0551	-67	120	126	EIQTAVR								Mascot		
	856.441	856.4662	0.0252	29	59	65	KSTETYK								Mascot		
	939.5873	939.5229	-0.0644	-69	127	135	LVLPGELAK								Mascot		
	942.5254	942.5745	0.0491	52	25	33	VAEKPAEK								Mascot		
	1180.6321	1180.5542	-0.0779	-66	74	84	QVHPDIGISSK								Mascot		
	1392.741	1392.624	-0.117	-84	60	70	STETYKIYFK								Mascot		
	1392.741	1392.624	-0.117	-84	60	70	STETYKIYFK								Mascot		
	1745.8237	1745.6953	-0.1284	-74	85	99	AMGIMNSFINDIFEK			Oxidation (M)[2]					Mascot		
	1761.8186	1761.6964	-0.1222	-69	85	99	AMGIMNSFINDIFEK			Oxidation (M)[2,5]					Mascot		
3	Histone H2B.9 OS=Arabidopsis thaliana GN=A15g02570 PE=1 SV=3						H2B9_ARATH	14535.1	10.06	6	88	99.994	59	99.976			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	802.4781	802.4175	-0.0606	-76	94	100	KPTITSR	38	96.882						Mascot		
	802.4781	802.4175	-0.0606	-76	94	100	KPTITSR								Mascot		
	816.4573	816.4022	-0.0551	-67	101	107	EIQTAVR	21	0						Mascot		
	816.4573	816.4022	-0.0551	-67	101	107	EIQTAVR								Mascot		
	856.441	856.4662	0.0252	29	40	46	KSTETYK								Mascot		
	939.5873	939.5229	-0.0644	-69	108	116	LVLPGELAK								Mascot		
	1392.741	1392.624	-0.117	-84	41	51	STETYKIYFK								Mascot		
	1392.741	1392.624	-0.117	-84	41	51	STETYKIYFK								Mascot		
	1745.8237	1745.6953	-0.1284	-74	66	80	AMGIMNSFINDIFEK			Oxidation (M)[2]					Mascot		
	1761.8186	1761.6964	-0.1222	-69	66	80	AMGIMNSFINDIFEK			Oxidation (M)[2,5]					Mascot		
4	Peptidyl-prolyl cis-trans isomerase OS=Lupinus luteus PE=2 SV=1						CYPH_LUPLU	18275	8.71	6	87	99.993	50	99.81			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	848.4148	848.3635	-0.0513	-60	126	132	TEWLDGK								Mascot		
	929.5203	929.4559	-0.0644	-69	49	56	SGKPLHYK	20	0						Mascot		
	929.5203	929.4559	-0.0644	-69	49	56	SGKPLHYK								Mascot		
	983.4832	983.4135	-0.0697	-71	90	97	FADENFIK								Mascot		
	1016.5557	1016.5284	-0.0273	-27	139	147	VIEGMNVVR								Mascot		
	1408.7141	1408.6184	-0.0957	-68	20	31	IVMELYADTTTPR								Mascot		
	1408.7141	1408.6184	-0.0957	-68	20	31	IVMELYADTTTPR	30	80.909						Mascot		
	2127.054	2126.9541	-0.0999	-47	20	37	IVMELYADTTTPRTAENFR								Mascot		
	2143.0488	2142.9451	-0.1037	-48	20	37	IVMELYADTTTPRTAENFR			Oxidation (M)[3]					Mascot		
5	Probable histone H2B.2 OS=Medicago truncatula PE=3 SV=3						H2B2_MEDTR	16288	10.02	6	87	99.993	59	99.976			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	802.4781	802.4175	-0.0606	-76	110	116	KPTITSR	38	96.882						Mascot		
	802.4781	802.4175	-0.0606	-76	110	116	KPTITSR								Mascot		
	816.4573	816.4022	-0.0551	-67	117	123	EIQTAVR	21	0						Mascot		
	816.4573	816.4022	-0.0551	-67	117	123	EIQTAVR								Mascot		
	933.4635	933.4448	-0.0155	-17	41	50	EGGSAAGEKK								Mascot		
	939.5873	939.5229	-0.0644	-69	124	132	LVLPGELAK								Mascot		
	1180.6321	1180.5542	-0.0779	-66	71	81	QVHPDIGISSK								Mascot		
	1745.8237	1745.6953	-0.1284	-74	82	96	AMGIMNSFINDIFEK			Oxidation (M)[2]					Mascot		
	1761.8186	1761.6964	-0.1222	-69	82	96	AMGIMNSFINDIFEK			Oxidation (M)[2,5]					Mascot		
6	Histone H2B.7 OS=Arabidopsis thaliana GN=A13g46030 PE=1 SV=3						H2B7_ARATH	15901.8	10.02	6	85	99.989	59	99.976			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	802.4781	802.4175	-0.0606	-76	107	113	KPTITSR	38	96.882						Mascot		
	802.4781	802.4175	-0.0606	-76	107	113	KPTITSR								Mascot		
	816.4573	816.4022	-0.0551	-67	114	120	EIQTAVR	21	0						Mascot		
	816.4573	816.4022	-0.0551	-67	114	120	EIQTAVR								Mascot		
	939.5873	939.5229	-0.0644	-69	121	129	LVLPGELAK								Mascot		
	944.5411	944.4663	-0.0748	-79	13	20	KPVEEKS								Mascot		
	1180.6321	1180.5542	-0.0779	-66	68	78	QVHPDIGISSK								Mascot		
	1745.8237	1745.6953	-0.1284	-74	79	93	AMGIMNSFINDIFEK			Oxidation (M)[2]					Mascot		
	1761.8186	1761.6964	-0.1222	-69	79	93	AMGIMNSFINDIFEK			Oxidation (M)[2,5]					Mascot		
7	Histone H2B.1 OS=Arabidopsis thaliana GN=A11g07790 PE=1 SV=3						H2B1_ARATH	16392.1	10.05	6	83	99.984	57	99.964			
Peptide Information																	
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification				Rank	Result Type		
	802.424	802.4175	-0.0065	-8	1	7	MAPRAEK								Mascot		
	802.4781	802.4175	-0.0606	-76	110	116	KPTITSR	38	96.882						Mascot		

		816.4573	816.4022	-0.0551	-67	117	123	EIQTAVR	21	0							Mascot
		816.4573	816.4022	-0.0551	-67	117	123	EIQTAVR									Mascot
		939.5873	939.5229	-0.0644	-69	124	132	LVLPGELAK									Mascot
		1180.6321	1180.5542	-0.0779	-66	71	81	QVHPDIGISSK									Mascot
		1745.8237	1745.6953	-0.1284	-74	82	96	AMGIMNSFINDIFEK									Mascot
		1761.8186	1761.6964	-0.1222	-69	82	96	AMGIMNSFINDIFEK									Mascot
8	Histone H2B.3 (Fragment) OS=Solanum lycopersicum GN=H2B-3 PE=2 SV=1	H2B3_SOLL	15035.4	10.11	5	82											
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	802.4781	802.4175	-0.0606	-76	99	105	KPTITSR	38	96.882				Mascot				
	802.4781	802.4175	-0.0606	-76	99	105	KPTITSR						Mascot				
	816.4573	816.4022	-0.0551	-67	106	112	EIQTAVR	21	0				Mascot				
	816.4573	816.4022	-0.0551	-67	106	112	EIQTAVR						Mascot				
	939.5873	939.5229	-0.0644	-69	113	121	LVLPGELAK						Mascot				
	1180.6321	1180.5542	-0.0779	-66	60	70	QVHPDIGISSK						Mascot				
	1745.8237	1745.6953	-0.1284	-74	71	85	AMGIMNSFINDIFEK						Mascot				
	1761.8186	1761.6964	-0.1222	-69	71	85	AMGIMNSFINDIFEK						Mascot				
9	Histone H2B.6 OS=Arabidopsis thaliana GN=H2B PE=1 SV=3	H2B6_ARATH	16426.1	10.02	6	82											
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	802.424	802.4175	-0.0065	-8	1	7	MAPRAEK						Mascot				
	802.4781	802.4175	-0.0606	-76	112	118	KPTITSR	38	96.882				Mascot				
	816.4573	816.4022	-0.0551	-67	119	125	EIQTAVR	21	0				Mascot				
	816.4573	816.4022	-0.0551	-67	119	125	EIQTAVR						Mascot				
	939.5873	939.5229	-0.0644	-69	126	134	LVLPGELAK						Mascot				
	1180.6321	1180.5542	-0.0779	-66	73	83	QVHPDIGISSK						Mascot				
	1745.8237	1745.6953	-0.1284	-74	84	98	AMGIMNSFINDIFEK						Mascot				
	1761.8186	1761.6964	-0.1222	-69	84	98	AMGIMNSFINDIFEK						Mascot				
10	Histone H2B.6 OS=Oryza sativa subsp. japonica GN=H2B.6 PE=3 SV=1	H2B6_ORYSJ	16462.1	10.02	6	82											
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	802.4781	802.4175	-0.0606	-76	115	121	KPTITSR	38	96.882				Mascot				
	802.4781	802.4175	-0.0606	-76	115	121	KPTITSR						Mascot				
	816.4573	816.4022	-0.0551	-67	122	128	EIQTAVR	21	0				Mascot				
	816.4573	816.4022	-0.0551	-67	122	128	EIQTAVR						Mascot				
	842.5093	842.452	-0.0573	-68	5	12	AEKKPAAK						Mascot				
	848.4108	848.3635	-0.0473	-66	44	52	GEKSGGEGK						Mascot				
	939.5873	939.5229	-0.0644	-69	129	137	LVLPGELAK						Mascot				
