

User	:	
Email	:	
Search title	:	
MS data file	:	E:\CAO Jing\20160619_Qe\20160616_SPX3P+.mgf
Database	:	TAIRArarp (35386 sequences; 14482855 residues)
Timestamp	:	19 Jun 2016 at 14:09:34 GMT
Enzyme	:	Trypsin
Fixed modifications	:	Cysteineamidomethyl (C)
Variable modifications	:	Deamidated (NQ),Oxidation (M)
Mass values	:	Monoisotopic
Protein Mass	:	Unrestricted
Peptide Mass Tolerance	:	± 20 ppm
Fragment Mass Tolerance:	:	± 0.2 Da
Max Missed Cleavages	:	2
Instrument type	:	ESI-TRAP
Number of queries	:	9030
Protein hits	:	<div><div>AT4G25500.1</div><div>Symbol: ATSP35, ATSP40, AT-SRP40, RSP35, RS40, At-RS40 arginine/serine-rich splicing factor 35 chr4:13025168-13027243 FORWARD LENGTH=350</div></div> <div><div>AT4G10320.1</div><div>Symbol: tRNA synthetase class 1 (I, L, M and V) family protein chr4:6397526-6404509 REVERSE LENGTH=1190</div></div> <div><div>AT2G45130.1</div><div>Symbol: ATPSP3, SPX3 SPX domain gene 3 chr2:18606489-18607754 FORWARD LENGTH=245</div></div> <div><div>AT5G27120.1</div><div>Symbol: NOP56-like pre RNA processing ribonucleoprotein chr5:9541287-9543684 FORWARD LENGTH=533</div></div> <div><div>AT5G35200.1</div><div>Symbol: EHTH/ANTH/VHS superfamily protein chr5:13462463-13465581 REVERSE LENGTH=544</div></div> <div><div>AT3G08590.1</div><div>Symbol: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent chr3:2608693-2611237 REVERSE LENGTH=560</div></div> <div><div>AT3G05060.1</div><div>Symbol: NOP56-like pre RNA processing ribonucleoprotein chr3:1413174-1415564 REVERSE LENGTH=533</div></div> <div><div>AT5G02500.1</div><div>Symbol: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 heat shock cognate protein 70-1 chr5:554055-556334 REVERSE LENGTH=651</div></div> <div><div>AT2G21660.1</div><div>Symbol: ATGRP7, CCR2, GR-RBP7, GRP7 cold, circadian rhythm, and rna binding 2 chr2:9265477-9266316 REVERSE LENGTH=176</div></div> <div><div>AT1G56070.1</div><div>Symbol: LOS1 Ribosomal protein S5/elongation factor G/III/V family protein chr1:20968245-20971077 REVERSE LENGTH=843</div></div> <div><div>AT1G07420.1</div><div>Symbol: glycine-rich protein chr4:11491519-11491934 FORWARD LENGTH=131</div></div> <div><div>AT5G58390.1</div><div>Symbol: RPT3 regulatory particle triple-A ATPase 3 chr5:23569155-23571116 FORWARD LENGTH=408</div></div> <div><div>AT3G04120.1</div><div>Symbol: GAPC, GAPC-1, GAPC1 glyceraldehyde-3-phosphate dehydrogenase C subunit 1 chr3:1081077-1083131 FORWARD LENGTH=338</div></div> <div><div>AT2G28000.1</div><div>Symbol: CPN60A, CH-CPN60A, SLP chaperonin-60alpha chr2:11926603-11929184 FORWARD LENGTH=586</div></div> <div><div>AT2G39730.1</div><div>Symbol: RCA rubisco activase chr2:16570951-16573345 REVERSE LENGTH=474</div></div> <div><div>AT5G58470.1</div><div>Symbol: TAF15B TBP-associated factor 15B chr5:23638566-23640854 REVERSE LENGTH=422</div></div> <div><div>AT5G42820.1</div><div>Symbol: ATU2AF35B, U2AF35B zinc finger C-x8-C-x5-C-x3-H type family protein chr5:17170445-17171296 REVERSE LENGTH=283</div></div> <div><div>AT5G26710.1</div><div>Symbol: Glutamyl glutaminy l-trna synthetase, class ic chr5:9305673-9308247 FORWARD LENGTH=719</div></div> <div><div>AT1G076010.1</div><div>Symbol: Alba DNA/RNA-binding protein chr1:28528505-28530488 REVERSE LENGTH=350</div></div> <div><div>AT2G20450.1</div><div>Symbol: Ribosomal protein L14 chr2:8813923-8815071 FORWARD LENGTH=134</div></div> <div><div>AT3G00120.1</div><div>Symbol: ATPA ATP synthase subunit alpha chr3:9938-11461 FORWARD LENGTH=507</div></div> <div><div>AT5G56740.1</div><div>Symbol: HAG2, HAC7, HAGG2, HAC07 histone acetyltransferase of the GNAT family 2 chr5:22953009-22955577 REVERSE LENGTH=467</div></div> <div><div>AT4G21280.1</div><div>Symbol: PSBQ, PSBQA, PSBQ-1 photosystem II subunit QA chr4:11334446-11335587 FORWARD LENGTH=223</div></div> <div><div>AT3G13570.1</div><div>Symbol: SCL30A, At-SCL30A SC35-like splicing factor 30A chr3:4429564-4431602 REVERSE LENGTH=262</div></div> <div><div>AT4G10340.1</div><div>Symbol: LHC85 light harvesting complex of photosystem II 5 chr4:24105713-24108780 FORWARD LENGTH=280</div></div> <div><div>AT1G07420.1</div><div>Symbol: CTP binding Elongation factor Tu family protein chr1:2455559-2457001 FORWARD LENGTH=449</div></div> <div><div>AT5G14040.1</div><div>Symbol: PHT31 phosphate transporter 31 chr5:4531059-4532965 REVERSE LENGTH=375</div></div> <div><div>AT3G44310.1</div><div>Symbol: NITI1, ATNIT1, NITI nitrilase 1 chr3:15986901-15988841 FORWARD LENGTH=346</div></div> <div><div>AT2G25670.1</div><div>Symbol: BEST Arabidopsis thaliana protein match is: copper ion binding (TAIR:AT4G32610.1); Has 43784 Blast hits to 26928 proteins in 1799 species: Archae - 86; Bacteria - 6347; Metazoa - 1597</div></div> <div><div>AT1G64880.1</div><div>Symbol: Ribosomal protein S5 family protein chr1:24105713-24108780 FORWARD LENGTH=515</div></div> <div><div>AT4G32610.1</div><div>Symbol: copper ion binding chr4:15728376-15729897 REVERSE LENGTH=315</div></div> <div><div>AT3G15730.1</div><div>Symbol: PLD4LPHAL, PLD phospholipase D alpha 1 chr3:5330835-5333474 FORWARD LENGTH=810</div></div> <div><div>AT3G000380.1</div><div>Symbol: RPS4 chloroplast ribosomal protein S4 chrC:45223-45828 REVERSE LENGTH=201</div></div> <div><div>AT2G33210.1</div><div>Symbol: HSP60-2 heat shock protein 60-2 chr2:14075093-14078568 REVERSE LENGTH=585</div></div> <div><div>AT4G39260.1</div><div>Symbol: CCR1, ATGRP8, GR-RBP8, GRP8 cold, circadian rhythm, and RNA binding chr4:18274166-18274958 REVERSE LENGTH=169</div></div> <div><div>AT2G35460.1</div><div>Symbol: SCL35A, At-SCL35A SC35-like splicing factor 30 chr3:20561024-20563502 FORWARD LENGTH=262</div></div> <div><div>AT1G64370.1</div><div>Symbol: unknown protein: Has 773 Blast hits to 375 proteins in 118 species: Archae - 0; Bacteria - 97; Metazoa - 421; Fungi - 108; Plants - 31; Viruses - 0; Other Eukaryotes - 116 (source: NCBI)</div></div> <div><div>AT4G45000.1</div><div>Symbol: AAA-type ATPase family protein chr1:17009220-17011607 FORWARD LENGTH=399</div></div> <div><div>AT2G27710.1</div><div>Symbol: 60S acidic ribosomal protein family chr2:11816929-11817670 FORWARD LENGTH=115</div></div> <div><div>AT5G26742.1</div><div>Symbol: emb1138 DEAD box RNA helicase (RH3) chr5:9285540-9288871 REVERSE LENGTH=747</div></div> <div><div>AT3G59510.1</div><div>Symbol: DEAD/DF-box RNA helicase family protein chr3:2164008-2164344 FORWARD LENGTH=612</div></div> <div><div>AT2G23390.1</div><div>Symbol: CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF482 (InterPro:IPR007434), Acyl-CoA N-acyltransferase (InterPro:IPR016181); Has 2165 Blast hits to 2163 proteins in 543 speci</div></div> <div><div>AT2G14880.1</div><div>Symbol: SWIB/MDM2 domain superfamily protein chr2:6393686-6394841 REVERSE LENGTH=141</div></div> <div><div>AT2G18220.1</div><div>Symbol: Nocp family chr2:7928254-7931851 FORWARD LENGTH=764</div></div> <div><div>AT3G09580.