



[illegible]

AT1G04732.1	Symbol: unknown protein with 388 amino acid residues [chrl1:16020337-16022277 REVERSE LENGTH=191]
AT1G04733.1	Symbol: IQ-domain 24 [chr5:2272028-2270551]
AT1G04734.1	Symbol: TMAP-like family protein [chrl1:14704-149156 REVERSE LENGTH=420]
AT1G04740.1	Symbol: transducin family protein / WD-40 repeat family protein [chr5:344889-346421 REVERSE LENGTH=757]
AT1G04741.1	Symbol: PSTRC-like family protein [chrl1:1033140-1033993 FORWARD LENGTH=854]
AT1G04750.1	Symbol: calcium-activated metallopeptidase superfamily protein [chr5:1025042-12060028 FORWARD LENGTH=1015]
AT1G04751.1	Symbol: Protein of unknown function, DDP42 [chr5:3446455-3446991 FORWARD LENGTH=536]
AT1G04752.1	Symbol: THAM1, THAM1:1 [chalcone synthase 1] [chr5:1945701-1946138 FORWARD LENGTH=766]
AT1G04753.1	Symbol: PAKRIL1, PAKRIL1-2 [pharmacoput-associated kinase-related protein, putative] [chr5:8619290-8620555 FORWARD LENGTH=1133]
AT1G04754.1	Symbol: PTA1, PTA1one H2A 4 [chr4:78351-783564 FORWARD LENGTH=118]
AT1G04746.1	Symbol: PTA1, PTA1one H2A protein 9 [chr1:1964540-1964622 FORWARD LENGTH=83]
AT1G04755.1	Symbol: csm31, csm31:1 [entry deleted 1745] [chr1:1449334-147273 REVERSE LENGTH=111]
AT1G04756.1	Symbol: PTA1, PTA1one H2A 8 [chr2:16211444-1622069 REVERSE LENGTH=136]

	tair	<a href="#">Decoy</a>	False discovery rate
Peptide matches above identity threshold	715	23	3.22 %
Peptide matches above homology or identity threshold	982	72	7.33 %

## Select Summary Repo

Select Summary (protein hits)		
Significance threshold $p <$		Max. number of hits
Standard scoring	MudPIT scoring	Ions score or expect cut-off
Show pop-ups	Suppress pop-ups	

All queries

Unassigned

Below homology threshold

Below identity threshold

1.

A070268.0.1

Name: 47546

Score: 4084

Hatches: 231(128)

Sequences: 14(126)

mpAI: 60.06

1 Symbol: PHR1 PHR1 phosphate starvation response 1 | chr4:14134131-14134491 REVERSE LIGNOT-10

Query

Observed

Hit (qval)

Hit (e10)

ppv

Hit (score)

Expect

Rank

Unique

Peptide

2

382.1841

702.3537

702.3537

-1.52

0

0.052

1

K.HISGK... [562 563 564 565 566 567 568](#)

3

374.2026

704.3906

704.3902

-2.26

0

0.019

1

K.HQSDG... [242 243 244](#)

4

432.2079

862.4012

862.4032

-2.26

16

1

K.HSQDQ... [7](#)

216

432.7435

861.4742

861.4726

-0.16

4

13

1

K.HAPVPS... [1](#)

217

434.2340

875.4775

874.4582

-0.77

20

0.071

1

K.LKQVQ... [140 141 142 143 144 145](#)

244

446.2421

890.4536

890.4531

0.53

0

0.021

1

K.LKQVQ... [51 52](#)

461

493.7855

985.5554

985.5556

0.74

0

58.584-005

1

K.KQGTDAIR... [1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 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3003 3004 3005 3006 3007 3008 3009 3010 3011 3012 3013 3014 3015 3016 3017 3018 3019 3020 3021 3022 3023 3024 3025 3026 3027 3028 3029 3030 3031 3032 3033 3034 3035 3036 3037 3038 3039 3040 3041 3042 3043 3044 3045 3046 3047 3048 3049 3050 3051 3052 3053 3054 3055 3056 3057 3058 3059 3060 3061 3062 3063 3064 3065 3066 3067 3068 3069 3070 3071 3072 3073 3074 3075 3076 3077 3078 3079 3080 3081 3082 3083 3084 3085 3086 3087 3088 3089 3090 3091 3092 3093 3094 3095 3096 3097 3098 3099 3100 3101 3102 3103 3104 3105 3106 3107 3108 3109 3110 3111 3112 3113 3114 3115 3116 3117 3118 3119 3120 3121 3122 3123 3124 3125 3126 3127 3128 3129 3130 3131 3132 3133 3134 3135 3136 3137 3138 3139 3140 3141 3142 3143 3144 3145 3146 3147 3148 3149 3150 3151 3152 3153 3154 3155 3156 3157 3158 3159 3160 3161 3162 3163 3164 3165 3166 3167 3168 3169 3170 3171 3172 3173 3174 3175 3176 3177 3178 3179 3180 3181 3182 3183 3184 3185 3186 3187 3188 3189 3190 3191 3192 3193 3194 3195 3196 3197 3198 3199 3200 3201 3202 3203 3204 3205 3206 3207 3208 3209 3210 3211 3212 3213 3214 3215 3216 3217 3218 3219 3220 3221 3222 3223 3224 3225 3226 3227 3228 3229 3230 3231 3232 3233 3234 3235 3236 3237 3238 3239 3240 3241 3242 3243 3244 3245 3246 3247 3248 3249 3250 3251 3252 3253 3254 3255 3256 3257 3258 3259 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270 3271 3272 3273 3274 3275 3276 3277 3278 3279 3280 3281 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292 3293 3294 3295 3296 3297 3298 3299 3300 3301 3302 3303 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3314 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324 3325 3326 3327 3328 3329 3330 3331 3332 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3352 3353 3354 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365 3366 3367 3368 3369 3370 3371 3372 3373 3374 3375 3376 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387 3388 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398 3399 3400 3401 3402 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3603 3604 3605 3606 3607 3608 3609 3610 3611 3612 3613 3614 3615 3616 3617 3618 3619 3620 3621 3622 3623 3624 3625 3626 3627 3628 3629 3630 3631 3632 3633 3634 3635 3636 3637 3638 3639 3640 3641 3642 3643 3644 3645 3646 3647 3648](#)

[illegible]

Proteins matching the same set of peptides:

AT5G52040.2 Mass: 41401 Score: 1069 Matches: 41(26) Sequences: 17(11)  
| Symbols: ATRSP41, RS41, At-RS41 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:21131081-21133318 FORWARD LENGTH=357

[illegible]

Proteins matching the same set of peptides:  
[AT7G44110.1](#) Mass: 38527 Score: 1049 Matches: 58(74) Sequences: 18(16)  
 | Symbols: NIT1, ATNIT1, NITI | nitrilase 1 | chr3:15986901-15988841 FORWARD LENGTH=346

[illegible]

Proteins matching the same set of peptides:  
[A7IQ25500.4](#) Mass: 40352 Score: 723 Matches: 27(18) Sequences: 11(6)  
 | Symbols: NBP35, NB40, At-NB40 | arginine/serine-rich splicing factor 35 | chr4:13025168-13027243 FORWARD LENGTH=350

Accession	Source	Score	681	Matches	48(19%)	Sequences	18(11)	emPAI	4.11
<p><b>Symbol:</b> GACP, GACP-1, GACP1   <b>glyceroldehyde-3-phosphate dehydrogenase (C subunit 1)</b>   chr3:1061077-1083131 FORWARD LENGTH=338</p>									
Observed	Replaced	Replaced	yes	Miss score	Expect	bank	Uniqe	Peptide	
<a href="#">A14</a>	384-2095	768.3864	768.3861	0.44	0	34	0.011	K.VTIPPAK-A	
<a href="#">A14</a>	406-7474	799.4803	799.4803	-0.07	0	55	0.0012	K.VTIPPAK-D <a href="#">A14</a> <a href="#">A14</a>	
<a href="#">A14</a>	606-2099	810.4053	810.4058	-0.57	0	151	0.018	K.LTQVDPG-I	
<a href="#">A14</a>	406-7476	831.4807	831.4803	0.42	0	19	0.16	K.VTIPPAK-G <a href="#">A14</a>	U
<a href="#">A14</a>	414-2078	826.4010	826.4007	0.29	0	36	0.042	K.LTQVDPG-I	
<a href="#">A14</a>	417-2346	832.4046	832.4055	-1.09	0	18	0.3	K.VTIPPAK-I	
<a href="#">A14</a>	417-7272	831.4198	831.4195	0.32	0	21	0.48	K.LTQVDPG-I	<a href="#">A14</a>
<a href="#">A14</a>	455-7286	909.4427	909.4443	-1.81	0	10	3.1	K.VTIPPAK-K	
<a href="#">A14</a>	695-7585	989.5025	989.5029	-0.46	1	2	94	R	

<a href="#">1441</a>	519.7768	1037.5391	1037.5393	-0.14	1	40	0.0033	1	K.AATDDEIK.A
<a href="#">1441</a>	373.8451	1118.5133	1118.5145	-1.06	0	(17)	0.65	1	K.YDSVQGR.H
<a href="#">1441</a>	560.2642	1118.5138	1118.5145	-0.63	0	36	0.0072	1	K.YDSVQGR.H
<a href="#">1441</a>	570.8208	1118.4770	1118.4373	-0.26	0	(4)	4.7	1	K.VDLVIGR.A
<a href="#">1441</a>	386.2180	1155.4322	1155.4322	-0.01	0	8	0	2	K.VDLVIGR.A
<a href="#">1441</a>	717.8840	1441.7514	1433.7514	1.40	0	30	0.083	1	K.AAPFIPIDISDAK.A <a href="#">1441</a>
<a href="#">1441</a>	749.9273	1447.8401	1447.8403	-1.16	0	82	1.7e-007	1	K.VQVYVQVQLTL.L <a href="#">1441</a> <a href="#">1442</a> <a href="#">1443</a> <a href="#">1444</a> <a href="#">1445</a> <a href="#">1446</a> <a href="#">1447</a> <a href="#">1448</a> <a href="#">1449</a> <a href="#">1450</a> <a href="#">1451</a> <a href="#">1452</a> <a href="#">1453</a> <a href="#">1454</a> <a href="#">1455</a> <a href="#">1456</a> <a href="#">1457</a> <a href="#">1458</a> <a href="#">1459</a> <a href="#">1460</a> <a href="#">1461</a> <a href="#">1462</a> <a href="#">1463</a> <a href="#">1464</a> <a href="#">1465</a> <a href="#">1466</a> <a href="#">1467</a> <a href="#">1468</a> <a href="#">1469</a> <a href="#">1470</a> <a href="#">1471</a> <a href="#">1472</a> <a href="#">1473</a> <a href="#">1474</a> <a href="#">1475</a> <a href="#">1476</a> <a href="#">1477</a> <a href="#">1478</a> <a href="#">1479</a> <a href="#">1480</a> <a href="#">1481</a> <a href="#">1482</a> <a href="#">1483</a> <a 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525.2674	1048.5202	1048.5189	1.28	0	41	0.0081	1	U	R.FLALSDKDN.R	
363.2132	1086.6177	1086.6186	-0.82	0	341	0.016	1	U	K.VYFFPVQR.H	
544.3164	1086.6182	1086.6186	-0.38	0	39	0.0045	1	U	K.VYFFPVQR.H	
549.3190	1096.6235	1096.6241	-0.53	0	31	0.013	1	U	R.OUVALVPTPLD.L	
559.8379	1117.6413	1117.6408	0.46	0	21	0.11	1	U	R.HAIVLLAR.D	
587.8241	1173.6336	1173.6184	-1.46	0	84	2.4e-005	1	U	R.VGSEDTLVGR.V <a href="#">2211</a>	
613.8585	1221.7025	1221.7030	-0.44	0	56	4.9e-005	1	U	R.TPIVLAVDVAR.Q <a href="#">1211</a>	
613.7846	1227.5547	1227.5631	9.39	0	38	0.005	1	U	R.DKAMQVDSGR.H	
620.8118	1239.6091	1239.6095	-0.33	0	39	0.0058	1	U	R.ELAQIDDKR.K	
660.8466	1313.6786	1313.6748	1.33	0	56	0.0016	1	U	R.SIMDLIAQR.K	
668.8246	1335.6346	1335.6315	2.32	0	49	0.00071	1	U	R.HLMDGPEPQK.K	
648.8955	1341.6467	1343.6577	-8.20	1	0		39	1	U	R.LITYGVDSRRF.G
656.9082	1367.7029	1367.7045	-1.16	1	3	21	4	U	R.KAGQVDSRRF.Y	
715.4255	1428.8364	1428.8340	1.65	0	21	0.13	1	U	R.TYVPLAVLPTPL.S	
745.8616	1489.7057	1489.7043	1.62	0	63	2.4e-005	1	U	R.WAGSDGVDSGR.H	
807.9511	1613.8876	1613.8889	-0.83	0	86	1.1e-007	1	U	R.VVVAYGTFPIHQLR.S	
592.3110	1773.9111	1773.9122	-0.60	0	(47)	0.0017	1	U	R.NEPAASRPVAPLAKDN.V	
887.9642	1773.9139	1773.9122	1.00	0	64	2.4e-005	1	U	R.NEPAASRPVAPLAKDN.V	

13. [AT1G056410.1](#) Mass: 68656 Score: 476 Matches: 21(13) Sequences: 14(9) mpAI: 0.92

[ Symbol: ERD2, RSP707-1 | bean\_ rhomb protein 70 (Rap 70) family protein | chr12:111747-1119241 FORWARD LENGTH=617

Query	Observed	Mr(Exp)	Mr(cale)	gpm	Misa	Score	Expect	Rank	Unique	Peptide
<a href="#">1201</a>	599.3516	1194.6887	1196.6877	0.81	0	3		15	1	K.DGVYIAGLAVLR.I
<a href="#">1241</a>	614.8180	1227.6213	1227.6207	0.49	0	87	6.8e-004	1	U	R.VLLIAQDQR.V
<a href="#">1261</a>	615.3096	1228.6048	1228.6048	-11.13	0	(50)	0.0092	1	U	R.VLLIAQDQR.V
<a href="#">1301</a>	639.8186	1277.6227	1277.6227	0.02	0	27		0.1	1	R.WDRNPVQPR.R
<a href="#">1311</a>	648.7987	1285.5767	1285.5856	-0.86	0	(0)		30	4	R.DGVYIAGLAVLR.I
<a href="#">1311</a>	719.3812	1434.7478	1436.7300	12.4	0	36	0.025	1	U	K.VGQLQDPFNGR.K
<a href="#">1321</a>	737.3458	1471.6771	1472.6783	-0.84	0	80	7.6e-007	1	U	R.TYVPLAVDVAR.Q <a href="#">1211</a>
<a href="#">1341</a>	693.2156	1482.6850	1482.6815	0.33	2	2		44	2	R.KAGQVDSRRF.D
<a href="#">1341</a>	825.4029	1648.7912	1648.7767	8.80	0	32	0.039	2	U	R.NVAVGQVPTVDMR.K
<a href="#">1341</a>	830.4509	1658.8873	1658.8879	-0.38	0	59	7.6e-005	1	U	R.LIIEPTAAVILGDLR.K
<a href="#">1341</a>	832.4094	1662.8841	1662.8838	0.35	0	(14)	2.8		1	K.NVAVGQVPTVDMR.R
<a href="#">1341</a>	839.3692	1674.7238	1674.7234	0.22	0	63	1.1e-005	1	U	R.ATAGQVHLDSGRDFM.M
<a href="#">1341</a>	559.2489	1674.7249	1674.7234	0.88	0	(48)	0.0028	1	U	R.AXDQVHLDSGRDFM.M
<a href="#">1341</a>	841.4218	1689.8291	1690.8107	10.9	0	61	0.00011	1	U	K.DAVYTPAPFDSGR.Q
<a href="#">1341</a>	595.6683	1786.9831	1786.9828	0.16	1	64	1.6e-005	1	U	R.LIIEPTAAVILGDLR.K
<a href="#">1341</a>	894.3933	1787.9840	1787.9839	0.58	1	(57)	8.6e-005	1	U	R.LIIEPTAAVILGDLR.K
<a href="#">1371</a>	777.0472	2132.1199	2132.1341	-6.09	2	2	38	1	U	K.GEISQPAKRISIQGLPR.E
<a href="#">1381</a>	1287.6468	2573.2790	2573.2693	7.06	0	32	0.038	1	U	R.SINDRQAVYAVQVAILSDGRK.V
<a href="#">1381</a>	859.0597	2574.2772	2574.2449	12.5	0	(29)	0.084	1	U	R.SINDRQAVYAVQVAILSDGRK.V
<a href="#">1381</a>	1701.5438	5101.6096	5101.5594	9.83	2	1	20	1	U	R.TIINGILGQVGLSGVPAFPGPIPTVQFDSDINGILVAKRQATK.K

14. [AT1G056410.1](#) Mass: 65327 Score: 442 Matches: 19(12) Sequences: 16(10) mpAI: 0.97

[ Symbol: DEAD(D)/Box RNA helicase family protein | chr3:2164668-2164164 FORWARD LENGTH=612

Query	Observed	Mr(Exp)	Mr(cale)	gpm	Misa	Score	Expect	Rank	Unique	Peptide
<a href="#">1211</a>	432.7253	861.6261	861.6261	0.60	0	18		44		K.VDRPRL.F
<a href="#">1211</a>	436.7453	871.4761	871.4763	-0.22	0	10		3.6	1	R.LINDLER.R
<a href="#">1241</a>	125.2674	1048.5202	1048.5189	1.28	0	41	0.0081	1	U	R.FLALSDKDN.R
<a href="#">1241</a>	372.5489	1114.6250	1114.6247	0.24	43	0.0023	1	U	K.VYFFPVQR.H	
<a href="#">1241</a>	558.3202	1114.6257	1114.6247	0.92	0	(32)	0.028	1	U	K.VYFFPVQR.H
<a href="#">1241</a>	566.8453	1131.6761	1131.6764	-0.23	0	19	0.18	1	U	R.HAIVLLAR.D
<a href="#">1261</a>	588.8144	1175.6143	1175.6146	-0.23	0	75	1.8e-006	1	U	R.VGSEDTLVGR.V
<a href="#">1271</a>	613.8585	1225.7025	1225.7030	-0.44	0	56	4.9e-005	1	U	R.TPIVLAVDVAR.Q <a href="#">1211</a>
<a href="#">1271</a>	613.7846	1227.5547	1227.5631	9.39	0	38	0.005	1	U	R.DKAMQVDSGR.H
<a href="#">1301</a>	660.8466	1313.6786	1313.6768	1.33	0	56	0.00016	1	U	R.SIMDLIAQR.R
<a href="#">1301</a>	668.8246	1335.6315	1335.6315	2.32	0	49	0.00071	1	U	R.HLMDGPEPQK.K
<a href="#">1301</a>	648.8955	1341.6467	1343.6577	-8.20	1	0		39	1	R.LITYGVDSRRF.G
<a href="#">1341</a>	760.4879	1519.6805	1519.6804	0.03	0	89	4.3e-008	1	U	R.WAPSDGVDSGRDFM.M
<a href="#">1341</a>	818.4586	1636.9026	1636.9049	-1.44	0	70	2.1e-006	1	U	R.VVVAYGTFPIHQLR.R
<a href="#">1341</a>	546.4425	1636.9058	1636.9049	0.50	0	(60)	2.4e-005	1	U	R.VVVAYGTFPIHQLR.S
<a href="#">1341</a>	877.9496	1753.8846	1753.8821	1.41	0	50	0.0056	1	U	R.QTHFATFPIHQLR.L
<a href="#">1341</a>	912.4557	1824.8968	1824.8962	0.36	0	19	0.4	1	U	R.GSLATAPFHHNAGLR.S
<a href="#">1341</a>	894.0256	2079.0551	2079.0497	2.57	1	2	36	1	U	R.GSLATAPFHHNAGLR.S

Proteins matching the same set of peptides:

AT1G056410.1 Mass: 65327 Score: 442 Matches: 19(12) Sequences: 16(10)

[ Symbol: DEAD(D)/Box RNA helicase family protein | chr3:2164668-2164164 FORWARD LENGTH=612

AT1G056410.1 Mass: 65327 Score: 442 Matches: 19(12) Sequences: 16(10)

[ Symbol: DEAD(D)/Box RNA helicase family protein | chr3:2164668-2164164 FORWARD LENGTH=612

15. [AT1G04320.1](#) Mass: 39340 Score: 421 Matches: 23(12) Sequences: 11(7) mpAI: 1.94

[ Symbol: NIT3, AKN273 | nitritease 3 | chr3:15993419-15995493 FORWARD LENGTH=346

Query	Observed	Mr(Exp)	Mr(Calc)	gpm	Misa	Score	Expect	Rank	Unique	Peptide	
<a href="#">1211</a>	351.2130	768.4115	768.4119	-0.55	0	49	0.0011	1	U	R.LAKELK.R	
<a href="#">1211</a>	595.2015	1186.5584	1188.5710	-2.11	0	51	0.00076	1	U	R.LGAKGQDNR.M	
<a href="#">1221</a>	630.8510	1381.6575	1383.6895	-1.48	0	49	0.00021	1	U	R.FGLAVQDNRK.D	
<a href="#">1241</a>	787.5149	1573.8152	1573.7948	13.0	0	27	0.13	1	U	K.NITGVQSRSTV.V	
<a href="#">1241</a>	965.4716	1919.8288	1930.8286	0.01	1	50	0.0087	1	U	R.FGLAVQDNRK.D	
<a href="#">1241</a>	644.6102	1930.8288	1930.8286	0.13	1	(49)	0.0058	1	U	R.FGLAVQDNRK.D <a href="#">1211</a> <a href="#">1211</a>	
<a href="#">1261</a>	644.9783	1931.8132	1931.8126	0.30	1	(28)	0.091	1	U	R.FGLAVQDNRK.D	
<a href="#">1261</a>	684.6842	2051.0247	2051.0423	0.74	0	(56)	0.00019	1	U	R.VTIVQSTVYDFTATLKR.L	
<a href="#">1281</a>	1026.5276	2051.0406	2051.0423	-0.80	0	59	7.4e-005	1	U	R.VTIVQSTVYDFTATLKR.L <a href="#">1211</a> <a href="#">1211</a>	
<a href="#">1281</a>	685.0158	2052.0256	2052.0283	-0.34	0	(3)		36	2	U	R.VTIVQSTVYDFTATLKR.L
<a href="#">1281</a>	1027.0213	2052.0286	2052.0282	0.46	0	(49)	0.0001	1	U	R.VTIVQSTVYDFTATLKR.L	
<a href="#">1281</a>	1027.0239	2052.0332	2052.0293	0.39	0	(52)	0.00047	1	U	R.VTIVQSTVYDFTATLKR.L	
<a href="#">1281</a>	694.6952	2081.0637	2081.0590	13.8	2	4	23	1	U	R.FVIVYVYDFTATLKR.L	
<a href="#">1281</a>	1082.9238	2183.0330	2183.0307	1.09	0	31	0.049	1	U	R.FVIVYVYDFTATLKR.L	
<a href="#">1281</a>	1118.0227	2234.0308	2234.0464	-15.01	1	2	36	1	U	R.FEPPFSDVYDFTATLKR.L	
<a href="#">1281</a>	784.0752	2379.2150	2379.2150	-0.44	1	57	0.00012	1	U	R.VTIVQSTVYDFTATLKRK.F	
<a href="#">1281</a>	1191.1098	2380.2050	2380.2059	1.72	1	(15)	2.1	1	U	R.VTIVQSTVYDFTATLKRK.F	
<a href="#">1281</a>	1191.1193	2380.2240	2380.2059	9.71	1	(28)	0.1	1	U	R.VTIVQSTVYDFTATLKRK.F	
<a href="#">1281</a>	1547.7324	3893.4502	3893.4787	-9.21	1	2	65	6	U	K.VPTVDSACTGQDSTVPTVDTGR.T	

16. [AT1G03910.1](#) Mass: 61141 Score: 413 Matches: 26(14) Sequences: 18(11) mpAI: 1.57

[ Symbol: RDC4, non-specific phospholipase C4 | chr3:84285-84470 REVERSE LENGTH=538

Query	Observed	Mr(Exp)	Mr(cale)	gpm	Misa	Score	Expect	Rank	Unique	Peptide
<a href="#">1211</a>	486.2448	970.4750	970.4760	-0.90	0	(24)	0.094	1	U	K.VYTRAEK.F
<a href="#">1211</a>	485.7372	971.4559	971.4600	-0.11	0	25	0.053	1	U	K.VYTRAEK.F
<a href="#">1211</a>	585.8459	1169.4773	1169.4768	0.44	0	72	1.7e-006	1	U	K.VTIVGVQNR.S <a href="#">2211</a>
<a href="#">1241</a>	608.8332	1215.6518	1215.6612	-7.68	0	4	20	4	U	K.LKRPVYQNR.V
<a href="#">1241</a>	637.3412	1272.6478	1272.6476	0.34	1	32	0.039	1	U	R.HAKEDVQNR.S
<a href="#">1261</a>	649.2294	1344.4645	1344.4673	-0.61	1	34	0.022	1	U	K.GDVNRELLRK.L
<a href="#">1261</a>	707.3410	1344.4675	1344.4673	0.09	1	(32)	0.034	1	U	K.GDVNRELLRK.L
<a href="#">1261</a>	684.8153	1367.4160	1367.4145	-0.31	0	79	1e-006	1	U	R.DVYVDSRELLR.V
<a href="#">1261</a>	694.8391	1387.4637	1387.4653	-1.20	0	58	7.4e-005	1	U	R.QDQVTFPIPK.L <a href="#">1211</a>
<a href="#">1261</a>	645.9125	1445.7156	1445.7150	0.36	0	31	0.044	1	U	R.DVYVDSRELLR.V
<a href="#">1281</a>	730.8672	1459.7199	1459.7208	-0.65	0	37	1.2e-006	1	U	R.WFAPVASTQPR.L
<a href="#">1281</a>	734.8980	1467.7014	1467.6994	1.34	0	46	0.0012	1	U	R.DKQVTFPIPK.L
<a href="#">1281</a>	510.8469	1529.8188	1529.8200	-0.87	1	11	4	1	U	K.HSLPVPVQNR.M
<a href="#">1281</a>	841.9291	1681.8436	1681.8253	10.9	5	18	1	1	U	K.VLTPRQVQIQPK.R
<a href="#">1281</a>	563.5714	1686.7926	1686.7962	-1.19	0	35	0.016	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	622.7055	1686.7926	1686.7962	-2.00	0	(25)	0.14	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	654.7288	1814.8859	1814.8911	-1.85	1	(29)	0.01	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	865.2695	1814.8857	1814.8911	-2.41	1	51	0.0049	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	905.4507	1814.8868	1814.9121	-2.38	1	(41)	0.0049	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	834.9948	2011.8684	2011.8721	-1.92	(2)	(2)	0.46	1	U	R.LVYVATSHATDNKR.K
<a href="#">1281</a>	717.6596	2011.8680	2011.8747	-0.45	0	59	7	1	U	K.GDSVAVGKPKLQVYV.R
<a href="#">1281</a>	736.0409	2205.1008	2205.0987	0.95	19	0	9	1	U	R.WKQAFQKQVTFKTHAGL.G
<a href="#">1281</a>	865.7198	2205.1008	2205.1076	1.26	36	0	0.15	1	U	R.WKQAFQKQVTFKTHAGL.G
<a href="#">1281</a>	1064.5172	3190.0048	3190.0049	7.78	2	6	3	1	U	QT.KQAFQKQVTFKTHAGL.G

1341	410.2358	818.4651	818.4850	0.10	0	12	2.8	1	U	R.FLYQNR.E
1341	445.7410	818.5075	818.5076	-0.13	0	51	0.00031	1	U	R.VYVNRH.L
1341	482.7597	963.5048	963.5025	2.40	0	29	0.059	1	U	R.SUTFLYR.A
1341	357.2127	1068.6182	1068.6179	-1.63	0	(31)	0.014	1	U	R.LGALPTDFE.A
1341	535.3163	1068.6180	1068.6179	0.11	0	58	1.7e-005	1	U	R.LGALPTDFE.A
1341	973.7941	1145.5737	1145.5751	-1.18	0	2	35	3	U	R.SLVCNDTLE.Y
1341	387.2140	1148.4801	1148.4807	-9.09	2	7	4.4	2	U	R.KLKGHMLV.E
1341	608.8237	1215.6329	1215.6347	-1.64	1	7	11	2	U	R.LANCTLEAV.A
1341	625.8037	1249.5929	1249.5939	-0.80	0	75	1.6e-004	1	U	R.ANDVVGAFR.E
1341	635.3319	1262.6481	1262.6506	-6.18	0	26	6.2e-1	1	U	R.RVYRNR.V
1341	643.3581	1281.7016	1281.7038	-1.65	0	38	0.0072	1	U	R.QLVVGQRH.D
1341	684.3694	1364.7243	1366.7245	-1.16	0	48	0.00073	1	U	R.FLNDITPTV.F
1341	471.5826	1411.7321	1411.7320	0.19	0	29	0.051	1	U	R.HMIDITPTSH.G
1341	490.2482	1467.7228	1467.6994	-0.59	0	(3)	53	7	U	R.KPLVDFRFE.E
1341	735.3460	1469.7032	1469.6934	23.4	0	23	0.054	1	U	R.KPLVDFRFE.E
1341	768.8668	1535.7191	1535.7256	-4.25	0	43	0.0024	1	U	R.SNSQVFPVVE.D
1341	565.2816	1692.8229	1692.8206	1.36	0	43	0.0028	1	U	R.KAGVDEADSTVLE.F
1341	985.0015	1975.8884	1975.8851	1.66	1	56	0.00017	1	U	R.KHSHVLYVDCGLTSE.I
1341	1010.0020	2017.9894	2017.9633	13.0	0	46	0.0015	1	U	R.RVTFPLVLEIDVAGVWL.V
1341	1088.0534	2154.0922	2174.0971	25.9	8	19	1	U	R.RVTFPLVLEIDVAGVWL.V	
1341	981.8104	2942.5393	2942.5331	-0.59	0	36	0.014	1	U	R.HSHGSLGLSLGSHVAVTCTATPTFE.E
1341	858.6895	3430.7290	3430.7238	1.53	0	51	0.00044	1	U	R.VNLTDEYTFDFVFAVLEFVHSLATFE.E
1341	1393.0388	3964.2476	3966.2463	5.44	0	23	0.1e-1	1	U	R.LSTVDFVFFVLEATVGLSHMLGSHVAVTCTATPTFE.E
1341	1076.9238	5379.5826	5379.6876	-19.52	1	3	22	2	U	R.RVDFVLEIGVTFVFDQSHVAVTCTATPTFEFVHSLATPTFE.V
1341	1077.1274	5380.6006	5380.6716	-13.20	1	(1)	32	2	U	R.RVDFVLEIGVTFVFDQSHVAVTCTATPTFEFVHSLATPTFE.V