	1180.6321	1180.5542	-0.0779	-66	76	86	QVHPDIGISSK						Mascot				
Gel Idx/Pos	160/G11						Instr./Gel Origin	BA2060/140227A					Process Statu	Analysis Succeeded			
Plate [#]	Name	[1] 31564					Instrument Sample Name						Spectra	11			
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %				
1	Photosystem I reaction center subunit II, chloroplastic OS=Solanum lycopersicum GN=psaD PE=2 SV=1	PSAD_SOLL	22903.9	9.71	6	254						100	220	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	906.4427	906.4193	-0.0234	-26	180	187	EGVGQNFR						Mascot				
	906.4427	906.4193	-0.0234	-26	180	187	EGVGQNFR						Mascot				
	1003.4995	1003.438	-0.0615	-61	148	154	INYOYFR						Mascot				
	1003.4995	1003.438	-0.0615	-61	148	154	INYOYFR	44	99.401				Mascot				
	1047.5251	1047.4597	-0.0654	-62	133	141	EQCLALGTR						Mascot				
	1175.6201	1175.5466	-0.0735	-63	132	141	KEQCLALGTR						Mascot				
	1527.7954	1527.6984	-0.097	-63	155	167	VFPNGEVQYLHPK	69	99.998		Carbamidomethyl (C)[3]		Mascot				
	1527.7954	1527.6984	-0.097	-63	155	167	VFPNGEVQYLHPK				Carbamidomethyl (C)[4]		Mascot				
	1650.7979	1650.6956	-0.1023	-62	107	121	EQIFEMPTGGAAIMR						Mascot				
	1650.7979	1650.6956	-0.1023	-62	107	121	EQIFEMPTGGAAIMR	108	100				Mascot				
	1666.7927	1666.6956	-0.0971	-58	107	121	EQIFEMPTGGAAIMR				Oxidation (M)[6]		Mascot				
	1682.7876	1682.6829	-0.1047	-62	107	121	EQIFEMPTGGAAIMR				Oxidation (M)[6,14]		Mascot				
2	Photosystem I reaction center subunit II-2, chloroplastic OS=Arabidopsis thaliana GN=psaD2 PE=1 SV=	PSAD2_ARATH	22292.7	9.78	6	211						100	177	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	1047.5251	1047.4597	-0.0654	-62	129	137	EQCLALGTR				Carbamidomethyl (C)[3]		Mascot				
	1175.6201	1175.5466	-0.0735	-63	128	137	KEQCLALGTR				Carbamidomethyl (C)[4]		Mascot				
	1527.7954	1527.6984	-0.097	-63	151	163	VFPNGEVQYLHPK	69	99.998				Mascot				
	1527.7954	1527.6984	-0.097	-63	151	163	VFPNGEVQYLHPK						Mascot				
	1650.7979	1650.6956	-0.1023	-62	103	117	EQIFEMPTGGAAIMR						Mascot				
	1650.7979	1650.6956	-0.1023	-62	103	117	EQIFEMPTGGAAIMR	108	100				Mascot				
	1666.7927	1666.6956	-0.0971	-58	103	117	EQIFEMPTGGAAIMR				Oxidation (M)[6]		Mascot				
	1682.7876	1682.6829	-0.1047	-62	103	117	EQIFEMPTGGAAIMR				Oxidation (M)[6,14]		Mascot				
	1972.0763	1971.8425	-0.2338	-119	23	39	LHLFSSSHRPKSLSFTK						Mascot				
	2211.1689	2210.9604	-0.2085	-94	1	22	MTQAAGIFSPAITTTTSA VKK				Oxidation (M)[1]		Mascot				
3	Photosystem I reaction center subunit II, chloroplastic OS=Nicotiana sylvestris GN=psaD PE=2 SV=1	PSAD_NICSY	22409.7	9.78	6	209						100	177	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	921.4346	921.3839	-0.0507	-55	47	55	AMAEAAATK						Mascot				
	1047.5251	1047.4597	-0.0654	-62	129	137	EQCLALGTR				Carbamidomethyl (C)[3]		Mascot				
	1175.6201	1175.5466	-0.0735	-63	128	137	KEQCLALGTR				Carbamidomethyl (C)[4]		Mascot				
	1527.7954	1527.6984	-0.097	-63	151	163	VFPNGEVQYLHPK	69	99.998				Mascot				
	1527.7954	1527.6984	-0.097	-63	151	163	VFPNGEVQYLHPK						Mascot				
	1650.7979	1650.6956	-0.1023	-62	103	117	EQIFEMPTGGAAIMR						Mascot				
	1650.7979	1650.6956	-0.1023	-62	103	117	EQIFEMPTGGAAIMR	108	100				Mascot				
	1666.7927	1666.6956	-0.0971	-58	103	117	EQIFEMPTGGAAIMR				Oxidation (M)[6]		Mascot				
	1682.7876	1682.6829	-0.1047	-62	103	117	EQIFEMPTGGAAIMR				Oxidation (M)[6,14]		Mascot				
	1994.0282	1993.8282	-0.2	-100	148	163	FYRVFPNGEVQYLHPK						Mascot				
4	Photosystem I reaction center subunit II, chloroplastic OS=Cucumis sativus GN=psaD PE=1 SV=1	PSAD_CUCCA	22706.8	9.54	5	202						100	177	100			
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		Modification	Rank	Result Type				
	906.4427	906.4193	-0.0234	-26	179	186	EGVGQNFR						Mascot				
	906.4427	906.4193	-0.0234	-26	179	186	EGVGQNFR						Mascot				
	1047.5251	1047.4597	-0.0654	-62	132	140	EQCLALGTR				Carbamidomethyl (C)[3]		Mascot				
	1175.6201	1175.5466	-0.0735	-63	131	140	KEQCLALGTR				Carbamidomethyl (C)[4]		Mascot				
	1527.7954	1527.6984	-0.097	-63	154	166	VFPNGEVQYLHPK	69	99.998				Mascot				

		1527.7954	1527.6984	-0.097	-63	154	168	VFPNGVEQYVYHPK									Mascot
		1650.7979	1650.6956	-0.1023	-62	106	120	EQIFEMPTGGAAIMR									Mascot
		1650.7979	1650.6956	-0.1023	-62	106	120	EQIFEMPTGGAAIMR	108	100							Mascot
		1666.7927	1666.6956	-0.0971	-58	106	120	EQIFEMPTGGAAIMR				Oxidation [M]6]					Mascot
		1682.7876	1682.6829	-0.1047	-62	106	120	EQIFEMPTGGAAIMR				Oxidation [M]6,14]					Mascot
5	Photosystem I reaction center subunit II-1, chloroplastic OS=Arabidopsis thaliana GN=psaD1 PE=1 SV=						PSAD1_ARATH	22583.8	9.78	4	195		100	177	100		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1047.5251	1047.4597	-0.0654	-62	133	141	EQCLALGTR					Carbamidomethyl (C)[3]			Mascot		
	1175.6201	1175.5466	-0.0735	-63	132	141	KEOCLALGTR					Carbamidomethyl (C)[4]			Mascot		
	1527.7954	1527.6984	-0.097	-63	155	167	VFPNGVEQYVYHPK			69	99.998				Mascot		
	1527.7954	1527.6984	-0.097	-63	155	167	VFPNGVEQYVYHPK								Mascot		
	1650.7979	1650.6956	-0.1023	-62	107	121	EQIFEMPTGGAAIMR								Mascot		
	1650.7979	1650.6956	-0.1023	-62	107	121	EQIFEMPTGGAAIMR			108	100				Mascot		
	1666.7927	1666.6956	-0.0971	-58	107	121	EQIFEMPTGGAAIMR					Oxidation [M]6]			Mascot		
	1682.7876	1682.6829	-0.1047	-62	107	121	EQIFEMPTGGAAIMR					Oxidation [M]6,14]			Mascot		
6	Photosystem I reaction center subunit II, chloroplastic OS=Spinacia oleracea GN=psaD PE=1 SV=2						PSAD_SPIOI	23088	9.76	3	119		100	108	100		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1047.5251	1047.4597	-0.0654	-62	137	145	EQCLALGTR					Carbamidomethyl (C)[3]			Mascot		
	1175.6201	1175.5466	-0.0735	-63	136	145	KEOCLALGTR					Carbamidomethyl (C)[4]			Mascot		
	1650.7979	1650.6956	-0.1023	-62	111	125	EQIFEMPTGGAAIMR								Mascot		
	1650.7979	1650.6956	-0.1023	-62	111	125	EQIFEMPTGGAAIMR			108	100				Mascot		
	1666.7927	1666.6956	-0.0971	-58	111	125	EQIFEMPTGGAAIMR					Oxidation [M]6]			Mascot		
	1682.7876	1682.6829	-0.1047	-62	111	125	EQIFEMPTGGAAIMR					Oxidation [M]6,14]			Mascot		
7	Photosystem I reaction center subunit II, chloroplastic OS=Chlamydomonas reinhardtii GN=psaD PE=1 S						PSAD_CHLRE	21328.2	10.31	3	117		100	108	100		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	889.4308	889.3958	-0.035	-39	166	173	VGANQNMR								Mascot		
	1566.7549	1566.6655	-0.0894	-57	1	14	MAVMVRTQAPAAATR					Oxidation [M][1,4]			Mascot		
	1650.7979	1650.6956	-0.1023	-62	93	107	EQIFEMPTGGAAIMR								Mascot		
	1650.7979	1650.6956	-0.1023	-62	93	107	EQIFEMPTGGAAIMR			108	100				Mascot		
	1666.7927	1666.6956	-0.0971	-58	93	107	EQIFEMPTGGAAIMR					Oxidation [M]6]			Mascot		
