
2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00546577 | AT3G05560.1;AT3G05560.2; | 60S ribosomal protein L22-2'

p2: IPI00540594 | AT5G27770.1; | 60S ribosomal protein L22-3'

s1: YFNIAENEGEEED, r1: 0.58

s2: YFNIAENEAEED, r2: 0.92

s3: NLYELR, r3: 0.73

QB1: 57.38, QA1: 33.50, R1: 0.58

QB2: 42.62, QA2: 39.26, R2: 0.92

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 6 peptides

cc =

p1	s1
p1	s3
p1	s4
p2	s2
p2	s3
p2	s4
p2	s6
p3	s3
p3	s5
p3	s6

p1: IPI00519609 | AT3G01290.1; | Band 7 family protein'

p2: IPI00546529 | AT5G62740.1; | Band 7 family protein'

p3: IPI00528838 | AT1G69840.1;AT1G69840.2;AT1G69840.3;AT1G69840.4; | Band 7 family protein'

s1: NGLLQANNAS, r1: 0.64
s2: DGLLQGSSANL, r2: 0.58
s3: QAIVDGLR, r3: 0.79
s4: AMNEINAAAR, r4: 0.83
s5: NSVLAFSESVPGTSSK, r5: 2.58
s6: EIGASSK, r6: 1.57

QB1: 84.47, QA1: 54.39, R1: 0.64
QB2: 7.82, QA2: 4.50, R2: 0.58
QB3: 7.71, QA3: 19.86, R3: 2.58

Objective: 21.55
LRD (Distance in peptide log ratios): 0.04

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00542239 | AT3G55610.1; | Delta 1-pyrroline-5-carboxylate synthetase B'
p2: IPI00529620 | AT2G39800.1;AT2G39800.2; | Delta 1-pyrroline-5-carboxylate synthetase A'
s1: TEAVENGI, r1: 0.81
s2: VIPIFNENDAISTR, r2: 1.32
s3: LDDVIDLVIPR, r3: 0.78

QB1: 100.00, QA1: 78.45, R1: 0.78
QB2: 0.00, QA2: 0.00, R2: NaN

Objective: 2.55
LRD (Distance in peptide log ratios): 0.10

4 proteins, 9 peptides

cc =

p1	s1
p1	s3
p1	s4
p1	s6
p1	s9
p2	s1
p2	s3
p2	s5
p2	s8
p3	s2
p3	s3
p3	s6
p3	s7
p3	s8
p3	s9
p4	s6
p4	s7

p1: IPI00522131 | AT3G14940.1; | Phosphoenolpyruvate carboxylase 3'
p2: IPI00541694 | AT1G53310.1;AT1G53310.2;AT1G53310.3; | Phosphoenolpyruvate carboxylase 1'
p3: IPI00530401 | AT2G42600.1;AT2G42600.2; | Phosphoenolpyruvate carboxylase 2'
p4: IPI00542747 | AT3G42628.1; | Phosphoenolpyruvate carboxylase-related'
s1: GIAAGLQNTG, r1: 0.71
s2: LLQLNK, r2: 1.40
s3: TPPTPQDEMR, r3: 0.90
s4: NIGIDER, r4: 0.57
s5: SIPTTEPYR, r5: 0.53
s6: MASIDAQLR, r6: 0.48
s7: LIEYDALLLDR, r7: 1.79
s8: QEWLLSELGK, r8: 0.96
s9: RPLFGPDLPK, r9: 0.70

QB1: 46.15, QA1: 26.38, R1: 0.57
QB2: 50.63, QA2: 42.68, R2: 0.84
QB3: 0.00, QA3: 5.76, R3: Inf
QB4: 3.21, QA4: 0.00, R4: 0.00

Objective: 66.34
LRD (Distance in peptide log ratios): 0.51

3 proteins, 5 peptides

cc =

p1	s1
p1	s4
p1	s5
p2	s2
p2	s5
p3	s3
p3	s4
p3	s5

p1: IPI00518050 | AT2G43090.1; | Aconitase C-terminal domain-containing protein'
p2: IPI00545682 | AT3G58990.1; | Aconitase C-terminal domain-containing protein'
p3: IPI00521882 | AT2G43100.1; | Aconitase C-terminal domain-containing protein'
s1: AGMIPSAAA, r1: 0.67
s2: DNIDTDQIIPAEYGTLPISIPEDR, r2: 1.86
s3: NSVATGEVFPLESEVR, r3: 0.27
s4: YSIIIGGENFGCGSSR, r4: 0.73
s5: EHAPVCLGAAGAK, r5: 1.07

QB1: 66.58, QA1: 44.72, R1: 0.67
QB2: 33.41, QA2: 61.99, R2: 1.86
QB3: 0.00, QA3: 0.00, R3: NaN

Objective: 5.74
LRD (Distance in peptide log ratios): 0.28

2 proteins, 3 peptides

cc =

p1	s1
p1	s3

p2 s2
p2 s3

p1: IPI00549147 | AT3G25860.1; | Dihydrolipoamide S-acetyltransferase (LTA2)'
p2: IPI00540464 | AT1G34430.1; | F12K21.24'
s1: IIENPDSLTL, r1: 0.96
s2: APPASPPTAAVEAPVSVEK, r2: 1.49
s3: GVTMTALLAK, r3: 1.29

QB1: 37.74, QA1: 36.32, R1: 0.96
QB2: 62.26, QA2: 92.69, R2: 1.49

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides
cc =

p1 s1
p1 s3
p2 s2
p2 s3

p1: IPI00540256 | AT2G19760.1; | Profilin-1'
p2: IPI00526887 | AT4G29350.1; | Profilin-2'
s1: LGDYLIESEL, r1: 0.87
s2: LGDYLIESGL, r2: 0.54
s3: GPGGVTIK, r3: 0.83