19. **AT0G01910\_1** Mass: 52347 Score: 382 Matches: 31(8) Sequences: 18(6) eBPAl: 0.53  
[ Symbol: RGA | rubisco activase | chr2:16570951-16573345 REVERSE LENGTH=474  
Query Observed Mr(egpt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
1341 380.2182 758.4179 758.4174 0.56 0 9 10 2 U R.SANLEL.K  
1341 384.2005 766.3864 766.1993 -14.32 1 8 4.7 2 U R.KSHGDF.V  
1341 445.2099 894.4852 894.4803 -5.42 0 44 0.0023 1 U R.VYDFVR.E  
1341 504.2738 1006.5330 1006.5335 -0.52 0 44 0.0032 1 U R.FVSELOVEK.L  
1341 539.7985 1077.5824 1077.5818 0.51 1 21 0.27 1 U R.VYKDAIK.L  
1341 564.3223 1134.6200 1134.6285 1.36 1 5 13 7 U R.RVYDFVR.E  
1341 849.3846 1694.7547 1696.7540 0.38 0 82 1.8e-007 1 U R.GLATVDSQDTR.G [1337](#)  
1341 971.5528 1771.7566 1771.7480 5.02 0 6 8.1 1 U R.KNCLTFVNDAGNR.M [1345](#) [1328](#) [8172](#) [8173](#) [8180](#) [8182](#) [8183](#)  
1341 971.9269 1772.7586 1772.7320 15.6 0 (2) 17 1 U R.KNCLTFVNDAGNR.M [1337](#)  
1341 890.9083 1979.8020 1979.8025 -0.27 0 41 0.0006 1 U R.RVDFVPEPTTE.L  
1341 899.4048 1796.7550 1796.7561 0.16 (148) 1.2 1 U R.RVDFVPEPTTE.L  
1341 717.3829 2149.1268 2149.1242 1.21 0 4 19 1 U R.VNLTCTSDSTVLAIR.D  
1341 731.7774 2192.3104 2192.3085 0.86 1 3 1.3 1 U R.KHPLTFVLEKVLIDNGR.G  
1341 1151.0415 2364.6084 2364.6035 10.8 0 74 2.2e-006 1 U R.KHPLTFVLEKVLIDNGR.G  
1341 1174.0865 2344.1784 2344.1815 -1.31 0 106 1.9e-009 1 U R.VGLATVLEKQALGSHVAVTCTATPTFE.E  
1341 1208.4991 2414.9836 2415.0221 -0.74 (88) 1.3e-004 1 U R.VGLATVLEKQALGSHVAVTCTATPTFE.E  
1341 1209.0000 2415.9894 2416.0061 -0.56 0 4 3.2 1 U R.QVLEKQVDFVIAFGRK.L  
1341 895.8343 2564.4812 2564.4730 3.20 2 1 6 5 U R.KHPLTFVLEKVLIDNGR.G  
1341 1526.6740 4577.0002 4577.0454 -9.69 1 3 25 5 U R.MSGTTFVYVNGVHATGLHATVGLPQGTKEKAR.V  
1341 1306.6133 5222.4241 5222.3721 5.95 2 3 18 8 U R.GLATVDSQDTRVGRGSHVFAQGTUTTHAVLSSTVYGLR.Q  
1341 1349.8216 5744.6716 5744.6849 1.97 2 0 18 1 U R.GSGTTFVYVNGVHATGLHATVGLPQGTKEKAR.V

Proteins matching the same set of peptides:  
**AT0G01910\_1** Mass: 49354 Score: 392 Matches: 31(8) Sequences: 18(6)  
[ Symbol: RGA | rubisco activase | chr2:16571045-16573345 REVERSE LENGTH=466  
**AT0G01910\_1** Mass: 48754 Score: 382 Matches: 31(8) Sequences: 18(6)  
[ Symbol: RGA | rubisco activase | chr2:16571174-16573345 REVERSE LENGTH=441

20. **AT0G02010\_1** Mass: 41937 Score: 381 Matches: 20(13) Sequences: 14(9) eBPAl: 1.48  
[ Symbol: ACT | actin T | chr5:3052809-3054220 FORWARD LENGTH=377  
Query Observed Mr(egpt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
1341 384.2240 768.4373 768.4377 0.53 0 9 10 2 U R.VYDFVR.E  
1341 572.7833 1143.5520 1143.5529 -0.82 0 13 1.8 1 U R.RVYVGVGSRQ.D  
1341 574.3056 1146.5507 1146.5504 1.08 0 46 0.0018 1 U R.KITLAFVIR.I  
1341 581.7721 1175.5295 1175.5281 0.23 0 38 0.0047 1 U R.CNPTFAIR.E  
1341 591.7468 1181.5191 1181.5200 -0.78 0 47 0.00054 1 U R.DAVYDQGRK.E  
1341 594.7699 1181.5252 1181.5230 1.84 0 (37) 0.0049 1 U R.QVPTFAIR.E  
1341 660.8178 1337.4210 1337.4211 -0.10 1 42 1.4e-005 1 U R.DAVYDQGRK.E  
1341 739.3415 1474.6484 1474.6488 -0.27 0 79 4.2e-007 1 U R.KVYDFSVIR.E  
1341 492.5638 1474.6496 1474.6510 0.53 0 (43) 1.6e-005 1 U R.KVYDFSVIR.E  
1341 758.3803 1514.7459 1514.7419 2.69 0 38 0.019 1 U R.HNITVIEL.V  
1341 487.9569 1773.8991 1773.8897 5.32 0 63 2.9e-005 1 U R.KHPLTFVLEKVLIDNGR.G  
1341 1161.1060 2324.1374 2324.1246 -11.07 0 0 54 4 U R.RVDFVLEKQVDFVIAFGRK.D  
1341 1051.2188 3150.6346 3150.6350 -0.13 0 (39) 0.0065 1 U R.PTVLEKQVDFVIAFGRK.L  
1341 785.6567 3150.6379 3150.6350 0.69 5 2e-005 2 U R.PTVLEKQVDFVIAFGRK.L  
1341 1589.7739 3177.5332 3177.5185 4.65 0 0 1.1e-002 9 U R.CPEVLEKQVDFVIAFGRK.L  
1341 1295.3071 3882.8995 3882.8994 0.02 2 1 45 3 U R.AGSHVLEKQVDFVIAFGRK.L  
1341 1300.9733 3889.8981 3889.8983 0.06 2 (0) 61 6 U R.AGSHVLEKQVDFVIAFGRK.L  
1341 1318.6084 3952.8034 3952.8355 -8.13 1 0 84 6 U R.CPEVLEKQVDFVIAFGRK.L

21. **AT0G02100\_1** Mass: 51883 Score: 377 Matches: 13(8) Sequences: 11(7) eBPAl: 0.64  
[ Symbol: AT0G02100\_1 | RAN GTPase homolog 12B | chr1:10970316-10971416 FORWARD LENGTH=476  
Query Observed Mr(egpt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
1341 412.2550 822.4955 822.4963 -0.52 0 20 0.072 1 U R.BILLAG.F  
1341 579.3299 1154.6432 1154.6432 0.04 0 20 0.41 1 U R.VNITVGLNR.E  
1341 695.3196 1388.4647 1388.4646 -0.09 0 29 0.057 1 U R.STVTVDFVQRK.I  
1341 479.2258 1434.6556 1434.6546 -0.94 1 (44) 0.0021 1 U R.KTDEIDAFNR.A  
1341 718.3385 1434.6624 1434.6626 -0.14 1 64 3.6e-005 1 U R.KTDEIDAFNR.A  
1341 841.4783 1680.8421 1680.8410 0.65 0 100 3.2e-009 1 U R.KLSDAGVIRVLE.E  
1341 905.8458 1689.8771 1689.8745 1.67 0 82 8.0e-007 1 U R.GTTFVATVDFR.E  
1341 954.0107 1906.0468 1906.0445 1.20 0 56 6.2e-005 1 U R.KTTLATVLAISGDSVAK.E  
1341 636.5867 1906.0482 1906.0485 1.92 0 (2) 18 2 U R.KTTLATVLAISGDSVAK.E  
1341 1022.0124 2050.0102 2050.0081 1.05 0 81 5.5e-007 1 U R.TVTFVAGVDFVIAFGRK.G  
1341 1068.0747 2134.1348 2134.1310 3.79 0 72 3.1e-006 1 U R.QVLEKQVDFVIAFGRK.L  
1341 1242.3793 2744.1413 2744.1408 18.9 2 0 9 1 U R.RVDFVLEKQVDFVIAFGRK.L  
1341 1454.7729 4361.2969 4361.2716 5.80 2 5 16 3 U R.BILLAGQVDFVIAFGRK.L

22. **AT0G02800\_1** Mass: 41563 Score: 368 Matches: 22(14) Sequences: 15(10) eBPAl: 2.16  
[ Symbol: AAC1 | ADP/ATP carrier 1 | chr3:12605708-12607030 REVERSE LENGTH=361  
Query Observed Mr(egpt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
1341 364.6897 727.3648 727.3633 -0.75 1 27 0.026 1 U R.DVDFR.L  
1341 735.3866 735.3793 735.3803 -1.26 0 26 0.076 1 U R.LAEVFE.G  
1341 368.6972 735.3798 735.3803 -0.64 0 (24) 0.13 1 U R.LAEVFE.G  
1341 384.2005 736.3879 736.3881 0.34 1 11 1.1 1 U R.SLDVFE.L  
1341 384.2273 770.4400 770.4399 -0.21 0 51 0.00044 1 U R.GAGATIR.A  
1341 386.7193 771.4241 771.4239 0.30 0 (2) 21 8 U R.GAGATIR.A  
1341 412.7421 823.4696 823.4704 -1.04 1 4 3.9 1 U R.HLVYR.E  
1341 414.7318 827.4490 827.4501 -1.28 0 49 0.00027 1 U R.TAAAFVIR.V  
1341 422.7358 841.4649 841.4663 0.82 0 46 0.0012 1 U R.GTTFVATVDFR.E  
1341 441.2056 880.3867 880.3862 0.65 0 9 9 1 U R.GTTFVATVDFR.E  
1341 483.2540 944.4935 944.4978 -1.44 0 77 2.4e-006 1 U R.TVDFVIRV.G  
1341 542.7459 1085.4773 1085.4763 0.99 0 56 5.2e-005 1 U R.HNITVIEL.V  
1341 550.7425 1099.4704 1099.4712 -0.68 0 (49) 0.00015 1 U R.HNITVIEL.V  
1341 550.7425 1099.4705 1099.4712 -0.59 0 (46) 0.00032 1 U R.HNITVIEL.V  
1341 620.7859 1239.5773 1239.5774 -0.06 1 31 0.429 1 U R.HNITVIEL.V  
1341 670.3537 1334.6928 1334.6932 -0.27 1 32 0.06 1 U R.QVDFVIRV.E  
1341 677.8633 1343.7121 1343.7119 0.22 0 52 0.00036 1 U R.KLSDAGVIRVLE.E  
1341 673.3632 1344.7118 1344.6959 51.6 0 (22) 0.73 1 U R.KLSDAGVIRVLE.E  
1341 680.8607 1359.7068 1359.7068 0.03 0 (38) 0.0099 1 U R.KLSDAGVIRVLE.E  
1341 732.8740 1445.7234 1445.7343 -0.61 0 44 0.0016 1 U R.TVDFVIRV.E  
1341 1016.5150 2031.0154 2031.0136 0.93 0 69 8.1e-006 1 U R.GTTFVATVDFR.E  
1341 1024.5111 2047.0076 2047.0085 -0.41 0 (41) 0.0059 1 U R.GTTFVATVDFR.E

Proteins matching the same set of peptides:  
**AT0G02800\_1** Mass: 41563 Score: 368 Matches: 22(14) Sequences: 15(10)  
[ Symbol: AAC1 | ADP/ATP carrier 1 | chr3:12605708-12607030 REVERSE LENGTH=361

23. **AT0G03100\_1** Mass: 69484 Score: 316 Matches: 19(12) Sequences: 13(10) eBPAl: 0.66  
[ Symbol: | P-loop containing nucleotide triphosphate hydrolase superfamily protein | chr3:12657099-12662352 FORWARD LENGTH=646  
Query Observed Mr(egpt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
1341 416.7385 831.4624 831.4637 -1.55 0 44 0.0022 1 U R.VLQVIR.F  
1341 416.7453 871.4763 872.4763 -1.22 0 20 3.6 1 U R.BILLAG.F  
1341 525.2674 1048.5202 1048.5189 1.20 0 41 0.0081 1 U R.FALDARH.M  
1341 363.2312 1086.4277 1086.4277 0.0006 0.82 0 (34) 0.016 1 U.RVDFVIRV.E  
1341 544.3164 1086.6192 1086.6186 -0.38 0 39 0.0065 1 U R.QVDFVIRV.E  
1341 569.3190 1096.6235 1096.6241 -0.53 0 31 0.013 1 U R.QVDFVIRV.E  
1341 587.8241 1173.6136 1173.6154 -1.46 0 64 2.4e-005 1 U R.TVDFVIRV.E  
1341 613.8585 1225.7025 1225.7030 -0.44 0 56 4.9e-005 1 U R.VDFVIRV.E  
1341 616.3648 1234.5949 1234.5993 -1.54 1 52 0.00044 1 U R.VDFVIRV.E  
1341 615.7846 1237.5547 1237.5431 -0.30 0 38 0.005 1 U R.HNITVIEL.V  
1341 660.8466 1319.6786 1319.6768 1.33 0 56 0.00016 1 U R.SLDAGVIRVLE.E  
1341 669.8146 1335.6346 1335.6315 0.32 0 49 0.00072 1 U R.HNITVIEL.V  
1341 970.4744 2904.4014 2904.4285 -9.34 2 (1) 97 1 U R.KIVQDFVIRVLE.E  
1341 970.4744 2904.4073 2904.4285 -7.30 2 (2) 41 2 U R.KIVQDFVIRVLE.E  
1341 1485.7069 2909.3992 2909.4126 -1.97 2 5 20 1 U R.KIVQDFVIRVLE.E  
1341 982.4824 2944.4254 2944.4431 -6.02 2 1 1.2e-002 5 U R.HNITVIEL.V  
1341 988.4832 2942.4278 2942.4561 7.34 2 (0) 73 1 U R.HNITVIEL.V

24. **AT0G04500\_1** Mass: 47785 Score: 310 Matches: 19(9) Sequences: 15(7) eBPAl: 1.38  
[ Symbol: PSAT | phosphoserine aminotransferase | chr4:16904205-16905497 FORWARD LENGTH=430

[illegible]



1146	469.3551	934.4956	934.4971	-1.59	0	22	0.62	1	U	K.TDTTVALK.V
1147	520.2885	1038.5625	1038.5611	1.44	0	20	0.33	1	U	K.TDNNVALK.V
1148	545.2638	1068.5130	1068.5138	-0.79	0	4	14	1	U	K.YVGVDFPK.V
1149	380.2633	1137.5879	1137.5891	-0.99	0	0	79	2	U	K.LADNVDFPK.H
1150	411.1952	1230.5639	1230.5638	0.08	0	2	16	2	U	K.SMKHMSPK.D
1151	667.3738	1332.7331	1332.7336	-0.38	0	(19)	5	1	U	K.AIPFATATPK.A
1152	645.2518	1332.7335	1332.7336	-0.36	0	10	3.9	1	U	K.AIPFATATPK.A
1153	675.3707	1346.7249	1346.7285	-1.21	0	(0)	37	1	U	K.AIPFATATPK.A
1154	470.2609	1467.7610	1467.7609	0.07	0	5	12	2	U	K.VVKKKATPK.V
1155	803.9462	1605.8779	1605.8614	10.3	1	30	0.037	1	U	K.VHGVDFKATPK.V
1156	839.6384	1676.8621	1676.8621	0.03	0	42	0.0077	1	U	K.TYGLDTTDEHKPK.F
1157	847.8798	1681.7450	1681.7485	-1.07	0	74	1.2e-004	1	U	K.LDGGHMMATPK.W.F
1158	933.4347	1864.8548	1864.8591	-1.30	0	40	0.012	1	U	K.RVQGVDFKATPK.S
1159	1005.5004	2008.9602	2008.9616	-0.34	0	30	0.058	1	U	K.LDGVDFKATPK.H
1160	780.4224	2338.2453	2338.2420	1.40	0	(2)	25	6	U	K.LDGVDFKATPK.H
1161	1170.1311	2338.2476	2338.2420	1.41	0	71	3.1e-006	1	U	K.LDGVDFKATPK.H
1162	797.4311	2349.2716	2349.2740	-1.02	1	36	0.011	1	U	K.VVKKKATPK.V
1163	1210.5975	4838.3609	4838.3522	1.79	0	18	0.69	1	U	K.NALALAVPVGVDFKATPK.H

33.	AT0G13430.1	Mass: 47060	Score: 255	Matches: 13(7)	Sequences: 10(5)	emPAI: 0.72				
[ Symbol:   Pyridinal-5-phosphate (P5P)-dependent transaminase superfamily protein   chr2:766637-766795 FORWARD LENGTH=122										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide				
214	354.7086	707.4227	707.4240	-1.78	0	22	0.11	1	U	K.LDGVDFK.V
215	379.7137	757.4088	757.4081	0.61	0	12	1.9	1	U	K.LDGVDFK.V
216	881.8446	1161.6746	1161.6757	-1.00	1	28	0.025	1	U	K.GRQGVDFK.V
217	654.7772	1307.5399	1307.5421	-1.66	0	45	4e-006	1	U	K.GRQGVDFK.V
218	436.8544	1307.5415	1307.5421	-0.45	0	(24)	0.063	1	U	K.GRQGVDFK.V
219	442.1857	1323.5353	1323.5370	-1.28	0	(41)	0.0068	1	U	K.GRQGVDFK.V
220	662.7753	1323.5358	1323.5370	-0.77	0	(26)	0.058	1	U	K.GRQGVDFK.V
221	662.9008	1323.7871	1323.7874	-0.27	0	88	1.5e-005	1	U	K.VGVDFKATPK.V
222	671.3409	1346.6472	1346.6511	-17.61	1	2	63	5	U	K.LDGVDFK.V
223	731.3621	1462.7197	1462.7195	0.53	0	11	6.1	1	U	K.LDGVDFK.V
224	761.3997	1526.7948	1526.7934	0.93	1	98	9.1e-009	1	U	K.LDGVDFK.V
225	919.0339	1836.2622	1836.2625	0.29	0	26	0.021	1	U	K.VVKKKATPK.V
226	1331.0732	2660.1318	2660.1417	-3.71	2	0	25	2	U	K.AGVDFKATPK.V

34.	AT0G13430.1	Mass: 41934	Score: 249	Matches: 15(11)	Sequences: 10(8)	emPAI: 1.31				
[ Symbol:   ACC   ADP-ATP carrier 2   chr4:413614-413779 FORWARD LENGTH=165										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect Rank Unique	Peptide			
21	184.6897	367.3648	367.3653	-0.75	1	27	0.126	U	K.DVDFK.V	
22	386.2273	770.4460	770.4399	0.21	0	51	0.0044	1	U	K.GRQGVDFK.V
23	386.7193	771.4241	771.4239	0.30	0	(2)	21	8	U	K.GRQGVDFK.V
24	412.7421	821.4656	821.4674	-1.04	1	4	1.9	3	U	K.LDGVDFK.V
25	414.7318	827.4490	827.4501	-1.28	0	49	0.00027	1	U	K.LDGVDFK.V
26	422.7358	841.4569	841.4563	0.82	0	46	0.0012	1	U	K.LDGVDFK.V
27	542.7459	1081.4973	1081.4963	0.99	0	56	5.2e-005	1	U	K.LDGVDFK.V
28	550.7425	1099.4704	1099.4712	-0.68	0	(49)	0.00015	1	U	K.LDGVDFK.V
29	550.7425	1099.4705	1099.4712	-0.59	0	(46)	0.00012	1	U	K.LDGVDFK.V
30	620.7959	1239.5773	1239.5774	-0.06	1	31	0.029	1	U	K.LDGVDFK.V
31	431.9018	1292.6835	1292.7088	-19.56	1	3	29	3	U	K.LDGVDFK.V
32	672.6833	1343.7121	1343.7119	0.22	0	52	0.00036	1	U	K.LDGVDFK.V
33	673.3632	1344.7118	1344.6959	11.8	0	(22)	0.73	1	U	K.LDGVDFK.V
34	680.8607	1359.7068	1359.7068	0.03	0	(38)	0.0099	1	U	K.LDGVDFK.V
35	733.8740	1465.7314	1465.7342	-0.61	0	46	0.0016	1	U	K.LDGVDFK.V

Proteins matching the same set of peptides:										
AT0G13430.1		Mass: 41934	Score: 249	Matches: 15(11)	Sequences: 10(8)	emPAI: 1.31				
[ Symbol:   ACC2   ADP-ATP carrier 2   chr4:413614-413779 FORWARD LENGTH=165										
35.	AT0G13430.1		Mass: 62205	Score: 236	Matches: 17(6)	Sequences: 15(6)	emPAI: 0.59			
[ Symbol:   CP9860A, CH-CP9860A, BCP   chaperonin-60alpha   chr2:1192663-1192814 FORWARD LENGTH=566										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect Rank	Unique	Peptide		
21	367.3648	732.3550	732.3555	-0.60	0	9	0.0051	1	U	K.LDGVDFK.V
22	383.7081	765.4017	765.4133	-15.11	1	9	4.1	10	U	K.LDGVDFK.V
23	405.7436	815.4724	815.4793	-5.33	0	36	0.003	1	U	K.LDGVDFK.V
24	551.7673	1101.5201	1101.5203	-0.20	0	36	0.0074	1	U	K.LDGVDFK.V
25	602.8146	1203.6146	1203.6136	0.89	0	1	49	2	U	K.LDGVDFK.V
26	645.8121	1289.6296	1289.6299	-0.25	0	78	7.8e-005	1	U	K.LDGVDFK.V
27	740.3768	1478.7391	1478.7405	-0.97	0	52	0.00092	1	U	K.LDGVDFK.V
28	781.3446	1566.6896	1566.6891	0.83	0	47	0.0011	1	U	K.LDGVDFK.V
29	790.4455	1578.6784	1578.6730	2.51	0	11	0.0011	1	U	K.LDGVDFK.V
30	825.9014	1649.7683	1649.7657	1.61	0	96	1.5e-008	1	U	K.LDGVDFK.V
31	571.5908	1712.7556	1712.7569	-0.67	0	4	11	3	U	K.LDGVDFK.V
32	691.0134	2070.0183	2069.9834	16.9	1	2	39	1	U	K.LDGVDFK.V
33	722.7004	2156.0793	2156.0448	16.0	1	2	46	2	U	K.LDGVDFK.V
34	1125.6551	2249.2256	2249.2852	-0.90	0	13	0.009	1	U	K.LDGVDFK.V
35	2913.2120	2916.4143	2916.5960	6.26	0	16	0.34	1	U	K.LDGVDFK.V

36.	AT0G13430.1	Mass: 38858	Score: 235	Matches: 14(11)	Sequences: 12(10)	emPAI: 1.46				
[ Symbol:   Adipocyte protein   chr3:1923743-1923874 REVERSE LENGTH=158										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide				
214	435.2580	865.4513	865.4528	-0.35	0	34	0.013	1	U	K.LDGVDFK.V
215	977.7887	1153.6428	1153.6615	-1.32	0	46	0.0011	1	U	K.LDGVDFK.V
216	387.8678	1160.5816	1160.5826	-0.63	1	(1)	0.051	1	U	K.LDGVDFK.V
217	981.2883	1160.5818	1160.5826	-0.53	1	38	0.0096	1	U	K.LDGVDFK.V
218	599.8180	1195.6214	1195.6197	1.40	0	33	0.019	1	U	K.LDGVDFK.V
219	666.8669	1335.7332	1335.7147	3.40	0	37	0.008	1	U	K.LDGVDFK.V
220	494.8391	1487.7953	1487.7944	0.45	1	34	2.1	1	U	K.LDGVDFK.V
221	763.3797	1524.7412	1524.7420	-0.49	1	40	0.0051	1	U	K.LDGVDFK.V
222	875.9559	1749.8972	1749.8937	0.00	0	46	0.0017	1	U	K.LDGVDFK.V
223	741.6884	2222.0434	2222.0352	3.72	0	67	1.2e-005	1	U	K.LDGVDFK.V
224	1112.5226	2223.0306	2223.0192	5.16	0	(4)	41	1	U	K.LDGVDFK.V
225	1165.1065	2328.1264	2328.1261	0.99	0	33	0.03	1	U	K.LDGVDFK.V
226	869.4222	2605.2449	2605.2355	3.59	1	40	0.014	1	U	K.LDGVDFK.V
227	1046.5334	3136.5784	3136.5638	4.64	0	1	1.1e+002	7	U	K.LDGVDFK.V

37.	AT0G13430.1	Mass: 53435	Score: 232	Matches: 12(6)	Sequences: 7(4)	emPAI: 0.71			
[ Symbol:   RBCL   ribulose-bisphosphate carboxylase   chr2:54958-56397 FORWARD LENGTH=479									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect	Rank	Unique	Peptide
214	435.7251	869.4357	869.4378	-0.32	0	22	0.18	0	U
215	396.5539	1186.4578	1186.4571	0.60	0	(32)	0.033	1	U
216	594.3373	1186.4601	1186.4571	0.57	0	69	8.4e-006	1	U
217	614.8140	1227.4534	1227.4459	0.12	0	12	2.3	1	U
218	362.6967	1446.7577	1446.7579	-0.18	0	(9)	7.6	1	U
219	481.2602	1446.7587	1446.7579	0.55	0	(20)	0.45	1	U
220	724.3487	1446.7588	1446.7579	0.61	0	43	0.0036	1	U
221	726.3153	1446.7581	1446.7547	0.98	0	26	0.04	1	U
222	489.2502	1446.7468	1446.7474	-0.30	0	(12)	3.9	1	U
223	733.3831	1446.7517	1446.7474	2.94	0	3	0.098	1	U
224	1085.4859	2168.9772	2168.9797	-1.13	1	95	1.2e-008	1	U
225	724.0056	2168.9801	2168.9797	0.20	1	(57)	7.1e-005	1	U

38.	AT0G13430.1	Mass: 37417	Score: 231	Matches: 11(6)	Sequences: 9(5)	emPAI: 0.97				
[ Symbol:   At1g18470.1   At1g18470.1   chr1:2552555-2553484 REVERSE LENGTH=150										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide				
214	433.7348	865.4513	865.4545	0.67	0	37	0.0081	1	U	K.LDGVDFK.V
215	651.7244	911.4342	911.4348	-0.74	0	20	0.3	1	U	K.LDGVDFK.V
216	473.7225	945.4305	945.4304	0.04	0	24	0.049	1	U	K.LDGVDFK.V
217	505.2406	1012.4656	1012.4676	-0.94	0	25	0.062	1	U	K.LDGVDFK.V
218	607.4084	1213.5950	1213.5939	0.93	0	46	0.00079	1	U	K.LDGVDFK.V
219	621.3468	1244.6790	1244.6799	-0.65	0	33	0.046	1	U	K.LDGVDFK.V
220	884.7943	2463.3611	2463.3629	-0.66	2	6	18	2	U	K.LDGVDFK.V
221	1227.5993	3680.7941	3680.7581	10.3	0	35	0.02	1	U	K.LDGVDFK.V
222	959.7318	3834.8981	3834.8912	1.80	1	131	5.4e-012	1	U	K.LDGVDFK.V
223	1279.4375	4873.8953	4873.8752	0.33	1	246	0.01	1	U	K.LDGVDFK.V

<a href="#">13845</a>	1238.6134	3712.8184	3712.7744	11.8	1	5	37	1	U	R.AYIPVDQVINGREVDQWELLKNNRPQQGSK.I
<a href="#">14308</a>	1284.5859	3850.7359	3850.7826	-12.12	1	1	63	8	U	R.GSDVHCILCPNRPDGGSSVGLQISTPWNK.I

<a href="#">40.</a>	<a href="#">AT1G07930.1</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	emPAI: 1.02
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2455559-245701 FORWARD LENGTH=449						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1384</a>	413.2215	824.4284	824.4280	0.82	0	(25) 0.082 1
<a href="#">1385</a>	825.4360	824.4288	824.4280	0.97	0	42 0.0017 1
<a href="#">1386</a>	481.2793	874.5443	874.5437	0.43	0	35 0.013 1
<a href="#">1387</a>	504.2792	1004.5438	1004.5447	-0.91	1	34 0.016 1
<a href="#">1388</a>	513.3091	1024.6636	1024.6030	0.64	0	21 0.137 1
<a href="#">1389</a>	374.2045	1119.5917	1119.5924	-0.62	0	(16) 1.5 1
<a href="#">1390</a>	560.8032	1119.5918	1119.5924	-0.51	0	46 0.0015 1
<a href="#">1391</a>	649.8767	1287.7389	1287.7394	-0.42	0	11 2 1
<a href="#">1392</a>	676.3254	1350.4362	1350.4415	-3.95	1	69 1.3e+005 1 U
<a href="#">1393</a>	451.2204	1350.4386	1350.4415	-1.52	1	(32) 0.033 1 U
<a href="#">1394</a>	484.5027	1450.4664	1450.4663	0.02	0	2 0.0000 1
<a href="#">1395</a>	754.3775	1504.7405	1504.7426	-1.41	2	66 1.5e+005 1 U
<a href="#">1396</a>	625.2992	1872.7527	1872.7661	-0.13	1	1 12 1
<a href="#">1397</a>	760.7179	2279.1319	2279.1330	-0.49	0	54 0.00025 1
<a href="#">1398</a>	1140.5750	2279.1324	2279.1330	1.07	0	(4) 53 1
<a href="#">1399</a>	1261.6448	2521.3150	2521.3179	-0.46	0	(15) 1.7 1
<a href="#">1400</a>	841.4465	2521.3176	2521.3172	0.17	0	15 1.5 1 U
<a href="#">1401</a>	1172.5691	3514.4855	3514.4556	8.50	1	0 1.2e+002 1

Proteins matching the same set of peptides:

<a href="#">AT1G07930.1</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2455559-245701 FORWARD LENGTH=449					
<a href="#">AT1G07940.1</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2463350-2464792 REVERSE LENGTH=449					
<a href="#">AT1G07950.2</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2463350-2464792 REVERSE LENGTH=449					
<a href="#">AT1G07960.1</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2429325-2429675 FORWARD LENGTH=449					
<a href="#">AT1G07970.1</a>	Mass: 49813	Score: 219	Matches: 18(8)	Sequences: 13(7)	
[ Symbol:   GTP binding Elongation factor Tu family protein   chr1:2429325-2429675 FORWARD LENGTH=449					