	1682.7876	1682.6829	-0.1047	-62	93	107	EQIFEMPTGGAAIMR					Oxidation [M]6,14]			Mascot		
8	Photosystem I reaction center subunit II, chloroplastic OS=Hordeum vulgare GN=psaD PE=1 SV=1						PSAD_HORVU	21919.4	9.81	3	81		99.974	69	99.998		
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1003.4989	1003.438	-0.0609	-61	130	138	EQCLALGNR								Mascot		
	1003.4989	1003.438	-0.0609	-61	130	138	EQCLALGNR								Mascot		
	1028.5048	1028.4534	-0.0514	-50	197	205	FTGKNSFDI								Mascot		
	1028.5048	1028.4534	-0.0514	-50	197	205	FTGKNSFDI								Mascot		
	1527.7954	1527.6984	-0.097	-63	152	164	VFPNGVEQYVYHPK			69	99.998				Mascot		
	1527.7954	1527.6984	-0.097	-63	152	164	VFPNGVEQYVYHPK								Mascot		
9	Probable protein phosphatase 2C 30 OS=Oryza sativa subsp. japonica GN=Os03g0268600 PE=2 SV=1						P2C30_ORYSJ	43255	5.64	12	48		44.167				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	842.5206	842.4492	-0.0714	-85	38	44	LRVVAER								Mascot		
	906.4573	906.4193	-0.038	-42	315	322	ACLRSSGR					Carbamidomethyl (C)[2]			Mascot		
	906.4573	906.4193	-0.038	-42	315	322	ACLRSSGR					Carbamidomethyl (C)[2]			Mascot		
	921.373	921.3839	0.0109	12	18	26	GPECDTGSR								Mascot		
	933.4723	933.452	-0.0203	-22	149	155	WRGVMER								Mascot		
	989.4509	989.5253	0.0744	75	78	86	YGFSTVCGR								Mascot		
	1156.5527	1156.5399	-0.0128	-11	203	213	HVVVANGGDSR								Mascot		
	1156.5527	1156.5399	-0.0128	-11	203	213	HVVVANGGDSR								Mascot		
	1670.9622	1670.9357	-0.2265	-136	371	386	ACAEAAVLLTKALAR					Carbamidomethyl (C)[2]			Mascot		
	1682.736	1682.6829	-0.0531	-32	2	17	AEICCEVVGSSSEGG					Carbamidomethyl (C)[4,5]			Mascot		
	1698.8527	1698.682	-0.1707	-100	203	218	HVVVANGGDSRAVLGR								Mascot		
	1756.755	1756.8169	0.0619	35	1	17	MAEICCEVVGSSSEGG					Carbamidomethyl (C)[5]			Mascot		
	1955.9983	1955.8425	-0.1558	-80	247	263	VIFWDGARVFGLMAMSR								Mascot		
	1971.9932	1971.8425	-0.1507	-76	247	263	VIFWDGARVFGLMAMSR					Oxidation [M][12]			Mascot		
	2995.4915	2995.4153	-0.0762	-25	219	246	GGAAIPLSDCHKPDRPDR ELERIHAAGGR					Carbamidomethyl (C)[9]			Mascot		
10	MLP-like protein 28 OS=Arabidopsis thaliana GN=MLP28 PE=1 SV=1						MLP28_ARATH	37590.9	5.2	9	45		0				
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	906.46	906.4193	-0.0407	-45	268	275	VIDGDLMK					Oxidation [M][7]			Mascot		
	906.46	906.4193	-0.0407	-45	268	275	VIDGDLMK					Oxidation [M][7]			Mascot		
	1028.5623	1028.4534	-0.1089	-106	178	187	TPETPSLVGK								Mascot		
	1028.5623	1028.4534	-0.1089	-106	178	187	TPETPSLVGK								Mascot		
	1644.8955	1644.7592	-0.1363	-83	92	105	IEAVEPKNLITFR								Mascot		
	1648.9091	1648.7155	-0.1936	-117	100	113	NLITFRVIEGDLMK					Oxidation [M][13]			Mascot		
	1650.8883	1650.6956	-0.1927	-117	262	275	NLITFRVIDGDLMK					Oxidation [M][13]			Mascot		
	1650.8883	1650.6956	-0.1927	-117	262	275	NLITFRVIDGDLMK					Oxidation [M][13]			Mascot		
	1666.9414	1666.6956	-0.2458	-147	276	289	EYKSFLLTIQVTPK								Mascot		
	1682.8119	1682.6829	-0.129	-77	164	177	EIDHLLAAEEVVK								Mascot		
	1732.7881	1732.7851	-0.023	-13	1	15	MADVATKHPMEDEVK					Oxidation [M][1,10]			Mascot		
	1956.0536	1955.8425	-0.2111	-108	178	195	TPETPSLVGKLETDVEIK								Mascot		
Get Idx/Pos	161/G12						Instr./Gel Origin	BA2060/140227A									
Plate #	Name	[1] 31564					Instrument Sample Name										
Rank	Protein Name						Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	Analysis Succeeded		
															11		
1	Ras-related protein RAB11b OS=Arabidopsis thaliana GN=RAB11B PE=2 SV=1						RAB11B_ARATH	23160.6	6.52	7	43	0					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	842.4301	842.4474	0.0173	21	121	127	CDLAHKR								Mascot		
	1045.5425	1045.5005	-0.042	-40	70	77	SITRSYYR								Mascot		
	1475.8329	1475.6541	-0.1788	-121	78	91	GAAGALLYVDITRR								Mascot		
	1866.7816	1866.7667	-0.0149	-8	192	211	TQGAAGGRDGTISGGGG CCG					Carbamidomethyl (C)[18,19]			Mascot		
	2284.2256	2284.0237	-0.2019	-88	9	29	YIIIGDTGVGKSCLLLOFT DK								Mascot		



2663.3611	2663.106	-0.2551	-96	47	69	MVTVDGRPIKLQIWDTAG QESFR					Oxidation (M)[1]	Mascot
3337.6204	3337.4851	-0.1353	-41	92	120	ETFNHLASWLEDARQHA NPNMSIMLIGNK						Mascot
3337.6204	3337.4851	-0.1353	-41	92	120	ETFNHLASWLEDARQHA NPNMSIMLIGNK						Mascot
3353.6152	3353.5134	-0.1018	-30	92	120	ETFNHLASWLEDARQHA NPNMSIMLIGNK					Oxidation (M)[21]	Mascot
Ras-related protein RAB1c OS=Arabidopsis thaliana GN=RAB1C PE=2 SV=1					RAB1C_ARATH	23149.6	6.96	7	40	0		
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
870.4362	870.4808	0.0446	51	121	127	CDLAHRR						Mascot
870.4362	870.4808	0.0446	51	121	127	CDLAHRR						Mascot
1028.3408	1028.3964	0.0956	93	200	211	DGSTSQGGGCCG						Mascot
1045.5425	1045.5005	-0.042	-40	70	77	SITRSYYR						Mascot
1475.8329	1475.6541	-0.1788	-121	78	91	GAGALLVVDITRR						Mascot
2284.2256	2284.0237	-0.2019	-88	9	29	YIIIGDTGVGKSCLLQFT DK						Mascot
2296.9668	2297.0283	0.0615	27	187	211	VGYGGIPGPSGGRDGST SQGGGCCG				Carbamidomethyl (C)[23,24]		Mascot
2720.4077	2720.083	-0.3247	-119	47	69	MITIDNKPIKLQIWDTAGQ ESFR				Oxidation (M)[1]		Mascot
Putative fucosyltransferase 10 OS=Arabidopsis thaliana GN=FUT10 PE=2 SV=2					FUT10_ARATH	59290.8	6.33	10	39	0		
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
842.4229	842.4474	0.0245	29	232	237	LFFCQK				Carbamidomethyl (C)[4]		Mascot
882.5406	882.5005	-0.0401	-45	354	361	VNISKPPK						Mascot
907.4341	907.433	-0.0011	-1	86	92	SYEMLHK						Mascot
933.4999	933.4578	-0.0421	-45	103	110	EATEKLSR						Mascot
1866.9265	1866.7667	-0.1598	-86	44	61	LIGLLTADFDEGSCLSR						Mascot
1911.952	1911.7775	-0.1745	-91	70	85	KPSPYMPSEYLVSEL				Oxidation (M)[6]		Mascot
1993.8129	1993.8184	0.0055	3	499	514	HCEDMMYGLKLYDDF				Carbamidomethyl (C)[2]		Mascot
2705.0813	2704.9307	-0.1506	-56	469	492	SMEPCYHTPPSHGCEAD WGTNSGK				Carbamidomethyl (C)[5,14]		Mascot
2807.3879	2807.1375	-0.2504	-89	36	61	ESERPVDKLIGLLTADF DEGSCLSR						Mascot
2807.3879	2807.1375	-0.2504	-89	36	61	ESERPVDKLIGLLTADF DEGSCLSR						Mascot
3794.7649	3794.499	-0.2659	-70	199	231	CYGTMLNHAINTSIPP HLYLHNHDSRDSK				Oxidation (M)[5]		Mascot
Transcription factor bHLH27 OS=Arabidopsis thaliana GN=BHLH27 PE=2 SV=1					BH027_ARATH	30261	5.1	8	37	0		
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
850.4127	850.4854	0.0727	85	171	177	VTWMGEK						Mascot
900.388	900.3427	-0.0453	-50	152	158	QMDYSTR						Mascot
1028.5735	1028.4364	-0.1371	-133	117	125	STLLENPVR						Mascot
1156.5377	1156.5282	-0.0095	-8	255	263	EYCTCLVLV				Carbamidomethyl (C)[3,5]		Mascot
1179.4987	1179.5338	0.0351	30	1	9	MEDLDHEYK						Mascot
2013.9806	2013.8258	-0.1548	-77	171	187	VTWMGEKTVVVCITCSK				Carbamidomethyl (C)[12,15], Oxidation (M)[4]		Mascot