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:6548955-6551150 REVERSE LENGTH=346</div></div> <div><div>AT3G20250.1</div><div>Symbol: APUms, PUMs pumilio 5 chr3:7059098-7062660 REVERSE LENGTH=961</div></div> <div><div>AT4G31580.1</div><div>Symbol: SRZ-22, SRZ22, RSPZ22, RSZ22, At-RSZ22 serine/arginine-rich 22 chr4:15306983-15308064 FORWARD LENGTH=200</div></div> <div><div>AT4G38680.1</div><div>Symbol: GRP2, CSPD2, CSP2, ATCSP2 glycine rich protein 2 chr4:18072240-18072851 REVERSE LENGTH=203</div></div> <div><div>AT4G35785.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953211-16955127 REVERSE LENGTH=238</div></div> <div><div>AT1G42470.1</div><div>Symbol: ATP4A-2 eIF4a-2 chr1:22040495-20262018 FORWARD LENGTH=412</div></div> <div><div>AT5G15300.1</div><div>Symbol: Ribosomal protein S4 chr5:4935124-4936334 REVERSE LENGTH=198</div></div> <div><div>AT2G09990.1</div><div>Symbol: Ribosomal protein S5 domain 2-like superfamily protein chr2:3781442-3781882 FORWARD LENGTH=146</div></div> <div><div>AT2G40660.1</div><div>Symbol: Nucleic acid-binding, OB-fold-like protein chr2:16966011-16968866 FORWARD LENGTH=389</div></div> <div><div>AT1G04270.1</div><div>Symbol: RPS15 cytosolic ribosomal protein S15 chr1:1141852-1142960 REVERSE LENGTH=152</div></div> <div><div>AT2G09760.1</div><div>Symbol: Protein kinase superfamily protein chr4:6548955-6551150 REVERSE LENGTH=346</div></div> <div><div>AT4G17520.1</div><div>Symbol: Hyaluronan / mRNA binding family chr4:9771496-9773313 FORWARD LENGTH=360</div></div> <div><div>AT5G57290.1</div><div>Symbol: 60S acidic ribosomal protein family chr5:23207049-23207835 REVERSE LENGTH=120</div></div> <div><div>AT1G69200.1</div><div>Symbol: FLN2 fructokinase-like 2 chr1:26016018-26018365 FORWARD LENGTH=616</div></div> <div><div>AT3G09680.1</div><div>Symbol: Ribosomal protein S12/S13 family protein chr3:2969197-2970291 REVERSE LENGTH=142</div></div> <div><div>AT3G06810.1</div><div>Symbol: IER3 acyl-CoA dehydrogenase-related chr3:2146594-2150654 FORWARD LENGTH=824</div></div> <div><div>AT3G00800.1</div><div>Symbol: structural constituent of ribosome chrC:82826-83482 REVERSE LENGTH=218</div></div> <div><div>AT3G11830.1</div><div>Symbol: TCP-1/cpn60 chaperonin family protein chr3:3732734-3736156 FORWARD LENGTH=557</div></div> <div><div>AT4G10840.1</div><div>Symbol: Tetratricopeptide repeat (TPR)-like superfamily protein chr4:6656614-6659033 FORWARD LENGTH=609</div></div> <div><div>AT2G39390.1</div><div>Symbol: Ribosomal L29 family protein chr2:16450803-16451762 REVERSE LENGTH=123</div></div> <div><div>AT1G29910.1</div><div>Symbol: CAB3, AB180, LHCB1.2 chlorophyll a/b binding protein 3 chr1:10472443-10473246 REVERSE LENGTH=267</div></div> <div><div>AT2G34420.1</div><div>Symbol: LHCB12, LHCB1.5 photosystem II light harvesting complex gene B1B2 chr2:14522716-14523513 REVERSE LENGTH=265</div></div> <div><div>AT3G44300.1</div><div>Symbol: NIT2, ATNIT2 nitrilase 2 chr3:15983351-15985172 FORWARD LENGTH=339</div></div> <div><div>AT5G15780.1</div><div>Symbol: Pollen Ole e 1 allergen and extensin family protein chr5:5144898-5146297 REVERSE LENGTH=401</div></div> <div><div>AT5G06850.1</div><div>Symbol: C2 calcium/lipid-binding plant phosphoribosyltransferase family protein chr5:2127200-2129584 REVERSE LENGTH=794</div></div> <div><div>AT2G29075.1</div><div>Symbol: glycine-rich protein chr3:11051645-1105269 REVERSE LENGTH=294</div></div> <div><div>AT3G05630.1</div><div>Symbol: PLDP2, PLD22, PLDZETA2 phospholipase D P2 chr3:1635321-1640105 FORWARD LENGTH=1046</div></div> <div><div>AT3G00490.1</div><div>Symbol: RBC1 ribulose-bisphosphate carboxylases chrC:54958-56397 FORWARD LENGTH=479</div></div> <div><div>AT3G10950.1</div><div>Symbol: Zinc-binding ribosomal protein family protein chr3:3423893-3424566 FORWARD LENGTH=92</div></div> <div><div>AT4G13850.1</div><div>Symbol: ATGRP2, GR-RBP2, GRP2 glycine-rich RNA-binding protein 2 chr4:8021314-8022065 FORWARD LENGTH=158</div></div> <div><div>AT1G34000.1</div><div>Symbol: Disease resistance protein (CC-NBS-LRR class) family chr1:21696165-21699118 REVERSE LENGTH=900</div></div> <div><div>AT2G47610.1</div><div>Symbol: Ribosomal protein L7Ae/L30e/S12e/Gad45 family protein chr2:19529854-19531401 FORWARD LENGTH=257</div></div> <div><div>AT1G28210.1</div><div>Symbol: ATJ1 DNAP heat shock family protein chr1:9854598-9859884 FORWARD LENGTH=408</div></div> <div><div>AT5G39500.1</div><div>Symbol: GNLI1, RRM01 GNOM-like 1 chr5:15815274-15819910 FORWARD LENGTH=1443</div></div> <div><div>AT5G10940.1</div><div>Symbol: Transducin family protein / WD-40 repeat family protein chr5:3448890-3454127 REVERSE LENGTH=757</div></div> <div><div>AT2G40650.1</div><div>Symbol: PRP18 family protein chr2:16963588-16965595 REVERSE LENGTH=355</div></div> <div><div>AT1G78950.1</div><div>Symbol: Terpenoid cyclase family protein chr1:29684558-29688673 REVERSE LENGTH=759</div></div> <div><div>AT5G56340.1</div><div>Symbol: ATCTRT RING/U-box superfamily protein chr5:22818254-22819444 FORWARD LENGTH=396</div></div> <div><div>AT3G54740.1</div><div>Symbol: Protein of unknown function, DUF593 chr3:20263093-20264466 FORWARD LENGTH=390</div></div> <div><div>AT2G39435.1</div><div>Symbol: Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related chr2:16464806-16466492 REVERSE LENGTH=464</div></div> <div><div>AT5G07240.1</div><div>Symbol: IQD24 IQ-domain 24 chr5:2272028-2274051 FORWARD LENGTH=401</div></div> <div><div>AT3G49790.1</div><div>Symbol: Carbohydrate-binding protein chr3:18468296-18469396 REVERSE LENGTH=366</div></div> <div><div>AT3G48730.1</div><div>Symbol: GS2A glutamate-1-semialdehyde 2,1-aminotase 2 chr3:18049697-18051550 FORWARD LENGTH=472</div></div> <div><div>AT3G46480.1</div><div>Symbol: 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein chr3:17103173-17105594 FORWARD LENGTH=286</div></div> <div><div>AT2G28620.1</div><div>Symbol: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr2:12265167-12270020 REVERSE LENGTH=1042</div></div>

