

User	:	
Email	:	
Search title	:	
MS data file	:	E:\CAO Jing\20160619_Qe\20160616_SFPX3-.mgf
Database	:	TAIRAraps (35386 sequences; 14482855 residues)
Timestamp	:	19 Jun 2016 at 14:04:07 GMT
Enzyme	:	Trypsin
Fixed modifications	:	Carbamidomethyl (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	:	19674
Protein hits	:	<div><div><div>ATG013320.1</div><div>Symbol: tRNA synthetase class I (I, L, M and V) family protein chr4:6397526-6404509 REVERSE LENGTH=1190</div></div><div><div>ATG245130.1</div><div>Symbol: ATSPX3, SFX3 SFX domain gene 3 chr2:18605489-18607754 FORWARD LENGTH=245</div></div><div><div>ATG525040.1</div><div>Symbol: ATSPF41, RS41, At-RS41 RNA-binding (RRM/RBD/RNP motifs) family protein chr5:21131081-2113318 FORWARD LENGTH=356</div></div><div><div>ATG535200.1</div><div>Symbol: ENTH/ANTH/VHS superfamily protein chr5:13462463-13465581 REVERSE LENGTH=544</div></div><div><div>ATG526710.1</div><div>Symbol: Glutamyl/glutaminyl-tRNA synthetase, class 1c chr5:9305673-9308247 FORWARD LENGTH=719</div></div><div><div>ATG042520.1</div><div>Symbol: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr2:17705382-17708744 FORWARD LENGTH=633</div></div><div><div>ATG502500.1</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>ATG131440.1</div><div>Symbol: GAPC-2, GAPC2 glyceraldehyde-3-phosphate dehydrogenase C2 chr1:4608465-4610494 REVERSE LENGTH=338</div></div><div><div>ATG435630.1</div><div>Symbol: PSAT phosphoserine aminotransferase chr4:16904205-16905497 FORWARD LENGTH=430</div></div><div><div>ATG358570.1</div><div>Symbol: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr3:21657099-21660352 FORWARD LENGTH=646</div></div><div><div>ATG041420.1</div><div>Symbol: GAPC-1, GAPC1 glyceraldehyde-3-phosphate dehydrogenase C subunit 1 chr3:9265477-9266316 REVERSE LENGTH=338</div></div><div><div>ATG358510.1</div><div>Symbol: DEA(D/H)-box RNA helicase family protein chr3:21640608-21643464 FORWARD LENGTH=612</div></div><div><div>ATG120220.1</div><div>Symbol: Alba DNA/RNA-binding protein chr1:7005090-7007285 REVERSE LENGTH=315</div></div><div><div>ATG308590.1</div><div>Symbol: Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent chr3:2608683-2611237 REVERSE LENGTH=560</div></div><div><div>ATG261460.1</div><div>Symbol: ATGRP7, CCR2, GR-RBP7, GRP7 cold, circadian rhythm, and rna binding 2 chr3:9265477-9266316 REVERSE LENGTH=176</div></div><div><div>ATG444310.1</div><div>Symbol: NIT1, ATNIT1, NIT1 nitrilase 1 chr3:15986901-15988841 FORWARD LENGTH=346</div></div><div><div>ATG19480.1</div><div>Symbol: DNA glycosylase superfamily protein chr1:6744520-6746144 FORWARD LENGTH=382</div></div><div><div>ATG107920.1</div><div>Symbol: GTP binding Elongation factor Tu family protein chr1:2455559-2457001 FORWARD LENGTH=449</div></div><div><div>ATG309440.1</div><div>Symbol: Heat shock protein 70 (Hsp 70) family protein chr3:2903434-2905632 REVERSE LENGTH=649</div></div><div><div>ATG357150.1</div><div>Symbol: NAPS7, ACNAP57, CBP5, ACNBP5 homologue of NAPS7 chr3:21154255-21155952 REVERSE LENGTH=565</div></div><div><div>ATG240460.1</div><div>Symbol: Nucleic acid-binding, OB-fold-like protein chr3:16966011-16968666 FORWARD LENGTH=389</div></div><div><div>ATG176010.1</div><div>Symbol: Alba DNA/RNA-binding protein chr1:28528505-28530488 REVERSE LENGTH=350</div></div><div><div>ATG439260.1</div><div>Symbol: CCR1, ATGRP8, GR-RBP8, GRP8 cold, circadian rhythm, and RNA binding 1 chr4:18274166-18274958 REVERSE LENGTH=169</div></div><div><div>ATG312580.1</div><div>Symbol: HSP70, ATHSP57 heat shock protein 70 chr3:3991487-3993689 REVERSE LENGTH=650</div></div><div><div>ATG228000.1</div><div>Symbol: CPN60A, CH-CPN60A, SLP chaperonin-60alpha chr2:11926603-11929184 FORWARD LENGTH=586</div></div><div><div>ATG217430.1</div><div>Symbol: Pyridoxal phosphate (PLP) dependent transferases superfamily protein chr2:766537-7667905 FORWARD LENGTH=422</div></div><div><div>ATG527120.1</div><div>Symbol: NOPS6-like pre RNA processing ribonucleoprotein chr5:9541287-9543684 FORWARD LENGTH=533</div></div><div><div>ATG464880.1</div><div>Symbol: Ribosomal protein S5 family protein chr1:24105713-24108780 FORWARD LENGTH=515</div></div><div><div>ATG43680.1</div><div>Symbol: GRP2, CSBP2, CSF2, ATCSP2 glycine rich protein 2 chr4:18072240-18072851 REVERSE LENGTH=203</div></div><div><div>ATG239730.1</div><div>Symbol: RCA rubisco activase chr2:16570951-16573345 REVERSE LENGTH=474</div></div><div><div>ATG31580.1</div><div>Symbol: RSZ-22, RSZ22, RSZ22, At-RSZ22 serine/arginine-rich 22 chr4:15306983-15308064 FORWARD LENGTH=200</div></div><div><div>ATG323930.1</div><div>Symbol: HSP60, HSP60-3B heat shock protein 60 chr1:8669031-8672278 FORWARD LENGTH=577</div></div><div><div>ATG502490.1</div><div>Symbol: Heat shock protein 70 (Hsp 70) family protein chr5:550296-552565 REVERSE LENGTH=653</div></div><div><div>ATG323450.1</div><div>Symbol: unknown protein: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 14 plant structures; EXPRESSED DURI</div></div><div><div>ATG354520.1</div><div>Symbol: THA3 threonine aldolase 2 chr3:1217397-1219571 REVERSE LENGTH=355</div></div><div><div>ATG537720.1</div><div>Symbol: ALX4 ALX4s family 4 chr5:149805-1498978 REVERSE LENGTH=98</div></div><div><div>ATG156670.1</div><div>Symbol: LOS1 Ribosomal protein S5/elongation factor G/III/V family protein chr1:20968245-20971077 REVERSE LENGTH=843</div></div><div><div>ATG344300.1</div><div>Symbol: NIT2, ACNIT2 nitrilase 2 chr3:15983351-15985172 FORWARD LENGTH=339</div></div><div><div>ATG303530.1</div><div>Symbol: NPC4 non-specific phospholipase C4 chr3:842686-844970 REVERSE LENGTH=538</div></div><div><div>ATG547210.1</div><div>Symbol: Hyaluronan / mRNA binding family chr5:19167022-19171012 REVERSE LENGTH=357</div></div><div><div>ATG175750.1</div><div>Symbol: CAS41 GAST1 protein homolog 1 chr1:28441813-28442284 REVERSE LENGTH=98</div></div><div><div>ATG135720.1</div><div>Symbol: ANNTA1, OXY5, ATOXR5 annexin 1 chr1:13225304-13226939 FORWARD LENGTH=317</div></div><div><div>ATG437800.1</div><div>Symbol: XTH7 xyloglucan endotransglucosylase/hydrolase 7 chr4:1775703-1777732 REVERSE LENGTH=293</div></div><div><div>ATG545490.1</div><div>Symbol: CPN60B, LEN1 chaperonin 60 beta chr1:2071517-20718673 REVERSE LENGTH=600</div></div><div><div>ATG126550.1</div><div>Symbol: FRKP-like peptidyl-prolyl cis-trans isomerase family protein chr1:9171800-9172716 FORWARD LENGTH=142</div></div><div><div>ATG31370.1</div><div>Symbol: SCL10A, At-SCL10A SC35-like splicing factor 30A chr4:1424956-1425116 REVERSE LENGTH=166</div></div><div><div>ATG233410.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr2:14156085-14157435 FORWARD LENGTH=404</div></div><div><div>ATG300490.1</div><div>Symbol: RBCL ribulose-bisphosphate carboxylases chrC:54958-56397 FORWARD LENGTH=479</div></div><div><div>ATG420360.1</div><div>Symbol: ATRABBD, ATRABE1B, RABE1b RAB ATPase homolog E1B chr4:10990036-10991466 FORWARD LENGTH=476</div></div><div><div>ATG315730.1</div><div>Symbol: PLDAB1, PLD1 phospholipase D alpha 1 chr3:5330835-5333474 FORWARD LENGTH=810</div></div><div><div>ATG556740.1</div><div>Symbol: HMG2, HMG7, HMG2, HMG7 histone acetyltransferase of the GMYT family 2 chr5:22953009-22955577 REVERSE LENGTH=467</div></div><div><div>ATG558470.1</div><div>Symbol: TAP15b TBP-associated factor 15B chr5:23638566-23640854 REVERSE LENGTH=422</div></div><div><div>ATG306810.1</div><div>Symbol: IBR3 acyl-CoA dehydrogenase-related chr3:2146534-2150654 FORWARD LENGTH=824</div></div><div><div>ATG141320.1</div><div>Symbol: SAC52, RPL10, RPL10A Ribosomal protein L16p/L10e family protein chr1:4888270-4889408 FORWARD LENGTH=220</div></div><div><div>ATG233210.1</div><div>Symbol: HSP60-2 heat shock protein 60-2 chr2:14075093-14078568 REVERSE LENGTH=585</div></div><div><div>ATG129250.1</div><div>Symbol: Alba DNA/RNA-binding protein chr1:10234631-10234592 REVERSE LENGTH=190</div></div><div><div>ATG352930.1</div><div>Symbol: Aldolase superfamily protein chr3:19627383-19628874 REVERSE LENGTH=358</div></div><div><div>ATG242590.1</div><div>Symbol: RSZ22a, At-RSZ22a RNA recognition motif and CCHC-type zinc finger domains containing protein chr2:10449837-10450860 FORWARD LENGTH=196</div></div><div><div>ATG435785.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:16953211-16955127 REVERSE LENGTH=238</div></div><div><div>ATG166260.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr1:24695895-24697883 REVERSE LENGTH=295</div></div><div><div>ATG18540.1</div><div>Symbol: Ribosomal protein L6 family protein chr1:6377448-6378548 REVERSE LENGTH=233</div></div><div><div>ATG149240.1</div><div>Symbol: ACT8 actin 8 chr1:18216539-18217947 FORWARD LENGTH=377</div></div><div><div>ATG20450.1</div><div>Symbol: Ribosomal protein L14 chr2:8813923-8815071 FORWARD LENGTH=134</div></div><div><div>ATG562690.1</div><div>Symbol: TUB2 tubulin beta chain 2 chr5:25181560-25183501 FORWARD LENGTH=450</div></div><div><div>ATG030380.1</div><div>Symbol: RPS4 chloroplast ribosomal protein S4 chrC:45223-45828 REVERSE LENGTH=201</div></div><div><div>ATG237270.1</div><div>Symbol: RPS19B, RPS19 ribosomal protein S9 chr2:15647883-15649042 REVERSE LENGTH=207</div></div><div><div>ATG421620.1</div><div>Symbol: glycine-rich protein chr4:11491519-11491914 FORWARD LENGTH=131</div></div><div><div>ATG542820.1</div><div>Symbol: ATU2A35B, U2AF35B Zinc finger C-x8-C-x5-C-x3-H-type family protein chr5:17170445-17171296 REVERSE LENGTH=283</div></div><div><div>ATG120620.1</div><div>Symbol: CAT3, SEN2, ATCAT3 catalase 3 chr1:7143142-7146193 FORWARD LENGTH=492</div></div><div><div>ATG164370.1</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: NC</div></div><div><div>ATG509810.1</div><div>Symbol: ACT7 actin 7 chr3:305809-3058249 FORWARD LENGTH=377</div></div><div><div>ATG131020.1</div><div>Symbol: EIF4B2 eukaryotic initiation factor 4B2 chr1:4440927-4443520 REVERSE LENGTH=549</div></div><div><div>ATG344320.1</div><div>Symbol: NIT3, ACNIT3 nitrilase 3 chr3:15993419-15995493 FORWARD LENGTH=346</div></div><div><div>ATG357560.1</div><div>Symbol: NAGK N-acetyl-L-glutamate kinase chr3:21311164-21312207 REVERSE LENGTH=347</div></div><div><div>ATG129910.1</div><div>Symbol: CAB3, ABI80, LHCRL2.1 chlorophyll a/b binding protein 3 chr1:10472434-10473246 REVERSE LENGTH=367</div></div><div><div>ATG234420.1</div><div>Symbol: LHB192, LHCRL5.5 photosystem II light harvesting complex gene B192 chr2:14527116-14523513 REVERSE LENGTH=265</div></div><div><div>ATG436690.1</div><div>Symbol: ATU2A65A U2 snRNP auxiliary factor, large subunit, splicing factor chr4:17294139-17297609 REVERSE LENGTH=573</div></div><div><div>ATG120010.1</div><div>Symbol: TUB5 tubulin beta-5 chain chr1:6938033-6940481 REVERSE LENGTH=449</div></div><div><div>ATG349430.1</div><div>Symbol: SRP34a, SR34a, At-SR34a SER/ARG-rich protein 34A chr3:18332668-18334829 FORWARD LENGTH=300</div></div><div><div>ATG353680.1</div><div>Symbol: Nucleic acid-binding, OB-fold-like protein chr3:13858152-13858589 REVERSE LENGTH=145</div></div><div><div>ATG16790.1</div><div>Symbol: DCP2 decapping 1 family chr5:5517784-5521566 REVERSE LENGTH=200</div></div><div><div>ATG502530.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr5:564332-565776 REVERSE LENGTH=292</div></div><div><div>ATG417520.1</div><div>Symbol: Hyaluronan / mRNA binding family chr4:9771496-9773313 FORWARD LENGTH=360</div></div><div><div>ATG225670.1</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>ATG217360.1</div><div>Symbol: Ribosomal protein S4 (RPS4A) family protein chr2:7546598-7548138 FORWARD LENGTH=261</div></div><div><div>ATG216940.1</div><div>Symbol: Splicing factor, CCI-like chr2:7342869-7347052 REVERSE LENGTH=561</div></div><div><div>ATG165440.1</div><div>Symbol: GTB1 global transcription factor group B1 chr1:24306945-24314327 REVERSE LENGTH=1647</div></div><div><div>ATG45470.1</div><div>Symbol: EIF4A-2 eif4a-2 chr1:20260495-20262018 FORWARD LENGTH=412</div></div><div><div>ATG539570.1</div><div>Symbol: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 14 growth stages;</div></div><div><div>ATG237230.1</div><div>Symbol: RPS19A, RPS19 ribosomal protein S9 chr2:15647883-15649042 REVERSE LENGTH=207</div></div><div><div>ATG421280.1</div><div>Symbol: PSBQ, PSBQA, PSBQ-1 photosystem II subunit QA chr4:11334446-11335587 FORWARD LENGTH=223</div></div><div><div>ATG538420.1</div><div>Symbol: Ribulose biphosphate carboxylase (small chain) family protein chr5:15381203-15381978 REVERSE LENGTH=181</div></div><div><div>ATG424680.1</div><div>Symbol: MOS1 modifier of sncl chr4:12733425-12739737 FORWARD LENGTH=1427</div></div><div><div>ATG326300.1</div><div>Symbol: alpha/beta-Hydrolases superfamily protein chr3:8473833-8475655 FORWARD LENGTH=239</div></div><div><div>ATG558280.1</div><div>Symbol: RPS1 regulatory particle triple-A ATPase 3 chr5:23569155-23571116 FORWARD LENGTH=408</div></div><div><div>ATG308580.1</div><div>Symbol: AAC1 ADP/ATP carrier 1 chr3:2605706-2607030 REVERSE LENGTH=381</div></div><div><div>ATG18020.1</div><div>Symbol: EMB2296 Ribosomal protein L2 family chr2:7837151-7838160 FORWARD LENGTH=258</div></div><div><div>ATG000480.1</div><div>Symbol: ATPB, PB ATP synthase subunit beta chr3:52660-54156 REVERSE LENGTH=498</div></div><div><div>ATG505660.1</div><div>Symbol: NOPS6-like pre RNA processing ribonucleoprotein chr3:1413174-1415564 REVERSE LENGTH=533</div></div><div><div>ATG10340.1</div><div>Symbol: LHCB5 light harvesting complex of photosystem II 5 chr4:6408200-6409496 FORWARD LENGTH=280</div></div><div><div>ATG145000.1</div><div>Symbol: AAA-type ATPase family protein chr1:17009220-17011607 FORWARD LENGTH=399</div></div><div><div>ATG528540.1</div><div>Symbol: BTP1 heat shock protein 70 (Hsp 70) family protein chr5:10540665-10543274 REVERSE LENGTH=669</div></div><div><div>ATG107630.1</div><div>Symbol: emb1473 Ribosomal protein L13 family protein chr1:29575997-29577406 FORWARD LENGTH=241</div></div><div><div>ATG355460.1</div><div>Symbol: SCL30, At-SCL30 SC35-like splicing factor 30 chr3:20561024-20563502 FORWARD LENGTH=262</div></div><div><div>ATG234160.1</div><div>Symbol: Alba DNA/RNA-binding protein chr2:14442681-14472220 FORWARD LENGTH=190</div></div><div><div>ATG565500.1</div><div>Symbol: TCP-1/cpn60 chaperonin family protein chr5:22874058-22876966 FORWARD LENGTH=597</div></div><div><div>ATG260450.1</div><div>Symbol: Nucleic acid-binding, OB-fold-like protein chr2:1574802-1575239 REVERSE LENGTH=145</div></div><div><div>ATG307070.1</div><div>Symbol: Alba DNA/RNA-binding protein chr3:2223001-2225254 REVERSE LENGTH=405</div></div><div><div>ATG489390.1</div><div>Symbol: EMB1080 Nucleic acid-binding, OB-fold-like protein chr3:1814017-18142189 REVERSE LENGTH=160</div></div><div><div>ATG220550.1</div><div>Symbol: DEL SMAD/PKA domain-containing protein chr3:7174695-7177600 REVERSE LENGTH=314</div></div><div><div>ATG513490.1</div><div>Symbol: AAC2 ADP/ATP carrier 2 chr5:4336034-4337379 FORWARD LENGTH=385</div></div><div><div>ATG514040.1</div><div>Symbol: PHT3.1 phosphate transporter 3.1 chr5:4531059-4532965 REVERSE LENGTH=375</div></div><div><div>ATG139650.1</div><div>Symbol: cyclin-related chr3:6823543-6825174 FORWARD LENGTH=302</div></div><div><div>ATG232860.1</div><div>Symbol: SRZ-21, SRZ21, RSZF21, RSZ21, At-RSZ21 RS-containing zinc finger protein 21 chr1:8428091-8429164 REVERSE LENGTH=187</div></div><div><div>ATG232420.1</div><div>Symbol: copper ion binding chr4:15728376-15729897 REVERSE LENGTH=215</div></div><div><div>ATG526742.1</div><div>Symbol: emb1138 DEAD box RNA helicase (RHS) chr5:9285540-9288871 REVERSE LENGTH=747</div></div><div><div>ATG252920.1</div><div>Symbol: RPL15 ribosomal protein L15 chr3:9491268-9492558 REVERSE LENGTH=277</div></div><div><div>ATG116610.1</div><div>Symbol: SR45, RNPS1 arginine/serine-rich 45 chr1:5675925-5678686 REVERSE LENGTH=414</div></div><div><div>ATG313860.1</div><div>Symbol: HSP60-3A heat shock protein 60-3A chr3:4561704-4565133 REVERSE LENGTH=572</div></div><div><div>ATG565130.1</div><div>Symbol: NOPS6-like pre RNA processing ribonucleoprotein chr3:2084544-20846693 REVERSE LENGTH=522</div></div><div><div>ATG555310.1</div><div>Symbol: SR33, ATSC133, SCL33, At-SCL33 SC35-like splicing factor 33 chr1:20630676-20632695 FORWARD LENGTH=287</div></div><div><div>ATG000120.1</div><div>Symbol: ATPA ATP synthase subunit alpha chrC:9938-11461 REVERSE LENGTH=507</div></div><div><div>ATG167090.1</div><div>Symbol: RBCS1A ribulose biphosphate carboxylase small chain 1A chr1:25048465-25049249 REVERSE LENGTH=180</div></div><div><div>ATG238540.1</div><div>Symbol: LPL, LTP1, ATLTP1 lipid transfer protein 1 chr2:16130418-16130893 FORWARD LENGTH=118</div></div><div><div>ATG233070.1</div><div>Symbol: Thiamine pyrophosphatase dependent pyruvate decarboxylase family protein chr4:15952519-15954676 REVERSE LENGTH=607</div></div><div><div>ATG304840.1</div><div>Symbol: Ribosomal protein S3Ac chr3:1329751-1331418 FORWARD LENGTH=262</div></div><div><div>ATG54410.1</div><div>Symbol: dehydrin family protein chr1:20310305-20310601 REVERSE LENGTH=98</div></div><div><div>ATG559950.1</div><div>Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr5:24140235-24141504 FORWARD LENGTH=244</div></div><div><div>ATG431700.1</div><div>Symbol: RPS6, RPS6A Ribosomal protein S6 chr1:15436306-15437714 REVERSE LENGTH=250</div></div><div><div>ATG238550.1</div><div>Symbol: NOPS6-like pre RNA processing ribonucleoprotein (PEARL 4) family chr4:1802586-18028546 FORWARD LENGTH=612</div></div><div><div>ATG535440.1</div><div>Symbol: unknown protein: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth</div></div><div><div>ATG126110.1</div><div>Symbol: DCP5 decapping 5 chr1:9024616-9027556 REVERSE LENGTH=611</div></div><div><div>ATG158380.1</div><div>Symbol: XM6 Ribosomal protein S5 family protein chr1:21689115-21690085 FORWARD LENGTH=284</div></div><div><div>ATG111830.1</div><div>Symbol: TCP-1/cpn60 chaperonin family protein chr3:3732734-3736156 FORWARD LENGTH=557</div></div><div><div>ATG564200.1</div><div>Symbol: RPS24, SC35, At-SC35 ortholog of human splicing factor SC35 chr5:25681849-25683553 REVERSE LENGTH=303</div></div><div><div>ATG131970.1</div><div>Symbol: STR81 DEA(D/H)-box RNA helicase family protein chr1:11479921-11482707 FORWARD LENGTH=537</div></div><div><div>ATG000800.1</div><div>Symbol: structural constituent of ribosome chrC:82826-83482 REVERSE LENGTH=218</div></div><div><div>ATG560400.1</div><div>Symbol: PSAN photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) chr5:25628724-25629409 REVERSE LENGTH=711</div></div><div><div>ATG506850.1</div><div>Symbol: C2 calcium/lipid-binding plant phospholipid-transferase family protein chr5:2127200-2129584 REVERSE LENGTH=794</div></div><div><div>ATG000160.1</div><div>Symbol: RPS2 ribosomal protein S2 chr1:150131-15729 REVERSE LENGTH=236</div></div><div><div>ATG131330.1</div><div>Symbol: PSAF photosystem I subunit F chr1:11215011-11215939 REVERSE LENGTH=221</div></div><div><div>ATG305670.1</div><div>Symbol: UI-70K, UISNRNP UI small nuclear ribonucleoprotein-70K chr3:18826476-18829492 REVERSE LENGTH=427</div></div><div><div>ATG000820.1</div><div>Symbol: RPS19 ribosomal protein S19 chrC:84005-84283 REVERSE LENGTH=92</div></div><div><div>ATG202220.1</div><div>Symbol: unknown protein: DUF2039 (InterPro:IPR019351); Has 215 Blast hits to 215 proteins in 94 species: Archae - 2; Bacteria - 2; Meta</div></div><div><div>ATG148920.1</div><div>Symbol: NTCU1-L1, PARL1, NUC-L1 nucleolin like 1 chr1:18098186-18101422 FORWARD LENGTH=557</div></div><div><div>ATG312390.1</div><div>Symbol: Nascent polypeptide-associated complex (NAC), alpha subunit family protein chr3:3942344-3943595 FORWARD LENGTH=203</div></div></div>

AT3G44690.1	Symbol: unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 295
AT2G27710.1	Symbol: 6Ss acidic ribosomal protein family chr2:11816929-1817670 FORWARD LENGTH=115
AT1G03070.1	Symbol: SRC2, [AT]SRC2 soybean gene regulated by cold-2 chr1:2927767-2928741 FORWARD LENGTH=324
AT3G24100.1	Symbol: Uncharacterised protein family SERF chr3:8703373-8704045 FORWARD LENGTH=69
AT2G31610.1	Symbol: Ribosomal protein S3 family protein chr2:13450384-13451669 FORWARD LENGTH=250
AT3G26060.1	Symbol: ATPRX Q Thioredoxin superfamily protein chr3:9524807-9526123 FORWARD LENGTH=216
AT1G29150.1	Symbol: ATPase 1 non-ATPase subfamily 9 chr3:10181240-10182499 FORWARD LENGTH=419
AT5G57370.1	Symbol: unknown protein: CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1777 (InterPro:IPR013957); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1
AT4G28990.1	Symbol: RNA-binding protein-related chr4:14291205-14293018 FORWARD LENGTH=347
AT5G52870.1	Symbol: PDLPH2 phospholipase D alpha 2 chr1:19583940-19586551 REVERSE LENGTH=810
AT1G02840.1	Symbol: SR1, ATRSP14, SRP34, SR34, AT-SR34 RNA-binding (RRM/RBD/RNP motifs) family protein chr1:626918-629583 FORWARD LENGTH=303
AT3G16160.1	Symbol: Ribosomal protein S11 family protein chr2:15169925-15171159 FORWARD LENGTH=150
AT1G12900.1	Symbol: GAPA-2 glyceraldehyde 3-phosphate dehydrogenase A subunit 2 chr1:4392634-4394283 REVERSE LENGTH=399
AT1G71080.1	Symbol: RNA polymerase II transcription elongation factor chr1:26809987-26811645 REVERSE LENGTH=326
ATCG00020.1	Symbol: PSBA photosystem II reaction center protein A chr3:383-1444 REVERSE LENGTH=353
ATCG00770.1	Symbol: RPS8 ribosomal protein S8 chr3:80068-80474 REVERSE LENGTH=134
AT3G05330.1	Symbol: PSFA, ATRS2 regulatory particle subunit-A ATPase 5A chr3:16033540-1605993 FORWARD LENGTH=424
AT1G07840.1	Symbol: Ssa10/Utp3/C1D family chr1:2424603-2424625 FORWARD LENGTH=312
AT2G38530.1	Symbol: LTP2, LP2, cdf3 lipid transfer protein 2 chr2:16128481-16128948 FORWARD LENGTH=118
AT3G13460.1	Symbol: ECT2 evolutionarily conserved C-terminal region 2 chr3:4385274-4388220 REVERSE LENGTH=667
AT3G60770.1	Symbol: Ribosomal protein S13/S15 chr3:22460525-22461656 REVERSE LENGTH=151
AT3G09630.1	Symbol: Ribosomal protein L4/L1 family chr3:2953813-2955444 FORWARD LENGTH=406
AT2G39390.1	Symbol: Ribosomal L29 family protein chr2:16450803-16451762 REVERSE LENGTH=123
AT4G00100.1	Symbol: ATRPS13A, RPS13, PFL2, RPS13A ribosomal protein S13A chr4:37172-38123 FORWARD LENGTH=151
AT1G70200.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr1:26432514-26434351 REVERSE LENGTH=538
AT3G63400.1	Symbol: Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein chr3:23412449-23415435 FORWARD LENGTH=570
AT3G1890.1	Symbol: ATRAP, RAP RNA-binding (RRM/RBD/RNP motifs) family protein chr2:11557100-11559715 REVERSE LENGTH=871
AT3G22310.1	Symbol: PMH1, ATRH9 putative mitochondrial RNA helicase 1 chr3:7887382-7889806 FORWARD LENGTH=610
AT3G1860.1	Symbol: ATRSP31, RSP31, AT-RS31, RS31 RNA-binding (RRM/RBD/RNP motifs) family protein chr3:22900311-22902159 REVERSE LENGTH=264
AT3G62530.1	Symbol: ARM repeat superfamily protein chr3:23132219-23133121 FORWARD LENGTH=221
AT1G04820.1	Symbol: TUA4, TOR2 tubulin alpha-4 chain chr1:1356421-1358266 REVERSE LENGTH=450
AT3G13480.1	Symbol: COX6B, beta subunit chr1:15264145-15267384 FORWARD LENGTH=948
AT5G62190.1	Symbol: PRH75 DEAD box RNA helicase (PRH75) chr5:24980542-24983879 REVERSE LENGTH=671
AT3G14310.1	Symbol: ATPME3, PME3 pectin methylesterase 3 chr3:4772214-4775095 REVERSE LENGTH=592
AT4G14300.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr4:8231179-8232785 FORWARD LENGTH=411
AT3G53500.1	Symbol: RS232, RS2232, AT-RS23 RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain chr3:19834557-19835896 REVERSE LENGTH=243
AT4G34460.1	Symbol: ATRSP10, RSP10 RNA-binding (RRM/RBD/RNP motifs) family protein chr1:4377987-14382624 FORWARD LENGTH=495
AT3G64420.1	Symbol: ATR2-1A RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain chr3:9671953-9673055 FORWARD LENGTH=245
AT3G45030.1	Symbol: Ribosomal protein S10p/S20e family protein chr3:16471606-16472312 REVERSE LENGTH=124
AT3G02080.1	Symbol: Ribosomal protein S19e family protein chr3:364138-365161 REVERSE LENGTH=143
AT1G29320.1	Symbol: Transducin/MD40 repeat-like superfamily protein chr1:10255355-10258218 FORWARD LENGTH=468
AT1G04580.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain chr1:22340089-22342148 FORWARD LENGTH=292
AT1G29030.1	Symbol: Apoptosis inhibitory protein 5 (API5) chr1:10129201-10133697 REVERSE LENGTH=556
AT5G27850.1	Symbol: Ribosomal protein L18e/L15 superfamily protein chr5:9873169-9874297 FORWARD LENGTH=187
AT4G2710.1	Symbol: unknown protein: Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI)
AT1G22780.1	Symbol: PFL, RPS18A, PFL1 Ribosomal protein S13/S18 family chr1:8067990-8069163 FORWARD LENGTH=152
AT5G39980.1	Symbol: Tetratricopeptide repeat (TPR)-like superfamily protein chr3:1601011-16003072 REVERSE LENGTH=678
AT3G15350.1	Symbol: Legume lectin family protein chr3:5174603-5175418 REVERSE LENGTH=271
AT2G39460.1	Symbol: ATRPL23A, RPL23A, RPL23AA ribosomal protein L23AA chr2:16475049-16475904 FORWARD LENGTH=154
AT1G19870.1	Symbol: Iqg32 IQ-domain 32 chr1:6895400-6898539 REVERSE LENGTH=794
AT2G07690.1	Symbol: ATPase, P1 complex, alpha subunit protein chr2:3361474-3364028 FORWARD LENGTH=777
AT5G15200.1	Symbol: Ribosomal protein S4 chr3:4935124-4936334 REVERSE LENGTH=198
AT3G58660.1	Symbol: Ribosomal protein L1p/L10e family chr3:21701574-21702814 FORWARD LENGTH=446
AT1G13950.1	Symbol: E1F-5A, ELF5A-1, ATRF5A-1, E1F5A eukaryotic elongation factor 5A-1 chr1:4773631-4774668 FORWARD LENGTH=158
AT5G15230.1	Symbol: GAS4 GASTI protein homolog 4 chr5:4945017-4946025 FORWARD LENGTH=106
AT2G38140.1	Symbol: PSR84 plastid-specific ribosomal protein 4 chr1:15880948-15981459 FORWARD LENGTH=118
AT5G2980.1	Symbol: TRAP-like family protein chr5:9208747-9210043 FORWARD LENGTH=350
AT3G23880.1	Symbol: BLI, KOS1 BLISTER chr1:8662818-8667440 REVERSE LENGTH=714
AT3G56880.1	Symbol: Ribosomal protein L21 chr1:13208777-13210246 FORWARD LENGTH=220
AT2G03680.1	Symbol: SPRI, SKU6 spirali chr2:1121398-1121850 FORWARD LENGTH=119
AT2G18040.1	Symbol: PIN1AT peptidylprolyl cis/trans isomerase, NIMA-interacting 1 chr2:7842346-7843537 FORWARD LENGTH=119
AT2G4400.1	Symbol: CRF1-interacting co-repressor CTR, N-terminal-Pro-ARM helical domain chr2:18276302-18278240 FORWARD LENGTH=493
AT1G07320.1	Symbol: RPL4 ribosomal protein L4 chr1:2249190-2250189 FORWARD LENGTH=282
AT2G23390.1	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 species
AT2G29560.1	Symbol: ENOC cytosolic enolase chr2:12646635-12649694 FORWARD LENGTH=475
AT2G01350.1	Symbol: Ribosomal protein L10/L7 family protein chr2:132943-134264 REVERSE LENGTH=242
AT5G6900.1	Symbol: DEAD/DEAD-box RNA helicase family protein chr5:26358328-26361244 FORWARD LENGTH=633
AT3G27830.1	Symbol: RPL12-A, RPL12 ribosomal protein L12-A chr3:10318576-10319151 FORWARD LENGTH=191
AT5G09510.1	Symbol: Ribosomal protein S19 family protein chr5:2955698-2956554 REVERSE LENGTH=152
AT5G23080.1	Symbol: TGH SNAP (Suppressor-of-White-Apricot)/surp domain-containing protein chr5:7743226-7748889 REVERSE LENGTH=930
AT2G01430.1	Symbol: AAA-type ATPase family protein chr2:8692736-8694837 FORWARD LENGTH=443
AT1G22300.1	Symbol: RPL10, RPL10B, RPL10A general regulatory factor 10 chr1:7879146-7881103 REVERSE LENGTH=254
ATCG00650.1	Symbol: RPS18 ribosomal protein S18 chr3:67917-68222 FORWARD LENGTH=101
AT4G19410.1	Symbol: Pectinacetylase family protein chr4:10582188-10584766 REVERSE LENGTH=391
AT5G05210.1	Symbol: Surfeit locus protein 6 chr5:1548198-1549534 FORWARD LENGTH=386
AT5G3560.1	Symbol: Tetratricopeptide repeat (TPR)-like superfamily protein chr5:900673-902719 REVERSE LENGTH=241
AT1G59610.1	Symbol: DCL2, CPT, DCL2B, DCL2 dynam-like 3 chr1:2192413-2190780 FORWARD LENGTH=200
AT5G10320.1	Symbol: unknown protein: Has 54 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK)
AT4G36500.1	Symbol: unknown protein: FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED During: 13
AT5G45775.1	Symbol: Ribosomal L5P family protein chr5:18565281-18566377 REVERSE LENGTH=172
AT5G60790.1	Symbol: ATGCN1, GCN1 ACR transporter family protein chr3:24453760-24455767 REVERSE LENGTH=595
AT5G04880.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain chr5:1192461-1195413 FORWARD LENGTH=310
AT3G09680.1	Symbol: Ribosomal protein S12/S23 family protein chr3:2969197-2970291 REVERSE LENGTH=142
AT5G40490.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr5:16225483-16227423 FORWARD LENGTH=423
AT5G17920.1	Symbol: ATCMS, ATMTS, ATMS1 Cobalamin-independent synthase family protein chr5:5935771-5939195 FORWARD LENGTH=765
AT3G54960.1	Symbol: ATPD11L-3, PD11, ATPD11, PD11L-3 PD1-like 1-3 chr3:20363514-20366822 REVERSE LENGTH=579
AT5G16470.1	Symbol: zinc finger (CH2 type) family protein chr5:5795916-5797490 FORWARD LENGTH=104
AT3G06560.1	Symbol: PAP83 poly(A) polymerase 3 chr3:2044443-2047034 FORWARD LENGTH=507
AT1G61520.1	Symbol: LHC43 photosystem I light harvesting complex gene 3 chr1:22700152-22701149 FORWARD LENGTH=273
AT1G60130.1	Symbol: Mannose-binding lectin superfamily protein chr1:22174179-22176321 FORWARD LENGTH=600
AT3G56990.1	Symbol: EAD7 embryo sac development arrest 7 chr3:21088358-21091976 REVERSE LENGTH=711
AT1G30420.1	Symbol: ATRP12, MRP12, ARP12 multidrug resistance-associated protein 12 chr1:1074816-10756316 FORWARD LENGTH=1495
AT1G69510.1	Symbol: cAMP-regulated phosphoprotein 19-related protein chr1:26126779-26127725 FORWARD LENGTH=137
AT5G43960.1	Symbol: Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain chr5:17689154-17691653 REVERSE LENGTH=450
AT3G28850.1	Symbol: Glutaredoxin family protein chr3:10848669-10849955 REVERSE LENGTH=428
AT3G53740.1	Symbol: Ribosomal protein L16e family protein chr1:19913921-19914813 REVERSE LENGTH=103
AT4G13850.1	Symbol: ATRP1, GR-RBP2, CRP2 glycine-rich RNA-binding protein 2 chr4:8021314-80221446 FORWARD LENGTH=158
AT1G04480.1	Symbol: Ribosomal protein L14p/L23e family protein chr1:1216110-1217257 FORWARD LENGTH=140
AT3G54230.1	Symbol: SUA suppressor of ab13-5 chr3:20073872-20080142 FORWARD LENGTH=1007
AT1G75350.1	Symbol: emb2184 ribosomal protein L31 chr1:28272163-28272687 FORWARD LENGTH=144
AT4G34370.1	Symbol: THY-2 thymidylate synthase 2 chr4:16511129-16514110 REVERSE LENGTH=565
AT2G47470.1	Symbol: ATPD12-1, UNP5, MEK10, ATPD12 thiodoxin family protein chr2:19481503-19483683 FORWARD LENGTH=361
AT3G56240.1	Symbol: CCH copper chaperone chr3:20863460-20864402 REVERSE LENGTH=121
AT1G58400.1	Symbol: Disease resistance protein (CC-NBS-LRR class) family chr1:21696165-21699118 REVERSE LENGTH=900
AT1G11430.1	Symbol: plastid developmental protein DAG, putative chr1:3847273-3848938 FORWARD LENGTH=232
AT1G16210.1	Symbol: unknown protein: CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1014 (InterPro:IPR010422); Has 16107 Blast hits to 8386 proteins in 1107 species: Archae - 26; Bacteria - 3
AT3G26580.1	Symbol: Tetratricopeptide repeat (TPR)-like superfamily protein chr3:2293217-22933619 FORWARD LENGTH=350
AT1G43170.1	Symbol: ARP1, emb2207, RPL3A, RPL1 ribosomal protein 1 chr1:16266992-16268631 FORWARD LENGTH=389
AT3G08940.1	Symbol: LHC84.2 light harvesting complex photosystem II chr3:2717717-2718400 FORWARD LENGTH=227
AT5G01530.1	Symbol: LHC84.1 light harvesting complex photosystem II chr3:209084-210243 FORWARD LENGTH=290
AT1G79850.1	Symbol: RPS17, CS17, RPS17 ribosomal protein S17 chr1:30041473-30041922 REVERSE LENGTH=149
AT4G22560.1	Symbol: ENTH/VMS/GAT family protein chr1:15799796-15803832 FORWARD LENGTH=675
AT5G14650.1	Symbol: Pectin lyase-like superfamily protein chr5:4724509-4726328 FORWARD LENGTH=435
AT4G10840.1	Symbol: Tetratricopeptide repeat (TPR)-like superfamily protein chr4:6656614-6659033 FORWARD LENGTH=609
AT3G17040.1	Symbol: HCF107 high chlorophyll fluorescent 107 chr3:5809378-5812605 REVERSE LENGTH=652
AT5G46020.1	Symbol: CONTAINS InterPro DOMAIN/s: Casein kinase substrate, phosphoprotein PP28 (InterPro:IPR019380); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Met
AT2G42680.1	Symbol: RPS14A, ATRP14 ribosomal protein L14 chr1:11324262-11327412 FORWARD LENGTH=142
AT5G45520.1	Symbol: Leucine-rich repeat (LRR) family protein chr5:18449509-18453012 REVERSE LENGTH=1167
AT1G15210.1	Symbol: PDY7, ATPD7 pleiotropic drug resistance 7 chr1:5231552-5236573 REVERSE LENGTH=1442
AT2G34480.1	Symbol: Ribosomal protein L18a/LX family protein chr2:14532916-14534611 REVERSE LENGTH=178
AT5G37030.1	Symbol: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr5:14634614-14636939 REVERSE LENGTH=638
AT5G5860.1	Symbol: GNC, CAT21 GATA type zinc finger transcription factor family protein chr2:22989630-22991351 REVERSE LENGTH=398
AT5G20290.1	Symbol: Ribosomal protein S8e family protein chr5:6851695-6853012 REVERSE LENGTH=222
AT1G70310.1	Symbol: SPDS2 spermidine synthase 2 chr1:26485497-26487352 REVERSE LENGTH=340
AT1G75280.1	Symbol: NmrA-like negative transcriptional regulator family protein chr1:28252030-28253355 FORWARD LENGTH=310
AT1G20230.1	Symbol: Pentatricopeptide repeat (PPR) superfamily protein chr1:7009570-7011852 FORWARD LENGTH=760
AT1G08260.1	Symbol: RML42, RML234, POLA1, TTI1, RML529, ARD4, EST1 DNA polymerase epsilon catalytic subunit chr1:2590944-2606892 FORWARD LENGTH=2161
AT3G10950.1	Symbol: Zinc-binding ribosomal protein family protein chr3:3423893-3424566 FORWARD LENGTH=92
AT3G60040.1	Symbol: F-box family protein chr3:22175937-22179728 REVERSE LENGTH=838
AT3G25520.1	Symbol: ATL5, PGV3, OLI5, RPL5A ribosomal protein L5 chr3:9269573-9271327 REVERSE LENGTH=301
AT3G04230.1	Symbol: Ribosomal protein S5 domain 2-like superfamily protein chr3:1113169-1113609 REVERSE LENGTH=146
AT4G30993.1	Symbol: Calceurin-like metallo-phosphoesterase superfamily protein chr4:15098201-15099422 FORWARD LENGTH=209
AT1G20440.1	Symbol: COR47, RD17, ATCOR47 cold-regulated 47 chr1:7084722-7085664 REVERSE LENGTH=265
AT4G08570.1	Symbol: Heavy metal transport/detoxification superfamily protein chr4:5455123-5455975 REVERSE LENGTH=150
AT3G13860.1	Symbol: ATRP84, RPS84 ribosomal protein L8 chr1:11324262-11327412 FORWARD LENGTH=705
AT5G5670.1	Symbol: RNA-binding (RRM/RBD/RNP motifs) family protein chr3:22544669-22546801 REVERSE LENGTH=710
AT1G17880.1	Symbol: BTTF3, ATBTTF3 basic transcription factor 3 chr1:6152572-6153425 REVERSE LENGTH=165
AT1G15270.1	Symbol: Translation machinery associated TMA7 chr1:5250833-5252020 REVERSE LENGTH=64
AT1G20020.1	Symbol: ATPFN22, FNR2 ferredoxin-NADP(+) -oxidoreductase 2 chr1:6942851-6944868 FORWARD LENGTH=369
AT5G41710.1	Symbol: ENTH/VMS family protein chr5:3729234-373765 FORWARD LENGTH=560
AT4G23440.1	Symbol: FtsH extracellular protease family chr4:12437108-12441841 FORWARD LENGTH=946
AT2G34350.1	Symbol: Scorpion toxin-like knottin superfamily protein chr2:18073263-18073651 FORWARD LENGTH=103
AT1G72370.1	Symbol: P40, AP40, RP40, RPSAA 40s ribosomal protein SA chr1:27243148-27244842 REVERSE LENGTH=298
AT1G27400.1	Symbol: Ribosomal protein L22e/L27e family protein chr1:9515230-9516725 FORWARD LENGTH=176
AT3G24530.1	Symbol: PPR8 family protein chr1:6969388-6969596 REVERSE LENGTH=355
AT3G13880.1	Symbol: AK-LYS1, AKL1, AK aspartate kinase 1 chr5:4249516-4252654 FORWARD LENGTH=569
AT1G6090.1	Symbol: U2 snRNP auxiliary factor, large subunit, splicing factor chr1:22424008-22427806 FORWARD LENGTH=589
AT1G08360.1	Symbol: Ribosomal protein L1p/L10e family chr1:2636231-2637694 FORWARD LENGTH=216
AT1G01490.1	Symbol: Heavy metal transport/detoxification superfamily protein chr1:180401-182066 REVERSE LENGTH=177
AT4G24820.1	Symbol: 26S proteasome, regulatory subunit Rpn7/Proteasome component (PCI) domain chr4:12790471-12792599 REVERSE LENGTH=387
AT1G11860.1	Symbol: Glycine cleavage T-protein family protein chr1:1801401245-18014245 FORWARD LENGTH=408
AT5G54900.1	Symbol: ATRBP45A, RBP45A RNA-binding protein 45A chr5:22295412-22298126 FORWARD LENGTH=387
AT4G04460.1	Symbol: Saposin-like aspartyl protease family protein chr4:2225232-2227746 FORWARD LENGTH=504
AT4G34620.1	Symbol: SR16 small subunit ribosomal protein 16 chr4:16535084-16536092 REVERSE LENGTH=113
AT1G05190.1	Symbol: emb2394 Ribosomal protein L6 family chr1:1502515-1503738 REVERSE LENGTH=223
AT2G5080.1	Symbol: SET domain-containing protein chr1:20411476-20414593 REVERSE LENGTH=353
AT3G29975.1	Symbol: glycine-rich protein chr3:11051645-11052629 REVERSE LENGTH=294
AT3G49990.1	Symbol: unknown protein: Has 1524 Blast hits to 1298 proteins in 225 species: Archae - 9; Bacteria - 84; Metazoa - 474; Fungi - 184; Plants - 98; Viruses - 17; Other Eukaryotes - 658 (source: NCBI)
AT1G18160.1	Symbol: Protein kinase superfamily protein chr1:6249126-6253835 FORWARD LENGTH=992
AT4G26590.1	Symbol: ATRPT5, OPT5 oligopeptide transporter 5 chr4:13414134-13416850 REVERSE LENGTH=753
AT4G29270.1	Symbol: HD superfamily, subfamily I1B acid phosphatase chr4:14421797-14424848 REVERSE LENGTH=256
AT3G22080.1	Symbol: TRAP-Like family protein chr3:7777818-7781718 REVERSE LENGTH=648
AT3G62330.1	Symbol: Zinc knuckle (CCHC-type) family protein chr3:23063329-23065419 REVERSE LENGTH=479
AT2G32460.1	Symbol: MYB101, ATMYB101, ATM1 myb domain protein 101 chr2:13782419-13784363 REVERSE LENGTH=490
AT5G10940.1	Symbol: transducin family protein / WD-40 repeat family protein chr5:3448890-3454127 REVERSE LENGTH=757
AT1G07890.1	Symbol: APX1, ME6E, CS1, ATAPX1, ATAPX01 ascorbate peroxidase 1 chr1:2438005-2439435 FORWARD LENGTH=250