<a href="#">41.</a>	<a href="#">AT1G07930.1</a>	Mass: 28280	Score: 217	Matches: 13(6)	Sequences: 6(3)	emPAI: 0.95
[ Symbol: CAB2, AB145, CAB145, LNCB1.3   chlorophyll A/B-binding protein 1   chr1:10478071-10478874 FORWARD LENGTH=267						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1402</a>	491.7687	981.5229	981.5243	-1.48	0	39 0.0036 1
<a href="#">1403</a>	492.2526	982.4906	982.4913	-0.64	0	19 0.46 1
<a href="#">1404</a>	418.2294	1251.6662	1251.6683	-1.70	1	(41) 0.0031 1
<a href="#">1405</a>	626.8408	1251.6670	1251.6683	-1.07	1	79 4.2e+007 1
<a href="#">1406</a>	633.2814	1264.5482	1264.5473	0.72	0	65 6.8e+006 1
<a href="#">1407</a>	614.9743	1853.8011	1853.8779	-0.77	(8)	40 4 U
<a href="#">1408</a>	615.9606	1853.8001	1853.8779	-0.43	(2)	37 4 U
<a href="#">1409</a>	624.3068	1869.8985	1869.9328	-18.35	1	5 17 1
<a href="#">1410</a>	1031.5114	3091.5124	3091.5152	-0.90	0	(22) 0.42 1
<a href="#">1411</a>	1032.1805	3093.5197	3093.4832	11.8	0	30 0.063 1

<a href="#">42.</a>	<a href="#">AT1G07930.1</a>	Mass: 28266	Score: 217	Matches: 12(6)	Sequences: 7(3)	emPAI: 0.95
[ Symbol: CAB2, AB145, LNCB1.2   chlorophyll A/B-binding protein 3   chr1:10478443-10479246 REVERSE LENGTH=267						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1412</a>	491.7687	981.5229	981.5243	-1.48	0	39 0.0036 1
<a href="#">1413</a>	492.2526	982.4906	982.4913	-0.64	0	19 0.46 1
<a href="#">1414</a>	418.2294	1251.6662	1251.6683	-1.70	1	(41) 0.0031 1
<a href="#">1415</a>	626.8408	1251.6670	1251.6683	-1.07	1	79 4.2e+007 1
<a href="#">1416</a>	633.2814	1264.5482	1264.5473	0.72	0	65 6.8e+006 1
<a href="#">1417</a>	614.9743	1853.8011	1853.8779	-0.77	(8)	40 4 U
<a href="#">1418</a>	615.9606	1853.8001	1853.8779	-0.43	(2)	37 4 U
<a href="#">1419</a>	624.3068	1869.8985	1869.9328	-18.35	1	5 17 1
<a href="#">1420</a>	1031.5114	3091.5124	3091.5152	-0.90	0	(22) 0.42 1
<a href="#">1421</a>	1032.1805	3093.5197	3093.4832	11.8	0	30 0.063 1

Proteins matching the same set of peptides:

Mass: 28266		Score: 217	Matches: 12(6)	Sequences: 7(3)		
[ Symbol: CAB2, AB145, LNCB1.2   chlorophyll A/B-binding protein 2   chr1:10475089-10475692 REVERSE LENGTH=267						
43.	Mass: 28093	Score: 217	Matches: 10(6)	Sequences: 5(3)	emPAI: 0.96	
[ Symbol: LNCB2, LNCB1.5   photosystem II light harvesting complex gene B102   chr2:14522716-14523513 REVERSE LENGTH=265						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1422</a>	491.7687	981.5229	981.5243	-1.48	0	39 0.0036 1
<a href="#">1423</a>	492.2526	982.4906	982.4913	-0.64	0	19 0.46 1
<a href="#">1424</a>	418.2294	1251.6662	1251.6683	-1.70	1	(41) 0.0031 1
<a href="#">1425</a>	626.8408	1251.6670	1251.6683	-1.07	1	79 4.2e+007 1
<a href="#">1426</a>	633.2814	1264.5482	1264.5473	0.72	0	65 6.8e+006 1
<a href="#">1427</a>	614.9743	1853.8011	1853.8779	-0.77	(8)	40 4 U
<a href="#">1428</a>	615.9606	1853.8001	1853.8779	-0.43	(2)	37 4 U
<a href="#">1429</a>	624.3068	1869.8985	1869.9328	-18.35	1	5 17 1
<a href="#">1430</a>	1031.5114	3091.5124	3091.5152	-0.90	0	(22) 0.42 1
<a href="#">1431</a>	1032.1805	3093.5197	3093.4832	11.8	0	30 0.063 1
K.PGLNLS						

Proteins matching the same set of peptides:

Symbol: LNCB2.1, LNCB2   photosystem II light harvesting complex gene 2.2   chr1:17994916-1800129 REVERSE LENGTH=265						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
1432	491.7687	981.5229	981.5243	-1.48	0	39 0.0035 1 R.ELEVINSR.V 1444
1433	492.2526	982.4906	982.4913	-0.64	0	19 0.46 1 K.FORAYR.V
1434	418.2294	1251.6662	1251.6683	-1.70	1	(41) 0.0031 1 K.NIELSENIR.V
1435	626.8408	1251.6670	1251.6683	-1.07	1	79 4.2e+007 1 K.NIELSENIR.V
1436	633.2814	1264.5482	1264.5473	0.72	0	65 6.8e+006 1 K.STQPIIR.V
1437	614.9743	1853.8011	1853.8013	-0.08	0	63 3e+005 1 U K.STQPIIR.V
1438	615.9606	1853.8012	1853.8013	-0.08	0	(47) 0.0013 1 U K.STQPIIR.V
1439	1185.9429	3534.7517	3534.7457	1.69	46	0.0014 1 U R.IODGLGLDGLDLPFGAFGLALMDAPAFKSL.V

Proteins matching the same set of peptides:

<a href="#">AT1G07930.1</a>	Mass: 28688	Score: 212	Matches: 8(7)	Sequences: 5(4)	
[ Symbol: LNCB2.1, LNCB2   photosystem II light harvesting complex gene 2.2   chr1:18234449-1824331 REVERSE LENGTH=265					
<a href="#">AT1G07930.1</a>	Mass: 28699	Score: 212	Matches: 8(7)	Sequences: 5(4)	
[ Symbol: LNCB2.4, LNCB2.3, LNCB2   photosystem II light harvesting complex gene 2.3   chr3:10256002-10256921 FORWARD LENGTH=266					

<a href="#">45.</a>	<a href="#">AT1G04480.1</a>	Mass: 60370	Score: 210	Matches: 22(8)	Sequences: 19(7)	emPAI: 0.89
[ Symbol:   Ribosomal protein S5 family protein   chr1:24105731-2410768 FORWARD LENGTH=515						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1442</a>	762.4520	761.4447	761.4436	1.45	0	17 0.44 1 U
<a href="#">1443</a>	394.7112	787.4018	787.4075	0.36	0	53 0.0024 1
<a href="#">1444</a>	472.2667	942.5189	942.5022	19.7	0	26 0.19 1 U
<a href="#">1445</a>	472.7613	941.5081	941.5087	-0.56	1	35 0.015 1 U
<a href="#">1446</a>	534.2517	1064.4889	1064.4931	-1.96	0	40 0.0074 1 U
<a href="#">1447</a>	573.7830	1141.5514	1141.5717	-19.70	0	14 1.7 1 U
<a href="#">1448</a>	594.3101	1186.4446	1186.4445	0.04	1	36 0.013 1 U
<a href="#">1449</a>	404.2430	1209.7071	1209.7081	-0.84	1	8 2.4 2 U
<a href="#">1450</a>	424.9032	1271.6879	1271.6874	0.37	1	3 27 1 U
<a href="#">1451</a>	637.8412	1271.6879	1271.6866	1.03	1	29 0.087 1
<a href="#">1452</a>	737.8272	1471.6399	1473.6444	-3.07	1	(32) 0.011 1 U
<a href="#">1453</a>	492.2210	1471.6413	1473.6444	-1.10	1	38 0.0024 1 U
<a href="#">1454</a>	739.8881	1477.7616	1477.7639	-0.24	0	28 0.11 1 U
<a href="#">1455</a>	534.6086	1540.8041	1540.8097	-0.61	(19)	0.51 1 U
<a href="#">1456</a>	771.4107	1540.8049	1540.8097	-0.81	1	44 0.0039 1 U
<a href="#">1457</a>	871.9303	1741.8460	1741.8192	15.4	2	0 57 1 U
<a href="#">1458</a>	882.9364	1761.8582	1761.8591	-0.47	0	(23) 0.37 1 U
<a href="#">1459</a>	588.9652	1761.8588	1761.8591	-0.15	0	29 0.081 1 U
<a href="#">1460</a>	903.4257	1804.8368	1804.8380	-0.68	0	71 3.6e+006 1 U
<a href="#">1461</a>	870.4294	2608.2463	2608.2795	-0.57	2	90 4 U
<a href="#">1462</a>	898.4551	2692.3436	2692.3101	12.4	2	0 1.3e+002 1 U
<a href="#">1463</a>	982.1278	2941.3616	2943.3549	2.28	1	9 7.9 1 U

<a href="#">46.</a>	<a href="#">AT1G04480.1</a>	Mass: 14064	Score: 209	Matches: 10(5)	Sequences: 8(4)	emPAI: 3.36
[ Symbol:   A16-090-090-binding protein   chr1:10223461-10224959 REVERSE LENGTH=10						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide
<a href="#">1464</a>	394.2481	786.4817	786.4816	-1.49	0	36 0.0028 1 U
<a href="#">1465</a>	504.2767	1004.5389	1004.5369	1.98	0	26 0.13 1 U
<a href="#">1466</a>	568.3223	1134.8300	1134.8318	-1.61	1	35 0.012 1
<a href="#">1467</a>	670.3927	1338.7708	1338.7700	0.65	0	1 18 1 U
<a href="#">1468</a>	684.3107	1364.6069	1364.6074	-0.39	0	18 0.95 1 U
<a href="#">1469</a>	740.8680	1479.7214	1479.7239	-1.69	1	105 1.9e+009 1 U
<a href="#">1470</a>	499.5790	1495.7152	1495.7188	-2.42	1	(86) 1.4e+007 1 U
<a href="#">1471</a>	856.3937	1710.7728	1710.7770	-2.46	1	51 0.00075 1 U
<a href="#">1472</a>	876.5944	1726.7715	1726.7719	0.82	1	(5) 10 1 U
<a href="#">1473</a>	894.7337	2681.1792	2681.1762	1.14	2	20 0.29 1 U

<a href="#">47.</a>	<a href="#">AT1G04480.1</a>	Mass: 37529	Score: 207	Matches: 17(10)	Sequences: 10(8)	emPAI: 1.54
[ Symbol: H1P2, H1P2T2   histidine 2   chr1:15993313-15993719 FORWARD LENGTH=39						
Query	Observed	Mr(Exp1)	Mr(calc)	ppm	Miss score	Expect Rank Unique Peptide

2346

1011.5243

2021.0340

2021.0317

1.17

0

43

0.0029

1

U

K.GRIPIVPPHAFIYDTYR.G

2347

1011.5243

2021.0340

2021.0317

1.17

0

44

1.8e-005

1

U

R.ATIVQSTVYDTPTLXK.A

2348

682.4796

2048.0149

2048.0079

4.40

2

5

22

1

U

R.PULGVGVHREHREPRK.Y

2349

1082.5218

2161.0130

2161.0307

1.09

0

31

0.049

1

U

R.CIQGQSGTTPVYTFPRK.L

49. **AT0G16210.1** Mass: 41996 Score: 200 Matches: 13(8) Sequences: 11(6) eMPI: 0.70

[ Symbol: | ACT12 | actin-12 | chr3:17128567-17129981 FORWARD LENGTH=177

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

2346

384.2240

766.4333

766.4337

-0.50

0

41

0.0015

1

U

K.VVADPR.K

2347

572.7833

1143.5520

1143.5529

-0.82

0

13

1.6

1

U

R.RTQVWQRK.D

2348

574.3056

1146.5907

1146.5954

1.08

0

46

0.0018

1

U

K.RITALASRME.I

2349

591.7668

1181.5191

1181.5200

-0.78

0

47

0.00054

1

U

K.DAVYDAQSR.R

2350

605.8178

1337.6210

1337.6211

-0.10

1

62

3.1e-005

1

U

K.DAVYDAQSR.G

2351

758.3803

1514.7459

1514.7419

2.69

0

38

0.019

1

U

K.IHMTVPHELR.V

2352

1167.1060

2324.1974

2324.2246

-11.67

1

0

54

4

U

R.APPFVIGAPRHDTQVQWQGD.D

2353

1051.2188

3150.6196

3150.6350

-0.13

0

39

0.0065

1

U

R.TGVILGSGDVSFVPIYEDALSHALLR.L

2354

788.6667

3150.6379

3150.6350

0.93

0

69

5.3e-006

2

U

R.TGVILGSGDVSFVPIYEDALSHALLR.L

2355

1176.5656

3526.4750

3526.4784

5

44

9

U

R.HNHYLGPFYTFYTAATGALVGLSDR.T

2356

1328.3003

3981.8791

3981.8079

17.9

1

7

13

9

U

R.CFVVLGPGHIGHGNGHIGHTTTSIGACVDVR.K

2357

1381.6597

4141.9573

4141.8927

15.6

2

1

91

10

U

R.CFVVLGPGHIGHGNGHIGHTTTSIGACVDVR.K

Proteins matching the same set of peptides:

AT0G16210.1

Mass: 41996

Score: 200

Matches: 13(8)

Sequences: 11(6)

[ Symbol: | ACT1 | actin 1 | chr3:23950109-23951586 FORWARD LENGTH=177

AT0G16210.1

Mass: 41996

Score: 200

Matches: 13(8)

Sequences: 11(6)

[ Symbol: | ACT4 | actin 4 | chr3:23950109-23951586 FORWARD LENGTH=177

49. **AT0G17420.1** Mass: 42056 Score: 200 Matches: 11(8) Sequences: 9(6) eMPI: 0.70

[ Symbol: | ACT1, ACT3 | actin 1 | chr2:15779761-15781241 FORWARD LENGTH=377

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

2346

384.2240

766.4333

766.4337

-0.50

0

41

0.0015

1

U

K.VVADPR.K

2347

572.7833

1143.5520

1143.5529

-0.82

0

13

1.6

1

U

R.RTQVWQRK.D

2348

574.3056

1146.5907

1146.5954

1.08

0

46

0.0018

1

U

K.RITALASRME.I

2349

591.7668

1181.5191

1181.5200

-0.78

0

47

0.00054

1

U

K.DAVYDAQSR.R

2350

605.8178

1337.6210

1337.6211

-0.10

1

62

3.1e-005

1

U

K.DAVYDAQSR.G

2351

758.3803

1514.7459

1514.7419

2.69

0

38

0.019

1

U

K.IHMTVPHELR.V

2352

1167.1060

2324.1974

2324.2246

-11.67

1

0

54

4

U

R.APPFVIGAPRHDTQVQWQGD.D

2353

1051.2188

3150.6196

3150.6350

-0.13

0

39

0.0065

1

U

R.TGVILGSGDVSFVPIYEDALSHALLR.L

2354

788.6667

3150.6379

3150.6350

0.93

0

69

5.3e-006

2

U

R.TGVILGSGDVSFVPIYEDALSHALLR.L

2355

1081.5127

3241.5163

3241.5185

-6.86

0

1

85

2

U

R.NTGLHPTPTGAPGATGALVGLSDR.T

Proteins matching the same set of peptides:

AT0G17420.1

Mass: 42056

Score: 200

Matches: 11(8)

Sequences: 9(6)

[ Symbol: | ACT1, ACT3 | actin 1 | chr2:15779761-15781241 FORWARD LENGTH=377

AT0G17420.1

Mass: 42056

Score: 200

Matches: 11(8)

Sequences: 9(6)

[ Symbol: | ACT3 | actin 3 | chr3:19915924-19917371 FORWARD LENGTH=377

50. **AT0G20260.1** Mass: 33850 Score: 199 Matches: 7(5) Sequences: 7(5) eMPI: 0.40

[ Symbol: | Actin DMS/DBP-binding protein | chr1:7050590-7057281 REVERSE LENGTH=115

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

2346

418.7296

835.4447

835.4440

0.85

0

21

0.29

1

U

K.INDVPEK.R

2347

614.6116

1227.6097

1227.6095

-0.48

0

43

0.0017

1

U

R.ADTYFAARME.I

2348

621.3468

1244.6790

1244.6759

-0.65

0

3

0.046

1

U

R.HVSGITTLSE.R

2349

836.4262

1679.8779

1679.8837

2.47

0

6

0.13

1

U

R.HYITTMALLQGR.S

2350

1003.4050

2004.7954

2004.7755

9.93

0

50

8.6e-005

1

U

R.GGCVYQGTGDSQGRQR.S

2351

1213.9388

3638.7946

3638.7952

-0.17

0

57

0.0004

1

U

R.IPLQKGTSTIGSTDTTQWTFEGRGQIETPR.H

2352

948.7340

3794.3609

3794.3863

2.79

1

93

2.6e-008

1

U

R.HPLQKGTSTIGSTDTTQWTFEGRGQIETPR.H

51. **AT0G48710.1** Mass: 81527 Score: 192 Matches: 17(6) Sequences: 17(6) eMPI: 0.27

[ Symbol: | Glutarylglutamyl-CoA synthetase, class II | chr5:1935673-1938247 FORWARD LENGTH=719

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

2346

811.3809

1621.3844

1621.3844

-0.41

0

41

0.0015

1

U

K.DVPEK.C

2347

446.7131

891.4317

891.4320

-0.27

0

20

0.33

1

U

K.HNIAFRRR.G

2348

454.2100

906.4054

906.4083

-0.28

0

3

13

2

U

K.FVDNRAR.H

2349

482.4972

965.0139

965.0185

1.48

0

34

0.018

1

U

K.YGVGVYR.F

2350

497.2246

992.0387

992.0386

0.16

0

4

10

1

U

K.FHQGRAR.A

2351

543.3379

1086.6813

1086.6804

-0.82

1

63

8.8e-006

1

U

K.HLADGVLYR.V

2352

585.7903

1169.5660

1169.5651

0.74

1

18

0.44

1

U

K.ANDQVYTR.C

2353

647.3207

1295.6269

1295.6248

1.62

0

21

1.1

1

U

K.EKRPQVNRK.D

2354

723.6088

1445.7250

1445.7184

1.60

1

48

1

U

R.HLACRQVGLAR.H

2355

741.3970

1480.7795

1480.7773

1.47

0

48

0.00074

1

U

R.GRPVDFPRAER.V

2356

815.3621

1631.8651

1631.8531

10.1

1

2

36

1

U

K.VYADYQGVTR.F

2357

883.4443

1704.8739

1704.8723

1.86

0

64

1.6e-005

1

U

K.VYLTIDQGVPR.H

2358

975.4407

1948.8669

1948.8902

-11.93

1

2

44

2

U

R.KLEKEDQVADVPQPRK

2359

1026.4521

2058.9894

2058.9894

-0.35

0

9

0.9

1

U

K.VYVDFVPELRAR.L

2360

693.3422

1387.0048

1387.0051

0.49

2

1

2.1

1

U

K.KLEKEDQVADVPQPRK

2361

1055.5479

2118.6219

2118.6193

0.81

0

60

5.5e-005

1

U

K.YLEKEDQVADVPQPRK

52. **AT0G48800.1** Mass: 76576 Score: 191 Matches: 14(6) Sequences: 10(6) eMPI: 0.34

[ Symbol: | cpim070-1 | chloroplast heat shock protein 70-1 | chr4:1259094-1259437 FORWARD LENGTH=718

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

2346

488.2483

916.4820

916.4801

-0.19

0

46

0.0093

1

U

R.VYVDFPELR.L

2347

485.7490

969.5235

969.5243

-0.81

0

8

2.9

1

U

K.HETFLER.A

2348

504.2929

1006.5712

1006.5660

15.1

1

5

6.6

2

U

K.QVDFVTR.D

2349

510.2719

1018.5292

1018.5295

-0.31

0

34

0.024

1

U

K.HSGDTQPR.D

2350

533.7920

1065.5713

1065.5706

0.63

0

33

0.018

1

U

R.TFVFAVTR.S

2351

616.5496

1236.6270

1236.6452

-13.95

1

17

12

1

U

R.HNKGDTQPR.S

2352

654.3209

1306.6273

1306.6452

-13.71

1

24

0.2

1

U

R.HNKGDTQPR.S

2353

691.3337

1386.6529

1386.6521

0.47

0

67

1e-005

1

U

R.HKQDVPQPR.G

2354

491.9365

983.8776

983.8786

-0.10

0

49

3

U

K.QGVITVQATPR.D

2355

737.4102

1472.8559

1472.8686

-1.85

1

17

2.5

1

U

K.QGVITVQATPR.D

2356

780.8808

1578.8015

1578.7995

1.27

0

42

0.004

1

U

K.AVYVQATPRK.T

2357

869.4431

1736.8717

1736.8733

-0.94

0

68

2.1e-005

1

U

R.HNPTASLQPRK.R

53. **AT0G48810.1** Mass: 58689 Score: 168 Matches: 12(7) Sequences: 9(5) eMPI: 0.30

[ Symbol: | Class-II DADP synthetase family protein | chr1:7912120-7914762 FORWARD LENGTH=827

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

2346

415.2580

830.5615

830.5615

-0.74

0

8

6.4

3

U

R.DVAGFLKE.V

2347

622.2979

1242.5811

1242.5815

-0.31

0

48

0.0013

1

U

R.AFATQVTAAR.V

2348

626.7763

1251.5380

1251.5368

0.97

0

33

0.011

1

U

R.GDNHGAARF.R

2349

627.0464

1252.5186

1252.5008

11.69

0

33

0.01

1

U

R.GDNHGAARF.R

2350

642.8185

1281.6625

1281.6622

0.22

0

42

0.0022

1

U

R.GLDANVFRL.G

2351

428.8955

857.6444

857.6422

2.18

1

14

15

1

U

R.GLDANVFRL.G

2352

706.9128

1413.8156

1413.8076

7.73

0

41

0.0019

1

U

R.LSLTANRMR.I

2353

656.0186

1310.0454

1310.0694

-23.97

1

1

33

2

U

R.HLNGHGLGDSVGEINR.Q

2354

631.4512

1267.3177

1267.3188

-0.43

0

44

0.0087

1

U

R.ITANGLAAATTTTATGTVQVQWRK.G

2355

1663.2161

3324.4176

3324.4629

-13.62

2

5

12

6

U

R.AFATQVTAARQVTVGLQVTFRRGRK.V

2356

1366.9739

2733.8999

2733.9251

-6.16

2

2

33

1

U

R.AVYQGAATLQLAATQVTAARQVTVGLQVTFRRGRK.V

54. **AT0G48820.1** Mass: 60654 Score: 162 Matches: 6(4) Sequences: 6(4) eMPI: 0.30

[ Symbol: | KPM/VMS family protein | chr3:3772981-377616 FORWARD LENGTH=560

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

2346

432.7388

865.4503

865.4502

0.18

0

0

0.028

1

U

K.VPQDPRK.R

2347

364.5206

729.0401

729.0407

-0.57

1

25

0.19

1

U

R.LSLTANRMR.I

2348

444.8412

889.6718

889.6713

0.61

0

60

0.0062

1

U

R.VGLGATVTR.S

2349

701.8091

1403.6037

1403.6048

-0.77

1

2

9.4

2

U

R.HKQDVPQPR.S

2350

643.1361

1286.2865

1286.2838

0.26

1

47

2.4e-005

1

U

R.HLADGVLYR.V

2351

669.1531

1338.3014

1338.2830

-0.23

0

82

4.2e-007

1

U

R.YGNTQVMPHPTALAGATYR.K

55. **AT0G54890.1** Mass: 61659 Score: 147 Matches: 12(6) Sequences: 12(6) eMPI: 0.42

[ Symbol: | CPM60, L2B1 | chaperonin 60 beta | chr1:10717157-10718473 REVERSE LENGTH=400

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

2346

407.1848

812.3550

812.3555

-0.60

0

19

0.0051

1

U

R.AQDPRK.R

2347

431.2884

862.5644

862.5644

-2.00

1

26

0.05

1

U

R.ALVYELR.K

2348

464.7288

927.4431

927.4450

-0.19

0

8

3.4

1

U

K.FYDARTRK.Y

2349

466.7328

930.4906

930.4924

-1.82

0

32

0.036

1

U

R.FYDALATK.A

2350

495.2613

988.5080

988.5077

0.26

1

14

4

1

U

R.FYVGLRME.A

2351

522.2961

1042.5777

1042.5771

0.59

0

61

3.3e-005

1

U

R.FYNDQVTR.R

2352

581.2907

1160.5668

1160.5673

-0.43

0

54

0.0004

1

U

R.HLADGVLYR.V

2353

591.8595

1181.7043

1181.7020

2.00

0

14

0.45

1

U

K.LADGVLYRQV.G

2354

600.3362

1198.6579

1198.6557

1.77

0

24

0.15

1

U

R.DGVLYDARK.D

2355

771.8779

1540.7613

1540.7620

-0.47

0

43

0.0029

1

U

R.FYVGLRME.A

2356

401.7141

802.8273

802.8478

-12.80

1

3

37

6

U

K.VGDFVINDQVTR.R

2357

776.7043

1539.5963

1539.5958

0.24

1

1

50

1

U

R.AFTPTATSSISQVYAWQGRK.R

Proteins matching the same set of peptides:

AT0G54890.1

Mass: 61659

Score: 147

Matches: 12(6)

Sequences: 12(6)

[ Symbol: | CPM60, L2B1 | chaperonin 60 beta | chr1:10717157-10718473 REVERSE LENGTH=400

56. **AT0G54890.1** Mass: 63762 Score: 147 Matches: 11(5) Sequences: 11(5) eMPI: 0.35

[ Symbol: | TCP-1/gp60 chaperonin family protein | chr3:4386685-4392624 FORWARD LENGTH=596

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

2346

407.1848

812.3550

812.3555

-0.60

0

19

0.0051

1

U

R.AQDPRK.R

2347

432.7388

865.4503

865.4502

0.18

0

0

0.028

1

U

K.FYDARTRK.Y

2348

444.8412

889.6718

889.6713

0.61

0

60

0.0062

1

U

R.VGLGATVTR.S

2349

701.8091

1403.6037

1403.6048

-0.77

1

2

9.4

2

U

R.HKQDVPQPR.S

2350

643.1361

1286.2865

1286.2838

0.26

1

47

2.4e-005

1

U

R.HLADGVLYR.V

23

Proteins matching the same set of peptides:

**AT0G16210.1** Mass: 41980 Score: 200 Matches: 13(8) Sequences: 11(6)

[ Symbol: | ACT1 | actin-4 | chr5:2395109-23951586 FORWARD LENGTH=177

**AT0G16210.2** Mass: 41980 Score: 200 Matches: 13(8) Sequences: 11(6)

[ Symbol: | ACT1 | actin-4 | chr5:2395109-23951586 FORWARD LENGTH=177

 49. **AT0G17240.1** Mass: 42056 Score: 200 Matches: 11(8) Sequences: 9(6) eMPI: 0.70  [ Symbol: | ACT1, Act1 | actin-1 | chr2:15779761-15781241 FORWARD LENGTH=177  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2346  384.2240  766.4333  766.4337  -0.50  0  41  0.0015  1  U  K.VVADPR.K  2347  572.7833  1143.5520  1143.5529  -0.82  0  13  1.6  1  U  R.RTQVWQRK.D  2348  574.3056  1146.5907  1146.5954  1.08  0  46  0.0018  1  U  K.RITALASRME.I  2349  591.7668  1181.5191  1181.5200  -0.78  0  47  0.00054  1  U  K.DAVYDAQSR.R  2350  605.8178  1337.6210  1337.6211  -0.10  1  62  3.1e-005  1  U  K.DAVYDAQSR.G  2351  758.3803  1514.7459  1514.7419  2.69  0  38  0.019  1  U  K.IHMTVPHELR.V  2352  1167.1060  2324.1974  2324.2246  -11.67  1  0  54  4  U  R.APPFVIGAPRHDTQVQWQGD.D  2353  1051.2188  3150.6196  3150.6350  -0.13  0  39  0.0065  1  U  R.TGVILGSGDVSFVPIYEDALSHALLR.L  2354  788.6667  3150.6379  3150.6350  0.93  0  69  5.3e-006  2  U  R.TGVILGSGDVSFVPIYEDALSHALLR.L  2355  1081.5127  3241.5163  3241.5185  -4.66  0  1  85  2  U  R.TGIMFTFPGHATGATGVLSDR.T |

Proteins matching the same set of peptides:

**AT0G17240.1** Mass: 42056 Score: 200 Matches: 11(8) Sequences: 9(6)

[ Symbol: | ACT1, Act1 | actin-1 | chr2:15779761-15781241 FORWARD LENGTH=177

**AT0G17240.2** Mass: 42056 Score: 200 Matches: 11(8) Sequences: 9(6)

[ Symbol: | ACT1 | actin-1 | chr3:18919524-19917371 FORWARD LENGTH=177

 50. **AT0G20490.1** Mass: 33800 Score: 199 Matches: 7(5) Sequences: 7(5) eMPI: 0.60  [ Symbol: | Kine DINK-like binding protein | chr1:7050590-7072785 REVERSE LENGTH=115  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2356  416.7296  835.4447  835.4440  0.85  0  21  0.29  1  U  K.SHEVPEK  2357  614.8116  1227.6887  1227.6988  -0.68  0  43  0.0057  1  U  K.ADTPLASRME.I  2358  623.3468  1244.6790  1244.6799  -0.65  0  33  0.046  1  U  R.HVIGITTLR.K  2359  636.4460  1470.8797  1470.8837  2.47  0  6  13  1  U  R.WITITALASRME.I  2360  1003.4050  2004.7954  2004.7755  9.93  0  50  8.6e-005  1  U  R.GGVYGVNGSGSGSR.S  2361  1213.9388  3638.7946  3638.7952  -0.17  0  57  0.00014  1  U  R.IPLGKQITVIGSDITDTNFTPTTQTITTR.H  2362  949.7340  3794.9069  3794.8963  2.79  1  93  2.8e-008  1  U  R.KIPGLQITVIGSDITDTNFTPTTQTITTR.H || 51. **AT0G26710.1** Mass: 81527 Score: 192 Matches: 17(6) Sequences: 17(6) eMPI: 0.27  [ Symbol: | glutamyl/glutamyl-LSDA synthetase, class Ic | chr5:9305671-9308247 FORWARD LENGTH=719  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2363  383.2157  764.4168  764.4181  -0.17  0  8  6.3  3  U  K.TQELVR.V  2364  406.6995  813.3849  813.3864  -0.25  0  41  0.0015  1  U  R.RVPTVR.V  2365  446.7131  893.4317  893.4320  -0.27  0  20  0.33  1  U  K.HNMGSGR.G  2366  454.2100  906.4054  906.4083  -0.25  0  3  13  2  U  R.FDTQWAK.H  2367  485.2072  969.3899  969.3888  1.48  0  34  0.018  1  U  R.TQTVLR.P  2368  497.2266  992.4387  992.4386  0.16  0  4  10  1  U  K.FHMGDPR.A  2369  543.3379  1086.6613  1086.6604  0.82  1  69  8.8e-006  1  U  R.RKQATVLR.Y  2370  581.7803  1169.5640  1169.5651  0.74  1  18  6.4e-1  U  K.AHGVTVLR.C  2371  647.3207  1292.6269  1292.6248  1.62  0  21  1.1  1  U  K.HSNEPVELK.D  2372  723.8696  1445.7230  1445.7184  4.69  1  1  48  1  U  R.RKQGVTVLR.K  2373  741.3970  1489.7785  1489.7773  1.47  0  48  0.00074  1  U  K.GGVYGVNGSGSR.V  2374  815.9231  1629.8316  1629.8351  10.1  1  2  36  1  U  K.VPMTGVTVLR.V  2375  853.4443  1706.8738  1706.8723  0.56  0  66  1.6e-005  1  U  R.NPFTLQGVTVLR.H  2376  975.4407  1948.8669  1948.8902  -11.93  1  2  44  2  U  K.KLEDDVDAPVGVTR.K  2377  1020.4521  2038.8836  2038.8804  -0.35  0  9  3.9  1  U  K.VTYYDVFELMSR.L  2378  691.3632  2077.0048  2076.9851  8.49  2  17  2.1  1  U  K.KLEDDVDAPVGVTR.K  2379  1050.5479  3147.6219  3148.4193  0.81  0  60  5.5e-005  1  U  K.VLESTPTVGHSLGVNVALAQDQW.W |
| 52. **AT0G41480.1** Mass: 76575 Score: 191 Matches: 14(6) Sequences: 10(6) eMPI: 0.34  [ Symbol: | cytochrome P-450 | chr1:12830034-1291837 FORWARD LENGTH=718  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2380  438.2483  944.4821  944.4821  -0.09  0  44  0.0093  1  U  R.TYVSRIR.D  2381  485.7690  969.5235  969.5243  -0.81  0  8  2.9  1  U  K.HETTLR.A  2382  504.2929  1006.5712  1006.5560  15.1  1  5  6.6  2  U  K.QVYVPR.D  2383  515.2719  1031.5292  1031.5295  -0.31  0  34  0.024  1  U  R.HMGVTVLR.D  2384  533.7929  1066.5713  1066.5706  0.43  0  33  0.018  1  U  R.TTPSVATPR.S  2385  436.1486  1306.4270  1306.4432  -11.95  1  17  12  1  U  R.HNMGGVTVLR.S  2386  454.3209  1306.4273  1306.4432  -11.71  1  24  6.2  2  U  R.HNMGGVTVLR.S  2387  491.3337  1380.6528  1380.6521  0.47  0  67  1e-005  1  U  K.WQADVGVTVTR.Q  2388  493.4955  1472.7876  1472.8086  -14.26  1  10  49  3  U  K.KGVITVASTLR.D  2389  737.4102  1472.8059  1472.8086  -1.85  1  17  1.5  1  U  K.KGVITVASTLR.D  2390  790.9080  1579.8015  1579.7995  1.27  0  42  0.004  2  U  K.KATVATVPRDQ.R  2391  869.4631  1736.8717  1736.8733  -0.54  0  68  2.1e-005  1  U  R.LHPTTALAVSR.K | | | | |
| 53. **AT0G22410.1** Mass: 58689 Score: 168 Matches: 12(7) Sequences: 9(5) eMPI: 0.39  [ Symbol: | class-12 DMBP synthetase family protein | chr1:7912120-7914742 FORWARD LENGTH=527  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2392  435.2580  868.5015  868.5018  -0.34  0  8  6.4  3  U  R.GVAGPLLR.V  2393  622.9979  1243.9811  1243.9823  -0.31  0  48  0.0013  1  U  R.AHATVATAPR.V  2394  626.7793  1251.5880  1251.5868  0.97  0  33  0.01  1  U  R.GHIVDMVR.S  2395  627.2466  1252.5186  1252.5208  -1.49  0  33  0.01  1  U  R.GHIVDMVR.S  2396  643.8180  1283.6458  1283.6423  0.23  0  42  0.0023  1  U  R.QDQAVTVLR.G  2397  428.8955  1283.6466  1283.6422  1.81  0  14  5  3  U  R.QDQAVTVLR.G  2398  726.9126  1451.8206  1451.8096  0.73  0  41  0.0019  1  U  R.LILILASDRR.E  2399  586.0186  2346.0454  2346.0494  -10.27  1  1  33  1  U  R.HLMLHRLGSLVPSGDMR.Q  2400  831.4532  2497.3377  2497.3388  -0.43  0  46  0.00087  1  U  R.KYPAASASATTPATLTPGVQWVR.S  2401  1463.2161  3241.4176  3241.4679  -13.62  4  5  12  4  U  R.AHATVATAPR.V  2402  1366.9739  4097.9399  4097.9251  -6.16  2  2  33  1  U  R.AYQSAATGLKAAATGTAATQVMTQVLYTR.S |
| 54. **AT0G17110.1** Mass: 60654 Score: 162 Matches: 6(4) Sequences: 6(4) eMPI: 0.30  [ Symbol: | ATPase family protein | chr5:3772881-3773516 FORWARD LENGTH=540  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2403  432.7326  863.4503  863.4501  0.18  0  32  0.028  1  U  K.VPQTVLR.E  2404  504.5206  1006.5403  1006.5407  -0.57  1  05  0.18  1  U  R.LGVTVLR.V  2405  644.8432  1287.6718  1287.6711  0.61  0  40  0.0062  1  U  K.VGLSLDTTR.S  2406  701.8091  1403.6037  1403.6048  -0.77  1  2  9.4  2  U  R.HNMGGVTVLR.S  2407  661.3361  1361.8945  1361.8938  0.36  1  67  8.4e-005  1  U  R.KALALGVVGLSDRDMR.A  2408  869.1011  2046.2814  2046.2820  -0.23  0  82  4.2e-007  1  U  K.VLQATDPVPPHATALAEATQYK.K |
| 55. **AT0G16140.1** Mass: 64149 Score: 147 Matches: 12(6) Sequences: 12(6) eMPI: 0.42  [ Symbol: | CPB60C\_LBD1 | chaperonin 60 beta | chr1:2071571-2071873 REVERSE LENGTH=400  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2409  307.1848  712.7850  712.7855  -0.40  0  39  0.0051  1  U  R.AQDPR.E  2410  451.2886  900.5626  900.5644  -2.00  0  26  0.05  1  U  K.ALVTRELK.Y  2411  484.7288  927.4431  927.4450  -0.09  0  8  3.4  1  U  K.FQVATQVR.V  2412  480.7526  958.4956  958.4924  0.62  0  32  0.036  1  U  R.VQDVALR.A  2413  495.2613  988.5080  988.5077  0.36  0  14  4  1  U  R.EVGLSLR.A  2414  522.2961  1042.5777  1042.5771  0.59  0  61  3.2e-005  1  U  R.HNMGVTVLR.V  2415  581.2907  1161.5648  1161.5673  -0.43  0  54  0.0024  1  U  R.HNMGVTVLR.V  2416  591.8595  1181.7043  1181.7020  2.00  0  14  0.45  1  U  K.LKALDVLTVLR.G  2417  600.3362  1198.6579  1198.6557  1.77  0  24  0.15  2  U  R.DAVYDAQSR.G  2418  771.3879  1540.7613  1540.7620  -0.47  0  43  0.0029  1  U  R.VLEEDVPVNGK.L  2419  401.7141  1602.8273  1602.8478  -12.80  1  3  37  6  U  K.YGSPVINDVTVAR.E  2420  770.7861  2305.0963  2305.0958  0.24  1  1  50  1  U  R.AATPTATGSGHATGATGATGKSR.K |
| Proteins matching the same set of peptides:  **AT0G16140.1** Mass: 64149 Score: 147 Matches: 12(6) Sequences: 12(6)  [ Symbol: | CPB60C\_LBD1 | chaperonin 60 beta | chr1:2071571-2071873 REVERSE LENGTH=400 | 56. **AT0G17470.1** Mass: 63702 Score: 146 Matches: 11(5) Sequences: 11(5) eMPI: 0.35  [ Symbol: | TCP-1/gp60 chaperonin family protein | chr3:4389685-4392624 FORWARD LENGTH=596  Query Observed Mr(expt) Mr(calc) ppm Miss score Expect Rank Unique Peptide  2421  307.1848  712.7850  712.7855  -0.40  0  39  0.0051  1  U  R.AQDPR.E  2422  484.7288  927.4431  927.4450  -0.09  0  8  3.4  1  U  K.FQVATQVR.V  2423  480.7526  958.4956  958.4924  0.62  0  32  0.036  1  U  R.VQDVALR.A  2424</ |

[illegible]

66.	<div> <div> <div>Mass:</div> <div>Score:</div> <div>Matches:</div> <div>Sequences:</div> <div>emPAI:</div> </div> <div> <div>[ Symbol: LH2A-1   light harvesting complex photosystem II   chr4:209084-212243 FORWARD LENGTH=290 ]</div> <div> <div>Query</div> <div>Observed</div> <div>Mr(exp)</div> <div>Mr(calc)</div> <div>ppm</div> <div>Miss</div> <div>Score</div> <div>Expect</div> <div>Rank</div> <div>Unique</div> <div>Peptide</div> </div> </div> <div> <div>2414</div> <div>508.2601</div> <div>1087.5141</div> <div>1087.5141</div> <div>-0.46</div> <div>0</div> <div>47</div> <div>0.00071</div> <div>1</div> <div>U</div> <div>R.HLADYDYS.T</div> </div> <div> <div>2414</div> <div>531.2643</div> <div>1060.5141</div> <div>1060.5149</div> <div>-0.49</div> <div>1</div> <div>20</div> <div>1.1</div> <div>1</div> <div>U</div> <div>R.HANLOSER.L</div> </div> <div> <div>2414</div> <div>557.8273</div> <div>1113.4400</div> <div>1113.4393</div> <div>0.58</div> <div>0</div> <div>16</div> <div>0.8</div> <div>1</div> <div>U</div> <div>R.YAGZANER.H</div> </div> <div> <div>2414</div> <div>710.7613</div> <div>1418.7081</div> <div>1418.7082</div> <div>-0.45</div> <div>0</div> <div>8</div> <div>7.2</div> <div>1</div> <div>U</div> <div>R.FYFVGLAWEK.T</div> </div> <div> <div>2414</div> <div>878.4377</div> <div>1754.8608</div> <div>1754.8628</div> <div>-1.15</div> <div>0</div> <div>62</div> <div>3.9e-005</div> <div>1</div> <div>U</div> <div>R.STYFQYVFGTQK.P <b>1111</b></div> </div> <div> <div>2414</div> <div>908.7821</div> <div>2723.3243</div> <div>2723.3191</div> <div>1.91</div> <div>0</div> <div>15</div> <div>2.4</div> <div>1</div> <div>U</div> <div>R.GPLNNATHLQDLETTIIDPESK.-</div> </div> </div>
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	<a href="#">AT061550.1</a>	Name: B5193	Score: 94	Matches: 4(2)	Sequences: 4(2)	eMSPAI: 0.18
	[ Symbol: BA12 ]	[ HMA topoisomerase-related   chr1:13197713-1424110 REVERSE LENGTH=774 ]				
Query	Observed	M(seqpt)	M(calc)	ppm	Misr Score	Expect Rank Unique Peptide
<a href="#">B001</a>	588,3144	1174,4143	1174,4130	-4.28	0	49 0.004 1 U K.RPPTSTFTQK.S
<a href="#">B002</a>	489,3088	1374,4031	1374,4035	-1.74	1	4 18 1 U K.VRRSGDRAAH.N
<a href="#">B003</a>	425,3145	1872,9216	1872,9177	-2.12	2	72 3.4e-006 1 U K.GLESLKWRGQANR.H
<a href="#">B102</a>	1584,7166	3167,4186	3167,4428	-7.53	2	0 62 4 U K.QRLSDVSRGDASAAHAKHKAER.H
<b>Proteins matching the same set of peptides:</b>						
	<a href="#">AT061550.1</a>	Name: B0925	Score: 94	Matches: 4(2)	Sequences: 4(2)	eMSPAI: 0.18
	[ Symbol: BA12 ]	[ HMA topoisomerase-related   chr1:13197713-1424110 REVERSE LENGTH=774 ]				
79.	<a href="#">AT061549.1</a>	Name: S0761	Score: 93	Matches: 11(2)	Sequences: 9(2)	eMSPAI: 0.14
	[ Symbol: TUBA ]	[ tubulin beta chain 4   chr5:17859442-17869994 REVERSE LENGTH=444 ]				
Query	Observed	M(seqpt)	M(calc)	ppm	Misr Score	Expect Rank Unique Peptide
<a href="#">B001</a>	359,4483	1076,5282	1076,5280	-1.72	1	29 1.2 U K.LDSRYVR.H
<a href="#">B002</a>	634,3986	1265,7826	1265,7812	1.08	1	0 7.1 1 U K.ELVNLIFFPR.L
<a href="#">B003</a>	739,8329	1477,6512	1477,6542	-1.93	0	6 6.8 1 U K.EYVDNRWIKGR.H
<a href="#">B004</a>	748,3314	1494,6483	1494,6330	10.2	0 (6)	13 3 U K.EYVDNRWIKGR.H
<a href="#">B005</a>	111,9296	1621,8447	1621,8439	0.50	0	60 5.9e-005 1 U K.LIRFVDFQAFILTR.G
<a href="#">B006</a>	824,4065	1646,7985	1646,8008	-1.37	0	56 5.00016 1 U K.AVALCIVLDTGSLA.S
<a href="#">B007</a>	848,9196	1695,8246	1695,8257	-0.59	0 (5)	20 1 U K.NSDTFVIMINNV.S
<a href="#">B008</a>	849,4154	1696,8163	1696,8097	1.89	0	17 2.2 1 U K.NSDTFVIMINNV.S
<a href="#">B009</a>	461,3184	1980,9333	1980,9687	-17.89	1	3 47 1 U K.REIILIQGLNQALQK.F
<a href="#">B010</a>	826,4028	2476,1867	2476,1589	11.2	2	1 94 8 U K.IENRTVFDMGTTFVPPFR.D
<a href="#">B103</a>	1202,5713	3604,4931	3604,4589	9.21	2	1 88 1 U K.LTYSRVGGAGTGQGFVVFWIKGVK.S
80.	<a href="#">AT061520.1</a>	Name: Z9163	Score: 92	Matches: 6(3)	Sequences: 5(3)	eMSPAI: 0.54
	[ Symbol: LHCX3 ]	[ photosystem 1 light harvesting complex gene 3   chr1:22700152-22701149 FORWARD LENGTH=273 ]				
Query	Observed	M(seqpt)	M(calc)	ppm	Misr Score	Expect Rank Unique Peptide
<a href="#">B001</a>	646,8345	1291,6545	1291,6561	-1.20	0	33 0.033 1 U R.MAVERIEGR.D
<a href="#">B002</a>	698,7588	1394,4270	1394,4189	-1.31	0	47 1.3e-005 1 U R.LIGNVFDISGR.D
<a href="#">B003</a>	815,4562	1628,8978	1628,8940	1.11	0	3 0.019 1 U R.PANGGAIGIAPIELQK.A <a href="#">B103</a>
<a href="#">B004</a>	1311,5585	2221,1024	2221,0957	3.06	0	12 4.2 1 U K.GLASGDPATGVPFFPDLPGR.D
<a href="#">B005</a>	865,7643	2384,2712	2384,2442	16.4	1	22 0.14 1 U K.GLASGDPATGVPFFPDLPGR.D
<b>Proteins matching the same set of peptides:</b>						
	<a href="#">AT061520.1</a>	Name: Z1845	Score: 92	Matches: 6(3)	Sequences: 5(3)	eMSPAI: 0.54
	[ Symbol: LHCX3 ]	[ photosystem 1 light harvesting complex gene 3   chr1:22700493-22701149 FORWARD LENGTH=218 ]				
	<a href="#">AT061520.1</a>	Name: Z9163	Score: 92	Matches: 6(3)	Sequences: 5(3)	eMSPAI: 0.54
	[ Symbol: LHCX3 ]	[ photosystem 1 light harvesting complex gene 3   chr1:22700152-22701149 FORWARD LENGTH=273 ]				
81.	<a href="#">AT061460.1</a>	Name: B8705	Score: 92	Matches: 8(4)	Sequences: 8(4)	eMSPAI: 0.39
	[ Symbol: A1 ]	[ Adonisase superfamily protein   chr2:15284929-15293187 REVERSE LENGTH=164 ]				
Query	Observed	M(seqpt)	M(calc)	ppm	Misr Score	Expect Rank Unique Peptide
<a href="#">B001</a>	405,4218	1070,6280	1070,6280	-1.23	1	29 0.145 1 U K.LGRDAEHLKW.D
<a href="#">B002</a>	486,9331	1487,7953	1487,7944	0.65	1	14 2.1 1 U K.GILANDSVTIQGR.L
<a href="#">B003</a>	748,3715	1484,7285	1484,7314	-1.95	1	10 11 1 U K.LNDRATLDY



90.	AT1G04820.1	Mass: 51417	Score: 79	Matches: 5(2)	Sequences: 5(2)	eMPAI: 0.13
[ Symbol: ] HORM high mobility group A5 [ chr11:17974148-17976101 REVERSE LENGTH=479						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	568.3140	1134.4135	1134.4145	-0.89	1	10 8.9 4 U
AAL	531.6287	1581.8554	1581.8570	-1.01	0	45 2 U
AAL	705.7145	2114.1218	2114.1219	-0.07	1	48 7.9e-004 1 U
AAL	985.8223	2954.4450	2954.4449	-0.65	0	34 0.025 1 U
AAL	1245.6494	3731.8664	3731.8667	7.36	0	8 10 1 U
91.	AT1G03750.1	Mass: 48286	Score: 78	Matches: 6(2)	Sequences: 6(2)	eMPAI: 0.14
[ Symbol: ] RPT1A regulatory particle triple-A 1A [ chr11:2065921-20668124 REVERSE LENGTH=426						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	370.2159	738.4173	738.4276	-13.89	0	1 22 3 U
AAL	544.2847	1086.5548	1086.5557	-0.42	0	56 0.0011 1 U
AAL	617.3029	1232.5913	1232.5707	16.7	0	4 46 1 U
AAL	794.3854	1586.7563	1586.7545	1.17	0	53 0.00058 1 U
AAL	970.9793	2469.8143	2469.8856	15.2	1	1 32 2 U
AAL	1555.7240	3109.4334	3109.4411	-2.47	1	7 16 1 U
92.	AT2G14160.1	Mass: 14607	Score: 77	Matches: 9(3)	Sequences: 7(3)	eMPAI: 1.31
[ Symbol: ] Kine DRA708-binding protein [ chr1:14126183-14127223 FORWARD LENGTH=110						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	504.2767	1004.5389	1004.5349	1.98	0	26 0.13 1 U
AAL	568.3223	1134.6300	1134.6318	-1.41	1	35 0.012 1 U
AAL	670.3927	1338.7708	1338.7700	0.65	0	1 18 1 U
AAL	684.3107	1384.6069	1384.6074	-0.39	0	18 0.95 1 U
AAL	732.8713	1463.7280	1463.7290	-0.47	1	47 0.0011 1 U
AAL	856.3937	1710.7728	1710.7770	-2.46	1	51 0.00075 1 U
AAL	976.5884	1726.7735	1726.7719	0.82	1	(5) 10 1 U
AAL	961.2592	1980.8757	1980.8470	14.5	0	(4) 12 1 U
AAL	998.4358	1994.8570	1994.8739	-8.45	0	7 5.1 1 U
93.	AT5G02080.1	Mass: 25592	Score: 76	Matches: 4(2)	Sequences: 4(2)	eMPAI: 0.46
[ Symbol: ] Ribosomal protein S8e family protein [ chr5:6851695-6853012 REVERSE LENGTH=222						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	400.1891	798.3634	798.3694	-7.18	1	3 14 2 U
AAL	781.3649	1560.7152	1560.7148	-1.06	0	18 1.2 1 U
AAL	619.9617	1856.0432	1856.0539	-0.40	1	38 0.0079 1 U
AAL	662.6559	1984.9577	1984.9589	-0.58	2	56 0.00016 1 U
94.	AT5G08280.1	Mass: 45894	Score: 75	Matches: 3(1)	Sequences: 3(1)	eMPAI: 0.07
[ Symbol: ] RPT1 regulatory particle triple-A subunit 3 [ chr1:21892155-21971116 FORWARD LENGTH=408						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	474.2817	1419.8233	1419.8139	2.49	0	2 8.5 2 U
AAL	1011.0143	2028.0540	2028.0527	0.45	0	75 1.6e-004 1 U
AAL	1181.5654	3541.6744	3541.6990	-6.95	2	0 1.2e+002 4 U
95.	AT4G1318.1	Mass: 28213	Score: 74	Matches: 2(1)	Sequences: 2(1)	eMPAI: 0.12
[ Symbol: ] RNA-binding (RBM/RBD/RBP motif) family protein [ chr4:16953211-16955127 REVERSE LENGTH=238						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	589.8127	1171.461	1171.469	1.45	0	74 2.3e-006 U
AAL	594.3104	1186.6043	1186.6056	0.60	0	6 11 1 U
Proteins matching the same set of peptides:						
AT4G1318.1	Mass: 28169	Score: 74	Matches: 2(1)	Sequences: 2(1)		
[ Symbol: ] RNA-binding (RBM/RBD/RBP motif) family protein [ chr4:16953211-16955127 REVERSE LENGTH=239						
AT4G1318.1	Mass: 24010	Score: 74	Matches: 2(1)	Sequences: 2(1)		
[ Symbol: ] RNA-binding (RBM/RBD/RBP motif) family protein [ chr4:16953708-16955127 REVERSE LENGTH=207						
AT4G1318.1	Mass: 23551	Score: 74	Matches: 2(1)	Sequences: 2(1)		
[ Symbol: ] RNA-binding (RBM/RBD/RBP motif) family protein [ chr4:16953404-16955127 REVERSE LENGTH=201						
AT4G1318.1	Mass: 28546	Score: 74	Matches: 2(1)	Sequences: 2(1)		
[ Symbol: ] RNA-binding (RBM/RBD/RBP motif) family protein [ chr4:16953404-16955127 REVERSE LENGTH=244						
96.	AT5G08020.1	Mass: 39025	Score: 73	Matches: 3(2)	Sequences: 3(2)	eMPAI: 0.18
[ Symbol: ] P88A photoreceptor L1 reaction center protein A [ chr7:383-1444 REVERSE LENGTH=353						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	643.8033	1285.5921	1285.5907	1.11	0	54 0.00012 1 U
AAL	1315.6028	1315.6555	1315.6772	-16.46	0	4 22 2 U
AAL	750.8166	1499.6186	1499.6012	11.6	0	39 0.0016 1 U
97.	AT5G13880.1	Mass: 78508	Score: 73	Matches: 13(4)	Sequences: 4(1)	eMPAI: 0.09
[ Symbol: ] Tetraepitope repeat (TPR)-like superfamily protein [ chr5:16001036-16003072 REVERSE LENGTH=678						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	495.7536	989.8926	989.8778	15.1	1	37 0.012 1 U
AAL	897.4312	1791.8519	1791.8566	-0.44	1	20 1.2 1 U
AAL	964.6646	1926.9187	1926.9509	-16.73	2	1 45 3 U
AAL	918.4612	3669.8159	3669.8211	-1.42	2	1 48 1 U
98.	AT1G17400.1	Mass: 31879	Score: 71	Matches: 4(1)	Sequences: 4(1)	eMPAI: 0.10
[ Symbol: ] Hsiaoa (2Pe-2S) domain-containing protein [ chr1:2693684-2693731 FORWARD LENGTH=287						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	437.7341	873.4536	873.4417	11.7	1	7 13 8 U
AAL	767.8689	1531.7233	1531.7423	-11.38	0	4 20 2 U
AAL	844.4345	1682.0545	1682.0588	-0.55	0	71 8.6e-004 1 U
AAL	901.9216	1801.8287	1801.8370	-4.59	1	0 39 7 U
99.	AT1G05410.2	Mass: 186590	Score: 71	Matches: 21(1)	Sequences: 13(1)	eMPAI: 0.02
[ Symbol: ] OTB1 global transcription factor group B1 [ chr1:24126595-24141327 REVERSE LENGTH=1642						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	352.1841	702.3537	702.3548	-1.55	0	21 0.44 4 U
AAL	435.7394	869.4641	869.4607	4.01	0	7 3.3 1 U
AAL	504.2212	1006.4279	1006.4203	7.52	1	1 13 3 U
AAL	597.3120	1192.6094	1192.6098	0.55	1	11 3.9 1 U
AAL	405.5060	1213.4962	1213.4921	3.36	0	4 3.6 2 U
AAL	419.2501	1254.7284	1254.7118	13.2	2	3 15 4 U
AAL	654.3111	1306.4777	1306.4599	13.6	2	3 64 5 U
AAL	502.2184	1503.6935	1503.6922	0.86	1	(6) 8.4 3 U
AAL	752.8544	1503.6942	1503.6922	1.12	1	9 5.1 3 U
AAL	751.8918	1505.7691	1505.7395	19.6	1	2 42 8 U
AAL	756.8937	1511.7728	1511.7692	2.38	0	71 3.6e-004 1 U
AAL	746.3605	2234.0596	2234.0383	9.53	3	58 1 U
AAL	801.7094	2402.1063	2402.1325	-10.90	2	3 27 1 U
AAL	1202.0625	2401.1104	2402.1325	-9.16	2	(1) 39 9 U
AAL	1202.5563	2401.0980	2403.1165	-7.67	2	(1) 82 1 U
AAL	989.1304	2964.3695	2964.4226	-17.94	2	2 32 1 U
100.	AT1G05410.1	Mass: 167204	Score: 71	Matches: 23(1)	Sequences: 13(1)	eMPAI: 0.02
[ Symbol: ] OTB1 global transcription factor group B1 [ chr1:24126595-24141327 REVERSE LENGTH=1654						
Query	Observed	Mr(empt)	Mr(calc)	ppm	Mise Score	Expect Rank Unique Peptide
AAL	352.1841	702.3537	702.3548	-1.55	0	21 0.44 4 U
AAL	435.7394	869.4641	869.4607	4.01	0	7 3.3 1 U
AAL	504.2212	1006.4279	1006.4203	7.52	1	1 13 3 U
AAL	597.3120	1192.6094	1192.6098	0.55	1	11 3.9 1 U
AAL	405.5060	1213.4962	1213.4921	3.36	0	4 3.6 2 U
AAL	419.2501	1254.7284	1254.7118	13.2	2	3 15 4 U
AAL	654.3111	1306.4777	1306.4599	13.6	2	3 64 5 U
AAL	751.8918	1505.7691	1505.7395	19.6	1	2 42 8 U
AAL	756.8937	1511.7728	1511.7692	2.38	0	71 3.6e-004 1 U
AAL	746.3605	2234.0596	2234.0383	9.53	3	58 1 U
AAL	801.7094	2402.1063	2402.1325	-10.90	2	3 27 1 U
AAL	1202.0625	2401.1104	2402.1325	-9.16	2	(1) 39 9 U
AAL	1202.5563	2401.0980	2403.1165	-7.67	2	(1) 82 1 U
AAL	921.9344	1845.4942	1845.4931	0.43	2	9 5.9 2 U
AAL	746.3605	2234.0596	2234.0383	9.53	3	58 1 U
AAL	801.7094	2402.1063	2402.1325	-10.90	2	3 27 1 U
AAL	1202.0625	2401.1104	2402.1325	-9.16	2	(1) 39 9 U
AAL	1202.5563	2401.0980	2403.1165	-7.67	2	(1) 82 1 U
AAL	989.1304	2964.3695	2964.4226	-17.94	2	2 32 1 U
AAL	1015.1617	3045.4633	3042.4106	17.5	2	(0) 64 4 U
AAL	1030.8090	3089.4052	3089.4108	-0.81	2	1 31 7 U
AAL	1593.7341	3165.4136	3165.4607	2.57	2	(0) 1 5 U
AAL	1562.7187	3123.4208	3123.3686	17.4	2	(1) 40 6 U

989.13042964.36952964.4226-17.9422321R.HQJHQAAYVYRVEALEA.V

160421411.56884231.68464231.633012.8281.21R.RDQHQKQDQNGWQGWGTQTADQNGGSGGGSSGSSEAK.V

102.AT004741.AMass: 42746Score: 71Matches: 2(1)Sequences: 1(1)eMFAI: 0.16

[ Symbol: ] TAF15b | TBP-associated factor 15b | chr5:23638566-23640854 REVERSE LENGTH=422

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A102749.34371496.67281496.6743-0.741494.7e-0561UR.QKASTYRDAAATE.V

A102499.89901494.67931494.67430.661(23)0.21UR.QKASTYRDAAATE.V

Proteins matching the same set of peptides:

AT004741.AMass: 42746Score: 71Matches: 2(1)Sequences: 1(1)

[ Symbol: ] TAF15b | TBP-associated factor 15b | chr5:23638566-23640854 REVERSE LENGTH=422

103.AT1002439.LMass: 23471Score: 71Matches: 5(3)Sequences: 5(3)eMFAI: 0.71

[ Symbol: ] ATOTPTP6, GDT1, BMD1, ATOTPTP3, GDTT6, ATOTPT1 | glutathione S-transferase 6 | chr1:661363-662191 REVERSE LENGTH=208

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A103492.2482902.4818902.4821-0.380480.00111UK.ONMLELPGF.D

A103515.77011029.52561029.52431.270470.00081UR.YLVDFVER.L

A103517.25611032.49771032.49750.160290.0561UK.TTVERRAE.L

A103381.86811142.58251142.5833-0.700141.71UK.VPDHFASATPR.N

A1031011.64402020.07342020.07031.5407101UK.VNWDQLPFLVHYTHK.T

Proteins matching the same set of peptides:

AT1002439.LMass: 23471Score: 71Matches: 5(3)Sequences: 5(3)

[ Symbol: ] GDTT6 | glutathione S-transferase 6 | chr1:661363-662191 REVERSE LENGTH=208

104.AT004894.MMass: 27805Score: 70Matches: 1(1)Sequences: 1(1)eMFAI: 0.13

[ Symbol: ] LHCb6, CP24 | light harvesting complex photosystem II subunit 6 | chr1:544685-544766 REVERSE LENGTH=258

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A104933.19161316.82481316.8289-2.275703.8e-0561UR.TSDVFANTQDQFGGR.F

Proteins matching the same set of peptides:

AT004894.MMass: 27805Score: 70Matches: 1(1)Sequences: 1(1)eMFAI: 0.13

[ Symbol: ] GDTT6 | glutathione S-transferase 6 | chr1:661363-662191 REVERSE LENGTH=208