Peptide matches above identity threshold	148	7	4.73 %
Peptide matches above homology or identity threshold	195	18	9.23 %

Select Summary Report

AT4G25500.1

Significance threshold < 0.05

Max. number of hits AUTO

Show Percolator scores

Standard scoring MudPIT scoring Ions score or expect cut-off 15

Show sub-sets 0

Show pop-ups Suppress pop-ups

Require bold red

Preferred taxonomy All entries

All queries Unassigned Below homology threshold Below identity threshold

1.	AT4G25500.1	Mass:	40352	Score:	654	Matches:	25 (22)	Sequences:	3 (3)	enPAI:	0.52
Symbol: ATSP35, ATSP40, AT-SRP40, RSP35, RS40, At-RS40 arginine/serine-rich splicing factor 35 chr4:13025168-13027243 FORWARD LENGTH=350											
Query	Observed	Nr(expt)	Nr(calcd)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
137	504.2876	1806.5607	1006.5699	-9.12	0	31	0.023	1	U	K.VISVETAYK.D	
2203	901.9124	1801.8103	1801.8971	-9.34	0	85	1e-007	1	U	R.NPAFIQTAEAGDATR.A 2202 2204 2205 2208 2209 2210 2212 2216 2217 2218 2219	
2220	902.4174	1802.8202	1802.8111	5.02	0	(76)	8.5e-007	1	U	R.NPAFIQTAEAGDATR.A 2222 2225	
3356	735.6677	2203.9813	2203.9844	-1.39	1	46	0.00085	1	U	K.AGFAPVYKDEKDAEDAIR.A 3351 3352 3353 3354 3355 3357 3359 3360	

Proteins matching the same set of peptides:											
AT4G25500.4 Mass: 40352 Score: 654 Matches: 25 (22) Sequences: 3 (3)											
Symbol: RSP35, RS40, At-RS40 arginine/serine-rich splicing factor 35 chr4:13025168-13027243 FORWARD LENGTH=350											
AT5G52040.1 Mass: 41314 Score: 654 Matches: 25 (22) Sequences: 3 (3)											
Symbol: ATSP41, RS41, At-RS41 RNA-binding (RRM/RBD/RNP motifs) family protein chr5:21131081-21133318 FORWARD LENGTH=356											
AT5G52040.2 Mass: 41401 Score: 654 Matches: 25 (22) Sequences: 3 (3)											
Symbol: ATSP41, RS41, At-RS41 RNA-binding (RRM/RBD/RNP motifs) family protein chr5:21131081-21133318 FORWARD LENGTH=357											

2.	AT4G10320.1	Mass:	136368	Score:	342	Matches:	12 (11)	Sequences:	8 (8)	enPAI:	0.37
Symbol: tRNA synthetase class I (I, L, M and V) family protein chr4:6397526-6404509 REVERSE LENGTH=1190											
Query	Observed	Nr(expt)	Nr(calcd)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
125	447.2375	892.4604	892.4654	-5.60	0	48	0.00079	1	U	K.FHGASLVGK.K	
914	444.2151	1329.6235	1329.6248	-0.97	0	46	0.00093	1	U	R.YQTMTHGHVTR.R	
2570	978.9621	1955.9096	1955.9153	-2.87	0	63	2.7e-005	1	U	R.QBEDVFLSPWTEIDAFK.T	
3333	725.7021	2174.0844	2174.0871	-1.20	0	60	6.3e-005	1	U	K.VMAFPPTFPPTETLYQNLR.K	
4162	828.0585	2481.1538	2481.1516	0.87	0	53	0.00032	1	U	R.TGDEDCHTALSTFLNPVLLTSCK.V	
4848	907.4185	2719.2336	2719.2389	-1.95	0	45	0.0014	1	U	K.SGLEPTDFVVFYQSLDEDSVSK.Q	

4849	1360.6249	2719.2352	2719.2389	-1.34	0	(34)	0.018	1	U	K.SGLEPTDFVEVFPQSLDEBSVK.Q
7779	1303.0217	3906.0434	3906.0163	6.92	0	33	0.015	1	U	R.LETGGVFPVPTDTQTSANILQDQWHSATQSLVR.F
7780	977.7607	3907.0139	3907.0004	3.46	0	(28)	0.054	1	U	R.LETGGVFPVPTDTQTSANILQDQWHSATQSLVR.F
8401	1355.3794	4063.1163	4063.1015	3.66	1	(51)	0.00026	1	U	K.RLETGGVFPVPTDTQTSANILQDQWHSATQSLVR.F
8402	1017.2897	4065.1296	4065.0695	14.8	1	52	0.00016	1	U	K.RLETGGVFPVPTDTQTSANILQDQWHSATQSLVR.F
8403	814.2310	4066.1184	4066.0535	16.0	1	(22)	0.17	1	U	K.RLETGGVFPVPTDTQTSANILQDQWHSATQSLVR.F

AT5G58470.2 **Mass:** 42746 **Score:** 102 **Matches:** 2(2) **Sequences:** 1(1)
| **Symbols:** TAF15b | TBP-associated factor 15B | chr5:23638566-23640854 REVERSE LENGTH=422

17. [A5G42820.1](#) Mass: 33611 Score: 94 Matches: 3(3) Sequences: 2(2) eMPAI: 0.29
 | Symbols: A02AF35B, U2AF35B | Zinc finger C-X8-C-X5-C-X3-H type family protein | chr5:17170445-17171296 REVERSE LENGTH=283

Query	Observed	M(expt)	M(calc)	ppm	M	q	Score	Expect	Rank	Unique	Peptide
2935	696.699	2087.059	2087.0476	1.58	0	49	0.0008	1	U	R.PYSGRPIADSPVDFR.E	
2936	777.6826	2330.0259	2330.0379	-5.17	0	44	0.0011	1	U	K.IQDHFQFQVDFR.F	3808

AT5G42820.2 Mass: 33611 Score: 94 Matches: 3(3) Sequences: 2(2)

Symbols: ATU2AF35B, U2AF35B	Zinc finger C-x8-C-x5-C-x3-H type family protein	chr5:17170445-17171296 REVERSE LENGTH=283
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18. [A7SG26710.1](#) Mass: 81527 Score: 92 Matches: 4(3) Sequences: 2(2) eMPAI: 0.11
 | Symbols: | Glutamyl/glutaminyl-tRNA synthetase, class Ic | chr5:9305673-9308247 FORWARD Length=719

Query	Observed	Rn(expt)	Rn(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
537	374.3558	1146.6970	1146.7012	-3.70	0	22	0.062	1	U	R.LNIVVTLSS.K.R
1805	553.9815	1658.9227	1658.9243	-0.95	0	51	0.00028	1	U	K.IEALIQVILIQEQASK.N
1806	380.4698	1658.9250	1658.9243	0.45	0	(37)	0.0065	1	U	K.IEALIQVILIQEQASK.N
4803	895.7711	2684.2915	2684.2945	-1.10	0	47	0.0012	1	U	K.IYPTDEACPFVDSLEGIHTALR.S

19. [AT1G76010.1](#) Mass: 37417 Score: 91 Matches: 4(4) Sequences: 3(3) eMPII: 0.41
 | Symbols: | Alpha DNA/RNA-binding protein | chr1:28528505-28530488 REVERSE LENGTH=350

Query	Observed	Nt(expt)	Nt(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
190	508,324.40	1014,6334	1014,6325	0.88	0	26	0.019	1	U	K.TVITVELIX.R
192	509,2406	1016,4666	1016,4675	-0.90	0	31	0.016	1	U	R.GYDPPFPGG.R
428	551,7700	1101,5254	1101,5316	-5.62	1	57	6e-005	1	R	R.GYDPPFPGG.R
428	568,1825	1101,5257	1101,5316	-5.34	1	(38)	0.0042	1	R	R.GYDPPFPGG.G

20. [AT2G20450.1](#) Mass: 15497 Score: 87 Matches: 1(1) Sequences: 1(1) emPAI: 0.31
| Symbols: | Ribosomal protein L14 | chr2:8813923-8815071 FORWARD LENGTH=134