2225.1006	2224.9739	-0.1267	-57	86	104	ASVIKDSIDYMOELIDQEK						Mascot
2225.1006	2224.9739	-0.1267	-57	86	104	ASVIKDSIDYMOELIDQEK						Mascot
2781.1152	2780.7417	-0.3735	-134	126	148	DYDCNFAETHLQDFSDN NDMRSK				Oxidation (M)[20]		Mascot
S-adenosylmethionine synthase 1 OS=Brassica juncea GN=SAMS1 PE=2 SV=1					METK1_BRAJU	43198.7	5.52	8	34	0		
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
842.5709	842.4474	-0.1235	-147	332	338	EILKIVK						Mascot
871.4784	871.4714	-0.007	-8	163	169	WLRPDGK						Mascot
1179.6481	1179.5338	-0.1143	-97	281	291	SGAVIVRQSAK						Mascot
1470.7332	1470.6871	-0.0461	-31	48	60	TNMVMVFGEITTK						Mascot
1502.7229	1502.6598	-0.0631	-42	48	60	TNMVMVFGEITTK				Oxidation (M)[3,5]		Mascot
2013.9773	2013.8258	-0.1515	-75	339	355	ESDFRPPGMMTINLDLK						Mascot
2170.0784	2169.9319	-0.1465	-68	339	356	ESDFRPPGMMTINLDLK						Mascot
2748.4163	2748.1221	-0.2942	-107	188	211	VHTVLISTQHDEVTNNEI ARDLK						Mascot
2748.4163	2748.1221	-0.2942	-107	188	211	VHTVLISTQHDEVTNNEI ARDLK						Mascot
3338.7671	3338.5256	-0.2415	-72	301	331	RALVQVSYAIGVPEPFSV FVDTYGTGLIPDK						Mascot
Pentatricopeptide repeat-containing protein At4g34830, chloroplastic OS=Arabidopsis thaliana GN=At4					PP349_ARATH	119696	8.06	13	33	0		
Peptide Information												
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type
1028.5483	1028.4364	-0.1119	-109	848	856	SGRPQIENK				Carbamidomethyl (C)[8]		Mascot
1448.6151	1448.8011	0.186	128	657	668	SGDWDFACSIYK				Carbamidomethyl (C)[13,14]		Mascot
1832.8339	1832.7693	-0.0646	-35	712	728	LGTISYSSLMGACCNAAK				Carbamidomethyl (C)[8], Oxidation (M)[14]		Mascot
1838.7723	1838.614	-0.1583	-86	657	671	SGDWDFACSIYKDMK						Mascot
1993.996	1993.8184	-0.1776	-89	35	51	RDFLCGCHSLRPPSHLR						Mascot
2221.0085	2220.9524	-0.0561	-25	712	731	LGTISYSSLMGACCAKAD WK				Carbamidomethyl (C)[13], Oxidation (M)[10]		Mascot
2239.1826	2238.9622	-0.2204	-98	777	796	TLGLKPNNTITYSMLMLAS ER						Mascot
2246.1353	2245.9878	-0.1475	-66	1045	1064	NWFQPKLDSFSGGKPG DLR						Mascot
2297.2751	2297.0283	-0.2468	-107	14	34	SSKYLTLTSYSPVILPAST LR						Mascot
2299.1321	2299.0217	-0.1104	-48	848	866	SGRPQIENKWTSMALMV YR				Oxidation (M)[13,16]		Mascot
3337.5935	3337.4851	-0.1084	-32	458	487	FTKLINPTMSTFNMLMS VCASSQDIEGAR				Oxidation (M)[10,15]		Mascot
3337.5935	3337.4851	-0.1084	-32	458	487	FTKLINPTMSTFNMLMS VCASSQDIEGAR				Oxidation (M)[10,15]		Mascot
3347.6936	3347.325	-0.3686	-110	768	796	AMEYLDKIKTLGLKPNITIT YSMLMLASER				Oxidation (M)[2]		Mascot
3353.5884	3353.5134	-0.075	-22	458	487	FTKLINPTMSTFNMLMS VCASSQDIEGAR				Oxidation (M)[10,15,17]		Mascot
3354.6677	3354.5237	-0.144	-43	461	491	LILNPTMSTFNMLMSVCA SSQDIEGARGLR						Mascot

7	Zinc finger CCOH domain-containing protein 19 OS=Arabidopsis thaliana GN=NERD PE=1 SV=3	C3H19_ARATH	194931	4.69	18	33	0					
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	856.4497	856.4681	0.0184	21	1752	1757	VCKFFR			Carbamidomethyl (C)[2]		Mascot
	900.4104	900.3427	-0.0677	-75	1758	1764	ENGHCRRK			Carbamidomethyl (C)[5]		Mascot
	907.4301	907.433	0.0029	3	852	859	SOVICDSR					Mascot
	933.4901	933.4578	-0.0323	-35	843	849	YNLRDPR					Mascot
	1165.532	1165.6603	0.1283	110	1755	1763	FFRENGHCR					Mascot
	1165.532	1165.6603	0.1283	110	1755	1763	FFRENGHCR					Mascot
	1448.6989	1448.8011	0.1022	71	1739	1751	QSGGQNNFKGQR					Mascot
	1475.6671	1475.6541	-0.013	-9	639	650	GKWNCGWHLCSK			Carbamidomethyl (C)[5]		Mascot
	1493.6624	1493.6644	0.002	1	618	630	GCTKAYHPSCVDR			Carbamidomethyl (C)[2]		Mascot
	1493.6624	1493.6644	0.002	1	618	630	GCTKAYHPSCVDR			Carbamidomethyl (C)[2]		Mascot
	1497.7175	1497.6715	-0.046	-31	434	446	ISEMSEVTETMIK					Mascot
	1557.5204	1557.6786	0.1582	102	1150	1162	MDPDCSEDEDEK			Oxidation (M)[1]		Mascot
	1838.8809	1838.614	-0.2669	-145	684	698	GLCETCMETVKLIER			Carbamidomethyl (C)[3,6]		Mascot
	1866.9537	1866.7667	-0.187	-100	1331	1345	WNNTGYFPAKLEIWK					Mascot
	2013.9124	2013.8258	-0.0866	-43	622	638	AYHPSCVDRDEAFFQTK					Mascot
	2220.9619	2220.9524	-0.0095	-4	654	672	TATLYCYTCMFSLCKGC AK			Carbamidomethyl (C)[6,9]		Mascot
	2238.8811	2238.9622	0.0811	36	598	616	EEDVCFMCFDGGDLVLC DR			Carbamidomethyl (C)[5], Oxidation (M)[7]		Mascot
	2299.0647	2299.0217	-0.043	-19	1026	1045	TEVISIDIISNQDFTDECK					Mascot
	2677.1531	2677.084	-0.0691	-26	468	491	DSSVADIEEGREDHEDM GVTETQK					Mascot
	2691.3308	2691.1179	-0.2129	-79	934	956	GRQSNLDDFAAVDMHNI NLIYLR			Oxidation (M)[14]		Mascot
	2691.3308	2691.1179	-0.2129	-79	934	956	GRQSNLDDFAAVDMHNI NLIYLR			Oxidation (M)[14]		Mascot
8	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic OS=Arabidopsis thaliana GN=At5g52970 PE=1 SV=2	TL15B_ARATH	24553.4	5.66	6	31	0					
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	1051.5684	1051.6415	0.0731	70	175	183	SFWSRLAGK					Mascot
	1051.5684	1051.6415	0.0731	70	175	183	SFWSRLAGK					Mascot
	1279.5549	1279.675	0.1201	94	37	47	TSGDEENWVSR					Mascot
	1475.7246	1475.6541	-0.0705	-48	2	13	AMLFRRPPPSQCR			Carbamidomethyl (C)[11], Oxidation (M)[2]		Mascot
	1493.7245	1493.6644	-0.0601	-40	180	191	LAKGYGNMFYWK			Oxidation (M)[8]		Mascot
	1493.7245	1493.6644	-0.0601	-40	180	191	LAKGYGNMFYWK			Oxidation (M)[8]		Mascot
	1838.8622	1838.614	-0.2482	-135	194	211	GEDASIEAAVMAISSCLR			Oxidation (M)[11]		Mascot
	2170.02	2169.9319	-0.0881	-41	14	32	SFSPPFVFNYSREVSSSS R					Mascot
9	Homeobox-leucine zipper protein HOX18 OS=Oryza sativa subsp. indica GN=HOX18 PE=2 SV=1	HOX18_ORYSI	27577.7	9.13	6	30	0					
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	882.5883	882.5005	-0.0878	-99	148	154	QLKLKPR					Mascot
	1165.5518	1165.6603	0.1085	93	237	249	VTVMGGGGGETGK			Oxidation (M)[4]		Mascot
	1165.5518	1165.6603	0.1085	93	237	249	VTVMGGGGGETGK			Oxidation (M)[4]		Mascot
	1537.6807	1537.5984	-0.0823	-54	222	236	AAAAAMVNVCPSCCK			Carbamidomethyl (C)[10], Oxidation (M)[6]		Mascot
	1892.0024	1891.7922	-0.2102	-111	203	221	LASAAAAAGSQLYVQF PR					Mascot
	2705.1606	2704.9307	-0.2299	-85	1	27	MEGEDLSGLWLGIGGG GYAYGGDDCR					Mascot
	3337.6489	3337.4851	-0.1638	-49	203	236	LASAAAAAGSQLYVQF PRAAAAAAMVNVCPSCCK					Mascot
	3337.6489	3337.4851	-0.1638	-49	203	236	LASAAAAAGSQLYVQF PRAAAAAAMVNVCPSCCK					Mascot
	3353.6438	3353.5134	-0.1304	-39	203	236	LASAAAAAGSQLYVQF PRAAAAAAMVNVCPSCCK			Oxidation (M)[25]		Mascot
10	Putative F-box/kelch-repeat protein At1g19930 OS=Arabidopsis thaliana GN=At1g19930 PE=4 SV=1	FK127_ARATH	38742.6	8.78	7	30	0					
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	864.4032	864.4407	0.0375	43	196	203	LHSCGGYK					Mascot
	996.5373	996.5191	-0.0182	-18	268	275	FARYANVR					Mascot
	1028.5847	1028.4364	-0.1483	-144	85	93	RPILASDR					Mascot
	1156.6797	1156.5282	-0.1515	-131	85	94	RPILASDR					Mascot