105.AT0054460.LMass: 29607Score: 70Matches: 9(2)Sequences: 8(2)eMFAI: 0.70

[ Symbol: ] SCL3b, Ar-SCL3b | SCY5-like splicing factor 3b | chr3:20561024-20563502 FORWARD LENGTH=262

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A105381.7114761.4092761.40721.920113.51UR.PVTTPR.D

A105395.2359794.4473794.442310.9720134UR.SDSPPVR.D

A105493.2226984.4305984.43010.460210.141UR.DVTSQGR.G

A105493.7136985.4126985.4141-1.540(18)0.151UR.DVTSQGR.G

A105594.74661011.54471011.54610.460340.0061UR.SDSPPVR.D

A105390.22291167.64681167.6472-0.421290.0321UR.SDSPPVR.D

A105588.81441175.61431175.6159-1.3428114UR.SDSPPVR.D

A105594.83161187.65261187.64446.4842105.99UR.SDSPPVR.D

A105595.32451187.63451188.6350-0.440300.0811UR.SDSPPVR.D

Proteins matching the same set of peptides:

AT0054460.LMass: 29607Score: 70Matches: 9(2)Sequences: 8(2)eMFAI: 0.70

[ Symbol: ] SCL3b, Ar-SCL3b | SCY5-like splicing factor 3b | chr3:20561024-20563502 FORWARD LENGTH=262

106.AT0062741.AMass: 34282Score: 68Matches: 6(2)Sequences: 6(2)eMFAI: 0.20

[ Symbol: ] SCL3b, Ar-SCL3b | SCY5-like splicing factor 3b | chr3:20561024-20563502 FORWARD LENGTH=262

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A106386.7119778.4484778.44840.2306144UR.PVTTPR.D

A106405.2295808.4445808.44430.280240.0851UR.PVTTPR.D

A106446.2440930.4752930.4751-1.940600.00112UR.PVTTPR.D

A106473.23061416.46981416.4732-2.311170.0121UR.PVTTPR.D

A106696.98542087.93432087.9371-1.330103.81UR.PVTTPR.D

A1061544.70464637.09204637.1733-17.3420725UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0062741.AMass: 34282Score: 68Matches: 6(2)Sequences: 6(2)eMFAI: 0.20

[ Symbol: ] SCL3b, Ar-SCL3b | SCY5-like splicing factor 3b | chr3:20561024-20563502 FORWARD LENGTH=262

107.AT0062741.AMass: 30761Score: 68Matches: 4(2)Sequences: 4(2)eMFAI: 0.36

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A107495.7644489.518289.5188-0.751970.00971UR.PVTTPR.D

A107505.76361049.51271049.5142-1.400540.000171UR.PVTTPR.D

A107923.46981042.51311042.5147-1.160210.0121UR.PVTTPR.D

A107725.00742172.00032172.0129-5.7825162UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0062741.AMass: 30761Score: 68Matches: 4(2)Sequences: 4(2)eMFAI: 0.36

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

108.AT0064130.LMass: 81345Score: 68Matches: 4(2)Sequences: 4(2)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=290

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A108392.7190783.4234783.4239-0.640490.00021UR.PVTTPR.D

A108623.21031244.60401244.60391.860390.00611UR.PVTTPR.D

A1081148.45162659.88662659.8836-9.37106610UR.PVTTPR.D

A1081009.84443026.51143026.455118.6232928UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064130.LMass: 81345Score: 68Matches: 4(2)Sequences: 4(2)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=290

109.AT0064271.AMass: 86196Score: 68Matches: 3(2)Sequences: 3(2)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A109392.7190783.4234783.4239-0.64490.00021UR.PVTTPR.D

A109623.21031244.60401244.60391.860390.00611UR.PVTTPR.D

A109975.82152924.44272924.412210.420661UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 86196Score: 68Matches: 3(2)Sequences: 3(2)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

110.AT0064271.AMass: 72198Score: 68Matches: 4(1)Sequences: 4(1)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A110615.81441218.61431218.6197-1.14030.00551UR.PVTTPR.D

A110660.28491318.57931318.57890.240564.8e-0051UR.PVTTPR.D

A110624.61361364.38491364.3836-0.130150.0121UR.PVTTPR.D

A110955.08932862.24602862.2481-0.7301269UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 72198Score: 68Matches: 4(1)Sequences: 4(1)eMFAI: 0.08

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

111.AT0064271.AMass: 27612Score: 68Matches: 4(1)Sequences: 4(1)eMFAI: 0.26

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A111499.2497916.5228916.5209-0.160150.0121UR.PVTTPR.D

A111712.33551422.65631422.6627-4.450590.00111UR.PVTTPR.D

A111772.87681543.73911543.73413.281280.0681UR.PVTTPR.D

A111501.19332021.95202021.93637.7728181UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 27612Score: 68Matches: 4(1)Sequences: 4(1)eMFAI: 0.26

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

112.AT0064271.AMass: 20556Score: 67Matches: 3(3)Sequences: 2(2)eMFAI: 0.58

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A112683.29161364.56871364.5745-4.270410.00281UR.PVTTPR.D

A112455.84471364.57221364.5745-1.680(00)0.0151UR.PVTTPR.D

A112774.90771547.80091547.8018-0.580340.0251UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 20556Score: 67Matches: 3(3)Sequences: 2(2)eMFAI: 0.58

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

113.AT0064271.AMass: 47083Score: 67Matches: 6(2)Sequences: 6(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A113417.7279811.4413811.4413-0.74480.0111UR.PVTTPR.D

A113479.7619957.5092957.5131-4.04084.11UR.PVTTPR.D

A113778.36021594.70581594.70580.010460.00891UR.PVTTPR.D

A113817.46051434.78451434.783813.919170.0121UR.PVTTPR.D

A113914.46881824.93311824.9315-4.620182.21UR.PVTTPR.D

A113511.72692042.87852042.8824-1.911360.00591UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 47083Score: 67Matches: 6(2)Sequences: 6(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

114.AT0064271.AMass: 46960Score: 67Matches: 5(2)Sequences: 5(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A114479.7619957.5092957.5131-4.04084.11UR.PVTTPR.D

A114592.83041103.64631103.64513.091150.631UR.PVTTPR.D

A114778.36021594.70581594.70580.010460.00891UR.PVTTPR.D

A114914.46881824.93311824.9315-4.620182.21UR.PVTTPR.D

A114511.72692042.87852042.8824-1.911360.00591UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 46960Score: 67Matches: 5(2)Sequences: 5(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

115.AT0064271.AMass: 47075Score: 67Matches: 5(2)Sequences: 5(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

QueryObservedMr(expt)Mr(calc)ppmMissScoreExpectRankUniquePeptide

A115479.7619957.5092957.5131-4.04084.11UR.PVTTPR.D

A115592.83041103.64631103.64513.091150.631UR.PVTTPR.D

A115778.36021594.70581594.70580.010460.00891UR.PVTTPR.D

A115914.46881824.93311824.9315-4.620182.21UR.PVTTPR.D

A115511.72692042.87852042.8824-1.911360.00591UR.PVTTPR.D

Proteins matching the same set of peptides:

AT0064271.AMass: 47075Score: 67Matches: 5(2)Sequences: 5(2)eMFAI: 0.23

[ Symbol: ] RHA-binding (RBM/RBD/RBP motifs) family protein | chr5:564332-565776 REVERSE LENGTH=292

[ Symbol: RIFA-2   wifa4-2   chr1:20260495-20262018 FORWARD LENGTH=412 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
1421	479.7619	957.5092	957.5131	-4.06	0	8	6.1	2		E.KIAQKKK.V
1422	774.3602	1584.7058	1584.7058	-0.01	0	48	0.0087	1		E.HYVLADKRLR.D
2441	914.4088	1826.9331	1826.9315	-4.62	0	18	2.2	1		E.GIYATGSLPSPHQA.QD.R
14211	511.7269	2042.8785	2042.8824	-1.91	1	36	0.0059	1		E.SHORVYATWQDQWY.D
1384	1236.6134	2475.2102	2475.2475	-15.06	2	4	47	1	U	E.VQDALVQGVYVHCVYVYR.E
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1B   chr4:14067082-14072357 REVERSE LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQDPFRLQK.I
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
10111	965.6358	1929.0370	1929.0427	7.39	0	1	45	2	U	E.HQGVYQGLPSPFVY.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
2021	1200.1899	5995.9131	5995.9784	-10.89	1	1	24	1	U	E.LPVLGQKAPLVPVLAALSLGKITVQCKHRYA.GIFALHGRSRLGLRFLP.R
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										
[ Symbol: R9PBI9, ATRPBI9   26S proteasome regulatory subunit S2 1A   chr2:8859211-8864699 FORWARD LENGTH=891 ]										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Misa	Score	Expect	Rank	Unique	Peptide
2311	449.7466	897.5184	897.5284	-10.88	2	1	13	4	U	E.K.VPDSKWK.K
2411	584.3038	1164.5931	1164.5931	-0.04	0	38	0.007	1		E.VQGVADVPQKQRLR.V
6211	740.9152	1479.8158	1479.8158	-0.02	0	48	0.0005	1		E.VQGVADVPQKQRLR.V
4411	667.3611	1999.0616	1999.0375	12.1	0	7	22	1		E.K.TITQPTQSTFVLLAAGR.A
Proteins matching the same set of peptides:										

144. [AT2G18560.1](#) Score: 55 Matches: 3(1) Sequences: 3(1) eBPFI: 0.08  
| Symbols: TP1IS | transcript elongation factor IIS | chr2:16134802-16136319 FORWARD LENGTH=37

Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	score	Expect	Rank	Unique	Peptide
<a href="#">A111</a>	594.8336	1187.45526	1187.4510	-1.33	2	19	0.78	2	U	R.GADGVEKVEK.D
<a href="#">A110</a>	650.8842	1299.7539	1299.7398	10.8	2	1	25	4	U	R.YVDTKVTGK.I
<a href="#">A111</a>	754.3775	1506.7405	1506.7348	3.82	2	55	0.0002	2	U	R.VIRGIGGGAPAK.A

145. [AT0G13800.1](#) Mass: 32682 Score: 55 Matches: 4(1) Sequences: 2(1) eMFAI: 0.10  
[ Symbol: | Ribosomal protein S5 family protein | chr2:14100925-14302352 REVERSE LENGTH=303  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 636.2356 1270.4387 1270.4378 -0.82 0 53 0.00012 1 U R.QGGRNALNAR.A [A111](#)  
[A112](#) 637.3172 1272.6199 1272.6058 11.1 0 (7) 9.1 9 U R.GLGRNGALNAR.A [A112](#)  
[A111](#) 908.4761 1814.9377 1814.9272 -16.26 2 1 36 3 U R.SALIDNRNVQVQGR.Y

146. [AT0G15100.1](#) Mass: 28208 Score: 55 Matches: 2(1) Sequences: 2(1) eMFAI: 0.12  
[ Symbol: | Ribosomal protein L2 family | chr3:19016606-19017547 REVERSE LENGTH=260  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 435.7738 869.5330 869.5195 15.5 1 4 6.5 5 U R.VQGTAAAR.T  
[A111](#) 508.7680 1015.5215 1015.5233 -1.80 0 55 0.00016 1 U R.AMIGQVADGR.T

147. [AT0G14100.1](#) Mass: 41582 Score: 55 Matches: 2(2) Sequences: 2(2) eMFAI: 0.17  
[ Symbol: | Protein of unknown function (D0F3411) | chr5:4044950-4047290 REVERSE LENGTH=386  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 421.7580 841.5014 841.5022 -0.91 0 32 0.004 1 U R.LIHDTYK.P  
[A111](#) 638.3560 1274.6975 1274.6983 -0.62 0 48 0.0012 1 U R.YQVAVDVGK.L

148. [AT0G17100.1](#) Mass: 63129 Score: 54 Matches: 5(2) Sequences: 3(1) eMFAI: 0.11  
[ Symbol: HAP57, H30507, CPM, ACMB8 | homologs of HAP57 | chr3:21154255-21155852 REVERSE LENGTH=565  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 551.7948 1105.2950 1105.2939 -0.12 1 4 25 4 U R.LGLNPPAKK.K  
[A111](#) 933.4159 1864.8172 1864.8174 -0.06 1 (34) 0.011 1 U R.SKDTAAVAQDAEAAK.S  
[A111](#) 622.6132 1264.8177 1264.8174 0.17 1 43 0.0013 1 U R.SKDTAAVAQDAEAAK.S  
[A111](#) 1391.0293 4370.1361 4370.0788 16.5 1 2 25 4 U R.HLVPVVCVCAQTITATGTVGLLLGVQVGGK.R [A111](#) [A111](#)

149. [AT0G07900.1](#) Mass: 67356 Score: 54 Matches: 3(1) Sequences: 3(1) eMFAI: 0.10  
[ Symbol: | ATOM1, GDM1 | ABC transporter family protein | chr5:24453760-24455767 REVERSE LENGTH=595  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 454.7453 907.4760 907.4763 -0.28 0 18 0.67 1 U R.LQETIKR.L  
[A11](#) 450.5494 1264.8264 1264.8292 -2.11 1 59 4.8e-005 1 U R.LDNRDRTAKR.A  
[A111](#) 531.2662 1090.7487 1090.7494 -1.72 1 1 76 7 U R.AQVWPGKADQGR.S

150. [AT0G14695.2](#) Mass: 10331 Score: 54 Matches: 2(1) Sequences: 2(1) eMFAI: 0.34  
[ Symbol: | Uncharacterized protein family (UPP0041) | chr4:8419833-8420845 FORWARD LENGTH=91  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 666.3640 1330.7133 1330.7146 -0.93 0 54 0.00042 1 U R.LQALNNHDAQK.T  
[A111](#) 1637.7662 3273.5178 3273.5144 1.04 0 6 24 7 U R.TNPQVFNHSTLQIATVTCNCKGR.C

151. [AT0G14695.1](#) Mass: 12385 Score: 54 Matches: 2(1) Sequences: 2(1) eMFAI: 0.28  
[ Symbol: | Uncharacterized protein family (UPP0041) | chr4:8419833-8420845 FORWARD LENGTH=109  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 666.3640 1330.7133 1330.7146 -0.93 0 54 0.00042 1 U R.LQALNNHDAQK.T  
[A111](#) 1553.2826 6209.1013 6209.1192 -2.88 2 1 16 1 U R.TIIPVATPFKMGISTANLAPQFPFNITLQIATVTCNCKGRQITTFK.N

152. [AT0G05600.1](#) Mass: 12173 Score: 54 Matches: 2(1) Sequences: 2(1) eMFAI: 0.29  
[ Symbol: | COMTAS InterPro DOMAM(a): Uncharacterized protein family (UPP0041) (TAIR:AT4022310.1): Has 30201 Blast hits to 17322 proteins in  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 666.3640 1330.7133 1330.7146 -0.93 0 54 0.00042 1 U R.LQALNNHDAQK.T  
[A111](#) 1706.8799 5117.6179 5117.6219 -0.78 1 1 56 4 U R.TIIPVATPFKMGISTANLAPQFPFNITLQIATVTCNCKGRQITTFK.N

153. [AT0G21100.1](#) Mass: 12054 Score: 54 Matches: 1(1) Sequences: 1(1) eMFAI: 0.28  
[ Symbol: | Uncharacterized protein family (UPP0041) | chr4:17914843-17928138 FORWARD LENGTH=108  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A111](#) 666.3640 1330.7133 1330.7146 -0.93 0 54 0.00042 1 U R.LQALNNHDAQK.T

154. [AT0G44500.1](#) Mass: 57028 Score: 53 Matches: 4(1) Sequences: 4(1) eMFAI: 0.06  
[ Symbol: | CYP71B38 | cytochrome P450, family 71, subfamily B, polypeptide 38 | chr3:15948505-15950224 REVERSE LENGTH=499  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 394.7112 787.4078 787.4075 0.36 0 53 0.00026 1 U R.LQETIKR.A  
[A111](#) 508.7680 1015.5215 1015.5120 9.30 1 17 0.92 2 U R.AMLGPKGR.I  
[A111](#) 581.8955 1428.8468 1428.8763 -30.10 2 16 2 1 U R.LTGLQETIKRQGR.S  
[A111](#) 663.9854 1368.9344 1368.9724 -19.10 2 3 29 1 U R.AMLGPKGRITTEDEK.V

155. [AT0G13100.1](#) Mass: 56804 Score: 53 Matches: 6(1) Sequences: 5(1) eMFAI: 0.06  
[ Symbol: | CYP71A20 | cytochrome P450, family 71, subfamily A, polypeptide 20 | chr4:7750453-7753049 FORWARD LENGTH=497  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 394.7112 787.4078 787.4075 0.36 0 53 0.00026 1 U R.LQETIKR.S  
[A11](#) 395.2209 788.4273 788.4280 -0.85 0 0 62 6 U R.VLQETIKR.L  
[A111](#) 459.7549 917.4952 917.5069 -12.81 0 3 29 3 U R.LLTGIDKIK.T  
[A111](#) 910.9106 1899.8507 1899.8810 -15.94 2 5 12 2 U R.LNRDNRQVTHLQK.L  
[A111](#) 697.6911 2090.0515 2090.0798 -13.56 2 (2) 47 1 U R.QMKSTCTQGLNGKGR.S  
[A111](#) 1055.0391 2108.0636 2108.0428 9.91 2 3 34 2 U R.QMKSTCTQGLNGKGR.S

Proteins matching the same set of peptides:  
[AT0G13100.2](#) Mass: 44710 Score: 53 Matches: 6(1) Sequences: 5(1)  
[ Symbol: | CYP71A20 | cytochrome P450, family 71, subfamily A, polypeptide 20 | chr4:7750453-7751856 FORWARD LENGTH=390

156. [AT0G21100.1](#) Mass: 81263 Score: 53 Matches: 6(1) Sequences: 4(1) eMFAI: 0.04  
[ Symbol: | LOC707870.10, chloplast: EXPRESSED IN: 15 plant structures: EXPRESSED DURING: 7 growth stages: BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2042320.2): Has 3369 Blast hits to 1516 proteins in 313 s  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 394.7112 787.4078 787.4075 0.36 0 53 0.00026 1 U R.LQETIKR.S  
[A111](#) 806.8686 1611.7225 1611.7198 1.67 1 2 18 3 U R.LSGTNRQVQGRK.V [A111](#)  
[A111](#) 806.8686 1611.7227 1611.7198 1.77 1 (1) 25 5 U R.LSGTNRQVQGRK.V  
[A111](#) 725.7027 2174.0843 2174.0827 -1.80 2 3 35 1 U R.LNRDNRQVQGRK.Q  
[A111](#) 751.3741 3001.4675 3001.5219 -16.13 1 4 25 1 U R.QVQVTPSPSCRLTIVAFPPYLE.L

157. [AT0G21100.1](#) Mass: 74907 Score: 53 Matches: 3(1) Sequences: 3(1) eMFAI: 0.04  
[ Symbol: | nucleolar protein gar2-related | chr2:17628102-17630457 FORWARD LENGTH=449  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 394.7112 787.4078 787.4075 0.36 0 53 0.00026 1 U R.LQETIKR.S  
[A111](#) 494.7416 991.8087 991.8120 -3.36 1 7 10 2 U R.LNTRQGR.Q  
[A111](#) 1199.2289 3594.6649 3594.7109 -12.81 2 0 57 7 U R.KLSEAFPTAAAGSVTPPTPTIARVAAAK.L

Proteins matching the same set of peptides:  
[AT0G21100.2](#) Mass: 74907 Score: 53 Matches: 3(1) Sequences: 3(1)  
[ Symbol: | nucleolar protein gar2-related | chr2:17628102-17630457 FORWARD LENGTH=469

158. [AT0G21100.1](#) Mass: 56623 Score: 53 Matches: 4(1) Sequences: 4(1) eMFAI: 0.06  
[ Symbol: | CYP71B38 | cytochrome P450, family 71, subfamily B, polypeptide 38 | chr3:15948505-15950224 REVERSE LENGTH=499  
Query Observed Mr(expect) Mr(calc) ppm Miss score Expect Rank Unique Peptide  
[A11](#) 394.7112 787.4078 787.4075 0.36 0 53 0.00026 1 U R.LQETIKR.A  
[A111](#) 972.8064 2915.3975 2915.4231 -8.79 0 1 52 3 U R.KLSTQVFLAVNAGSTIKNTWTELR.R  
[A111](#) 1773.8438 3545.7090 3545.7187 -1.86 2 2 46 1 U R.LTSDIPIQGVIPQIPQIT

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect	Rank	Unique	Peptide						
<a href="#">4441</a>	633.3304	1300.4462	1300.4412	3.88	0	52	0.00076	1	U	R.VAAYVDEHGR.L						
144.	<a href="#">AT0G000279.1</a>	Mass: 39750	Score: 51	Matches: 3(1)	Sequences: 2(1)	emPAI: 0.08										
[ Symbols: PSB0   photosystem II reaction center protein D   chrC132711-13772 FORWARD LENGTH=163 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1441</a>	1042.5937	1041.5864	1041.5818	4.42	0	10	2.9	2	U	R.KHILAGDIR.A						
<a href="#">1442</a>	521.8008	1041.5870	1041.5818	4.94	0	(0)	12	0	U	R.KHILAGDIR.A						
<a href="#">1443</a>	614.3024	1224.5903	1224.5931	-2.31	0	51	0.00064	1	U	R.AATPVQDIR.A						
145.	<a href="#">AT0G02100.1</a>	Mass: 39269	Score: 51	Matches: 3(1)	Sequences: 2(1)	emPAI: 0.08										
[ Symbols: MT24, ADR74   nitritease 4   chrS7379401-7391764 FORWARD LENGTH=355 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1451</a>	358.8703	1071.5890	1071.5903	-1.16	1	(13)	3.3	3	U	R.LGAPVALGR.L						
<a href="#">1452</a>	537.8019	1071.5883	1071.5903	-0.81	1	17	1.3	3	U	R.LGAPVALGR.L						
<a href="#">1453</a>	595.2915	1188.5684	1188.5710	-2.11	0	51	0.00076	1	U	R.LGACVCHGR.M						
146.	<a href="#">AT0G04670.1</a>	Mass: 94743	Score: 51	Matches: 9(2)	Sequences: 8(2)	emPAI: 0.07										
[ Symbols: L201   Ribosomal protein O111V family protein   chr1:20968245-20971077 REVERSE LENGTH=843 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1461</a>	478.2491	994.5236	994.1247	-1.09	0	19	0.27	1	U	R.DGGVTVFAR.R						
<a href="#">1462</a>	973.2634	1144.5143	1144.5182	-1.47	0	35	0.018	1	U	R.NQVLAHGR.D						
<a href="#">1463</a>	436.5553	1306.4441	1306.4452	-0.87	0	5	18	2	U	R.NNVVIAYVQGR.S						
<a href="#">1464</a>	737.4000	1472.7854	1472.7809	3.06	1	4	20	8	U	R.VLVHGVYVGR.E						
<a href="#">1465</a>	491.9365	1472.7876	1472.7809	4.53	1	(3)	24	1	U	R.VLVHGVYVGR.E						
<a href="#">1466</a>	1129.1084	2284.2022	2286.1361	2.71	0	16	1.2	1	U	R.STYDTEVAAGTIAQGVADGR.H						
<a href="#">1467</a>	800.7409	2389.1390	2389.1393	8.20	1	36	0.016	1	U	R.VTVHDLFGVLAQGVADGR.H						
<a href="#">1468</a>	860.4200	2578.2381	2578.2342	1.53	2	11	9.8	1	U	R.NCQPPFLVGLYVQENIFASQGR.F						
<a href="#">1469</a>	1742.3174	3522.4202	3522.4858	-18.61	1	1	39	5	U	R.QTVTVFVCGTFVAVVGLGFTTQNTATVGR.H						
147.	<a href="#">AT0G17380.1</a>	Mass: 43168	Score: 51	Matches: 4(2)	Sequences: 4(2)	emPAI: 0.16										
[ Symbols: MT03, SAM3, MT4   S-adenosylmethionine synthetase family protein   chr3:5952484-5953655 REVERSE LENGTH=393 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1471</a>	383.2337	764.4168	764.4181	-1.71	0	36	0.013	1	U	R.SGVTVV.Q						
<a href="#">1472</a>	437.2407	872.5069	872.5080	-1.17	0	14	2.8	1	U	R.STVAVGLAR.R						
<a href="#">1473</a>	571.3101	1160.6057	1160.6040	1.49	0	38	0.011	1	U	R.TVTHVQGR.F						
<a href="#">1474</a>	866.0957	2595.2654	2595.2863	-8.06	2	2	42	3	U	R.RSFVPPQGLINLKLQVQGR.F						
148.	<a href="#">AT0G02100.1</a>	Mass: 43587	Score: 51	Matches: 6(2)	Sequences: 6(2)	emPAI: 0.16										
[ Symbols: SAM1, SAM-1, MAT1, AICSAM1   S-adenosylmethionine synthetase 1   chr1:519037-520218 FORWARD LENGTH=393 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1481</a>	381.2157	764.4168	764.4181	-1.71	0	36	0.013	1	U	R.SGVTVV.Q						
<a href="#">1482</a>	571.3101	1160.6057	1160.6040	1.49	0	38	0.011	1	U	R.TVTHVQGR.F						
<a href="#">1483</a>	660.8281	1319.4417	1319.4503	-6.52	1	11	4.6	1	U	R.QAKKVFVQGR.S						
<a href="#">1484</a>	487.2480	1458.7822	1458.7725	6.66	2	1	84	10	U	R.QAKKVFVQGR.S						
<a href="#">1485</a>	1423.1573	2844.3000	2844.3368	-13.64	2	0	54	7	U	R.KQTCVAGVCGTGVTVVGR.D						
<a href="#">1486</a>	869.9458	3475.7540	3475.7617	-2.21	2	1	46	2	U	R.GAGVTVVTVLSTQMDTVTQETLQGR.E						
Proteins matching the same set of peptides:																
<a href="#">AT0G04670.1</a>	Mass: 43587	Score: 51	Matches: 6(2)	Sequences: 6(2)												
[ Symbols: SAM1, SAM-1, MAT1, AICSAM1   S-adenosylmethionine synthetase 1   chr1:519037-520218 FORWARD LENGTH=393 ]																
149.	<a href="#">AT0G04080.1</a>	Mass: 31461	Score: 51	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10										
[ Symbols:   KIMD-U-box superfamily protein   chr3:22187635-2218855 FORWARD LENGTH=306 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1491</a>	583.2670	1104.5195	1104.5233	-3.47	0	51	0.00072	1	U	R.VVIGQSRM.D						
150.	<a href="#">AT0G04670.1</a>	Mass: 17075	Score: 50	Matches: 3(1)	Sequences: 3(1)	emPAI: 0.43										
[ Symbols: PSB0   photosystem I subunit 0   chr1:20802874-2083356 REVERSE LENGTH=160 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1501</a>	426.2470	856.4734	856.4800	-6.49	0	0	45	4	U	R.STVGLK.S						
<a href="#">1502</a>	486.2427	970.4707	970.4720	-1.24	0	22	0.13	1	U	R.QQLPQGR.Y						
<a href="#">1503</a>	667.6414	1999.9085	1999.8871	10.7	1	43	0.0022	1	U	R.QQLPQGRYTVQADGR.A						
151.	<a href="#">AT0G16160.1</a>	Mass: 16304	Score: 49	Matches: 2(1)	Sequences: 2(1)	emPAI: 0.21										
[ Symbols:   Ribosomal protein S11 family protein   chr2:15169925-15171159 FORWARD LENGTH=150 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1511</a>	721.3638	1442.7331	1442.7353	-1.50	0	49	0.0013	1	U	R.VVTVTVPTQGR.R						
<a href="#">1512</a>	1141.9951	2281.9756	2282.0121	-15.95	1	2	15	5	U	R.AGDSVFVTAALAGVQGR.C						
Proteins matching the same set of peptides:																
<a href="#">AT0G16160.1</a>	Mass: 16320	Score: 49	Matches: 2(1)	Sequences: 2(1)												
[ Symbols:   Ribosomal protein S11 family protein   chr3:3623757-3624866 REVERSE LENGTH=150 ]																
<a href="#">AT0G04670.1</a>	Mass: 15285	Score: 49	Matches: 2(1)	Sequences: 2(1)												
[ Symbols:   Ribosomal protein S11 family protein   chr3:19503324-19504701 FORWARD LENGTH=150 ]																
152.	<a href="#">AT0G04670.1</a>	Mass: 42748	Score: 49	Matches: 6(2)	Sequences: 4(2)	emPAI: 0.16										
[ Symbols: GAPB, GAPB-1   glyceraldehyde 3-phosphate dehydrogenase A subunit   chr3:9795226-9796848 FORWARD LENGTH=396 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1521</a>	417.7279	831.4413	831.4395	2.14	0	18	0.85	2	U	R.VAIVQGR.I <a href="#">1521</a> <a href="#">153</a>						
<a href="#">1522</a>	641.7822	927.4649	927.4629	0.19	0	49	0.00071	1	U	R.LQVTVV.V						
<a href="#">1523</a>	692.8943	1383.7740	1383.7722	1.32	0	33	0.017	1	U	R.AAALIVVPTQGR.A						
<a href="#">1524</a>	519.2311	1554.6716	1554.6733	-1.09	0	35	0.013	1	U	R.QNTVTVYVQGR.L						
153.	<a href="#">AT0G16160.1</a>	Mass: 48086	Score: 49	Matches: 6(2)	Sequences: 4(2)	emPAI: 0.14										
[ Symbols: GAPB   glyceraldehyde 3-phosphate dehydrogenase B subunit   chr1:1517552-15129584 FORWARD LENGTH=447 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1531</a>	406.7660	811.5215	811.5247	0.94	0	4	U	U	R.VETTRAR.G							
<a href="#">1532</a>	417.7279	831.4413	831.4395	2.14	0	18	0.85	2	U	R.VAIVQGR.I <a href="#">1521</a> <a href="#">153</a>						
<a href="#">1533</a>	692.8943	1383.7740	1383.7722	1.32	0	33	0.017	1	U	R.AAALIVVPTQGR.A						
<a href="#">1534</a>	519.2311	1554.6716	1554.6733	-1.09	0	35	0.013	1	U	R.QNTVTVYVQGR.L						
154.	<a href="#">AT0G04670.1</a>	Mass: 119882	Score: 49	Matches: 10(1)	Sequences: 8(1)	emPAI: 0.03										
[ Symbols:   DEAD box RNA helicase family protein   chr3:1985697-1996666 REVERSE LENGTH=1088 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1541</a>	491.7687	981.5229	981.5216	1.25	2	3	14	7	U	R.SRSPRGR.D						
<a href="#">1542</a>	528.2913	1054.5680	1054.5971	-6.68	0	4	24	4	U	R.GAIVVAVGR.L						
<a href="#">1543</a>	411.8823	1232.4250	1232.4336	-6.91	0	1	51	8	U	R.GAQLVAVPR.D						
<a href="#">1544</a>	668.8246	1315.8346	1315.8315	2.32	0	49	0.00071	1	U	R.MLQDPFQGR.E						
<a href="#">1545</a>	787.8154	1573.4942	1573.4865	4.22	0	(3)	12	1	U	R.APHQDQTLQGR.S						
<a href="#">1546</a>	787.8170	1573.4995	1573.4865	8.28	0	4	9	1	U	R.APHQDQTLQGR.S <a href="#">1546</a>						
<a href="#">1547</a>	800.8180	1589.4534	1589.4484	-18.41	1	2	5.9	1	U	R.FQDQVTVVQGR.H						
<a href="#">1548</a>	1390.1307	2778.2468	2778.2460	2.40	1	2	25	3	U	R.SFQGVTFVTAALAGVTAALQGR.C						
<a href="#">1549</a>	1526.6740	4577.0002	4577.0533	-11.60	1	3	25	5	U	R.CQVTVQAVTVQVQVGLTQGLQGRVAVVQVTVVQGR.D						
155.	<a href="#">AT0G16160.1</a>	Mass: 76566	Score: 49	Matches: 5(1)	Sequences: 5(1)	emPAI: 0.04										
[ Symbols:   DEAD box RNA helicase family protein   chr5:471271-474713 FORWARD LENGTH=712 ]																
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	score	Expect <td>Rank</td> <td>Unique</td> <td>Peptide</td>	Rank	Unique	Peptide						
<a href="#">1551</a>	605.8246	1252.2446	1252.2525	-0.79	0	49	0.00071	1	U	R.MLQDPFQGR.E						
<a href="#">1552</a>	789.8741	1571.7296	1571.7434	-6.74	1	2	29	4	U	R.GAQLVAVPR.D						
<a href="#">1553</a>	828.4848	1850.9520	1850.9632	-4.40	0	2	67	1	U	R.LSLAQGVTVLQDADRLMLQSPFQGR.K						
<a href="#">1554</a>	1059.5250	3175.5532	3175.5682	-4.72	1	8	21	1	U	R.LSLAQGVTVLQDADRLMLQSPFQGR.K						
<a href="#">1555</a>	1546.7461	4637.2165	4637.2406	-5.20	1	4	50	7	U	R.CFVAAGPVTFLVAVGRGVTAQVTA						