AT2047640.1	Symbols:	Small nuclear ribonucleoprotein family protein chr2:19537393-19538431 FORWARD LENGTH=109
AT2047640.1	Symbols:	U-box domain-containing protein kinase family protein chr4:12903360-12906659 REVERSE LENGTH=835
AT4262150.1	Symbols:	SESA2, AT252 seed storage albumin 2 chr4:13609396-13609908 FORWARD LENGTH=170
AT5267040.1	Symbols:	Protein of unknown function (DUF295) chr5:26757896-26758475 REVERSE LENGTH=165
AT1021610.1	Symbols:	wound-responsive family protein chr1:7574104-7578643 FORWARD LENGTH=684
AT3051880.1	Symbols:	HMGBl, NF01 high mobility group B1 chr3:19247241-19248491 REVERSE LENGTH=178
AT2647000.1	Symbols:	MDR4, FGF4, ABCB4, ATP6F4 ATP binding cassette subfamily B4 chr2:19310008-19314750 REVERSE LENGTH=1286
AT4262480.1	Symbols:	cpHsc70-1 chloroplast heat shock protein 70-1 chr4:12590094-12593437 FORWARD LENGTH=718
AT1271100.1	Symbols:	Actin cross-linking protein chr1:9407557-9411074 REVERSE LENGTH=519
AT3061690.1	Symbols:	nucleotidyltransferases chr3:22828349-22833477 FORWARD LENGTH=1303
AT3023220.1	Symbols:	Ribosomal L27e protein family chr2:13678945-13679352 FORWARD LENGTH=135
AT5061110.1	Symbols:	zinc ion binding chr5:24581078-24581991 REVERSE LENGTH=161
AT5004690.1	Symbols:	Ankyrin repeat family protein chr5:1349781-1352525 REVERSE LENGTH=625
AT5255660.1	Symbols:	DEK domain-containing chromatin associated protein chr5:22539375-22543142 FORWARD LENGTH=778
AT1072140.1	Symbols:	NagB/RpiA/COA transferase-like superfamily protein chr1:27236898-27238482 FORWARD LENGTH=382
AT1045207.2	Symbols:	Remorin family protein chr1:17130703-17133548 REVERSE LENGTH=555
AT1065470.1	Symbols:	PAS1, NPB2 chromatin assembly factor-1 (PASCITAT) (PAS1) chr1:24319906-24323879 REVERSE LENGTH=815
AT3058250.1	Symbols:	TRAP-like family protein chr3:21507045-21527143 REVERSE LENGTH=317
AT2325625.1	Symbols:	unknown protein: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.06
AT2028240.1	Symbols:	ATP-dependent helicase family protein chr2:12039649-12041970 FORWARD LENGTH=660
AT5039500.1	Symbols:	GNLI1, ERMOL GNOM-like 1 chr5:15815274-15819910 FORWARD LENGTH=1443
AT3013782.1	Symbols:	NPA04, NAPI4, NPA4 nucleosome assembly protein14 chr3:4526660-4528398 FORWARD LENGTH=317
AT5222650.1	Symbols:	HD2B, HD202, HD2T, ATHD2B, HDMA4, HD2, ATHD2 histone deacetylase 2B chr5:7534120-7536054 FORWARD LENGTH=306
AT50207240.1	Symbols:	IQD24 IQ-domain 24 chr5:2272028-2274051 FORWARD LENGTH=401
AT3064620.1	Symbols:	ATBZIP25, BZOZM4, BZIP25 basic leucine zipper 25 chr3:20218085-20220341 REVERSE LENGTH=403
AT3039350.1	Symbols:	VPS2.3 vacuolar protein sorting-associated protein 2.3 chr1:1011388-1013212 REVERSE LENGTH=210
AT1051120.1	Symbols:	family enzyme family protein chr1:19186812-19188638 REVERSE LENGTH=252
AT1013560.1	Symbols:	AAPI1, AATAPI1 aminoalcoholphosphotransferase 1 chr1:4638834-4641691 REVERSE LENGTH=389
AT3232580.1	Symbols:	Protein of unknown function (DUF1068) chr2:13827849-13829135 FORWARD LENGTH=183

TAIRArapr [Decoy](#) False discovery rate

Peptide matches above identity threshold	836	37	4.43 %
Peptide matches above homology or identity threshold	1041	83	7.97 %

Select Summary Report

Select Summary (protein hits)

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Significance threshold Max. number of hits Show Percolator scores ☒

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off Show sub-sets

Show pop-ups ☒ Suppress pop-ups ☐ Require bold red ☒

Preferred taxonomy

☒ All queries ☐ Unassigned ☐ Below homology threshold ☐ Below identity threshold

1.	AT4610320.1	Mass: 136368	Score: 1717	Matches: 73(62)	Sequences: 42(39)	emPAI: 3.11
	Symbols:	tRNA synthetase class I (I, L, M and V) family protein chr4:6397526-6404509 REVERSE LENGTH=1190				
Query	Observed	Mr(expt)	Mr(calcd)	ppm	Miss Score	Expect Rank Unique Peptide
3	350.7208	699.4270	699.4279	-1.34	0	32 0.022 1 U K.IIDLAR.N
5	353.2015	704.3885	704.3891	-0.87	0	37 0.0075 1 U K.SMGLVAK.E
79	374.1921	746.3697	746.3711	-1.95	0	20 0.63 1 U R.DNAISR.S
244	391.6920	781.3695	781.3759	-8.11	27	0.041 1 U K.EFSPFR.Q 243
353	409.2423	816.4699	816.4705	-0.68	0	37 0.01 1 U R.IELSVTR.N
358	410.2395	818.4645	818.4650	-0.63	0	35 0.012 1 U R.FLVQNAK.R
663	446.7292	891.4438	891.4450	-1.42	0	29 0.072 1 U R.GDEFGVLR.R
664	446.7469	891.4792	891.4814	-2.45	42	0.0029 1 U K.FNGASLVGK.K
667	447.2396	892.4646	892.4654	-0.96	0 (37)	0.0097 1 U K.FNGASLVGK.K
726	457.1884	912.3623	912.3647	-2.64	0	25 0.015 1 U R.EMDAYR.L
771	462.7263	923.4380	923.4389	-0.90	0	23 0.18 1 U R.YVASEK.V
811	468.7606	935.5066	935.5076	-1.12	0	51 0.00027 1 U K.VTVIASER.L
932	482.7565	963.4984	963.5025	-4.30	0	53 0.00025 1 U R.SDTPLIYR.A
1436	529.7341	1057.4536	1057.4573	-3.47	0	34 0.0039 1 U K.VMPYSTGCK.R
1466	531.7753	1061.5361	1061.5393	-3.03	0	31 0.048 1 U K.AEPDFSVLGR.K 1464
1495	535.3147	1068.6148	1068.6179	-2.85	0	48 0.0003 1 U R.LSALPTDKPK.A
2235	573.7938	1145.5730	1145.5751	-1.82	0	32 0.037 1 U R.SLVFCDNTLK.Y
2482	396.1957	1185.5653	1185.5679	-2.21	0 (29)	0.04 1 U R.FHNLENAR.D
2483	593.7909	1185.5673	1185.5679	-0.48	0	54 0.00012 1 U R.FHNLENAR.D
2790	608.8230	1215.6314	1215.6347	-2.64	1	40 0.0051 1 U K.DAKKDIEAVK.A
2791	406.2182	1215.6329	1215.6347	-1.48	1 (23)	0.34 1 U K.DAKKDIEAVK.A
3181	632.3269	1262.6392	1262.6506	-9.08	0	39 0.008 1 U R.ETVLEELNVR.S 3182
3313	643.3583	1284.7021	1284.7038	-1.26	0	58 7.4e-005 1 U K.QVLVSQGNIK.D
3598	658.3069	1314.5992	1314.6026	-2.62	1	39 0.003 1 U R.FVREMDAYR.L
3599	439.2076	1314.6011	1314.6026	-1.18	1 (26)	0.065 1 U R.FVREMDAYR.L
3674	665.8172	1329.6198	1329.6248	-3.74	0	65 1e-005 1 U R.YQTMTHHIVR.R
3675	444.2142	1329.6208	1329.6248	-3.04	0 (47)	0.00072 1 U R.YQTMTHHIVR.R
3939	684.3678	1366.7210	1366.7245	-2.52	0	58 7.4e-005 1 U K.FLDNLTHIVR.F
4193	471.5834	1411.7284	1411.7320	-2.60	0	44 0.0016 1 U R.HHIDHITPSSR.G 4194
4195	353.9402	1411.7318	1411.7320	-0.19	0 (27)	0.076 1 U R.HHIDHITPSSR.G 4197
4196	706.8734	1411.7323	1411.7320	0.16	0 (28)	0.066 1 U R.HHIDHITPSSR.G
4210	472.2045	1413.5918	1413.6017	-7.00	1 (58)	2e-005 1 U K.MGIDKYNECK.R
4212	707.8662	1413.5977	1413.6017	-2.76	1	77 3.1e-007 1 U K.MGIDKYNECK.R 4211
4379	715.8041	1429.5937	1429.5966	-1.99	1 (55)	3.4e-005 1 U K.MGIDKYNECK.R
5110	768.8695	1535.7245	1535.7256	-0.75	0	45 0.0016 1 U K.SNEGTWVPGTVK.D
5736	539.9153	1616.7242	1616.7253	-0.68	0	51 0.00026 1 U K.GSEESVHYCSIPPA.E 5735
5737	809.3715	1616.7284	1616.7253	1.90	0 (30)	0.028 1 U K.GSEESVHYCSIPPA.E
5985	827.9179	1653.8213	1653.8250	-2.25	0	54 0.00023 1 U K.FNEASVALYSGDVK.S 5984
6040	833.3906	1664.7666	1664.7795	-7.75	0	59 4.9e-005 1 U K.NFGDFVAGLDQTR.G
6043	833.9014	1665.7882	1665.7635	14.8	0 (40)	0.006 1 U K.NFGDFVAGLDQTR.G
6154	847.4159	1692.8172	1692.8206	-1.99	0	68 1.1e-005 1 U K.GAKPESAASDEVLEK.F
6155	565.2805	1692.8197	1692.8206	-0.51	0 (53)	0.00032 1 U K.GAKPESAASDEVLEK.F
7644	978.9633	1955.9120	1955.9153	-1.69	0	56 0.00013 1 U R.QEEDVLFWTEIDAFK.T
7708	988.9968	1975.9791	1975.9851	-3.03	1	51 0.00053 1 U K.KGENLVAVDDGLFTR.I
7956	1009.4999	2016.9852	2016.9792	2.95	0	74 2.4e-006 1 U R.NYPPFLEVIDEGADAVR.L 7953 7954 7955
8314	695.0397	2082.0974	2082.0997	-1.12	0	75 1.7e-006 1 U K.DILAFERAGEVTIANHLLK.E
9047	725.7025	2174.0855	2174.0871	-0.70	0 (45)	0.0023 1 U K.VMAFFTFFFTETLYQNLK.R
9048	1088.5546	2175.0946	2175.0711	10.8	0	45 0.0021 1 U K.VMAFFTFFFTETLYQNLK.R
9653	1124.5115	2247.0084	2247.0160	-3.40	1 (45)	0.0011 1 U K.KYEPFLDYPSDFSSRAFR.V
9654	750.0128	2247.0166	2247.0160	0.26	1	58 6.5e-005 1 U K.KYEPFLDYPSDFSSRAFR.V
9687	752.0554	2253.1443	2253.1464	-0.94	0	70 6.9e-006 1 U K.EMIVVHPDADFNDITGVLR.E
9688	1127.5797	2253.1449	2253.1464	-0.66	0 (52)	0.00037 1 U K.EMIVVHPDADFNDITGVLR.E
9736	757.7228	2270.1465	2270.1253	9.35	0 (22)	0.45 1 U K.EMIVVHPDADFNDITGVLR.E
10680	828.0580	2481.1523	2481.1516	0.28	0	48 0.00082 1 U R.TGDDCHTALSTFLNVLTSCK.V
12046	1360.6271	2719.2396	2719.2389	0.27	0	44 0.0018 1 U K.SGLEPTDFVYFQSLDEDESVK.Q
16282	858.6901	3430.7314	3430.7238	2.22	0	33 0.026 1 U R.TENLPEIFYDGGPPFATGLPHYGHILAGTIK.D
16283	1144.9147	3431.7222	3431.7078	4.20	0 (20)	0.63 1 U R.TENLPEIFYDGGPPFATGLPHYGHILAGTIK.D
17728	1303.0129	3906.0170	3906.0163	0.17	0	47 0.00078 1 U R.LETBGGVFPVPTDLATIQSANILDQWHSATQSLVR.F
17739	978.0150	3908.0307	3907.9844	11.9	0 (37)	0.0068 1 U R.LETBGGVFPVPTDLATIQSANILDQWHSATQSLVR.F
18572	1016.5380	4062.1230	4062.1174	1.36	1 (66)	7.1e-006 1 U K.RLETBGGVFPVPTDLATIQSANILDQWHSATQSLVR.F
18573	813.4319	4062.1230	4062.1174	1.37	1 (43)	0.0013 1 U K.RLETBGGVFPVPTDLATIQSANILDQWHSATQSLVR.F
18580	1356.0499	4065.1280	4065.0695	14.4	1	67 5.7e-006 1 U K.RLETBGGVFPVPTDLATIQSANILDQWHSATQSLVR.F

2.	AT2045110.1	Mass: 29246	Score: 1399	Matches: 48(35)	Sequences: 16(13)	emPAI: 8.48
	Symbols:	ATSPK3, SPK3 SPK domain gene 3 chr2:18606489-18607754 FORWARD LENGTH=245				
Query	Observed	Mr(expt)	Mr(calcd)	ppm	Miss Score	Expect Rank Unique Peptide
34	360.2072	718.3997	718.4014	-2.25	0	19 0.64 1 U R.SPPIQK.V
551	430.7261	859.4376	859.4399	-2.70	0	67 1e-005 1 U R.ENISEIR.K 550 552 553
1024	494.7738	987.5330	987.5349	-1.84	1	29 0.069 1 U R.ENISEIR.K
1147	508.2887	1014.5629	1014.5651	-2.15	0	23 0.25 1 U K.VLHQPFKK.T 1146 1148
1178	512.2393	1022.4640	1022.4669	-2.83	0	64 1.3e-005 1 U K.VAEADYER.C 1177 1179 1180
1457	531.3008	1060.5871	1060.5950	-7.49	0 (48)	0.00073 1 U R.NTVALLTMK.E 1454 1456
1467	531.7965	1061.5783	1061.5791	-0.67	0	49 0.00065 1 U R.NTVALLTMK.E
1535	539.3018	1076.5891	1076.5900	-0.80	0 (44)	0.0018 1 U R.NTVALLTMK.E 1534
4782	740.8565	1479.6983	1479.7140	-10.58	0	103 2.4e-009 1 U R.CAAVTSAAAGGIFR.N 4781 4785
4783	494.2404	1479.6993	1479.7140	-9.97	0 (60)	5.2e-005 1 U R.CAAVTSAAAGGIFR.N
5108	768.8471	1535.6797	1535.6814	-1.12	0	73 1.2e-006 1 U R.EMETTHDAVDPVK.V 5109
5889	828.4280	1654.8414	1654.8678	-15.97	1 (75)	1.6e-006 1 U R.IKEQIQESLPENW.D 5895
5890	552.6223	1654.8449	1654.8678	-13.84	1	91 4e-008 1 U R.IKEQIQESLPENW.D 5891
8918	538.2631	2149.0234	2149.0269	-1.63	0	44 0.0024 1 U K.FNAFFVEQEDFIHKK.E 8919 8920 8922
10525	1213.6600	2425.3055	2425.3104	-2.02	0	56 7.8e-005 1 U K.NLISAPVESIFVGLMARIDK.F
10526	809.4437	2425.3094	2425.3104	-0.43	0 (50)	0.00027 1 U K.NLISAPVESIFVGLMARIDK.F 10527
10571	814.0714	2439.1924	2439.1918	0.26	0 (59)	8.3e-005 1 U R.GSSTYSAPSLPLNIDSQDNVLR.S 10572
10573	1220.6036	2439.1927	2439.1918	0.39	0	129 8.4e-012 1 U R.GSSTYSAPSLPLNIDSQDNVLR.S 10570
10825	842.3854	2524.1345	2524.1428	-3.28	1 (41)	0.0032 1 U R.EMETTHDAVDPVKVAEADYER.C
10826	1263.0764	2524.1383	2524.1428	-1.77	1	64 1.5e-005 1 U R.EMETTHDAVDPVKVAEADYER.C
11114	866.1034	2595.2885	2595.2929	-1.68	1	57 0.00013 1 U R.RGSSTYSAPSLPLNIDSQDNVLR.S

11115	1298.6541	2595.2935	2595.2929	0.26	1	(54)	0.00029	1	U	R.RGSSTYSAPSLPPLNISDSDNVLR.S
12598	942.1505	2823.4297	2823.4265	1.12	0	(21)	0.5	1	U	K.DIVNFHGMVLLVYNNINYTLGLK.I
12766	947.8223	2840.4450	2840.4055	13.9	0	43	0.003	1	U	K.DIVNFHGMVLLVYNNINYTLGLK.I
19275	912.4758	4557.3428	4557.3107	7.03	1	55	9.4e-005	1	U	K.NLISSAPVSEIFVGLLNARIDKFNAPFVBQREDFIHNK.E
19277	1140.8424	4559.3405	4559.2788	13.5	1	(21)	0.24	1	U	K.NLISSAPVSEIFVGLLNARIDKFNAPFVBQREDFIHNK.E

3.	ATSG52040_1	Mass: 41314	Score: 1054	Matches: 39(31)	Sequences: 10(8)	emPAI: 1.80
Symbols: ATRSP41, RS41, AC-RS41 RNA-binding (RRM/RBD/RNP motifs) family protein chr5:21131081-21133318 FORWARD LENGTH=356						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
615	439.2129	876.4112	876.4130	-2.08	0	26 0.11 1 U R.HPEFYTK.I
791	466.2708	930.5270	930.5287	-1.80	1	16 1.5 1 U R.LREVMTK.N
1082	500.7535	999.4924	999.4985	-6.10	0	45 0.0007 1 U R.VASPENGAVR.W
1115	504.2933	1006.5720	1006.5699	2.15	0	41 0.0019 1 U R.VISVEYAVK.D 1108 1110 1111 1112 1113 1116 1117
1400	525.7448	1049.4751	1049.4778	-2.59	0	29 0.05 1 U R.GTGDGSPTR.E
2046	563.7849	1125.5551	1125.5567	-1.37	1	31 0.031 1 U R.ALDRFEYCR.T
2047	376.1924	1125.5553	1125.5567	-1.22	1	(26) 0.1 1 U R.ALDRFEYCR.T
5610	532.6000	1594.7781	1594.7839	-3.60	1	64 2.2e-005 1 U R.VISVEYAVKDDSR.G 5611 5612
6315	867.3908	1732.7671	1732.7701	-1.77	0	69 3.6e-006 1 U --MKPVFCGNFEYDAR.E
6316	578.5966	1732.7679	1732.7701	-1.32	0	(59) 3.3e-005 1 U --MKPVFCGNFEYDAR.E 6317
6362	583.9290	1748.7652	1748.7651	0.10	0	(49) 0.00034 1 U --MKPVFCGNFEYDAR.E
6782	901.9094	1801.8042	1801.8271	-12.73	0	90 2.9e-008 1 U R.NFAPIQTEAQEDATR.A 6783 6786 6787 6791
6785	601.6111	1801.8116	1801.8271	-8.59	0	(53) 0.00014 1 U R.NFAPIQTEAQEDATR.A
6796	902.4213	1802.8281	1802.8111	9.43	0	(75) 1.2e-006 1 U R.NFAPIQTEAQEDATR.A 6797
9130	735.6688	2203.9845	2203.9844	0.02	1	50 0.00031 1 U K.AGFAFVTEMDERDAIR.A 9123 9124 9125 9126 9127 9128 9129 9131 9132

Proteins matching the same set of peptides:

ATSG52040_2	Mass: 41401	Score: 1054	Matches: 39(31)	Sequences: 10(8)
Symbols: ATRSP41, RS41, AC-RS41 RNA-binding (RRM/RBD/RNP motifs) family protein chr5:21131081-21133318 FORWARD LENGTH=357				

4.	ATSG35200_1	Mass: 61369	Score: 640	Matches: 22(20)	Sequences: 17(16)	emPAI: 2.26
Symbols: ENTH/ANTH/VHS superfamily protein chr5:13462463-13465581 REVERSE LENGTH=544						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
115	384.6889	767.3632	767.3636	-0.52	0	32 0.0082 1 U K.ALDMYTR.R
517	426.2761	850.5376	850.5389	-1.52	0	42 0.00023 1 U K.TLIVYTR.A
528	426.2491	854.4836	854.4861	-2.97	0	32 0.01 1 U K.EAPLAAGVR.K
802	468.2559	934.4973	934.4971	-0.23	0	55 0.00017 1 U K.DTTTVSLAK.V 803
1670	545.2629	1088.5113	1088.5138	-2.31	0	52 0.00021 1 U K.YDVVDVDFP.D
2885	411.1945	1230.5616	1230.5638	-1.73	0	35 0.0081 1 U R.SBMLNHSYF.D
3896	680.3432	1358.6718	1358.6765	-3.41	0	(22) 0.32 1 U R.ADVAYCHALAR.R
3897	453.8983	1358.6731	1358.6765	-2.47	0	40 0.0048 1 U R.ADVAYCHALAR.R
6086	839.4363	1676.8580	1676.8621	-2.44	0	70 6.5e-006 1 U K.IYQALTGDIDNLVDR..F 6087
6163	847.8811	1693.7476	1693.7485	-0.49	0	56 7.4e-005 1 U K.DDSGPNMAYSAWVR.F
7140	933.4286	1864.8426	1864.8591	-8.86	0	53 0.00019 1 U R.EVDQTFHEEVINTSR.S
7930	670.6671	2008.9793	2008.9816	-1.11	0	31 0.054 1 U K.IEQPPTSFLLQAEETVK.E
9643	1122.5243	2243.0340	2243.0337	0.14	0	39 0.0064 1 U K.QPDLSSMDQFAPMVELEK.N
10000	780.4202	2338.2389	2338.2420	-1.34	0	77 7.3e-007 1 U K.DLDTFLLLEQLPALQELLFR.V
10001	1170.1309	2338.2472	2338.2420	2.21	0	(70) 4e-006 1 U K.DLDTFLLLEQLPALQELLFR.V
10264	598.3238	2389.2663	2389.2740	-3.23	1	42 0.0027 1 U K.VVEEKASPEFVRAAEKPVK.Q
10720	834.7500	2501.2282	2501.2261	0.84	1	(34) 0.03 1 U K.IYQALTGDIDNLVDRKFFDMQR.N
10761	840.0808	2517.2206	2517.2210	-0.15	1	69 9.1e-006 1 U K.IYQALTGDIDNLVDRKFFDMQR.N
11022	856.8040	2567.3901	2567.3846	2.11	1	77 5.3e-007 1 U R.TKDLDTFLLLEQLPALQELLFR.V
15697	1051.2078	3150.6015	3150.6053	-1.22	0	54 0.00021 1 U R.VLDCQFEGAAVQNHIIQLASHVISESTR.I

5.	ATSG26710_1	Mass: 81527	Score: 636	Matches: 31(27)	Sequences: 24(21)	emPAI: 2.34
Symbols: Glutamyl/glutamyl-tRNA synthetase, class Ic chr5:9305673-9308247 FORWARD LENGTH=719						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
113	383.2141	764.4137	764.4181	-5.77	0	30 0.036 1 U K.YQSLVR.W
279	397.2435	792.4725	792.4745	-2.56	0	24 0.038 1 U K.VLATYTK.X
348	408.7444	815.4743	815.4753	-1.20	0	29 0.084 1 U K.DIGTLGIK.Y 349
556	432.7170	863.4195	863.4211	-1.87	0	42 0.0028 1 U R.CDVFPVK.S
662	446.7087	891.4029	891.4055	-2.95	0	29 0.048 1 U R.GLQCCVR.G
796	466.7475	931.4804	931.4797	0.81	0	45 0.0019 1 U K.VLEDMGLR.Q 794 795
809	468.7238	935.4329	935.4349	-2.04	0	38 0.0055 1 U K.AYVDOTPR.E
858	474.7440	947.4735	947.4746	-1.18	0	(45) 0.0018 1 U K.VLEDMGLR.L
912	479.2899	956.5652	956.5655	-0.31	0	49 0.00045 1 U K.LNGATVLLR.Y
928	482.2663	962.5181	962.5185	-0.43	0	49 0.00058 1 U R.YQGEVIVR.F
956	485.2606	968.5067	968.5113	-4.80	0	34 0.01 1 U R.IIDPVCPH.R
1041	497.2270	992.4394	992.4386	0.88	0	21 0.2 1 U K.FNMQDPNK.A
1156	508.7924	1015.5702	1015.5815	-11.14	0	38 0.0087 1 U R.FPTVQIVR.R
1618	542.8447	1083.6748	1083.6764	-1.49	1	(44) 0.00036 1 U R.KLNGATVLLR.Y
1637	543.3367	1084.6588	1084.6604	-1.50	1	58 3.5e-005 1 U R.KLNGATVLLR.Y
1672	545.2714	1088.5282	1088.5284	-0.25	0	63 2.2e-005 1 U K.CGDVTQLER.K
2257	574.3575	1146.7005	1146.7012	-0.61	0	51 4.8e-005 1 U R.LNLVFTLLEK.R
2407	585.7888	1169.5630	1169.5651	-1.86	1	29 0.033 1 U K.AMRDPVYTR.C
4799	741.3929	1480.7712	1480.7773	-4.11	0	45 0.0016 1 U K.GKPEVLPFAEIGK.V
4930	505.9546	1514.8420	1514.8457	-2.40	0	54 0.00015 1 U K.SSEKPVLFSTPDGR.A
5813	541.9467	1622.8183	1622.8205	-1.34	0	44 0.0022 1 U R.FAPEPSGYLHIGNAK.A
5814	406.7122	1622.8197	1622.8205	-0.53	0	(33) 0.034 1 U R.FAPEPSGYLHIGNAK.A
6014	553.9821	1658.9244	1658.9243	0.04	0	64 1.3e-005 1 U K.IEALIQFILEQGAK.N
6015	830.4700	1658.9254	1658.9243	0.66	0	(55) 0.0001 1 U K.IEALIQFILEQGAK.N
6207	853.4432	1704.8718	1704.8723	-0.30	0	94 2.5e-008 1 U R.VLFTLDGDEPFVVR.M
7087	928.9562	1855.8978	1855.8992	-0.75	0	36 0.015 1 U R.WFNISILDEYSEVLNK.V
7482	635.3283	1902.9629	1902.9662	-1.70	1	20 0.64 1 U K.NLNLMEWDELNSINK.R
11903	895.7717	2684.2934	2684.2945	-0.42	0	59 8.1e-005 1 U K.IYPTYDFACPFVDSLEGITHALR.S

6.	AT2G42520_1	Mass: 67813	Score: 633	Matches: 19(15)	Sequences: 15(12)	emPAI: 1.41
Symbols: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr2:17705382-17708744 FORWARD LENGTH=633						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
1396	525.2612	1048.5078	1048.5189	-10.60	0	56 0.00012 1 R.PLALDEADR.M
1658	363.2120	1086.6142	1086.6186	-4.03	0	(24) 0.15 1 K.YVYKPTPVQR.H
1659	544.3144	1086.6142	1086.6186	-4.00	0	28 0.062 1 K.YVYKPTPVQR.H
1711	549.3127	1096.6109	1096.6241	-11.98	0	42 0.0014 1 R.GVDILVATGRL.L
2426	587.8226	1173.6306	1173.6354	-4.07	0	105 2e-009 1 R.VGSSLDLIVQR.V
2856	613.8502	1225.6858	1225.7030	-14.09	0	45 0.00071 1 R.TPILVATDVAAK.G
2913	619.7775	1237.5404	1237.5431	-2.20	0	(62) 1.5e-005 1 R.DLMACQATGSGK.T
3128	627.7750	1253.5355	1253.5380	-2.02	0	78 3.2e-007 1 R.DLMACQATGSGK.T
3638	440.8994	1319.6765	1319.6768	-0.25	0	22 0.39 1 R.SHMLDLHAGK.E
3696	668.8212	1335.6279	1335.6315	-2.70	0	56 0.00015 1 R.MLDMGFEQTR.K
3943	456.9076	1367.7009	1367.7045	-2.63	1	15 1.3 1 U R.ELASQIHDAKK.F
4378	715.4236	1428.8327	1428.8340	-0.91	0	67 3.8e-006 1 U R.VYFVLAVLSPTR.E
4837	745.8602	1489.7059	1489.7063	-0.24	0	81 3.6e-007 1 U R.WAPGGGVGVGGGGYR.A
5273	778.4040	1554.7934	1554.7938	-0.26	0	46 0.0014 1 K.TAAPCFPIISGIM.D
5322	786.4026	1570.7906	1570.7888	1.19	0	(42) 0.0031 1 K.TAAPCFPIISGIM.D
5726	807.9374	1613.8603	1613.8889	-17.73	0	84 2.2e-007 1 U K.VVVGQGFPIINQLR.E
6617	592.3107	1773.9102	1773.9122	-1.11	0	56 0.00015 1 U R.NHFASEFVAFLPANDR.V
13108	718.3609	2869.4145	2869.4148	-0.09	0	60 7.5e-005 1 R.GLDIFHVRHVVNFDLPNDIDTVHR.I
13109	574.8909	2869.4180	2869.4148	1.12	0	(40) 0.007 1 R.GLDIFHVRHVVNFDLPNDIDTVHR.I