	1179.5892	1179.5338	-0.0554	-47	159	169	EYPSASLLDGK					Mascot
	2170.2131	2169.9319	-0.2812	-130	94	113	KSSGYVLATIPHPSPPLH R					Mascot
	2807.2876	2807.1375	-0.1501	-53	178	203	LTFHGCQDQTDNVVVDG KLHSCGGYK			Carbamidomethyl (C)[6]		Mascot
	2807.2876	2807.1375	-0.1501	-53	178	203	LTFHGCQDQTDNVVVDG KLHSCGGYK			Carbamidomethyl (C)[6]		Mascot
Gel Idx/Pos		162/G13		Instr./Gel Origin		BA2060/140227A		Process Statu		Analysis Succeeded		
Plate [#] Name		[1] 31564		Instrument Sample Name				Spectra		11		
Rank	Protein Name	Accession No.		Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Total Ion Score	Total Ion C. I. %		
1	Ribulose biphosphate carboxylase small chain 3, chloroplastic OS=Solanum tuberosum GN=RBCS-3 PE=3	RBS3_SOLTU		20424.2	8.29	7	126	100	83	100		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	907.4883	907.4315	-0.0568	-63	31	39	SAASFVPYTK					Mascot
	914.4002	914.345	-0.0552	-60	116	123	SPGYVDGR	50	99.838			Mascot
	914.4002	914.345	-0.0552	-60	116	123	SPGYVDGR					Mascot
	933.5151	933.4582	-0.0569	-61	159	166	IIGFDNVR	35	95.243			Mascot
	933.5151	933.4582	-0.0569	-61	159	166	IIGFDNVR					Mascot
	1350.7046	1350.5835	-0.1211	-90	1	14	MASSIVSSAAVATR			Carbamidomethyl (C)[3]		Mascot
	1658.8328	1658.7137	-0.1191	-72	56	68	VRCMQVWPPINMK					Mascot
	2027.022	2026.9668	-0.0552	-27	70	86	YETLSYLPDLSDEQLLK					Mascot
	2691.2407	2691.1047	-0.136	-51	94	115	NGVWPCLFEFTEHGFVY RENHK					Mascot
2	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Pyruis pyrifolia GN=RBCS PE=2 SV=1	RBS_PYRPPY		20513.3	9.04	6	117	100	83	100		
Peptide Information												
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
	907.4883	907.4315	-0.0568	-63	89	95	EVDYLLR					Mascot

	914.4002	914.345	-0.0552	-60	118	125	SPGYDGR	50	99.838								Mascot
	914.4002	914.345	-0.0552	-60	118	125	SPGYDGR										Mascot
	933.5151	933.4582	-0.0569	-61	161	168	IIGFDNVR	35	95.243								Mascot
	933.5151	933.4582	-0.0569	-61	161	168	IIGFDNVR										Mascot
	1555.8124	1555.6759	-0.1365	-88	58	70	VQCMQVWPPLGLK										Mascot
	1582.7604	1582.6509	-0.1095	-69	132	145	LPMFGCTDSSQVLK										Mascot
	2225.0828	2224.9448	-0.138	-62	132	151	LPMFGCTDSSQVLKELE EAK										Mascot
3	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Capsicum annuum GN=RBCS PE=2 SV=1				RBS_CAPAN	21185.5	6.82	6	116	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR	50	99.838			Mascot					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR					Mascot					
	1446.7183	1446.653	-0.0653	-45	41	54	QDLDTISASNGGR					Mascot					
	1485.7593	1485.6699	-0.0894	-60	55	66	VECMILVWPPINK			Carbamidomethyl (C)[3]		Mascot					
	1485.7593	1485.6699	-0.0894	-60	55	66	VECMILVWPPINK			Carbamidomethyl (C)[3]		Mascot					
	2027.022	2026.9668	-0.0552	-27	69	85	YETLSYLPDLSDEQLLK					Mascot					
	2125.98	2125.9319	-0.0481	-23	94	110	GWVPCLEFETEHGFVYR			Carbamidomethyl (C)[5]		Mascot					
4	Ribulose biphosphate carboxylase small chain 2B, chloroplastic OS=Solanum tuberosum GN=RBCS-2B PE=				RBSB_SOLTU	20288.1	7.6	6	116	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR	50	99.838			Mascot					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR					Mascot					
	1350.7046	1350.5835	-0.1211	-90	1	14	MASSIVSSAAVATR					Mascot					
	1658.8328	1658.7137	-0.1191	-72	55	67	VRCMQVWPPINMK			Carbamidomethyl (C)[3]		Mascot					
	2027.022	2026.9668	-0.0552	-27	69	85	YETLSYLPDLSDEQLLK					Mascot					
	2225.0464	2224.9448	-0.1016	-46	129	148	LPMFGCTADTQVLAEVE EAK			Carbamidomethyl (C)[6], Oxidation (M)[3]		Mascot					
5	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Hevea brasiliensis GN=RBCS PE=2 SV=				RBS_HEVBR	20707.3	8.7	6	113	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	914.4002	914.345	-0.0552	-60	117	124	SPGYDGR	50	99.838			Mascot					
	914.4002	914.345	-0.0552	-60	117	124	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	160	167	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	160	167	IIGFDNVR					Mascot					
	944.393	944.4698	0.0768	81	152	159	AYPCYGR					Mascot					
	1485.7454	1485.6699	-0.0755	-51	57	68	VQCMQVWPPRGK			Carbamidomethyl (C)[3]		Mascot					
	1485.7454	1485.6699	-0.0755	-51	57	68	VQCMQVWPPRGK			Carbamidomethyl (C)[3]		Mascot					
	2034.9741	2034.8591	-0.115	-57	96	112	GWVPCLEFELEHGTVYR					Mascot					
	2691.2976	2691.1047	-0.1929	-72	43	66	TTTDTISASNGGRVQCM QVWPPR			Carbamidomethyl (C)[17], Oxidation (M)[18]		Mascot					
6	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Glycine tabacina GN=RBCS PE=3 SV=1				RBS_GLYTA	20005	8.87	5	109	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	882.4138	882.5104	0.0966	109	30	37	SMAGFPTR					Mascot					
	914.4002	914.345	-0.0552	-60	113	120	SPGYDGR	50	99.838	Oxidation (M)[2]		Mascot					
	914.4002	914.345	-0.0552	-60	113	120	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	156	163	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	156	163	IIGFDNVR					Mascot					
	1566.7655	1566.6611	-0.1044	-67	127	140	LPMFGCTDASQVLK			Carbamidomethyl (C)[6]		Mascot					
	1582.7604	1582.6509	-0.1095	-69	127	140	LPMFGCTDASQVLK			Carbamidomethyl (C)[6], Oxidation (M)[3]		Mascot					
	2691.4133	2691.1047	-0.3086	-115	2	29	ASSMISSPAVTTVNRAGA GTVAPFTGLK					Mascot					
7	Ribulose biphosphate carboxylase small chain 1, chloroplastic OS=Solanum tuberosum GN=RBCS-1 PE=3				RBS1_SOLTU	20543.2	8.23	5	108	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	914.4002	914.345	-0.0552	-60	116	123	SPGYDGR	50	99.838			Mascot					
	914.4002	914.345	-0.0552	-60	116	123	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	159	166	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	159	166	IIGFDNVR					Mascot					
	1350.7046	1350.5835	-0.1211	-90	1	14	MASSIVSSAAVATR					Mascot					
	1658.8328	1658.7137	-0.1191	-72	56	68	VRCMQVWPPINMK			Carbamidomethyl (C)[3]		Mascot					
	2691.2407	2691.1047	-0.136	-51	94	115	NGWVPCLEFETEHGFVY RENHK					Mascot					
8	Ribulose biphosphate carboxylase small chain 2C, chloroplastic OS=Solanum tuberosum GN=RBCS-2C PE=				RBSC_SOLTU	20306	7.6	5	107	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR	50	99.838			Mascot					
	914.4002	914.345	-0.0552	-60	115	122	SPGYDGR					Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR	35	95.243			Mascot					
	933.5151	933.4582	-0.0569	-61	158	165	IIGFDNVR			Carbamidomethyl (C)[3]		Mascot					
	1658.8328	1658.7137	-0.1191	-72	55	67	VRCMQVWPPINMK					Mascot					
	2027.022	2026.9668	-0.0552	-27	69	85	YETLSYLPDLSDEQLLK					Mascot					
	2225.0464	2224.9448	-0.1016	-46	129	148	LPMFGCTADTQVLAEVE EAK			Carbamidomethyl (C)[6], Oxidation (M)[3]		Mascot					