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
971	686.3938	1370.7730	1370.7769	-2.82	0	87	7.4e-008	1	U	R.LSGLDIV

AT4G27090.1 **Mass:** 15496 **Score:** 87 **Matches:** 1(1) **Sequences:** 1(1)

Symbols: Ribosomal protein Li4 chr4:13594104-13595187 REVERSE LENGTH=134

21. [ATCG0120_1](#) Mass: 55351 Score: 80 Matches: 2(2) Sequences: 1(1) eMPI: 0.08
 | Symbols: ATPA | ATP synthase subunit alpha | chr9:9938-11461 REVERSE LENGTH=507

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
3680	1137.1115	2272.2081	2272.2137	-2.35	0	(44)	0.0019	1	U	R. SVYPLQQTGLIADSNIP .GIG.G
3681	758.4113	2272.2121	2272.2137	-0.68	0	54	0.00018	1	U	R. SVYPLQQTGLIADSNIP .GIG.G

22. [A7SG56740.1](#) Mass: 52876 Score: 79 Matches: 3(3) Sequences: 2(2) eMPI: 0.17
 | Symbols: HAG2, HAC7, HAG20, HAC07 | histone acetyltransferase of the GNAT family 2 | chr5:22953009-22955577 reverse length=467
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[188](#) 506.2949 1010.5753 1010.5801 -4.67 0 25 0.049 1 U R.IVGPTAIYK.F
[6283](#) 1001.5040 3001.4901 3001.5033 -4.40 1 49 0.00085 1 U K.SALQNIFAETIVDTKDEFLTFSTQR.D
[6284](#) 751.3843 3001.5080 3001.5033 1.58 1 (47) 0.0014 1 U K.SALQNIFAETIVDTKDEFLTFSTQR.D

23.	AT4G21280.1	Mass: 23781	Score: 76	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.19
Symbols: PSBQ, PSBQA, PSBQ-1 photosystem II subunit QA chr4:11334446-11335587 FORWARD LENGTH=223						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique
2655	995.4794	1988.9442	1988.9552	-5.54	0 76	1.3e-006 1 U
						K.VGPPAPSGGLPGTNSDQAR.D

24. [A37G13570.1](#) Mass: 30265 Score: 71 Matches: 3(3) Sequences: 2(2) emPAI: 0.52
 | Symbols: SLC30A, ALC-SLC30A | SC3=like splicing factor 30A | chr3:4429564-4431602 REVERSE LENGTH=262

Query	Observed	Rn(expt)	SC3=like	ppm	Miss	Score	Expect	Rank	Unique	Peptide
704	608.3259	1214.6372	1214.6507	-11.10	0	41	0.0034	1	U	R.DSDLTSLTLVR.N
2243	907.9176	1813.8206	1818.8345	-7.65	0	(32)	0.022	1	U	R.GFGFIQFNDPADAAEAK.H
2101	915.9155	1829.8164	1829.8294	-7.13	0	36	0.0073	1	U	R.GFGFIQFNDPADAAEAK.H

25. [AT4G10340.1](#) Mass: 30195 Score: 69 Matches: 1(1) Sequences: 1(1) emPAI: 0.15
| Symbols: LWCB5 | light harvesting complex of photosystem II 5 | chr4:6408200-6409496 FORWARD LENGTH=280
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
3212 709.0389 2124.0948 2124.0964 -0.73 0 69 6.4e-006 1 U K.H.LSDPFGNNLLTVIAGTAER.A

26. [ATIG07920.1](#) Mass: 49813 Score: 67 Matches: 2(2) Sequences: 2(2) emPAI: 0.19
 | Symbols: | GTP binding Elongation factor Tu family protein | chr1:2455559-2457001 FORWARD LENGTH=449

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3713	760.7119	2279.1137	2279.1330	-8.46	0	57	0.00012	1	K	K.NPTPKFMVVFVESEYPLGFR.F
7638	764.5761	3817.8439	3817.8659	-6.02	0	30	0.059	1	K	K.GAANFYSYLDINNHGQIGNGYAPVLDCSHIAVNF.F

AT1G07930.1	Mass: 49813	Score: 67	Matches: 2(2)	Sequences: 2(2)	
Symbol:	GTP binding Elongation factor Tu family protein chr1:2459014-2460458 FORWARD LENGTH=449				
AT1G07940.1	Mass: 49813	Score: 67	Matches: 2(2)	Sequences: 2(2)	
Symbol:	GTP binding Elongation factor Tu family protein chr1:2463350-2464792 REVERSE LENGTH=449				
AT1G07940.2	Mass: 49813	Score: 67	Matches: 2(2)	Sequences: 2(2)	
Symbol:	GTP binding Elongation factor Tu family protein chr1:2463350-2464792 REVERSE LENGTH=449				
AT5G06390.1	Mass: 49813	Score: 67	Matches: 2(2)	Sequences: 2(2)	
Symbol:	GTP binding Elongation factor Tu family protein chr5:24289226-24290675 FORWARD LENGTH=449				
AT5G06390.3	Mass: 49813	Score: 67	Matches: 2(2)	Sequences: 2(2)	
Symbol:	GTP binding Elongation factor Tu family protein chr5:24289226-24290675 FORWARD LENGTH=449				

27. [ATSG14040.1](#) Mass: 40466 Score: 66 Matches: 2(2) Sequences: 2(2) emPAI: 0.23
 | Symbols: PHT3:1 | phosphate transporter 3:1 | chr5:4531059-4532965 REVERSE LENGTH=375

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
112	435.2054	868.4863	868.4919	-6.45	0	31	0.013	1	U	K.GLAPLNGR.Q
119	497.2788	992.5431	992.5477	-4.64	0	55	0.00011	1	U	K.IGVNGLEFR.TG

28. [A73G44310.1](#) Mass: 38527 Score: 64 Matches: 2(1) Sequences: 2(1) emPAI: 0.12
 | Symbols: NIT1, ATNIT1, NIT1 | nitrilase 1 | chr3:15986901-15988841 FORWARD LENGTH=346

Query	Observed	Nr(expt)	Nr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2285	911.44809	1820.9472	1820.9461	0.62	0	53	0.00028	1	U	K.GAEVLVVFVGGIGGYP.G
2549	914.6462	1930.9167	1930.9286	-6.14	1	27	0.11	1	U	R.FGLAVLGVNNEGRDEFK.R

AT3G44310.3 Mass: 38527 Score: 64 Matches: 2(1) Sequences: 2(1)
| Symbols: NIT1, ATNIT1, NITI | nitrilase 1 | chr3:15986901-15988841 FORWARD LENGTH=346

29. [AT2925670.1](#) Mass: 35108 Score: 64 Matches: 1 Sequences: 1(1) eMPAI: 0.13
 Symbols: | BEST Arabidopsis thaliana protein match is: copper ion binding (TAIR:AT4G32610.1); Has 43784 Blast hits to 26928 proteins in 1799 species: Archaea - 86; Bacteria - 6347; Metazoa - 15971; Fungi - 5398; Plants - 19311
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Uniq Peptide
 2138 595.2926 1784.9560 1784.9560 0.01 .0 .64 2e-905 1 U K.EUAELEALLADPGVAPK.E

Proteins matching the same set of peptides:
[AT2G25670.2](#) Mass: 35108 Score: 64 Matches: 1(1) Sequences: 1(1)
 Symbols: BEST Arabidopsis thaliana protein match is: copper ion binding (TAIR:AT4G32610.1); Has 43784 Blast hits to 26928 proteins in 1799 species: Archae - 86; Bacteria - 6347; Metazoa - 15971; Fungi - 5398; Plants - 1931

30. [AT1G64880.1](#) Mass: 60370 Score: 63 Matches: 2(1) Sequences: 2(1) emPAI: 0.07
| Symbols: | Ribosomal protein S5 family protein | chr1:24105713-24108780 FORWARD LENGTH=515
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1239](#) 492.2190 1473.6351 1473.6444 -6.28 1 24 0.061 1 U R.DNVQGGGGEERER.L
[2227](#) 903.4191 1804.8237 1804.8380 -7.92 0 57 8.6e-005 1 U K.EAFDPNNFANYGVIER.D

