Peptide No.1

AAAASSWSDNSGTESSPR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of AAAASSWSDNSGTESSPR
Found in AT1G59610.1, ADL3 (ARABIDOPSIS DYNAMIN–LIKE 3)

Match to Query 2614: 1859.731432 from(930.872992,2+)
Elution from: 24.716 to 24.716 scan no 1886 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1859.7323
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 1e-009
Matched b ions: b(5), b(7), b(9), b(10), b(11), b(13), b(14), b(15), b(16)−98, b(16)+, b(17)−98++
Matched y ions: y(2), y(3), y(4)−98, y(6), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)+, y(12), y(13), y(14), y(14)+, y(15)+, y(16)+, y(17)−98++
Precursor origin neutral loss: +

Peptide No.2

AAAAVTTTTTDLSASDDDR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AAAAVTTTTTDLSASDDDR
Found in AT1G66680.1, AR401

Match to Query 3289: 1960.825062 from(981.419807,2+)
Elution from: 30.046 to 30.046 scan no 2718 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1960.8263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 Expect: 1.2e-009
Matched b ions: b(6), b(8), b(9), b(11), b(12), b(13), b(14), b(16)-98, b(17)-98++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(8)-98, y(8), y(9), y(10), y(10)-98, y(11)-98++, y(11), y(11)-98, y(12), y(13), y(13)-98++, y(14), y(15), y(15)-98, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.3

AAEQGSALAAAVEGVEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AAEQGSALAAAVEGVEK
Found in AT3G52950.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 2425: 1679.775602 from(840.895077,2+)
Elution from: 47.307 to 47.307 scan no 4934 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1679.7766
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 2.1e-005
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11), b(11)-98, b(12)++, b(12)-98, b(12), b(13)-98, b(14)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(13)
Precursor origin neutral loss: +

Peptide No.4

AAGLADSPPPNSPTR
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of AAGLADSPPPNSPTR
Found in AT4G10930.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to expressed protein

Match to Query 2264: 1512.598288 from(757.306420,2+) Elution from: 27.672 to 27.672 scan no 2223 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1512.6011
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00055
Matched b ions: b(7)-98
Matched y ions: y(3), y(4), y(7), y(8)-98, y(9), y(9)-98, y(10), y(10)+, y(11)-98++, y(11)+, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.5

AAGLADSPPNSPTR
Confirmed sites: @S:7
Ambiguous sites: @S:11orT:13

MS/MS Fragmentation of AAGLADSPPNSPTR
Found in AT4G10930.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to expressed protein

Match to Query 2332: 1512.599578 from(757.307065,2+)
Elution from: 26.413 to 26.413 scan no 2220 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1512.6011
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.039
Matched b ions: b(7)-98, b(7), b(8)-98
Matched y ions: y(5), y(6)-98, y(7), y(8), y(9)-98, y(10), y(12)+, y(12)-98+
Precursor origin neutral loss: +

Peptide No.6

AALVLNASR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AALVLNASR
Found in AT5G57110.1, ACA8 (AUTOINHIBITED CA2+ ATPASE, ISOFORM 8); calcium-transporting ATPase/ calmodulin binding

Match to Query 467: 993.499244 from(497.756898,2+)
Elution from: 30.289 to 30.289 scan no 2686 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 993.5008
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.001
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7)
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(7), y(7)++, y(8)−98++, y(8)++
Precursor origin neutral loss: +

Peptide No.7
AASFQPER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASFQPER
Found in AT4G32350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79910.1); similar to hypothetical prote

Match to Query 450: 984.406726 from(493.210639,2+)
Elution from: 22.533 to 22.533 scan no 1544 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 984.4066
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 Expect: 0.06
Matched b ions: b(4), b(5), b(6)-98
Matched y ions: y(3), y(4), y(6), y(6)-98, y(6)-98++, y(7)++
Precursor origin neutral loss: +

Peptide No.8

AASGSLAPPNADR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASGSLAPPNADR
Found in AT4G11740.1, SAY1