QB1: 86.80, QA1: 75.53, R1: 0.87
QB2: 13.20, QA2: 7.07, R2: 0.54

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00521979 | AT5G58440.1; | Phox (PX) domain-containing protein'

p2: IPI00546538 | AT5G07120.1; | Phox (PX) domain-containing protein'

s1: ANDMKNLATAAVK, r1: 2.69

s2: TNLSDYGGSEFSVR, r2: 0.88

s3: ELNSQTVK, r3: 1.07

QB1: 10.36, QA1: 27.92, R1: 2.69

QB2: 89.64, QA2: 78.89, R2: 0.88

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 6 peptides

cc =

p1	s1
p1	s4
p1	s5
p1	s6
p2	s2
p2	s5
p2	s6
p3	s3
p3	s4
p3	s6

p1: IPI00540817 | AT5G57110.1;AT5G57110.2; | Calcium-transporting ATPase 8, plasma membrane-type'

p2: IPI00520370 | AT4G29900.1; | Putative calcium-transporting ATPase 10, plasma membrane-type'

p3: IPI00548670 | AT3G21180.1; | Calcium-transporting ATPase'

s1: NSSGEGSL, r1: 3.39

s2: SESGEIQVSGSPTER, r2: 0.95
s3: MVTGDNLQTAK, r3: 0.61
s4: QSLQFQNLNDEK, r4: 2.85
s5: YTLDLK, r5: 1.86
s6: SVYANIQK, r6: 1.94

QB1: 34.27, QA1: 116.05, R1: 3.39
QB2: 57.51, QA2: 54.84, R2: 0.95
QB3: 8.22, QA3: 5.05, R3: 0.61

Objective: 18.19
LRD (Distance in peptide log ratios): 0.02

4 proteins, 9 peptides

cc =

p1	s1
p1	s5
p1	s7
p1	s9
p2	s2
p2	s4
p2	s5
p2	s6
p3	s2
p3	s4
p3	s5
p3	s7
p3	s8
p4	s3
p4	s4
p4	s5
p4	s6
p4	s9

p1: IPI00538665 | AT1G79550.1;AT1G79550.2; | Phosphoglycerate kinase'

p2: IPI00530695 | AT1G56190.1; | Phosphoglycerate kinase, chloroplast precursor'
p3: IPI00534991 | AT1G56190.1; | Phosphoglycerate kinase'
p4: IPI00535490 | AT3G12780.1; | Phosphoglycerate kinase'
s1: VDLNVPLDDNSNITDDTR, r1: 1.61
s2: ADLNVPLDDNQNITDDTR, r2: 0.77
s3: ADLNVPLDDNQITDDTR, r3: 1.56
s4: FSLAPLVPR, r4: 1.23
s5: GVTTIIGGGDSVAAVEK, r5: 1.33
s6: GVSLLLPTDVVVADK, r6: 1.34
s7: GVSLLLPTDVVIADK, r7: 0.98
s8: GTEAVANK, r8: 0.96
s9: NDPEFAK, r9: 1.25

QB1: 0.61, QA1: 0.98, R1: 1.61
QB2: 11.79, QA2: 3.45, R2: 0.29
QB3: 29.91, QA3: 28.81, R3: 0.96
QB4: 57.70, QA4: 89.89, R4: 1.56

Objective: 27.50
LRD (Distance in peptide log ratios): 0.03

4 proteins, 8 peptides

cc =

p1	s1
p1	s7
p2	s2
p2	s4
p2	s6
p2	s7
p2	s8
p3	s3
p3	s6
p3	s8
p4	s4
p4	s5
p4	s6

p4 s7

p1: IPI00518654 | AT4G31570.1; | Expressed protein'
p2: IPI00516481 | AT1G64190.1; | 6-phosphogluconate dehydrogenase family protein'
p3: IPI00519564 | AT3G02360.1;AT3G02360.2; | 6-phosphogluconate dehydrogenase family protein'
p4: IPI00545955 | AT5G41670.1;AT5G41670.2; | 6-phosphogluconate dehydrogenase family protein'
s1: EDVQTGTSSDDL, r1: 1.46
s2: AAVEGNLPVSGQYSPR, r2: 0.69
s3: WTVQQAAELSVPAPTIESSLDAR, r3: 0.11
s4: VDETLDR, r4: 0.82
s5: LPVAGQYSPR, r5: 0.81
s6: LPANLVQAQR, r6: 1.02
s7: DILEK, r7: 0.88
s8: IGLAGLAVMGQNLALNIAEKGFPISVYNR, r8: 1.32

QB1: 9.55, QA1: 13.93, R1: 1.46
QB2: 0.00, QA2: 0.00, R2: NaN
QB3: 0.00, QA3: 0.00, R3: NaN
QB4: 90.45, QA4: 74.08, R4: 0.82

Objective: 19.86
LRD (Distance in peptide log ratios): 0.39

2 proteins, 3 peptides
cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00549121 | AT3G55440.1; | Triosephosphate isomerase, cytosolic'
p2: IPI00524641 | AT2G21170.1; | Triosephosphate isomerase, chloroplast precursor'
s1: NVSADVAATTR, r1: 0.89
s2: GPEFATIVNSVTSK, r2: 1.40
s3: FFVGGNWK, r3: 0.94