31. [AT4G32610.1](#) Mass: 34758 Score: 62 Matches: 1(1) Sequences: 1(1) emPAI: 0.13
| Symbols: | copper ion binding | chr4:15728376-15729897 REVERSE LENGTH=315
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2141](#) 597.3242 1788.9507 1788.9509 -0.14 0 62 3.8e-005 1 U K.ELAELEALLDFGVATK.D

32. [AT3G15730.1](#) Mass: 92246 Score: 61 Matches: 2(1) Sequences: 2(1) emPAI: 0.05
| Symbols: | PLD4LPHAL, PLD | phospholipase D alpha 1 | chr3:5330835-5333474 FORWARD LENGTH=810
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1523](#) 784.8488 1567.6831 1567.6977 -9.31 0 50 0.00028 1 U R.CWEIDPDIAISNAK.W
[7466](#) 1238.2802 3711.8186 3711.7904 7.61 1 29 0.071 1 U R.ATIFVDQVINGEEVDQWVELDNRNPIQGSK.I

33. [ATCG00380.1](#) Mass: 23340 Score: 56 Matches: 2(2) Sequences: 2(2) emPAI: 0.44
| Symbols: | RPS4 | chloroplast ribosomal protein S4 | chrC:45223-45828 REVERSE LENGTH=201
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[124](#) 445.7548 889.4951 889.5021 -7.92 0 37 0.0084 1 U R.LDNILFLR.L
[1519](#) 780.9209 1559.8272 1559.8341 -4.41 0 43 0.0029 1 U K.GSTQVLLQLLEMR.L

34. [AT2G33210.1](#) Mass: 62339 Score: 55 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
| Symbols: | HSP60-2 | heat shock protein 60-2 | chr2:14075093-14078568 REVERSE LENGTH=585
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[76](#) 413.7520 825.4895 825.4960 -7.82 0 55 2.3e-005 1 U K.AGIDPLK.V

Proteins matching the same set of peptides:
[AT2G33210.2](#) Mass: 61781 Score: 55 Matches: 1(1) Sequences: 1(1)
| Symbols: | HSP60-2 | heat shock protein 60-2 | chr2:14075093-14078568 REVERSE LENGTH=580
[AT3G23990.1](#) Mass: 61584 Score: 55 Matches: 1(1) Sequences: 1(1)
| Symbol: | HSP60, HSP60-3B | heat shock protein 60 | chr3:8669013-8672278 FORWARD LENGTH=577

35. [AT4G39260.1](#) Mass: 16626 Score: 55 Matches: 1(1) Sequences: 1(1) emPAI: 0.29
| Symbols: | CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=169
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[921](#) 672.3238 1342.6331 1342.6405 -5.49 0 55 0.0001 1 U R.TFSQSGVDISK.I

Proteins matching the same set of peptides:
[AT4G39260.2](#) Mass: 12856 Score: 55 Matches: 1(1) Sequences: 1(1)
| Symbols: | CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=126
[AT4G39260.3](#) Mass: 10281 Score: 55 Matches: 1(1) Sequences: 1(1)
| Symbols: | CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=92
[AT4G39260.4](#) Mass: 10914 Score: 55 Matches: 1(1) Sequences: 1(1)
| Symbols: | CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=105

36. [AT3G5460.1](#) Mass: 29607 Score: 54 Matches: 2(1) Sequences: 2(1) emPAI: 0.15
| Symbols: | SCL30, At-SCL30 | SC35-like splicing factor 30 | chr3:20561024-20563502 FORWARD LENGTH=262
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1522](#) 781.8404 1561.6662 1561.6757 -6.06 1 47 0.00024 1 U R.GGPPRGEKEDENYSR.R
[2657](#) 996.9562 1991.8978 1991.8901 3.86 0 25 0.13 1 U R.GFAPVFVFDAYDAEAGR.S

37. [AT1G64370.1](#) Mass: 19685 Score: 53 Matches: 2(2) Sequences: 1(1) emPAI: 0.24
| Symbol: | unknown protein; Has 773 Blast hits to 375 proteins in 118 species: Archae - 0; Bacteria - 97; Metazoa - 421; Fungi - 108; Plants - 31; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLINK). | chr1:23888967-238
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[3376](#) 740.9815 2219.9227 2219.9329 -4.58 0 (34) 0.0048 1 U R.NGYQSQSHNHGYQSQSR.G
[3378](#) 555.9886 2219.9253 2219.9329 -3.43 0 34 0.0044 1 U R.NGYQSQSHNHGYQSQSR.G

38. [AT1G45000.1](#) Mass: 44898 Score: 52 Matches: 1(1) Sequences: 1(1) emPAI: 0.10
| Symbols: | AAA-type ATPase family protein | chr1:17009220-17011607 FORWARD LENGTH=399
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2200](#) 900.9835 1799.9524 1799.9491 1.81 0 52 0.00035 1 U R.ESIELPLNNPELFLR.V

Proteins matching the same set of peptides:
[AT1G45000.2](#) Mass: 37720 Score: 52 Matches: 1(1) Sequences: 1(1)
| Symbols: | AAA-type ATPase family protein | chr1:17009220-17011607 FORWARD LENGTH=335
[AT5G43010.1](#) Mass: 44960 Score: 52 Matches: 1(1) Sequences: 1(1)
| Symbols: | RPT4A | regulatory particle triple-A ATPase 4A | chr5:17248563-17251014 REVERSE LENGTH=399

39. [AT2G27710.1](#) Mass: 11437 Score: 51 Matches: 1(1) Sequences: 1(1) emPAI: 0.44
| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=115
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[201](#) 514.7862 1027.5578 1027.5662 -8.16 0 51 0.00023 1 U K.DLAELIAGR.E

Proteins matching the same set of peptides:
[AT2G27710.2](#) Mass: 11437 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=115
[AT2G27710.3](#) Mass: 11437 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=115
[AT2G27710.4](#) Mass: 10237 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=98
[AT2G27720.1](#) Mass: 11445 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=115
[AT2G27720.2](#) Mass: 13137 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=130
[AT2G27720.3](#) Mass: 12757 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=127

40. [AT5G26742.1](#) Mass: 81293 Score: 51 Matches: 1(1) Sequences: 1(1) emPAI: 0.05
| Symbols: | emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540-9288871 REVERSE LENGTH=747
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[154](#) 481.7659 961.5172 961.5233 -6.33 0 51 0.00042 1 U K.IFLIADDR.I

Proteins matching the same set of peptides:
[AT5G26742.2](#) Mass: 81449 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbols: | emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540-9288871 REVERSE LENGTH=748
[AT5G26742.3](#) Mass: 71192 Score: 51 Matches: 1(1) Sequences: 1(1)
| Symbol: | emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540-9288618 REVERSE LENGTH=655

41. [AT3G58510.1](#) Mass: 66327 Score: 50 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
| Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:21640608-21643464 FORWARD LENGTH=612
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1756](#) 546.9747 1637.9022 1637.8889 8.08 0 50 0.00025 1 U K.VVAVYGTFPIHQLR.E

Proteins matching the same set of peptides:
[AT3G58510.2](#) Mass: 66327 Score: 50 Matches: 1(1) Sequences: 1(1)
| Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:21640608-21643464 FORWARD LENGTH=612
[AT3G58510.3](#) Mass: 66327 Score: 50 Matches: 1(1) Sequences: 1(1)
| Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:21640608-21643464 FORWARD LENGTH=612

42. [AT2G23390.1](#) Mass: 54902 Score: 48 Matches: 1(1) Sequences: 1(1) emPAI: 0.08
| Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF482 (InterPro:IPR007434), Acyl-CoA N-acyltransferase (InterPro:IPR016181); Has 2165 Blast hits to 2163 proteins in 543 species: Archae - 0; Bacteria - 104
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2322](#) 613.6451 1837.9134 1837.9131 0.14 0 48 0.0011 1 U K.QVQVDAIVSAMTELAK.L

43. [AT2G19740.1](#) Mass: 13750 Score: 45 Matches: 1(1) Sequences: 1(1) emPAI: 0.35
| Symbols: | Ribosomal protein L31e family protein | chr2:8513577-8514346 FORWARD LENGTH=119
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[8621](#) 1061.5179 3181.5320 3181.5190 4.07 1 45 0.0024 1 U R.NDEDAKEFFSLVTVAIRPAGLSGLTK.V