Match to Query 1622: 1305.570724 from(653.792638,2+)
Elution from: 25.542 to 25.542 scan no 2032 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1305.5714
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 4.9e-005
Matched b ions: b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(12), b(12)++
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11)-98++
Precursor origin neutral loss: +

Peptide No.9

AASGSLAPPNADR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AASGSLAPPNADR
Found in AT4G11740.1, SAY1

Match to Query 1588: 1305.570196 from(653.792374,2+)
Elution from: 25.535 to 25.535 scan no 2023 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1305.5714
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.024
Matched b ions: b(6)−98, b(7)−98, b(7), b(8)−98
Matched y ions: y(6), y(7), y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.10

AASGLAPPNADRSR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of AASGLAPPNADRSR
Found in AT4G11740.1, SAY1

Match to Query 2145: 1548.704892 from(517.242240,3+)  
Elution from: 21.407 to 21.407 scan no 1484 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1548.7045
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 4.1e-005
Matched b ions: b(6), b(7), b(11)++
Matched y ions: y(6)++, y(7)++, y(7)−98++, y(8)++, y(8)−98++, y(9)++, y(9)−98++, y(10)++, y(10)−98++, y(11)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss:

Peptide No.11

AASPDPLGESSSSGTAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASPDPLGESSSSGTAR
Found in AT4G35980.1, similar to hypothetical protein MtrDRAFT_AC148217g8v1 [Medicago truncatula] (GB:ABE88169.1); contai

Match to Query 1935: 1668.697488 from(835.356020,2+) Elution from: 26.432 to 26.432 scan no 2139 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1668.6992
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 1.2e-008
Matched b ions: b(5)-98, b(5), b(7)-98, b(7), b(9)-98, b(9), b(10)-98, b(11)+, b(13)+, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)+, y(12)+, y(12), y(13), y(13)+, y(14)++ , y(14), y(15)-98++, y(15)-98, y(15)+, y(16)++
Precursor origin neutral loss: +

Peptide No.12
AATTLESLVLASTKTAAAKITNLK
Confirmed sites: "@S:7,@S:12,@T:13"
Ambiguous sites: @T:3orT:4

MS/MS Fragmentation of AATTLESLVLASTKTAAAKITNLK
Found in AT5G46960.1, invertase/pectin methylesterase inhibitor family protein

Match to Query 4214: 2735.266227 from(912.762685,3+)
Elution from: 50.295 to 50.295 scan no 5123 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2735.2601

Fixed modifications: Carbamidomethyl (C)

Variable modifications:

T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 26 Expect: 0.032

Matched b ions: b(4), b(6), b(7), b(8)−98++, b(8), b(8)−98, b(9)++, b(9), b(9)−98, b(9)−196, b(10), b(11), b(12)−294, b(13)++, b(15)−98++, b(16)−392++, b(17)−294, b(17)−392++, b(19)−392++, b(20)−294++

Matched y ions: y(13)++, y(14)++, y(15)++, y(16)−98++, y(17)++, y(22)−392++

Precursor origin neutral loss:

Peptide No.13

AAVEGNLPVSGQYSPR

Confirmed sites: @S:14

Ambiguous sites:

MS/MS Fragmentation of AAVEGNLPVSGQYSPR

Found in AT1G64190.1, 6-phosphogluconate dehydrogenase family protein

Match to Query 2563: 1723.790334 from(862.902443,2+)

Elution from: 36.809 to 36.809 scan no 3560 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1723.7930
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.025
Matched b ions: b(7), b(10), b(12), b(13), b(14)−98, b(15)++
Matched y ions: y(4), y(6)−98, y(6), y(7)−98, y(8), y(9)−98, y(9), y(12), y(13)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.14

ACCQGAEILSGSPSK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ACCQGAEILSGSPSK
Found in AT5G44070.1, CAD1 (CADMIUM SENSITIVE 1)

Match to Query 2602: 1643.667304 from(822.840928,2+) Elution from: 31.715 to 31.715 scan no 2654 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1643.6684
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 8.4e-007
Matched b ions: b(3), b(4), b(5)+, b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12)+, b(12)-98, b(13)-98++, b(13)+, b(13)-98++, b(14)-98 b(14)-98++
Matched y ions: y(3), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12), y(13)-98, y(13), y(13)+, y(13)-98++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.15
ACCQGAEILSGPSK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of ACCQGAEILSGPSK
Found in AT5G44070.1, CAD1 (CADMIUM SENSITIVE 1)