9	Ribulose biphosphate carboxylase small chain 1, chloroplastic OS=Glycine max GN=RBCS-1 PE=3 SV=1				RBS1_SOYBN	20060	8.87	5	106	100	83	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type					
	882.4138	882.5104	0.0966	109	30	37	SMAGFPTR					Mascot					
	914.4002	914.345	-0.0552	-60	113	120	SPXYDGR	50	99.838			Mascot					
	914.4229	914.345	-0.0779	-85	121	126	YWTMWK					Mascot					
	933.5151	933.4582	-0.0569	-61	156	163	IIGFDNVR	35	95.243			Mascot					

	933.5151	933.4582	-0.0569	-61	158	163	IGFDNVR										Mascot
	1568.7655	1568.6811	-0.1044	-67	127	140	LPMFQCTDASQVLK										Mascot
	1582.7604	1582.6509	-0.1095	-69	127	140	LPMFQCTDASQVLK										Mascot
10	Ribulose biphosphate carboxylase small chain 6, chloroplatic OS=Flaveria pringlei GN=RBCS6 PE=2 S																
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	907.4883	907.4315	-0.0568	-63	79	85	EVDYLLR									Mascot	
	914.4002	914.345	-0.0552	-60	108	115	SPGYDGR			50	99.838					Mascot	
	914.4002	914.345	-0.0552	-60	108	115	SPGYDGR									Mascot	
	933.5151	933.4582	-0.0569	-61	151	158	IGFDNVR			35	95.243					Mascot	
	933.5151	933.4582	-0.0569	-61	151	158	IGFDNVR									Mascot	
	1491.755	1491.6578	-0.0972	-65	34	47	KVNDFTLPSNGGR									Mascot	
	1555.7317	1555.6759	-0.0558	-36	122	135	LPMFQCTDSVQVMK									Mascot	
Gel Idx/Pos	163/G14					Instr./Gel Origin		BA2060/140227A					Process Status		Analysis Succeeded		
Plate [#] Name	[1] 31564					Instrument Sample Name							Spectra		11		
Rank	Protein Name				Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score	Total Ion Score	Total Ion C. I. %					
1	putative cold-inducible protein-like protein [Helleborus orientalis]				gi 317454922	15598.2	0	2	114	100	106	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1261.6787	1261.6533	-0.0254	-20	20	31	LPEQSTPPPAK									Mascot	
	1492.7432	1492.6633	-0.0799	-54	39	52	FSDVLAFSGPAPER									Mascot	
	1492.7432	1492.6633	-0.0799	-54	39	52	FSDVLAFSGPAPER			106						Mascot	
2	putative early light induced protein 2 [Camellia sinensis]				gi 259018355	18779.7	0	2	113	100	106	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1492.7432	1492.6633	-0.0799	-54	66	79	FSDVLAFSGPAPER									Mascot	
	1492.7432	1492.6633	-0.0799	-54	66	79	FSDVLAFSGPAPER			106						Mascot	
	2077.1072	2076.8745	-0.2327	-112	2	21	ATSMATMQSVLARPVTSVT TR									Mascot	
3	uncharacterized protein LOC100306375 [Glycine max]				gi 351724919	19363.8	0	2	113	100	106	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1492.7432	1492.6633	-0.0799	-54	82	95	FSDVLAFSGPAPER									Mascot	
	1492.7432	1492.6633	-0.0799	-54	82	95	FSDVLAFSGPAPER			106						Mascot	
	1638.8594	1638.7327	-0.1267	-77	100	115	LMAMFGVGAMAVEIAK					Oxidation (M)[3,10]				Mascot	
4	unknown [Glycine max]				gi 255627107	20260.6	0	2	113	100	106	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1492.7432	1492.6633	-0.0799	-54	83	96	FSDVLAFSGPAPER									Mascot	
	1492.7432	1492.6633	-0.0799	-54	83	96	FSDVLAFSGPAPER			106						Mascot	
	2077.1296	2076.8745	-0.2551	-123	97	116	INGRLAMIGFVAAMAVEV AK					Oxidation (M)[7]				Mascot	
5	putative early light induced protein [Arachis hypogaea]				gi 28194659	20200.3	0	1	106	99.997	106	100					
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	1492.7432	1492.6633	-0.0799	-54	83	96	FSDVLAFSGPAPER									Mascot	
	1492.7432	1492.6633	-0.0799	-54	83	96	FSDVLAFSGPAPER			106						Mascot	
6	unknown [Zea mays]				gi 223942337	47205.4	0	13	53	0							
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	830.4804	830.3941	-0.0863	-104	297	304	VATPMALK									Mascot	
	870.4104	870.4948	0.0844	97	273	279	EAAFNYR									Mascot	
	870.4104	870.4948	0.0844	97	273	279	EAAFNYR									Mascot	
	1002.5764	1002.5151	-0.0613	-61	297	305	VATPMALKR					Oxidation (M)[5]				Mascot	
	1002.5764	1002.5151	-0.0613	-61	296	304	RVATPMALK					Oxidation (M)[6]				Mascot	
	1005.5146	1005.5482	0.0336	33	305	312	RMOALQDK			8		Oxidation (M)[2]				Mascot	
	1045.5103	1045.5045	-0.0058	-6	259	268	OFFPNVPEK									Mascot	
	1106.5146	1106.4534	-0.0612	-55	192	200	EMIGEIENR					Oxidation (M)[2]				Mascot	
	1129.6324	1129.6097	-0.0227	-20	4	13	EGDARVTLRL									Mascot	
	1504.7755	1504.6682	-0.1073	-71	113	126	VNPQNPNTSTQPK									Mascot	
	1530.7482	1530.5967	-0.1515	-99	391	404	IHLQALGGFDEGCRK									Mascot	
	1546.782	1546.5684	-0.2136	-138	42	55	QGISLLEGOETNKR									Mascot	
	1546.782	1546.5684	-0.2136	-138	42	55	QGISLLEGOETNKR									Mascot	
	1671.8234	1671.811	-0.2124	-127	132	147	EGCMAPPPPPPLPSK					Carbamidomethyl (C)[3]				Mascot	
	1687.8182	1687.6038	-0.2144	-127	132	147	EGCMAPPPPPPLPSK					Carbamidomethyl (C)[3], Oxidation (M)[4]				Mascot	
	1687.8182	1687.6038	-0.2144	-127	132	147	EGCMAPPPPPPLPSK					Carbamidomethyl (C)[3], Oxidation (M)[4]				Mascot	
	2211.1365	2210.9189	-0.2176	-98	35	54	HOVSQKLQGISLLEGE TNK									Mascot	
7	conserved hypothetical protein [Ricinus communis]				gi 255656962	5720.1	0	5	51	0							
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	856.4774	856.4799	0.0025	3	22	29	APEGLELEK									Mascot	
	856.4774	856.4799	0.0025	3	22	29	APEGLELEK									Mascot	
	870.4064	870.4948	0.0884	102	30	37	VTADHDGR									Mascot	
	870.4064	870.4948	0.0884	102	30	37	VTADHDGR			13						Mascot	
	1045.6252	1045.5045	-0.1207	-115	12	21	TLAVVTKADK									Mascot	
	1116.6736	1116.5238	-0.1498	-134	8	18	TGARTLAVVTK									Mascot	
	1707.8661	1707.6409	-0.2252	-132	22	37	APEGLELEKVTADHDGR									Mascot	
8	uncharacterized protein LOC100280291 [Zea mays]				gi 226530632	51206.7	0	12	51	0							
	Peptide Information																
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence			Ion Score	C. I. %	Modification		Rank	Result Type		
	856.4233	856.4799	0.0566	66	1	8	MAVFSASK					Oxidation (M)[1]				Mascot	
	856.4384	856.4799	0.0415	48	36	42	TRHADTR									Mascot	
	1002.5466	1002.5151	-0.0315	-31	164	173	VGELADLGTK									Mascot	
	1002.5466	1002.5151	-0.0315	-31	164	173	VGELADLGTK									Mascot	
	1037.6102	1037.4384	-0.1718	-166	120	130	APLAPAAAVTR									Mascot	
	1320.7134	1320.5882	-0.2052	-155	186	196	NKLFETHYVYK									Mascot	
	1446.6527	1446.6527	-0.0657	-45	260	276	GGAGGAIDEATGSKAGK									Mascot	
	1474.8489	1474.6676	-0.1813	-123	100	112	LRLSLAFNSGLLQR									Mascot	
	1530.7395	1530.5967	-0.1428	-93	83	97	KAVSTAPADAADER									Mascot	
	1671.8337	1671.611	-0.2227	-133	2	17	AVFSASKAVSDSAFR									Mascot	
	1701.9395	1701.609	-0.3305	-194	113	130	GDPAAPRAPLAPAAAVT R									Mascot	
	2173.0454	2172.929	-0.1164	-54	38	56	HADTRIVPNPFCEISSS					Carbamidomethyl (C)[12]				Mascot	

	2173.0454	2172.929	-0.1164	-54	38	56	HADTRIVPPNFCSEISS							Carbamidomethyl (C)[12]		Mascot
	2232.9866	2232.8948	-0.0918	-41	241	259	LEFPKEFQNDGTTADCD									Mascot