Proteins matching the same set of peptides:
[AT4G26230.1](#) Mass: 13869 Score: 45 Matches: 1(1) Sequences: 1(1)
| Symbols: | Ribosomal protein L31e family protein | chr4:13286026-13286553 FORWARD LENGTH=119

	AT5G56710.1	Mass: 13852	Score: 45	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.30
	Symbols: Ribosomal protein L31e family protein chr5:22944003-22944767 REVERSE LENGTH=119					
44.	AT2G14880.1	Mass: 16007	Score: 44	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.30
	Symbols: SWIB/MDM2 domain superfamily protein chr2:6393686-6394841 REVERSE LENGTH=141					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	122	438.7606	875.5066	875.5116	-5.73	0 44 0.0011 1 U R.VQFLSIK.L
Proteins matching the same set of peptides:						
	AT4G34290.1	Mass: 16102	Score: 44	Matches: 1(1)	Sequences: 1(1)	
	Symbols: SWIB/MDM2 domain superfamily protein chr4:16410883-16412122 FORWARD LENGTH=144					
45.	AT2G18220.1	Mass: 87591	Score: 44	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
	Symbols: Noc2p family chr2:7928254-7931851 FORWARD LENGTH=764					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	1639	400.2001	1596.7714	1596.7743	-1.80	2 44 0.0021 1 U K.KARAREHEELK.R
46.	AT3G08580.1	Mass: 41563	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
	Symbols: AAC1 ADP/ATP carrier 1 chr3:2605706-2607030 REVERSE LENGTH=381					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	1040	470.2431	1407.7074	1407.7147	-5.17	1 42 0.0034 1 U R.TIKDEGFGSLNR.G
Proteins matching the same set of peptides:						
	AT3G08580.2	Mass: 41563	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols: AAC1 ADP/ATP carrier 1 chr3:2605706-2607030 REVERSE LENGTH=381					
47.	AT3G20250.1	Mass: 107384	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04
	Symbols: APUM5, PUM5 pumilio 5 chr3:7059098-7062660 REVERSE LENGTH=961					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	160	487.2675	972.5205	972.5240	-3.60	0 42 0.0039 1 U K.LELSDIAGR.V
48.	AT4G31580.1	Mass: 22615	Score: 42	Matches: 2(1)	Sequences: 2(1)	emPAI: 0.20
	Symbols: SRZ-22, SRZ22, RSZP22, RSZ22, At-RSZ22 serine/arginine-rich 22 chr4:15306983-15308064 FORWARD LENGTH=200					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	138	469.2134	936.4123	936.4189	-6.97	0 42 0.0016 1 U R.ELEDEFR.A
	1834	560.6060	1678.7962	1678.8103	-8.41	0 16 1.3 1 U R.RPPGYAFLLDFEDPR.D
Proteins matching the same set of peptides:						
	AT4G31580.2	Mass: 22615	Score: 42	Matches: 2(1)	Sequences: 2(1)	
	Symbols: SRZ-22, SRZ22, RSZP22, RSZ22, At-RSZ22 serine/arginine-rich 22 chr4:15306983-15308064 FORWARD LENGTH=200					
49.	AT4G38680.1	Mass: 19484	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.24
	Symbols: GRP2, CSPD2, CSP2, ATCSP2 glycine rich protein 2 chr4:18072240-18072851 REVERSE LENGTH=203					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	3966	794.3777	2380.1112	2380.0972	5.90	0 42 0.0042 1 U K.GPGFITPDGGDGLFVQGSIR.S
50.	AT4G35785.1	Mass: 28213	Score: 41	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.16
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953211-16955127 REVERSE LENGTH=238					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	909	662.8154	1323.6163	1323.6315	-11.50	0 41 0.003 1 U K.VASCFLYMEPR.T
Proteins matching the same set of peptides:						
	AT4G35785.2	Mass: 28369	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953211-16955127 REVERSE LENGTH=239					
	AT4G35785.3	Mass: 24010	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953708-16955127 REVERSE LENGTH=207					
	AT4G35785.4	Mass: 23551	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953404-16955127 REVERSE LENGTH=201					
	AT4G35785.5	Mass: 28546	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953404-16955127 REVERSE LENGTH=244					
51.	AT1G54270.1	Mass: 47075	Score: 41	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
	Symbols: EIF4A-2 eif4a-2 chr1:20260495-20262018 FORWARD LENGTH=412					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	2733	507.7277	2026.8817	2026.8875	-2.90	1 41 0.0024 1 U R.RKDHTVSATHGMDQWTR.D
Proteins matching the same set of peptides:						
	AT1G54270.2	Mass: 46508	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: EIF4A-2 eif4a-2 chr1:20260495-20262018 FORWARD LENGTH=407					
	AT1G72710.1	Mass: 47083	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: DEA(D/H)-box RNA helicase family protein chr1:27378040-27379593 REVERSE LENGTH=414					
	AT3G13920.1	Mass: 46960	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: EIF4A1, RH4, TIF4A1 eukaryotic translation initiation factor 4A1 chr3:4592635-4594128 REVERSE LENGTH=412					
	AT3G13920.2	Mass: 47376	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: EIF4A1, RH4, TIF4A1 eukaryotic translation initiation factor 4A1 chr3:4592586-4594128 REVERSE LENGTH=415					
	AT3G13920.3	Mass: 46014	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: EIF4A1, RH4, TIF4A1 eukaryotic translation initiation factor 4A1 chr3:4592635-4594094 REVERSE LENGTH=402					
	AT3G13920.4	Mass: 46393	Score: 41	Matches: 1(1)	Sequences: 1(1)	
	Symbols: EIF4A1 eukaryotic translation initiation factor 4A1 chr3:4592635-4594128 REVERSE LENGTH=407					
52.	AT5G15200.1	Mass: 23079	Score: 40	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.20
	Symbols: Ribosomal protein S4 chr5:4935124-4936334 REVERSE LENGTH=198					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	275	524.2923	1046.5700	1046.5760	-5.71	0 40 0.0058 1 U R.IFGEALLR.R
Proteins matching the same set of peptides:						
	AT5G15200.2	Mass: 19090	Score: 40	Matches: 1(1)	Sequences: 1(1)	
	Symbols: Ribosomal protein S4 chr5:4935602-4936334 REVERSE LENGTH=156					
	AT5G39850.1	Mass: 23203	Score: 40	Matches: 1(1)	Sequences: 1(1)	
	Symbols: Ribosomal protein S4 chr5:15950053-15951171 FORWARD LENGTH=197					
53.	AT2G09990.1	Mass: 16849	Score: 39	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.28
	Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr2:3781442-3781882 FORWARD LENGTH=146					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	529	571.8597	1141.7049	1141.7111	-5.37	0 39 0.0013 1 U K.IFEPILLGK.H
54.	AT2G04660.1	Mass: 42290	Score: 39	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
	Symbols: Nucleic acid-binding, OB-fold-like protein chr2:16966011-16968866 FORWARD LENGTH=389					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	727	619.7717	1237.5288	1237.5397	-8.84	0 39 0.0022 1 U K.FCSPEDLTNR.L
55.	AT1G04270.1	Mass: 17118	Score: 38	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.28
	Symbols: RPS15 cytosolic ribosomal protein S15 chr1:1141852-1142960 REVERSE LENGTH=152					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	916	446.2299	1335.6680	1335.6783	-7.66	0 38 0.0099 1 U R.EAPQGEKPEPVR.T
Proteins matching the same set of peptides:						
	AT1G04270.2	Mass: 17047	Score: 38	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RPS15 cytosolic ribosomal protein S15 chr1:1141852-1142960 REVERSE LENGTH=151					
56.	AT4G09760.1	Score: 37	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12	
	Symbols: Protein kinase superfamily protein chr4:6148955-6151150 REVERSE LENGTH=346					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	154	481.7659	961.5172	961.5055	12.1	0 37 0.0098 2 U R.IMLINDR.M
Proteins matching the same set of peptides:						
	AT4G09760.2	Score: 37	Matches: 1(1)	Sequences: 1(1)		
	Symbols: Protein kinase superfamily protein chr4:6148955-6151150 REVERSE LENGTH=346					
	AT4G09760.3	Score: 37	Matches: 1(1)	Sequences: 1(1)		
	Symbols: Protein kinase superfamily protein chr4:6149592-6151150 REVERSE LENGTH=255					
57.	AT4G17520.1	Mass: 38882	Score: 37	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
	Symbols: Hyaluronan / mRNA binding family chr4:9771496-9773313 FORWARD LENGTH=360					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	2184	599.9269	1796.7590	1796.7674	-4.66	1 37 0.0031 1 U R.RGSYENGGDGDSEPR.K

ATSG57290.1

Mass: 11913

Score: 37

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.12

| Symbols: | 60S acidic ribosomal protein family | chr5:23207049-23207835 REVERSE LENGTH=120

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

140

472.2362

942.4578

942.4633

-5.88

0

37

0.0032

1

U

M.GVFSVPCK.S

Proteins matching the same set of peptides:

ATSG57290.2

Mass: 8996

Score: 37

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.30

| Symbols: | 60S acidic ribosomal protein family | chr5:23207089-23207835 REVERSE LENGTH=89

ATSG57290.3

Mass: 11814

Score: 37

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.30

| Symbols: | 60S acidic ribosomal protein family | chr5:23207049-23207835 REVERSE LENGTH=119

59.