QB1: 89.77, QA1: 79.49, R1: 0.89
QB2: 10.23, QA2: 14.33, R2: 1.40

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00522866 | AT1G70410.1;AT1G70410.2;AT1G70410.3; | Carbonic anhydrase'
p2: IPI00524264 | AT1G23730.1; | Carbonic anhydrase'
s1: ELDSSNSDAIER, r1: 0.46
s2: GLMAIEDNTAPTK, r2: 0.84
s3: GTFDLWELDFK, r3: 0.70

QB1: 35.11, QA1: 15.98, R1: 0.46
QB2: 64.89, QA2: 54.21, R2: 0.84

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00538993 | AT2G17200.1; | Ubiquitin family protein'
p2: IPI00531268 | AT2G17190.1; | Ubiquitin family protein'

s1: ELVAQSSDVPANQQR, r1: 0.96
s2: ELIAQNSDVPANQQR, r2: 0.61
s3: ALLATNGNVNAAVER, r3: 0.96

QB1: 99.72, QA1: 95.77, R1: 0.96
QB2: 0.28, QA2: 0.17, R2: 0.61

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

3 proteins, 5 peptides

cc =

p1	s1
p1	s4
p2	s2
p2	s5
p3	s3
p3	s4
p3	s5

p1: IPI00536631 | AT5G65770.1; | Putative nuclear matrix constituent protein 1-like protein'
p2: IPI00524495 | AT4G12590.1; | Expressed protein'
p3: IPI00517532 | IPI00517532 | Putative non-LTR retroelement reverse transcriptase'
s1: VTTLDCSESPSEAGR, r1: 0.80
s2: GLFSLILGDENAIDDTQR, r2: 1.23
s3: ADALAK, r3: 0.79
s4: IQSLK, r4: 1.20
s5: SLGAEK, r5: 1.51

QB1: 41.04, QA1: 32.92, R1: 0.80
QB2: 58.96, QA2: 72.71, R2: 1.23
QB3: 0.00, QA3: 16.39, R3: Inf

Objective: 20.68
LRD (Distance in peptide log ratios): 1.07

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00542856 | AT3G16480.1; | Probable mitochondrial processing peptidase alpha subunit 2, mitochondrial precursor'

p2: IPI00546705 | AT1G51980.1; | Probable mitochondrial processing peptidase alpha subunit 1, mitochondrial precursor'

s1: EIEAIGGNTSASASR, r1: 1.13

s2: SAVLMNLESR, r2: 0.75

s3: TVDQLTLK, r3: 1.15

QB1: 95.62, QA1: 109.74, R1: 1.15

QB2: 4.38, QA2: 3.30, R2: 0.75

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 5 peptides

cc =

p1	s1
p1	s5
p2	s2
p2	s3
p2	s5
p3	s2
p3	s4

p1: IPI00543676 | " PWWP domain-containing protein, hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606" | PWWP domain-containing protein, hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606'

p2: IPI00519778 | AT3G52990.1; | Pyruvate kinase'
p3: IPI00523591 | AT2G36580.1; | Pyruvate kinase'
s1: SLSVSSSDATVENAR, r1: 1.56
s2: GLYPVETISTVGR, r2: 0.86
s3: ADGLVTLTPNQDQEASSEVLPINFNGLAK, r3: 0.53
s4: ADGLVTLTPSQDQEASSEVLPINFNFDGLAK, r4: 1.11
s5: TNQLK, r5: 1.31

QB1: 58.23, QA1: 91.00, R1: 1.56
QB2: 18.35, QA2: 9.68, R2: 0.53
QB3: 23.43, QA3: 26.06, R3: 1.11

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00520435 | AT5G27120.1; | SAR DNA-binding protein'
p2: IPI00543036 | AT3G05060.1; | SAR DNA-binding protein'
s1: CDALGDSQDNTMGVENR, r1: 0.46
s2: VDALGDSQDNTMGLENR, r2: 0.87
s3: MNTIAPNLTALVGELVGAR, r3: 0.53

QB1: 83.58, QA1: 38.86, R1: 0.46
QB2: 16.42, QA2: 14.35, R2: 0.87

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00522647 | AT1G65590.1; | Glycosyl hydrolase family 20 protein'

p2: IPI00538209 | AT3G55260.1; | Beta-N-acetylhexosaminidase-like protein'

s1: GVAAAPLVGGGR, r1: 0.48

s2: GLLIDTSR, r2: 0.95

s3: GVPAAPVDNFYAR, r3: 1.57

QB1: 57.01, QA1: 27.40, R1: 0.48

QB2: 42.99, QA2: 67.67, R2: 1.57

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 7 peptides

cc =

p1	s1
p1	s4
p1	s5
p1	s6
p2	s2
p2	s4
p2	s5
p2	s7
p3	s3
p3	s4
p3	s6
p3	s7

p1: IPI00533300 | AT1G02780.1; | 60S ribosomal protein L19-1'

p2: IPI00538939 | AT3G16780.1; | 60S ribosomal protein L19-2'

p3: IPI00542800 | AT4G02230.1; | 60S ribosomal protein L19-3'
s1: GPGGDVAPVAAPAPAATPAPTAAVVK, r1: 0.44
s2: LAQGPGGGETTTTPAGAPQQPEVTK, r2: 0.62
s3: VWLDPNEGSDISMANSR, r3: 0.85
s4: DGFIIIR, r4: 1.02
s5: LAASVMK, r5: 1.15
s6: TLSDQFEAK, r6: 1.25
s7: HMYHDMYMK, r7: 0.76