9	phospholipase D zeta [Arabidopsis thaliana]					gi 15239403	93303.3	0	10	50	0	34	0			
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type				
	830.4366	830.3941	-0.0425	-51	33	40	GNKEPTGK					Mascot				
	842.4843	842.4641	-0.0202	-24	141	148	RPIQGGSK					Mascot				
	870.4791	870.4948	0.0157	18	615	622	KGLDANPR					Mascot				
	870.4791	870.4948	0.0157	18	615	622	KGLDANPR	34				Mascot				
	1002.5336	1002.5151	-0.0185	-18	311	318	VRCVLCPR			Carbamidomethyl (C)[3]		Mascot				
	1002.5336	1002.5151	-0.0185	-18	311	318	VRCVLCPR			Carbamidomethyl (C)[3]		Mascot				
	1037.5197	1037.4384	-0.0813	-78	27	35	FNLCGKGNK			Carbamidomethyl (C)[4]		Mascot				
	1045.5889	1045.5045	-0.0844	-81	490	500	EAASIGLISGK					Mascot				
	1480.837	1480.6287	-0.2083	-141	2	14	TEQLLLHGTLEVK					Mascot				
	1639.7461	1639.6941	-0.052	-32	218	230	CWEEIFDAIWEAK					Mascot				
	1707.964	1707.6409	-0.3231	-189	541	555	DINLNEINALQLPK					Mascot				
	2195.0835	2194.9141	-0.1694	-77	670	688	MMIVDDEVYIIGSANINQR					Mascot				
	2211.0784	2210.9189	-0.1595	-72	670	688	MMIVDDEVYIIGSANINQR			Oxidation (M)[1]		Mascot				
10	PREDICTED: uncharacterized protein LOC101265358 [Solanum lycopersicum]					gi 460365253	41151.6	0	7	49	0	27	0			
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type				
	830.4003	830.3941	-0.0062	-7	241	247	DEGERPK					Mascot				
	1002.5367	1002.5151	-0.0216	-22	54	61	WAVLQETR					Mascot				
	1002.5367	1002.5151	-0.0216	-22	54	61	WAVLQETR					Mascot				
	1045.5571	1045.5045	-0.0526	-50	103	110	NLLVRCDR			Carbamidomethyl (C)[6]		Mascot				
	1480.7795	1480.6287	-0.1508	-102	31	43	QIAKDVQVLFQAEK					Mascot				
	1492.7239	1492.6633	-0.0606	-41	15	30	SPGVASMGNSISSTK					Mascot				
	1492.7239	1492.6633	-0.0606	-41	15	30	SPGVASMGNSISSTK	27				Mascot				
	1514.8439	1514.6323	-0.2116	-140	49	61	GLVSRWAVLQETR					Mascot				
	1552.8582	1552.5677	-0.2905	-187	89	102	GLEPEDIANILLQK					Mascot				
Gel Idx/Pos		164/G15				Instr./Gel Origin		BA2060/140227A				Process Statu		Analysis Succeeded		
Plate [#] Name		[1] 31564				Instrument Sample Name						Spectra		11		
Rank	Protein Name					Accession No.	Protein MW	Protein PI	Pep. Count	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %			
1	Stromal 70 kDa heat shock-related protein, chloroplastic OS=Pisum sativum GN=HSP70 PE=2 SV=1					HSP7S_PEA	75469.3	5.22	19	685	100	573	100			
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type				
	869.509	869.4707	-0.0383	-44	529	536	GVPIQIEVK					Mascot				
	870.5406	870.4975	-0.0431	-50	226	233	IAGLEVLR	38	97.508			Mascot				
	870.5406	870.4975	-0.0431	-50	226	233	IAGLEVLR					Mascot				
	915.4894	915.4329	-0.0565	-62	379	386	TPVENSRL					Mascot				
	915.4894	915.4329	-0.0565	-62	379	386	TPVENSRL	10	0			Mascot				
	935.5308	935.4725	-0.0583	-62	520	528	LDGIPPAPR					Mascot				
	970.5316	970.4815	-0.0501	-52	356	363	HIETTLTR					Mascot				
	970.5316	970.4815	-0.0501	-52	356	363	HIETTLTR	46	99.584			Mascot				
	996.6088	996.5535	-0.0553	-55	407	415	IPAVQELVK					Mascot				
	1197.5304	1197.5936	0.0632	53	142	151	KMSEVDEESK			Oxidation (M)[2]		Mascot				
	1199.5725	1199.5826	0.0101	8	576	585	MVSEAEERFSK			Oxidation (M)[1]		Mascot				
	1373.7271	1373.6526	-0.0745	-54	394	406	DIDEVLVGGSTR	123	100			Mascot				
	1373.7271	1373.6526	-0.0745	-54	394	406	DIDEVLVGGSTR					Mascot				
	1381.6594	1381.584	-0.0754	-55	598	609	NOADSVVYQTEK					Mascot				
	1396.6412	1396.5957	-0.0455	-33	366	376	FEELCSDLLR			Carbamidomethyl (C)[5]		Mascot				
	1566.791	1566.7075	-0.0835	-53	204	217	AVVTVPAYFNDSQR	85	100			Mascot				
	1566.791	1566.7075	-0.0835	-53	204	217	AVVTVPAYFNDSQR					Mascot				
	1579.8114	1579.7135	-0.0979	-62	123	136	QAVVNPENTFFSVK					Mascot				
	1595.7733	1595.6854	-0.0879	-55	364	376	AKFEELCSDLLR			Carbamidomethyl (C)[7]		Mascot				
	1735.9126	1735.8113	-0.1013	-58	123	137	QAVVNPENTFFSVKR					Mascot				
	1745.9644	1745.7725	-0.1919	-110	630	646	LGELKEAITGGSTQTIK					Mascot				
	1815.0222	1814.9183	-0.1039	-57	390	406	LSIKDIDEVLVGGSTR					Mascot				
	1815.0222	1814.9183	-0.1039	-57	390	406	LSIKDIDEVLVGGSTR	95	100			Mascot				
	2437.1841	2437.0327	-0.1514	-62	484	506	SEVFSTAADGQTSVEINV LQGER					Mascot				
	2437.1841	2437.0327	-0.1514	-62	484	506	SEVFSTAADGQTSVEINV LQGER	187	100			Mascot				
	3070.5837	3070.3535	-0.2302	-75	70	100	VVGIDLGTTNSAVAAMEG GKPTIITNAEGQR					Mascot				
	3086.5786	3086.3999	-0.1787	-58	70	100	VVGIDLGTTNSAVAAMEG GKPTIITNAEGQR			Oxidation (M)[16]		Mascot				
2	Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=1 SV=1					HSP7G_ARATH	76949.7	5.17	14	568	100	502	100			
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type				
	869.509	869.4707	-0.0383	-44	539	546	GVPIQIEVK					Mascot				
	870.5406	870.4975	-0.0431	-50	236	243	IAGLEVLR	38	97.508			Mascot				
	870.5406	870.4975	-0.0431	-50	236	243	IAGLEVLR					Mascot				
	915.4894	915.4329	-0.0565	-62	389	396	TPVENSRL					Mascot				
	915.4894	915.4329	-0.0565	-62	389	396	TPVENSRL	10	0			Mascot				
	935.5308	935.4725	-0.0583	-62	530	538	LDGIPPAPR					Mascot				
	970.5316	970.4815	-0.0501	-52	366	373	HIETTLTR					Mascot				
	970.5316	970.4815	-0.0501	-52	366	373	HIETTLTR	46	99.584			Mascot				
	1138.6942	1138.5833	-0.1109	-97	417	426	IPAVQDLVRK					Mascot				
	1155.6481	1155.5764	-0.0717	-62	366	375	HIETTLTRGK					Mascot				
	1373.7271	1373.6526	-0.0745	-54	404	416	DIDEVLVGGSTR	123	100			Mascot				
	1373.7271	1373.6526	-0.0745	-54	404	416	DIDEVLVGGSTR					Mascot				
	1381.6594	1381.584	-0.0754	-55	608	619	NOADSVVYQTEK			Carbamidomethyl (C)[5]		Mascot				
	1396.6412	1396.5957	-0.0455	-33	376	386	FEELCSDLLR					Mascot				
	1461.7695	1461.6926	-0.0769	-53	185	197	QFAAEIEIAQVLR					Mascot				
	1461.7695	1461.6926	-0.0769	-53	185	197	QFAAEIEIAQVLR	109	100			Mascot				
	1579.8114	1579.7135	-0.0979	-62	133	146	QAVVNPENTFFSVK					Mascot				
	1735.9126	1735.8113	-0.1013	-58	133	147	QAVVNPENTFFSVKR					Mascot				
	2437.1841	2437.0327	-0.1514	-62	494	516	SEVFSTAADGQTSVEINV LQGER					Mascot				
	2437.1841	2437.0327	-0.1514	-62	494	516	SEVFSTAADGQTSVEINV LQGER	187	100			Mascot				
3	Heat shock 70 kDa protein 6, chloroplastic OS=Arabidopsis thaliana GN=HSP70-6 PE=1 SV=1					HSP7F_ARATH	76461.4	5.07	13	561	100	502	100			
	Peptide Information															
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type				

				Seq.		Seq.		Score									
		869.509	869.4707	-0.0383	-44	539	546	GVPOIEVK							Mascot		
		870.5406	870.4975	-0.0431	-50	236	243	IAGLEVLR	38	97.508					Mascot		
		870.5406	870.4975	-0.0431	-50	236	243	IAGLEVLR							Mascot		
		915.4894	915.4329	-0.0565	-62	389	396	TPVENSRLR	10	0					Mascot		
		915.4894	915.4329	-0.0565	-62	389	396	TPVENSRLR							Mascot		