Match to Query 2376: 1643.667016 from(822.840784,2+)
Elution from: 30.157 to 30.157 scan no 2668 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1643.6684
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 Expect: 6.7e-008
Matched b ions: b(3), b(4), b(5)++, b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(12)++, b(12)−98, b(12), b(13)−98++, b(13)+, b(14)
Matched y ions: y(3), y(4), y(4)−98, y(5)−98, y(5), y(6)−98, y(6), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(9)++, y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)−98, y(12)−98++, y(13)−98, y(13), y(13)−98++, y(13)+, y(14)+, y(14)−98++
Precursor origin neutral loss: +

Peptide No.16

ACCQGAELSGSPSK
Confirmed sites:
Ambiguous sites: @S:12orS:14

MS/MS Fragmentation of **ACCQGAELSGSPSK**
Found in **AT5G44070.1**, CAD1 (CADMIUM SENSITIVE 1)

Match to Query 2917: 1643.666468 from(822.840510,2+)
Elution from: 30.108 to 30.108 scan no 2695 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1643.6684
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00015
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10), b(10)++, b(14)-98, b(14)-98++
Matched y ions: y(5), y(5)-98, y(6)-98, y(6), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(11)-98, y(13)-98, y(13)++, y(13)-98++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.17

ADGSDSEEACLEVSEEAIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ADGSDSEEACLEVSEEAIK
Found in AT3G19750.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50150.1); similar to hypothetical prote

Match to Query 2965: 2117.832218 from(1059.923385,2+)
Elution from: 44.582 to 44.582 scan no 4421 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2117.8347
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 2.1e-005
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(18)-98, b(18)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14)
Precursor origin neutral loss: +

Peptide No.18

ADGSDSEEACLEVSEEAIK
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of ADGSDSEEACLEVSEEAIK
Found in AT3G19750.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50150.1);
similar to hypothetical prote

Match to Query 3689: 2197.796862 from(1099.905707,2+)
Elution from: 48.551 to 48.551 scan no 5034 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2197.8010
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.016
Matched b ions: b(13)-196, b(13)-98
Matched y ions: y(6), y(7), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.19

ADGSDSEEACLEVSEEAIK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of ADGSDSEEACLEVSEEAIK
Found in AT3G19750.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50150.1); similar to hypothetical prote

Match to Query 3009: 2117.833058 from(1059.923805,2+) Elution from: 44.452 to 44.452 scan no 4418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2117.8347
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00036
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(13), b(13)-98, b(16)-98, b(18)-98
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(15)-98, y(16), y(17)-98++
Precursor origin neutral loss: +

Peptide No.20
ADSDEEAEDVEGR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of ADSDEEAEDVEGR
Found in AT2G34357.1, binding
Match to Query 2171: 1647.591364 from(824.802958,2+)
Elution from: 37.657 to 37.657 scan no 3602 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1647.5937
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 2.4e-007
Matched b ions: b(5)-98, b(6), b(6)-98, b(7)-98, b(9)-98, b(9), b(10), b(11), b(12)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.21
ADSDGEDDESDAEHPGK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ADSDGEDDESDAEHPGK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 2592: 1852.626153 from(618.549327,3+)
Elution from: 17.691 to 17.691 scan no 964 polarity:+

Peptide No.21
ADSDGEDDESDAEHPGK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ADSDGEDDESDAEHPGK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 2592: 1852.626153 from(618.549327,3+)
Elution from: 17.691 to 17.691 scan no 964 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.6272  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 31 Expect: 0.0017  
Matched b ions: b(10)++, b(15)++  
Matched y ions: y(11)++, y(13)++, y(14)++, y(15)++  
Precursor origin neutral loss:

Peptide No.22

ADSVTFTILISGSCR  
Confirmed sites: "@S:3,@T:5,@S:11,@S:13"  
Ambiguous sites:

MS/MS Fragmentation of ADSVTFTILISGSCR  
Found in AT2G41720.1, EMB2654 (EMBRYO DEFECTIVE 2654); binding  

Match to Query 2581: 1945.678323 from(649.566717,3+)  
Elution from: 22.841 to 22.841 scan no 1663 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1945.6736
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.044
Matched b ions: b(3), b(5), b(6)−196, b(7), b(10)+++, b(13)−392++
Matched y ions: y(5)−98, y(7)+++, y(7)−98, y(8)+++, y(9)+++, y(11)+++, y(11)−98++, y(11)−294++, y(12)−98++, y(12)−196++, y(12)+
Precursor origin neutral loss: +

Peptide No.23

ADTPIAENEIR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of ADTPIAENEIR
Found in AT1G20220.1, nucleic acid binding

Match to Query 1100: 1307.575796 from(654.795174,2+)
Elution from: 30.527 to 30.527 scan no 2671 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1307.5758
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 39 Expect: 0.00062
Matched b ions: b(3), b(3)-98, b(5), b(5)-98, b(6)-98, b(7)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.24
ADTPIDANEIR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of ADTPIDANEIR
Found in AT1G76010.1, nucleic acid binding

Match to Query 1111: 1293.560018 from (647.787285,2+)
Elution from: 30.467 to 30.467 scan no 2673 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1293.5602
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 22 Expect: 0.035
Matched b ions: b(3), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(9)-98
Matched y ions: y(4), y(5), y(6), y(8)+, y(8), y(9)-98++, y(9)+
Precursor origin neutral loss: +

Peptide No.25

ADVEDFLASGSK
Confirmed sites:
Ambiguous sites: @S:11 or S:9

MS/MS Fragmentation of ADVEDFLASGSK
Found in AT3G13930.1, dihydrolipoamide S-acetyltransferase, putative

Match to Query 1357: 1317.548828 from(659.781690,2+)
Elution from: 44.926 to 44.926 scan no 4633 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1317.5489
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.019
Matched b ions: b(7), b(8)
Matched y ions: y(5), y(6), y(7), y(8), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.26

ADVLSEDSPGEGR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ADVLSEDSPGEGR
Found in AT3G54760.1, dentin sialophosphoprotein-related

Match to Query 1401: 1410.565986 from(706.290269,2+) Elution from: 28.083 to 28.083 scan no 2241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1410.5664
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.022
Matched b ions: b(3), b(5)++, b(10)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(9), y(10)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.27

ADVLSEDSPGGRK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ADVLSEDSPGGRK
Found in AT3G54760.1, dentin sialophosphoprotein-related

Match to Query 2354: 1538.660823 from(513.894217,3+)
Elution from: 23.304 to 23.304 scan no 1722 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1538.6613
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0064
Matched b ions: b(2), b(3), b(4), b(5)--98, b(7), b(7)++, b(12)++
Matched y ions: y(6)++, y(6), y(7)++, y(8)++, y(10)++, y(10)--98++, y(11)++, y(11)--98++, y(12)++, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.28

ADVLSEDSPGEGRK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ADVLSEDSPGEGRK
Found in AT3G54760.1, dentin sialophosphoprotein-related

Match to Query 1821: 1538.660109 from(513.893979,3+)
Elution from: 22.050 to 22.050 scan no 1531 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1538.6613
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00034
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(9), b(11)−98++, b(12)++
Matched y ions: y(3), y(6)++, y(6), y(7)−98++, y(7)++, y(8)−98, y(8)−98++, y(8)++, y(9)++, y(10)++, y(10)−98++, y(11)++, y(11)−98++, y(12)−98++, y(12)++, y(13)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.29

ADYEGSPVREHR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of ADYEGSPVREHR
Found in AT5G16780.1, SART−1 family protein

Match to Query 1972: 1494.626076 from(499.215968,3+)
Elution from: 18.395 to 18.395 scan no 1089 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1494.6252
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0084
Matched b ions: b(8)++, b(10)++
Matched y ions: y(6)++, y(7)++, y(8)−98++, y(8)++, y(9)++, y(10)++, y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.30