179.	AT2G04360.1	Score: 48	Matches: 2(1)	Sequences: 2(1)	emPAI: 0.15	[ Symbol: ] Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein   chr5:25280151-25281463 REVERSE LENGTH=301					
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211	394.7112	787.4078	787.4075	0.36	0	48	0.00098	6	K.LDAQGR.D	
	132A	776.7136	2327.1190	2327.0985	8.84	2	2	46	10	U	K.EASARYSDAVKALMGSTQGR.R
180.	AT2G04382.2	Mass: 38891	Score: 46	Matches: 4(1)	Sequences: 4(1)	emPAI: 0.09	[ Symbol: ] Adiponectin superfamily protein   chr3:953389-954852 REVERSE LENGTH=159				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	212A	495.5791	1487.7953	1487.7944						K.LLILANADDTQGR.P	
	2483	875.9559	1749.8972	1749.8937	2.00	0	46	0.0017	1	K.FADELLANAAVIGTQGR.G	
	1725A	501.7633	2003.0239	2003.0548	-15.41	2	1	53	3	U	K.PVQIVGVGVEERAAAR.R
	242A	1246.5314	3136.5784	3136.5638	6.64	0	1	1.1e+002	7	U	K.TAVTQVQGLGVGVVETRIIDSDSDIK.C
181.	AT2G04520.1	Mass: 38684	Score: 45	Matches: 5(2)	Sequences: 5(2)	emPAI: 0.18	[ Symbol: ] TM22   threonine aldolase 2   chr3:1217397-1219571 REVERSE LENGTH=355				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	241	408.7264	815.4383	815.4389	-0.72	0	38	0.0085	1	K.EVATIAQR.R	
	2411	586.2962	1110.5778	1110.5781	-0.28	2	0	31	8	U	K.LKDNDKAR.V
	2441	872.4888	1742.9570	1742.9567	0.17	0	31	0.032	1	U	K.SLSDVVGVVTPATPA.T
	248A	730.4801	2189.0185	2188.9906	12.7	0	1	45	1	U	K.FAGANAVGVGVVDFGTFAR.L
	248	907.4786	2719.4179	2718.4175	0.17	2	0	87	2	U	K.VTFTTFTVGLAGVGVVFTPTGR.S
182.	AT2G04540.2	Mass: 38555	Score: 45	Matches: 5(2)	Sequences: 5(2)	emPAI: 0.03	[ Symbol: ] TM22   threonine aldolase 2   chr3:1217397-1219571 REVERSE LENGTH=354				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	212A	594.3177	1186.6208	1186.6194						K.VAAKATITQYV.N	
	531A	712.8374	1423.6602	1423.6831	-16.02	1	4	17	1	U	K.SIGSGVGVSPGAR.D
	15011	889.1059	2664.2959	2664.2588	13.9	1	1	97	9	U	K.ARMKQGLTFEDGLGDLAAAR.V.15011.15012
183.	AT2G04510.1	Mass: 58865	Score: 45	Matches: 5(1)	Sequences: 4(1)	emPAI: 0.06	[ Symbol: ] BOP56   homolog of nuclear protein BOP56   chr1:20984844-20986893 REVERSE LENGTH=622				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	605.2701	1208.5257	1208.5230	2.24	1	5	17	5	U	K.MNTATARRGR.S
	2411	420.8180	1239.6224	1239.6248	-1.89	0	45	0.0015	1	U	K.TVNTYIAR.V
	15011	781.3790	2201.1153	2201.1042	4.81	0	1	1.1e+002	1	U	K.ARMKQGLTFEDGLGDLAAAR.V.15011.15012
184.	AT2G04510.1	Mass: 58865	Score: 45	Matches: 5(1)	Sequences: 4(1)	emPAI: 0.06	[ Symbol: ] BOP56   homolog of nuclear protein BOP56   chr1:20984844-20986893 REVERSE LENGTH=622				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	605.2701	1208.5257	1208.5230	2.24	1	5	17	5	U	K.MNTATARRGR.S
	2411	420.8180	1239.6224	1239.6248	-1.89	0	45	0.0015	1	U	K.TVNTYIAR.V
	15011	781.3790	2201.1153	2201.1042	4.81	0	1	1.1e+002	1	U	K.ARMKQGLTFEDGLGDLAAAR.V.15011.15012
185.	AT2G04540.2	Mass: 38555	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.12	[ Symbol: ] PSAM   photosystem 2 reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAM)   chr5:25628724-25629409 REVERSE LENGTH=171				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	481.7442	961.4739	961.4716	2.40	1	1	42	3	U	K.TPTEKAR.R
	248A	488.2713	974.5279	974.5293	-1.37	0	8	8.1	3	U	K.QLSHVIR.A
	248A	488.2703	974.5441	974.5293	15.2	0	33	20	8	U	K.QMSNVIR.A
186.	AT2G04540.2	Mass: 38555	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.12	[ Symbol: ] PSAM   photosystem 2 reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAM)   chr5:25628690-25629409 REVERSE LENGTH=181				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	481.7442	961.4739	961.4716	2.40	1	1	42	3	U	K.TPTEKAR.R
	248A	488.2713	974.5279	974.5293	-1.37	0	8	8.1	3	U	K.QLSHVIR.A
	248A	488.2703	974.5441	974.5293	15.2	0	33	20	8	U	K.QMSNVIR.A
187.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
188.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
189.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
190.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
191.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
192.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
193.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
194.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
195.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
196.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
197.	AT2G04560.1	Mass: 31136	Score: 44	Matches: 4(1)	Sequences: 3(1)	emPAI: 0.11	[ Symbol: ] ATRP1, RSP1, At-RSP1, RSP1   RNA-binding (RBM/RBP/RBP motif) family protein   chr3:22900311-22902159 REVERSE LENGTH=264				
	Query	Observed	Mr(Exp)	Mr(Calc)	ppm	Miss Score	Expect	Rank	Unique	Peptide	
	211A	389.1894	776.3822	776.3851	-3.64	0	(8)	7.7	4	K.KPTTGR.T.25A.27A.27B.28B	
	211A	423.6444	904.4742	904.4800	-6.42	1	3	51	9	K.KPTTGR.T	
	211A	497.7186	985.4126	985.4161	-1.56	0	18	0.15	1	K.KPTTGR.T	
198.											

	<b>Proteins matching the same set of peptides:</b> <b>AT0G01466.1</b> Mass: 8448 Score: 41 Matches: 2(1) Sequences: 2(1)   Symbol:   AT0G01466.1   Cobalamin-independent synthase family protein   chr5:5935771-5939155 FORWARD LENGTH=765									
193.	<b>AT0G00890.1</b> Mass: 17347 Score: 43 Matches: 2(1) Sequences: 2(1) eMFAI: 0.43   Symbol:   RPS7.1   Ribosomal protein S7p/S6e family protein   chrC9:9748-9748 REVERSE LENGTH=155 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 916.7830 1031.9515 1031.9499 1.05 0 24 0.014 1 U K.LSRLVDAAG.G 1112 598.9833 1793.9280 1793.9272 0.45 0 36 0.014 1 U R.VGGSTQQYQKIGDTFOOK.A									
	<b>Proteins matching the same set of peptides:</b> <b>AT0G01466.1</b> Mass: 17347 Score: 43 Matches: 2(1) Sequences: 2(1)   Symbol:   RPS7.1   ribosomal protein S7   chrC:140704-141171 FORWARD LENGTH=155									
194.	<b>AT0G01488.1</b> Mass: 62182 Score: 42 Matches: 2(1) Sequences: 2(1) eMFAI: 0.37   Symbol:   GNT7.1   galactose-4-epimerase 1   chrB1:1336144-1336908 FORWARD LENGTH=137 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 373.2158 744.6131 744.6130 0.12 0 42 0.0044 1 U R.SGLAKTS.S 1112 1280.6216 2559.2086 2559.2129 -1.65 2 0 1.2e+02 7 U R.AYTPFGTSGDITSEFVEVPPE.Y									
195.	<b>AT0G01496.1</b> Mass: 73714 Score: 42 Matches: 4(2) Sequences: 4(2) eMFAI: 0.09   Symbol:   WUC70.2, WUC70.3   wicohandrin1 WUC70.2   chrU:2973722-2973858 FORWARD LENGTH=682 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 520.8119 1239.8176 1239.8149 0.81 1 30 0.031 1 U K.HETAYVGR.G 1112 478.3391 1384.6637 1384.6616 0 36 0.031 1 U K.NPACTYPTIVIK.S 1113 744.9104 1487.8462 1487.8308 10.4 2 10 2.6 1 U K.DHTTVYQQLTIR.S 1114 1178.4314 2395.3162 2395.1740 17.9 1 4 40 4 U K.QYGVQRAVPAALGGSLHDKVK.R									
196.	<b>AT0G01499.1</b> Mass: 40463 Score: 42 Matches: 5(0) Sequences: 5(0) eMFAI: 0.25   Symbol:   PTH1.1   phosphate transporter 1   chrU5:4531059-4532945 REVERSE LENGTH=737 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 427.6886 851.2626 851.3640 -1.40 0 9 1.4 1 U R.QSDPKP.K 1112 435.2504 868.4843 868.4849 -0.45 0 0 0.15 1 U K.BAQAAPR.G 1113 487.2353 972.4550 972.4552 0.82 0 25 0.061 1 U K.ESSVLGYLKG.G 1114 708.3386 1414.6527 1414.6516 0.76 0 25 0.11 1 U K.TYLGLADREYAT.Y 1115 599.5317 2094.5333 2094.5317 -0.76 2 0 64 8 U K.VLVGVGTAFANGDPVF.F									
197.	<b>AT0G01499.1</b> Mass: 96722 Score: 42 Matches: 3(1) Sequences: 3(1) eMFAI: 0.03   Symbol:   heat shock protein 70 (Hsp 70) family protein   chrE1:9377225-9381232 FORWARD LENGTH=867 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 371.2161 740.4176 740.4181 -0.69 0 1 7.2 2 U K.QGVPRM.M 1112 593.7081 705.4817 705.4821 -0.44 0 42 0.0119 1 U R.VTLGGR.L 1113 1116.8421 3347.5645 3347.6216 -17.06 2 0 58 2 U K.RSLQDAQNNAHTTAAREPAVALGTEKLE.K									
198.	<b>AT0G01508.1</b> Mass: 53020 Score: 42 Matches: 4(1) Sequences: 4(1) eMFAI: 0.13   Symbol:   ATP9B, HSP9 non-intrinsic ABC protein B   chrU1:1750091-1751994 REVERSE LENGTH=475 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 412.2314 1233.8724 1233.8942 -0.76 1 0 62 2 U K.IILHWRRGR.G 1112 467.8438 1333.8724 1333.8739 -1.12 0 33 0.038 0 U R.PACCTAGGLTG.S 1113 487.3527 1372.4909 1372.4946 -2.73 0 32 0.077 1 U R.SQIEPISTOQN.N 1114 619.1927 1854.8263 1854.8372 -5.80 0 1 51 1 U R.QMSERTIEFTVTGK.L									
199.	<b>AT0G05580.1</b> Mass: 20970 Score: 41 Matches: 1(1) Sequences: 1(1) eMFAI: 0.16   Symbol:   RPL18 ribosomal protein L18   chrU3:1621111-1622775 FORWARD LENGTH=187 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 693.4050 1384.7954 1384.7926 2.02 0 41 0.0029 1 U K.IAVLVGITDLR.V									
	<b>Proteins matching the same set of peptides:</b> <b>AT0G01508.1</b> Mass: 21011 Score: 41 Matches: 1(1) Sequences: 1(1)   Symbol:   Ribosomal protein L18/L15 superfamily protein   chrU5:9873169-9874297 FORWARD LENGTH=187									
200.	<b>AT0G01560.1</b> Mass: 27871 Score: 41 Matches: 1(1) Sequences: 1(1) eMFAI: 0.12   Symbol:   Tetrahydrogolate repeat (THR)-like superfamily protein   chrU5:900573-902719 REVERSE LENGTH=241 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 122.2489 1022.5032 1022.4955 17.3 0 41 0.0035 1 U K.Q1ZNVVR.Y									
201.	<b>AT0G01569.1</b> Mass: 122850 Score: 41 Matches: 20(1) Sequences: 13(1) eMFAI: 0.03   Symbol:   EMP1 embryonic E1one 1 (EMP1)   chrU5:1897140-1700390 FORWARD LENGTH=1096 Query Observed Mr(exp) Mr(cal) psn Miss Score Expect Rank Unique Peptide 1111 354.3503 710.2840 710.2873 -1.54 0 19 0.091 4 U K.SDPR.C 1112 363.2129 724.6132 724.3980 18.3 1 6 4.3 3 U K.BHQRTR.R 1113 475.2425 948.4754 948.4699 0.55 1 3 59 6 U K.QMAQTYR.K 1114 425.8975 1274.6707 127									

[illegible]



[illegible]





<a href="#">AT4G00030.2</a>	Mass: 17477	Score: 31	Matches: 41 (2)
Symbol: Histone superfamily protein			chr4:18555840-18555827 REVERSE LENGTH=13
<a href="#">AT4G00030.3</a>	Mass: 15454	Score: 31	Matches: 41 (2)
Symbol: Histone superfamily protein			chr4:18555840-18556147 REVERSE LENGTH=13
<a href="#">AT4G00040.1</a>	Mass: 15454	Score: 31	Matches: 41 (2)
Symbol: Histone superfamily protein			chr4:18557539-18558236 REVERSE LENGTH=13
<a href="#">AT4G00040.2</a>	Mass: 15454	Score: 31	Matches: 41 (2)
Symbol: Histone superfamily protein			chr4:18557539-18558236 REVERSE LENGTH=13
<a href="#">AT5G01980.1</a>	Mass: 15454	Score: 31	Matches: 41 (2)
Symbol: Histone superfamily protein			chr5:3472591-3473349 REVERSE LENGTH=136

Proteins matching the same set of peptides

[AT3G05620.2](#) Mass: 21536 Score: 30 Matches: 4(1) Sequences: 3(1)  
 [ Symbols: | winged-helix DNA-binding transcription factor family protein | chr2:13045360-13046267 FORWARD LENGTH: 202 ]

[AT3G05440.1](#) Score: 30 Matches: 2(1) Sequences: 2(1) smPAI: 0.08  
 [ Symbols: DMDP82 | dihydronicotinamide synthase | chr2:18731294-18732867 FORWARD LENGTH: 365 ]

Query	Observed	Nr(expt)	Nr(calc)	ppm	Miss	Score	Expect	Rank	Unim	Peptide
<a href="#">10567</a>	459.7520	917.4894	917.4971	-8.31	1	30	0.052	3	U	R.SKKVSPK.A
<a href="#">2185</a>	54.7425	1106.5345	1106.5204	12.7	0	5	16	3	U	K.VTIGTQNGTR.E

[AT2G29560.1](#)    **Match:** 52080    **Score:** 30

Symbol	RNC	[cytosine]	smiles	chr	pos	score	expect	rank	unique	Aptide
Query	Observed	Mt(exp)	Mt(calc)			%				
876	403.7291	805.4437	805.4446	-1.12	0	3.038	1			K.YNDLIR.L
876	851.4758	1700.9371	1700.9171	11.7	0	2	39	U		A.GNVLVPVPTVLGGK.N
13337	1175.0619	2348.1092	2348.1028	2.73	0	2	10	U		K.YFSSIGIQGVVDGGLSSEK.R
14725	1572.4113	3174.2139	3174.2497	-7.60	2	42	9	U		R.FEALQGSSTETLVLLKLSISEGLDGLGVDDGLASDISL.N

[AT3G18190.1](#)      Mass: 58195      Score: 30

Query	Accession	Score	Matrix	Ch1	Query	Accession	Score	Matrix	Ch2
Symbol	TCF	cpn	chaperonin	family	ch1	62322222	6233835	FORWARD	LEU08-536
Observed	Exp(art)	W(alc)	p	Miss	Score	Expect	Mass	Peptide	
45	359.2050	716.3954	716.3817	19.4	0	36	10.1	U	R.AVDVDAV.T
2355	585.3350	1168.6554	1168.686	14.4	0	6	0.021	U	M.AVAANVAKMKPKR.G <a href="#">2355</a>
3029	595.8854	1184.6343	1184.6335	0.62	0	(3)	20	3	M.AVAANVAKMKPKR.G
18100	835.4536	3337.7134	3337.6752	11.4	1	2	30	2	K.IAVIGQVIGSPKDEKREGIVSDTDT

AT2G20400.1      Name: 44312      Score: 30

MASS: 44312    SCORE: 30    MATCHES: 9(1)    SEQUENCES: 2(1)    EMBL: 0.07  
 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:8799624-8801621 FORWARD LENGTH:397  
 Query    Observed    Mr(expt)    Mr(calc)    ppm    Miss    Score    Expect    Rank    Unique    Peptide  
 7    352.1841    702.3537    702.3548    -1.52    0    0    0.052    1    R.IKRGQKN.A 5 6 8 9 10 11 12  
 10893    1015.4946    702.3620    704.4233    12.7    1    0    1.2e+02    5    U    R.NRWKGVHVPFDVAVGLGSSNEATPK

[AT3G25920.1](#)      Name: 29860      Score: 30

Symbol: RPL15		ribosomal protein L15		chr3:9491268-9492558		REVERSE		LENGTH:277		
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<u>2068</u>	357.2127	1068.6162	1068.6040	11.4	1	1	15	8	U	K.QKGL
<u>3212</u>	599.7945	1197.5744	1197.5778	-2.84	0	30	0.032	1	U	R.GPRG

Seq1	Ratio	Mass	Score	Score	Matches	Score	Sequences	3(0)	emPA: 0.07
57440		LUC7	related protein		chr5:5749849-5753415	FORMED LENGTH=404			
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Uniq
2126	551.3120	1100.6094	1100.6077	1.59	1	30	0.06	1	K.AKKAALKK.L
3156	618.3144	1852.0025	1851.9690	1.8	2	5	26	2	K.KADLHDLGKTDLKIR.A
3564	1059.0114	2116.0056	2116.0331	-12.91	1	1	47	3	K.QLDVIGANNRNDGTVKIR.A

**AF360887.1** Mass: 62816 Score: 29 Matches: 2(1) Sequences: 2(1) eMFI: 0.05  
 | Symbol: ATYR23A, TMS1 | TMS2 | TMS3 | TMS4 | TMS5 | TMS6 | TMS7 | TMS8 | TMS9 | TMS10 | TMS11 | TMS12 | TMS13 | TMS14 | TMS15 | TMS16 | TMS17 | TMS18 | TMS19 | TMS20 | TMS21 | TMS22 | TMS23 | TMS24 | TMS25 | TMS26 | TMS27 | TMS28 | TMS29 | TMS30 | TMS31 | TMS32 | TMS33 | TMS34 | TMS35 | TMS36 | TMS37 | TMS38 | TMS39 | TMS40 | TMS41 | TMS42 | TMS43 | TMS44 | TMS45 | TMS46 | TMS47 | TMS48 | TMS49 | TMS50 | TMS51 | TMS52 | TMS53 | TMS54 | TMS55 | TMS56 | TMS57 | TMS58 | TMS59 | TMS60 | TMS61 | TMS62 | TMS63 | TMS64 | TMS65 | TMS66 | TMS67 | TMS68 | TMS69 | TMS70 | TMS71 | TMS72 | TMS73 | TMS74 | TMS75 | TMS76 | TMS77 | TMS78 | TMS79 | TMS80 | TMS81 | TMS82 | TMS83 | TMS84 | TMS85 | TMS86 | TMS87 | TMS88 | TMS89 | TMS90 | TMS91 | TMS92 | TMS93 | TMS94 | TMS95 | TMS96 | TMS97 | TMS98 | TMS99 | TMS100 | TMS101 | TMS102 | TMS103 | TMS104 | TMS105 | TMS106 | TMS107 | TMS108 | TMS109 | TMS110 | TMS111 | TMS112 | TMS113 | TMS114 | TMS115 | TMS116 | TMS117 | TMS118 | TMS119 | TMS120 | TMS121 | TMS122 | TMS123 | TMS124 | TMS125 | TMS126 | TMS127 | TMS128 | TMS129 | TMS130 | TMS131 | TMS132 | TMS133 | TMS134 | TMS135 | TMS136 | TMS137 | TMS138 | TMS139 | TMS140 | TMS141 | TMS142 | TMS143 | TMS144 | TMS145 | TMS146 | TMS147 | TMS148 | TMS149 | TMS150 | TMS151 | TMS152 | TMS153 | TMS154 | TMS155 | TMS156 | TMS157 | TMS158 | TMS159 | TMS160 | TMS161 | TMS162 | TMS163 | TMS164 | TMS165 | TMS166 | TMS167 | TMS168 | TMS169 | TMS170 | TMS171 | TMS172 | TMS173 | TMS174 | TMS175 | TMS176 | TMS177 | TMS178 | TMS179 | TMS180 | TMS181 | TMS182 | TMS183 | TMS184 | TMS185 | TMS186 | TMS187 | TMS188 | TMS189 | TMS190 | TMS191 | TMS192 | TMS193 | TMS194 | TMS195 | TMS196 | TMS197 | TMS198 | TMS199 | TMS200 | TMS201 | TMS202 | TMS203 | TMS204 | TMS205 | TMS206 | TMS207 | TMS208 | TMS209 | TMS210 | TMS211 | TMS212 | TMS213 | TMS214 | TMS215 | TMS216 | TMS217 | TMS218 | TMS219 | TMS220 | TMS221 | TMS222 | TMS223 | TMS224 | TMS225 | TMS226 | TMS227 | TMS228 | TMS229 | TMS230 | TMS231 | TMS232 | TMS233 | TMS234 | TMS235 | TMS236 | TMS237 | TMS238 | TMS239 | TMS240 | TMS241 | TMS242 | TMS243 | TMS244 | TMS245 | TMS246 | TMS247 | TMS248 | TMS249 | TMS250 | TMS251 | TMS252 | TMS253 | TMS254 | TMS255 | TMS256 | TMS257 | TMS258 | TMS259 | TMS260 | TMS261 | TMS262 | TMS263 | TMS264 | TMS265 | TMS266 | TMS267 | TMS268 | TMS269 | TMS270 | TMS271 | TMS272 | TMS273 | TMS274 | TMS275 | TMS276 | TMS277 | TMS278 | TMS279 | TMS280 | TMS281 | TMS282 | TMS283 | TMS284 | TMS285 | TMS286 | TMS287 | TMS288 | TMS289 | TMS290 | TMS291 | TMS292 | TMS293 | TMS294 | TMS295 | TMS296 | TMS297 | TMS298 | TMS299 | TMS300 | TMS301 | TMS302 | TMS303 | TMS304 | TMS305 | TMS306 | TMS307 | TMS308 | TMS309 | TMS310 | TMS311 | TMS312 | TMS313 | TMS314 | TMS315 | TMS316 | TMS317 | TMS318 | TMS319 | TMS320 | TMS321 | TMS322 | TMS323 | TMS324 | TMS325 | TMS326 | TMS327 | TMS328 | TMS329 | TMS330 | TMS331 | TMS332 | TMS333 | TMS334 | TMS335 | TMS336 | TMS337 | TMS338 | TMS339 | TMS340 | TMS341 | TMS342 | TMS343 | TMS344 | TMS345 | TMS346 | TMS347 | TMS348 | TMS349 | TMS350 | TMS351 | TMS352 | TMS353 | TMS354 | TMS355 | TMS356 | TMS357 | TMS358 | TMS359 | TMS360 | TMS361 | TMS362 | TMS363 | TMS364 | TMS365 | TMS366 | TMS367 | TMS368 | TMS369 | TMS370 | TMS371 | TMS372 | TMS373 | TMS374 | TMS375 | TMS376 | TMS377 | TMS378 | TMS379 | TMS380 | TMS381 | TMS382 | TMS383 | TMS384 | TMS385 | TMS386 | TMS387 | TMS388 | TMS389 | TMS390 | TMS391 | TMS392 | TMS393 | TMS394 | TMS395 | TMS396 | TMS397 | TMS398 | TMS399 | TMS400 | TMS401 | TMS402 | TMS403 | TMS404 | TMS405 | TMS406 | TMS407 | TMS408 | TMS409 | TMS410 | TMS411 | TMS412 | TMS413 | TMS414 | TMS415 | TMS416 | TMS417 | TMS418 | TMS419 | TMS420 | TMS421 | TMS422 | TMS423 | TMS424 | TMS425 | TMS426 | TMS427 | TMS428 | TMS429 | TMS430 | TMS431 | TMS432 | TMS433 | TMS434 | TMS435 | TMS436 | TMS437 | TMS438 | TMS439 | TMS440 | TMS441 | TMS442 | TMS443 | TMS444 | TMS445 | TMS446 | TMS447 | TMS448 | TMS449 | TMS450 | TMS451 | TMS452 | TMS453 | TMS454 | TMS455 | TMS456 | TMS457 | TMS458 | TMS459 | TMS460 | TMS461 | TMS462 | TMS463 | TMS464 | TMS465 | TMS466 | TMS467 | TMS468 | TMS469 | TMS470 | TMS471 | TMS472 | TMS473 | TMS474 | TMS475 | TMS476 | TMS477 | TMS478 | TMS479 | TMS480 | TMS481 | TMS482 | TMS483 | TMS484 | TMS485 | TMS486 | TMS487 | TMS488 | TMS489 | TMS490 | TMS491 | TMS492 | TMS493 | TMS494 | TMS495 | TMS496 | TMS497 | TMS498 | TMS499 | TMS500 | TMS501 | TMS502 | TMS503 | TMS504 | TMS505 | TMS506 | TMS507 | TMS508 | TMS509 | TMS510 | TMS511 | TMS512 | TMS513 | TMS514 | TMS515 | TMS516 | TMS517 | TMS518 | TMS519 | TMS520 | TMS521 | TMS522 | TMS523 | TMS524 | TMS525 | TMS526 | TMS527 | TMS528 | TMS529 | TMS530 | TMS531 | TMS532 | TMS533 | TMS534 | TMS535 | TMS536 | TMS537 | TMS538 | TMS539 | TMS540 | TMS541 | TMS542 | TMS543 | TMS544 | TMS545 | TMS546 | TMS547 | TMS548 | TMS549 | TMS550 | TMS551 | TMS552 | TMS553 | TMS554 | TMS555 | TMS556 | TMS557 | TMS558 | TMS559 | TMS560 | TMS561 | TMS562 | TMS563 | TMS564 | TMS565 | TMS566 | TMS567 | TMS568 | TMS569 | TMS570 | TMS571 | TMS572 | TMS573 | TMS574 | TMS575 | TMS576 | TMS577 | TMS578 | TMS579 | TMS580 | TMS581 | TMS582 | TMS583 | TMS584 | TMS585 | TMS586 | TMS587 | TMS588 | TMS589 | TMS590 | TMS591 | TMS592 | TMS593 | TMS594 | TMS595 | TMS596 | TMS597 | TMS598 | TMS599 | TMS600 | TMS601 | TMS602 | TMS603 | TMS604 | TMS605 | TMS606 | TMS607 | TMS608 | TMS609 | TMS610 | TMS611 | TMS612 | TMS613 | TMS614 | TMS615 | TMS616 | TMS617 | TMS618 | TMS619 | TMS620 | TMS621 | TMS622 | TMS623 | TMS624 | TMS625 | TMS626 | TMS627 | TMS628 | TMS629 | TMS630 | TMS631 | TMS632 | TMS633 | TMS634 | TMS635 | TMS636 | TMS637 | TMS638 | TMS639 | TMS640 | TMS641 | TMS642 | TMS643 | TMS644 | TMS645 | TMS646 | TMS647 | TMS648 | TMS649 | TMS650 | TMS651 | TMS652 | TMS653 | TMS654 | TMS655 | TMS656 | TMS657 | TMS658 | TMS659 | TMS660 | TMS661 | TMS662 | TMS663 | TMS664 | TMS665 | TMS666 | TMS667 | TMS668 | TMS669 | TMS670 | TMS671 | TMS672 | TMS673 | TMS674 | TMS675 | TMS676 | TMS677 | TMS678 | TMS679 | TMS680 | TMS681 | TMS682 | TMS683 | TMS684 | TMS685 | TMS686 | TMS687 | TMS688 | TMS689 | TMS

AT1G60900.1 Mass: 66446 Score: 29

chr24:99861 | Raw: 66446 | Score: 29 | Matches: 5(1) | Sequences: 5(1) | eBPAT: 0.05  
| Symbols: | U2 snRNP auxiliary factor, large subunit, splicing factor | chr1:22424008-22427806 FORWARD LENGTH=588

[illegible]

[http://gary.mascot.cgi/master\\_results.pl?file=...%2Fdata%2F20160426%2FF004493.dmg](http://gary.mascot.cgi/master_results.pl?file=...%2Fdata%2F20160426%2FF004493.dmg) [2016/4/26 14:34:11]