		935.5308	935.4725	-0.0583	-62	530	538	LDGIPPAPR							Mascot		
		970.5316	970.4815	-0.0501	-52	366	373	HIETTLTR							Mascot		
		970.5316	970.4815	-0.0501	-52	366	373	HIETTLTR	46	99.584					Mascot		
		1373.7271	1373.6526	-0.0745	-54	404	416	DIDEVILVGGSTR	123	100					Mascot		
		1373.7271	1373.6526	-0.0745	-54	404	416	DIDEVILVGGSTR							Mascot		
		1381.6594	1381.584	-0.0754	-55	608	619	NQADSVVYQTEK							Mascot		
		1396.6412	1396.5957	-0.0455	-33	376	386	FEELCSDLLDR				Carbamidomethyl (C)[5]			Mascot		
		1461.7695	1461.6926	-0.0769	-53	185	197	QFAAEISIAQVLR							Mascot		
		1461.7695	1461.6926	-0.0769	-53	185	197	QFAAEISIAQVLR	109	100					Mascot		
		1579.8114	1579.7135	-0.0979	-62	133	146	QAVNPENTFFSVK							Mascot		
		1595.7733	1595.6854	-0.0879	-55	374	386	AKFEECSDLLDR				Carbamidomethyl (C)[7]			Mascot		
		1735.9126	1735.8113	-0.1013	-58	133	147	QAVNPENTFFSVKLR							Mascot		
		2437.1841	2437.0327	-0.1514	-62	494	516	SEVFSTAADGQTSVEINV LOGER							Mascot		
		2437.1841	2437.0327	-0.1514	-62	494	516	SEVFSTAADGQTSVEINV LOGER	187	100					Mascot		
4	Stromal 70 kDa heat shock-related protein, chloroplastic (Fragment) OS=Spinacia oleracea GN=CHSP70					HSP7S_SPIOI		64860.7	4.87	10	510	100	464	100			
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type			
		870.5406	870.4975	-0.0431	-50	106	113	IAGLEVLR		38	97.508			Mascot			
		870.5406	870.4975	-0.0431	-50	106	113	IAGLEVLR						Mascot			
		915.4894	915.4329	-0.0565	-62	259	266	TPVENSRLR						Mascot			
		915.4894	915.4329	-0.0565	-62	259	266	TPVENSRLR	10	0				Mascot			
		935.5308	935.4725	-0.0583	-62	400	408	LDGIPPAPR						Mascot			
		970.5316	970.4815	-0.0501	-52	236	243	HIETTLTR						Mascot			
		970.5316	970.4815	-0.0501	-52	236	243	HIETTLTR	46	99.584				Mascot			
		1155.5714	1155.5764	0.005	4	456	465	MYSEAEKFAK				Oxidation (M)[1]		Mascot			
		1381.6594	1381.584	-0.0754	-55	478	489	NQADSVVYQTEK						Mascot			
		1461.7695	1461.6926	-0.0769	-53	55	67	QFAAEISIAQVLR						Mascot			
		1461.7695	1461.6926	-0.0769	-53	55	67	QFAAEISIAQVLR	109	100				Mascot			
		1566.791	1566.7075	-0.0835	-53	84	97	AVVTVPAYFNDSSQR	85	100				Mascot			
		1566.791	1566.7075	-0.0835	-53	84	97	AVVTVPAYFNDSSQR						Mascot			
		1723.8901	1723.7856	-0.1045	-61	114	129	INEPTAASLAYGFEK						Mascot			
		2437.1841	2437.0327	-0.1514	-62	384	386	SEVFSTAADGQTSVEINV LOGER						Mascot			
		2437.1841	2437.0327	-0.1514	-62	384	386	SEVFSTAADGQTSVEINV LOGER	187	100				Mascot			
5	Heat shock 70 kDa protein OS=Chlamydomonas reinhardtii GN=HSP70 PE=2 SV=2					HSP70_CHLRE		70953.2	5.2	6	94	99.999	85	100			
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type			
		949.4481	949.4984	0.0503	53	318	325	KCMDPVEK						Mascot			
		949.4481	949.4984	0.0503	53	318	325	KCMDPVEK						Mascot			
		1197.6626	1197.5936	-0.069	-58	465	475	FELTGIPPAPR						Mascot			
		1228.6281	1228.5688	-0.0593	-48	27	37	VEIIANDQGNR				Oxidation (M)[6]		Mascot			
		1318.5806	1318.6521	0.0715	54	308	317	FEELCMDLFR						Mascot			
		1487.7013	1487.6327	-0.0686	-46	38	50	TPPSVYAFDTTER						Mascot			
		1566.791	1566.7075	-0.0835	-53	146	159	AVVTVPAYFNDSSQR	85	100				Mascot			
		1566.791	1566.7075	-0.0835	-53	146	159	AVVTVPAYFNDSSQR						Mascot			
6	Putative cytochrome c oxidase subunit II PS17 (Fragments) OS=Pinus strobus PE=1 SV=1					PS17_PINST		1707	9.63	2	78	99.943	56	99.955			
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type			
		856.525	856.4809	-0.0441	-51	1	8	SPTVIALR						Mascot			
		856.525	856.4809	-0.0441	-51	1	8	SPTVIALR	35	95.196				Mascot			
		870.5043	870.4975	-0.0068	-8	9	16	VVEALSPR	20	0				Mascot			
		870.5043	870.4975	-0.0068	-8	9	16	VVEALSPR						Mascot			
7	Acetyl-CoA carboxylase 2 OS=Arabidopsis thaliana GN=ACC2 PE=2 SV=1					ACC2_ARATH		262562.8	6.65	26	52	80.64					
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type			
		856.5363	856.4809	-0.0554	-65	1643	1649	NRLNVK						Mascot			
		856.5363	856.4809	-0.0554	-65	1643	1649	NRLNVK						Mascot			
		865.4665	865.4686	0.0021	2	944	950	EFEIISK						Mascot			
		869.4297	869.4707	0.041	47	1033	1038	MRQQYK				Oxidation (M)[1]		Mascot			
		915.5006	915.4329	-0.0677	-74	2164	2171	ANIQDAKR						Mascot			
		915.5006	915.4329	-0.0677	-74	2164	2171	ANIQDAKR						Mascot			
		935.4985	935.4725	-0.026	-28	1965	1972	WLGGIFDK						Mascot			
		949.4481	949.4984	0.0503	53	781	788	LMIAETPCK				Carbamidomethyl (C)[7]		Mascot			
		949.4481	949.4984	0.0503	53	781	788	LMIAETPCK				Carbamidomethyl (C)[7]		Mascot			
		982.5316	982.4754	-0.0562	-57	55	63	TFKVGSSIR						Mascot			
		1045.5537	1045.5105	-0.0432	-41	328	338	ASWGGGGKGIR						Mascot			
		1094.5333	1094.525	-0.0083	-8	2146	2154	KELCECMGR				Oxidation (M)[7]		Mascot			
		1156.6249	1156.6012	-0.0237	-20	942	950	YKEFEISK						Mascot			
		1162.5773	1162.5629	-0.0144	-12	738	748	DGGLLMQLDGK				Oxidation (M)[6]		Mascot			
		1228.6532	1228.5688	-0.0844	-69	845	855	LDLDDPSAVRK						Mascot			
		1318.595	1318.6521	0.0571	43	160	170	TWAYETFGSEK						Mascot			
		1444.7351	1444.6608	-0.0743	-51	2130	2142	GNVLPEGMIEIK				Oxidation (M)[9]		Mascot			
		1473.7195	1473.6217	-0.0978	-66	560	571	SKPNMWSYFSVK						Mascot			
		1499.8369	1499.6481	-0.1888	-126	2051	2062	EQLPLFIANNWR						Mascot			
		1579.7057	1579.7135	0.0078	5	1940	1952	TVYEPENSCDPR				Carbamidomethyl (C)[10]		Mascot			
		1601.7952	1601.7128	-0.0824	-51	724	737	MSNSEVVAEIHTRL				Oxidation (M)[1]		Mascot			
		1623.7618	1623.704	-0.0578	-36	2203	2216	FAELHDTSMRMAAK						Mascot			
		1657.8142	1657.6973	-0.1169	-71	1714	1728	EDAFPLAVTELACTK				Oxidation (M)[9]		Mascot			
		1677.675	1677.7311	0.0561	33	496	509	FYGMHHGGGYDSWR				Oxidation (M)[4]		Mascot			
		1678.8224	1678.7622	-0.0602	-36	2221	2234	SVVEWSGSRFFYK						Mascot			
		1680.8414	1680.7458	-0.0956	-57	1064	1077	LMEOQLYPNPAAYR				Oxidation (M)[2]		Mascot			
		1791.8806	1791.7186	-0.162	-90	1557	1571	TCTVHYREVEATGR				Carbamidomethyl (C)[2]		Mascot			
		1814.972	1814.9183	-0.0537	-30	247	264	GIIFLGPPADSMIALGDK						Mascot			
		1814.972	1814.9183	-0.0537	-30	247	264	GIIFLGPPADSMIALGDK						Mascot			
		2046.0721	2045.9342	-0.1379	-67	2147	2163	ELLECMMGLDLDTLINLK				Carbamidomethyl (C)[5]		Mascot			
8	CDT1-like protein a, chloroplastic OS=Arabidopsis thaliana GN=CDT1A PE=1 SV=1					CDT1A_ARATH		63700.4	9.27	9	48	46.679	21	0			
Peptide Information																	
		Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence		Ion Score	C. I. %	Modification	Rank	Result Type			
		870.5407	870.4975	-0.0432	-50	548	555	LASPLTIR	21	0				Mascot			
		870.5407	870.4975	-0.0432	-50	548	555	LASPLTIR						Mascot			
		1162.683	1162.5629	-0.1201	-103	166	175	HILPEAIEIK						Mascot			
		1197.6222	1197.5936	-0.0286	-24	503	513	IIAGHSIDTDR						Mascot			