QB1: 0.00, QA1: 22.41, R1: Inf
QB2: 42.24, QA2: 26.17, R2: 0.62
QB3: 57.76, QA3: 49.76, R3: 0.86

Objective: 55.02
LRD (Distance in peptide log ratios): 0.90

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00522739 | AT5G16450.1;AT5G16450.2; | Regulator of ribonuclease-like protein 2'
p2: IPI00542180 | AT3G02770.1; | Regulator of ribonuclease-like protein 1'
s1: DVDEINGCDIGVR, r1: 0.97
s2: ALQPVFQIYGR, r2: 0.80
s3: ALQPIFQIYGR, r3: 1.28

QB1: 35.34, QA1: 45.24, R1: 1.28
QB2: 64.66, QA2: 51.80, R2: 0.80

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00519575 | AT1G74910.1;AT1G74910.2;AT1G74910.3; | ADP-glucose pyrophosphorylase family protein'

p2: IPI00524585 | AT2G04650.1; | ADP-glucose pyrophosphorylase family protein'

s1: LTSPQLLASGDGTR, r1: 1.17

s2: LDQDILSPLAGK, r2: 1.10

s3: QLYTYENK, r3: 0.60

QB1: 88.07, QA1: 103.16, R1: 1.17

QB2: 11.93, QA2: 7.17, R2: 0.60

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00532313 | AT1G19870.1; | F6F9.8 protein'

p2: IPI00530126 | AT3G18190.1; | Chaperonin'

s1: VEPEESESDDVIIIVR, r1: 1.45

s2: TDIEQSIVVSDYTQMDR, r2: 0.87

s3: VENAK, r3: 1.14

QB1: 47.42, QA1: 68.56, R1: 1.45

QB2: 52.58, QA2: 45.53, R2: 0.87

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00531081 | AT1G09780.1; | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1'

p2: IPI00520882 | AT3G08590.1;AT3G08590.2; | Probable 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 2'

s1: YLVSPPEIDR, r1: 0.52

s2: GVDAQVASGGGR, r2: 1.32

s3: LEEYVEIPSDSGISFNVQPK, r3: 0.95

QB1: 45.94, QA1: 23.79, R1: 0.52

QB2: 54.06, QA2: 71.14, R2: 1.32

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00520520 | AT2G38700.1; | Mevalonate diphosphate decarboxylase (MVD1)'

p2: IPI00521560 | AT3G54250.1; | Mevalonate diphosphate decarboxylase'

s1: LMNVNEDPSQLSAIAR, r1: 0.57
s2: ETSSTSGMR, r2: 0.72
s3: EDGSDSVAVQLADEK, r3: 1.20

QB1: 76.14, QA1: 43.62, R1: 0.57
QB2: 23.86, QA2: 28.55, R2: 1.20

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00533390 | AT2G41220.1; | Ferredoxin-dependent glutamate synthase 2, chloroplast precursor'
p2: IPI00539225 | AT5G04140.1;AT5G04140.2; | Splice Isoform Long of Ferredoxin-dependent glutamate
synthase 1, chloroplast precursor'
s1: FAQVTNPAIDPLR, r1: 0.68
s2: ASDSANLDSAAELLIR, r2: 0.62
s3: AVNAGLLK, r3: 1.29

QB1: 91.78, QA1: 57.02, R1: 0.62
QB2: 8.22, QA2: 10.63, R2: 1.29

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1 s1
p1 s2
p2 s1
p2 s3

p1: IPI00524653 | AT1G23310.1;AT1G23310.2; | Glutamate:glyoxylate aminotransferase 1 (GGT1)'
p2: IPI00539634 | AT1G70580.1;AT1G70580.2;AT1G70580.3;AT1G70580.4; | Glutamate:glyoxylate
aminotransferase 2 (GGT2)'
s1: AMVIINPGNPTGQCLSEANIR, r1: 0.92
s2: LPTGALQAAK, r2: 1.86
s3: VLMDMGAPISK, r3: 0.77

QB1: 13.71, QA1: 25.49, R1: 1.86
QB2: 86.29, QA2: 66.39, R2: 0.77

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides
cc =

p1 s1
p1 s3
p2 s2
p2 s3

p1: IPI00543912 | AT4G34670.1; | 40S ribosomal protein S3a'
p2: IPI00520872 | AT3G04840.1; | 40S ribosomal protein S3A (RPS3aA)'
s1: VDRPADETMVEEPTTEIIGA, r1: 2.69
s2: VDRPADEMAVEEPTTEIIGA, r2: 1.56
s3: FIPEAIGR, r3: 0.99

QB1: 0.00, QA1: 0.00, R1: NaN
QB2: 100.00, QA2: 99.23, R2: 0.99

Objective: 56.75
LRD (Distance in peptide log ratios): 0.48

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00528096 | AT2G27720.1; | 60S acidic ribosomal protein P2-B'

p2: IPI00537053 | AT2G27710.1;AT2G27710.2;AT2G27710.3; | 60S acidic ribosomal protein P2-A'

s1: DLAEILIAAGR, r1: 0.93

s2: LASVPSGGGGVAVASATSGGGGGGASAAESK, r2: 0.46

s3: LASVPSGGGGVAVASATSGGGGGGAPAAESK, r3: 1.90

QB1: 32.58, QA1: 61.87, R1: 1.90

QB2: 67.42, QA2: 31.15, R2: 0.46

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00528468 | AT3G28715.1; | Probable vacuolar ATP synthase subunit d 2'

p2: IPI00535838 | AT3G28710.1; | Probable vacuolar ATP synthase subunit d 1'

s1: AVNITINSIGTELTR, r1: 0.81

s2: AYLEDFYK, r2: 0.86

s3: AYLEDFYNFCQK, r3: 0.50

QB1: 14.61, QA1: 7.36, R1: 0.50

QB2: 85.39, QA2: 73.55, R2: 0.86

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00541299 | AT2G45030.1; | Mitochondrial elongation factor'