7.	ATSG02500_1	Mass: 71712	Score: 569	Matches: 22(17)	Sequences: 18(14)	emPAI: 1.59
Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 heat shock cognate protein 70-1 chr5:554055-556334 REVERSE LENGTH=651						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
921	481.2606	960.5067	960.5127	-6.30	1	33 0.033 1 R.LSKDEIEK.M
2786	608.3262	1214.6379	1214.6441	-5.13	0	67 9.9e-006 1 K.DAGVIAGLVNMR.I
2869	614.8176	1227.6207	1227.6207	-0.03	0	67 5.8e-006 1 R.VEIANDQGNR.T
3072	623.7652	1245.5158	1245.5183	-2.00	0	60 9.7e-006 1 U R.FSDSSVSQDMK.L 3073
3269	426.8809	1277.6208	1277.6227	-1.44	0	(17) 1 1 R.MVNHFQGEFR.R
3270	639.8182	1277.6208	1277.6227	-0.59	0	34 0.02 1 R.MVNHFQGEFR.R
3584	657.3129	1312.6113	1312.6122	-0.64	0	60 3.5e-005 1 R.FEELNMDLFR.K
3887	679.8048	1357.5951	1357.6084	-9.84	0	62 1.2e-005 1 K.NALENYATNMR.N
3977	687.8053	1373.5960	1373.6033	-5.31	0	(48) 0.00025 1 K.NALENYATNMR.N
4367	476.2593	1425.7561	1425.7576	-1.07	0	24 0.17 1 U K.STVHDVVLVVGSTR.I
5119	514.2563	1539.7470	1539.7504	-2.16	1	42 0.0031 1 R.ARFPEELNMDLFR.K
5311	783.9070	1565.7995	1565.8011	-0.98	0	43 0.0031 1 U K.EFAAEISGMVLK.M
5945	549.2828	1644.8265	1644.8578	-19.05	1	16 1.8 1 K.MKELESICNPFAK.M
5959	825.3954	1648.7763	1648.7767	-0.19	0	24 0.2 2 K.NQVMANFVNPTVDAK.R
6018	830.9491	1659.8836	1659.8719	7.08	0	66 1.3e-005 1 R.IETNEPTAAIAYGLDK.R
11001	1280.6262	2559.2379	2559.2425	-2.87	0	20 0.63 1 U K.SINDPEADAEAGVQAGAILSGEGNEK.V
11731	1329.6323	2657.2501	2657.2609	-4.08	0	46 0.0015 1 K.QQVTSFVSTPQVQLGVQYR.R
12141	917.0535	2748.1388	2748.1392	-0.16	0	24 0.052 1 U K.MYQGAAGEAGGAPGAGDEKAPGAGGAPG.I

15157	1012.5675	3034.6807	3034.6988	-5.98	0	71	1.3e-006	1	U	K.VQDLLLLDVTPLSIGLETAGGVMTTLIP.R
15209	1017.9131	3050.7174	3050.6937	7.77	0	(48)	0.00014	1	U	K.VQDLLLLDVTPLSIGLETAGGVMTTLIP.R
15691	1050.1685	3147.4836	3147.4884	-1.53	1	88	1.1e-007	1	U	K.KIEDSIEQAIQWLEGNQLAEDEFDK.M

[474035630.1]		Mass: 47785	Score: 467	Matches: 18(14)	Sequences: 12(11)	emPAI: 1.92				
[Symbol: PSAT]		phosphoserine aminotransferase chr4:16904205-16905497 FORWARD LENGTH=430								
Query	Observed	M(expt)	M(calc)	p-sm	Miss	Score	Expect	Rank	Unique	Peptide
12	354.7084	707.4023	707.4040	-2.37	0	(22)	0.1	1		K.VLAFNM.D
31	359.6907	717.3669	717.3697	-3.94	0	25	0.18	1	U	K.DYVPVE.N
46	362.7062	723.3979	723.3989	-1.46	0	27	0.019	1		K.VLAFNM.D
697	542.7475	903.4804	903.4814	-1.14	0	35	0.021	1		K.PNVIYVIG.S 696
1313	520.2813	1038.5479	1038.5498	-1.82	0	43	0.0017	1	U	K.UYVIOGAQK.N
1482	533.2755	1064.5365	1064.5390	-2.34	0	37	0.012	1		K.DELRAEPIK.E
2131	568.7761	1135.5376	1135.5410	-3.05	0	49	0.00063	1	U	K.AALADFTK.N
3271	639.8398	1277.6650	1277.6689	-3.08	0	42	0.0034	1		R.SLMGVPTFLK.S
3558	654.7765	1307.5384	1307.5421	-2.77	0	75	3.7e-007	1		R.GSGMSVSEHSR.G
3650	662.8964	1323.7782	1323.7874	-7.01	0	69	1.4e-006	1		K.NVGSQGVITIR.K
7424	634.3556	1900.0451	1900.0458	-0.37	0	36	0.0078	1		R.VVNFAGPATLVNLLK.A
7425	951.0316	1900.0487	1900.0458	1.51	(25)	0.09	0.1	1	U	VVNFAGPATLVNLLK.A
7488	635.9515	1904.9527	1904.9554	-1.38	0	36	0.02	1		K.DLIGNAQDTFVMDLK.I
7831	931.9975	1985.9804	1985.9847	-2.12	1	81	4.4e-007	1		R.KADLLNAATESNGFFR.C
7832	663.0016	1985.9829	1985.9847	-0.86	1	(68)	9.8e-006	1		R.KADLLNAATESNGFFR.C
7838	663.3305	1986.9697	1986.9687	0.53	1	(67)	1.2e-005	1	U	KADLLNAATESNGFFR.C 7837

273058570.1	Mass: 69484	Score: 449	Matches: 15(12)	Sequences: 11(9)	enPAI: 0.97				
Symbols: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr3:21657099-21660352 FC									
Query	Observed	Mr(expT)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
1396	525.2612	1048.5078	1048.5189	-10.60	0	56	0.0012	1	R. FIALDEADR.SL
1658	363.2120	1086.6142	1086.6186	-4.03	0	(24)	0.15	1	K. YVYKPTVPQR.N
1659	544.3144	1086.6142	1086.6186	-4.00	0	28	0.062	1	K. YVYKPTVPQR.N
1711	549.3127	1096.6109	1096.6241	-11.98	0	42	0.0014	1	R. GVDIVLATQGR.L
2426	587.8226	1173.6306	1173.6354	-4.07	0	105	2e-009	1	R. VGSDTLQGR.V
2856	613.8502	1225.6858	1225.7030	-14.09	0	45	0.0071	1	R. TPVILATDVAAR.G
2911	619.7175	1237.5404	1237.5431	-2.20	0	(62)	1.5e-005	1	R. DLMAACQTSGSK.T
3128	627.7750	1253.5355	1253.5380	-2.02	0	78	3.2e-007	1	R. DIHAACQTSGSK.T
3638	404.8994	1319.6765	1319.6768	-0.25	0	22	0.39	1	R. SHMDLLHAQR.G
3696	668.8212	1335.6279	1335.6315	-2.70	0	56	0.00015	1	R. RLMDFGPQIR.E
4050	693.4101	1384.8056	1384.8078	-1.58	0	46	0.0062	1	U R. GYVPIALVPSTR.E
5273	778.4040	1554.7934	1554.7938	-0.26	0	46	0.0014	1	K. TAAFCPTFIISGK.D
5277	786.4026	1570.7906	1570.7888	1.19	0	(42)	0.0031	1	K. TAAFCPTFIISGK.D
13108	718.3690	2869.4145	2869.4148	-0.09	0	60	7.5e-005	1	R. GLDIFRVHVVNFDLPNDIDYVHR.I
13109	574.8909	2869.4180	2869.4148	1.12	0	(40)	0.007	1	R. GLDIFRVHVVNFDLPNDIDYVHR.I

#37040120.1		Mass: 37005	Score: 441	Matches: 17(14)	Sequences: 11(9)	enPA1: 2.15					
Symbols: GACP, GACP-1, GACP1		glyceroldehyde 3-phosphate dehydrogenase C subunit 1 chr3:1081077-1083131 FOR									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique		
293	400.7451	799.4756	799.4803	-5.90	0	33	0.019	1			K.VVISAPSD
325	406.2650	810.4955	810.4963	-0.98	0	(20)	0.051	2			K.V.PALNKGK.L
329	406.7471	811.4797	811.4803	-0.77	0	41	0.0012	1	U		K.V.PALNKGK.L 330
467	417.2338	832.4530	832.4555	-3.08	0	(41)	0.0038	1			R.IGIMGGR.I
471	417.7267	833.4388	833.4395	-0.88	0	67	1.2e-005	1			R.IGIMGGR.I 470
785	464.7938	927.5730	927.5753	-2.52	1	62	1.5e-005	1			K.KVISAPSD
1310	519.7756	1037.5366	1037.5393	-2.61	1	21	0.25	1			K.AATYDEIKK.A
4394	717.8813	1433.7480	1433.7514	-2.37	0	33	0.029	1			R.AASPN1PSSGAAK.A
4871	749.9210	1497.8275	1497.8403	-8.55	0	74	1.2e-006	1			R.VPTVDSVDLTV.L
6084	838.9896	1675.9647	1675.9661	-0.87	0	72	7.7e-007	1			K.TLLGPKPKVTPGIR.N
6085	559.6623	1675.9650	1675.9661	-0.66	0	(51)	0.00011	1			R.TLLGPKPKVTPGIR.N 6081
8030	768.3619	2032.0640	2032.0663	-1.15	0	80	5.9e-007	1			R.FGIVGIVGIVSTATQK.T
9464	1125.5629	2439.0392	2439.0668	-12.27	0	59	6.2e-005	1			K.SLDVIDSNCTTCLAPLAK.V
19877	985.4616	2953.3630	2953.3658	4.22	1	23	0.25	1	U		K.NPDIINAEAGDVTTCVGFVDDK.K

AF30550.1	Mass: 66327	Score: 420	Matches: 15(11)	Sequences: 11(8)	EMPAI: 0.90					
Symbols: DEAD(D/H)-box RNA helicase family protein chr3:21640608-21643646 FORWARD LENGTH=612										
Query	Observed	M(exp.)	M(calc)	ppm	Miss	Score	Expect	Rank	Uniq	Peptide
1396	525.2612	1048.5078	1048.5189	-10.60	0	56	0.00012	1	U	R.FLALDEAD.R
1890	558.3186	1114.6226	1114.6247	-1.86	0	(24)	0.16	1	U	K.YVRPTFPVQR.H
1891	372.5482	1114.6226	1114.6247	-1.78	0	28	0.065	1	U	K.YVRPTFPVQR.H
2429	588.8316	1175.6126	1175.6146	-1.68	0	77	1.4e-006	1	U	R.VGSSDTLITQR.V
2856	613.8502	1225.6858	1225.7030	-14.09	0	45	0.00071	1	U	R.TPLIVATDVAAR.G
2913	619.7775	1237.5404	1237.5431	-2.20	0	(62)	1.5e-005	1	R	R.DLMACQTGSGK.T
3128	627.7750	1253.5355	1253.5380	-2.02	0	78	3.2e-007	1	R	R.DLMACQTGSGK.T
3638	404.8994	1319.6765	1319.6768	-0.25	22	0.39	1		R	R.SHLMDLHAQR.E
3666	668.8122	1335.6279	1335.6315	-2.70	56	0.00015	1		R	R.SLMDGFEPQIR.K
5273	778.4040	1554.7934	1554.7938	-0.26	46	0.0014	1		K	K.TAACFPFIISGIMK.D
5322	786.4026	1570.7906	1570.7888	1.19	0	(42)	0.0031	1	K	K.TAACFPFIISGIMK.D
5905	546.6418	1636.9035	1636.9049	-0.87	0	68	3.6e-006	1	U	K.VVVAYGPTIQLQAR.E
11551	879.4020	2635.1843	2635.1319	-19.9	16	1	1	U	R	R.GADTLNLEKSNFEPATISGDR.T
13108	718.3609	2869.4145	2869.4148	-0.09	0	60	7.5e-005	1	R	R.GLDPIHVVVNFDFNPIDDIYVHR.I
13109	574.8909	2869.4180	2869.4148	1.12	0	(40)	0.007	1	R	R.GLDPIHVVVNFDFNPIDDIYVHR.I

Proteins matching the same set of peptides:

TFID2020_1		Mass: 33800	Score: 412	Matches: 15(11)	Sequences: 9(7)	emPAI: 2.96				
> > > >		Alba	DNA/RNA-binding protein	chr1:7005090-7007285	REVERSE	LENGTH=315				
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Rank	Unique	Peptide	
473	418.7284	835.4423	835.4440	-1.99	0	45	0.0012	1	U	K.SNEVTFK.A
588	505.7235	899.4323	899.4348	-2.76	0	28	0.029	1	U	K.SNGAPIQAAA..
1084	501.1300	1000.6055	1000.6168	-11.32	0	18	0.33	2	U	K.SVTIVELIK.R1085
2867	614.8107	1227.6069	1227.6095	-2.11	0	47	0.00066	1	U	K.ADTPIAENIK.I
4986	765.3138	1528.6130	1528.6179	-3.17	0	71	5se-007	1	U	R.GGVGVNNEYDGDGR.G
4994	765.8602	1529.5979	1529.6019	-2.62	0	(68)	5.9e-007	1	U	R.GGVGVNNEYDGDGR.G
4997	766.3072	1530.5998	1530.5859	9.12	0	(61)	3.4e-006	1	U	R.GGVGVNNEYDGDGR.G
6058	955.8517	1670.8332	1670.8337	-0.35	0	(43)	0.0028	1	U	R.NVIYTAMALQENK.S
6122	984.4206	1686.8266	1686.8287	-1.20	0	46	0.0014	1	U	R.NVIYTAMALQENK.S 6123
7914	1002.9022	2003.7899	2003.7915	-0.82	0	85	1.5e-008	1	U	R.GSGVGVNNEYDGDGR.DS
7970	1011.3999	2020.7852	2020.7705	7.32	(49)	4.9e-005	1	U	R.GSGVGVNNEYDGDGR.DS	
16879	1214.6019	3640.7840	3640.7632	5.70	29	0.083	1	U	R.IPLGILQITIGSDITDWTPEETREGILQTLET	
17471	497.7355	3794.9128	3794.8963	4.35	1	55	0.00017	1	U	R.RIPLGILQITIGSDITDWTPEETREGILQTLET

AF370680.9	Mass: 60897	Score: 397	Matches: 4(1/10)	Sequences: 10(8)	eMAnI: 0.88					
[Symbola] Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent chr3:2606863-611237 REVERSE LENGTH=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
720	1555.7575	909.5003	909.5032	-3.16	0	39	0.0028	1	U	R.VHILLTDGR.D
811	471.7190	941.4235	941.4243	-0.86	1	30	0.015	1	U	R.KDFPDRPQGR
1218	1393.7777	985.5801	985.5801	0.00	0	53	0.00018	53	U	R.VHILLTDGR.D 1017
1515	37.2694	1072.5241	1072.5262	1.87	0	49	0.00048	1	U	R.GYDVNQAQSGGR.N
1550	435.2169	1302.6289	1302.6317	-2.09	0	44	0.002	1	U	R.TSGEYLANGVGR.T
9180	1139.8937	2276.1529	2276.1536	-0.30	0	107	1.4e-009	1	U	R.DYSLDGSGYFVEETLADLAALR.A

9781	759.7256	2276.1549	2276.1536	0.59	0	(84)	2.5e-007	1	U	R.DVLDDSGVGVETLEADLAALR.A
11469	877.4231	2629.2475	2629.2483	-0.30	0	22	0.39	1	U	K.TIGLIVLDGWGSDPDQNCIHK.A
12041	680.5596	2718.2094	2718.2416	-11.84	0	66	8.7e-006	1	U	K.AHGTAIVGLPSEDDMGNSFVHNAAGLR.I
12112	913.0846	2736.2319	2736.2045	10.0	0	(32)	0.026	1	U	K.AHGTAIVGLPSEDDMGNSFVHNAAGLR.I
12936	953.4784	2857.4135	2857.4168	-1.14	0	23	0.33	1	U	R.TILDATIEQVGGIYVVTADHGNADMVK.R
12940	953.8139	2858.4199	2858.4008	6.68	0	(20)	0.62	1	U	R.TILDATIEQVGGIYVVTADHGNADMVK.R
18846	1066.5443	4262.1481	4262.1093	9.12	1	52	0.00027	1	U	R.FRQDIETPLGLNVAATVMNLHGFVAPSDYETSLIEVVEK.-
Proteins matching the same set of peptides:										
AT3G08590.2 Mass: 60897 Score: 397 Matches: 14(10) Sequences: 10(8)										
Symbols: Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent chr3:2608683-2611237 REVERSE LENGTH=560										
15.	AT2G21660.1	Mass: 16937	Score: 364	Matches: 9(6)	Sequences: 5(4)	emPAI: 2.43				
Symbols: ATGRP7, CCR2, GR-RBP7, GRP7 cold, circadian rhythm, and rna binding 2 chr2:9265477-9266316 REVERSE LENGTH=176										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
693	451.7399	901.4653	901.4698	-5.00	0	28	0.071	1		R.GGFGVTFK.D 694
4675	734.3370	1466.6594	1466.6613	-1.27	0	50	0.00034	1	U	R.CFVGGLAWATDDR.A
4845	746.3218	1490.6290	1490.6307	-1.15	0	(16)	0.31	1	U	K.DAIEGNNQDLDGR.S
4897	753.8262	1505.6379	1505.6416	-2.47	0	91	1.3e-008	1	U	K.DAIEGNNQDLDGR.S
4899	754.3189	1506.6233	1506.6256	-1.58	0	(91)	1e-008	1	U	K.DAIEGNNQDLDGR.S
5290	780.8223	1559.6300	1559.6350	-3.19	0	86	1.7e-008	1	U	R.SGGGGTSGGGGSGGGGGGR.R
6283	864.4242	1726.8338	1726.8414	-4.37	0	87	1.2e-007	1	U	R.ALETAFAQTGDVIDSK.T 6284
16.	AT3G44310.1	Mass: 38527	Score: 362	Matches: 17(15)	Sequences: 10(9)	emPAI: 1.70				
Symbols: NIT1, ATNIT1, NITI nitrilase 1 chr3:15986901-15988841 FORWARD LENGTH=346										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
544	440.7414	879.4682	879.4702	-2.21	0	41	0.0028	1	U	K.YIVDEASK.G 645
854	473.7546	945.4947	945.4953	-0.70	0	(30)	0.076	1		K.LMPTSLER.C
925	481.7515	961.4884	961.4902	-1.87	0	45	0.0016	1		K.LMPTSLER.C 924
1524	358.8698	1073.5876	1073.5903	-2.50	1	(38)	0.0092	1		R.KLMPISLER.C
1525	537.8014	1073.5882	1073.5903	-1.92	1	48	0.00095	1		R.KLMPISLER.C
2499	595.2878	1188.5610	1188.5710	-8.37	0	44	0.0014	1		K.LGALICWNR.M
4796	741.3378	1480.6611	1480.6868	-17.34	0	33	0.017	1		K.GIELYCAPTAGDSEK.E
5651	401.7136	1602.8255	1602.8267	-0.73	0	(31)	0.051	1	U	K.YHASAIHVPGPEVAR.L
5652	535.2825	1602.8258	1602.8267	-0.56	0	43	0.0032	1	U	K.YHASAIHVPGPEVAR.L
5653	802.4292	1602.8438	1602.8267	10.7	0	(31)	0.047	1	U	K.YHASAIHVPGPEVAR.L
6307	433.7371	1730.9193	1730.9216	-1.36	1	52	0.00034	1	U	R.KYHASAIHVPGPEVAR.L
6928	911.4791	1820.9437	1820.9461	-1.33	0	64	2.5e-005	1	U	K.GAELVLPFEGFIGOTPR.G
6929	607.9888	1820.9445	1820.9461	-0.90	0	(48)	0.00093	1	U	K.GAELVLPFEGFIGOTPR.G
7571	644.6458	1930.9156	1930.9286	-6.72	1	26	0.15	1		R.PGLAVGVNNEGRDFR.K
8993	1082.5199	2163.0252	2163.0307	-2.51	0	71	4.9e-006	1		R.CIWQGDGSTVPTVDPIGK.L
Proteins matching the same set of peptides:										
AT3G44310.3 Mass: 38527 Score: 362 Matches: 17(15) Sequences: 10(9)										
Symbols: NIT1, ATNIT1, NITI nitrilase 1 chr3:15986901-15988841 FORWARD LENGTH=346										
17.	AT1G19480.1	Mass: 42154	Score: 339	Matches: 12(11)	Sequences: 9(9)	emPAI: 1.48				
Symbols: DNA glycosylase superfamily protein chr1:6744520-6746144 FORWARD LENGTH=382										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
789	465.7912	929.5678	929.5698	-2.19	0	34	0.0087	1	U	K.TPFLALIR.N
1339	523.2723	1044.5300	1044.5352	-4.99	0	30	0.046	1	U	K.ASYLHDLAR.K
2420	391.8798	1172.6175	1172.6302	-10.77	1	(23)	0.27	1	U	R.KASYLHDLAR.K
2421	587.3204	1172.6262	1172.6302	-3.40	1	64	2.7e-005	1	U	R.KASYLHDLAR.K
3667	664.8546	1327.6947	1327.6983	-2.76	0	49	0.00055	1	U	R.ITELGNVSSPPEK.I
4811	742.9056	1483.7967	1483.7994	-1.83	1	50	0.00045	1	U	R.RITELGNVSSPPEK.I
4812	495.6066	1483.7981	1483.7994	-0.93	1	(46)	0.00096	1	U	R.RITELGNVSSPPEK.I
8064	681.0009	2039.9809	2039.9721	4.34	1	84	2e-007	1	U	R.KYQNGILSDSAILNDEK.S
10266	798.0897	2391.2473	2391.2474	-0.04	0	38	0.0079	1	U	R.NADPLAALIDVHPPTFESFK.T
12204	923.8226	2768.4459	2768.4531	-2.61	0	68	7.9e-006	1	U	R.FVSLCGENLVVPEVLELNPQQLR.Q
12205	1385.2336	2768.4527	2768.4531	-0.14	0	(55)	0.00014	1	U	R.FVSLCGENLVVPEVLELNPQQLR.Q
12334	696.6036	2782.3855	2782.3894	-1.43	1	40	0.0068	1	U	R.KGVQLLYGLDLPFRPSQMEQHCAR.W
Proteins matching the same set of peptides:										
AT1G19480.2 Mass: 41625 Score: 339 Matches: 12(11) Sequences: 9(9)										
Symbols: DNA glycosylase superfamily protein chr1:6744520-6745653 FORWARD LENGTH=377										
18.	AT1G07920.1	Mass: 49813	Score: 335	Matches: 18(12)	Sequences: 12(8)	emPAI: 0.98				
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
378	413.2206	824.4265	824.4280	-1.72	0	15	0.88	1	U	K.EVSSYLK.K
475	419.2387	836.4628	836.4644	-1.85	0	23	0.095	1	U	K.PSEILTK.I
749	457.7868	913.5590	913.5597	-0.75	0	25	0.1	1	U	R.QTVAVGVIK.S
975	488.2745	974.5344	974.5437	-9.50	0	38	0.0073	1	U	R.LPLQDVYK.I 976
1210	513.3080	1024.6015	1024.6030	-1.39	0	60	1.3e-005	1	U	K.IGIGITVPGVR.V
1211	513.7440	1025.4734	1025.4818	-8.22	0	35	0.0085	1	U	R.STNLNLYK.Q 1212 1213
2012	374.2042	1119.5907	1119.5924	-1.50	0	22	0.34	1	U	K.STTGHLYK.L
3406	649.8754	1297.7363	1297.7394	-2.39	0	55	8.8e-005	1	U	R.HALLAFTLVQK.Q
3824	676.3257	1350.6369	1350.6415	-3.42	1	69	6.8e-006	1	U	R.GYVANSKDDPAK.G
3825	451.2198	1350.6375	1350.6415	-3.03	1	(53)	0.00024	1	U	R.GYVANSKDDPAK.G
4587	484.5621	1450.6644	1450.6663	-1.35	0	(46)	0.0011	1	U	K.YYCTVIDAQRH.D
4588	726.3400	1450.6655	1450.6663	-0.57	0	51	0.00036	1	U	K.YYCTVIDAQRH.D
9784	760.7165	2279.1278	2279.1330	-2.28	0	76	1.8e-006	1	U	K.MPTKPMVFVETSEYPLGR.F
17516	764.7802	3818.8644	3818.8509	3.54	0	34	0.028	1	U	K.GAANFTSQVINNHPPQIGNGYAPVLDCHTSHIAV.F
17517	764.7806	3818.8665	3818.8509	4.10	0	(25)	0.19	1	U	K.GAANFTSQVINNHPPQIGNGYAPVLDCHTSHIAV.F
Proteins matching the same set of peptides:										
AT1G07930.1 Mass: 49813 Score: 335 Matches: 18(12) Sequences: 12(8)										
Symbols: GTP binding Elongation factor Tu family protein chr1:2459014-2460458 FORWARD LENGTH=449										
AT1G07940.1 Mass: 49813 Score: 335 Matches: 18(12) Sequences: 12(8)										
Symbols: GTP binding Elongation factor Tu family protein chr1:2463350-2464792 REVERSE LENGTH=449										
AT1G07940.2 Mass: 49813 Score: 335 Matches: 18(12) Sequences: 12(8)										
Symbols: GTP binding Elongation factor Tu family protein chr1:2463350-2464792 REVERSE LENGTH=449										
AT5G60390.1 Mass: 49813 Score: 335 Matches: 18(12) Sequences: 12(8)										
Symbols: GTP binding Elongation factor Tu family protein chr5:24289226-24290675 FORWARD LENGTH=449										
AT5G60390.3 Mass: 49813 Score: 335 Matches: 18(12) Sequences: 12(8)										
Symbols: GTP binding Elongation factor Tu family protein chr5:24289226-24290675 FORWARD LENGTH=449										
19.	AT3G09440.1	Mass: 71559	Score: 327	Matches: 13(11)	Sequences: 11(10)	emPAI: 0.93				
Symbols: Heat shock protein 70 (Hsp 70) family protein chr3:2903434-2905632 REVERSE LENGTH=649										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
921	481.2606	960.5067	960.5127	-6.30	1	33	0.033	1		R.LSKDEIEK.M
2786	608.3262	1214.6379	1214.6441	-5.13	0	67	9.9e-006	1		K.DAGVIAGLNVNR.I
2839	613.7980	1225.5815	1225.5827	-0.94	0	42	0.0023	1	U	R.FTDSVSQDIK.L
2869	614.8176	1227.6207	1227.6207	-0.03	0	67	5.8e-006	1		R.VEIANDQNR.T
3269	426.8809	1277.6208	1277.6227	-1.44	0	(17)		1		R.MVNHVFQEFK.R
3270	639.8182	1277.6219	1277.6227	-0.59	0	34	0.02	1		R.MVNHVFQEFK.R
3887	679.8048	1357.5951	1357.6084	-9.84	0	62	1.2e-005	1		K.NALENTAYNNR.N
3977	687.8053	1373.5960	1373.6033	-5.31	0	(48)	0.00025	1		K.NALENTAYNNR.N
5945	549.2828	1644.8265	1644.8578	-19.05	1	16	1.8	1		K.MKELEICNPIAK.M
6018	830.9491	1659.8836	1659.8719	7.08	0	66	1.3e-005	1		R.IIIEPTAAIAVGLDK.K
6033	832.3921	1662.7696	1662.7923	-13.63	0	34	0.02	1	U	K.NQVAMHPIFIVDAK.R
11044	858.7606	2573.2600	2573.2609	-0.33	0	57	0.00012	1		K.SINPDEAVTAGAAVQAALISGEENEK.V
11731	1329.6323	2657.2501	2657.2609	-4.08	0	46	0.0015	1		K.RQVFTSYSDNQGVLIQYVEGER.A
Proteins matching the same set of peptides:										
AT3G09440.2 Mass: 71559 Score: 327 Matches: 13(11) Sequences: 11(10)										
Symbols: Heat shock protein 70 (Hsp 70) family protein chr3:2903434-2905632 REVERSE LENGTH=649										
20.	AT3G57150.1	Mass: 63329	Score: 326	Matches: 8(8)	Sequences: 5(5)	emPAI: 0.40				
Symbols: NAP57, AINAP57, CBP5, AICBP5 homologue of NAP57 chr3:21154255-21155952 REVERSE LENGTH=565										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3982	688.3311	1374.6477	1374.6514	-2.71	1	65	1.5e-005	1	U	K.EVREGEAREKKVK.S
3983	459.2238	1374.6495	1374.6514	-1.36	1	(42)	0.0026	1	U	K.EVREGEAREKKVK.S
4618	486.2220	1455.6442	1455.6478	-2.44	0	(48)	0.00047	1	U	K.HDSDSDSPAPVTTK.K
4619	728.8296	1455.6446	1455.6478	-2.17	0	68	3.9e-006	1	U	K.HDSDSDSPAPVTTK.K
5656	401.9545	1603.7888	1603.7941	-3.29	2	51	0.0005	1	U	K.TKREGEAREKKVK.S
7138	933.4128	1864.8111	1864.8174	-3.35	1	73	1.2e-006	1	U	K.SKDEAAVDAEDSAAEK.S
7139	622.6119	1864.8140	1864.8174	-1.81	1	(71)	1.9e-006	1	U	K.SKDEAAVDAEDSAAEK.S
9149	737.3355	2208.9847	2208.9869	-1.01	2	66	9.3e-006	1	U	K.SKDEAAVDAEDSAAEK.S

21.	AT2G40660.1	Mass: 42290	Score: 313	Matches: 15(9)	Sequences: 13(8)	emPAI: 1.23
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
296	401.2438	800.47751	800.47756	-3.09	0	25 0.16 1 U R.QVVGSLAK.F
817	469.2708	936.5271	936.5280	-1.01	0	20 0.21 1 U K.TILYDNVLA.A
1047	498.2453	994.4761	994.4760	0.13	0	24 0.15 1 U K.DWFSALEK.L
2789	608.8107	1215.6068	1215.6095	-2.24	0	(19) 0.62 1 U K.EVSAQNNDVLK.W
3798	609.3130	1216.6114	1216.5935	14.7	0	51 0.00047 1 U K.EVSAQNNDVLK.W
3100	626.8966	1251.7787	1251.7914	-10.21	0	(25) 0.016 1 U R.LVALITNVKPK.L
3101	418.2701	1251.7883	1251.7914	-2.49	0	45 9.3e-005 1 U R.LVALITNVKPK.L
5645	534.6346	1600.8819	1600.8865	-2.84	0	47 0.00085 1 U K.LPESFEVTKPAIK.V
6338	871.4272	1740.8399	1740.8570	-9.81	0	58 8.5e-005 1 U K.ITPOLYTDENVATTK.G
6744	899.4191	1796.8236	1796.8437	-11.20	0	34 0.017 1 U K.GIQPTTACGCTTSIPK.A
7904	667.9846	2000.9320	2000.9480	-7.97	0	65 1.5e-005 1 U K.HFSLDPEPVVGAGSEDIK.T
8299	693.0463	2076.1170	2076.1215	-2.20	0	53 0.0002 1 U K.AABGVKPKVDFVQVQLQTK.K
9136	552.0612	2204.2158	2204.2165	-0.32	1	26 0.061 1 U K.KAABGVKPKVDFVQVQLQTK.K
9143	736.7031	2207.0876	2207.1070	-8.80	1	75 1.9e-006 1 U K.HPSADSLVKEIDVQEKVR.Q
10637	822.3825	2464.1257	2464.1223	1.38	1	17 1.1 1 U K.WLDPARQFSSDKWFSALEK.L
22.	AT1G76010.1	Mass: 37417	Score: 308	Matches: 19(14)	Sequences: 10(9)	emPAI: 2.11
Symbols: Alba DNA/RNA-binding protein chr1:28528505-28530488 REVERSE LENGTH=350						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
723	456.7250	911.4355	911.4349	0.67	0	29 0.037 1 U R.RDGPPVQAAA.- 722
852	473.7208	945.4271	945.4304	-3.53	0	45 0.00058 1 U R.GYDGPPQGR.G
1150	508.3221	1014.6297	1014.6325	-2.78	0	30 0.0092 1 U K.TVTIVELIK.R 1149 1151
1157	509.2394	1016.4641	1016.4676	-3.36	0	25 0.063 1 U R.GGYDAPPQGR.G
1825	551.7704	1101.5263	1101.5316	-4.73	1	57 6e-005 1 U R.RGYDAPPQGR.G
1826	368.1829	1101.5269	1101.5316	-4.20	1	(37) 0.0054 1 U R.RGYDAPPQGR.G
2785	607.8019	1213.5893	1213.5939	-3.73	0	52 0.00021 1 U K.ADTPIDANEIR.I
5348	525.2687	1572.7842	1572.7858	-0.98	0	(33) 0.028 1 U R.NYITTYAMTLQDK.G
5349	787.4004	1572.7863	1572.7858	0.38	0	50 0.00055 1 U R.NYITTYAMTLQDK.G
5484	795.3989	1588.7833	1588.7807	1.66	0	(18) 1.1 1 U R.NYITTYAMTLQDK.G
16204	1132.2275	3393.6608	3393.6472	4.00	0	(49) 0.00092 1 U K.IELNTSSVGVQCPIPIELVKPMGDIYGR.E
16205	849.4239	3393.6665	3393.6472	5.67	0	(16) 1.6 1 U K.IELNTSSVGVQCPIPIELVKPMGDIYGR.E
16247	1137.2280	3408.6623	3408.6581	1.21	0	57 0.00013 1 U K.IELNTSSVGVQCPIPIELVKPMGDIYGR.E
17108	1227.9364	3680.7874	3680.7581	7.95	0	30 0.059 1 U R.IPDLMQNTSIGSTDITDTWEPTBGLLPLETR.H 17107
17536	1279.9694	3836.8863	3836.8592	7.05	1	34 0.027 1 U R.RIPDLMQNTSIGSTDITDTWEPTBGLLPLETR.H
23.	AT4G39260.1	Mass: 16626	Score: 289	Matches: 12(10)	Sequences: 4(3)	emPAI: 2.51
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
623	451.7399	901.4643	901.4698	-5.00	0	48 0.071 1 U R.GFGVFTFK.D 624
1094	503.7281	1005.4417	1005.4437	-1.98	0	(54) 0.0001 1 U R.DAIEEMNGK.E
1101	504.2204	1006.4263	1006.4277	-1.37	0	56 4.1e-005 1 U R.DAIEEMNGK.E 1102
1899	558.8031	1115.5916	1115.5935	-1.64	0	60 5.5e-005 1 U R.VITVNEAQSQK.G 1898 1900 1901 1902
5416	789.3574	1576.7003	1576.7039	-2.26	1	62 1.8e-005 1 U R.DAIEEMNGKELDGR.V
5593	531.9068	1592.6986	1592.6988	-0.13	1	(36) 0.006 1 U R.DAIEEMNGKELDGR.V
Proteins matching the same set of peptides:						
AT4G39260.1 Mass: 12856 Score: 289 Matches: 12(10) Sequences: 4(3)						
Symbols: CCR1, ATGRP8, GR-RBP8, GRP8 cold, circadian rhythm, and RNA binding 1 chr4:18274166-18274958 REVERSE LENGTH=126						
AT4G39260.3 Mass: 10281 Score: 289 Matches: 12(10) Sequences: 4(3)						
Symbols: CCR1, ATGRP8, GR-RBP8, GRP8 cold, circadian rhythm, and RNA binding 1 chr4:18274166-18274958 REVERSE LENGTH=92						
24.	AT3G12580.1	Mass: 71456	Score: 281	Matches: 10(9)	Sequences: 8(8)	emPAI: 0.71
Symbols: HSP70, ATHSP70 heat shock protein 70 chr3:3991487-3993689 REVERSE LENGTH=650						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
2869	614.8176	1227.6207	1227.6207	-0.03	0	67 5.8e-006 1 R.VELIANDQNR.T
3269	426.8809	1277.6208	1277.6227	-1.44	0	(17) 1 1 R.MVNHVQEFK.R
3270	639.8182	1277.6219	1277.6227	-0.59	0	34 0.02 1 R.MVNHVQEFK.R
3584	657.3129	1312.6113	1312.6122	-0.64	0	60 3.5e-005 1 R.FEELNMDLFR.K
3887	679.8048	1357.5951	1357.6084	-9.84	0	62 1.2e-005 1 K.NALENYAYNMR.N
3977	687.8053	1373.5960	1373.6033	-5.31	0	(48) 0.00025 1 K.NALENYAYNMR.N
5119	514.2563	1539.7470	1539.7504	-2.16	1	42 0.0031 1 R.ARPEELNMDLFR.K
5959	825.3954	1648.7763	1648.7879	-7.01	0	31 0.039 1 U K.NQVAMNPTNTVFDK.R
6018	830.9491	1659.8836	1659.8719	7.08	0	66 1.3e-005 1 R.IIIEPTAAALYGLDK.K
11044	858.7606	2573.2600	2573.2609	-0.33	0	57 0.00012 1 K.SINPDEAVYGAQVAILSGEGNEK.V
25.	AT2G28000.1	Mass: 62205	Score: 274	Matches: 9(9)	Sequences: 8(8)	emPAI: 0.73
Symbols: CPN60A, CH-CPN60A, SLP chaperonin-60alpha chr2:11926603-11929184 FORWARD LENGTH=586						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
497	422.2495	842.4845	842.4862	-1.94	0	42 0.0023 1 U R.LGADIVQK.A
686	449.7878	897.5609	897.5648	-4.24	0	52 7.9e-005 1 U R.GLVNVAVK.A
826	470.7870	939.5595	939.5641	-4.86	0	29 0.015 1 U K.DIIPILEK.T
2578	602.8043	1203.5940	1203.6136	-16.27	0	44 0.002 1 U R.NVVLDFGSPK.V
3150	629.3548	1256.6950	1256.6976	-2.03	0	43 0.0026 1 U K.TVQGLTEELQK.K
3358	645.8096	1289.6046	1289.6099	-4.13	0	73 2.2e-006 1 U K.VGATATELEDR.K
6379	877.4672	1752.9198	1752.9192	0.33	0	67 1.1e-005 1 U R.AIELPNAMENAGALIR.E
9665	750.7703	2249.2891	2249.2882	0.40	0	61 6.4e-006 1 U R.APLLTIAEDVTGEALATLVNKK.L
9666	1125.6528	2249.2911	2249.2882	1.28	0	(32) 0.0055 1 U R.APLLTIAEDVTGEALATLVNKK.L
26.	AT2G17630.1	Mass: 47060	Score: 368	Matches: 10(9)	Sequences: 9(9)	emPAI: 1.26
Symbols: Pyridoxal phosphate (PLP)-dependent transferases superfamily protein chr2:7666637-7667905 FORWARD LENGTH=422						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
12	354.7084	707.4023	707.4040	-2.37	0	(22) 0.1 K.LVAFMK.D
46	362.7062	723.3979	723.3989	-1.46	0	27 0.019 1 K.LVAFMK.D
1411	527.2899	1052.5652	1052.5655	-0.29	0	41 0.00019 1 U K.PGVIVAGAK.N
1482	533.2755	1064.5365	1064.5390	-2.34	0	37 0.012 1 K.SELAEFIK.E
2290	576.7696	1151.5247	1151.5360	-9.73	0	48 0.0005 1 U K.AQSDLVNMR.G
3271	639.8398	1277.6650	1277.6689	-3.08	0	42 0.0034 1 R.SLQNVPTLEK.S
3558	654.7765	1307.5384	1307.5421	-2.77	0	75 3.7e-007 1 R.GSGMSVMTNMR.G
3650	662.8964	1323.7782	1323.7874	-7.01	0	69 1.4e-006 1 K.NVQSGVMTVIRIIR.E
4965	761.3922	1520.7697	1520.7834	-8.99	1	64 2.3e-005 1 U R.KAEFLYNADISR.G
6988	919.0323	1836.0501	1836.0509	-0.40	0	29 0.017 1 U R.VINFAGYPAALFENVLLK.A
27.	AT5G27120.1	Mass: 58947	Score: 261	Matches: 11(9)	Sequences: 7(6)	emPAI: 0.54
Symbols: NOP56-like pre RNA processing ribonucleoprotein chr5:9541287-9543684 FORWARD LENGTH=533						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
4141	701.3201	1400.6256	1400.6307	-3.63	0	65 7.3e-006 1 U K.TEAEPTAEPAK.K
4620	486.5563	1456.6470	1456.6504	-2.32	1	42 0.0017 1 U R.KHEEETEMPAK.K
4987	765.3679	1528.7213	1528.7256	-2.84	1	52 0.00024 1 U K.TEAEPTAEPAKK.E
4988	510.5812	1528.7218	1528.7256	-2.51	1	(48) 0.00071 1 U K.TEAEPTAEPAKK.E
5412	526.5640	1576.6701	1576.6740	-2.50	1	63 7.2e-006 1 K.ADDEEAKTEPSK.K
5413	789.3426	1576.6706	1576.6740	-2.14	1	(36) 0.0039 1 U K.ADDEEAKTEPSK.K
5723	404.1944	1612.7485	1612.7515	-1.84	2	22 0.25 1 U K.RKHEEETEMPAK.K
6004	553.2798	1656.8175	1656.8206	-1.84	2	(55) 0.00016 1 U K.KTEAEPTAEPAKK.E
6005	415.2119	1656.8183	1656.8206	-1.38	2	57 0.00011 1 U K.KTEAEPTAEPAKK.E
6205	853.3880	1704.7614	1704.7690	-4.40	2	(21) 0.28 1 U K.KADDEEAKTEPSK.K
6206	569.2617	1704.7632	1704.7690	-3.40	2	37 0.0069 1 U K.KADDEEAKTEPSK.K
28.	AT1G64880.1	Mass: 60370	Score: 261	Matches: 20(14)	Sequences: 15(10)	emPAI: 1.03
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
106	381.7288	761.4431	761.4436	-0.64	0	17 0.66 1 U K.PVLQKK.L
791	466.2547	930.4948	930.4957	-0.88	0	35 0.029 1 U R.VIGELMNR.L
833	471.7645	941.5145	941.5182	-3.89	0	43 0.0011 1 U K.ALNAVETPK.D 834
843	472.7604	943.5061	943.5087	-2.65	1	32 0.037 1 U K.RLEEIR.E
856	474.2530	946.4914	946.4906	0.83	0	(20) 0.68 1 U R.VIGELMNR.L
979	488.3148	974.6150	974.6164	-1.45	0	37 0.00062 1 U K.TILLLAGFK.N 982
1489	534.2521	1066.4897	1066.4931	-3.15	0	40 0.0031 1 U K.SETLDAFPA.W
2234	382.8641	1145.5705	1145.5717	-1.03	0	23 0.26 1 U K.LELSDHTFK.Q
2492	396.5547	1186.6422	1186.6445	-1.88	1	35 0.018 1 U R.ELIAETFEK.K
2773	404.2427	1209.7064	1209.7081	-1.41	1	17 0.28 1 U R.HKELLQTLK.S
3417	651.3226	1300.6306	1300.6371	-5.02	1	38 0.0061 1 U K.QNLKDDGELNR.R
3928	455.8835	1364.6286	1364.6295	-0.69	0	37 0.0084 1 U K.CFQNLHYER.H
4621	486.5851	1456.7335	1456.7382	-3.24	2	18 0.67 1 U K.QNLKDDGELNR.E
4712	492.2193	1473.6362	1473.6444	-5.59	1	23 0.09 1 U R.DNVQGGEEEREER.L