ATIG69200.1

Mass: 69842

Score: 36

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.06

| Symbols: | FLN2 | fructokinase-like 2 | chr1:26016018-26018365 FORWARD LENGTH=616

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

7633

763.2065

3810.9963

3811.0030

-1.75

2

36

0.0089

1

U

K.VVVKDEPLETSEFLVNDDVDLKEISIVALKPK.K

60.

AT3G09680.1

Mass: 15931

Score: 36

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.30

| Symbols: | Ribosomal protein S12/S23 family protein | chr3:2969197-2970291 REVERSE LENGTH=142

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

521

567.3494

1132.6843

1132.6856

-1.13

0

36

0.0023

1

U

K.VSGVSLALFK.E

Proteins matching the same set of peptides:

ATSG02960.1

Mass: 15840

Score: 36

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.30

| Symbols: | Ribosomal protein S12/S23 family protein | chr5:693280-694396 REVERSE LENGTH=142

61.

AT3G06810.1

Mass: 92282

Score: 35

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.05

| Symbols: | IBR3 | acyl-CoA dehydrogenase-related | chr3:2146534-2150654 FORWARD LENGTH=824

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1837

842.4586

1682.9027

1682.8879

8.79

0

35

0.015

1

U

K.EQISEWLPLLEGR.I

62.

ATCG00800.1

Mass: 25344

Score: 34

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.18

| Symbols: | structural constituent of ribosome | chrC:82826-83482 REVERSE LENGTH=218

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1305

1080.5703

2159.1261

2159.1262

-0.08

0

34

0.019

1

U

R.ISNPYGGPNILAEFIAGQLK.N

63.

AT3G11830.1

Mass: 60195

Score: 34

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.07

| Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732734-3736156 FORWARD LENGTH=557

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

3793

773.0770

2316.2093

2316.1882

9.08

0

34

0.022

1

U

K.INAINAATEAACILLSVDETvk.N

Proteins matching the same set of peptides:

AT3G11830.2

Mass: 59935

Score: 34

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.07

| Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732734-3736156 FORWARD LENGTH=555

64.

AT4G10840.1

Mass: 66866

Score: 34

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.07

| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:6656614-6659033 FORWARD LENGTH=609

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1325

756.9296

1511.8447

1511.8446

0.05

0

34

0.012

1

U

R.EDATEILEQVLK.L

65.

AT3G19390.1

Score: 33

Matches: 2(1)

Sequences: 2(1)

eMPIAI: 0.36

| Symbols: | Ribosomal L29 family protein | chr2:16450803-16451762 REVERSE LENGTH=123

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

66

393.2462

784.4779

784.4807

-3.50

0

30

0.027

1

U

K.AKLALLR.V

151

478.2362

954.4578

954.4633

-5.76

0

26

0.062

1

U

K.ENMYFFIR.K

Proteins matching the same set of peptides:

AT3G09500.1

Score: 33

Matches: 2(1)

Sequences: 2(1)

eMPIAI: 0.36

| Symbols: | Ribosomal L29 family protein | chr3:2917047-2917895 FORWARD LENGTH=123

66.

ATIG29910.1

Mass: 28266

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.16

| Symbols: | CAB3, AB180, LHCB1.2 | chlorophyll A/B binding protein 3 | chr1:10472443-10473246 REVERSE LENGTH=267

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

7172

1211.2684

3630.7835

3630.7617

5.99

0

33

0.029

1

U

R.VAGDGLGEADLLYPGGSPDPLGLATDPEAFARLK.V

Proteins matching the same set of peptides:

ATIG29920.1

Mass: 28266

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.16

| Symbols: | CAB2, AB165, LHCB1.1 | chlorophyll A/B-binding protein 2 | chr1:10475089-10475892 REVERSE LENGTH=267

ATIG29930.1

Mass: 28280

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.16

| Symbols: | CAB1, AB140, CAB140, LHCB1.3 | chlorophyll A/B binding protein 1 | chr1:10478071-10478874 FORWARD LENGTH=267

67.

AT3G34420.1

Mass: 28093

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.16

| Symbols: | LHCB1B2, LHCB1.5 | photosystem II light harvesting complex gene B1B2 | chr2:14522716-14523513 REVERSE LENGTH=265

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

7172

1211.2684

3630.7835

3630.7617

5.98

0

33

0.029

1

U

R.VAGDGLGEADLLYPGGSPDPLGLATDPEAFARLK.V

Proteins matching the same set of peptides:

AT3G34430.1

Mass: 28209

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.16

| Symbols: | LHCB1B1, LHCB1.4 | light-harvesting chlorophyll-protein complex II subunit B1 | chr2:14524818-14525618 FORWARD LENGTH=266

68.

AT3G44300.1

Mass: 37529

Score: 33

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.12

| Symbols: | NIT2, AKNIT2 | nitrilase 2 | chr3:15983351-15985172 FORWARD LENGTH=339

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2316

919.4730

1836.9315

1836.9410

-5.20

0

33

0.034

1

U

K.GSELVVFPPAFIYGPR.G

69.

ATSG15780.1

Mass: 43293

Score: 32

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.10

| Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:5144898-5146297 REVERSE LENGTH=401

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

4871

685.8485

2739.3649

2739.3650

-0.02

0

32

0.038

1

U

K.EPMHLISGALVAVECIDENSKPSFR.Q

70.

ATSG06850.1

Mass: 91629

Score: 32

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.05

| Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:2127200-2129584 REVERSE LENGTH=794

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

519

566.8329

1131.6513

1131.6539

-2.30

0

32

0.018

1

U

R.LISPLSVFEK.R

71.

AT3G29075.1

Mass: 34488

Score: 29

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.13

| Symbols: | glycine-rich protein | chr3:11051645-11052629 REVERSE LENGTH=294

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2575

655.9262

1964.7566

1964.7660

-4.78

1

29

0.0038

1

U

K.EQYKEHHDDDDYDEK.K

72.

AT3G05610.1

Score: 28

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.04

| Symbols: | PLDP2, PDL22, PLDZETA2 | phospholipase D P2 | chr3:1635321-1640105 FORWARD LENGTH=1046

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

134

463.3003

924.5860

924.5684

19.0

0

28

0.0059

1

U

K.IYIILYK.E

73.

ATCG00490.1

Mass: 53435

Score: 28

Matches: 1(0)

Sequences: 1(0)

eMPIAI: 0.47

| Symbols: | RBCL | ribulose-bisphosphate carboxylases | chrC:54958-56397 FORWARD LENGTH=479

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

3668

568.2883

2269.1240

2269.1226

0.59

2

28

0.1

1

U

R.ESTLGFVLLRDDYVEKDR.S

74.

AT3G10950.1

Mass: 10667

Score: 28

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.47

| Symbols: | Zinc-binding ribosomal protein family protein | chr3:3423893-3424566 FORWARD LENGTH=92

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

432

555.7214

1109.4282

1109.4310

-2.58

0

28

0.0086

1

U

K.YFCFCQK.Y

Proteins matching the same set of peptides:

AT3G0245.1

Mass: 10462

Score: 28

Matches: 1(1)

Sequences: 1(1)

eMPIAI: 0.47

| Symbols: | Zinc-binding ribosomal protein family protein | chr3:2226803-22269750 FORWARD LENGTH=92

75.