p2: IPI00549153 | AT1G45332.1; | Probable elongation factor G, mitochondrial precursor'

s1: FLNDEPVSAAELEEAIR, r1: 0.77

s2: VTLTGSPDGPLVALAFK, r2: 1.41

s3: ATIAQTFVFPVFMGSAFK, r3: 1.87

QB1: 42.14, QA1: 32.60, R1: 0.77

QB2: 57.86, QA2: 107.92, R2: 1.87

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00540360 | AT2G25970.1; | KH domain-containing protein'

p2: IPI00531611 | AT4G34030.1; | Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor'

s1: AEQLITDVLQEAEAGNTAGSGGGGGR, r1: 2.41

s2: AQEIAAR, r2: 1.00

s3: GGTYYPITIK, r3: 0.81

QB1: 11.42, QA1: 27.52, R1: 2.41

QB2: 88.58, QA2: 72.11, R2: 0.81

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1 s1

p1 s2

p2 s2

p2 s3

p1: IPI00547943 | AT1G01960.1; | Guanine nucleotide exchange family protein'

p2: IPI00544005 | AT3G60860.1; | Guanine nucleotide exchange family protein'

s1: QDVDPSEDDSTDQR, r1: 0.51

s2: TLIGDYLGER, r2: 0.89

s3: LAEGDLNSPSTNK, r3: 1.07

QB1: 33.23, QA1: 17.09, R1: 0.51

QB2: 66.77, QA2: 71.50, R2: 1.07

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1 s1

p1 s2

p2 s2
p2 s3

p1: IPI00522047 | AT5G47910.1; | Respiratory burst oxidase protein D (RbohD) '
p2: IPI00522565 | AT5G51060.1; | Respiratory burst oxidase protein C (RbohC) '
s1: GANSDTNSDTEIASDR, r1: 4.29
s2: VLIDGPYGAPAQDYK, r2: 1.52
s3: LTSVSGGIGGR, r3: 0.74

QB1: 22.04, QA1: 94.61, R1: 4.29
QB2: 77.97, QA2: 57.87, R2: 0.74

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides
cc =

p1 s1
p1 s2
p2 s2
p2 s3

p1: IPI00518294 | AT4G17330.1; | Agenet domain-containing protein '
p2: IPI00540433 | IPI00540433 | Hypothetical protein dl4700c '
s1: NTTASDMESDESAENR, r1: 1.58
s2: SSFSPSIFGGNLVR, r2: 1.37
s3: TDDGQEQVLVK, r3: 0.98

QB1: 64.38, QA1: 101.98, R1: 1.58
QB2: 35.62, QA2: 35.02, R2: 0.98

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00536297 | AT5G52920.1; | Pyruvate kinase'

p2: IPI00519857 | AT1G32440.1; | Pyruvate kinase'

s1: GDLGAELPIEEVPILQEEIINLCR, r1: 0.48

s2: LAEAGMNVAR, r2: 1.11

s3: LNMSHGDDHASHQITIDLVK, r3: 1.14

QB1: 3.49, QA1: 1.67, R1: 0.48

QB2: 96.51, QA2: 109.65, R2: 1.14

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00517047 | AT1G31070.1;AT1G31070.2; | UDP-N-acetylglucosamine pyrophosphorylase-related'

p2: IPI00520340 | AT2G35020.1; | Probable UDP-N-acetylglucosamine pyrophosphorylase'

s1: NVNGSNFDTPE SAR, r1: 1.46

s2: YVDCYGV DNV LVR, r2: 0.56

s3: NANGSNYDTPE SAR, r3: 0.17

QB1: 30.36, QA1: 44.41, R1: 1.46

QB2: 69.64, QA2: 11.60, R2: 0.17

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

3 proteins, 5 peptides

cc =

p1	s1
p1	s2
p1	s5
p2	s2
p2	s4
p3	s3
p3	s5

p1: IPI00540778 | AT1G43170.1;AT1G43170.2;AT1G43170.3; | 60S ribosomal protein L3'

p2: IPI00524843 | AT1G61580.1; | 60S ribosomal protein L3'

p3: IPI00532859 | AT4G09950.1; | Avirulence-responsive family protein'

s1: QSLLTQTSR, r1: 0.98

s2: GYEGVVTR, r2: 0.81

s3: VLFDNSYNAPVSK, r3: 2.33

s4: QVPVDAIFQK, r4: 1.88

s5: TELNK, r5: 0.84

QB1: 97.93, QA1: 79.18, R1: 0.81

QB2: 0.00, QA2: 0.00, R2: NaN

QB3: 2.07, QA3: 4.83, R3: 2.33

Objective: 16.85

LRD (Distance in peptide log ratios): 0.16

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2

p2 s3

p1: IPI00539973 | AT3G48890.1; | Putative steroid binding protein 2'
p2: IPI00522918 | AT5G52240.1; | Membrane steroid binding protein 1'
s1: GQIYDVSQSR, r1: 0.73
s2: SDDAPAETVLK, r2: 1.36
s3: MFYGPGGPYALFAGK, r3: 0.84

QB1: 82.99, QA1: 60.46, R1: 0.73
QB2: 17.01, QA2: 23.09, R2: 1.36

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00530352 | AT4G34230.1;AT4G34230.2; | Probable cinnamyl-alcohol dehydrogenase'
p2: IPI00517601 | AT3G19450.1; | Cinnamyl-alcohol dehydrogenase'
s1: ETGPEDVNIR, r1: 1.46
s2: DPSGVLSPYSYTLR, r2: 0.51
s3: GGILGLGGVGHMGVK, r3: 1.04