5122 771.4114 1540.8082 1540.8097 -0.94 1 45 0.0014 1 U K.ALNAVETPKDVQEK.F

5123 514.6107 1540.8102 1540.8097 0.32 1 (31) 0.036 1 U K.ALNAVETPKDVQEK.F

523 588.9596 1763.8569 1763.8591 -1.21 0 (43) 0.0041 1 U R.HEHTIAHAIQTSTYK.K

524 441.9716 1763.8573 1763.8591 -1.03 0 43 0.0037 1 U R.HEHTIAHAIQTSTYK.K

29. AT4G38680.1 Mass: 19484 Score: 258 Matches: 4(4) Sequences: 1(1) emPAI: 0.24

| Symbols: GRP2, CSDP2, 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

10239 794.0436 2379.1091 2379.1132 -1.72 0 99 7.1e-009 1 U K.GFGFIFTPDDGGDLFVHQSSIR.S 10237 10238 10240

30. AT2G39730.1 Mass: 52347 Score: 255 Matches: 10(6) Sequences: 9(6) emPAI: 0.63

| Symbols: RCA | rubisco activase | chr2:16570951-16573345 REVERSE LENGTH=474

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

670 448.2095 894.4045 894.4083 -4.25 0 40 0.0025 1 U R.VYDDEV.R

1105 504.2732 1006.5318 1006.5335 -1.67 0 47 0.00092 1 U K.FVSESLGVEK.I

1447 530.3127 1058.6108 1058.6124 -1.51 0 20 0.36 1 U K.NFLTLFNK.V

2296 576.8608 1151.7071 1151.7067 0.40 0 45 0.00016 1 U K.VPLILGIWGK.G

6177 849.8826 1697.7506 1697.7380 7.39 0 63 1.3e-005 1 U R.GLAYDTSDQQDITR.G

6231 856.8781 1711.7417 1711.7480 -3.72 0 81 2.1e-007 1 U K.MCCLFINDLDAGAGR.M

6642 890.8995 1779.7844 1779.8025 -10.19 0 15 0.87 1 U R.EGFPVFQEPTEMYK.L

8925 1075.5689 2149.1231 2149.1242 -0.47 0 79 6.2e-007 1 U R.VFICTGNGDFSTLYAPLIR.D

16082 832.4016 3325.5771 3325.5384 11.6 0 24 0.27 1 U K.GMVDVFGAPMGDTGTHAVLSSEYFVSQGLR.Q 16081

Proteins matching the same set of peptides:

AT2G39730.2 Mass: 49354 Score: 255 Matches: 10(6) Sequences: 9(6)

| Symbols: RCA | rubisco activase | chr2:16571046-16573345 REVERSE LENGTH=446

AT2G39730.3 Mass: 48754 Score: 255 Matches: 10(6) Sequences: 9(6)

| Symbols: RCA | rubisco activase | chr2:16571174-16573345 REVERSE LENGTH=441

31. AT4G31580.1 Mass: 22615 Score: 252 Matches: 15(11) Sequences: 7(6) emPAI: 2.68

| 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

30 359.2054 716.3962 716.3970 -1.05 0 29 0.085 1 R.SVWVR.R

814 469.2155 936.4165 936.4189 -2.53 0 44 0.0011 1 R.ELEDEFR.A 813 815

1291 516.7758 1031.5371 1031.5400 -2.82 0 31 0.054 1 R.VYVGNLDPK.V

1362 646.3100 1290.6054 1290.6092 -2.88 0 (16) 1 1 U R.ERVFYANGQLK.E

1367 646.8001 1291.5857 1291.5932 -5.81 0 39 0.0045 1 U R.ERVFYANGQLK.E

4817 743.7926 1485.5706 1485.5765 -3.96 0 (55) 1e-005 1 U K.CYCOGETGHFAR.E

4818 496.1978 1485.5716 1485.5765 -3.32 0 61 2.5e-006 1 U K.CYCOGETGHFAR.E

4941 506.9226 1517.7461 1517.7474 -0.85 1 (39) 0.0078 1 U R.AREVFYANGQLK.E

4946 760.3704 1518.7263 1518.7314 -3.36 1 49 0.00063 1 U R.AREVFYANGQLK.E

4947 507.2499 1518.7278 1518.7314 -2.35 1 (46) 0.0013 1 U R.AREVFYANGQLK.E

6092 560.6009 1678.7808 1678.8103 -17.58 0 31 0.038 1 U R.RPGGYALDFEDPR.D 6093 6094

Proteins matching the same set of peptides:

AT4G31580.2 Mass: 22615 Score: 252 Matches: 15(11) Sequences: 7(6)

| Symbols: SRZ-22, SRZ22, RSZP22, RSZ22, At-RSZ22 | serine/arginine-rich 22 | chr4:15306983-15308064 FORWARD LENGTH=200

32. AT3G23990.1 Mass: 61584 Score: 250 Matches: 8(7) Sequences: 8(7) emPAI: 0.62

| Symbols: HSP60, HSP60-3B | heat shock protein 60 | chr3:8669013-8672278 FORWARD LENGTH=577

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

391 413.7550 825.4955 825.4960 -0.56 0 29 0.012 1 K.AGIDPLK.V

672 448.2200 894.4255 894.4269 -1.59 0 20 0.3 1 U R.AIFAROCK.S

2233 573.7838 1145.5531 1145.5564 -2.92 0 87 8.7e-008 1 U K.IGGASAEVQEK.K

2544 598.8697 1195.7249 1195.7288 -3.25 0 38 0.0013 1 K.IGVQIQLNALK.T

3257 425.5564 1273.6474 1273.6514 -3.14 1 39 0.0072 1 U K.IGGASAEVQEK.D

4900 754.8863 1507.7581 1507.7592 -0.71 0 82 3.5e-007 1 K.TLPNLELVQGMK.L

7555 643.0263 1926.0571 1926.0574 -0.17 0 73 1.5e-006 1 U K.AAEVPELPGGVALLYAAR.E

12129 915.1502 2742.4288 2742.4109 6.52 1 36 0.013 1 U R.KANLQDLAALTGGVITDELGMNLEK.V

33. AT5G02490.1 Mass: 71741 Score: 238 Matches: 10(7) Sequences: 8(6) emPAI: 0.52

| Symbols: | Heat shock protein 70 (Hsp 70) family protein | chr5:550296-552565 REVERSE LENGTH=653

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

921 481.2606 960.5067 960.5127 -6.30 1 29 0.1 2 U R.LSKEDIK.M

2869 614.8176 1227.6207 1227.6207 -0.03 0 67 5.8e-006 1 R.VEIIANDQNR.T

3269 426.8809 1277.6208 1277.6227 -1.44 0 (17) 1 1 R.MVNHVPQEFK.R

3270 639.8182 1277.6219 1277.6227 -0.59 0 34 0.02 1 R.MVNHVPQEFK.R

3887 679.8048 1357.5951 1357.6084 -9.84 0 62 1.2e-005 1 K.NALENYANNR.N

3977 687.8053 1373.5960 1373.6033 -5.31 0 (48) 0.00025 1 K.NALENYANNR.N

5311 783.9070 1565.7995 1565.8011 -0.98 0 40 0.0062 2 U K.QFAAEISSVVLK.M

5959 825.3954 1648.7763 1648.7767 -0.19 0 24 0.2 2 K.NQVAMPEVNTVVDAR.K

6018 830.9491 1659.8836 1659.8719 7.08 0 66 1.3e-005 1 R.IIHEPTAAALYGLEK.K

11044 858.7606 2573.2600 2573.2609 -0.33 0 57 0.00012 1 K.SINPDEAVYGAQAILSGEGNEK.V

34. AT3G23450.1 Mass: 34902 Score: 232 Matches: 8(8) Sequences: 4(4) emPAI: 0.63

| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; Has 694543

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

116 386.7183 771.4221 771.4239 -2.30 0 44 0.0011 1 U K.OGGIOGGIKK.G

311 403.7102 805.4059 805.4083 -2.99 0 33 0.027 1 U K.OGGIOGGQPK.G

765 460.7322 919.4498 919.4512 -1.53 0 66 1.2e-005 1 U K.OGGIOGGQGGPK.G 763 764 766 767

890 477.7247 953.4348 953.4356 -0.76 0 53 0.00013 1 U K.OGGFOGGQGGPK.G

35. AT3G04520.1 Mass: 38684 Score: 229 Matches: 9(8) Sequences: 6(6) emPAI: 0.93

| Symbols: THA2 | threonine aldolase 2 | chr3:1217397-1219571 REVERSE LENGTH=355

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

261 394.2365 786.4585 786.4600 -1.90 0 30 0.059 1 U M.VTPTTR.T

610 436.2511 870.4877 870.4923 -5.27 0 37 0.0059 1 U R.VLAELGNR.I

3826 451.2198 1350.6376 1350.6449 -5.40 0 (38) 0.0085 1 U R.SDTVTKTESMR.S

3827 676.3278 1350.6410 1350.6449 -2.93 0 55 0.00016 1 U R.SDTVTKTESMR.S

3935 456.5509 1366.6309 1366.6398 -6.57 0 (27) 0.083 1 U R.SDTVTKTESMR.S

5663 803.3765 1604.7384 1604.7399 -0.95 0 66 1e-005 1 U K.LICLHQIQANCOGR.C

10853 633.3218 2529.2580 2529.2574 0.26 0 (48) 0.0011 1 U R.IVLNHQISDDVYVLSCFEK.I

10854 844.0949 2529.2629 2529.2574 2.19 0 50 0.00064 1 U R.IVLNHQISDDVYVLSCFEK.I

11665 884.0871 2649.2395 2649.2237 5.96 0 59 8.5e-005 1 U K.EAMFVPSGTGNLISLVHCDER.G

36. AT5G37720.1 Mass: 30417 Score: 228 Matches: 6(5) Sequences: 5(4) emPAI: 0.74

| Symbols: ALY4 | ALWAYS EARLY 4 | chr5:14981805-14983978 REVERSE LENGTH=288

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

714 455.2257 908.4368 908.4392 -2.63 0 20 0.34 1 R.YAIHYDK.N

1304 518.2825 1034.5504 1034.5509 -0.47 1 30 0.052 1 U R.RSDAPQALK.K

1522 537.7792 1073.5438 1073.5465 -2.56 0 87 1.1e-007 1 U R.AAGASGVQVTR.L

5657 802.9057 1603.7968 1603.7995 -1.62 0 49 0.00087 1 U R.SLPQSGSLFDGLR.A

6937 608.6440 1822.9101 1822.9173 -3.97 0 (70) 6.1e-006 1 U R.LHVTNLDQGVNTEDIR.E

6938 912.4664 1822.9183 1822.9173 0.53 0 97 1.3e-008 1 U R.LHVTNLDQGVNTEDIR.E

Proteins matching the same set of peptides:

AT5G37720.2 Mass: 29692 Score: 228 Matches: 6(5) Sequences: 5(4)

| Symbols: ALY4 | ALWAYS EARLY 4 | chr5:14981805-14983978 REVERSE LENGTH=280

37. AT1G56070.1 Mass: 94743 Score: 227 Matches: 3(3) Sequences: 2(2) emPAI: 0.09

| Symbols: LOS1 | Ribosomal protein S5/Elongation factor G/III/V family protein | chr1:20968245-20971077 REVERSE LENGTH=843

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

2231 573.2659 1144.5172 1144.5182 -0.91 0 52 0.00013 1 U K.RUPLARENMR.G

9702 1129.1055 2256.1964 2256.1961 0.11 0 (96) 1.2e-008 1 U K.STLTDLSVAAGIIAQEVAGDVR.M

9703 753.0734 2256.1985 2256.1961 1.03 0 122 2.5e-011 1 U K.STLTDLSVAAGIIAQEVAGDVR.M

38. AT3G44300.1 Mass: 37529 Score: 227 Matches: 11(10) Sequences: 8(8) emPAI: 1.47

| Symbols: NIT2, ATNIT2 | nitrilase 2 | chr3:15983351-15985172 FORWARD LENGTH=339

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

525 427.7322 853.4498 853.4545 -5.53 0 34 0.0082 1 U K.VPQPEVEK.L

557 432.7442 863.4738 863.4752 -1.62 0 42 0.0021 1 K.FIVRAASK.G

854 473.7546 945.4947 945.4953 -0.70 0 (30) 0.076 1 K.LMPTSLER.C

925 481.7515 961.4884 961.4902 -1.87 0 45 0.0016 1 K.LMPTSLER.C 924

1524 358.8698 1073.5876 1073.5903 -2.50 1 (38) 0.0092 1 R.KLMPTSLER.C

1525 537.8014 1073.5882 1073.5903 -1.92 1 48 0.00095 1 R.KLMPTSLER.C

2499 595.2878 1188.5610 1188.5710 -8.37 0 44 0.0014 1 K.LGAAICWENR.M

4796 741.3378 1480.6611 1480.6668 -17.34 0 33 0.017 1 K.GIELYCAPTADSGK.E

5991	919.4788	1836.9431	1836.9410	1.11	0	32	0.035	1	U	K.GSELVVFPEAFIGGTFR.G
8993	1082.5199	2163.0252	2163.0307	-2.51	0	71	4.9e-006	1	U	R.CIWQGGDSTIPVYDTPIGK.L

39.

AT3G03530.1

Mass: 61141

Score: 221

Matches: 7(5)

Sequences: 6(5)

emPAI: 0.42

| Symbols: NPC4 | non-specific phospholipase C4 | chr3:842686-844970 REVERSE LENGTH=538

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
641	440.2315	878.4485	878.4498	-1.46	0	23	0.25	1	U	K.EVYEALR.S
2792	608.8282	1215.6418	1215.6612	-15.90	0	77	1e-006	1	U	K.LPNYVVVEGR.W
3923	682.8327	1363.6508	1363.6554	-3.36	0	51	0.0004	1	U	K.ELVQYFAICDR.W
3934	684.3226	1366.6307	1366.6324	-1.27	0	68	7.2e-006	1	U	K.SMTVSSSDTNSLR.V
4059	694.8376	1387.6606	1387.6653	-3.39	0	57	7.7e-005	1	U	R.QDCELTSTPIK.L
9140	736.0371	2205.0895	2205.0987	-4.17	0	58	0.00012	1	U	K.ENAQLSEFGEDLVIMAAGLK.G
9143	736.7031	2207.0876	2207.0667	9.45	0	(17)	1.3	2	U	K.ENAQLSEFGEDLVIMAAGLK.G

40.

AT5G47210.1

Mass: 37977

Score: 206

Matches: 7(6)

Sequences: 6(5)

emPAI: 0.96

| Symbols: | Hyaluronan / mRNA binding family | chr5:19169222-19171012 REVERSE LENGTH=357

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1855	554.7797	1107.5448	1107.5448	-0.02	0	(31)	0.038	1	U	K.NTDERIFIK.L
1859	555.2789	1108.5432	1108.5288	13.0	0	48	0.00063	1	U	K.NTDERIFIK.L
2489	594.2600	1186.5053	1186.5063	-0.83	0	28	0.022	1		R.EMTLEYEKK.I
4117	465.9293	1394.7660	1394.7670	-0.77	0	35	0.0096	1	U	K.PFTKPAFPSPQAVR.E
4943	506.9425	1517.8057	1517.8089	-2.15	0	55	0.0002	1		K.SLSINEFLKPADGK.R
6047	834.8536	1667.6926	1667.6924	0.12	0	100	1.3e-009	1	U	R.NNDAPGNENGSGGTGR.R
6373	584.9606	1751.8601	1751.8663	-3.56	1	26	0.15	1	U	R.RGVVANGESGVVERPFR.N

41.

AT1G75750.1

Mass: 11422

Score: 197

Matches: 6(6)

Sequences: 3(3)

emPAI: 1.96

| Symbols: GASAL | GAST1 protein homolog 1 | chr1:28441813-28442284 REVERSE LENGTH=98

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2905	412.8654	1235.5743	1235.5751	-0.59	1	(59)	5.4e-005	1	U	K.KIDCGSACVAR.C
2906	618.7946	1235.5747	1235.5751	-0.31	1	65	1.5e-005	1	U	K.KIDCGSACVAR.C
4902	755.8271	1509.6396	1509.6453	-3.75	0	60	1.5e-005	1	U	K.QCCYASLTTHOGR.R
4904	504.2215	1509.6426	1509.6453	-1.80	0	(41)	0.0013	1	U	K.QCCYASLTTHOGR.R 4903
5942	822.8411	1643.6677	1643.6708	-1.90	0	34	0.0036	1	U	R.CNCPVPGTGYNDK.C

Proteins matching the same set of peptides:

AT1G75750.2

Mass: 11323

Score: 197

Matches: 6(6)

Sequences: 3(3)

| Symbols: GASAL | GAST1 protein homolog 1 | chr1:28441813-28442284 REVERSE LENGTH=97

42.

AT1G35720.1

Mass: 36296

Score: 195

Matches: 8(6)

Sequences: 7(6)

emPAI: 1.02

| Symbols: ANNAT1, OXY5, ATOXY5 | annexin 1 | chr1:13225304-13226939 FORWARD LENGTH=317

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2284	575.8395	1149.6644	1149.6758	-9.87	0	66	3.5e-006	1	U	K.LLVSLVTSYR.Y
2567	601.3323	1200.6501	1200.6462	3.26	1	49	0.00068	1	U	R.DALLANEATKR.W
3761	673.8143	1345.6141	1345.6150	-0.66	0	16	0.9	1	U	R.YQDNGREILK.S
4125	699.3924	1396.7702	1396.7714	-0.84	0	33	0.014	1	U	R.AILLWLEPGER.D
4680	734.3601	1466.7055	1466.6889	11.4	1	44	0.002	1	U	K.TLDELKSNDFR.A
6114	843.4040	1684.7934	1684.7904	1.79	0	53	0.00024	1	U	K.VSDSVPAISDDAEQLR.T
9150	1105.5851	2209.1556	2209.1565	-0.42	0	(30)	0.054	1	U	R.STIQCITRPELYFVDVLR.S
9151	737.3928	2209.1566	2209.1565	0.05	0	35	0.016	1	U	R.STIQCITRPELYFVDVLR.S

43.

AT4G37800.1

Mass: 34002

Score: 188

Matches: 7(6)

Sequences: 6(5)

emPAI: 0.87

| Symbols: XTH7 | xyloglucan endotransglucosylase/hydrolase 7 | chr4:17775703-17777372 REVERSE LENGTH=293

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1175	511.7516	1021.4887	1021.4909	-2.16	0	31	0.035	1	U	R.AFFYATYK.D
2111	567.2907	1132.5669	1132.5665	0.29	0	17	1.1	1	U	R.VNLMFDPDR.D
3688	667.8752	1333.7359	1333.7394	-2.62	0	60	3.4e-005	1	U	R.IVFYVNVPIR.V
5131	772.8276	1543.6406	1543.6436	-1.91	0	46	0.00031	1	U	R.VNHHVYDYCTDK.S
5132	515.5550	1543.6431	1543.6436	-0.27	0	(33)	0.0064	1	U	R.VNHHVYDYCTDK.S
6318	578.6249	1732.8530	1732.8533	-0.18	0	40	0.0071	1	U	R.SGQPTVYVQNVFAHKG.G
9751	1137.5158	2273.0169	2273.0099	3.09	0	68	4.9e-006	1	U	R.FQMGVYSTLWEADQWATR.G

44.

AT1G55490.1

Mass: 64169

Score: 186

Matches: 5(4)

Sequences: 4(4)

emPAI: 0.30

| Symbols: CPN60B, LEN1 | chaperonin 60 beta | chr1:20715717-20718673 REVERSE LENGTH=600

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2562	600.3350	1198.6555	1198.6557	-0.22	0	68	5.2e-006	1	U	R.DLVGLEDAIR.G
3279	640.8756	1279.7367	1279.7612	-19.18	0	81	1.2e-007	1	U	K.VVAAGANFVLIR.G
7709	659.7034	1976.0885	1976.0942	-2.92	1	72	2.1e-006	1	U	R.KSQGLDDIALTGATVIR.E
11026	857.1414	2568.4024	2568.4050	-1.01	0	31	0.017	1	U	R.GGYPILIIARDIEQEALATLVNKK.L
11027	1285.2128	2568.4110	2568.4050	2.32	0	(18)	0.36	1	U	R.GGYPILIIARDIEQEALATLVNKK.L

Proteins matching the same set of peptides:

AT1G55490.2

Mass: 64169

Score: 186

Matches: 5(4)

Sequences: 4(4)

| Symbols: CPN60B, LEN1 | chaperonin 60 beta | chr1:20715717-20718673 REVERSE LENGTH=600

AT3G13470.1

Mass: 63702

Score: 186

Matches: 5(4)

Sequences: 4(4)

| Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:4389685-4392624 FORWARD LENGTH=596

45.

AT1G26550.1

Mass: 15019

Score: 185

Matches: 6(4)

Sequences: 4(4)

emPAI: 2.04

| Symbols: | PKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr1:9171800-9172716 FORWARD LENGTH=142

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2105	378.2004	1131.5793	1131.5825	-2.85	1	37	0.012	1	U	K.KGUGLGNWFR.G
3570	656.2953	1310.5761	1310.5812	-3.88	0	92	1.6e-008	1	U	K.IAARSISCFPSK.K
4686	490.5871	1468.7395	1468.7423	-1.90	0	64	1.7e-005	1	U	K.STWGHILISEGR.K
9785	761.0468	2280.1186	2280.1249	-2.77	0	38	0.0099	1	U	K.MAGFPQDVAFNTPFVGTSAPFK.S
9786	1141.0674	2280.1202	2280.1249	-2.07	0	(25)	0.22	1	U	K.MAGFPQDVAFNTPFVGTSAPFK.S
9865	1149.0686	2296.1226	2296.1198	1.22	0	(22)	0.44	1	U	K.MAGFPQDVAFNTPFVGTSAPFK.S

46.

AT3G13570.1

Mass: 30265

Score: 174

Matches: 7(7)

Sequences: 5(5)

emPAI: 1.31

| Symbols: SCL30A, At-SCL30A | SC35-like splicing factor 30A | chr3:4429564-4431602 REVERSE LENGTH=262

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1013	493.7126	985.4106	985.4141	-3.55	0	44	0.00049	1		R.DYTTGDPR.G
2580	602.8263	1203.6380	1203.6400	-1.68	0	42	0.0034	1	U	R.RPFEGPFPVK.D
2788	608.3315	1214.6484	1214.6507	-1.86	0	62	3.4e-005	1	U	R.DSDLPTSLLR.V 2787
3420	434.8887	1301.6442	1301.6550	-8.33	0	33	0.027	1	U	K.HQMDQYLLLR.E
6864	907.9246	1813.8346	1813.8345	0.03	0	(36)	0.01	1	U	R.GGFGFIQFMDPADAABAK.H
6963	915.9217	1829.8289	1829.8294	-0.27	0	45	0.001	1	U	R.GGFGFIQFMDPADAABAK.H

47.

AT2G33410.1

Mass: 41303

Score: 173

Matches: 4(4)

Sequences: 3(3)

emPAI: 0.36

| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:14156085-14157435 FORWARD LENGTH=404

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
992	490.2316	978.4487	978.4519	-3.27	0	45	0.001	1	U	R.NFDSGANVR.T
5634	799.4030	1596.7915	1596.7937	-1.37	0	42	0.003	1	U	R.GGFGFVAFSDRAVIDR.V
6261	859.9575	1717.9005	1717.9039	-2.00	0	82	3.9e-007	1	U	K.IFVGGLPALTSDEPR.A 6262

48.

ATCG00490.1

Mass: 53435

Score: 173

Matches: 8(6)

Sequences: 8(6)

emPAI: 0.61

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
718	455.7264	909.4382	909.4378	0.43	0	27	0.067	1	U	R.AVYCELR.G
1172	511.2679	1020.5212	1020.5240	-2.74	0	42	0.0032	1	U	K.DTDILAAFR.V
1897	558.7934	1115.5722	1115.5757	-3.11	0	41	0.0043	1	U	R.VALEACQVAK.N
4166	704.3361	1406.6577	1406.6605	-2.03	0	36	0.011	1	U	K.LTYTTPETETK.D
4579	483.2584	1446.7533	1446.7579	-3.19	0	16	1.7	1	U	R.LSGGDHIAHTVVGK.L
4659	489.2557	1464.7454	1464.7474	-1.35	0	51	0.00052	1	U	K.TFQGPPIHGIQVER.D
7680	656.3099	1965.9080	1965.9037	2.21	1	60	4.9e-005	1	U	K.GHYLNATAGTCRHHKR.A
15163	760.3663	3037.4360	3037.4426	-2.19	0	42	0.0042	1	U	R.ELGLNFIHVDYLTGGTANTSLSHYCR.D

49.

AT4G20360.1

Mass: 51883

Score: 172

Matches: 5(5)

Sequences: 4(4)

emPAI: 0.51

| Symbols: ATRAB8D, ATRAB8B, RAB8B | RAB GTPase homolog E1B | chr4:10990036-10991466 FORWARD LENGTH=476

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4397	479.2263	1434.6570	1434.6626	-3.90	1	34	0.018	1	U	K.KYDEIDAAPER.A
7497	636.3552	1906.0437	1906.0445	-0.44	0	(50)	0.00029	1	U	K.TTLTAALTHALISIGSVAK.K
7544	641.6873	1922.0401	1922.0394	0.37	0	57	7.1e-005	1	U	K.TTLTAALTHALISIGSVAK.K
8205	1026.0120	2050.0094	2050.0081	0.62	0	78	1.1e-006	1	U	K.IYELMDAVIDYTIPIQR.Q
16287	1145.9235	3434.7486	3434.7344	4.11	0	40	0.0049	1	U	R.ELLSYEFKNGDIPITISGALLAVETLTENPK.V

50.

AT3G15730.1

Mass: 92246

Score: 165

Matches: 9(7)

Sequences: 8(6)

emPAI: 0.32

Symbols: PLDALPHA1, PLD phospholipase D alpha 1 chr3:5330835-5333474 FORWARD LENGTH=810												
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
1141	507.7441	1013.4737	1013.4778	-4.05	0	23	0.1	1	U	R.AQGLEEDPR.N		
3324	429.5598	1285.6574	1285.6779	-15.89	0	44	0.0019	1		R.SIQDAYTHAIR.R		
3338	643.8447	1285.6748	1285.6779	-2.39	0	(33)	0.025	1		R.SIQDAYTHAIR.R		
5315	784.8549	1567.6952	1567.6977	-1.60	0	40	0.0033	1	U	R.CWEDIPTAISNAK.H		
5429	527.3086	1578.9039	1578.9093	-3.41	0	41	0.0014	1	U	R.RPKPGDVTIGLELK.K		
7582	645.6342	1933.8808	1933.8853	-2.32	0	40	0.0043	1	U	R.DSEIANGGYQHHLNR.Q		
7682	984.4698	1966.9250	1966.9247	0.16	0	39	0.008	1	U	R.LEGPIAMDVHYNFKR.W		
10634	616.7937	2463.1457	2463.1495	-1.55	0	34	0.022	1	U	R.KYDVFYSSELSLEHDLPHLLR.Y		
10641	617.3009	2465.1745	2465.1612	5.40	0	19	0.87	1	U	R.TLDTVHDDFQPNFTGAATK.G		

51. [AT5G56740.1](#) Mass: 52876 Score: 157 Matches: 5(4) Sequences: 4(3) emPAI: 0.38
| Symbols: HAG2, HAC7, HAG02, 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		
829	471.2586	940.5027	940.5018	0.92	0	27	0.043	1	U	K.IYVGQGLK.I		
2057	565.3077	1128.6009	1128.6179	-15.03	0	24	0.14	1	U	R.FTPPLNAIEK.V		
7706	659.0168	1974.0287	1974.0310	-1.14	0	47	0.0011	1	U	R.SFDPFKPIDSAVQTLTK.G		
15034	751.3834	3001.5043	3001.5033	0.35	1	(53)	0.00034	1	U	K.SALQNFARTIVDTKDEPLQTFSTQR.D		
15044	1001.8435	3002.5087	3002.4873	7.13	1	83	3.1e-007	1	U	K.SALQNFARTIVDTKDEPLQTFSTQR.D		

52. [AT5G58470.1](#) Mass: 42746 Score: 154 Matches: 5(5) Sequences: 4(4) emPAI: 0.49
| Symbols: TAF15b | TBP-associated factor 15b | chr5:23638566-23640854 REVERSE LENGTH=422

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
4848	746.8235	1491.6324	1491.6347	-1.54	0	48	0.00024	1	U	R.CPNPSCGVNVPAR.R		
4865	499.8963	1496.6670	1496.6743	-4.87	1	(51)	0.00028	1	U	R.RQEASVEDAAATEK.V		
4866	749.3413	1496.6681	1496.6743	-4.14	1	69	4.6e-006	1	U	R.RQEASVEDAAATEK.V		
6285	864.7840	1727.5534	1727.5570	-2.06	0	19	0.012	1	U	K.QCDDACDDNCDNAR.I		
7642	652.5775	1954.7107	1954.7204	-4.95	1	38	0.00022	1	U	K.VKQDADCDNCDNAR.I		

Proteins matching the same set of peptides:
[AT5G58470.2](#) Mass: 42746 Score: 154 Matches: 5(5) Sequences: 4(4)
| Symbols: TAF15b | TBP-associated factor 15b | chr5:23638566-23640854 REVERSE LENGTH=422

53. [AT3G06810.1](#) Mass: 92282 Score: 153 Matches: 5(4) Sequences: 5(4) emPAI: 0.20
| Symbols: IIR3 | acyl-CoA dehydrogenase-related | chr3:2146534-2150654 FORWARD LENGTH=824

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
636	439.2289	876.4431	876.4454	-2.52	0	27	0.12	1	U	R.GFEIAQGR.L		
2821	612.8058	1223.5970	1223.6009	-3.14	0	45	0.0014	1	U	K.HFELVDMLE.R		
6076	837.4365	1672.8585	1672.8573	0.71	0	50	0.00056	1	U	R.BGLNMLFVPVDSAAAR.A		
6099	841.9567	1681.8989	1681.9039	-2.96	0	52	0.00025	1	U	K.BQISEMLPLLEGR.I		
7916	669.0160	2004.0261	2004.0276	-0.72	0	72	4.1e-006	1	U	R.NTVQVANELVESALGTIAR.R		

54. [AT1G14320.1](#) Mass: 25357 Score: 152 Matches: 2(2) Sequences: 2(2) emPAI: 0.40
| Symbols: SAC52, RPL10, RPL10A | Ribosomal protein L16p/L10e family protein | chr1:4888270-4889408 FORWARD LENGTH=220

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
2317	577.8659	1153.7173	1153.7183	-0.89	0	74	2.6e-007	1	U	R.VAIGGVLLSR.C		
3261	638.3128	1274.6111	1274.6102	0.67	0	102	3.1e-009	1	U	K.ENVVSLEALEAR.I		

Proteins matching the same set of peptides:
[AT1G26910.1](#) Mass: 25349 Score: 152 Matches: 2(2) Sequences: 2(2)
| Symbols: RPL10B | Ribosomal protein L16p/L10e family protein | chr1:9321709-9322813 FORWARD LENGTH=221

[AT1G66580.1](#) Mass: 25312 Score: 152 Matches: 2(2) Sequences: 2(2)
| Symbols: SAG24, RPL10C | senescence associated gene 24 | chr1:24839208-24840439 FORWARD LENGTH=221

55. [AT2G33210.1](#) Mass: 62339 Score: 150 Matches: 4(4) Sequences: 4(4) emPAI: 0.31
| 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		
321	413.7550	825.4955	825.4960	-0.56	0	29	0.012	1		K.AGIDPLK.V		
2544	598.8697	1195.7249	1195.7288	-3.25	0	38	0.0013	1		K.IGVQIQNALK.T		
2603	603.7946	1205.5746	1205.5775	-2.47	0	73	2.7e-006	1	U	K.IGGASRTVESEK.K		
4900	754.8863	1507.7581	1507.7592	-0.71	0	82	3.5e-007	1		K.TLPLELEVVEGK.I		

Proteins matching the same set of peptides:
[AT2G33210.2](#) Mass: 61781 Score: 150 Matches: 4(4) Sequences: 4(4)
| Symbols: HSP60-2 | heat shock protein 60-2 | chr2:14075093-14078568 REVERSE LENGTH=580

56. [AT1G29250.1](#) Mass: 14564 Score: 148 Matches: 6(5) Sequences: 4(3) emPAI: 3.19
| Symbols: | Alba DNA/RNA-binding protein | chr1:10223461-10224592 REVERSE LENGTH=130

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
262	394.2488	786.4831	786.4851	-2.48	0	42	0.0024	1	U	K.IEITLAK.S		
1106	504.2749	1006.5352	1006.5369	-1.62	0	(37)	0.0088	1		K.IMTSTVDIK.D		
1184	512.2730	1022.5315	1022.5318	-0.32	0	58	6.8e-005	1		K.IMTSTVDIK.D		
4787	494.2478	1479.7217	1479.7239	-1.52	1	60	5.5e-005	1	U	K.IMTSTVDIKDDSR.G		
4863	748.8638	1495.7131	1495.7188	-3.82	1	(51)	0.0004	1	U	K.IMTSTVDIKDDSR.G		
15376	773.1504	3088.5725	3088.5712	0.40	0	21	0.5	1	U	R.YMQQYTVDELALQGAIAIVTVVAILK.N		

57. [AT3G52930.1](#) Mass: 38858 Score: 141 Matches: 5(4) Sequences: 5(4) emPAI: 0.55
| Symbols: | Aldolase superfamily protein | chr3:19627383-19628874 REVERSE LENGTH=358

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
507	424.2664	846.5182	846.5215	-3.85	0	34	0.0039	1	U	K.LFVDILK.E		
2540	399.5472	1195.6197	1195.6197	0.02	0	28	0.069	1	U	K.LGDGAASLRVK.D		
3699	668.8658	1335.7171	1335.7147	1.85	0	39	0.0047	1	U	K.VSPVEIAETVR.A		
9180	556.5144	2222.0285	2222.0352	-3.00	0	64	2.2e-005	1	U	K.IGNEPSEHSIHENAYGLAR.Y		
9960	1165.1085	2328.2025	2328.1961	2.73	0	47	0.001	1	U	R.TVPAAPVAVFLSGGQSEERAT.N		

58. [AT2G24590.1](#) Mass: 22073 Score: 141 Matches: 8(6) Sequences: 6(4) emPAI: 1.14
| Symbols: RSZ22a, At-RSZ22a | RNA recognition motif and CCHC-type zinc finger domains containing protein | chr2:10449837-10450860 FORWARD LENGTH=196

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
30	359.2054	716.3962	716.3970	-1.05	0	29	0.085	1		R.SYVVAR.R		
814	469.2155	936.4165	936.4189	-2.53	0	44	0.0011	1		R.ELKEDEFR.S 813 815		
1281	516.7758	1031.5371	1031.5400	-2.82	0	31	0.054	1		R.VYVGNLDR.V		
4696	491.5262	1471.5568	1471.5609	-2.77	0	58	3.4e-006	1	U	K.CYKCOESGNFAR.E		
4894	502.5784	1504.7133	1504.7157	-1.64	1	29	0.067	1	U	R.AREFVVTANQSLK.D		
6051	557.2662	1668.7767	1668.7896	-7.75	0	33	0.019	1	U	R.RPFGVAFLEDSDR.D		

59. [AT4G35785.1](#) Mass: 28213 Score: 140 Matches: 5(4) Sequences: 4(4) emPAI: 0.82
| 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		
2441	589.8133	1177.6120	1177.6091	2.47	0	69	6.3e-006	1	U	K.YLNGSVLEGR.Y		
2472	395.2189	1182.6350	1182.6397	-4.01	0	30	0.026	1	U	R.TPTPGHYLGLE.S		
2473	592.3262	1182.6378	1182.6397	-1.62	0	(16)	0.84	1	U	R.TPTPGHYLGLE.S		
2491	594.3082	1186.6019	1186.6056	-3.14	0	49	0.00064	1	U	R.GFAPVTMSLEK.D		
3649	662.8230	1323.6314	1323.6315	-0.06	0	53	0.00022	1	U	K.VASCFVLMPEPR.T		