	<b>AT1G13410.2</b>	Mass: 1311009	Score: 25	Matches: 5(0)	Sequences: 5(0)	
	[ Symbol: ] UNP3   ubiquitin-specific protease 33   chr3:3761758-3770295 REVERSE LENGTH=1114					
319.	<b>AT1G13410.2</b>	Mass: 41973	Score: 24	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.08
	[ Symbol: ] unknown protein  RUST Arabidopsis thaliana protein match 1st   unknown protein (TAIR ATG313980.1); Has 1064 Blast hits to 581 proteins in 136 species  Archae - 0; Bacteria - 72; Metazoa - 212; Fungi - 78; Plants - 102; Viruses - 0; Other					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>241</b>	385.1936	768.3726	768.3878	-19.84	0	24 0.22 1 0 R.STLNN.V
320.	<b>AT1G27260.1</b>	Mass: 70037	Score: 24	Matches: 3(0)	Sequences: 3(0)	emPAI: 0.05
	[ Symbol: ] GH1.5, WEI1   Auxin-responsive GH1 family protein   chr4:1365704-1365892 FORWARD LENGTH=612					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>241</b>	708.8452	1415.6798	1415.7031	-19.29	0	4 15 6 0 K.KQGRVLDVGVK.L
<b>424</b>	1178.6154	2355.2152	2355.1893	-8.81	2	24 0.37 1 0 K.SPQGLDLEHTDNDQDK.Q
<b>424</b>	1719.9236	3437.8236	3437.7941	-14.1	1	1 40 7 0 R.HLVTLADVQGVQVPLSDNDCTFLFK.S
321.	<b>AT5G06430.1</b>	Mass: 40112	Score: 24	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.08
	[ Symbol: ] CSD2-type zinc finger family protein   chr5:1239166-1240254 FORWARD LENGTH=362					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>5541</b>	718.8230	1435.6315	1435.6327	-0.88	1	24 0.1 1 0 K.QGRSGHQDK.Q
322.	<b>AT1G57410.1</b>	Mass: 73813	Score: 24	Matches: 3(1)	Sequences: 3(1)	emPAI: 0.04
	[ Symbol: ] Commensal-like kinase family protein   chr3:2287079-2289058 REVERSE LENGTH=659					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>244</b>	547.7166	1093.4464	1093.4159	-9.54	0	24 0.612 1 0 K.HVYBNGD.L
<b>1103</b>	686.0011	2040.9815	2040.9513	-14.7	0	2 38 1 0 K.RNLVLYCFGRSHSLD.C
<b>424</b>	1280.9194	3839.7164	3839.7855	-12.65	1	1 34 1 0 K.QGSGHGFVFPSTGLGAFQGLFPRTHQK.A
323.	<b>AT1G13860.1</b>	Mass: 43913	Score: 24	Matches: 6(0)	Sequences: 2(0)	emPAI: 0.16
	[ Symbol: ] AAP71, ATAP71   aminocobolophosphotransferase 1   chr1:4618834-4641693 REVERSE LENGTH=389					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>434</b>	795.4101	2386.2084	2386.1687	-6.25	0	8 29 0 1 K.TNQCGLLYFPFALAGALTAR.L
<b>244</b>	796.7446	2387.2121	2387.1687	-18.2	0	(18) 1.1 1 0 K.TNQCGLLYFPFALAGALTAR.L
<b>434</b>	1357.3199	4008.9379	4009.0007	-15.67	2	0 59 6 0 R.KILAHCEPRGLATNGRLLYLPFALAGALTAR.L
Proteins matching the same set of peptides:						
	<b>AT1G13860.1</b>	Mass: 38792	Score: 24	Matches: 6(0)	Sequences: 2(0)	
	[ Symbol: ] AAP71, ATAP71   aminocobolophosphotransferase 2   chr1:4638834-4641563 REVERSE LENGTH=346					
	<b>AT1G13861.1</b>	Mass: 44047	Score: 24	Matches: 6(0)	Sequences: 2(0)	
	[ Symbol: ] AAP72, ATAP72   aminocobolophosphotransferase   chr3:9295856-9298271 FORWARD LENGTH=389					
	<b>AT1G13862.1</b>	Mass: 44047	Score: 24	Matches: 6(0)	Sequences: 2(0)	
	[ Symbol: ] AAP72, ATAP72   aminocobolophosphotransferase   chr3:9295856-9298271 FORWARD LENGTH=389					
	<b>AT1G13863.1</b>	Mass: 38952	Score: 24	Matches: 6(0)	Sequences: 2(0)	
	[ Symbol: ] AAP72, ATAP72   aminocobolophosphotransferase   chr3:9298023-9298271 FORWARD LENGTH=137					
	<b>AT1G13864.1</b>	Mass: 44047	Score: 24	Matches: 6(0)	Sequences: 2(0)	
	[ Symbol: ] AAP72, ATAP72   aminocobolophosphotransferase   chr3:9295856-9298271 FORWARD LENGTH=389					
324.	<b>AT1G14110.1</b>	Mass: 47042	Score: 24	Matches: 4(0)	Sequences: 4(0)	emPAI: 0.07
	[ Symbol: ] AT23, AT2   GHM1 homologous 3   chr3:15866115-15871059 REVERSE LENGTH=420					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>241</b>	383.8940	1148.6262	1148.6262	-0.03	1	18 0.41 2 0 R.HSDGVGVK.V
<b>314</b>	597.2748	1192.5350	1192.5473	-10.27	1	4 25 4 0 K.HSDGKGVK.F
<b>241</b>	710.3583	1418.7020	1418.7041	-1.49	0	24 0.28 1 0 K.HSDGVVGVGVK.A
<b>424</b>	704.7347	3218.6373	3218.6875	-14.27	1	0 55 1 0 K.QHQLGCTFPGKGLVTVGVGVGVK.Q
Proteins matching the same set of peptides:						
	<b>AT1G14110.1</b>	Mass: 36154	Score: 24	Matches: 4(0)	Sequences: 4(0)	
	[ Symbol: ] AT23, AT2   GHM1 homologous 3   chr3:15866179-15871059 REVERSE LENGTH=343					
325.	<b>AT1G31330.1</b>	Mass: 24329	Score: 23	Matches: 3(0)	Sequences: 3(0)	emPAI: 0.14
	[ Symbol: ] PSAP   photosystem 2 subunit P   chr1:11215011-11215939 REVERSE LENGTH=221					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>451</b>	402.7389	801.4652	801.4792	-12.10	1	9 3 4 4 K.HARDEK.L
<b>3041</b>	590.3193	1178.6239	1178.6237	0.25	0	10 4.3 1 0 R.GFVWPAAYR.R
<b>345</b>	613.3622	1234.7098	1234.7078	1.67	0	23 0.08 1 0 K.KIIVDPLAH.L
326.	<b>AT1G08139.1</b>	Mass: 42451	Score: 23	Matches: 2(0)	Sequences: 2(0)	emPAI: 0.08
	[ Symbol: ] RING/U-box superfamily protein   chr5:2616487-2617617 FORWARD LENGTH=376					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>424</b>	492.7424	983.4702	983.4634	6.91	0	23 0.11 1 0 R.TGTPTNVL.-
<b>1264</b>	1600.2992	3198.5838	3198.5217	19.4	1	0 64 10 0 R.BRAGSGHGRVRLHLELTPGVGGK.E
327.	<b>AT1G13860.1</b>	Mass: 18045	Score: 23	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.19
	[ Symbol: ] Ribosomal protein L31 family protein   chr2:1563959-1562059 REVERSE LENGTH=166					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>640</b>	672.8648	1362.7151	1362.7092	4.34	0	23 0.5 1 0 R.VTGGVGAASLAK.I
Proteins matching the same set of peptides:						
	<b>AT1G13860.1</b>	Mass: 18073	Score: 23	Matches: 1(0)	Sequences: 1(0)	
	[ Symbol: ] Ribosomal protein L31 family protein   chr3:15809895-15810395 REVERSE LENGTH=166					
	<b>AT1G06410.2</b>	Mass: 17946	Score: 23	Matches: 1(0)	Sequences: 1(0)	
	[ Symbol: ] Ribosomal protein L31 family protein   chr5:24381066-24381564 REVERSE LENGTH=166					
328.	<b>AT1G13430.1</b>	Mass: 21681	Score: 23	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.16
	[ Symbol: ] unknown protein  Has 21 Blast hits to 21 proteins in 6 species  Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI NLink).   chr3:4457038-4457989 FORWARD LENGTH=193					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>114</b>	466.2750	930.5294	930.5433	-14.34	1	23 0.43 1 0 K.RGLIAYR.R
Proteins matching the same set of peptides:						
	<b>AT1G13430.1</b>	Mass: 18970	Score: 23	Matches: 1(0)	Sequences: 1(0)	
	[ Symbol: ] unknown protein  FUNCTIONS DE: molecular_function unknown; BIOLOGY DE: biological_process unknown; LOCATED DE: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species  Archae - 12; Bacteria - 1396; Metazoa -					
329.	<b>AT1G13430.1</b>	Mass: 67074	Score: 25	Matches: 3(0)	Sequences: 2(0)	emPAI: 0.02
	[ Symbol: ] Auxin-responsive GH3 family protein   chr5:4278884-4282287 FORWARD LENGTH=587					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>223</b>	628.3702	1254.7255	1254.7163	5.99	2	(11) 0.4 2 0 R.HMGIGDLEIK.V
<b>484</b>	419.2501	1254.7284	1254.7183	8.01	2	22 0.19 1 0 R.HMGIGDLEIK.V
<b>1584</b>	939.8608	2816.5005	2816.4629	13.3	2	2 24 2 0 R.QEVLLSLHMYTREDLKAVTGAR.L
330.	<b>AT1G09990.1</b>	Mass: 16849	Score: 22	Matches: 2(0)	Sequences: 1(0)	emPAI: 0.20
	[ Symbol: ] Ribosomal protein S5 domain 2-like superfamily protein   chr2:3781442-3781882 FORWARD LENGTH=146					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>111</b>	487.2419	1458.7518	1458.7215	-12.15	0	(3) 39 2 0 R.VGGHNTGVQVAYR.Q
<b>131</b>	487.2491	1458.7254	1458.7215	2.65	0	22 0.53 1 0 R.VGGHNTGVQVAYR.Q
Proteins matching the same set of peptides:						
	<b>AT1G09990.1</b>	Mass: 16835	Score: 22	Matches: 2(0)	Sequences: 1(0)	
	[ Symbol: ] Ribosomal protein S5 domain 2-like superfamily protein   chr5:6090253-6090693 REVERSE LENGTH=146					
	<b>AT1G1380.2</b>	Mass: 16819	Score: 22	Matches: 2(0)	Sequences: 1(0)	
	[ Symbol: ] Ribosomal protein S5 domain 2-like superfamily protein   chr5:6090128-6090693 REVERSE LENGTH=144					
	<b>AT1G1380.1</b>	Mass: 16772	Score: 22	Matches: 2(0)	Sequences: 1(0)	
	[ Symbol: ] Ribosomal protein S5 domain 2-like superfamily protein   chr5:6090128-6090693 REVERSE LENGTH=139					
331.	<b>AT1G13690.1</b>	Mass: 67683	Score: 22	Matches: 4(0)	Sequences: 3(0)	emPAI: 0.05
	[ Symbol: ] AT1G2AF65A   U2 snRNP auxiliary factor, large subunit, splicing factor   chr4:17294139-17297609 REVERSE LENGTH=573					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>434</b>	1141.0848	2482.1798	2482.2126	-31.59	2	(3) 19 1 1 K.EFQGVAVVYTFKRPQGVLA.-
<b>434</b>	895.0844	2482.2314	2482.2126	7.02	2	22 0.3 1 0 K.EFQGVAVVYTFKRPQGVLA.-
<b>223</b>	1335.0400	4670.1216	4670.2895	-46.12	1	0 2 11.1 0 2 15 1 0 R.VGGVAVVAVKAAKAAATVGGVAVVAVTTLGAGVGGVPPVLTGGVPSGLGGVGGTGAQYR.R
<b>203</b>	1455.5152	7272.5396	7272.4294	15.1	2	0 16 1 0 K.QVGGVGMFAPFAPKAAAGAVTGVVAPPTLVGGVPPVLTGGVPSGLGGVGGTGAQYR.R
Proteins matching the same set of peptides:						
	<b>AT1G13690.1</b>	Mass: 60799	Score: 22	Matches: 4(0)	Sequences: 3(0)	
	[ Symbol: ] AT1G2AF65A   U2 snRNP auxiliary factor, large subunit, splicing factor   chr4:17294139-17297609 REVERSE LENGTH=551					
332.	<b>AT1G54110.1</b>	Mass: 32983	Score: 22	Matches: 3(0)	Sequences: 3(0)	emPAI: 0.10
	[ Symbol: ] ATP8P1, ATP, P8P1, ATP8P1, UCP1   plant uncoupling mitochondrial protein   chr3:20038890-20040996 FORWARD LENGTH=306					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>211</b>	450.7616	899.5087	899.5188	-11.25	1	5 11 3 0 K.VRLQAKD.L
<b>424</b>	529.3217	1056.6289	1056.6292	-0.25	0	24 0.22 1 0 R.GLITGVQYAR.R
<b>424</b>	1284.2378	2564.4004	2564.4880	-10.74	2	4 14 1 0 K.KILAGTDLGLGLVAMPDVLVGVYR.L
333.	<b>AT1G11580.1</b>	Mass: 22694	Score: 22	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15
	[ Symbol: ] RING/U-box superfamily protein   chr2:6797687-6798612 FORWARD LENGTH=196					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>154</b>	376.2504	750.4863	750.4864	-0.15	1	22 0.013 1 0 R.LRIPVR.T
Proteins matching the same set of peptides:						
	<b>AT1G11580.1</b>	Mass: 14554	Score: 22	Matches: 1(1)	Sequences: 1(1)	
	[ Symbol: ] RING/U-box superfamily protein   chr2:6797687-6798612 FORWARD LENGTH=130					
334.	<b>AT1G19190.1</b>	Mass: 47389	Score: 22	Matches: 7(0)	Sequences: 6(0)	emPAI: 0.07
	[ Symbol: ] RPS2A, ATD201   regulatory particle subunit A ATPase 6A   chr5:475144-4754918 FORWARD LENGTH=419					
Query	Observed	Mr(calc)	Mr(calc)	ppm	Mis	Score Expect Rank Unique Peptide
<b>24</b>	367.6691	733.3236	733.3242	-0.84	0	2 14 2 0 K.TYNNQD.L

4272

473.7636

945.5127

945.5131

-0.44

0

22

0.37

1

U

K.VGSSRLQV.V

4273

495.2613

986.5080

986.4937

14.5

1

3

54

4

U

R.QTJLADN.L

4274

619.1245

1286.4145

1286.4132

17.2

2

3

57

1

U

K.KVDFQNGA.R

4281

810.1878

1618.7610

1618.7661

-3.18

0

1

96

4

U

R.VVVTQGVQVAK.V.2481

4281

881.4382

2641.2929

2641.3136

-7.83

2

7

15

1

U

K.GAAAGQVHLEQVYTGHLRGP.Q

335.

A0081339.1

Mass: 199620

Score: 22

Matches: 18(0)

Sequences: 4(0)

emPAI: 0.03

[ Symbol: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:115182-13009 REVERSE LENGTH=1797

Query

Observed

Mr(Exp)

Mr(Calc)

ppm

Mis

Score

Expect

Rank

Unique

Peptide

4282

685.7001

1369.5059

1369.5238

-13.24

0

1

1.1

1

U

K.LHQGAQCSASQD.Q.4831

4283

905.2329

1512.4768

1512.4805

-2.46

0

19

0.37

1

U

K.TPQNDLDTSSR.R

4284

757.1449

1512.4792

1512.4805

-0.36

0

(127)

1

1

U

K.TPQNDLDTSSR.R

4285

967.1341

2898.3806

2898.3474

11.5

2

8

11

2

U

K.TKQTFGLTRGKQVIGLHLEK.V.16487.16490.16493.16494.16485.16507.16516.16514.16513.16491

4286

967.4489

2899.3849

2899.3324

18.5

2

(6)

15

1

U

K.TKQTFGLTRGKQVIGLHLEK.V.R

4287

1162.5413

3544.6039

3544.5608

12.1

1

2

29

2

U

K.KGVGVAVAGTQGVQVNGVAVASSTDSQW.K

336.

A0081339.1

Mass: 62339

Score: 22

Matches: 11(0)

Sequences: 9(0)

emPAI: 0.05

[ Symbol: | HSP60-2 | heat shock protein 60-2 | chr1:14075093-14078568 REVERSE LENGTH=585

Query

Observed

Mr(Exp)

Mr(Calc)

ppm

Mis

Score

Expect

Rank

Unique

Peptide

4288

496.2654

990.0162

990.0050

10.8

0

22

0.37

1

U

K.LIGLIMAK.V.1442

4289

618.2548

1234.5705

1234.5798

-3.85

0

21

0.79

1

U

K.FVAGNMMK.R

4290

431.9517

1292.4834

1292.4974

-11.03

1

6

14

2

U

K.LQVYKSTIRK.D

4291

831.4349

1660.7932

1660.7944

-0.73

0

5

38

1

U

K.LLQGVQVIGTDAK.G

4292

1087.9988

2173.9630

2173.9606

1.13

1

1

18

1

U

R.AIFTRVCSVAGNADSLR.R

4293

1158.5877

2329.1428

2329.0977

19.4

2

14

2.8

2

U

R.AIFTRVCSVAGNADSLR.G.13113

4294

601.5133

3052.3302

3052.5091

7.00

1

1

50

4

U

K.RVVALRQVNAIVNDVQDTCAVTLR.A

4295

1135.8876

3404.6410

3404.7061

-19.12

2

0

42

3

U

K.LLQGVQVIGTDAKGVVQVIGLHLEK.V

4296

984.9700

3935.8507

3935.8478

0.74

1

1

47

4

U

K.ANLKKAALTAQVITRLGRLGRLGRLGQVQK.V

Proteins matching the same set of peptides:

A0081339.1

Mass: 61781

Score: 22

Matches: 11(0)

Sequences: 9(0)

[ Symbol: | HSP60-2 | heat shock protein 60-2 | chr1:14075093-14078568 REVERSE LENGTH=580

337.

A0081432.1

Mass: 43844

Score: 21

Matches: 31(0)

Sequences: 1(0)

emPAI: 0.08

[ Symbol: | YDCC1 | Flavon-binding monooxygenase family protein | chr1:750845-7522186 FORWARD LENGTH=391

Query

Observed

Mr(Exp)

Mr(Calc)

ppm

Mis

Score

Expect

Rank

Unique

Peptide

4297

721.3512

1440.7679

1440.7401

15.2

1

21

0.3

1

U

K.SAVFQGVQV.V.5588.5590.5591.5593.5594.5595.5598.5599.5600.5601.5603.5604.5605.5606.5608.5610.5611.5612.5613.5614.5615.5616.5617.5618.5619.5620.5621.5622.5623.5624.5625.5626.5627.5628.5629.5630.5631.5632.5633.5634.5635.5636.5637.5638.5639.5640.5641.5642.5643.5644.5645.5646.5647.5648.5649.5650.5651.5652.5653.5654.5655.5656.5657.5658.5659.5660.5661.5662.5663.5664.5665.5666.5667.5668.5669.5670.5671.5672.5673.5674.5675.5676.5677.5678.5679.5680.5681.5682.5683.5684.5685.5686.5687.5688.5689.5690.5691.5692.5693.5694.5695.5696.5697.5698.5699.5700.5701.5702.5703.5704.5705.5706.5707.5708.5709.5710.5711.5712.5713.5714.5715.5716.5717.5718.5719.5720.5721.5722.5723.5724.5725.5726.5727.5728.5729.5730.5731.5732.5733.5734.5735.5736.5737.5738.5739.5740.5741.5742.5743.5744.5745.5746.5747.5748.5749.5750.5751.5752.5753.5754.5755.5756.5757.5758.5759.5760.5761.5762.5763.5764.5765.5766.5767.5768.5769.5770.5771.5772.5773.5774.5775.5776.5777.5778.5779.5780.5781.5782.5783.5784.5785.5786.5787.5788.5789.5790.5791.5792.5793.5794.5795.5796.5797.5798.5799.5800.5801.5802.5803.5804.5805.5806.5807.5808.5809.5810.5811.5812.5813.5814.5815.5816.5817.5818.5819.5820.5821.5822.5823.5824.5825.5826.5827.5828.5829.5830.5831.5832.5833.5834.5835.5836.5837.5838.5839.5840.5841.5842.5843.5844.5845.5846.5847.5848.5849.5850.5851.5852.5853.5854.5855.5856.5857.5858.5859.5860.5861.5862.5863.5864.5865.5866.5867.5868.5869.5870.5871.5872.5873.5874.5875.5876.5877.5878.5879.5880.5881.5882.5883.5884.5885.5886.5887.5888.5889.5890.5891.5892.5893.5894.5895.5896.5897.5898.5899.5900.5901.5902.5903.5904.5905.5906.5907.5908.5909.5910.5911.5912.5913.5914.5915.5916.5917.5918.5919.5920.5921.5922.5923.5924.5925.5926.5927.5928.5929.5930.5931.5932.5933.5934.5935.5936.5937.5938.5939.5940.5941.5942.5943.5944.5945.5946.5947.5948.5949.5950.5951.5952.5953.5954.5955.5956.5957.5958.5959.5960.5961.5962.5963.5964.5965.5966.5967.5968.5969.5970.5971.5972.5973.5974.5975.5976.5977.5978.5979.5980.5981.5982.5983.5984.5985.5986.5987.5988.5989.5990.5991.5992.5993.5994.5995.5996.5997.5998.5999.6000.6001.6002.6003.6004.6005.6006.6007.6008.6009.6010.6011.6012.6013.6014.6015.6016.6017.6018.6019.6020.6021.6022.6023.6024.6025.6026.6027.6028.6029.6030.6031.6032.6033.6034.6035.6036.6037.6038.6039.6040.6041.6042.6043.6044.6045.6046.6047.6048.6049.6050.6051.6052.6053.6054.6055.6056.6057.6058.6059.6060.6061.6062.6063.6064.6065.6066.6067.6068.6069.6070.6071.6072.6073.6074.6075.6076.6077.6078.6079.6080.6081.6082.6083.6084.6085.6086.6087.6088.6089.6090.6091.6092.6093.6094.6095.6096.6097.6098.6099.6100.6101.6102.6103.6104.6105.6106.6107.6108.6109.6110.6111.6112.6113.6114.6115.6116.6117.6118.6119.6120.6121.6122.6123.6124.6125.6126.6127.6128.6129.6130.6131.6132.6133.6134.6135.6136.6137.6138.6139.6140.6141.6142.6143.6144.6145.6146.6147.6148.6149.6150.6151.6152.6153.6154.6155.6156.6157.6158.6159.6160.6161.6162.6163.6164.6165.6166.6167.6168.6169.6170.6171.6172.6173.6174.6175.6176.6177.6178.6179.6180.6181.6182.6183.6184.6185.6186.6187.6188.6189.6190.6191.6192.6193.6194.6195.6196.6197.6198.6199.6200.6201.6202.6203.6204.6205.6206.6207.6208.6209.6210.6211.6212.6213.6214.6215.6216.6217.6218.6219.6220.6221.6222.6223.6224.6225.6226.6227.6228.6229.6230.6231.6232.6233.6234.6235.6236.6237.6238.6239.6240.6241.6242.6243.6244.6245.6246.6247.6248.6249.6250.6251.6252.6253.6254.6255.6256.6257.6258.6259.6260.6261.6262.6263.6264.6265.6266.6267.6268.6269.6270.6271.6272.6273.6274.6275.6276.6277.6278.6279.6280.6281.6282.6283.6284.6285.6286.6287.6288.6289.6290.6291.6292.6293.6294.6295.6296.6297.6298.6299.6300.6301.6302.6303.6304.6305.6306.6307.6308.6309.6310.6311.6312.6313.6314.6315.6316.6317.6318.6319.6320.6321.6322.6323.6324.6325.6326.6327.6328.6329.6330.6331.6332.6333.6334.6335.6336.6337.6338.6339.6340.6341.6342.6343.6344.6345.6346.6347.6348.6349.6350.6351.6352.6353.6354.6355.6356.6357.6358.6359.6360.6361.6362.6363.6364.6365.6366.6367.6368.6369.6370.6371.6372.6373.6374.6375.6376.6377.6378.6379.6380.6381.6382.6383.6384.6385.6386.6387.6388.6389.6390.6391.6392.6393.6394.6395.6396.6397.6398.6399.6400.6401.6402.6403.6404.6405.6406.6407.6408.6409.6410.6411.6412.6413.6414.6415.6416.6417.6418.6419.6420.6421.6422.6423.6424.6425.6426.6427.6428.6429.6430.6431.6432.6433.6434.6435.6436.6437.6438.6439.6440.6441.6442.6443.6444.6445.6446.6447.6448.6449.6450.6451.6452.6453.6454.6455.6456.6457.6458.6459.6460.6461.6462.6463.6464.6465.6466.6467.6468.6469.6470.6471.6472.6473.6474.6475.6476.6477.6478.6479.6480.6481.6482.6483.6484.6485.6486.6487.6488.6489.6490.6491.6492.6493.6494.6495.6496.6497.6498.6499.6500.6501.6502.6503.6504.6505.6506.6507.6508.6509.6510.6511.6512.6513.6514.6515.6516.6517.6518.6519.6520.6521.6522.6523.6524.6525.6526.6527.6528.6529.6530.6531.6532.6533.6534.6535.6536.6537.6538.6539.6540.6541.6542.6543.6544.6545.6546.6547.6548.6549.6550.6551.6552.6553.6554.6555.6556.6557.6558.6559.6560.6561.6562.6563.6564.6565.6566.6567.6568.6569.6570.6571.6572.6573.6574.6575.6576.6577.6578.6579.6580.6581.6582.6583.6584.6585.6586.6587.6588.6589.6590.6591.6592.6593.6594.6595.6596.6597.6598.6599.6600.6601.6602.6603.6604.6605.6606.6607.6608.6609.6610.6611.6612.6613.6614.6615.6616.6617.6618.6619.6620.6621.6622.6623.6624.6625.6626.6627.6628.6629.6630.6631.6632.6633.6634.6635.6636.6637.6638.6639.6640.6641.6642.6643.6644.6645.6646.6647.6648.6649.6650.6651.6652.6653.6654.6655.6656.6657.6658.6659.6660.6661.6662.6663.6664.6665.6666.6667.6668.6669.6670.6671.6672.6673.6674.6675.6676.6677.6678.6679.6680.6681.6682.6683.6684.6685.6686.6687.6688.6689.6690.6691.6692.6693.6694.6695.6696.6697.6698.6699.6700.6701.6702.6703.6704.6705.6706.6707.6708.6709.6710.6711.6712.6713.6714.6715.6716.6717.6718.6719.6720.6721.6722.6723.6724.6725.6726.6727.6728.6729.6730.6731.6732.6733.6734.6735.6736.6737.6738.6739.6740.6741.6742.6743.6744.6745.6746.6747.6748.6749.6750.6751.6752.6753.6754.6755.6756.6757.6758.6759.6760.6761.6762.6763.6764.6765.6766.6767.6768.6769.6770.6771.6772.6773.6774.6775.6776.6777.6778.6779.6780.6781.6782.6783.6784.6785.6786.6787.6788.6789.6790.6791.6792.6793.6794.6795.6796.6797.6798.6799.6800.6801.6802.6803.6804.6805.6806.6807.6808.6809.6810.6811.6812.6813.6814.6815.6816.6817.6818.6819.6820.6821.6822.6823.6824.6825.6826.6827.6828.6829.6830.6831.6832.6833.6834.6835.6836.6837.6838.6839.6840.6841.6842.6843.6844.6845.6846.6847.6848.6849.6850.6851.6852.6853.6854.6855.6856.6857.6858.6859.6860.6861.6862.6863.6864.6865.6866.6867.6868.6869.6870.6871.6872.6873.6874.6875.6876.6877.6878.6879.6880.6881.6882.6883.6884.6885.6886.6887.6888.6889.6890.6891.6892.6893.6894.6895.6896.6897.6898.6899.6900.6901.6902.6903.6904.6905.6906.6907.6908.6909.6910.6911.6912.6913.6914.6915.6916.6917.6918.6919.6920.6921.6922.6923.6924.6925.6926.6927.6928.6929.6930.6931.6932.6933.6934.6935.6936.6937.6938.6939.6940.6941.6942.6943.6944.6945.6946.6947.6948.6949.6950.6951.6952.6953.6954.6955.6956.6957.6958.6959.6960.6961.6962.6963.6964.6965.6966.6967.6968.6969.6970.6971.6972.6973.6974.6975.6976.6977.6978.6979.6980.6981.6982.6983.6984.6985.6986.6987.6988.6989.6990.6991.6992.6993.6994.6995.6996.6997.6998.6999.7000.7001.7002.7003.7004.7005.7006.7007.7008.7009.7010.7011.7012.7013.7014.7015.7016.7017.7018.7019.7020.7021.7022.7023.7024.7025.7026.7027.7028.7029.7030.7031.7032.7033.7034.7035.7036.7037.7038.7039.7040.7041.7042.7043.7044.7045.7046.7047.7048.7049.7050.7051.7052.7053.7054.7055.7056.7057.7058.7059.7060.7061.7062.7063.7064.7065.7066.7067.7068.7069.7070.7071.7072.7073.7074.7075.7076.7077.7078.7079.7080.7081.7082.7083.7084.7085.7086.7087.7088.7089.7090.7091.7092.7093.7094.7095.7096.7097.7098.7099.7100.7101.7102.7103.7104.7105.7106.7107.7108.7109.7110.7111.7112.7113.7114.7115.7116.7117.7118.7119.7120.7121.7122.7123.7124.7125.7126.7127.7128.7129.7130.7131.7132.7133.7134.7135.7136.7137.7138.7139.7140.7141.7142.7143.7144.7145.7146.7147.7148.7149.7150.7151.7152.7153.7154.7155.7156.7157.7158.7159.7160.7161.7162.7163.7164.7165.7166.7167.7168.7169.7170.7171.7172.7173.7174.7175.7176.7177.7178.7179.7180.7181.7182.7183.7184.7185.7186.7187.7188.7189.7190.7191.7192.7193.7194.7195.7196.7197.7198.7199.7200.7201.7202.7203.7204.7205.7206.7207.7208.7209.7210.7211.7212.7213.7214.7215.7216.7217.7218.7219.7220.7221.7222.7223.7224.7225.7226.7227.7228.7229.7230.7231.7232.7233.7234.7235.7236.7237.7238.7239.7240.7241.7242.7243.7244.7245.7246.7247.7248.7249.7250.7251.7252.7253.7254.7255.7256.7257.7258.7259.7260.7261.7262.7263.7264.7265.7266.7267.7268.7269.7270.7271.7272.7273.7274.7275.7276.7277.7278.7279.7280.7281.7282.7283.7284.7285.7286.7287.7288.7289.7290.7291.7292.7293.7294.7295.7296.7297.7298.7299.7300.7301.7302.7303.7304.7305.7306.7307.7308.7309.7310.7311.7312.7313.7314.7315.7316.7317.7318.7319.7320.7321.7322.7323.7324.7325.7326.7327.7328.7329.7330.7331.7332.7333.7334.7335.7336.7337.7338.7339.7340.7341.7342.7343.7344.7345.7346.7347.7348.7349.7350.7351.7352.7353.7354.7355.7356.7357.7358.7359.7360.7361.7362.7363.7364.7365.7366.7367.7368.7369.7370.7371.7372.7373.7374.7375.7376.7377.7378.7379.7380.7381.7382.7383.7384.7385.7386.7387.7388.7389.7390.7391.7392.7393.7394.7395.7396.7397.7398.7399.7400.7401.7402.7403.7404.7405.7406.7407.7408.7409.7410.7411.7412.7413.7414.7415.7416.7417.7418.7419.7420.7421.7422.7423.7424.7425.7426.7427.7428.7