QB1: 55.98, QA1: 81.50, R1: 1.46
QB2: 44.02, QA2: 22.49, R2: 0.51

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00517477 | AT1G76090.1; | 24-methylenesterol C-methyltransferase 3'

p2: IPI00540275 | AT1G20330.1; | 24-methylenesterol C-methyltransferase 2'

s1: GDALPGLR, r1: 0.77

s2: ANVVGITINEYQVNR, r2: 0.84

s3: LEEVYSEIFR, r3: 0.49

QB1: 19.29, QA1: 9.47, R1: 0.49

QB2: 80.71, QA2: 67.90, R2: 0.84

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00518863 | AT5G44020.1; | Acid phosphatase class B family protein'

p2: IPI00540435 | AT1G04040.1; | Acid phosphatase class B family protein'

s1: YMTSSQYEDDVER, r1: 0.30

s2: IFLISSR, r2: 0.49

s3: GLGSSSSQNGIVSK, r3: 1.33

QB1: 81.67, QA1: 24.41, R1: 0.30

QB2: 18.33, QA2: 24.44, R2: 1.33

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00538860 | AT2G45300.1; | 3-phosphoshikimate 1-carboxyvinyltransferase, chloroplast precursor'

p2: IPI00518245 | AT1G48860.1;AT1G48860.2; | 3-phosphoshikimate 1-carboxyvinyltransferase'

s1: LGLNVETDSENNR, r1: 1.61

s2: VSWTENSVTVTGPSR, r2: 1.11

s3: ASEIVLQPIR, r3: 1.21

QB1: 21.00, QA1: 33.80, R1: 1.61

QB2: 79.00, QA2: 87.37, R2: 1.11

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00526329 | AT1G17890.1;AT1G17890.2;AT1G17890.3; | Putative GDP-L-fucose synthase 2'

p2: IPI00540212 | AT1G73250.1; | Encodes a bifunctional 3, 5-epimerase-4-reductase in L-fucose synthesis and converts GDP-D-mannose to GDP-L-fucose in vitro along with MUR1 (GDP-D-mannose 4,6-dehydratase)'

s1: GLVGSIVR, r1: 0.80

s2: ANNADEVVVWGSPLR, r2: 0.90

s3: LQEQGFTNLVLK, r3: 0.52

QB1: 75.25, QA1: 67.49, R1: 0.90

QB2: 24.75, QA2: 12.80, R2: 0.52

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00523537 | AT3G02350.1; | Probable glycosyltransferase At3g02350'

p2: IPI00522399 | AT3G25140.1; | Glycosyltransferase QUASIMODO1'

s1: SAVSDNGNALEEDSFR, r1: 0.77

s2: FYLPEMYPK, r2: 0.84

s3: DLTGLWEIDMDGK, r3: 1.25

QB1: 87.02, QA1: 67.32, R1: 0.77

QB2: 12.98, QA2: 16.19, R2: 1.25

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 6 peptides

cc =

p1	s1
p1	s2
p1	s4
p2	s1

p2 s3
p2 s5
p3 s2
p3 s5
p3 s6

p1: IPI00516663 | AT2G42790.1; | Citrate synthase 3, peroxisomal precursor'
p2: IPI00545433 | AT3G58750.1; | Citrate synthase 2, peroxisomal precursor'
p3: IPI00541007 | AT3G58740.1; | Citrate synthase 1, peroxisomal precursor'
s1: LYDPGYLNTAPVR, r1: 0.83
s2: SSISYIDGDEGILR, r2: 0.73
s3: LADEVFSIVGR, r3: 0.82
s4: VPVSDDGTVK, r4: 1.06
s5: AALSDEYFVK, r5: 0.68
s6: LSGFGHRIYK, r6: 1.27

QB1: 19.72, QA1: 20.91, R1: 1.06
QB2: 71.49, QA2: 54.57, R2: 0.76
QB3: 8.79, QA3: 0.00, R3: 0.00

Objective: 16.02
LRD (Distance in peptide log ratios): 0.80

2 proteins, 3 peptides
cc =

p1 s1
p1 s3
p2 s1
p2 s2

p1: IPI00518174 | AT3G25220.1; | FK506-binding protein 2-1 precursor'
p2: IPI00540512 | AT5G48580.1; | FK506-binding protein 2-2 precursor'
s1: LTDGTVFDSSFER, r1: 1.03
s2: LGSGQVIK, r2: 1.22
s3: SGDVTTELQIGVK, r3: 0.74

QB1: 38.79, QA1: 28.55, R1: 0.74
QB2: 61.21, QA2: 74.92, R2: 1.22

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

4 proteins, 9 peptides
cc =

p1	s1
p1	s3
p1	s6
p1	s7
p2	s2
p2	s7
p2	s9
p3	s2
p3	s3
p3	s5
p3	s6
p3	s7
p3	s8
p4	s2
p4	s3
p4	s4
p4	s5
p4	s7

p1: IPI00517370 | IPI00517370 | F19P19.11 protein'
p2: IPI00521270 | AT5G14430.1;AT5G14430.2; | Dehydration-responsive protein-related'
p3: IPI00522341 | AT3G23300.1; | Dehydration-responsive protein-related'
p4: IPI00531513 | AT4G14360.1;AT4G14360.2; | Ankyrin like protein'
s1: DGLLLLELDR, r1: 1.69
s2: DGILLLELDR, r2: 1.69
s3: GSGLAPWPAR, r3: 1.23
s4: VDTYWDLLSPR, r4: 1.11
s5: DVWVMNVVPEDGPNTLK, r5: 1.74

s6: GIPAYLGVLGTK, r6: 1.60
s7: IDWLQR, r7: 1.44
s8: VDTYWDLSPK, r8: 1.08
s9: KLWVSLPAISVS, r9: 0.96

QB1: 75.01, QA1: 119.78, R1: 1.60
QB2: 24.99, QA2: 23.91, R2: 0.96
QB3: 0.00, QA3: 0.00, R3: NaN
QB4: 0.00, QA4: 0.00, R4: NaN