Proteins matching the same set of peptides:
[AT4G35785.2](#) Mass: 28369 Score: 140 Matches: 5(4) Sequences: 4(4)
| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:16953211-16955127 REVERSE LENGTH=239

60. [AT1G66260.1](#) Mass: 31299 Score: 140 Matches: 5(4) Sequences: 5(4) emPAI: 0.72
| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:24695895-24697883 REVERSE LENGTH=295

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
714	455.2257	908.4368	908.4392	-2.63	0	20	0.34	1		R.YAHYDK.N		
788	465.7536	929.4926	929.4930	-0.42	0	68	9e-006	1	U	R.VNVVTGLNGR.M		
3639	440.9078	1319.7015	1319.7085	-5.27	1	42	0.0034	1	U	R.ELTAIEGELER.Y		
5636	799.4199	1596.8252	1596.8471	-13.69	0	53	0.00024	1	U	K.LEILGNTESAPVAAR.V		
7917	1003.4670	2004.9194	2004.9541	-17.30	0	46	0.0011	1	U	R.SLFWQNGNDLYETLR.A		

Proteins matching the same set of peptides:
[AT1G66260.2](#) Mass: 31299 Score: 140 Matches: 5(4) Sequences: 5(4)
| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:24695895-24697883 REVERSE LENGTH=295

61. [AT1G18540.1](#) Mass: 26136 Score: 138 Matches: 5(3) Sequences: 4(3) emPAI: 0.63
| Symbols: | Ribosomal protein L6 family protein | chr1:6377448-6378548 REVERSE LENGTH=233

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide		
75	373.7004	745.3863	745.3871	-1.16	0	(18)	0.97	1	U	K.NGVVFR.H		
78	374.1912	746.3678	746.3711	-4.44	0	31	0.06	1	U	K.NGVVFR.H		

1412	351.8680	1052.5822	1052.5866	-4.17	0	34	0.01	1	U	K.VDAPVEKPAK.F
3278	640.8445	1279.6744	1279.6772	-2.19	0	65	1.2e-005	1	U	R.VNQAVVIGTSTK.I
4800	741.4546	1480.8946	1480.8977	-2.08	0	78	8.9e-008	1	U	K.ASITPGTVLILAGR.F

62. AT1G49240.1

Mass: 42064

Score: 136

Matches: 3(3)

Sequences: 3(3)

emPAI: 0.35

| Symbols: ACT8 | actin 8 | chr1:18216539-18217947 FORWARD LENGTH=377

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4209	471.8965	1412.6677	1412.6684	-0.51	0	70	3.9e-006	1	U	K.ARYDEAGPGIVHR.K
4929	505.9199	1514.7379	1514.7419	-2.60	0	36	0.012	1		K.IWHHTFYNELR.I
6618	888.4551	1774.8956	1774.8737	12.3	0	65	1.9e-005	1		K.NYELPDQGVITIGAER.F

Proteins matching the same set of peptides:

AT3G18780.2

Mass: 42078

Score: 136

Matches: 3(3)

Sequences: 3(3)

| Symbols: ACT2, DER1, LSR2, ENL2 | actin 2 | chr3:6475535-6476832 FORWARD LENGTH=377

63. AT2G20450.1

Mass: 15497

Score: 135

Matches: 4(4)

Sequences: 3(3)

emPAI: 1.93

| Symbols: | Ribosomal protein L14 | chr2:8813923-8815071 FORWARD LENGTH=134

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1894	558.7718	1115.5290	1115.5281	0.84	0	43	0.0015	1	U	R.ALVDAPDIMER.I
2102	566.7681	1131.5216	1131.5230	-1.26	0	(28)	0.048	1	U	R.ALVDAPDIMER.I
3970	686.3944	1370.7741	1370.7769	-2.02	0	93	2e-008	1	U	R.LSLTDIVIDINKR.V
6168	566.0037	1694.9893	1694.9931	-2.20	1	39	0.0015	1	U	R.LSLTDIVIDINKRVPK.X

Proteins matching the same set of peptides:

AT4G27090.1

Mass: 15496

Score: 135

Matches: 4(4)

Sequences: 3(3)

| Symbols: | Ribosomal protein L14 | chr4:13594104-13595187 REVERSE LENGTH=134

64. AT5G62690.1

Mass: 51385

Score: 132

Matches: 5(3)

Sequences: 5(3)

emPAI: 0.28

| Symbols: TUB2 | tubulin beta chain 2 | chr5:25181560-25183501 FORWARD LENGTH=450

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1479	533.2162	1064.4178	1064.4201	-2.17	0	16	0.16	1		K.NMCAADPR.H
1531	359.8478	1076.5216	1076.5250	-3.19	1	22	0.34	1		K.IKEEYFDR.M
2156	570.3497	1138.6849	1138.6862	-1.18	0	56	2.9e-005	1		K.LAVNLVFPFR.L
4536	723.8274	1445.6402	1445.6245	10.9	0	52	0.00014	1	U	R.IHYVYNASGCR.F
5950	824.4065	1646.7984	1646.8008	-1.42	0	70	6.4e-006	1	U	R.AVLMDLEPGTMDSLR.S

Proteins matching the same set of peptides:

AT5G62700.1

Mass: 51385

Score: 132

Matches: 5(3)

Sequences: 5(3)

| Symbols: TUB3 | tubulin beta chain 3 | chr5:25184501-25186426 FORWARD LENGTH=450

65. ATCG00380.1

Mass: 23340

Score: 131

Matches: 3(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
5134	772.9245	1543.8344	1543.8392	-3.08	0	99	6.9e-009	1	U	K.GSTGQVLLQLLEMR.L
5293	780.9200	1559.8254	1559.8341	-5.59	0	(30)	0.064	1	U	K.GSTGQVLLQLLEMR.L
18631	1030.5321	4118.0993	4118.0960	0.80	0	49	0.00057	1	U	R.TLVQNLLDSAPFELPHNHLTHTFPQYGLVQNQIIDR.K

66. AT2G37270.1

Mass: 23090

Score: 129

Matches: 3(3)

Sequences: 2(2)

emPAI: 0.44

| Symbols: ATRP5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2528	398.5434	1192.6084	1192.6102	-1.49	0	45	0.0016	1	U	K.HATVPFHTAGR.Y
5854	816.4195	1630.8244	1630.8236	0.52	0	72	4.7e-006	1	U	K.TIARCLADELINAAR.G
5855	544.6154	1630.8244	1630.8236	0.52	0	(57)	0.00013	1	U	K.TIARCLADELINAAR.G

Proteins matching the same set of peptides:

AT2G37270.2

Mass: 23090

Score: 129

Matches: 3(3)

Sequences: 2(2)

| Symbols: ATRP5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207

AT3G11940.1

Mass: 23021

Score: 129

Matches: 3(3)

Sequences: 2(2)

| Symbols: ATRP5A, AML1, RPS5A | ribosomal protein 5A | chr3:3778175-3779354 REVERSE LENGTH=207

AT3G11940.2

Mass: 23021

Score: 129

Matches: 3(3)

Sequences: 2(2)

| Symbols: ATRP5A, AML1, RPS5A | ribosomal protein 5A | chr3:3778175-3779354 REVERSE LENGTH=207

67. AT4G21620.1

Mass: 13307

Score: 124

Matches: 2(2)

Sequences: 2(2)

emPAI: 0.87

| Symbols: | glycine-rich protein | chr4:11491519-11491914 FORWARD LENGTH=131

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2422	587.3227	1172.6308	1172.6336	-2.37	0	31	0.044	1	U	K.GGVVRPTVTKR.E
4834	745.7742	1489.5338	1489.5385	-3.15	0	109	1.2e-011	1	U	K.GYGSGGGGGCTMDCK.K

Proteins matching the same set of peptides:

AT4G21620.2

Mass: 10497

Score: 124

Matches: 2(2)

Sequences: 2(2)

| Symbols: | glycine-rich protein | chr4:11491519-11491914 FORWARD LENGTH=98

68. AT5G42820.1

Mass: 33611

Score: 123

Matches: 6(4)

Sequences: 5(4)

emPAI: 0.66

| Symbols: ATU2AF35B, U2AF35B | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:17170445-17171296 REVERSE LENGTH=283

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
500	423.2148	844.4151	844.4191	-4.81	0	18	0.48	1	U	R.IEQWNR.E
1521	537.7496	1073.4846	1073.5004	-14.77	0	30	0.017	1	U	R.VNCPFFPK.I
5426	790.3814	1578.7483	1578.7750	-16.93	0	(28)	0.086	1	U	K.EDHAAALQALQGR.F
5427	527.2586	1578.7540	1578.7750	-13.30	0	54	0.00023	1	U	K.EDHAAALQALQGR.F
8330	696.6918	2087.0535	2087.0476	2.80	0	47	0.0012	1	U	R.FYSGRFIADFSPTDGR.E
9966	777.6873	2330.0401	2330.0379	0.96	0	40	0.0037	1	U	K.IQDHFEDFYEDIFEELNK.F

Proteins matching the same set of peptides:

AT5G42820.2

Mass: 33611

Score: 123

Matches: 6(4)

Sequences: 5(4)

| Symbols: ATU2AF35B, U2AF35B | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:17170445-17171296 REVERSE LENGTH=283

69. AT1G20620.1

Mass: 57059

Score: 123

Matches: 5(4)

Sequences: 5(4)

emPAI: 0.35

| Symbols: CAT3, SEN2, ATCAT3 | catalase 3 | chr1:7143142-7146193 FORWARD LENGTH=492

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
282	399.7444	797.4743	797.4759	-2.05	0	25	0.037	1	U	R.LNVRPSI.-
2134	568.8431	1135.6716	1135.6714	0.22	0	57	1.9e-005	1	U	R.AFGVQTPVIIVR.F
4976	762.4302	1522.8459	1522.8507	-3.16	0	47	0.00049	1	U	R.LGPNYLQLPQNAK.C
5860	816.9583	1631.9021	1631.9035	-0.89	0	27	0.062	1	U	K.INPDILPLQPVGR.L
7592	969.9905	1937.9665	1937.9636	1.52	0	35	0.021	1	U	R.BGNFDLVGNTPVFFIR.D

Proteins matching the same set of peptides:

AT1G20620.5

Mass: 56331

Score: 123

Matches: 5(4)

Sequences: 5(4)

| Symbols: CAT3, SEN2, ATCAT3 | catalase 3 | chr1:7143142-7146193 FORWARD LENGTH=485

70. AT1G64370.1

Mass: 19685

Score: 122

Matches: 6(6)

Sequences: 5(5)

emPAI: 1.91

| Symbols: | 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
2435	393.2037	1176.5892	1176.5928	-3.05	0	37	0.011	1	U	R.SHGGLDGLFK.G
3668	443.9011	1328.6816	1328.6837	-1.58	0	31	0.041	1	U	K.QQSGLTFLQGRK.S
4816	743.3494	1484.6842	1484.6895	-3.61	1	46	0.00076	1	U	R.EKDYVEAQQGR.N
9168	740.9827	2219.9262	2219.9329	-3.02	0	28	0.019	1	U	R.NGYQSQSQSHNHBTGQSQSR.G
9169	555.9888	2219.9262	2219.9329	-3.00	0	(24)	0.049	1	U	R.NGYQSQSQSHNHBTGQSQSR.G
10232	594.7944	2375.1486	2375.1618	-5.55	0	44	0.0027	1	U	R.EGYSQSQSRPVYGLSPTLNHR.S

71. AT5G09810.1

Mass: 41937

Score: 121

Matches: 3(3)

Sequences: 3(3)

emPAI: 0.36

| Symbols: ACT7 | actin 7 | chr5:3052809-3054220 FORWARD LENGTH=377

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4722	492.5628	1474.6665	1474.6688	-1.59	0	56	6.7e-005	1	U	K.SYDEGSPSIVHR.K
4929	505.9199	1514.7379	1514.7419	-2.60	0	36	0.012	1		K.IWHHTFYNELR.V
6618	888.4551	1774.8956	1774.8737	12.3	0	65	1.9e-005	1		K.NYELPDQGVITIGAER.F

72. AT1G13020.1

Mass: 59289

Score: 121

Matches: 5(3)

Sequences: 5(3)

emPAI: 0.24

| Symbols: EIF4B2 | eukaryotic initiation factor 4B2 | chr1:4440927-4443520 REVERSE LENGTH=549

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
102	380.7207	759.4269	759.4279	-1.33	0	30	0.063	1	U	R.LVTFPR.K
1303	517.7678	1033.5210	1033.5193	1.64	0	29	0.069	1	U	R.VSDFPQVSR.E
1721	367.5328	1099.5767	1099.5774	-0.68	0	38	0.0054	1	U	R.VNPFQDAKPR.A
2345	580.2347	1158.4548	1158.4578	-2.58	0	60	5.1e-006	1	U	R.GYQGFDDQGR.G
3096	626.3189	1250.6233	1250.6255	-1.79	0	60	5.4e-005	1	U	K.GAYTAPASAGLTR.E

73. AT3G44320.1

Mass: 38340

Score: 121

Matches: 4(3)

Sequences: 4(3)

emPAI: 0.39

| Symbols: NIT3, ATNIT3 | nitrilase 3 | chr3:15993419-15995493 FORWARD LENGTH=346

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
557	432.7442	863.4738	863.4752	-1.62	0	42	0.0021	1		K.FIVEAASK.G
2499	595.2878	1188.5610	1188.5710	-8.37	0	44	0.0014	1	U	K.IGAAICWNR.M
7571	644.6458	1930.9156	1930.9286	-6.72	1	26	0.15	1		R.FGLAVGVHNEGRDEF.N
8993	1082.5199	2163.0252	2163.0307	-2.51	0	71	4.9e-006	1		R.CIWGGDGSITFVYDTPIGK.I

74. [AT3G57560.1](#) Mass: 36800 Score: 114 Matches: 3(2) Sequences: 3(2) emPAI: 0.26
| Symbols: NAGK | N-acetyl-L-glutamate kinase | chr3:21311164-21312207 REVERSE LENGTH=347
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[4882](#) 751.9270 1501.8394 1501.8392 0.18 0 39 0.0039 1 U R.VEILSELFPFIQK.F
[8377](#) 698.3753 2092.1041 2092.1025 0.76 0 84 1.7e-007 1 U K.NLVSLINAGATAVGLSGHNGR.L
[19582](#) 1241.1438 4960.5461 4960.4869 11.9 0 26 0.065 1 U R.VDPSVLRLVYGVYPIVASVAADDSGQAYHNTADTVAGELAAALGAEK.L

75. [AT1G29910.1](#) Mass: 28266 Score: 110 Matches: 5(3) Sequences: 5(3) emPAI: 0.57
| 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
[1002](#) 491.7686 981.5225 981.5243 -1.81 0 47 0.00049 1 R.ELEVHSR.W
[1007](#) 492.2486 982.4826 982.4913 -8.82 0 40 0.0035 1 K.FGEAVWFK.A
[3183](#) 633.2782 1264.5418 1264.5473 -4.29 0 52 0.00012 1 K.GPSSPFWYSDR.V
[15417](#) 1031.5150 3091.5232 3091.5152 2.60 0 18 1.1 1 U K.GPIENLHADLPVNNNAWAFATNFVPGK.-
[16848](#) 1211.2687 3630.7842 3630.7617 6.20 0 28 0.1 1 U R.VAGNPLGEAEEDLLYPGGSFDPGLGLATDPEAFAEK.V

Proteins matching the same set of peptides:
[AT1G29920.1](#) Mass: 28266 Score: 110 Matches: 5(3) Sequences: 5(3)
| Symbols: CAB2, AB165, LHCB1.1 | chlorophyll A/B-binding protein 2 | chr1:10475089-10475892 REVERSE LENGTH=267
[AT1G29930.1](#) Mass: 28280 Score: 110 Matches: 5(3) Sequences: 5(3)
| Symbols: CAB1, AB140, CAB140, LHCB1.3 | chlorophyll A/B binding protein 1 | chr1:10478071-10478874 FORWARD LENGTH=267

76. [AT2G34420.1](#) Mass: 28093 Score: 110 Matches: 5(3) Sequences: 5(3) emPAI: 0.57
| Symbols: LHB1B2, 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
[1002](#) 491.7686 981.5225 981.5243 -1.81 0 47 0.00049 1 R.ELEVHSR.W
[1007](#) 492.2486 982.4826 982.4913 -8.82 0 40 0.0035 1 K.FGEAVWFK.A
[3183](#) 633.2782 1264.5418 1264.5473 -4.29 0 52 0.00012 1 K.GPSSPFWYSDR.V
[15417](#) 1031.5150 3091.5232 3091.5152 2.60 0 18 1.1 1 U K.GPIENLHADLPVNNNAWAFATNFVPGK.-
[16848](#) 1211.2687 3630.7842 3630.7617 6.19 0 28 0.1 1 U R.VAGDPLGEAEEDLLYPGGSFDPGLGLATDPEAFAEK.V

77. [AT4G36690.1](#) Mass: 63683 Score: 107 Matches: 3(1) Sequences: 3(1) emPAI: 0.07
| Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294139-17297609 REVERSE LENGTH=573
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[9717](#) 1132.5580 2263.1014 2263.1042 -1.23 0 18 1 1 U R.SVERASNMSLDGIIFGAPVK.V
[12088](#) 910.4780 2728.4123 2728.4140 -0.63 0 93 3e-008 1 U R.VMLQGAIVATTVVCLTQVVTEDEL.R.D
[19026](#) 1082.7564 4326.9963 4327.0004 -0.96 1 28 0.06 1 U R.VMLQGAIVATTVVCLTQVVTEDELRDDEYGDIMEDMR.Q

Proteins matching the same set of peptides:
[AT4G36690.2](#) Mass: 60815 Score: 107 Matches: 3(1) Sequences: 3(1)
| Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294591-17297609 REVERSE LENGTH=542
[AT4G36690.3](#) Mass: 63701 Score: 107 Matches: 3(1) Sequences: 3(1)
| Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294422-17297609 REVERSE LENGTH=565
[AT4G36690.4](#) Mass: 60799 Score: 107 Matches: 3(1) Sequences: 3(1)
| Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294139-17297609 REVERSE LENGTH=551

78. [AT1G20010.1](#) Mass: 50880 Score: 105 Matches: 4(2) Sequences: 4(2) emPAI: 0.18
| Symbols: TUB5 | tubulin beta-5 chain | chr1:6938033-6940481 REVERSE LENGTH=449
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1479](#) 533.2162 1064.4178 1064.4201 -2.17 0 16 0.16 1 K.NNMCAADPR.H
[1533](#) 359.8478 1076.5216 1076.5250 -3.19 1 22 0.34 1 K.IREYTPDR.M
[2156](#) 570.3497 1138.6849 1138.6862 -1.18 0 56 2.9e-005 1 K.LAVNLIPFPR.L
[5950](#) 824.4065 1646.7984 1646.8008 -1.42 0 70 6.4e-006 1 U R.AVLMDLEFGTMDSIR.S

Proteins matching the same set of peptides:
[AT1G15780.1](#) Mass: 50755 Score: 105 Matches: 4(2) Sequences: 4(2)
| Symbols: TUB1 | tubulin beta-1 chain | chr1:28451378-28453602 REVERSE LENGTH=447

79. [AT3G49430.1](#) Mass: 33807 Score: 105 Matches: 6(5) Sequences: 5(5) emPAI: 0.87
| Symbols: SRp34a, SR34a, At-SR34a | SER/ARG-rich protein 34A | chr3:18332668-18334829 FORWARD LENGTH=300
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[421](#) 415.2502 828.4858 828.4957 -11.88 0 31 0.032 1 U R.IVDIELK.V
[671](#) 448.2100 894.4054 894.4083 -3.22 0 39 0.003 1 K.LDDTEFR.N
[1183](#) 512.2570 1022.4995 1022.5033 -3.69 1 39 0.0056 1 R.KLDDTEFR.N [1182](#)
[1493](#) 535.2214 1068.4282 1068.4295 -1.19 0 35 0.0021 1 U R.DGYNLDCGR.L
[3643](#) 441.5410 1321.6010 1321.6190 -13.61 0 45 0.0011 1 U R.EHEIDETIFYK.Y

Proteins matching the same set of peptides:
[AT3G49430.2](#) Mass: 33727 Score: 105 Matches: 6(5) Sequences: 5(5)
| Symbols: SRp34a, SR34a, At-SR34a | SER/ARG-rich protein 34A | chr3:18332668-18334617 FORWARD LENGTH=297
[AT3G49430.3](#) Mass: 33807 Score: 105 Matches: 6(5) Sequences: 5(5)
| Symbols: SRp34a, SR34a, At-SR34a | SER/ARG-rich protein 34A | chr3:18332668-18334829 FORWARD LENGTH=300

80. [AT5G35680.1](#) Mass: 16750 Score: 105 Matches: 3(3) Sequences: 3(3) emPAI: 1.11
| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr5:13858152-13858589 REVERSE LENGTH=145
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2272](#) 575.2805 1148.5464 1148.5462 0.17 0 56 0.00011 1 K.AYGELENTR.L
[2539](#) 598.7518 1195.4891 1195.5036 -12.10 0 55 3.3e-005 1 U R.CDVICIDGVK.R
[4248](#) 711.8586 1421.7027 1421.7038 -0.76 1 42 0.0043 1 R.DYQDKADVILK.Y

Proteins matching the same set of peptides:
[AT5G35680.2](#) Mass: 16750 Score: 105 Matches: 3(3) Sequences: 3(3)
| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr5:13858152-13858589 REVERSE LENGTH=145
[AT5G35680.3](#) Mass: 17182 Score: 105 Matches: 3(3) Sequences: 3(3)
| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr5:13858085-13858589 REVERSE LENGTH=150

81. [AT5G16780.1](#) Mass: 94086 Score: 103 Matches: 3(2) Sequences: 3(2) emPAI: 0.10
| Symbols: DOT2, MDF | SART-1 family | chr5:5517784-5521566 REVERSE LENGTH=820
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1694](#) 547.7781 1093.5417 1093.5403 1.27 0 21 0.39 1 U R.SNAYQRAIAK.A
[1896](#) 558.7863 1115.5579 1115.5571 0.79 0 45 0.0013 1 U K.EASALDLQNR.I
[4835](#) 745.8380 1489.6615 1489.6645 -2.02 0 79 3.2e-007 1 U R.GLNEGGDNVDAASQK.E

82. [AT5G02530.1](#) Mass: 30761 Score: 103 Matches: 3(3) Sequences: 3(3) emPAI: 0.51
| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1401](#) 525.7628 1049.5110 1049.5142 -3.04 0 53 0.00023 1 U R.YNNVQDLK.L
[2460](#) 590.8184 1179.6222 1179.6248 -2.22 1 41 0.003 1 U R.SKGTARVFPVSR.R
[3371](#) 431.5662 1291.6767 1291.6772 -0.42 1 51 0.00041 1 U K.ELFSEVQDLKR.Y

Proteins matching the same set of peptides:
[AT5G02530.2](#) Mass: 30548 Score: 103 Matches: 3(3) Sequences: 3(3)
| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=290

83. [AT4G17520.1](#) Mass: 38882 Score: 103 Matches: 4(4) Sequences: 4(4) emPAI: 0.55
| Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[725](#) 456.7786 911.5426 911.5440 -1.53 0 39 0.0018 1 U K.VVAPVQTAQK.S
[2489](#) 594.2600 1186.5053 1186.5063 -0.83 0 28 0.022 1 K.EMTLEYEK.V
[4943](#) 506.9425 1517.8057 1517.8089 -2.15 0 55 0.0002 1 K.SLSINEFLKPADGK.S
[6741](#) 599.9276 1796.7608 1796.7674 -3.64 1 35 0.0048 1 U R.RGYSVNGGDSERPR.K

84. [AT2G25670.1](#) Mass: 35108 Score: 101 Matches: 3(3) Sequences: 2(2) emPAI: 0.27
| 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
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[6022](#) 831.3638 1660.7130 1660.7176 -2.77 0 39 0.0024 1 U K.NNGLEESQEAQEK.K
[6679](#) 595.9927 1784.9564 1784.9560 0.23 0 60 5.4e-005 1 U K.ELALEALLADFGVAPK.E
[6680](#) 893.4857 1784.9569 1784.9560 0.51 0 (51) 0.00036 1 U K.ELALEALLADFGVAPK.E

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8018	1015.0344	2028.0542	2028.0527	0.71	0	91	4.1e-008	1	U	K.ENAPAIIFIDEVDIAIATAR.F

96. [AT3G08580.1](#) Mass: 41563 Score: 91 Matches: 3(3) Sequences: 3(3) emPAI: 0.36
| 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
647	441.1995	880.3845	880.3862	-1.89	0	34	0.0064	1	U	K.GIGDCFGR.T
758	459.2929	916.5713	916.5746	-3.55	0	44	0.00026	1		K.LQLIVFGK.K
3741	672.8613	1343.7081	1343.7119	-2.79	0	57	0.00011	1	U	K.LLIGNQDEMIK.A

Proteins matching the same set of peptides:
[AT3G08580.2](#) Mass: 41563 Score: 91 Matches: 3(3) Sequences: 3(3)
| Symbols: AAC1 | ADP/ATP carrier 1 | chr3:2605706-2607030 REVERSE LENGTH=381

97. [AT2G18020.1](#) Mass: 28013 Score: 90 Matches: 2(2) Sequences: 2(2) emPAI: 0.35
| Symbols: EMB2296 | Ribosomal protein L2 family | chr2:7837151-7838160 FORWARD LENGTH=258

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1154	508.7683	1015.5221	1015.5233	-1.15	0	51	0.0004	1	U	R.AMIGQVAGGGR.T
3097	626.3908	1250.7671	1250.7711	-3.19	0	63	2.5e-006	1	U	K.ATLVVGVNPLRL.S

Proteins matching the same set of peptides:
[AT4G36130.1](#) Mass: 28159 Score: 90 Matches: 2(2) Sequences: 2(2)
| Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258

98. [ATCG00480.1](#) Mass: 53957 Score: 87 Matches: 3(2) Sequences: 3(2) emPAI: 0.17
| Symbols: ATPB, PB | ATP synthase subunit beta | chrC:52660-54156 REVERSE LENGTH=498

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
277	488.2795	974.5445	974.5549	-10.74	0	40	0.0042	1	U	K.IGLPQAGVVK.T
4223	708.3586	1414.7026	1414.7052	-1.84	0	71	3.7e-006	1	U	R.TNPTTSNPVEVIR.R
4695	736.4305	1470.8464	1470.8479	-1.05	0	15	0.71	1	U	K.TVLIMELINIAK.A

99. [AT3G05060.1](#) Mass: 59195 Score: 86 Matches: 5(3) Sequences: 4(2) emPAI: 0.16
| Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr3:1413174-1415564 REVERSE LENGTH=533

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6118	844.3762	1686.7379	1686.7471	-5.49	0	37	0.0057	1	U	K.VVEEKPEEKEPSEK.K
6889	605.9525	1814.8357	1814.8421	-3.53	1	49	0.00056	1	U	K.KVEEKPEEKEPSEK.K
6890	908.4258	1814.8371	1814.8421	-2.74	1	(45)	0.0014	1	U	K.KVEEKPEEKEPSEK.K
7606	486.7402	1942.9317	1942.9371	-2.76	2	26	0.13	1	U	K.KVEEKPEEKEPSEK.K
7607	486.6516	1942.9330	1942.9371	-2.09	2	27	0.11	1	U	K.KVVEEKPEEKEPSEK.K

100. [AT4G10340.1](#) Mass: 30195 Score: 85 Matches: 2(2) Sequences: 2(2) emPAI: 0.32
| Symbols: LHCB5 | 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
3076	416.5495	1246.6267	1246.6458	-15.37	0	36	0.016	1	U	K.YQAFELIAR.W
8780	709.0382	2124.0928	2124.0964	-1.67	0	68	8e-006	1	U	K.HLSDPPGNLLTVIAGTAER.A

101. [AT1G45000.1](#) Mass: 44898 Score: 85 Matches: 2(2) Sequences: 1(1) emPAI: 0.21
| 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
6771	900.9825	1799.9504	1799.9491	0.72	0	62	3.1e-005	1	U	R.ESELPLANPELFLR.V
6778	901.4815	1800.9485	1800.9331	8.52	0	(43)	0.0026	1	U	R.ESELPLANPELFLR.V

Proteins matching the same set of peptides:
[AT1G45000.2](#) Mass: 37720 Score: 85 Matches: 2(2) Sequences: 1(1)
| Symbols: | AAA-type ATPase family protein | chr1:17009220-17011607 FORWARD LENGTH=335
[AT5G43010.1](#) Mass: 44960 Score: 85 Matches: 2(2) Sequences: 1(1)
| Symbols: RPT4A | regulatory particle triple-A ATPase 4A | chr5:17248563-17251014 REVERSE LENGTH=399

102. [AT5G28540.1](#) Mass: 73869 Score: 84 Matches: 2(2) Sequences: 2(2) emPAI: 0.12
| Symbols: BIP1 | heat shock protein 70 (Hsp 70) family protein | chr5:10540665-10543274 REVERSE LENGTH=669

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5305	782.9156	1563.8166	1563.8218	-3.31	0	41	0.0045	1	U	K.VFSPERISAMILTK.M
6018	830.9491	1659.8836	1659.8719	7.08	0	66	1.3e-005	1		R.IIIEPTAAAIAYGLDK.K

Proteins matching the same set of peptides:
[AT5G42020.1](#) Mass: 73801 Score: 84 Matches: 2(2) Sequences: 2(2)
| Symbols: BIP, BIP2 | Heat shock protein 70 (Hsp 70) family protein | chr5:16807697-16810480 REVERSE LENGTH=668
[AT5G42020.2](#) Mass: 67644 Score: 84 Matches: 2(2) Sequences: 2(2)
| Symbols: BIP | Heat shock protein 70 (Hsp 70) family protein | chr5:16807697-16810480 REVERSE LENGTH=613

103. [AT1G78630.1](#) Mass: 26886 Score: 84 Matches: 1(1) Sequences: 1(1) emPAI: 0.17
| Symbols: emb1473 | Ribosomal protein L13 family protein | chr1:29575997-29577406 FORWARD LENGTH=241

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1702	365.8798	1094.6176	1094.6196	-1.81	0	84	7.1e-008	1	U	R.LASTIANHIR.G

104. [AT3G55460.1](#) Mass: 29607 Score: 82 Matches: 6(3) Sequences: 4(2) emPAI: 0.33
| 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
105	381.7106	761.4066	761.4072	-0.70	0	23	0.29	1	U	R.DVIYPR.D 104
1012	493.2208	984.4270	984.4301	-3.18	0	21	0.14	1	U	R.DYYSQGPR.G
1712	549.7206	1097.4267	1097.4261	0.56	0	46	0.00016	1	U	R.GEEDENYSR.R
5301	521.5642	1561.6706	1561.6757	-3.25	1	(26)	0.034	1	U	R.GGPPGREEDENYSR.R
5302	781.8445	1561.6744	1561.6757	-0.82	1	43	0.00071	1	U	R.GGPPGREEDENYSR.R

105. [AT2G34160.1](#) Mass: 14607 Score: 82 Matches: 3(3) Sequences: 2(2) emPAI: 1.35
| Symbols: | Alba DNA/RNA-binding protein | chr2:14426283-14427220 FORWARD LENGTH=130

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
346	408.2594	814.5042	814.5164	-14.90	0	38	0.0047	1	U	K.IEITLVK.S
1106	504.2749	1006.5352	1006.5369	-1.62	0	(37)	0.0088	1		K.IMTSTVDIK.D
1184	512.2730	1022.5315	1022.5318	-0.32	0	58	6.8e-005	1		K.IHTSTVDIK.D

106. [AT5G56500.1](#) Mass: 63627 Score: 81 Matches: 2(1) Sequences: 2(1) emPAI: 0.07
| Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:22874058-22876966 FORWARD LENGTH=597

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2879	615.3439	1228.6733	1228.6914	-14.75	0	20	0.54	1	U	R.DIIISILEDIAIK.G
3279	640.8756	1279.7367	1279.7612	-19.18	0	81	1.2e-007	1		K.VVAAGANPVLITR.G

Proteins matching the same set of peptides:
[AT5G56500.2](#) Mass: 63627 Score: 81 Matches: 2(1) Sequences: 2(1)
| Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:22874058-22876966 FORWARD LENGTH=597

107. [AT2G04520.1](#) Mass: 16798 Score: 80 Matches: 3(3) Sequences: 3(3) emPAI: 1.11
| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:1574802-1575239 REVERSE LENGTH=145

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2272	575.2805	1148.5464	1148.5462	0.17	0	56	0.00011	1		K.AYGELEPENTR.L
2475	592.7373	1183.4600	1183.4672	-6.01	0	28	0.0083	1	U	R.CEMACIDGTK.R
4248	711.8586	1421.7027	1421.7038	-0.76	1	42	0.0043	1		R.DVQDDKADVILK.Y

108. [AT3G07030.1](#) Mass: 42476 Score: 79 Matches: 4(3) Sequences: 4(3) emPAI: 0.35
| Symbols: | Alba DNA/RNA-binding protein | chr3:2223001-2225254 REVERSE LENGTH=405

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3317	643.7756	1285.5366	1285.5436	-5.45	1	27	0.024	1	U	R.YGGGRDDGYGGGR.D
4989	765.3976	1528.7807	1528.7773	2.25	0	38	0.0095	1	U	R.WYISTATSLLEK.S
5344	787.3129	1572.6112	1572.6190	-4.94	1	41	0.00032	1	U	R.DGYGGGRDDGYGGGR.N
11806	888.0801	2661.2184	2661.2055	4.84	0	27	0.095	1	U	K.DSPGYQAQSDGSKPQFPQGGGR.Q

109. [AT3G48930.1](#) Mass: 18174 Score: 79 Matches: 1(1) Sequences: 1(1) emPAI: 0.26
| Symbols: EMB1080 | Nucleic acid-binding, OB-fold-like protein | chr3:18141017-18142189 REVERSE LENGTH=160

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2133	568.8012	1135.5877	1135.5873	0.36	0	79	7.4e-007	1	U	K.VIPAGSSSPGK.K

110. [AT3G20550.1](#) Mass: 37102 Score: 76 Matches: 3(2) Sequences: 3(2) emPAI: 0.26
| Symbols: DDL | SMAD/FHA domain-containing protein | chr3:7174695-7177600 REVERSE LENGTH=314

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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1039	496.2354	990.4563	990.4698	-13.66	0	25	0.12	1	U	R.YYELFEK.D
4547	723.8647	1445.7149	1445.7150	-0.05	0	45	0.0019	1	U	K.TYINESPIEQR.Y
5354	787.8482	1573.6819	1573.6856	-2.37	0	46	0.00046	1	U	R.GGSEEPNVEEDSVAR.M

111.	AT5G13490.1	Mass: 41834	Score: 76	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.23				
Symbols: AAC2 ADP/ATP carrier 2 chr5:4336034-4337379 FORWARD LENGTH=385										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
758	459.2929	916.5713	916.5746	-3.55	0	44	0.00026	1	U	K.LQLIVFGK.K
3741	672.8613	1343.7081	1343.7119	-2.79	0	57	0.00011	1	U	K.LLIQNGDEMLK.A

Proteins matching the same set of peptides:

AT5G13490.2	Mass: 41834	Score: 76	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.23
Symbols: AAC2 ADP/ATP carrier 2 chr5:4336034-4337379 FORWARD LENGTH=385					

112.	AT5G14040.1	Mass: 40463	Score: 75	Matches: 3(2)	Sequences: 3(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
303	401.7259	801.4373	801.4385	-1.46	0	41	0.0052	1	U	K.YAIPNPK.S
1044	497.2775	992.5405	992.5477	-7.28	0	50	0.00035	1	U	K.IGMVGLPTR.G
4222	708.3394	1414.6643	1414.6616	1.90	0	22	0.21	1	U	K.TYSDLAGPEYTA.Y

113. [AT3G19650.1](#) Mass: 35261 Score: 75 Matches: 1(1) Sequences: 1(1) emPAI: 0.13
| Symbols: | cyclin-related | chr3:6823543-6825174 FORWARD LENGTH=302

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2418	589.7656	1177.5166	1177.5211	-3.85	0	75	8e-007	1	U	R.ESDQTQALSR.K

114.	AT1G23860.1	Mass: 21695	Score: 75	Matches: 7(3)	Sequences: 6(3)	emPAI: 0.79				
Symbols: SRZ-21, SRZ21, RSZP21, RSZ21, At-RSZ21 RS-containing zinc finger protein 21 chr1:8428091-8429164 REVERSE LENGTH=187										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
72	372.7108	743.4071	743.4079	-0.95	0	28	0.088	1	U	R.NVNVAR.R
713	455.2133	908.4120	908.4127	-0.81	0	31	0.02	1	U	R.ELDEEFA.A
1291	516.7758	1031.5371	1031.5400	-2.82	0	31	0.054	1	U	R.VYVGNLDP.V
4105	697.8378	1393.6610	1393.6725	-8.26	1	15	1.5	7	U	R.VTERELEDEFA.A
4869	500.2106	1497.6101	1497.6129	-1.91	0	45	0.0003	1	U	K.CYCEGELGHFA.E
14966	596.9016	2979.4717	2979.4726	-0.32	2	24	0.29	1	U	R.RPPGYAFLEFDUERDALDAISALDRK.N
14967	745.8756	2979.4733	2979.4726	0.24	2	(19)	0.86	1	U	R.RPPGYAFLEFDUERDALDAISALDRK.N

Proteins matching the same set of peptides:

AT1G23860.2	Mass: 21695	Score: 75	Matches: 7(3)	Sequences: 6(3)	emPAI: 0.79
Symbols: SRZ-21, SRZ21, RSZ21, At-RSZ21 RS-containing zinc finger protein 21 chr1:8428091-8429164 REVERSE LENGTH=187					
AT1G23860.3	Mass: 19030	Score: 75	Matches: 7(3)	Sequences: 6(3)	emPAI: 0.79
Symbols: SRZ-21, SRZ21, RSZ21, At-RSZ21 RS-containing zinc finger protein 21 chr1:8428091-8429164 REVERSE LENGTH=164					
AT1G23860.4	Mass: 21149	Score: 75	Matches: 7(3)	Sequences: 6(3)	emPAI: 0.79
Symbols: RSZP21, RSZ21, At-RSZ21 RS-containing zinc finger protein 21 chr1:8428091-8429164 REVERSE LENGTH=183					

115.	AT4G32610.1	Mass: 34758	Score: 73	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
6695	895.4827	1788.9509	1788.9509	0.01	0	73	2.9e-006	1	U	K.ELAELEALLADFGVATK.D

116.	AT5G26742.1	Mass: 81293	Score: 72	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.11				
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
3700	668.8895	1335.7645	1335.7650	-0.33	0	58	3e-005	1	U	R.TILSDLITVYAK.G
4991	765.4127	1528.8108	1528.8137	-1.91	0	40	0.0056	1	U	R.IQGAVDLPETIAK.E

Proteins matching the same set of peptides:

AT5G26742.2	Mass: 81449	Score: 72	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.11
Symbols: emb1138 DEAD box RNA helicase (RH3) chr5:9285540-9288871 REVERSE LENGTH=748					
AT5G26742.3	Mass: 71192	Score: 72	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.11
Symbols: emb1138 DEAD box RNA helicase (RH3) chr5:9285540-9288618 REVERSE LENGTH=655					

117.	AT3G25920.1	Mass: 29860	Score: 70	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.33				
Symbols: RPL15 ribosomal protein L15 chr3:9491268-9492558 REVERSE LENGTH=277										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
332	407.2325	812.4504	812.4504	-0.04	0	28	0.028	1	U	K.GLENSGR.E
2551	599.7930	1197.5714	1197.5778	-5.38	0	66	8.5e-006	1	U	R.GFGGQTALY.R

118. [AT1G16610.1](#) Mass: 45322 Score: 70 Matches: 1(1) Sequences: 1(1) emPAI: 0.10
| Symbols: SR45, RNPS1 | arginine/serine-rich 45 | chr1:5675925-5678686 REVERSE LENGTH=414
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[4172](#) 705.3303 1408.6461 1408.6656 -13.89 0 70 3.6e-006 1 U K.AQLYMDGAQIDGK.V

Proteins matching the same set of peptides:

AT1G16610.2	Mass: 44622	Score: 70	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Symbols: SR45, RNPS1 arginine/serine-rich 45 chr1:5675925-5678686 REVERSE LENGTH=407					
AT1G16610.3	Mass: 46570	Score: 70	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Symbols: SR45 arginine/serine-rich 45 chr1:5675925-5678686 REVERSE LENGTH=425					

119. [AT3G13860.1](#) Mass: 60771 Score: 70 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
| Symbols: HSP60-3A | heat shock protein 60-3A | chr3:4561704-4565133 REVERSE LENGTH=572

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5135	773.3609	1544.7072	1544.7067	0.39	0	70	2.9e-006	1	U	K.ALDNLQTENEDQR.R

120.	AT1G56110.1	Mass: 58865	Score: 70	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08				
Symbols: NOP56 homolog of nucleolar protein NOP56 chr1:20984544-20986893 REVERSE LENGTH=522										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
16781	1200.9427	3599.8064	3599.7930	3.73	0	70	5.7e-006	1	U	R.VVQLTAPHPFESALDALNQVNAVSEGVMTDEL.R.S

121.	AT1G55310.1	Mass: 33333	Score: 70	Matches: 3(3)	Sequences: 3(3)	emPAI: 0.46				
Symbols: SR33, ATSC133, SCL33, At-SCL33 SC35-like aplicing factor 33 chr1:20630676-20632695 FORWARD LENGTH=287										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1013	493.7126	985.4106	985.4141	-3.55	0	44	0.00049	1	U	R.DYTTGDP.R
1140	507.3010	1012.5875	1012.5917	-4.13	0	36	0.0047	1	U	R.DLPTSLR.N
6681	893.9076	1785.8007	1785.8032	-1.39	0	29	0.043	1	U	R.GFGFVQPMDDAAADAK.H

Proteins matching the same set of peptides:

AT1G55310.2	Mass: 25570	Score: 70	Matches: 3(3)	Sequences: 3(3)	emPAI: 0.46
Symbols: SR33, ATSC133, SCL33, At-SCL33 SC35-like aplicing factor 33 chr1:20630676-20632567 FORWARD LENGTH=220					

122.	ATCG00120.1	Mass: 351	Score: 70	Matches: 3(2)	Sequences: 3(2)	emPAI: 0.17				
Symbols: ATPA ATP synthase subunit alpha chrC:9938-11461 REVERSE LENGTH=507										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
344	408.2329	814.4513	814.4548	-4.32	0	26	0.12	2	U	R.ELIIGDR.Q
554	430.7526	859.4906	859.4949	-5.01	0	44	0.0022	1	U	R.QMSLLLR.R
9748	758.4099	2272.2079	2272.2137	-2.54	0	53	0.0002	1	U	R.SVVEPLQTGLLAIDSNPIGR.G

123.	AT1G67090.1	Mass: 20488	Score: 70	Matches: 3(3)	Sequences: 3(3)	emPAI: 0.85				
Symbols: RBCS1A ribulose biphosphate carboxylase small chain 1A chr1:25048465-25049249 REVERSE LENGTH=180										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
709	454.2473	906.4800	906.4811	-1.16	0	34	0.018	1	U	K.EVDYLIR.N
801	468.2497	934.4848	934.4872	-2.57	0	40	0.0046	1	U	R.IIGFDNTR.Q
5148	774.9054	1547.7962	1547.8018	-3.57	0	45	0.0019	1	U	K.LPLFGCTDSAQVLK.E

124.	AT2G38540.1	Mass: 12317	Score: 70	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.40				
Symbols: LPI1, LTP1, ATLTP1 lipid transfer protein 1 chr2:16130418-16130893 FORWARD LENGTH=118										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
751	458.2520	914.4893	914.4934	-4.39	0	70	4.2e-006	1	U	R.ALIGSLNAGR.A

125.	AT4G33070.1	Mass: 67253	Score: 70	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07				
Symbols: Thiamine pyrophosphate dependent pyruvate decarboxylase family protein chr4:15952519-15954676 REVERSE LENGTH=607										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2910	619.3157	1236.6168	1236.6211	-3.47	0	70	6e-006	1	U	R.VSAANSRFPNPQ.-

Proteins matching this same set of peptides:

AT5G54960.1	Mass: 66802	Score: 70	Matches: 1(1)	Sequences: 1(1)
Symbols: PDC2 pyruvate decarboxylase-2 chr5:22310858-22312681 REVERSE LENGTH=607				

| Symbols: | Ribosomal protein S3ae | chr3:1329751-1331418 FORWARD LENGTH=262

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
108	382.2019	762.3892	762.3912	-2.65	0	46	0.001	1	U	K.AVDFFSK.K
5749	810.4484	1618.8822	1618.8831	-0.59	0	43	0.0023	1	U	K.ATQGIYPLQNVFIR.K

Proteins matching the same set of peptides:
AT4G34670.1 Mass: 29956 Score: 69 Matches: 2(2) Sequences: 2(2)
 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262

Symbols: | dehydrin family protein | chr1:20310305-20310601 REVERSE LENGTH=98

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2287	576.3113	1150.6080	1150.6095	-1.27	0	60	3.9e-005	1	U	K.IGDALHIGGGNK.E
2288	384.5433	1150.6082	1150.6095	-1.13	0	(34)	0.016	1	U	K.IGDALHIGGGNK.E

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3361	430.8995	1289.6768	1289.6979	-16.38	1	52	0.00043	1	U	K.ELFPAEVGELK.R.Y
5876	545.8972	1634.6698	1634.6784	-5.22	0	36	0.0023	1	U	K.APESTGWGHMFSDR.S

Proteins matching the name of peptides:

ATG509950.4	Mass: 23565	Score: 67	Matches: 2(2)	Sequences: 2(2)
Symbols: RNA-binding (RM/RBD/RNF motifs) family protein chr5:24140235-24141410 FORWARD LENGTH=211				
ATG509950.5	Mass: 25827	Score: 67	Matches: 2(2)	Sequences: 2(2)
Symbols: RNA-binding (RM/RBD/RNF motifs) family protein chr5:24140235-24141504 FORWARD LENGTH=245				

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1314	520.8250	1039.6355	1039.6390	-3.38	0	45	0.0026	1	U	R.LVTPLTQQR.K
3695	668.8188	1335.6230	1335.6241	-0.84	0	45	0.0016	1	U	K.FNVANPTTGQCK.K

Proteins matching the same set of peptides:

<u>AT5G0360.1</u>	Mass: 28373	Score: 66	Matches: 2(2)	Sequences: 2(2)
Symbols: EMB3010, RPS6b Ribosomal protein S6e chr5:3258734-3260142 REVERSE LENGTH=249				
<u>AT5G0360.2</u>	Mass: 22311	Score: 66	Matches: 2(2)	Sequences: 2(2)
Symbols: EMB3010 Ribosomal protein S6e chr5:3258734-3260142 REVERSE LENGTH=197				

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2886	616.3107	1230.6069	1230.6105	-2.95	0	34	0.021	1	U	K.STPGSPAHPPGAR.S
3648	442.2121	1323.6145	1323.6208	-4.76	0	55	0.00012	1	U	R.SPSPSPFHTPDR.R

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3232	578.7812	1155.5477	1155.5520	-3.68	0	26	0.083	1	U	R.SIEVEETGHR.N
3248	637.7816	1273.5486	1273.5535	-3.83	0	61	1.4e-005	1	U	K.VENNNDLNDAR.N

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4374	715.3500	1428.6854	1428.6885	-2.17	1	64	1.7e-005	1	U	R.KLDLTETFGFEFSR.F

[AT1G26110.2](#) Mass: 63621 Score: 64 Matches: 1(1) Sequences: 1(1)
 | Symbols: DCP5 | decapping 5 | chr1:9024616-9027556 REVERSE LENGTH=605

Symbols: XWB		Ribosomal protein S5 family protein		cNR1:21689115-21690085 FORWARD LENGTH=284					
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
5986	827.9231	1653.8316	1653.8363	-2.79	0.63	2.8e-005	1	U	K.VLQFAGIDVFTSSR.G

AT5G08684.1	Name: 30980	Score: 63	Matches: 1(1)	Sequences: 1(1)
[Symbols]	Ribosomal protein S5 family protein	chr1:21770021-21771217	REVERSE	LENGTH=284
AT5G58983.1	Name: 30980	Score: 63	Matches: 1(1)	Sequences: 1(1)
[Symbols]	Ribosomal protein S5 family protein	chr1:21806279-21807475	REVERSE	LENGTH=284
AT5G59359.1	Name: 30980	Score: 63	Matches: 1(1)	Sequences: 1(1)
[Symbols]	Ribosomal protein S5 family protein	chr1:21842537-21843733	REVERSE	LENGTH=284
AT2G41840.1	Name: 31087	Score: 63	Matches: 1(1)	Sequences: 1(1)
[Symbols]	Ribosomal protein S5 family protein	chr2:17460016-17461398	REVERSE	LENGTH=285
AT3G57490.1	Name: 30325	Score: 63	Matches: 1(1)	Sequences: 1(1)
[Symbols]	Ribosomal protein S5 family protein	chr3:21279824-21280887	REVERSE	LENGTH=276

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
9929	772.7424	2315.2053	2315.2042	0.46	0	62	3.3e-005	1	U	K.INAINAATEAACILLSVDETVK.N

AT3G11830.2	Mass: 59935	Score: 62	Matches: 1(1)	Sequences: 1(1)
Symbols:	TCP-1/cpn60 chaperonin family protein chr3:3732734-3736156 FORWARD LENGTH=555			

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<u>805</u>	468.2630	934.5115	934.5124	-0.93	0	36	0.0092	1	U	R.EITVQFAK.Y
<u>3851</u>	677.8464	1353.6783	1353.6816	-2.44	0	55	0.00016	1	U	R.TTADDELYPLFAK.Y

Protein matching the same set of peptides:
ATSG64200.2 Mass: 35149 Score: 62 Matches: 2(2) Sequences: 2(2)
 | Symbols: ATSC35, SC35, At-SC35 | ortholog of human splicing factor SC35 | chr5:25681849-25683553 REVERSE LENGTH=303

Query		Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
291	400.2671	798.5196	798.5215	-2.29	0	33	0.0086	1	U		R.LIALLEK.Y
2161	570.8389	1139.6633	1139.6662	-2.58	0	52	0.00011	1	U		K.GLAGELVNVLR.E

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Uniq	Peptide
347	408.7360	815.4575	815.4654	-9.58	0	47	0.00092	1	U	K.INPGLFR.L
8977	1080.5686	2159.1226	2159.1262	-1.66	0	36	0.014	1	U	R.ISNPYDGNILAEFIAGQLK.N

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
976	488.2778	974.5411	974.5293	12.1	0	20	0.53	2	U	K. <u>Q</u> IMPVK.A 97
1104	504.2666	1006.5186	1006.5196	-0.92	0	61	3.9e-005	1	U	R.LATSGANFAR.A

Proteins matching the same set of peptides:

AT5G64040.2	Mass: 19563	Score: 61	Matches: 3(1)	Sequences: 2(1)
Symbols: PSAN photoavstem I reaction center subunit PSI-N. chloroplast. putative / PSI-N. putative (PSAN) chr5:25628690-25629409 REVERSE LENGTH=181				

139. [AT5G06850.1](#) Mass: 91629 Score: 61 Matches: 3(2) Sequences: 3(2) emPAI: 0.10
| 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

1077

499.8039

997.5932

997.5920

1.20

0

15

0.46

1

U

K.VGVNQILK.T

2197

566.8323

1131.6500

1131.6539

-3.48

0

32

0.019

1

U

R.LISLPSVFEK.R

2800

406.8750

1217.6033

1217.6074

-3.42

1

52

0.00037

1

U

K.VTPAKDEVQGR.L

140.

ATCG00160.1

Mass: 27172

Score: 61

Matches: 3(2)

Sequences: 3(2)

emPAI: 0.36

| Symbols: RPS2 | ribosomal protein S2 | chrC:15013-15723 REVERSE LENGTH=236

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

704

453.2698

904.5250

904.5382

-14.59

0

41

0.002

1

U

K.QFLIVGK.N

1045

497.2842

992.5538

992.5542

-0.43

0

22

0.14

1

U

R.LETYLGGIK.Y

6187

850.9019

1699.7892

1699.7876

0.94

0

41

0.0033

1

U

R.FLSEACDLVFDASR.G

141.

AT1G31130.1

Mass: 24329

Score: 60

Matches: 2(2)

Sequences: 2(2)

emPAI: 0.41

| Symbols: PSAP | photosystem I | chrI:11215011-1121939 REVERSE LENGTH=221

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1550

540.7943

1079.5741

1079.5862

-13.28

0

40

0.0036

1

U

R.SVLTAISGEK.K

2836

613.3583

1224.7021

1224.7078

-4.60

0

44

0.00072

1

U

K.EIIVDPLASR.I

142.

AT3G50670.1

Mass: 50415

Score: 60

Matches: 2(1)

Sequences: 2(1)

emPAI: 0.09

| Symbols: UI-70K, ULSNRNP | UI small nuclear ribonucleoprotein-70K | chr3:18826476-18829492 REVERSE LENGTH=427

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

420

415.2422

828.4698

828.4705

-0.84

0

28

0.061

1

U

R.VLVDVER.G

5916

820.4050

1638.7954

1638.7962

-0.48

0

60

6.1e-005

1

U

R.VGGGEIVGEQQPQGR.T

143.

ATCG00820.1

Mass: 10570

Score: 59

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.48

| Symbols: RPS19 | ribosomal protein S19 | chrC:84005-84283 REVERSE LENGTH=92

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

3277

640.8304

1279.6463

1279.6561

-7.62

0

59

6.2e-005

1

U

K.LGEFSPITNFR.G

144.

AT3G02220.1

Mass: 26113

Score: 59

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.18

| Symbols: | unknown protein: CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2039 (InterPro:IPR019351); Has 215 Blast hits to 215 proteins in 94 species: Archae - 2; Bacteria - 2; Metazoa - 125; Fungi - 4; Plants -

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

973

487.7473

973.4800

973.4829

-2.93

0

59

5.1e-005

1

U

K.INITEVGQR.F

145.

AT1G48920.1

Mass: 58796

Score: 59

Matches: 2(2)

Sequences: 2(2)

emPAI: 0.16

| Symbols: ATNUC-11, PARL1, NUC-L1 | nucleolin like 1 | chr1:18098186-18101422 FORWARD LENGTH=557

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

498

422.7299

843.4453

843.4450

0.33

0

29

0.042

1

U

R.LDIAQER.G

1452

531.2346

1060.4546

1060.4560

-1.39

0

53

5.6e-005

1

U

R.EPEDIDTK.V

146.

AT3G12390.1

Mass: 21969

Score: 59

Matches: 2(2)

Sequences: 2(2)

emPAI: 0.47

| Symbols: | Nascent polypeptide-associated complex (NAC), alpha subunit family protein | chr3:3942344-3943595 FORWARD LENGTH=203

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2144

386.8938

1157.6565

1157.6591

-2.25

0

52

0.00028

1

U

K.LGMGPITGVSR.S

4951

760.4462

1518.8779

1518.8810

-2.03

0

28

0.027

1

U

K.NILFVSKPDVFR.S

Proteins matching the same set of peptides:

AT5G13850.1

Mass: 22044

Score: 59

Matches: 2(2)

Sequences: 2(2)

| Symbols: NACA3 | nascent polypeptide-associated complex subunit alpha-like protein 3 | chr5:4471361-4472676 FORWARD LENGTH=204

147.

AT3G44690.1

Mass: 138560

Score: 59

Matches: 2(1)

Sequences: 2(1)

emPAI: 0.03

| Symbols: | unknown protein: Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLINK). | chr3

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1907

559.2432

1116.4718

1116.4724

-0.52

0

20

0.089

1

U

K.YYDSGIDER.M

3213

635.3065

1268.5985

1268.5997

-0.94

0

59

5.1e-005

1

U

K.SDLVLHEDAR.G

148.

AT2G27710.1

Mass: 11437

Score: 59

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

1217

514.7895

1027.5644

1027.5662

-1.70

0

59

4.3e-005

1

U

K.DLAELIAAGR.E

Proteins matching the same set of peptides:

AT2G27710.2

Mass: 11437

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=115

AT2G27710.3

Mass: 11437

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=115

AT2G27710.4

Mass: 10237

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=98

AT2G27720.1

Mass: 11445

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=115

AT2G27720.2

Mass: 13137

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=130

AT2G27720.3

Mass: 12757

Score: 59

Matches: 1(1)

Sequences: 1(1)

| Symbols: | 60S acidic ribosomal protein family | chr2:11818696-11819370 FORWARD LENGTH=127

149.

AT1G09070.1

Mass: 34282

Score: 59

Matches: 2(1)

Sequences: 2(1)

emPAI: 0.13

| Symbols: SRC2, (AT)SRC2 | soybean gene regulated by cold-2 | chr1:2927767-2928741 FORWARD LENGTH=324

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

790

466.2448

930.4750

930.4771

-2.20

0

59

7e-005

1

U

K.LTYDDAAR.D

4232

473.2308

1416.6707

1416.6732

-1.80

1

16

1

1

U

K.ELLQNKQDEEK.T

150.

AT3G24100.1

Mass: 7248

Score: 59

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.75

| Symbols: | Uncharacterised protein family SERP | chr3:8703373-8704045 FORWARD LENGTH=69

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

3235

636.8093

1271.6040

1271.6106

-5.18

1

51

0.00025

1

U

K.NKDDGLTFEQR.R

3236

424.8767

1271.6083

1271.6106

-1.79

1

(30)

0.033

1

U

K.NKDDGLTFEQR.R

151.

AT2G31610.1

Mass: 27673

Score: 58

Matches: 4(1)

Sequences: 4(1)

emPAI: 0.17

| Symbols: | Ribosomal protein S3 family protein | chr2:13450384-13451669 FORWARD LENGTH=250

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

757

459.2662

916.5179

916.5229

-5.53

0

20

0.5

1

U

R.ELTSLVQK.R

810

468.7422

935.4698

935.4712

-1.49

0

20

0.47

1

U

K.EYIDAAVR.H

2791

406.2182

1215.6329

1215.6571

-19.97

1

18

1

2

U

R.ATRTQNLVGEK.G

3349

644.8270

1287.6395

1287.6605

-16.30

0

58

7.7e-005

1

U

R.GLCAIAQESLSL.Y

Proteins matching the same set of peptides:

AT5G15530.1

Mass: 27612

Score: 58

Matches: 4(1)

Sequences: 4(1)

| Symbols: | Ribosomal protein S3 family protein | chr5:13710355-13712192 REVERSE LENGTH=248

152.

AT3G26060.1

Mass: 23834

Score: 58

Matches: 3(2)

Sequences: 3(2)

emPAI: 0.42

| Symbols: ATPRX Q | Thioredoxin superfamily protein | chr3:9524807-9526123 FORWARD LENGTH=216

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

564

433.7315

865.4485

865.4545

-6.93

0

17

0.88

1

U

R.QTYVLDK.N

1384

524.2811

1046.5477

1046.5397

7.69

0

38

0.0088

1

U

K.GQAAPDFTLK.D

5278

778.8970

1555.7794

1555.7784

0.67

0

42

0.0035

1

U

K.DWGVGDLFGALPGR.Q

Proteins matching the same set of peptides:

AT3G26060.2

Mass: 23962

Score: 58

Matches: 3(2)

Sequences: 3(2)

| Symbols: ATPRX Q | Thioredoxin superfamily protein | chr3:9524807-9526123 FORWARD LENGTH=217

153.

AT1G29150.1

Mass: 47005

Score: 57

Matches: 2(2)

Sequences: 1(1)

emPAI: 0.09

| Symbols: AT59, RPN6 | non-ATPase subunit 9 | chr1:10181240-10182499 FORWARD LENGTH=419

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

8389

524.7987

2095.1657

2095.1677

-0.94

0

(31)

0.017

1

U

R.VEAIHIAELIGLPLDRVEK.K

8390

699.3986

2095.1739

2095.1677

2.93

0

40

0.002

1

U

R.VEAIHIAELIGLPLDRVEK.K

154.

AT5G57370.1

Mass: 26026

Score: 56

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.18

| Symbols: | unknown protein: CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1777 (InterPro:IPR013957); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi -

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2855

613.8455

1225.6764

1225.6779

-1.24

0

56

5.6e-005

1

U

K.GKPVAGADVSGIR.A

155.

AT4G28990.1

Mass: 39987

Score: 56

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.11

| Symbols: | RNA-binding protein-related | chr4:14291205-14293018 FORWARD LENGTH=347

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	3920	682.8065	1363.5984	1363.6004	-1.49	0	56	5.9e-005	1	U R.NAAGDYRPEVSR.D
Proteins matching the same set of peptides:										
	AT4G28990.2	Mass:	45584	Score:	56	Matches:	1(1)	Sequences:	1(1)	
	Symbols:	RNA-binding protein-related chr4:14291205-14293018 FORWARD LENGTH=395								
156.	AT1G52570.1	Mass:	92167	Score:	56	Matches:	3(2)	Sequences:	2(1)	emPAI: 0.05
	Symbols:	PLDAPHIA2 phospholipase D alpha 2 chr1:19583940-19586551 REVERSE LENGTH=810								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	2790	608.8230	1215.6314	1215.6347	-2.67	0	17	1.1	3	U K.QQGVDTVGELLK.K
	3324	429.5598	1285.6574	1285.6779	-15.89	0	44	0.0019	1	R.SIQDAYHAIR.R
	3338	643.8447	1285.6748	1285.6779	-2.39	0	(33)	0.025	1	R.SIQDAYHAIR.R
157.	AT1G02840.1	Mass:	33823	Score:	56	Matches:	4(3)	Sequences:	3(3)	emPAI: 0.46
	Symbols:	SR1, ATSRP34, SRP34, SR34, At-SR34 RNA-binding (RRM/RBD/RNP motifs) family protein chr1:626918-629583 FORWARD LENGTH=303								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	671	448.2100	894.4054	894.4083	-3.22	0	39	0.003	1	K.LDDTEFR.N
	1183	512.2570	1022.4995	1022.5033	-3.69	1	39	0.0056	1	K.KLDDTEFR.N182
	1551	541.2202	1080.4259	1080.4261	-0.22	0	22	0.036	1	U R.DGYDPDGR.H
Proteins matching the same set of peptides:										
	AT1G02840.2	Mass:	32062	Score:	56	Matches:	4(3)	Sequences:	3(3)	
	Symbols:	SR1, ATSRP34, SRP34, SR34, At-SR34 RNA-binding (RRM/RBD/RNP motifs) family protein chr1:626918-628995 FORWARD LENGTH=285								
	AT1G02840.3	Mass:	33823	Score:	56	Matches:	4(3)	Sequences:	3(3)	
	Symbols:	SR1, ATSRP34, SRP34, SR34, At-SR34 RNA-binding (RRM/RBD/RNP motifs) family protein chr1:626918-629583 FORWARD LENGTH=303								
158.	AT2G36160.1	Mass:	16304	Score:	55	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.29
	Symbols:	Ribosomal protein S11 family protein chr2:15169925-15171159 FORWARD LENGTH=150								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	1417	527.7850	1053.5554	1053.5567	-1.25	0	55	9.9e-005	1	U K.TPGDAQSALR.A
Proteins matching the same set of peptides:										
	AT3G11510.1	Mass:	16320	Score:	55	Matches:	1(1)	Sequences:	1(1)	
	Symbols:	Ribosomal protein S11 family protein chr3:3623757-3624866 REVERSE LENGTH=150								
	AT3G52580.1	Mass:	16285	Score:	55	Matches:	1(1)	Sequences:	1(1)	
	Symbols:	Ribosomal protein S11 family protein chr3:19503324-19504701 FORWARD LENGTH=150								
159.	AT1G12900.1	Score:	55	Matches:	3(2)	Sequences:	1(1)	emPAI:	0.10	
	Symbols:	GAPA-2 glyceraldehyde 3-phosphate dehydrogenase A subunit 2 chr1:4392634-4394283 REVERSE LENGTH=399								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	467	417.2338	832.4530	832.4555	-3.08	0	(27)	0.1	2	U K.VAINGFGR.I
	471	417.7267	833.4388	833.4395	-0.88	0	50	0.00065	2	U K.VAINGFGR.I 470
Proteins matching the same set of peptides:										
	AT1G12900.3	Score:	55	Matches:	3(2)	Sequences:	1(1)			
	Symbols:	GAPA-2 glyceraldehyde 3-phosphate dehydrogenase A subunit 2 chr1:4392634-4393850 REVERSE LENGTH=350								
	AT1G12900.4	Score:	55	Matches:	3(2)	Sequences:	1(1)			
	Symbols:	GAPA-2 glyceraldehyde 3-phosphate dehydrogenase A subunit 2 chr1:4392634-4393850 REVERSE LENGTH=350								
	AT1G42970.1	Score:	55	Matches:	3(2)	Sequences:	1(1)			
	Symbols:	GAPB glyceraldehyde-3-phosphate dehydrogenase B subunit chr1:16127552-16129584 FORWARD LENGTH=447								
	AT3G26650.1	Score:	55	Matches:	3(2)	Sequences:	1(1)			
	Symbols:	GAPA, GAPA-1 glyceraldehyde 3-phosphate dehydrogenase A subunit chr3:9795226-9796848 FORWARD LENGTH=396								
160.	AT1G71080.1	Mass:	34868	Score:	55	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.13
	Symbols:	RNA polymerase II transcription elongation factor chr1:26809987-26811645 REVERSE LENGTH=326								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	3834	676.8719	1351.7292	1351.7347	-4.07	0	55	0.00012	1	U R.SLLDPVPEVER.I
161.	ATCG00020.1	Mass:	39025	Score:	54	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.11
	Symbols:	PSBA photosystem II reaction center protein A chrC:383-1444 REVERSE LENGTH=353								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	3591	657.8605	1313.7065	1313.7092	-2.02	0	54	0.00018	1	U R.VINTWADIIMR.A
162.	ATCG00770.1	Mass:	15527	Score:	54	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.31
	Symbols:	RPS8 ribosomal protein S8 chrC:80068-80472 REVERSE LENGTH=134								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	3172	631.3430	1260.6714	1260.6925	-16.78	0	54	0.00026	1	U R.IGSTNITESIVK.I
163.	AT3G05530.1	Mass:	47735	Score:	54	Matches:	3(2)	Sequences:	3(2)	emPAI: 0.20
	Symbols:	RPT5A, AT56A.2 regulatory particle triple-A ATPase 5A chr3:1603540-1605993 FORWARD LENGTH=424								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	7042	617.3470	1849.0193	1849.0019	9.43	0	26	0.065	1	U K.QIGELVEAIVLPMTHK.E
	8029	678.3556	2032.0451	2032.0551	-4.89	1	41	0.0055	1	U K.EKAPCIIFIIDEIDAIQTK.R
	12048	907.5112	2719.5117	2719.5161	-1.61	0	29	0.018	1	U R.QTIFLPVVGVLVDPSLKGDLGVGNK.D
164.	AT1G07840.1	Mass:	36168	Score:	53	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.12
	Symbols:	Sas10/Utp3/CID family chr1:2424603-2426425 FORWARD LENGTH=312								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	2579	402.2138	1203.6195	1203.6248	-4.37	1	53	0.00034	1	U K.FLIDKGEKPR.S
Proteins matching the same set of peptides:										
	AT1G07840.2	Mass:	36168	Score:	53	Matches:	1(1)	Sequences:	1(1)	
	Symbols:	Sas10/Utp3/CID family chr1:2424603-2426425 FORWARD LENGTH=312								
165.	AT2G38530.1	Mass:	12500	Score:	53	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.39
	Symbols:	LTP2, LP2, cdf3 lipid transfer protein 2 chr2:16128481-16128948 FORWARD LENGTH=118								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	2813	611.7949	1221.5752	1221.5772	-1.65	0	53	0.00027	1	U K.ISASTNCTVR.-
166.	AT3G13460.1	Mass:	72716	Score:	52	Matches:	2(1)	Sequences:	2(1)	emPAI: 0.06
	Symbols:	ECT2 evolutionarily conserved C-terminal region 2 chr3:4385274-4388220 REVERSE LENGTH=667								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	3618	660.2958	1318.5770	1318.5789	-1.47	0	52	0.00013	1	U R.SALGYSGSGSDSR.T
	7699	658.6573	1972.9502	1972.9490	0.60	0	17	1	1	U K.YSDVQRPVSGGVASYSK.S
Proteins matching the same set of peptides:										
	AT3G13460.2	Mass:	72438	Score:	52	Matches:	2(1)	Sequences:	2(1)	
	Symbols:	ECT2 evolutionarily conserved C-terminal region 2 chr3:4385274-4388220 REVERSE LENGTH=664								
	AT3G13460.3	Mass:	54999	Score:	52	Matches:	2(1)	Sequences:	2(1)	
	Symbols:	ECT2 evolutionarily conserved C-terminal region 2 chr3:4385934-4388220 REVERSE LENGTH=508								
	AT3G13460.4	Mass:	72614	Score:	52	Matches:	2(1)	Sequences:	2(1)	
	Symbols:	ECT2 evolutionarily conserved C-terminal region 2 chr3:4385274-4388220 REVERSE LENGTH=666								
167.	AT3G60770.1	Mass:	17142	Score:	52	Matches:	1(1)	Sequences:	1(1)	emPAI: 0.28
	Symbols:	Ribosomal protein S13/S15 chr3:22460525-22461656 REVERSE LENGTH=151								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	4093	696.8196	1391.6246	1391.6239	0.53	0	52	0.00018	1	U K.TTPQDVDESICK.F
168.	AT3G09630.1	Mass:	44788	Score:	52	Matches:	3(2)	Sequences:	2(1)	emPAI: 0.10
	Symbols:	Ribosomal protein L4/L1 family chr3:2953813-2955444 FORWARD LENGTH=406								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide
	1303	517.7678	1033.5210	1033.5226	-1.58	0	21	0.5	2	U R.MSLLAQAQR.V
	2575	401.5710	1201.6913	1201.6918	-0.40	1	43	0.0015	1	U K.TVTKERAIAIK.A
	2576	601.8531	1201.6916	1201.6918	-0.12	1	(35)	0.01	1	U K.TVTKERAIAIK.A
169.	AT2G39390.1	Score:	52	Matches:	1(1)	Sequences:	1(1)	emPAI:	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
	258	393.2431	784.4716	784.4807	-11.55	0	52	0.00011	1	U K.AELALLR.V
Proteins matching the same set of peptides:										
	AT3G09500.1	Score:	52	Matches:	1(1)	Sequences:	1(1)			
	Symbols:	Ribosomal L29 family protein chr3:2917047-2917895 FORWARD LENGTH=123								
	AT5G02610.1	Mass:	14322	Score:	52	Matches:	1(1)	Sequences:	1(1)	

	Symbols:	Ribosomal L29 family protein	chr5:587611-588547	FORWARD LENGTH=123	
	AT5G02610.2	Mass: 17068	Score: 52	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Ribosomal L29 family protein	chr5:587611-588547	FORWARD LENGTH=146	
170.	AT4G00100.1	Mass: 17132	Score: 51	Matches: 1(1) Sequences: 1(1) emPAI: 0.28	
	Symbols:	ATRPS13A, RPS13, PFL2, RPS13A	ribosomal protein S13a	chr4:37172-38123	FORWARD LENGTH=151
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	4027	691.8077	1381.6008	1381.6031	-1.68 0 51 0.00017 1 0 K.TTSQDVDESICK.F
171.	AT1G70200.1	Mass: 60587	Score: 51	Matches: 1(1) Sequences: 1(1) emPAI: 0.07	
	Symbols:	RNA-binding (RRM/RBD/RNP motifs)	family protein	chr1:26432514-26434351	REVERSE LENGTH=538
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	424	415.7337	829.4528	829.4545	-2.01 0 51 0.00047 1 0 K.IEIPGSXK.R
172.	AT3G63400.1	Mass: 63674	Score: 51	Matches: 1(1) Sequences: 1(1) emPAI: 0.07	
	Symbols:	Cyclophilin-like peptidyl-prolyl	cis-trans isomerase family protein	chr3:23412449-23415435	FORWARD LENGTH=570
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	3363	646.3184	1290.6223	1290.6238	-1.17 0 51 0.00044 1 0 K.IIDGSETSQIR.A
	Proteins matching the same set of peptides:				
	AT3G63400.2	Mass: 42395	Score: 51	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Cyclophilin-like peptidyl-prolyl	cis-trans isomerase family protein	chr3:23412449-23415435	FORWARD LENGTH=387
	AT3G63400.3	Mass: 63674	Score: 51	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Cyclophilin-like peptidyl-prolyl	cis-trans isomerase family protein	chr3:23412449-23415435	FORWARD LENGTH=570
173.	AT2G1890.1	Mass: 76259	Score: 50	Matches: 1(1) Sequences: 1(1) emPAI: 0.06	
	Symbols:	ATRAP, RAP	RAP	chr2:13557100-13559715	REVERSE LENGTH=671
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	10856	844.1168	2529.3286	2529.3247	1.55 0 50 0.00042 1 0 K.AIIIAQTAREVLEVTARTINAVAK.G
174.	AT3G22310.1	Mass: 63798	Score: 50	Matches: 2(2) Sequences: 2(2) emPAI: 0.14	
	Symbols:	PWH1, ATRH9	putative mitochondrial RNA helicase 1	chr3:7887382-7889806	FORWARD LENGTH=610
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	683	449.2856	896.5565	896.5695	-14.43 0 23 0.04 1 0 R.ASIIIGPLVK.E
	2495	594.3550	1186.6954	1186.6962	-0.63 0 44 0.00088 1 0 K.TLAFGIPIDIK.I
175.	AT3G61860.1	Mass: 31136	Score: 50	Matches: 2(1) Sequences: 2(1) emPAI: 0.15	
	Symbols:	ATRSP31, RSP31, At-RS31, RS31	RNA-binding (RRM/RBD/RNP motifs)	family protein	chr3:22900311-22902159
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	636	439.2129	876.4112	876.4130	-2.08 0 26 0.11 1 0 K.HFEPTGK.V
	1416	352.1812	1053.5217	1053.5243	-2.46 1 45 0.00093 1 0 R.YKGPAAAYER.R
176.	AT3G62530.1	Mass: 24659	Score: 50	Matches: 1(1) Sequences: 1(1) emPAI: 0.19	
	Symbols:	ARM repeat superfamily protein	chr3:23132219-23133121	FORWARD LENGTH=221	
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	2103	566.7755	1131.5365	1131.5408	-3.79 0 50 0.0004 1 0 R.GAIDSSAPAEK.A
177.	AT1G04820.1	Mass: 50194	Score: 50	Matches: 1(1) Sequences: 1(1) emPAI: 0.09	
	Symbols:	TUA4, TOR2	tubulin alpha-4 chain	chr1:1356421-1358266	REVERSE LENGTH=450
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	6191	851.4596	1700.9046	1700.8985	3.59 0 50 0.00059 1 0 R.AVFVDLEPTVIDEVR.T
	Proteins matching the same set of peptides:				
	AT1G50010.1	Mass: 50194	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	TUA2	tubulin alpha-2 chain	chr1:18517737-18519729	FORWARD LENGTH=450
	AT4G14960.1	Mass: 47889	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	TUA6	Tubulin/FtsZ family protein	chr4:8548753-8550319	REVERSE LENGTH=427
	AT4G14960.2	Mass: 50191	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	TUA6	Tubulin/FtsZ family protein	chr4:8548769-8550319	REVERSE LENGTH=450
	AT5G19770.1	Mass: 50250	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	TUA3	tubulin alpha-3	chr5:6682761-6684474	REVERSE LENGTH=450
	AT5G19780.1	Mass: 50250	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	TUA5	tubulin alpha-5	chr5:6687212-6688926	FORWARD LENGTH=450
178.	AT4G31480.1	Mass: 107161	Score: 50	Matches: 1(1) Sequences: 1(1) emPAI: 0.04	
	Symbols:	Coatomer, beta subunit	chr4:15264145-15267384	FORWARD LENGTH=948	
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	3067	622.8273	1243.6400	1243.6521	-9.70 0 50 0.00056 1 0 K.VAVVTIQNER.E
	Proteins matching the same set of peptides:				
	AT4G31480.2	Mass: 107161	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Coatomer, beta subunit	chr4:15264145-15267384	FORWARD LENGTH=948	
	AT4G31490.1	Mass: 107094	Score: 50	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Coatomer, beta subunit	chr4:15269460-15272693	FORWARD LENGTH=948	
179.	AT5G62190.1	Mass: 73187	Score: 49	Matches: 1(1) Sequences: 1(1) emPAI: 0.06	
	Symbols:	PRH75	DEAD box RNA helicase (PRH75)	chr5:24980542-24983879	REVERSE LENGTH=671
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	4630	730.3889	1458.7631	1458.7678	-3.20 0 49 0.00068 1 0 K.VQVSELSGLLDQSR.A
180.	AT3G14310.1	Mass: 64729	Score: 49	Matches: 2(1) Sequences: 2(1) emPAI: 0.07	
	Symbols:	ATPME3, PME3	pectin methylesterase 3	chr3:4772214-4775095	REVERSE LENGTH=592
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	16543	888.4262	3549.6755	3549.6821	-1.86 0 36 0.014 1 0 K.TALHDLCLTIDETLDELHETVEDLHLYPTK.K
	17097	736.5642	3677.7847	3677.7771	2.07 1 27 0.12 1 0 K.TALHDLCLTIDETLDELHETVEDLHLYPTK.T
181.	AT4G14300.1	Mass: 42328	Score: 48	Matches: 1(1) Sequences: 1(1) emPAI: 0.11	
	Symbols:	RNA-binding (RRM/RBD/RNP motifs)	family protein	chr4:8231179-8232785	FORWARD LENGTH=411
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	8219	685.9924	2054.9553	2054.9586	-1.60 0 48 0.00088 1 0 R.GPGFVPSDEDAVSVLHK.T
182.	AT3G53500.1	Score: 48	Matches: 1(1) Sequences: 1(1) emPAI: 0.17		
	Symbols:	RS232, RS2232, At-RS22	RNA-binding (RRM/RBD/RNP motifs)	family protein with retrovirus zinc finger-like domain	chr3:19834557-19835896
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	119	388.2176	774.4207	774.4236	-3.70 0 48 0.00011 1 0 R.ITVEASR.G
	Proteins matching the same set of peptides:				
	AT3G53500.2	Score: 48	Matches: 1(1) Sequences: 1(1)		
	Symbols:	RS232, RS2232, At-RS22	RNA-binding (RRM/RBD/RNP motifs)	family protein with retrovirus zinc finger-like domain	chr3:19834557-19836507
183.	AT2G34040.1	Mass: 61948	Score: 48	Matches: 2(2) Sequences: 2(2) emPAI: 0.15	
	Symbols:	Apoptosis inhibitory protein 5 (API5)	chr2:14377957-14382246	REVERSE LENGTH=553	
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	965	486.7573	971.5000	971.5036	-3.69 0 29 0.04 1 0 K.IVTGQPSDR.L
	3099	626.8961	1251.7776	1251.7802	-2.10 0 40 0.00048 1 0 R.QLLPSIVELLK.I
	Proteins matching the same set of peptides:				
	AT2G34040.2	Mass: 50360	Score: 48	Matches: 2(2) Sequences: 2(2)	
	Symbols:	Apoptosis inhibitory protein 5 (API5)	chr2:14378571-14382246	REVERSE LENGTH=442	
184.	AT3G26420.1	Mass: 27135	Score: 48	Matches: 1(1) Sequences: 1(1) emPAI: 0.17	
	Symbols:	ATRZ-1A	RNA-binding (RRM/RBD/RNP motifs)	family protein with retrovirus zinc finger-like domain	chr3:9671953-9673055
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	2362	580.7835	1159.5525	1159.5550	-2.18 0 48 0.00061 1 0 R.GFGFITFDEK.K
185.	AT3G45030.1	Mass: 13984	Score: 48	Matches: 1(1) Sequences: 1(1) emPAI: 0.35	
	Symbols:	Ribosomal protein S10p/S20e	family protein	chr3:16471606-16472312	REVERSE LENGTH=124
	Query	Observed	Mr(expt)	Mr(calc)	ppm Miss Score Expect Rank Unique Peptide
	3617	659.8640	1317.7135	1317.7180	-3.46 0 48 0.00089 1 0 R.VIDLFSPPVVK.Q
	Proteins matching the same set of peptides:				
	AT3G47370.1	Mass: 13799	Score: 48	Matches: 1(1) Sequences: 1(1)	
	Symbols:	Ribosomal protein S10p/S20e	family protein	chr3:17453671-17454437	REVERSE LENGTH=122