352.	AT1G13440.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		6644	770.3800	1336.7494	1338.7464	0	9	-1.5	0	1	K.VTIGSDSLVDVGV.V	
		1414	614.2797	1226.5448	1226.5439	-15.58	2	19	0.28	1	R.KKHRRGGGR.T	
		[Symbol]:   P:hm and associated interaction domain containing protein   chr1:11701985-11702903 FORWARD LENGTH=302										
353.	AT1G58180.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	385.2505	769.4864	768.4858	0.82	0	19	0.11	1	R.LGVVTVR.R	
		1414	618.2678	1224.5211	1224.5380	-12.10	1	7	3.2	2	R.LAKRGGRRAM.G	
		1414	929.8318	2786.4736	2786.4603	4.76	2	2	28	0	R.VVQGVVTVVTSSTSTLQNVF.A	
354.	AT1G18720.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	802.2788	1002.5451	1002.5570	-11.87	2	7	11	1	R.SELRRQR.S	
		1414	508.7610	1015.5075	1015.4943	13.0	1	19	0.43	1	R.HKCDLPPV.F	
		1414	680.8229	1359.6312	1359.6050	19.3	1	3	18	3	R.KNVTIRQVSEK.Y	
355.	AT1G41670.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	640.4132	1678.8097	1678.8348	-14.98	2	(7)	29	9	R.LAKRGGRRAM.G	
		1414	640.4132	1678.8097	1678.8348	-14.98	2	18	2.1	1	R.LAKRGGRRAM.G	
		[Symbol]:   Uipi protease family protein   chr5:18472301-18475574 FORWARD LENGTH=921										
356.	AT1G14330.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	387.8678	1160.5816	1160.5972	-13.40	1	(6)	14	3	R.MANKATADALA.A	
		1414	581.2983	1160.5819	1160.5972	-13.10	1	(9)	7.1	3	R.MANKATADALA.A	
		1414	589.3151	1176.6156	1176.5921	20.0	1	19	1.5	1	R.MANKATADALA.A	
357.	AT1G13120.1	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	573.7687	1145.5229	1145.5200	2.54	0	1	16	1	R.HPGKGTPLR.G	
		1414	717.8926	1433.7504	1433.7515	-0.60	0	19	0.9	1	R.VVYVQGVQGVVTVV.F	
		Proteins matching the same set of peptides: [Symbol]: JAL31   Jacalin-related lectin 31   chr3:5581830-5582959 FORWARD LENGTH=296										
358.	AT1G24510.2	Query	Observed	Mr(expect)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1414	476.7626	951.5107	951.5138	-3.21	0	18	0.45	1	R.VAVHELR.I	
		1414	1480.7386	4439.1940	4439.1360	13.1	2	4	50	5	R.DVVGQVLAIVLSEGV	



14601 875.0979 2622.2718 2622.3211 -18.80 1 1 51 4 U R.TPOVLTKIDGPGQPTGAVDLESH.G 14761 14784

348.	AT1G03410.1	Mass: 94740	Score: 17	Matches: 5(0)	Sequences: 5(0)	emPAI: 0.03
[ Symbol:   p-loop containing nucleoside triphosphate hydrolases superfamily protein   chr1:2790341-2794059 FORWARD LENGTH=500 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1461	484.7252	947.4358	947.4359	-0.10	0	17 5.49 1 U R.HDHGSRP.D
1462	359.8483	1076.5232	1076.5033	18.5	2	4 22 4 U K.RKSGKGRNR.F
1463	562.8251	1123.6355	1123.6284	6.35	1	2 11 5 U R.QICHVALER.D
1464	594.8336	1187.6506	1187.6371	11.1	2	9 6.7 10 U R.HHSGGELHAR.S
1465	631.8541	1261.6936	1261.6918	1.41	0	1 37 5 U K.SPLPVIDPRAVE.R
349.	AT1G07110.1	Mass: 28745	Score: 17	Matches: 8(0)	Sequences: 1(0)	emPAI: 0.12
[ Symbol:   Dinucleoside co-synthesizing enzyme family protein   chr1:1318812-1318835 REVERSE LENGTH=252 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1466	1294.045	2386.114	2386.125	-5.81	0	(6) 14 1 U R.LAGASRGLQGAMITTVSSAE.D
1467	801.7094	2402.1063	2402.1232	-7.06	0	(1) 40 3 U K.LAGASRGLQGAMITTVSSAE.D 14724
1468	1202.0625	2402.1104	2402.1232	-5.32	0	20 0.48 1 U K.LAGASRGLQGAMITTVSSAE.D
1469	1210.6607	2416.1306	2416.1181	-4.47	0	(17) 6.95 1 U K.LAGASRGLQGAMITTVSSAE.D 14651 14655 14658
370.	AT1G14850.1	Mass: 132549	Score: 17	Matches: 4(0)	Sequences: 3(0)	emPAI: 0.02
[ Symbol:   ATPDR1, TERT (telomerase reverse transcriptase [chr1:5533832-553444 REVERSE LENGTH=112] ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1470	396.5599	1186.6578	1186.6380	16.7	1	11 3.6 2 U K.SDHGLGLDH.N
1471	594.3373	1186.6401	1186.6380	18.7	1	(1) 40 9 U K.SDHGLGLDH.N
1472	1137.5001	2273.6896	2273.6973	-6.12	1	17 1.3 1 U R.KLVTTGGQVVFPAJCH.Y
1473	1298.5963	2595.1780	2595.2129	-13.44	1	2 56 2 U K.DIGLEKPFVLGGVTFHSDQFR.W
371.	AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)	emPAI: 0.12
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1474	670.3437	1338.6470	1338.6469	4.75	1	4 47 1 U R.DVPVAMQILANER.D
1475	1140.5370	2279.0594	2279.0535	2.61	0	17 1.1 1 U R.SQPGAMTDFILPDSYFE.R
1476	1308.6719	2615.3292	2615.3456	-6.23	1	1 45 1 U R.PDAGAMTDFILPDSYFE.R
Proteins matching the same set of peptides:						
AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)		
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)		
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)		
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)		
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
AT1G07100.1	Mass: 27829	Score: 17	Matches: 3(0)	Sequences: 3(0)		
[ Symbol:   APX1, MERS, CSI1, ATAPX1, ATAPX01   ascorbate peroxidase 1   chr1:2438005-2439435 FORWARD LENGTH=250 ]						
372.	AT1G09410.1	Mass: 17425	Score: 17	Matches: 12(0)	Sequences: 2(0)	emPAI: 0.19
[ Symbol:   ATELP5A-3, ELPSA-3   eukaryotic elongation factor 5A-3   chr1:26089301-2609104 FORWARD LENGTH=158 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1477	425.6975	1274.6707	1274.6731	-1.87	1	(5) 19 10 U K.TPFGQNIKE.G
1478	638.2438	1274.6731	1274.6731	-0.03	1	(3) 53 2 U K.TPFGQNIKE.G
1479	638.8360	1275.6574	1275.6574	0.26	1	21 0.45 1 U K.TPFGQNIKE.G 1484 1487 1491 1495 1498 1499 1502 1505 1508 1511
1480	705.3362	1212.9867	1212.9564	14.4	0	1 47 1 U K.DPVVYVMSGRPQCALE.R
373.	AT1G1310.1	Mass: 118788	Score: 17	Matches: 3(0)	Sequences: 3(0)	emPAI: 0.03
[ Symbol:   F180 PFYFED (F180 superfamily protein   chr1:1181810-1181843 FORWARD LENGTH=1048 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1481	382.2293	722.4440	722.4351	-15.46	1	17 0.12 1 U R.PPVPR.N
1482	393.7167	781.4149	781.4256	-11.60	2	20 0.00 1 U R.HSGHR.T
1483	638.3572	1274.6399	1274.6351	3.79	1	2 46 5 U K.LKLLGPHNR.R
374.	AT1G1410.1	Mass: 94742	Score: 16	Matches: 12(0)	Sequences: 3(0)	emPAI: 0.03
[ Symbol:   Laminin-rich repeat protein kinase family protein   chr1:1018179-1030440 REVERSE LENGTH=853 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1484	493.7955	985.5565	985.555	-0.01	0	20 0.39 3 U R.HHGLDYN.N 1473 1474 1475 1476 1477 1478 1480 1481 1484
1485	858.4601	2572.2986	2572.2842	5.57	0	0 58 5 U R.HHGLDYN.NSGTGLDITR.R
1486	931.7754	2792.3043	2792.2909	4.82	2	0 59 3 U K.HHGLDYN.NSGTGLDITR.R
375.	AT1G09210.1	Mass: 173642	Score: 16	Matches: 17(0)	Sequences: 6(0)	emPAI: 0.02
[ Symbol:   XIH, AXI18   Myosin family protein with b11 domain   chr4:14172280-14181771 FORWARD LENGTH=1516 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1487	401.2320	800.4695	800.4617	-15.17	1	6 23 2 U R.LAMTRR.K
1488	487.2680	1458.7622	1458.8055	-15.98	2	6 32 4 U K.KAATTCGAWRAR.L
1489	859.9108	1715.8470	1715.8478	-0.50	0	16 1.4 1 U K.DVYVAMQILANER.D 1492 1493 1494 1495 1496 1497
1490	872.9578	1715.8506	1715.8478	1.62	0	(13) 2.6 1 U K.DVYVAMQILANER.D 1492 1493 1494
1491	859.4211	1716.8276	1716.8118	-2.47	0	(13) 6 1 U K.DVYVAMQILANER.D 1492
1492	643.9044	1868.8643	1868.8678	-0.11	2	1 49 1 U R.PDGMALHGRNR.D
1493	1269.1877	2536.3008	2536.2890	4.68	2	8 11 1 U K.VATHSGAVGQSLPFLGR.R
1494	962.7081	3846.8033	3846.8035	-0.05	1	1 49 2 U R.LPHLTHGPGQVKGQPGLEPWFPAVDATR.Q
376.	AT1G04560.1	Mass: 119405	Score: 16	Matches: 17(0)	Sequences: 6(0)	emPAI: 0.03
[ Symbol:   Protein kinase superfamily protein   chr1:17084115-17092277 REVERSE LENGTH=1042 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1495	516.7830	1031.5515	1031.5433	7.87	5	5 18 5 U R.KCCAGLYK.W
1496	682.8633	1363.7121	1363.7320	-14.59	2	16 1.3 1 U R.KGPTVFWGRK.T 1498 1499
1497	1575.6937	1574.4654	1574.4610	0.24	0	(1) 15 2 U K.GPTFGVGRK.T
1498	788.3506	1574.4807	1574.7001	-8.50	0	6 13 1 U K.GPTFGVGRK.T 1498 1499 1500 1501 1502 1503
1499	1277.1010	2552.1874	2552.1835	0.77	1	0 55 1 U R.HHGLDYN.NSGTGLDITR.R
1500	1001.4744	3061.4014	3061.3948	1.18	1	1 53 2 U K.HHGLDYN.NSGTGLDITR.R
1501	1224.8481	3671.5225	3671.5816	-16.11	2	(0) 10 2 U K.HHGLDYN.NSGTGLDITR.R
1502	1230.1855	3687.5247	3687.5765	-11.35	2	2 6 1 U K.HHGLDYN.NSGTGLDITR.R 1498
1503	1230.1881	3687.5425	3687.5765	-9.23	2	(2) 7.5 4 U K.HHGLDYN.NSGTGLDITR.R
1504	1230.1892	3687.5458	3687.5765	-8.34	2	(2) 7.9 2 U K.HHGLDYN.NSGTGLDITR.R
Proteins matching the same set of peptides:						
AT1G04560.1	Mass: 119405	Score: 16	Matches: 17(0)	Sequences: 6(0)		
[ Symbol:   Protein kinase superfamily protein   chr1:17083814-17092277 REVERSE LENGTH=1067 ]						
377.	AT1G13170.1	Mass: 57913	Score: 16	Matches: 7(0)	Sequences: 6(0)	emPAI: 0.06
[ Symbol:   CYP94B   cytochrome P450, family 96, subfamily A, polypeptide 2   chr4:1553772-15539292 FORWARD LENGTH=506 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1505	596.3400	1190.6655	1190.6485	-15.95	0	7 6 1 U R.IIICLALGR.N
1506	920.8490	1839.8835	1839.8850	-0.62	0	5 18 1 U R.KGPTFGVGRK.T
1507	927.0155	1852.0564	1852.0426	7.41	1	5 6.1 1 U K.HHGLDYN.NSGTGLDITR.R
1508	1330.0696	2658.1246	2658.1400	-0.78	1	16 0.71 1 U K.HHGLDYN.NSGTGLDITR.R
1509	887.0509	2658.1309	2658.1400	-2.43	1	(1) 18 1 U K.HHGLDYN.NSGTGLDITR.R
1510	1213.9388	2658.7946	2658.7497	12.3	2	0 63 4 U R.HHGLDYN.NSGTGLDITR.R
1511	1595.2636	6389.0213	6388.9266	14.6	2	1 10 1 U R.HHGLDYN.NSGTGLDITR.R
378.	AT1G1920.1	Mass: 45521	Score: 16	Matches: 5(0)	Sequences: 4(0)	emPAI: 0.07
[ Symbol:   unknown protein: BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G04230.1): Has 217 Blast hits to 217 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukar ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1512	660.3108	1318.6070	1318.6049	1.58	1	6 23 2 U R.KYGFAMGRK.I
1513	840.4121	1678.8097	1678.8108	-12.59	1	7 25 8 U R.HHGLDYN.NSGTGLDITR.R
1514	798.0899	2391.2778	2391.2328	18.8	0	16 1 1 U R.HHGLDYN.NSGTGLDITR.R
1515	803.4085	2407.2035	2407.2278	-10.08	0	(3) 76 2 U R.HHGLDYN.NSGTGLDITR.R
1516	1072.1692	3213.4858	3213.5330	-14.70	2	0 52 6 U R.HHGLDYN.NSGTGLDITR.R
379.	AT2G00110.1	Mass: 23748	Score: 16	Matches: 2(0)	Sequences: 1(0)	emPAI: 0.14
[ Symbol:   AC17.1   Rhodopsin protein whose expression is responsive to nematode infection.   chr2:164014-165068 FORWARD LENGTH=215 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1517	761.4401	2280.1256	2280.1419	-7.18	2	16 1.9 1 U R.HHGLDYN.NSGTGLDITR.R
380.	AT1G02160.1	Mass: 65449	Score: 15	Matches: 20(0)	Sequences: 7(0)	emPAI: 0.05
[ Symbol:   MAP5-4   microtubule-associated protein 65-2   chr4:1347834-1348130 REVERSE LENGTH=578 ]						
Query	Observed	Mr(egpt)	Mr(calcd)	ppm	Mis	Score Expect Rank Unique Peptide
1518	497.7984	993.5923	993.5881	14.2	3	5.5 1 U R.HHGLDYN.NSGTGLDITR.R
1519	709.3582	1416.7019	1416.6779	16.9	1	3 62 2 U R.HHGLDYN.NSGTGLDITR.R
1520	628.3401	1881.9986	1881.9843	7.60	1	1 51 3 U K.KYGFAMGRK.I
1521	680.7600	2039.0961	2039.0994	13.1	2	(2) 22 2 U K.KYGFAMGRK.I 1523 1524
1522	681.3608	2040.0905	2040.0848	5.90	2	(1) 47 1 U K.KYGFAMGRK.I
1523	515.0244	2056.0686	2056.0484	9.85	2	4 24 1 U K.KYGFAMGRK.I
1524	911.7813	2673.3260	2673.3140	-0.73	2	16 1.7 1 U R.HHGLDYN.NSGTGLDITR.R 1518 1519 1521 1522 1524 1525
1525	1469.7047	2937.3948	2937.4104	-5.29	1	5 41 4 U K.KYGFAMGRK.I
1526	782.8836	3007.5054	3007.4695	11.9	2	4 23 1 U R.HHGLDYN.NSGTGLDITR.R
1527	1001.5104	3007.5094	3007.4695	13.2	2	(3) 29 2 U R.HHGLDYN.NSGTGLDITR.R
381.	AT1G19180.1	Mass: 20353	Score: 15	Matches: 73(0)	Sequences: 1(0)	emPAI: 0.17
[ Symbol:   Protein of unknown function (DUF1068)   chr2:13827849-13829135 FORWARD LENGTH=183 ]						

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1312

216,044

2370.114

2370.114

79

2

121

0

1

0

R.EYALLETRELKQGRRAARVF.V

1313

593,533

2370.114

2370.114

4.20

2

1

48

5

0

R.KYALLETRELKQGRRAARVF.V

1314

791,074

2370.1210

2370.1240

-2.09

2

16

1.6

1

0

R.KYALLETRELKQGRRAARVF.V

Proteins matching the same set of peptides:

AT0G1386.2

Mass: 13847

Score: 15

Matches: 73(0)

Sequences: 1(0)

[Symbol]: Protein of unknown function (DUF1048) | chr2:1382862-1382915 FORWARD LENGTH=121

382.

AT0G1386.2

Mass: 68219

Score: 15

Matches: 4(0)

Sequences: 3(0)

msPAI: 0.05

[Symbol]: unknown protein: Rat 2 blast hits to 1 proteins in 11 species: Archaea - 0; Bacteria - 0; Metazoa - 0; Pungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK). | chr2:17977619-1797846 FORWARD LENGTH=625

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1315

503,753

1005.4480

1005.5025

-14.44

1

3

24

9

0

R.AEGDQV.L

1316

523,2858

1044.5570

1044.5451

11.4

0

3

28

1

0

R.TQDAITSLR.Q

1317

745,3308

2232.9707

2232.9805

-4.38

1

(5)

8.1

1

0

R.NGDSSTRTVQPSQSEK.R

1318

1137,4938

2232.9710

2232.9805

-4.21

1

15

0.74

1

0

R.NGDSSTRTVQPSQSEK.R

383.

AT0G148730.1

Mass: 21266

Score: 15

Matches: 1(0)

Sequences: 1(0)

msPAI: 0.16

[Symbol]: unknown protein: Rat 1 blast hits to 1 proteins in 11 species: Archaea - 0; Bacteria - 0; Metazoa - 0; Pungi - 0; Plants - 1; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK). | chr1:18020337-18022277 REVERSE LENGTH=191

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1319

436,7032

871.3919

871.3745

19.9

0

15

0.34

1

0

R.SAARATK.A

384.

AT0G17480.1

Mass: 43283

Score: 15

Matches: 9(0)

Sequences: 4(0)

msPAI: 0.07

[Symbol]: IQG24 | IQ-domain 24 | chr5:2272028-2274031 FORWARD LENGTH=401

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1320

465,2433

928

928.4839

-12.76

1

3

12

4

0

R.GQAPAGR.L

1321

481,7525

961.4904

961.5015

-11.47

1

5

20

9

0

R.KQVATMLR.L

1322

603,7508

1005.4870

1005.5025

-15.47

0

0

7.79

5

0

R.QVATMLR.L

1323

860,3075

1118.5977

1118.5866

11.7

2

0

87

3

0

R.KQVATMLR.L

1324

804,3444

1406.7143

1406.7434

-18.16

2

15

1

1

0

R.QVATMLR.L

1325

1022,1271

2703.3584

2703.3454

6.37

2

4

31

3

0

R.SGLVYVTFVQPSQATRTSSQSSK.R

385.

AT0G18710.1

Mass: 44491

Score: 15

Matches: 2(0)

Sequences: 1(0)

msPAI: 0.07

[Symbol]: TRAP-like family protein | chr2:1417404-1419156 REVERSE LENGTH=420

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1326

882,4613

1762.9080

1762.9043

2.12

0

15

2.2

1

0

R.VTFISPPNPTVTK.L

1327

883,4554

1764.8967

1764.8723

13.8

0

(3)

60

1

0

R.VTFISPPNPTVTK.L

Proteins matching the same set of peptides:

AT0G18710.1

Mass: 44491

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr2:1417404-1419156 REVERSE LENGTH=420

AT0G18710.1

Mass: 33855

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr2:1417404-1418712 REVERSE LENGTH=298

AT0G18710.1

Mass: 33855

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr2:1417404-1418712 REVERSE LENGTH=298

AT0G18710.1

Mass: 33123

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr2:1417404-1419156 REVERSE LENGTH=369

AT0G18710.1

Mass: 44505

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr2:1417404-1419156 REVERSE LENGTH=411

AT0G18710.1

Mass: 39421

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr5:9208724-9210403 FORWARD LENGTH=350

AT0G18710.1

Mass: 36852

Score: 15

Matches: 2(0)

Sequences: 1(0)

[Symbol]: TRAP-like family protein | chr5:9208724-9210403 FORWARD LENGTH=327

386.

AT0G18960.1

Mass: 44804

Score: 15

Matches: 37(0)

Sequences: 3(0)

msPAI: 0.04

[Symbol]: transducin family protein / WD-40 repeat family protein | chr5:348890-3484127 REVERSE LENGTH=757

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1328

384,2005

765.3864

765.3861

0.14

0

8

1.6

0

R.LIKSLPR.L

1329

465,6483

1209.4760

1209.4829

-5.73

2

15

0.8

1

0

R.GSKAKALDPK.Q

1330

404,2327

1209.4762

1209.4829

-5.36

2

(15)

0.83

1

0

R.GSKAKALDPK.Q

1331

529,4327

1585.4164

1585.7852

17.8

1

12

1.4

1

0

R.NSLPGLVLAQK.F

Proteins matching the same set of peptides:

AT0G18960.1

Mass: 44444

Score: 15

Matches: 37(0)

Sequences: 3(0)

[Symbol]: transducin family protein / WD-40 repeat family protein | chr5:348890-3484127 REVERSE LENGTH=754

387.

AT0G190430.1

Mass: 47735

Score: 14

Matches: 4(0)

Sequences: 2(0)

msPAI: 0.07

[Symbol]: RPTSA, ATSEA.2 | regulatory particle triple-A ATase 5A | chr3:1603540-1605993 FORWARD LENGTH=424

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1332

407,3335

9715.5186

9715.5141

0.49

0

54

0.4

1

0

R.GTFYFVLVQPSKQLVLPVWKE.D

1333

1361,2481

2720.5216

2720.5001

7.93

0

(0)

12

2

0

R.GTFYFVLVQPSKQLVLPVWKE.D

1334

1444,7059

4325.0959

4325.0959

0.00

0

2

7

2

0

R.VYATGVQKPTHTDYGDLGSLGSLVVALVFWKE.E

1335

1443,7170

4326.1292

4326.1331

-0.90

2

(2)

82

1

0

R.VYATGVQKPTHTDYGDLGSLGSLVVALVFWKE.E

388.

AT0G19300.1

Mass: 118221

Score: 14

Matches: 7(0)

Sequences: 5(0)

msPAI: 0.03

[Symbol]: calcium-binding-like superfamily protein / WD-40 repeat family protein | chr4:1205541-1206028 FORWARD LENGTH=1015

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1336

561,8386

1125.24

1125.1859

-5.23

1

0

14

9

0

R.TVTPVSR.L

1337

402,2053

1203.5940

1203.6070

-10.76

1

2

40

3

0

R.FIANGKGR.V

1338

487,8460

1373.7175

1373.7415

-17.48

2

2

39

3

0

R.AQKQVPIKKK.H

1339

561,4441

1585.4164

1585.7852

18.41

0

2

58

1

0

R.NAMLVYGVFFPIRSHGSLVWKE.L

1340

1084,3042

3416.4844

3416.5817

-17.93

2

14

1.3

1

0

R.TILTYTFYFPIRSHAMLVGVGVFFPIRSHGSLVWKEQK.W

1341

1087,5352

3416.4886

3416.5746

-14.02

2

(7)

7.3

1

0

R.TILTYTFYFPIRSHAMLVGVGVFFPIRSHGSLVWKEQK.W

1342

1346,4449

5462.5005

5462.5885

-8.78

2

(3)

15

6

0

R.TILTYTFYFPIRSHAMLVGVGVFFPIRSHGSLVWKEQK.W

389.

AT0G11420.1

Mass: 39900

Score: 14

Matches: 11(0)

Sequences: 2(0)

msPAI: 0.08

[Symbol]: protein of unknown function, DUF42 | chr1:364455-364493 FORWARD LENGTH=366

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1343

614,3514

1226.6883

1226.6493

15.5

0

1

22

3

0

R.QGKELVVPKQ.F

1344

761,3414

2227.0036

2226.9974

34.3

1

(2)

43

1

0

R.QGKELVVPKQ.F

1345

1122,0042

2241.9938

2241.9783

6.94

1

14

1.6

1

0

R.QGKELVVPKQ.F

1346

1122,5040

2242.9934

2242.9623

13.9

1

(0)

65

6

0

R.QGKELVVPKQ.F

Proteins matching the same set of peptides:

AT0G11420.1

Mass: 40181

Score: 14

Matches: 11(0)

Sequences: 2(0)

[Symbol]: protein of unknown function, DUF42 | chr5:5865310-5865394 FORWARD LENGTH=369

390.

AT0G14810.1

Mass: 89001

Score: 15

Matches: 4(0)

Sequences: 4(0)

msPAI: 0.04

[Symbol]: TMAD, TMAD.1 | thalidomide synthase 1 | chr1:1947001-1948158 FORWARD LENGTH=766

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1347

895,3884

1474.7628

1474.7479

0.19

0

13

2.2

1

0

R.AKMLKAKDEK.S

1348

1329,6222

2857.2298

2857.1870

16.1

0

3

60

3

0

R.GSHTPVQVQALGVLPVWKE.D

1349

976,7785

2897.1359

2897.1305

-8.48

0

2

24

5

0

R.AAGVLPVQVQALGVLPVWKE.D

1350

1461,7687

5042.4709

5042.4252

9.07

1

3

11

1

0

R.NAMLVYGVFFPIRSHGSLVVALVFWKE.E

391.

AT0G148730.1

Mass: 148003

Score: 13

Matches: 6(0)

Sequences: 6(0)

msPAI: 0.02

[Symbol]: PABP1L, KENB1B-12B | polyomavirus-associated kinase-related protein, putative | chr3:8519290-8520555 FORWARD LENGTH=1313

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1351

425,7467

849.5189

849.5184

0.57

0

13

0.37

1

0

R.HKQKAR.D

1352

437,7341

871.4516

871.4668

-15.07

1

17

1.2

2

0

R.AKQKAR.D

1353

709,3588

1416.7030

1416.7118

-6.21

1

3

30

9

0

R.KFPPFPAKIL.D

1354

963,9781

1505.4657

1505.4676

-11.40

1

4

27

1

0

R.HKQKAR.D

1355

1126,9907

2251.9468

2251.9442

10.1

1

1

20

1

0

R.HKQKAR.D

1356

1250,9304

3749.7494

3749.7214

12.8

1

4

23

4

0

R.AKQKAR.D

392.

AT0G13720.1

Mass: 13249

Score: 13

Matches: 4(0)

Sequences: 3(0)

msPAI: 0.26

[Symbol]: HTAF | histone H2A 9 | chr4:7885116-7885644 FORWARD LENGTH=118

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1357

425,7467

849.5189

849.5184

0.57

0

13

0.37

1

0

R.HKQKAR.D

1358

489,2476

1464.7810

1464.7972

16.2

1

(1)

34

2

0

R.VYATGVQVQALGVLPVWKE.D

1359

1329,6222

2857.2298

2857.1870

16.1

0

3

60

3

0

R.GSHTPVQVQALGVLPVWKE.D

1360

976,7785

2897.1359

2897.1305

-8.48

0

2

24

5

0

R.AAGVLPVQVQALGVLPVWKE.D

393.

AT0G13720.1

Mass: 14263

Score: 13

Matches: 3(0)

Sequences: 3(0)

msPAI: 0.24

[Symbol]: HTAF | histone H2A protein 9 | chr1:1948409-1948421 FORWARD LENGTH=14

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1361

425,7467

849.5189

849.5184

0.57

0

13

0.37

1

0

R.HKQKAR.D

1362

472,7692

943.5238

943.5240

-0.11

0

1

40

2

0

R.AKQKAR.D

1363

846,0098

1890.0050

1890.0155

-6.20

2

2

6.5

1

0

R.AKQKAR.D

394.

AT0G13720.1

Mass: 69939

Score: 13

Matches: 2(0)

Sequences: 2(0)

msPAI: 0.05

[Symbol]: emb745 | embryo defective 745 | chr1:4483334-4472775 REVERSE LENGTH=611

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1364

425,7467

849.5189

849.5184

0.57

0

13

0.37

1

0

R.HKQKAR.D

1365

745,8904

1489.7653

1489.7558

7.06

2

2

40

8

0

R.HKQKAR.D

395.

AT0G13720.1

Mass: 14361

Score: 13

Matches: 2(0)

Sequences: 2(0)

msPAI: 0.24

[Symbol]: HTAF | histone H2A 9 | chr1:1631944-1632079 REVERSE LENGTH=116

Query

Observed

Mr(expect)

Mr(calcd)

ppm

Misa

Score

Expect

Rank

Unique

Peptide

1366

425,7467

849.5189

849.5184

0.57

0

13

0.37

1

0

R.HKQKAR.D

1367

472,7692

943.5238

943.5240

-0.11

0

1

40

2

0

R.AKQKAR.D

[ Symbol: HTAS | histone H2A 8 | chr2:16219444-16220679 REVERSE LENGTH=136  
[ATGAGAGGAA](#) Mass: 14361 Score: 13 Matches: 2(0) Sequence: 2(0)  
[ Symbol: HTAS | histone H2A 8 | chr2:16219444-16220679 REVERSE LENGTH=136  
[ATGAGAGGAA](#) Mass: 14332 Score: 13 Matches: 2(0) Sequence: 2(0)  
[ Symbol: HTAL1 | histone H2A 11 | chr3:22196532-22197466 FORWARD LENGTH=136

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