Objective: 52.52
LRD (Distance in peptide log ratios): 0.18

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00525984 | AT2G22230.1; | Beta-hydroxyacyl-ACP dehydratase'
p2: IPI00536187 | AT5G10160.1; | Beta-hydroxyacyl-ACP dehydratase'
s1: FPAFPTVMDINQIR, r1: 0.40
s2: FPFLLVDR, r2: 0.56
s3: YEAFPTVMDINK, r3: 0.75

QB1: 56.41, QA1: 22.78, R1: 0.40
QB2: 43.59, QA2: 32.78, R2: 0.75

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00535198 | AT4G22810.1; | DNA-binding protein-related'

p2: IPI00522782 | AT2G45430.1; | DNA-binding protein-related'

s1: NQTDGDQGGSGGNR, r1: 0.35

s2: QPASVPGGGSSVVNLHGR, r2: 1.54

s3: NPKPPIIIITR, r3: 0.70

QB1: 70.67, QA1: 24.71, R1: 0.35

QB2: 29.33, QA2: 45.27, R2: 1.54

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00518513 | Hypothetical protein | Hypothetical protein'

p2: IPI00530629 | AT3G27310.1; | Expressed protein'

s1: EAEEAAR, r1: 0.80

s2: DDGGSSTPYLNEEILSLK, r2: 1.64

s3: ATLYEK, r3: 0.41

QB1: 68.45, QA1: 27.84, R1: 0.41

QB2: 31.55, QA2: 51.88, R2: 1.64

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00519228 | AT1G52070.1; | Jacalin lectin family protein'

p2: IPI00523814 | AT1G52060.1; | Jacalin lectin family protein'

s1: DGQVVTR, r1: 0.30

s2: TSEVIGYPK, r2: 0.41

s3: ALNSIGAYLTK, r3: 0.73

QB1: 74.22, QA1: 21.92, R1: 0.30

QB2: 25.78, QA2: 18.71, R2: 0.73

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

3 proteins, 6 peptides

cc =

p1	s1
p1	s3
p1	s5
p1	s6
p2	s1
p2	s4
p2	s6
p3	s2
p3	s5
p3	s6

p1: IPI00528962 | AT5G66510.1; | Bacterial transferase hexapeptide repeat-containing protein'
p2: IPI00530525 | IPI00530525 | F18O14.34'
p3: IPI00544889 | AT1G47260.1; | Bacterial transferase hexapeptide repeat-containing protein'
s1: ETGQALDR, r1: 1.13
s2: SFEQIEVER, r2: 0.80
s3: DTEYDSVLDDLTLPENVPK, r3: 0.82
s4: IPSGEVWGGNPAR, r4: 1.16
s5: IPSGEVWGGNPAK, r5: 0.82
s6: TLMNVFDK, r6: 1.08

QB1: 8.16, QA1: 6.65, R1: 0.82
QB2: 76.90, QA2: 89.31, R2: 1.16
QB3: 14.94, QA3: 11.91, R3: 0.80

Objective: 0.44
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00540937 | AT5G47690.1; | Similar to expressed protein'
p2: IPI00522015 | AT1G18720.1; | Expressed protein'
s1: VVGLVGELFSLPGR, r1: 0.47
s2: VESDIK, r2: 1.30
s3: LGSSLALK, r3: 1.48

QB1: 18.07, QA1: 8.49, R1: 0.47
QB2: 81.93, QA2: 121.59, R2: 1.48

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00544398 | AT3G60900.1; | Fasciclin-like arabinogalactan protein 10 precursor'

p2: IPI00549138 | AT2G45470.1; | Fasciclin-like arabinogalactan protein 8 precursor'

s1: LADEINSR, r1: 1.20

s2: DAISTLATNGAGK, r2: 0.75

s3: AEGVPDLTK, r3: 1.32

QB1: 22.21, QA1: 16.69, R1: 0.75

QB2: 77.79, QA2: 102.82, R2: 1.32

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00531458 | AT1G72160.1; | Patellin-3'

p2: IPI00538227 | AT4G09160.1; | Patellin-5'

s1: LVFAGPSR, r1: 0.85

s2: IWGIPLLEDDR, r2: 0.82

s3: SEVLNHAEDSEQPR, r3: 1.82

QB1: 97.42, QA1: 80.10, R1: 0.82

QB2: 2.58, QA2: 4.70, R2: 1.82

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00535082 | AT3G21190.1; | Expressed protein'

p2: IPI00532409 | AT1G51630.1; | Expressed protein'

s1: FIAVDLR, r1: 2.29

s2: SDVFVPAIPGLFYANTVGK, r2: 1.10

s3: HLGATLVLPDIR, r3: 1.17

QB1: 5.97, QA1: 13.66, R1: 2.29

QB2: 94.03, QA2: 103.60, R2: 1.10

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00538325 | AT2G47800.1; | Glutathione-conjugate transporter (MRP4)'

p2: IPI00543716 | AT3G62700.1; | Glutathione-conjugate transporter'

s1: QFTDIPSESEWER, r1: 0.98
s2: SQGCDGNVAVEIK, r2: 1.63
s3: FGIIPQEPVLFEGTVR, r3: 1.34

QB1: 44.61, QA1: 43.70, R1: 0.98
QB2: 55.39, QA2: 90.06, R2: 1.63

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00530933 | AT5G37475.1; | Translation initiation factor-related'
p2: IPI00518471 | AT1G66070.1; | Translation initiation factor-related'
s1: SESDFLDYAELISQR, r1: 1.30
s2: DVASSITTIANEK, r2: 0.58
s3: EAAAGK, r3: 0.95