	AT3G47370.2	Mass: 13799	Score: 48	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein S10p/S20e family protein	chr3:17453671-17454437 REVERSE LENGTH=122								
	AT3G47370.3	Mass: 13799	Score: 48	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein S10p/S20e family protein	chr3:17453671-17454437 REVERSE LENGTH=122								
	AT5G62300.1	Mass: 13984	Score: 48	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein S10p/S20e family protein	chr5:25021388-25022235 REVERSE LENGTH=124								
	AT5G62300.2	Mass: 13984	Score: 48	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein S10p/S20e family protein	chr5:25021388-25022235 REVERSE LENGTH=124								
186.	AT3G02080.1	Mass: 15875	Score: 48	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.69					
	Symbols:	Ribosomal protein S19e family protein	chr3:364138-365161 REVERSE LENGTH=143								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	623	437.2251	872.4356	872.4352	0.45	0	40	0.0022	1	U	R.DLDQVAGR.I
	3593	657.8682	1313.7219	1313.7231	-0.91	0	30	0.046	1	U	K.IELPTWTDIVK.T
187.	AT1G29320.1	Mass: 52809	Score: 47	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08					
	Symbols:	Transducin/WD40 repeat-like superfamily protein	chr1:10255355-10258238 FORWARD LENGTH=468								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3359	430.8756	1289.6049	1289.6099	-3.86	1	47	0.00082	1	U	K.VSSEGEKDEL.R.S
188.	AT1G60650.1	Mass: 34605	Score: 47	Matches: 2(1)	Sequences: 2(1)	emPAI: 0.13					
	Symbols:	RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain	chr1:22340089-22342148 FORWARD LENGTH=292								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2362	580.7835	1159.5525	1159.5662	-11.88	0	47	0.00076	2	U	R.GGFGFITFDDR.R
	6077	419.4381	1673.7232	1673.7256	-1.42	0	15	0.64	1	U	R.YGMPFHHLENEYR.G
	Proteins matching the same set of peptides:										
	AT1G60650.2	Mass: 34605	Score: 47	Matches: 2(1)	Sequences: 2(1)						
	Symbols:	RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain	chr1:22340089-22342148 FORWARD LENGTH=292								
189.	AT1G29030.1	Mass: 62583	Score: 46	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.15					
	Symbols:	Apoptosis inhibitory protein 5 (API5)	chr1:10129201-10133697 REVERSE LENGTH=556								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	965	486.7573	971.5000	971.5036	-3.69	0	29	0.04	1	U	K.IVTGQPSDDR.L
	3099	626.8961	1251.7776	1251.7802	-2.10	0	38	0.00068	2	U	R.QILPSIVQLLK.K
190.	AT5G27850.1	Mass: 21011	Score: 46	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.22					
	Symbols:	Ribosomal protein L18e/L15 superfamily protein	chr5:9873169-9874297 FORWARD LENGTH=187								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	7649	491.0086	1960.0053	1960.0068	-0.73	0	46	0.0015	1	U	K.HFGPAGVPHSNTEPKFYVR.H
191.	AT5G42710.1	Mass: 93100	Score: 46	Matches: 3(1)	Sequences: 1(1)	emPAI: 0.05					
	Symbols:	unknown protein: Has 1807 Blast hits to 1807 proteins in 277 species: Archaea - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLINK).	chr5:17125578-17125578-1								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	8372	698.0230	2091.0472	2091.0531	-2.81	1	33	0.037	1	U	K.GAQLNQIINACNSGLSFR.K 8369
	8381	698.6858	2093.0357	2093.0211	6.98	1	(23)	0.34	1	U	K.GAQLNQIINACNSGLSFR.K
	Proteins matching the same set of peptides:										
	AT5G42710.2	Mass: 92614	Score: 46	Matches: 3(1)	Sequences: 1(1)						
	Symbols:	unknown protein: INVOLVED IN: biological_process unknown.	chr5:17125578-17128696 FORWARD LENGTH=803								
192.	AT1G22780.1	Mass: 17591	Score: 46	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.27					
	Symbols: PFL, RPS18A, PFL1	Ribosomal protein S13/S18 family	chr1:8067990-8069163 FORWARD LENGTH=152								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1185	512.2974	1022.5802	1022.5834	-3.18	0	46	0.00055	1	U	K.IMFALTSIK.G
	Proteins matching the same set of peptides:										
	AT1G34030.1	Mass: 17591	Score: 46	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein S13/S18 family	chr1:12370285-12371465 REVERSE LENGTH=152								
	AT4G09800.1	Mass: 17591	Score: 46	Matches: 1(1)	Sequences: 1(1)						
	Symbols: RPS18C	S18 ribosomal protein	chr4:6173818-6174963 FORWARD LENGTH=152								
193.	AT5G39980.1	Mass: 78508	Score: 45	Matches: 7(0)	Sequences: 1(0)						
	Symbols:	Tetratricopeptide repeat (TPR)-like superfamily protein	chr5:16001036-16003072 REVERSE LENGTH=678								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1037	495.7533	989.4920	989.4778	14.4	1	30	0.059	1	U	R.ADKLINDASR.V 1031 1032 1033 1034 1035 1036
194.	AT3G15356.1	Mass: 29788	Score: 45	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15					
	Symbols:	Legume lectin family protein	chr3:5174603-5175418 REVERSE LENGTH=271								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2810	611.3288	1220.6429	1220.6554	-10.17	0	45	0.0016	1	U	K.AGYVQVLVGK.R
195.	AT2G39460.1	Mass: 17430	Score: 45	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.27					
	Symbols: ATRPL23A, RPL23A, RPL23AA	ribosomal protein L23AA	chr2:16475049-16475904 FORWARD LENGTH=154								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4391	717.8476	1433.6806	1433.7038	-16.16	0	45	0.0018	1	U	R.LTPDYDALDVANK.I
	Proteins matching the same set of peptides:										
	AT2G39460.2	Mass: 17430	Score: 45	Matches: 1(1)	Sequences: 1(1)						
	Symbols: ATRPL23A, RPL23A, RPL23AA	ribosomal protein L23AA	chr2:16475049-16475904 FORWARD LENGTH=154								
	AT3G5280.1	Mass: 17385	Score: 45	Matches: 1(1)	Sequences: 1(1)						
	Symbols: RPL23AB	ribosomal protein L23AB	chr3:20500667-20501519 FORWARD LENGTH=154								
	AT3G5280.2	Mass: 17385	Score: 45	Matches: 1(1)	Sequences: 1(1)						
	Symbols: RPL23AB	ribosomal protein L23AB	chr3:20500667-20501519 FORWARD LENGTH=154								
	AT3G5280.3	Mass: 16733	Score: 45	Matches: 1(1)	Sequences: 1(1)						
	Symbols: RPL23AB	ribosomal protein L23AB	chr3:20500667-20501519 FORWARD LENGTH=148								
196.	AT1G19870.1	Mass: 87115	Score: 44	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05					
	Symbols: igd32 IQ-domain 32	chr1:6895400-6898539 REVERSE LENGTH=794									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2417	587.2612	1172.5079	1172.5098	-1.62	0	44	0.0005	1	U	R.TSPGYDQEAR.E
197.	AT2G07698.1	Score: 44	Matches: 2(1)	Sequences: 2(1)	emPAI: 0.05						
	Symbols:	ATPase, F1 complex, alpha subunit protein	chr2:3361474-3364028 FORWARD LENGTH=777								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	344	408.2329	814.4513	814.4548	-4.32	0	26	0.12	2	U	R.ELLIGDR.Q
	554	430.7526	859.4906	859.4949	-5.01	0	44	0.0022	1		R.QMSLLLR.R
198.	AT5G15200.1	Mass: 23079	Score: 44	Matches: 3(2)	Sequences: 3(2)	emPAI: 0.44					
	Symbols:	Ribosomal protein S4	chr5:4935124-4936334 REVERSE LENGTH=198								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	707	453.7542	905.4938	905.4971	-3.59	0	32	0.027	1	U	K.LVGEYGLR.N
	853	473.7504	945.4862	945.5019	-16.51	0	35	0.017	1	U	R.DLLTLDEK.S
	3630	660.3587	1318.7028	1318.7067	-2.95	0	26	0.14	1	U	K.QLVNI PSF HVR.L
199.	AT3G58660.1	Mass: 50224	Score: 44	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09					
	Symbols:	Ribosomal protein L1p/L10e family	chr3:21701574-21702914 FORWARD LENGTH=446								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	5525	530.9382	1589.7929	1589.7970	-2.62	1	44	0.0024	1	U	K.EVSEVASEKPMKK.A
200.	AT1G13950.1	Mass: 17521	Score: 44	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.27					
	Symbols: EIF-5A, ELPSA-1, ATELP5A-1, EIF5A	eukaryotic elongation factor 5A-1	chr1:4773631-4774668 FORWARD LENGTH=158								
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	9161	555.0269	2216.0783	2216.0644	6.29	1	44	0.0028	1	U	K.KLEDIVPSSHNCDVPHVNR.T
	Proteins matching the same set of peptides:										
	AT1G26630.1	Mass: 17358	Score: 44	Matches: 1(1)	Sequences: 1(1)						
	Symbols: FBR12, ATELP5A-2, ELPSA-2	Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) protein	chr1:9205968-9207098 FORWARD LENGTH=159								
	AT1G26630.2	Mass: 15322	Score: 44	Matches: 1(1)	Sequences: 1(1)						
	Symbols: FBR12, ATELP5A-2, ELPSA-2	Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) protein	chr1:9205968-9207013 FORWARD LENGTH=138								
	AT1G69410.1	Mass: 17425	Score: 44	Matches: 1(1)	Sequences: 1(1)						
	Symbols: ATELP5A-3, ELPSA-3	eukaryotic elongation factor 5A-3	chr1:26089301-26090194 FORWARD LENGTH=158								
201.	AT5G15230.1	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.42						

	Symbols: GAS44	GAST1 protein homolog 4	chr5:4945017-4946025	FORWARD	LENGTH=106	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>39</u>	361.1969	720.3793	720.3806	-1.84	0 43 0.0017 1 U R.YGPGSLK.R
Proteins matching the same set of peptides:						
	<u>AT5G15230.2</u>	Score: 43	Matches: 1(1)	Sequences: 1(1)		
	Symbols: GAS44	GAST1 protein homolog 4	chr5:4945286-4946025	FORWARD	LENGTH=83	
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202.	<u>AT2G38140.1</u>	Mass: 12890	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.38
	Symbols: PSRP4	plastid-specific ribosomal protein 4	chr2:15980948-15981459	FORWARD	LENGTH=118	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>787</u>	465.2817	928.5487	928.5494	-0.74	0 43 0.002 1 U R.VPVPFAPPR.K
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203.	<u>AT5G26280.1</u>	Mass: 39421	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
	Symbols:	TRAF-like family protein	chr5:9208724-9210403	FORWARD	LENGTH=350	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>1856</u>	554.8094	1107.6043	1107.6176	-11.95	0 43 0.0013 1 U K.YLTVTDLGVK.R
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Proteins matching the same set of peptides:						
	<u>AT5G26280.2</u>	Mass: 36852	Score: 43	Matches: 1(1)	Sequences: 1(1)	
	Symbols:	TRAF-like family protein	chr5:9208724-9210403	FORWARD	LENGTH=327	
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204.	<u>AT3G23980.1</u>	Mass: 78394	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
	Symbols: BLI, KOS1	BLISTER	chr3:8662818-8667440	REVERSE	LENGTH=714	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>1685</u>	546.3078	1090.6010	1090.6056	-4.19	1 43 0.0019 1 U K.KVLQTMVQK.A
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205.	<u>AT1G35680.1</u>	Mass: 24195	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.19
	Symbols:	Ribosomal protein L21	chr1:13208777-13210246	FORWARD	LENGTH=220	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>994</u>	490.2634	978.5123	978.5287	-16.75	0 43 0.0021 1 U R.QYIVFPGR.Y
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206.	<u>AT2G03680.1</u>	Mass: 11970	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.41
	Symbols: SPRI, SKU6	spiral1	chr2:1121398-1121850	FORWARD	LENGTH=119	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>799</u>	467.7405	933.4664	933.4668	-0.43	0 43 0.0027 1 U K.TPVNNYAR.A
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Proteins matching the same set of peptides:						
	<u>AT2G03680.2</u>	Mass: 11970	Score: 43	Matches: 1(1)	Sequences: 1(1)	
	Symbols: SPRI, SKU6	spiral1	chr2:1121398-1121850	FORWARD	LENGTH=119	
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207.	<u>AT2G18040.1</u>	Mass: 13064	Score: 43	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.89
	Symbols: FIN1AT	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	chr2:7842346-7843537	FORWARD	LENGTH=119	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>354</u>	409.2601	816.5057	816.5069	-1.46	0 36 0.0027 1 U K.IILTTRT.E
	<u>1830</u>	368.5405	1102.5997	1102.5982	1.32	1 33 0.031 1 U K.S1REDIVSGK.A
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208.	<u>AT2G44200.1</u>	Mass: 57750	Score: 43	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
	Symbols:	CBP1-interacting co-repressor CIR, N-terminal/Pre-mRNA splicing factor	chr2:18276302-18278240	FORWARD	LENGTH=493	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>7110</u>	621.9660	1862.8762	1862.8758	0.19	1 43 0.0029 1 U R.KAEKLDGKPFNEYQNR.R
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209.	<u>AT1G07320.1</u>	Mass: 30540	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15
	Symbols: RPL4	ribosomal protein L4	chr1:2249190-2250189	FORWARD	LENGTH=282	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>3988</u>	688.8736	1375.7326	1375.7347	-1.50	0 42 0.0031 1 U R.T1NLFDILNADE.L
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Proteins matching the same set of peptides:						
	<u>AT1G07320.2</u>	Mass: 30396	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RPL4	ribosomal protein L4	chr1:2249190-2250189	FORWARD	LENGTH=280	
	<u>AT1G07320.3</u>	Mass: 30124	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RPL4	ribosomal protein L4	chr1:2249190-2250026	FORWARD	LENGTH=278	
	<u>AT1G07320.4</u>	Mass: 30124	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RPL4	ribosomal protein L4	chr1:2249190-2250173	FORWARD	LENGTH=278	
<hr/>						
210.	<u>AT2G23390.1</u>	Mass: 54902	Score: 42	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
	<u>6995</u>	613.6448	1837.9127	1837.9131	-0.25	0 42 0.0036 1 U K.EQVFDATVSAMTELASK.L
<hr/>						
211.	<u>AT2G29560.1</u>	Mass: 52080	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
	Symbols: ENOC	cytosolic enolase	chr2:12646635-12649694	FORWARD	LENGTH=475	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>6189</u>	850.9742	1699.9338	1699.9331	0.40	0 42 0.0022 1 U R.ANHVLFPVPAFTVLSGGE.H
<hr/>						
212.	<u>AT2G01250.1</u>	Mass: 28210	Score: 42	Matches: 3(2)	Sequences: 3(2)	emPAI: 0.35
	Symbols:	Ribosomal protein L30/L7 family protein	chr2:132943-134264	REVERSE	LENGTH=242	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>88</u>	378.2589	754.5032	754.5065	-4.34	0 36 0.00054 1 U K.L1QLLL.L
	<u>1485</u>	533.3099	1064.6053	1064.6019	3.25	0 27 0.044 1 U R.Q1FNGVFLK.V
	<u>4898</u>	753.8898	1505.7650	1505.7667	-1.12	0 20 0.63 1 U K.EANNFLMPFQLK.A
<hr/>						
Proteins matching the same set of peptides:						
	<u>AT2G44120.1</u>	Mass: 27979	Score: 42	Matches: 3(2)	Sequences: 3(2)	
	Symbols:	Ribosomal protein L30/L7 family protein	chr2:18249227-18250402	REVERSE	LENGTH=242	
	<u>AT2G44120.2</u>	Mass: 28559	Score: 42	Matches: 3(2)	Sequences: 3(2)	
	Symbols:	Ribosomal protein L30/L7 family protein	chr2:18249227-18250417	REVERSE	LENGTH=247	
	<u>AT3G13580.1</u>	Mass: 28473	Score: 42	Matches: 3(2)	Sequences: 3(2)	
	Symbols:	Ribosomal protein L30/L7 family protein	chr3:4433809-4435109	FORWARD	LENGTH=244	
	<u>AT3G13580.2</u>	Mass: 28473	Score: 42	Matches: 3(2)	Sequences: 3(2)	
	Symbols:	Ribosomal protein L30/L7 family protein	chr3:4433809-4435109	FORWARD	LENGTH=244	
	<u>AT3G13580.3</u>	Mass: 28473	Score: 42	Matches: 3(2)	Sequences: 3(2)	
	Symbols:	Ribosomal protein L30/L7 family protein	chr3:4433809-4435109	FORWARD	LENGTH=244	
<hr/>						
213.	<u>AT5G65900.1</u>	Mass: 72293	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
	Symbols:	DEA(D/H)-box RNA helicase family protein	chr5:26358328-26361244	FORWARD	LENGTH=633	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>1711</u>	549.3127	1096.6109	1096.6241	-11.97	0 42 0.0014 1 U K.GVHLLVATPGR.L
<hr/>						
214.	<u>AT3G27830.1</u>	Mass: 20063	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.23
	Symbols: RPL12-A, RPL12	ribosomal protein L12-A	chr3:10318576-10319151	FORWARD	LENGTH=191	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>351</u>	408.7620	815.5095	815.5116	-2.55	0 42 0.0013 1 U R.ALTSIALK.E
<hr/>						
Proteins matching the same set of peptides:						
	<u>AT3G27850.1</u>	Mass: 19671	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols: RPL12-C	ribosomal protein L12-C	chr3:10324905-10325468	FORWARD	LENGTH=187	
<hr/>						
215.	<u>AT5G09510.1</u>	Mass: 17061	Score: 42	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.28
	Symbols:	Ribosomal protein S19 family protein	chr5:2955698-2956554	REVERSE	LENGTH=152	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>3275</u>	427.2254	1278.6544	1278.6568	-1.89	0 42 0.0036 1 U R.EAPAGKEPEPVR.T
<hr/>						
Proteins matching the same set of peptides:						
	<u>AT5G09510.2</u>	Mass: 13403	Score: 42	Matches: 1(1)	Sequences: 1(1)	
	Symbols:	Ribosomal protein S19 family protein	chr5:2955698-2956353	REVERSE	LENGTH=118	
<hr/>						
216.	<u>AT5G23080.1</u>	Mass: 104985	Score: 41	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04
	Symbols: TGH	SWAP (Suppressor-of-White-Fluorocot)/surp domain-containing protein	chr5:7743226-7748889	REVERSE	LENGTH=930	
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<u>3177</u>	631.8531	1261.6916	1261.6918	-0.13	0 41 0.0037 1 U R.L1AGDFLESIGE.E
<hr/>						
Proteins matching the same set of peptides:						
	<u>AT5G23080.2</u>	Mass: 101551	Score: 41	Matches: 1(1)	Sequences: 1(1)	

	Symbols: RPL16A ribosomal protein large subunit 16A chr2:17791794-17792946 FORWARD LENGTH=182
	AT3G58700.1 Mass: 21019 Score: 39 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal L5P family protein chr3:21711661-21712816 FORWARD LENGTH=182
	AT4G18730.1 Mass: 21019 Score: 39 Matches: 1(1) Sequences: 1(1)
	Symbols: RPL16B ribosomal protein L16B chr4:10302238-10303206 FORWARD LENGTH=182
	AT5G45775.2 Mass: 21019 Score: 39 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal L5P family protein chr5:18565281-18566496 REVERSE LENGTH=182
227.	AT5G60790.1 Score: 39 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
	Symbols: ATGCM1, GCM1 ABC transporter family protein chr5:24453760-24455767 REVERSE LENGTH=595
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	712 454.7446 907.4746 907.4763 -1.82 0 39 0.005 1 U R.LQSIYER.L
228.	AT5G04280.1 Mass: 33694 Score: 39 Matches: 2(1) Sequences: 2(1) emPAI: 0.13
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain chr5:1192461-1195413 FORWARD LENGTH=310
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1022 494.7374 987.4602 987.4621 -1.96 0 39 0.0023 1 U R.DIAPSAGSDR.Y
	1828 368.5246 1102.5519 1102.5519 -0.04 0 16 1.5 1 U R.AGAPYERPSR.S
229.	AT3G09680.1 Mass: 15931 Score: 38 Matches: 1(1) Sequences: 1(1) emPAI: 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
	2119 567.3496 1132.6845 1132.6856 -0.92 0 38 0.0012 1 U K.VSGVSLALFK.E
	Proteins matching the same set of peptides:
	AT5G02960.1 Mass: 15840 Score: 38 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal protein S12/S23 family protein chr5:693280-694396 REVERSE LENGTH=142
230.	AT5G40490.1 Mass: 42382 Score: 37 Matches: 2(1) Sequences: 2(1) emPAI: 0.11
	Symbols: RNA-binding (RRM/RBD/RNP motifs) family protein chr5:16225483-16227423 FORWARD LENGTH=423
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	466 416.7563 831.4980 831.4967 1.43 0 23 0.11 1 U K.IFYVGLAR.E
	1205 513.2611 1024.5077 1024.5077 -0.01 0 37 0.007 1 U R.ETTSAEFLK.W
231.	AT5G17920.1 Mass: 84646 Score: 37 Matches: 1(1) Sequences: 1(1) emPAI: 0.05
	Symbols: ATCIMS, ATMETS, ATMS1 Cobalam-in-dependent synthase family protein chr5:5935771-5939195 FORWARD LENGTH=765
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	2241 573.8419 1145.6692 1145.6696 -0.36 0 37 0.0039 1 U K.SFELLSLLPK.I
	Proteins matching the same set of peptides:
	AT5G17920.2 Mass: 84646 Score: 37 Matches: 1(1) Sequences: 1(1)
	Symbols: ATCIMS Cobalam-in-dependent synthase family protein chr5:5935771-5939195 FORWARD LENGTH=765
232.	AT3G54960.1 Mass: 64400 Score: 37 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
	Symbols: ATPDIL1-3, PDIL1, ATPDIL1, PDIL1-3 PDI-like 1-3 chr3:20363514-20366822 REVERSE LENGTH=579
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	4129 700.3196 1398.6246 1398.6263 -1.21 0 37 0.0058 1 U K.SDPLPENNDGVK.V
	Proteins matching the same set of peptides:
	AT3G54960.2 Mass: 57883 Score: 37 Matches: 1(1) Sequences: 1(1)
	Symbols: ATPDIL1-3, PDIL1-3 PDI-like 1-3 chr3:20363895-20366822 REVERSE LENGTH=518
233.	AT5G16470.1 Mass: 11346 Score: 37 Matches: 2(1) Sequences: 2(1) emPAI: 0.44
	Symbols: zinc finger (C2H2 type) family protein chr5:5379516-5379830 FORWARD LENGTH=104
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	257 393.2414 784.4682 784.4695 -1.64 0 30 0.019 1 U K.IIVPDLK.T
	8322 418.0337 2085.1322 2085.1330 -0.39 0 27 0.076 1 U R.NLHEALAAPASSEKPKQIR.G
234.	AT3G06560.1 Score: 36 Matches: 1(1) Sequences: 1(1) emPAI: 0.08
	Symbols: PAPS3 poly(A) polymerase 3 chr3:2044443-2047034 FORWARD LENGTH=507
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	346 408.2594 814.5042 814.5164 -14.90 0 36 0.0071 2 U R.IQLTLVK.A
235.	AT1G61520.1 Mass: 29163 Score: 36 Matches: 1(1) Sequences: 1(1) emPAI: 0.16
	Symbols: LHCA3 photosystem I light harvesting complex gene 3 chr1:22700152-22701149 FORWARD LENGTH=273
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	5849 815.4545 1628.8945 1628.8960 -0.90 0 36 0.012 1 U R.FAMLAGAGATAPEILG.A
	Proteins matching the same set of peptides:
	AT1G61520.2 Mass: 23845 Score: 36 Matches: 1(1) Sequences: 1(1)
	Symbols: LHCA3 photosystem I light harvesting complex gene 3 chr1:22700493-22701149 FORWARD LENGTH=218
	AT1G61520.3 Mass: 29163 Score: 36 Matches: 1(1) Sequences: 1(1)
	Symbols: LHCA3 photosystem I light harvesting complex gene 3 chr1:22700152-22701149 FORWARD LENGTH=273
236.	AT1G60130.1 Mass: 67421 Score: 36 Matches: 2(1) Sequences: 2(1) emPAI: 0.07
	Symbols: Mannose-binding lectin superfamily protein chr1:22174179-22176321 FORWARD LENGTH=600
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1319 521.7659 1041.5173 1041.5131 4.05 1 18 0.4 1 U K.FLYDKDK.F
	7089 619.6492 1855.9257 1855.9356 -5.34 0 36 0.015 1 U K.QPVLYSVIQETVNR.G
237.	AT3G56990.1 Mass: 79960 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.05
	Symbols: EDA7 embryo sac development arrest 7 chr3:21088358-21091976 REVERSE LENGTH=711
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	297 401.2442 800.4738 800.4756 -2.19 0 35 0.016 1 U R.GVQSLGLK.S
238.	AT1G30420.1 Mass: 169023 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.03
	Symbols: ATMRP12, MRP12, ABCG11 multidrug resistance-associated protein 12 chr1:10748816-10756316 FORWARD LENGTH=1495
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	432 416.2503 830.4861 830.4974 -13.54 1 35 0.016 1 U K.LRLRLTK.A
239.	AT1G69510.1 Mass: 15144 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.32
	Symbols: cAMP-regulated phosphoprotein 19-related protein chr1:26126779-26127725 FORWARD LENGTH=137
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	2517 596.8234 1191.6323 1191.6360 -3.11 0 34 0.021 1 U K.LQPTPQQPR.A
	Proteins matching the same set of peptides:
	AT1G69510.2 Mass: 15144 Score: 34 Matches: 1(1) Sequences: 1(1)
	Symbols: cAMP-regulated phosphoprotein 19-related protein chr1:26126779-26127725 FORWARD LENGTH=137
	AT1G69510.3 Mass: 15144 Score: 34 Matches: 1(1) Sequences: 1(1)
	Symbols: cAMP-regulated phosphoprotein 19-related protein chr1:26126779-26127725 FORWARD LENGTH=137
240.	AT5G43960.1 Mass: 50149 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
	Symbols: Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain chr5:17689154-17691653 REVERSE LENGTH=450
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	15918 814.1649 3252.6306 3252.6190 3.56 1 34 0.026 1 U R.NLPDSIASRIEIEEFKMFQIKPDGVFLR.T
	Proteins matching the same set of peptides:
	AT5G43960.2 Mass: 43515 Score: 34 Matches: 1(1) Sequences: 1(1)
	Symbols: Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain chr5:17689154-17691220 REVERSE LENGTH=391
241.	AT3G28850.1 Score: 33 Matches: 2(1) Sequences: 1(1) emPAI: 0.09
	Symbols: Glutaredoxin family protein chr3:10848669-10849955 FORWARD LENGTH=428
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	308 402.7136 803.4127 803.4025 12.8 1 33 0.027 1 U R.KLNEDGK.L 307
242.	AT3G53740.1 Mass: 11673 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.43
	Symbols: Ribosomal protein L36e family protein chr3:19913921-19914813 REVERSE LENGTH=103
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1683 546.2704 1090.5262 1090.5295 -2.97 0 33 0.024 1 U K.EVAGQAPYEK.R
	Proteins matching the same set of peptides:
	AT3G53740.2 Mass: 12668 Score: 33 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal protein L36e family protein chr3:19913921-19914813 REVERSE LENGTH=112
	AT3G53740.3 Mass: 12668 Score: 33 Matches: 1(1) Sequences: 1(1)

	Symbols:	Ribosomal protein L36e family protein	chr3:19913921-19914813	REVERSE LENGTH=112							
	AT3G53740.4	Mass: 12668	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein L36e family protein	chr3:19913921-19914813	REVERSE LENGTH=112							
	AT5G02450.1	Mass: 12182	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein L36e family protein	chr5:533501-534394	FORWARD LENGTH=108							
243.	AT4G13850.1	Mass: 15750	Score: 33	Matches: 2(0)	Sequences: 2(0)						
	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
	3374	431.8918	1292.6534	1292.6585	-3.95	0	21	0.43	1	U	R.VNPANDRPSAPR.A
	6217	854.4346	1706.8546	1706.8628	-4.81	0	29	0.082	1	U	K.LFIGGLSWGTDASLR.D
	Proteins matching the same set of peptides:										
	AT4G13850.2	Mass: 15464	Score: 33	Matches: 2(0)	Sequences: 2(0)						
	Symbols:	ATGRP2	glycine-rich RNA-binding protein 2	chr4:8021314-8022065	FORWARD LENGTH=153						
	AT4G13850.3	Mass: 14739	Score: 33	Matches: 2(0)	Sequences: 2(0)						
	Symbols:	ATGRP2	glycine-rich RNA-binding protein 2	chr4:8021314-8022065	FORWARD LENGTH=144						
244.	AT1G04480.1	Mass: 15188	Score: 33	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.32					
	Symbols:	Ribosomal protein L14p/L23e family protein	chr1:1216110-1217257	FORWARD LENGTH=140							
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	691	450.7615	899.5084	899.5076	0.84	0	33	0.019	1	U	K.GSAITGPIGK.E
	Proteins matching the same set of peptides:										
	AT2G33370.1	Mass: 15188	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	Ribosomal protein L14p/L23e family protein	chr2:14143718-14144644	REVERSE LENGTH=140							
	AT3G04400.1	Mass: 15188	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	emb2171	Ribosomal protein L14p/L23e family protein	chr3:1167339-1168308	FORWARD LENGTH=140						
	AT3G04400.2	Mass: 13568	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	emb2171	Ribosomal protein L14p/L23e family protein	chr3:1167611-1168308	FORWARD LENGTH=125						
245.	AT3G54230.1	Mass: 113011	Score: 33	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04					
	Symbols:	SUA	suppressor of abi3-5	chr3:20073872-20080142	FORWARD LENGTH=1007						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	4978	763.8846	1525.7546	1525.7565	-1.27	0	33	0.032	1	U	R.GFAFIDFPFVDAAR.T
	Proteins matching the same set of peptides:										
	AT3G54230.2	Mass: 113098	Score: 33	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	SUA	suppressor of abi3-5	chr3:20073872-20080142	FORWARD LENGTH=1008						
246.	AT1G75350.1	Mass: 16194	Score: 32	Matches: 2(0)	Sequences: 1(0)						
	Symbols:	emb2184	Ribosomal protein L31	chr1:28272163-28272687	FORWARD LENGTH=144						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	5146	773.9302	1545.8458	1545.8476	-1.18	0	27	0.092	1	U	R.PAGLSEIMEIPVLK.G
	5304	781.9287	1561.8429	1561.8425	0.21	0	(24)	0.19	1	U	R.PAGLSEIMEIPVLK.G
247.	AT4G34570.1	Score: 32	Matches: 5(2)	Sequences: 2(1)	emPAI: 0.07						
	Symbols:	THY-2	thymidylate synthase 2	chr4:16511129-16514110	REVERSE LENGTH=565						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	551	430.7261	859.4376	859.4440	-7.41	0	31	0.041	2	U	K.TWESIPK.K 550 552 553
	1024	494.7738	987.5330	987.5389	-5.94	1	22	0.36	2	U	K.TWESIPKK.Y
248.	AT2G47470.1	Mass: 39815	Score: 32	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11					
	Symbols:	ATPDIL2-1, UNR5, MRE30, PDI11, ATPD11	thioredoxin family protein	chr2:19481503-19483683	FORWARD LENGTH=361						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2801	406.8770	1217.6091	1217.6139	-3.94	1	32	0.039	1	U	K.ELVAASEDEKK.A
	Proteins matching the same set of peptides:										
	AT2G47470.3	Mass: 35997	Score: 32	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	ATPDIL2-1, UNR5, MRE30, PDI11, ATPD11	thioredoxin family protein	chr2:19481503-19483571	FORWARD LENGTH=323						
	AT2G47470.4	Mass: 36884	Score: 32	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	ATPDIL2-1, UNR5, MRE30, PDI11, ATPD11	thioredoxin family protein	chr2:19481503-19483683	FORWARD LENGTH=335						
249.	AT3G56240.1	Mass: 13077	Score: 32	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.37					
	Symbols:	CCH	copper chaperone	chr3:20863460-20864402	REVERSE LENGTH=121						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2069	565.7858	1129.5571	1129.5615	-3.88	0	32	0.023	1	U	K.AAAEATKPSQV.-
250.	AT1G58400.1	Mass: 105437	Score: 32	Matches: 9(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
	8512	1055.0376	2108.0606	2108.0459	6.99	2	(17)	1.4	1	U	R.KYVWMQLQNLTSRETK.D 8477 8481 8494 8522
	8523	703.6946	2108.0619	2108.0459	7.59	2	27	0.12	1	U	R.KYVWMQLQNLTSRETK.D 8471 8505 8551
251.	AT1G11430.1	Mass: 26355	Score: 32	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.17					
	Symbols:	plastid developmental protein DAG, putative	chr1:3847273-3848938	FORWARD LENGTH=232							
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	11030	857.7606	2570.2600	2570.2608	-0.28	1	32	0.044	1	U	R.DQMDITYLNTLATVLGSMEEAKK.N
252.	AT1G16210.1	Mass: 26810	Score: 32	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.17					
	Symbols:	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1014 (InterPro:IPR010422); Has 16107 Blast hits to 8386 proteins in 1107 species: Archae - 26; Bacteria - 3370; Metazoa - 4013; Fungi - 1!									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3590	438.9077	1313.7012	1313.7051	-2.98	2	32	0.031	1	U	R.RREEDQVALAK.K
253.	AT3G26580.1	Score: 31	Matches: 4(2)	Sequences: 1(1)	emPAI: 0.12						
	Symbols:	Tetratricopeptide repeat (TPR)-like superfamily protein	chr3:9758933-9760349	FORWARD LENGTH=350							
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	551	430.7261	859.4376	859.4511	-15.77	1	(31)	0.045	3	U	R.RQASELR.Y 550 552 553
254.	AT1G43170.1	Score: 31	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10						
	Symbols:	ARP1, emb2207, RPL3A, RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	345	408.2470	814.4793	814.4800	-0.78	0	31	0.036	1	U	R.LALEEIK.L
	Proteins matching the same set of peptides:										
	AT1G43170.2	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	ARP1, RPL3A, RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.3	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	ARP1, RPL3A, RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.4	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	ARP1, RPL3A, RP1	ribosomal protein 1	chr1:16267519-16268631	FORWARD LENGTH=306						
	AT1G43170.5	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.6	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.7	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.8	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
	AT1G43170.9	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Symbols:	RP1	ribosomal protein 1	chr1:16266992-16268631	FORWARD LENGTH=389						
255.	AT3G08940.1	Mass: 25157	Score: 31	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18					
	Symbols:	LHCb4.2	light harvesting complex photosystem II	chr3:2717717-2718400	FORWARD LENGTH=227						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	6380	878.4351	1754.8556	1754.8628	-4.12	0	31	0.043	1	U	K.STPFPQPYSEVFLQQR.F
	Proteins matching the same set of peptides:										
	AT3G08940.2	Mass: 31231	Score: 31	Matches: 1(1)	Sequences: 1(1)						
	Symbols:	LHCb4.2	light harvesting complex photosystem II	chr3:2717717-2718665	FORWARD LENGTH=287						
256.	AT5G01530.1	Mass: 31177	Score: 31	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15					
	Symbols:	LHCb4.1	light harvesting complex photosystem II	chr5:209084-210243	FORWARD LENGTH=290						
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	6380	878.4351	1754.8556	1754.8628	-4.12	0	31	0.043	1	U	K.STPFPQPYSEVFGIQR.F