AT4G13850.1

Mass: 15750

Score: 28

Matches: 1(0)

Sequences: 1(0)

eMPIAI: 0.47

| Symbols: | ATGRP2, GR-RBP2, GRP2 | glycine-rich RNA-binding protein 2 | chr4:8021314-8022065 FORWARD LENGTH=158

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

834

431.8918

1292.6535

1292.6585

-3.88

0

28

0.1

1

U

R.VNPANDRPSAPR.A

Proteins matching the same set of peptides:

[AT4G13850.2](#) Mass: 15464 Score: 28 Matches: 1(0) Sequences: 1(0)
| Symbols: | ATGRP2 | glycine-rich RNA-binding protein 2 | chr4:8021314-8022065 FORWARD LENGTH=153
[AT4G13850.1](#) Mass: 14739 Score: 28 Matches: 1(0) Sequences: 1(0)
| Symbols: | ATGRP2 | glycine-rich RNA-binding protein 2 | chr4:8021314-8022065 FORWARD LENGTH=144

76. [AT1G58400.1](#) Mass: 105437 Score: 26 Matches: 3(0) Sequences: 1(0)
| Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:21696165-21699118 REVERSE LENGTH=900
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2994](#) 1054.5436 2107.0726 2107.0619 5.08 2 26 0.17 1 U R.KYVWQMIQLNLTSTRETK.D
[3072](#) 1055.0413 2108.0680 2108.0459 10.5 2 (16) 1.5 1 U R.KYVWQMIQLNLTSTRETK.D [3073](#)

Proteins matching the same set of peptides:

[AT1G62870.1](#) Mass: 29187 Score: 24 Matches: 1(0) Sequences: 1(0)
| Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256

78. [AT1G28210.1](#) Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.10
| Symbols: | DNAJ heat shock family protein | chr1:9854598-9859884 FORWARD LENGTH=408
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[76](#) 413.7520 825.4895 825.4960 -7.82 0 24 0.034 2 U K.IQLDIPK.G

Proteins matching the same set of peptides:

[AT1G28210.2](#) Score: 24 Matches: 1(1) Sequences: 1(1)
| Symbols: | DNAJ heat shock family protein | chr1:9854598-9859977 FORWARD LENGTH=427

79. [AT5G39500.1](#) Mass: 163675 Score: 24 Matches: 1(0) Sequences: 1(0)
| Symbols: | GNL1, ERM01 | GNOM-like 1 | chr5:15815274-15819910 FORWARD LENGTH=1443
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[4802](#) 895.7480 2684.2221 2684.2309 -3.26 2 24 0.2 1 U R.WSQEAKYSIGETDAMKMLSEDIQK.M

80. [AT5G10940.1](#) Mass: 84804 Score: 23 Matches: 6(0) Sequences: 1(0)
| Symbols: | transducin family protein / WD-40 repeat family protein | chr5:3448890-3454127 REVERSE LENGTH=757
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[695](#) 605.8452 1209.6759 1209.6829 -5.84 2 20 0.24 1 U R.SGAKRALADPPK.Q [650](#) [656](#) [662](#) [671](#) [679](#)

Proteins matching the same set of peptides:

[AT5G10940.2](#) Mass: 84444 Score: 23 Matches: 6(0) Sequences: 1(0)
| Symbols: | transducin family protein / WD-40 repeat family protein | chr5:3448890-3454127 REVERSE LENGTH=754

81. [AT2G40650.1](#) Mass: 43317 Score: 21 Matches: 1(0) Sequences: 1(0)
| Symbols: | PRP38 family protein | chr2:16963588-16965596 REVERSE LENGTH=355
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2460](#) 625.0026 1871.9859 1871.9880 -1.17 0 21 0.43 1 U K.FSLTHVDVIEKLLTK.D

82. [AT1G78950.1](#) Mass: 87923 Score: 21 Matches: 1(0) Sequences: 1(0)
| Symbols: | Terpenoid cyclases family protein | chr1:2968458-29688673 REVERSE LENGTH=759
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[7055](#) 1192.5886 3574.7440 3574.7838 -11.12 2 21 0.55 1 U K.QDPERLHDSVNIILLQSKNGMTAWEPAGAPK.W

83. [AT5G56340.1](#) Mass: 44902 Score: 20 Matches: 1(0) Sequences: 1(0)
| Symbols: | ATCRT1 | RING/U-box superfamily protein | chr5:22818254-22819444 FORWARD LENGTH=396
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[6856](#) 1161.2451 3480.7135 3480.6653 13.8 2 20 0.68 1 U R.DVQDSSTDFGTDRALSNAWILLQAMSSPRR.R

84. [AT1G54740.1](#) Mass: 44317 Score: 17 Matches: 1(0) Sequences: 1(0)
| Symbols: | Protein of unknown function, DUF593 | chr3:20263093-20264466 FORWARD LENGTH=390
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[6060](#) 1462.7022 2923.3897 2923.3514 13.1 1 17 1.4 1 U R.QNKTYVELSANNQMIILGEGSGTR.R

Proteins matching the same set of peptides:

[AT1G54740.2](#) Mass: 49897 Score: 17 Matches: 1(0) Sequences: 1(0)
| Symbols: | Protein of unknown function, DUF593 | chr3:20262949-20264466 FORWARD LENGTH=438

85. [AT2G39435.1](#) Mass: 53281 Score: 16 Matches: 1(0) Sequences: 1(0)
| Symbols: | Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related | chr2:16464806-16466492 REVERSE LENGTH=464
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1005](#) 693.8469 1385.6793 1385.7051 -18.66 2 16 0.98 1 U K.QNQPFRFRQK.E

Proteins matching the same set of peptides:

[AT2G39435.2](#) Mass: 53256 Score: 16 Matches: 1(0) Sequences: 1(0)
| Symbols: | Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related | chr2:16464446-16466492 REVERSE LENGTH=464

86. [AT5G07240.1](#) Mass: 45293 Score: 16 Matches: 1(0) Sequences: 1(0)
| Symbols: | IQD24 | IQ-domain 24 | chr5:2272028-2274051 FORWARD LENGTH=401
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1653](#) 804.3651 1606.7157 1606.7434 -17.28 2 16 0.81 1 U R.GVSDGLDRNQSDKSK.M

87. [AT1G49790.1](#) Mass: 40599 Score: 16 Matches: 1(0) Sequences: 1(0)
| Symbols: | Carbohydrate-binding protein | chr3:18468296-18469396 REVERSE LENGTH=366
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[6054](#) 975.1396 2922.3969 2922.4465 -16.96 2 16 1.8 1 U R.ASRKFPQLNRSSSQDSSQTLTVGSTK.Q

88. [AT3G48730.1](#) Mass: 50452 Score: 15 Matches: 1(0) Sequences: 1(0)
| Symbols: | GSA2 | glutamate-1-semialdehyde 2,1-aminomutase 2 | chr3:18049697-18051550 FORWARD LENGTH=472
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[7114](#) 1197.9266 3590.7581 3590.7241 9.46 1 15 1.9 1 U R.RDIMEKVAPAGPHYQAGTLGONPLANTAGIHTLK.R

Proteins matching the same set of peptides:

[AT5G63570.1](#) Mass: 50737 Score: 15 Matches: 1(0) Sequences: 1(0)
| Symbols: | GSA1 | glutamate-1-semialdehyde-2,1-aminomutase | chr5:25451957-25453620 FORWARD LENGTH=474

89. [AT1G46480.1](#) Mass: 32911 Score: 15 Matches: 1(0) Sequences: 1(0)
| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:17103173-17105594 FORWARD LENGTH=286
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1871](#) 857.9774 1713.9403 1713.9097 17.9 2 15 1.2 1 U K.VHQEALRVCKAIAR.L

Proteins matching the same set of peptides:

[AT1G46500.1](#) Mass: 28913 Score: 15 Matches: 1(0) Sequences: 1(0)
| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:17120793-17122602 FORWARD LENGTH=251

90. [AT2G28620.1](#) Mass: 116835 Score: 15 Matches: 1(0) Sequences: 1(0)
| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12265167-12270020 REVERSE LENGTH=1042
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1875](#) 858.9682 1715.9218 1715.9393 -10.14 1 15 1.4 1 U K.KPLALMEDGGGVFVR.G