QB1: 51.00, QA1: 66.36, R1: 1.30
QB2: 49.00, QA2: 28.47, R2: 0.58

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s2

p2 s3

p1: IPI00548267 | AT3G48000.1; | Aldehyde dehydrogenase (ALDH2) '
p2: IPI00533796 | AT1G23800.1; | Aldehyde dehydrogenase, mitochondrial (ALDH3) '
s1: VVGDPFR, r1: 1.00
s2: TAEQTPLSALLVGK, r2: 0.61
s3: VYDEFVEK, r3: 0.89

QB1: 71.03, QA1: 71.36, R1: 1.00
QB2: 28.97, QA2: 17.61, R2: 0.61

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides
cc =

p1	s1
p1	s3
p2	s2
p2	s3

p1: IPI00518457 | AT2G21270.1;AT2G21270.2; | Ubiquitin fusion degradation UFD1 family protein '
p2: IPI00516874 | AT4G38930.1;AT4G38930.2; | Ubiquitin fusion degradation UFD1 family protein '
s1: LVFGANGNR, r1: 0.97
s2: EVDVAEAEPK, r2: 1.60
s3: NVTLPK, r3: 1.16

QB1: 70.81, QA1: 68.97, R1: 0.97
QB2: 29.19, QA2: 46.83, R2: 1.60

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00518012 | AT5G16390.1;AT5G16390.2; | Biotin carboxyl carrier protein 1 (BCCP1)'

p2: IPI00518381 | IPI00518381 | Biotin carboxyl carrier protein-like protein'

s1: SPMAGTFYR, r1: 0.54

s2: TNVPEPAELSEFMAK, r2: 0.41

s3: DIVELQLK, r3: 1.11

QB1: 18.12, QA1: 20.10, R1: 1.11

QB2: 81.88, QA2: 33.91, R2: 0.41

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00528722 | AT2G18770.1; | Expressed protein'

p2: IPI00518957 | AT5G05670.1;AT5G05670.2; | Expressed protein'

s1: LEEYLPR, r1: 0.83

s2: TVLFYQLR, r2: 0.99

s3: SNTVLLSGLTGSGK, r3: 1.40

QB1: 71.19, QA1: 58.74, R1: 0.83

QB2: 28.81, QA2: 40.47, R2: 1.40

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00526496 | AT2G31060.1;AT2G31060.2; | Putative GTP-binding protein'
p2: IPI00656641 | AT2G31060.1;AT2G31060.2; | Elongation factor family protein'
s1: ETDLDLNPVK, r1: 0.99
s2: DNELNMVDTPGHADFGGEVER, r2: 0.55
s3: GPLGNVRK, r3: 7.11

QB1: 93.23, QA1: 51.22, R1: 0.55
QB2: 6.77, QA2: 48.15, R2: 7.11

Objective: 0.00

LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00544466 | AT2G15430.1; | DNA-directed RNA polymerase II 36 kDa polypeptide A'
p2: IPI00547850 | AT2G15400.1; | DNA-directed RNA polymerase II 36 kDa polypeptide B'
s1: IDLIESSPTK, r1: 1.38
s2: LGLIPLTSER, r2: 1.56
s3: VMISEVPTMAIHLVK, r3: 0.19

QB1: 87.17, QA1: 136.01, R1: 1.56
QB2: 12.83, QA2: 2.39, R2: 0.19

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s3
p2	s1
p2	s2

p1: IPI00522443 | AT2G36620.1; | 60S ribosomal protein L24 (RPL24A) '
p2: IPI00547637 | AT3G53020.1; | 60S ribosomal protein L24 '
s1: SIVGATLEVIQK, r1: 1.17
s2: AAAASK, r2: 1.96
s3: VEYASK, r3: 1.02

QB1: 83.97, QA1: 85.43, R1: 1.02
QB2: 16.03, QA2: 31.45, R2: 1.96

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s1
p2	s3

p1: IPI00533016 | AT2G42680.1; | Ethylene-responsive transcriptional coactivator'
p2: IPI00547930 | AT3G58680.1; | Ethylene-responsive transcriptional coactivator'
s1: AIPNQIISK, r1: 1.15
s2: MLDDDTENLTER, r2: 0.63
s3: KFNAGSNK, r3: 1.35

QB1: 28.61, QA1: 18.15, R1: 0.63
QB2: 71.39, QA2: 96.62, R2: 1.35

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00

2 proteins, 3 peptides

cc =

p1	s1
p1	s2
p2	s2
p2	s3

p1: IPI00533120 | AT1G12780.1; | UDP-glucose 4-epimerase'
p2: IPI00534992 | AT1G63180.1; | Uridine diphosphate glucose epimerase, putative; 80611-78786'
s1: DIQKAEPEWR, r1: 0.16
s2: LFLEEIAR, r2: 0.93
s3: LEFNLGDLR, r3: 2.48

QB1: 66.59, QA1: 10.53, R1: 0.16
QB2: 33.41, QA2: 82.77, R2: 2.48

Objective: 0.00
LRD (Distance in peptide log ratios): 0.00