257.	AT1G79850.1	Mass: 16329	Score: 31	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.29
Symbols: RPS17, CS17, PRPS17 ribosomal protein S17 chr1:30041473-30041922 REVERSE LENGTH=149						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	1508	536.8285	1071.6424	1071.6441	-1.52	0 31 0.016 1 U K.SPVALPVIAR.A
258.	AT4G32760.1	Mass: 73146	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
Symbols: ENTH/VHS/GAT family protein chr4:15799376-15803832 FORWARD LENGTH=675						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	4977	763.4811	1524.9477	1524.9491	-0.87	0 30 0.0028 1 U K.AQLLALTLLLETIVK.N
Proteins matching the same set of peptides:						
	AT4G32760.2	Mass: 73275	Score: 30	Matches: 1(1)	Sequences: 1(1)	
Symbols: ENTH/VHS/GAT family protein chr4:15799376-15803832 FORWARD LENGTH=676						
259.	AT5G14650.1	Mass: 47477	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
Symbols: Pectin lyase-like superfamily protein chr5:4724509-4726328 FORWARD LENGTH=435						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	344	408.2329	814.4513	814.4661	-18.13	1 30 0.042 1 U K.KGGLIDGR.G
260.	AT4G10840.1	Mass: 66866	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 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
	4909	756.9301	1511.8455	1511.8446	0.60	0 30 0.027 1 U R.IEDAITEILEQVLK.L
261.	AT3G17040.1	Mass: 73882	Score: 30	Matches: 1(0)	Sequences: 1(0)	
Symbols: HCF107 high chlorophyll fluorescent 107 chr3:5809378-5812605 REVERSE LENGTH=652						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	1448	530.7811	1059.5477	1059.5560	-7.84	1 30 0.063 1 U K.LDVNLDSEKR.L
Proteins matching the same set of peptides:						
	AT3G17040.2	Mass: 70184	Score: 30	Matches: 1(0)	Sequences: 1(0)	
Symbols: HCF107 high chlorophyll fluorescent 107 chr3:5809378-5812605 REVERSE LENGTH=618						
262.	AT5G46020.1	Mass: 18966	Score: 30	Matches: 1(0)	Sequences: 1(0)	
Symbols: CONTAINS InterPro DOMAIN/s: Casein kinase substrate, phosphoprotein PP28 (InterPro:IPR019380); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Pl						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	6139	564.2894	1689.8463	1689.8798	-19.84	0 30 0.066 1 U R.FSSAADILAGTSAARPR.S
263.	AT2G42690.1	Mass: 15610	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.31
Symbols: MBF1A, ATMBF1A multiprotein bridging factor 1A chr2:17774972-17776116 FORWARD LENGTH=142						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	1870	556.3271	1110.6396	1110.6397	-0.05	0 30 0.022 1 U K.AIIPNQILSK.L
Proteins matching the same set of peptides:						
	AT3G58680.1	Mass: 15572	Score: 30	Matches: 1(1)	Sequences: 1(1)	
Symbols: MBF1B, ATMBF1B multiprotein bridging factor 1B chr3:21707367-21708625 FORWARD LENGTH=142						
264.	AT5G45520.1	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03	
Symbols: Leucine-rich repeat (LRR) family protein chr5:18449509-18453012 REVERSE LENGTH=1167						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	291	400.2671	798.5196	798.5215	-2.29	0 30 0.018 2 U K.LIALILQK.K
265.	AT1G15210.1	Mass: 163321	Score: 30	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03
Symbols: PDR7, ATPDR7 pleiotropic drug resistance 7 chr1:5231552-5236573 REVERSE LENGTH=1442						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	4378	715.8041	1429.5937	1429.5966	-1.99	1 30 0.011 2 U R.WNNWMSQNSTTR.L
266.	AT2G34480.1	Mass: 21407	Score: 29	Matches: 2(0)	Sequences: 2(0)	
Symbols: Ribosomal protein L18ae/LX family protein chr2:14532916-14534161 REVERSE LENGTH=178						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	1023	494.7632	987.5119	987.5138	-1.86	0 29 0.062 1 U K.LMATNEVR.A
	1166	509.7887	1017.5629	1017.5681	-5.12	0 27 0.11 1 U R.FPCIQIIT.K
267.	AT5G37030.1	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06	
Symbols: P-loop containing nucleoside triphosphate hydrolases superfamily protein chr5:14634614-14636939 REVERSE LENGTH=638						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	391	413.7550	825.4955	825.5112	-19.04	0 29 0.012 1 U K.LINGPLK.T
268.	AT5G58680.1	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10	
Symbols: GNC, GATA21 GATA type zinc finger transcription factor family protein chr5:22989630-22991351 REVERSE LENGTH=398						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	391	413.7550	825.4955	825.4960	-0.56	0 29 0.012 1 U R.VQGLPLK.K
269.	AT5G20290.1	Mass: 25092	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18
Symbols: Ribosomal protein S8e family protein chr5:6851695-6853012 REVERSE LENGTH=222						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	5294	781.3658	1560.7171	1560.7168	0.18	0 29 0.048 1 U R.SLDSHIEDQFASGR.L
270.	AT1G70310.1	Mass: 37630	Score: 29	Matches: 1(0)	Sequences: 1(0)	
Symbols: SPDS2 spermidine synthase 2 chr1:26485497-26487352 REVERSE LENGTH=340						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	625	437.7462	873.4779	873.4920	-16.04	2 29 0.097 1 U K.KVIDSKAN.-
271.	AT1G75280.1	Mass: 33773	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.13
Symbols: NmrA-like negative transcriptional regulator family protein chr1:28252030-28253355 FORWARD LENGTH=310						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	557	432.7442	863.4738	863.4752	-1.62	0 28 0.052 2 U K.FLVEASAK.A
272.	AT1G20230.1	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05	
Symbols: Pentatricopeptide repeat (PPR) superfamily protein chr1:7009570-7011852 FORWARD LENGTH=760						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	826	470.7870	939.5595	939.5641	-4.86	0 28 0.018 2 U K.QVLPLIEK.I
273.	AT1G08260.1	Mass: 251874	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02
Symbols: EMB142, EMB2284, POL2A, TIL1, EMB529, ABO4, ESD7 DNA polymerase epsilon catalytic subunit chr1:2590944-2606892 FORWARD LENGTH=2161						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	713	455.2133	908.4120	908.4127	-0.81	0 28 0.042 2 U K.IGEDQFK.K
274.	AT3G10950.1	Mass: 10667	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 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
	1863	555.7233	1109.4320	1109.4310	0.85	0 28 0.0091 1 U K.YPCEFCGK.Y
Proteins matching the same set of peptides:						
	AT3G60245.1	Mass: 10462	Score: 28	Matches: 1(1)	Sequences: 1(1)	
Symbols: Zinc-binding ribosomal protein family protein chr3:22268803-22269750 FORWARD LENGTH=92						
275.	AT3G60040.1	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05	
Symbols: F-box family protein chr3:22175937-22179728 REVERSE LENGTH=838						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	346	408.2594	814.5042	814.5164	-14.90	0 28 0.051 3 U K.LETLIVK.D
276.	AT3G25520.1	Mass: 34394	Score: 27	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.13
Symbols: ATL5, PGY3, OLI5, RPL5A ribosomal protein L5 chr3:9269573-9271327 REVERSE LENGTH=301						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
	958	485.3057	968.5968	968.6019	-5.19	0 27 0.018 1 U R.ALLDVGLIR.T
Proteins matching the same set of peptides:						
	AT3G25520.2	Mass: 21532	Score: 27	Matches: 1(1)	Sequences: 1(1)	

	Symbols: ATL5 ribosomal protein L5 chr3:9269573-9270434 REVERSE LENGTH=190
	AT5G39740.1 Mass: 34473 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: OL17, RPL5B ribosomal protein L5 B chr5:15903365-15905185 FORWARD LENGTH=301
	AT5G39740.2 Mass: 34473 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: RPL5B ribosomal protein L5 B chr5:15903484-15905185 FORWARD LENGTH=301
277.	AT3G04230.1 Mass: 16747 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.28
	Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr3:1113169-1113609 REVERSE LENGTH=146
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	2054 564.8549 1127.6953 1127.6954 -0.12 0 27 0.024 1 U K.IFEPVLLGK.H
	Proteins matching the same set of peptides:
	AT5G18380.1 Mass: 16835 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:6090253-6090693 REVERSE LENGTH=146
	AT5G18380.2 Mass: 16819 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:6090128-6090693 REVERSE LENGTH=144
	AT5G18380.3 Mass: 16272 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: Ribosomal protein S5 domain 2-like superfamily protein chr5:6090128-6090693 REVERSE LENGTH=139
278.	AT4G30993.1 Score: 27 Matches: 1(0) Sequences: 1(0)
	Symbols: Calcineurin-like metallo-phosphoesterase superfamily protein chr4:15098201-15099422 FORWARD LENGTH=209
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	761 459.7710 917.5274 917.5368 -10.18 1 27 0.062 1 U R.LLRIMKK.V
	Proteins matching the same set of peptides:
	AT4G30993.2 Score: 27 Matches: 1(0) Sequences: 1(0)
	Symbols: Calcineurin-like metallo-phosphoesterase superfamily protein chr4:15098201-15099935 FORWARD LENGTH=285
279.	AT1G20440.1 Mass: 29879 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.15
	Symbols: COR47, RD17, ATCOR47 cold-regulated 47 chr1:7084722-7085664 REVERSE LENGTH=265
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	680 448.7472 895.4798 895.4804 -0.66 0 27 0.048 1 U R.GLDFDLGK.K
	Proteins matching the same set of peptides:
	AT1G76180.1 Mass: 20774 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: ERD14 Dehydrin family protein chr1:28587013-28587657 REVERSE LENGTH=185
	AT1G76180.2 Mass: 20774 Score: 27 Matches: 1(1) Sequences: 1(1)
	Symbols: ERD14 Dehydrin family protein chr1:28587013-28587657 REVERSE LENGTH=185
280.	AT4G08570.1 Mass: 17064 Score: 27 Matches: 1(0) Sequences: 1(0)
	Symbols: Heavy metal transport/detoxification superfamily protein chr4:5455123-5455975 REVERSE LENGTH=150
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	2080 565.8312 1129.6479 1129.6343 12.1 1 27 0.075 1 U K.SVDVDVLQK.V
281.	AT1G31360.1 Mass: 80117 Score: 26 Matches: 2(0) Sequences: 1(0)
	Symbols: RECQL2, ATRECQ2, MED34 RECQ helicase L2 chr1:11232422-11237412 FORWARD LENGTH=705
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	10541 1215.0612 2428.1078 2428.1257 -7.37 0 26 0.11 1 U R.QSSMVFYYSGLQNLNIDIVR.Y 10542
	Proteins matching the same set of peptides:
	AT1G31360.2 Mass: 66351 Score: 26 Matches: 2(0) Sequences: 1(0)
	Symbols: RECQL2, MED34 RECQ helicase L2 chr1:11233174-11237412 FORWARD LENGTH=580
282.	AT5G55670.1 Mass: 76614 Score: 26 Matches: 2(0) Sequences: 2(0)
	Symbols: RNA-binding (RBM/RBD/RNP motifs) family protein chr5:22544669-22546801 REVERSE LENGTH=710
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	3218 636.8481 1271.6816 1271.6894 -1.37 0 28 0.089 1 U R.TQQAQSVYIAQK.R
	3992 689.3212 1376.6279 1376.6167 8.11 2 16 0.96 1 U K.KNDEAGSRNEEK.E
	Proteins matching the same set of peptides:
	AT5G55670.2 Mass: 64214 Score: 26 Matches: 2(0) Sequences: 2(0)
	Symbols: RNA-binding (RBM/RBD/RNP motifs) family protein chr5:22544669-22546801 REVERSE LENGTH=585
283.	AT1G17880.1 Mass: 17935 Score: 26 Matches: 1(0) Sequences: 1(0)
	Symbols: BTF3, ATBTF3 basic transcription factor 3 chr1:6152572-6153425 REVERSE LENGTH=165
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	15077 1004.5516 3010.6329 3010.6379 -1.67 1 26 0.061 1 U R.TGVNSIPAIEEVNIFKDDVVIQFINPK.V
284.	AT1G15270.1 Mass: 6974 Score: 26 Matches: 1(0) Sequences: 1(0)
	Symbols: Translation machinery associated TMA7 chr1:5250833-5252020 REVERSE LENGTH=64
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	4414 719.8377 1437.6609 1437.6623 -1.01 0 26 0.092 1 U K.EYDETDLANIQK.K
285.	AT1G20020.1 Mass: 41484 Score: 26 Matches: 1(0) Sequences: 1(0)
	Symbols: ATLFNR2, FNR2 ferredoxin-NADP(+)-oxidoreductase 2 chr1:6942851-6944868 FORWARD LENGTH=369
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	3932 683.8481 1365.6817 1365.6776 3.01 0 26 0.14 1 U R.LVYTNDQGETVK.G
	Proteins matching the same set of peptides:
	AT1G20020.2 Mass: 39550 Score: 26 Matches: 1(0) Sequences: 1(0)
	Symbols: ATLFNR2 ferredoxin-NADP(+)-oxidoreductase 2 chr1:6942851-6944868 FORWARD LENGTH=350
	AT1G20020.3 Mass: 41483 Score: 26 Matches: 1(0) Sequences: 1(0)
	Symbols: ATLFNR2 ferredoxin-NADP(+)-oxidoreductase 2 chr1:6942851-6944868 FORWARD LENGTH=369
286.	AT5G11710.1 Mass: 60654 Score: 26 Matches: 2(0) Sequences: 2(0)
	Symbols: ENTH/VHS family protein chr5:3772981-3776316 FORWARD LENGTH=560
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	2316 577.8405 1153.6663 1153.6707 -3.73 0 23 0.085 1 U R.GLIDNLNTAPK.K
	5751 810.9337 1619.8529 1619.8519 0.64 0 20 0.57 1 U K.ALAVIDYLIISGSR.A
287.	AT4G23940.1 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.04
	Symbols: FtsH extracellular protease family chr4:12437108-12441841 FORWARD LENGTH=946
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	727 457.2075 912.4005 912.4011 -0.68 0 26 0.036 1 U K.MGLEDFR.K
288.	AT2G43550.1 Score: 25 Matches: 1(0) Sequences: 1(0)
	Symbols: Scorpion toxin-like knottin superfamily protein chr2:18073263-18073651 FORWARD LENGTH=103
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	825 470.7377 939.4608 939.4637 -3.00 0 25 0.081 1 U K.FFPTLCR.Q
289.	AT1G72370.1 Mass: 32499 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.14
	Symbols: P40, AP40, RP40, RPSAA 40s ribosomal protein SA chr1:27243148-27244842 REVERSE LENGTH=298
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	827 470.7900 939.5654 939.5753 -10.57 0 25 0.032 1 U R.LLLITDPK.T
	Proteins matching the same set of peptides:
	AT1G72370.2 Mass: 32189 Score: 25 Matches: 1(1) Sequences: 1(1)
	Symbols: P40, AP40, RP40, RPSAA 40s ribosomal protein SA chr1:27243148-27244842 REVERSE LENGTH=294
	AT3G04770.1 Mass: 37618 Score: 25 Matches: 1(1) Sequences: 1(1)
	Symbols: RPSAB 40s ribosomal protein SA B chr3:1309465-1310846 REVERSE LENGTH=332
	AT3G04770.2 Mass: 30805 Score: 25 Matches: 1(1) Sequences: 1(1)
	Symbols: RPSAB 40s ribosomal protein SA B chr3:1309544-1310846 REVERSE LENGTH=280
290.	AT1G27400.1 Mass: 20056 Score: 25 Matches: 2(0) Sequences: 2(0)
	Symbols: Ribosomal protein L22p/L17e family protein chr1:9515230-9516725 FORWARD LENGTH=176
Query	Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	433 416.7347 831.4549 831.4603 -6.51 0 23 0.38 1 U K.QAIPFTR.F
	2116 567.3317 1132.6488 1132.6492 -0.36 0 25 0.09 1 U K.SAQVFDLLK.N
	Proteins matching the same set of peptides:
	AT1G67430.1 Mass: 20013 Score: 25 Matches: 2(0) Sequences: 2(0)
	Symbols: Ribosomal protein L22p/L17e family protein chr1:25262209-25263627 FORWARD LENGTH=175
	AT1G67430.2 Mass: 14872 Score: 25 Matches: 2(0) Sequences: 2(0)
	Symbols: Ribosomal protein L22p/L17e family protein chr1:25262209-25263627 FORWARD LENGTH=131

AT5G04050.1

Mass: 43317

Score: 25

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

1719 550.2891 1098.5636 1098.5669 -3.06 0 25 0.096 1 U R.GTNPQNLVKE.I

292.

AT5G13280.1

Mass: 62658

Score: 25

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.07

| Symbols: | AK-LYS1, AK1, AK | aspartate kinase 1 | chr5:4249516-4252654 FORWARD LENGTH=569

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

6211 853.5129 1705.0113 1704.9808 17.9 2 25 0.019 1 U K.TRDMTKSILTSIVLK.R

293.

AT1G09060.1

Mass: 66446

Score: 25

Matches: 1(0)

Sequences: 1(0)

| Symbols: | U2 snRNP auxiliary factor, large subunit, splicing factor | chr1:22424008-22427806 FORWARD LENGTH=589

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

9478 1121.5868 2241.1590 2241.1562 1.25 0 25 0.18 1 U R.SVERASNAHALDOILBOVPVK.V

294.

AT1G08360.1

Mass: 24624

Score: 25

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.19

| Symbols: | Ribosomal protein L1p/L10e family | chr1:2636231-2637694 FORWARD LENGTH=216

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

325 406.2550 810.4955 810.4963 -0.98 0 25 0.017 1 U R.LLGLPGLNK.A

Proteins matching the same set of peptides:

AT2G27530.1 Mass: 24580 Score: 25 Matches: 1(1) Sequences: 1(1)
| Symbols: | PGY1 | Ribosomal protein L1p/L10e family | chr2:11763443-11764570 REVERSE LENGTH=216

AT2G27530.2 Mass: 24580 Score: 25 Matches: 1(1) Sequences: 1(1)
| Symbols: | PGY1 | Ribosomal protein L1p/L10e family | chr2:11763443-11764570 REVERSE LENGTH=216

AT5G22440.1 Mass: 24744 Score: 25 Matches: 1(1) Sequences: 1(1)
| Symbols: | Ribosomal protein L1p/L10e family | chr5:7435328-7436486 REVERSE LENGTH=217

AT5G22440.2 Mass: 24744 Score: 25 Matches: 1(1) Sequences: 1(1)
| Symbols: | Ribosomal protein L1p/L10e family | chr5:7435328-7436486 REVERSE LENGTH=217

295.

AT1G01490.1

Mass: 19882

Score: 24

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:180401-182066 REVERSE LENGTH=177

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

2566 601.3111 1200.6076 1200.5986 7.55 2 24 0.16 1 U K.KEGAAPKEKG.K

Proteins matching the same set of peptides:

AT1G01490.2 Mass: 19882 Score: 24 Matches: 1(0) Sequences: 1(0)
| Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:180401-182066 REVERSE LENGTH=177

296.

AT4G24820.1

Mass: 44425

Score: 24

Matches: 1(0)

Sequences: 1(0)

| Symbols: | 26S proteasome, regulatory subunit Rpn7/Proteasome component (PCI) domain | chr4:12790471-12792599 REVERSE LENGTH=387

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

5886 546.3019 1635.8838 1635.8872 -2.08 0 24 0.13 1 U K.LFLTLTHPVDIEK.V

Proteins matching the same set of peptides:

AT4G24820.2 Mass: 44425 Score: 24 Matches: 1(0) Sequences: 1(0)
| Symbols: | 26S proteasome, regulatory subunit Rpn7/Proteasome component (PCI) domain | chr4:12790471-12792599 REVERSE LENGTH=387

297.

AT1G1860.1

Mass: 44759

Score: 24

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.10

| Symbols: | Glycine cleavage T-protein family | chr1:4001801-4003245 FORWARD LENGTH=408

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

7692 657.3974 1969.1704 1969.1724 -1.03 0 24 0.019 1 U R.SLLALQGPAAVPLVQLTK.E

Proteins matching the same set of peptides:

AT1G1860.2 Mass: 44759 Score: 24 Matches: 1(1) Sequences: 1(1)
| Symbols: | Glycine cleavage T-protein family | chr1:4001801-4003245 FORWARD LENGTH=408

AT1G1860.3 Mass: 44759 Score: 24 Matches: 1(1) Sequences: 1(1)
| Symbols: | Glycine cleavage T-protein family | chr1:4001801-4003245 FORWARD LENGTH=408

298.

AT5G54900.1

Mass: 42411

Score: 24

Matches: 1(0)

Sequences: 1(0)

| Symbols: | ATRBP45A, RBP45A | RNA-binding protein 45A | chr5:22295412-22298126 FORWARD LENGTH=387

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

4716 492.2726 1473.7961 1473.7980 -1.30 0 24 0.24 1 U K.SIFQPGELLHVK.I

299.

AT4G04460.2

Mass: 55865

Score: 23

Matches: 17(0)

Sequences: 1(0)

| Symbols: | Saposin-like aspartyl protease family protein | chr4:2225232-2227746 FORWARD LENGTH=504

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

1968 560.3070 1118.5995 1118.6005 -0.93 0 23 0.22 1 U K.TMNSLLAQK.V 1945 1948 1954 1957 1975 1980 1987 1988 1992 1996 1997 1998 2001 2004 2006 2008

300.

AT4G34620.1

Mass: 12748

Score: 23

Matches: 1(0)

Sequences: 1(0)

| Symbols: | SSR16 | small subunit ribosomal protein 16 | chr4:16535084-16536092 REVERSE LENGTH=113

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

5678 803.9276 1605.8405 1605.8403 0.18 0 23 0.27 1 U K.QIEVLGFDPLQKK.E

301.

AT1G05190.1

Score: 23

Matches: 1(0)

Sequences: 1(0)

| Symbols: | emb2394 | Ribosomal protein L6 family | chr1:1502515-1503738 REVERSE LENGTH=223

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

648 441.2210 880.4275 880.4290 -1.78 0 23 0.15 1 U K.YGDEIVR.R

302.

AT3G55080.2

Score: 23

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.11

| Symbols: | SET domain-containing protein | chr3:20411476-20414595 REVERSE LENGTH=353

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

88 378.2589 754.5032 754.5065 -4.34 0 23 0.01 4 U M.LAAVLIR.E

303.

AT3G29075.1

Mass: 34488

Score: 23

Matches: 1(0)

Sequences: 1(0)

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

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

10936 510.4293 2547.1102 2547.1150 -1.87 1 23 0.13 1 U R.IEEDYVKPSYGGHEDGGDGHKK.H

304.

AT3G49990.1

Mass: 56611

Score: 23

Matches: 1(0)

Sequences: 1(0)

| Symbols: | unknown protein; Has 1524 Blast hits to 1298 proteins in 225 species: Archae - 9; Bacteria - 84; Metazoa - 474; Fungi - 184; Plants - 98; Viruses - 17; Other Eukaryotes - 658 (source: NCBI BLINK). | chr3:18532492-18532492

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

2328 579.2576 1156.5006 1156.5005 0.07 0 23 0.086 1 U K.MLYGGETQR.A

305.

AT1G18160.1

Mass: 108663

Score: 22

Matches: 1(1)

Sequences: 1(1)

emPAI: 0.04

| Symbols: | Protein kinase superfamily protein | chr1:6249126-6253835 FORWARD LENGTH=992

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

1129 505.8031 1009.5916 1009.6032 -11.48 0 22 0.05 1 U K.QQKPIQR.A

306.

AT4G26590.1

Mass: 85405

Score: 22

Matches: 1(0)

Sequences: 1(0)

| Symbols: | ATOPT5, OPT5 | oligopeptide transporter 5 | chr4:13414134-13416850 REVERSE LENGTH=753

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

637 439.2517 876.4888 876.4916 -3.23 1 22 0.19 1 U K.ATLTTKDK.F

307.

AT4G29270.1

Score: 22

Matches: 1(0)

Sequences: 1(0)

| Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:14423797-14424848 REVERSE LENGTH=256

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

643 440.7231 879.4317 879.4338 -2.33 0 22 0.27 1 U K.YNEVVEK.G

308.

AT3G22080.1

Mass: 74708

Score: 21

Matches: 1(0)

Sequences: 1(0)

| Symbols: | TRAF-like family protein | chr3:7777818-7781718 REVERSE LENGTH=648

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

2807 610.8541 1219.6937 1219.6747 15.6 2 21 0.16 1 U R.MIIVPKGNRK.D

309.

AT3G62330.1

Mass: 56212

Score: 21

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Zinc knuckle (CWC-type) family protein | chr3:23063329-23065419 REVERSE LENGTH=479

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

4967 508.2303 1521.6691 1521.6709 -1.15 1 21 0.22 1 U K.GRYPMHGNYSR.H

310.

AT2G32460.1

Mass: 54745

Score: 21

Matches: 1(0)

Sequences: 1(0)

| Symbols: | MYB101, ATMYB101, ATM1 | myb domain protein 101 | chr2:13782419-13784363 REVERSE LENGTH=490

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

9077

1095.0183

2188.0221

2188.0391

-7.80

1

21

0.45

1

U

K.KDIDAMSYSLLMGDLEIR.S

Proteins matching the same set of peptides:

AT2G32460.2

Mass: 53623

Score: 21

Matches: 1(0)

Sequences: 1(0)

| Symbols: MYB101, ATMYB101, ATM1 | myb domain protein 101 | chr2:13782419-13784359 REVERSE LENGTH=478

311.

AT5G10940.1

Mass: 84804

Score: 21

Matches: 7(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

2754

605.8452

1209.6759

1209.6829

-5.84

2

20

0.23

1

U

R.SGAKRALADPFK.Q

2640

2690

2701

2724

2741

2746

Proteins matching the same set of peptides:

AT5G10940.2

Mass: 84444

Score: 21

Matches: 7(0)

Sequences: 1(0)

| Symbols: | transducin family protein / WD-40 repeat family protein | chr5:3448890-3454127 REVERSE LENGTH=754

312.

AT1G07890.1

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

8714

537.9736

1610.8991

1610.9032

-2.56

0

20

0.3

1

U

K.ALLDDPVFRPLVEK.Y

Proteins matching the same set of peptides:

AT1G07890.2

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

AT1G07890.3

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

AT1G07890.4

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

AT1G07890.5

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

AT1G07890.6

Mass: 27788

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439349 FORWARD LENGTH=249

AT1G07890.7

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

AT1G07890.8

Mass: 27829

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: APX1, MEE6, CSI, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250

313.

AT2G47640.1

Mass: 12741

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr2:19537393-19538431 FORWARD LENGTH=109

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2887

616.3136

1230.6126

1230.6139

-1.01

0

20

0.56

1

U

K.NNTQVLINCR.N

Proteins matching the same set of peptides:

AT2G47640.2

Mass: 12613

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr2:19537393-19538431 FORWARD LENGTH=108

AT2G47640.3

Mass: 12613

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr2:19537393-19538431 FORWARD LENGTH=108

AT2G47640.4

Mass: 12741

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr2:19537393-19538431 FORWARD LENGTH=109

AT3G62840.1

Mass: 12741

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr3:23235727-23236615 REVERSE LENGTH=109

AT3G62840.2

Mass: 12613

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Small nuclear ribonucleoprotein family protein | chr3:23235727-23236615 REVERSE LENGTH=108

314.

AT4G25160.1

Mass: 94322

Score: 20

Matches: 1(0)

Sequences: 1(0)

| Symbols: | U-box domain-containing protein kinase family protein | chr4:12903360-12906669 REVERSE LENGTH=835

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

7031

615.9815

1844.9225

1844.9097

6.94

0

20

0.75

1

U

R.LFQVNSPPLFWFER.F

315.

AT4G27150.1

Mass: 19919

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: SESA2, AT2S2 | seed storage albumin 2 | chr4:13609396-13609908 FORWARD LENGTH=170

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2415

391.5313

1171.5720

1171.5734

-1.19

0

19

0.35

1

U

K.EFQQQLR.A

Proteins matching the same set of peptides:

AT4G27160.1

Mass: 19320

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: AT2S3, SESA3 | seed storage albumin 3 | chr4:13611836-13612330 FORWARD LENGTH=164

316.

AT5G67040.1

Mass: 18978

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Protein of unknown function (DUF295) | chr5:26757896-26758475 REVERSE LENGTH=165

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

5461

794.3870

1586.7594

1586.7722

-8.09

1

19

0.6

1

U

-.MGSLHLNNNNLEK.Y

317.

AT1G21610.1

Mass: 76511

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: | wound-responsive family protein | chr1:7574104-7578643 FORWARD LENGTH=684

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

9749

758.4200

2272.2381

2272.1950

19.0

1

19

0.43

1

U

R.VIPAPQHLNIPRTTPDLNLP.S.-

Proteins matching the same set of peptides:

AT1G21610.2

Mass: 76383

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: | wound-responsive family protein | chr1:7574104-7578643 FORWARD LENGTH=683

AT1G21610.3

Mass: 76610

Score: 19

Matches: 1(0)

Sequences: 1(0)

| Symbols: | wound-responsive family protein | chr1:7574104-7578643 FORWARD LENGTH=685

318.

AT3G51880.1

Mass: 20253

Score: 18

Matches: 1(0)

Sequences: 1(0)

| Symbols: HMGBl, NFD1 | high mobility group Bl | chr3:19247241-19248491 REVERSE LENGTH=178

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

2904

618.7627

1235.5108

1235.5153

-3.62

0

18

0.22

1

U

K.NLEBGSDESEK.S

Proteins matching the same set of peptides:

AT3G51880.2

Mass: 20977

Score: 18

Matches: 1(0)

Sequences: 1(0)

| Symbols: HMGBl, NFD1 | high mobility group Bl | chr3:19247241-19248491 REVERSE LENGTH=185

AT3G51880.3

Mass: 20253

Score: 18

Matches: 1(0)

Sequences: 1(0)

| Symbols: HMGBl, NFD1 | high mobility group Bl | chr3:19247241-19248491 REVERSE LENGTH=178

AT3G51880.4

Mass: 18308

Score: 18

Matches: 1(0)

Sequences: 1(0)

| Symbols: HMGBl | high mobility group Bl | chr3:19247241-19248491 REVERSE LENGTH=161

319.

AT2G47090.1

Mass: 139397

Score: 18

Matches: 2(0)

Sequences: 1(0)

| Symbols: MDR4, POP4, ABCM4, ATPOP4 | ATP binding cassette subfamily B4 | chr2:19310008-19314750 REVERSE LENGTH=1286

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

7765

991.4434

1980.8723

1980.8631

4.64

1

18

0.53

1

U

R.TVASPCAEKDVQKNYSK.K

7788

320.

AT4G24280.1

Mass: 76575

Score: 17

Matches: 1(0)

Sequences: 1(0)

| Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12590094-12593437 FORWARD LENGTH=718

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

3553

436.5500

1306.6281

1306.6452

-13.06

1

17

0.98

1

U

R.NLNGKGGTFMPR.S

321.

AT1G27100.1

Mass: 57877

Score: 17

Matches: 2(0)

Sequences: 1(0)

| Symbols: | Actin cross-linking protein | chr1:9407557-9411074 REVERSE LENGTH=519

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

1206

513.2791

1024.5437

1024.5553

-11.34

1

17

0.59

1

U

K.TESAKAPPK.T

1209

322.

AT3G61690.1

Mass: 145454

Score: 17

Matches: 1(0)

Sequences: 1(0)

| Symbols: | nucleotidyltransferases | chr3:22828349-22833477 FORWARD LENGTH=1303

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

13804

581.8661

2904.2941

2904.2865

2.60

2

17

0.75

1

U

R.SNPQSQQNNCGTEITSRVYQTQKSR.G

323.

AT3G32220.1

Mass: 15632

Score: 17

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Ribosomal L27e protein family | chr2:13678945-13679352 FORWARD LENGTH=135

Query

Observed

Mr(expt)

Mr(calc)

ppm

Miss

Score

Expect

Rank

Unique

Peptide

576

435.2810

868.5475

868.5494

-2.18

0

17

0.18

1

U

K.AVILLQQR.Y

Proteins matching the same set of peptides:

AT3G22230.1

Mass: 15719

Score: 17

Matches: 1(0)

Sequences: 1(0)

| Symbols: | Ribosomal L27e protein family | chr3:7844136-7844543 REVERSE LENGTH=135

AT4G15000.1

Mass: 15712

Score: 17

Matches: 1(0)

Sequences: 1(0)

	Symbols: Ribosomal L27e protein family chr4:8571896-8572303 FORWARD LENGTH=135
	AT4G15000.2 Mass: 15139 Score: 17 Matches: 1(0) Sequences: 1(0)
	Symbols: Ribosomal L27e protein family chr4:8571896-8572387 FORWARD LENGTH=131
324.	AT5G61110.1 Mass: 17637 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: zinc ion binding chr5:24581078-24581991 REVERSE LENGTH=161
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	17900 1314.5874 3940.7404 3940.7106 7.55 2 16 0.68 1 0 K.KPCEVCGSHANDHAIMTCFLCRDTRHHYCAR.V
325.	AT5G04690.1 Mass: 71032 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: Ankyrin repeat family protein chr5:1349781-1352525 REVERSE LENGTH=625
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	12767 948.1340 2841.3803 2841.3776 0.95 0 16 1.7 1 1 U K.LLEIPGNNGEIPVVVAVENTQHEMAR.Y
326.	AT5G55660.1 Mass: 87212 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: DEK domain-containing chromatin associated protein chr5:22539375-22543142 FORWARD LENGTH=778
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	8196 683.3142 2046.9206 2046.9229 -1.10 1 16 0.93 1 1 U K.NEASLAREEETNKGREVK.E
327.	AT1G72340.1 Mass: 42393 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: NagB/RpIA/CoA transferase-like superfamily protein chr1:27236898-27238482 FORWARD LENGTH=382
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	3111 627.3467 1252.6789 1252.6775 1.12 0 16 0.64 1 1 U K.QPDLAEEAAAIR.A
328.	AT1G45207.2 Mass: 61390 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: Remorin family protein chr1:17130703-17133548 REVERSE LENGTH=555
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1992 689.3212 1376.6279 1376.6168 8.09 1 16 0.96 1 1 U K.KDDESQMLDSAR.S
329.	AT1G65470.1 Mass: 94315 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: FAS1, NFB2 chromatin assembly factor-1 (FASCIAT1) (FAS1) chr1:24319906-24323879 REVERSE LENGTH=815
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1992 689.3212 1376.6279 1376.6419 -10.17 2 16 0.96 1 1 U K.KQDSESEKQK.R
	Proteins matching the same set of peptides:
	AT1G65470.2 Mass: 93349 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: FAS1 chromatin assembly factor-1 (FASCIAT1) (FAS1) chr1:24319906-24323879 REVERSE LENGTH=807
330.	AT1G58250.1 Mass: 36559 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: TRAF-like family protein chr3:21570745-21572143 REVERSE LENGTH=317
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1992 689.3212 1376.6279 1376.6547 -19.46 1 16 0.96 1 1 U R.KETHWPCCK.V
331.	AT2G25625.1 Mass: 16550 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	983 488.7205 975.4264 975.4145 12.2 0 16 0.56 1 1 U R.TENETEPR.K
	Proteins matching the same set of peptides:
	AT2G25625.2 Mass: 16420 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four
332.	AT2G28240.1 Mass: 71037 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: ATP-dependent helicase family protein chr2:12039649-12041970 FORWARD LENGTH=660
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	4972 762.3654 1522.7163 1522.7263 -6.58 1 16 1.4 1 1 U K.SGRVDAAAYNAQAKK.N
333.	AT5G39500.1 Mass: 163675 Score: 16 Matches: 1(0) Sequences: 1(0)
	Symbols: GNL1, ERW01 GNOM-like 1 chr5:15815274-15819910 FORWARD LENGTH=1443
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	11902 895.7527 2684.2362 2684.2309 1.99 2 16 1.4 1 1 U R.WSQEAKXSTIGETDAMHLSKDIGK.M
334.	AT3G13782.1 Mass: 36623 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: NFA04, NAP14, NFA4 nucleosome assembly protein1;4 chr3:4526660-4528398 FORWARD LENGTH=317
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	753 458.7541 915.4937 915.4848 9.80 0 15 1.6 1 1 U K.VNNIPMTK.T
335.	AT5G22650.1 Mass: 32386 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: HD2B, HDT02, HDT2, ATHD2B, HDA4, HD2, ATHD2 histone deacetylase 2B chr5:7534120-7536054 FORWARD LENGTH=306
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	1316 521.2713 1040.5280 1040.5251 2.88 0 15 0.88 1 1 U K.SPYNANGSPK.S
	Proteins matching the same set of peptides:
	AT5G22650.2 Mass: 32257 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: HD2B, HDT02, HDT2, ATHD2B, HDA4, HD2 histone deacetylase 2B chr5:7534120-7536054 FORWARD LENGTH=305
336.	AT5G07240.1 Mass: 45293 Score: 15 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
	5690 804.3676 1606.7207 1606.7434 -14.17 2 15 1 1 1 U R.GVSDGLDRNQSDSK.M
337.	AT3G54620.1 Mass: 44361 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: ATBZIP25, BZO2H4, BZIP25 basic leucine zipper 25 chr3:20218085-20220341 REVERSE LENGTH=403
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	6997 920.4238 1838.8331 1838.8105 12.3 0 15 1.2 1 1 U K.QBXNNEPDTQVQQLR.A
338.	AT1G03950.1 Mass: 23012 Score: 15 Matches: 3(0) Sequences: 1(0)
	Symbols: VPS2.3 vacuolar protein sorting-associated protein 2.3 chr1:1011388-1013212 REVERSE LENGTH=210
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	4608 485.2722 1452.7947 1452.8048 -6.94 2 (15) 0.92 1 1 U K.KPNPREVLRESK.R
	4610 727.4057 1452.7968 1452.8048 -5.49 2 19 0.35 1 1 U K.KPNPREVLRESK.R 4609
339.	AT1G51730.1 Mass: 28745 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: Ubiquitin-conjugating enzyme family protein chr1:19186812-19188638 REVERSE LENGTH=252
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	10250 1194.0513 2386.0880 2386.1283 -16.90 0 15 1.5 1 1 U K.LERGEASENLGMAMITVLSSAK.D
340.	AT1G13560.1 Mass: 43913 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT1, ATAAPPT1 aminoalcoholphosphotransferase 1 chr1:4638834-4641691 REVERSE LENGTH=389
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	10258 796.4081 2386.2026 2386.1847 7.50 0 15 2 1 1 U K.TNMCMGLLYLPPALANALTAR.L
	Proteins matching the same set of peptides:
	AT1G13560.2 Mass: 38792 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT1, ATAAPPT1 aminoalcoholphosphotransferase 1 chr1:4638834-4641563 REVERSE LENGTH=346
	AT3G25585.1 Mass: 44067 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT2, ATAAPPT2 aminoalcoholphosphotransferase chr3:9295856-9298271 FORWARD LENGTH=389
	AT3G25585.2 Mass: 44067 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT2, ATAAPPT2 aminoalcoholphosphotransferase chr3:9295856-9298271 FORWARD LENGTH=389
	AT3G25585.3 Mass: 38052 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT2, ATAAPPT2 aminoalcoholphosphotransferase chr3:9296203-9298271 FORWARD LENGTH=337
	AT3G25585.4 Mass: 44067 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: AAPPT2, ATAAPPT2 aminoalcoholphosphotransferase chr3:9295856-9298271 FORWARD LENGTH=389
341.	AT2G32580.1 Mass: 20353 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: Protein of unknown function (DUF1068) chr2:13827849-13829135 FORWARD LENGTH=183
	Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
	10147 1186.0647 2370.1148 2370.1260 -4.70 2 15 1.8 1 1 U K.NYAKLITELKQREAAAMEK.H
	Proteins matching the same set of peptides:
	AT2G32580.2 Mass: 13847 Score: 15 Matches: 1(0) Sequences: 1(0)
	Symbols: Protein of unknown function (DUF1068) chr2:13828662-13829135 FORWARD LENGTH=121