AEAVEGAATSDDDLK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AEAVEGAATSDDDLK
Found in AT1G75950.1, SKP1 (ARABIDOPSIS SKP1 HOMOLOGUE); ubiquitin–protein ligase

Match to Query 1702: 1570.638316 from(786.326434,2+)  
Elution from: 26.486 to 26.486 scan no 2146 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1570.6399
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.5e-006
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9)+, b(9), b(12), b(13), b(13)+, b(14)
Matched y ions: y(2), y(4), y(6)+98, y(7), y(7)+98, y(8), y(8)+, y(8)+98, y(9), y(10), y(10)+98, y(11), y(12), y(12)+98, y(12)+, y(13)+
Precursor origin neutral loss:

Peptide No.31

AEGNESGEDDDFLR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AEGNESGEDDDFLR
Found in AT3G24080.1, KRR1 family protein

Match to Query 2633: 1632.593292 from(817.303922,2+)
Elution from: 38.515 to 38.515 scan no 3680 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.5940
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 1.9e-007
Matched b ions: b(4), b(5), b(6), b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98++, b(9)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(11)-98, b(12)-98, b(12), b(13)-98, b(13)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(12), y(12)++, y(12)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.32
AEIKSGSEFGAMIQSMIAEGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AEIKSGSEFGAMIQSMIAEGR
Found in AT3G60180.1, uridylate kinase, putative / uridine monophosphate kinase, putative / UMP kinase, putative

Match to Query 3704: 2323.019061 from(775.346963,3+)
Elution from: 40.870 to 40.870 scan no 3990 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2323.0224
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M16 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 24 Expect: 0.046
Matched b ions: b(5), b(6), b(7), b(8), b(10)++, b(10)--98++, b(11)--98++, b(16)++, b(16)--98++, b(18)++
Matched y ions: y(14)++, y(17)--98++
Precursor origin neutral loss:

Peptide No.33

AEKDEVSDDEATIEQTLK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AEKDEVSDDEATIEQTLK
Found in AT1G58200.1, MSL3 (MSCS-LIKE 3)

Match to Query 2913: 2099.912056 from(1050.963304,2+)
Elution from: 45.157 to 45.157 scan no 4485 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2099.9147
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00025
Matched b ions: b(6), b(8)—98, b(8), b(9)—98, b(12), b(13), b(13)—98, b(17)—98++
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(12), y(13)—98, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.34

AEPSFESGASFGETK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AEPSFESGASFGETK
Found in AT5G27630.1, ACBP5 (ACYL–COA BINDING PROTEIN 5, ACYL–COA–BINDING DOMAIN 5); acyl–CoA binding

Match to Query 2237: 1622.650508 from(812.332530,2+)  
Elution from: 38.532 to 38.532 scan no 3790 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1622.6501
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0007
Matched b ions: b(5), b(6), b(7), b(9), b(10)–98, b(11)–98, b(13)–98
Matched y ions: y(5), y(6), y(7)–98, y(8), y(8)–98, y(9), y(10), y(12)++, y(13)++, y(13), y(13)–98++
Precursor origin neutral loss: +

Peptide No.35

AEPSFESGASFGETK
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of AEPSFESGASFGETK
Found in AT5G27630.1, ACBP5 (ACYL-COA BINDING PROTEIN 5, ACYL-COA-BINDING DOMAIN 5); acyl-CoA binding

Match to Query 2616: 1622.648362 from(812.331457,2+) 
Elution from: 39.788 to 39.788 scan no 3956 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1622.6501
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.0001
Matched b ions: b(5), b(6), b(7), b(9), b(10)
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(12)+, y(13)+, y(13), y(13)−98++, y(14) ++
Precursor origin neutral loss: +

Peptide No.36
AESDSEEEEIIDELPR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of AESDSEEEEIIDELPR
Found in AT4G37090.1, similar to Os02g0186700 [Oryza sativa (japonica cultivar−group)]
(GB:NP_001046122.1); similar to vi

Match to Query 2964: 2019.757922 from(1010.886237,2+)
Elution from: 64.179 to 64.179 scan no 6148 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2019.7598
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00046
Matched b ions: b(10)-98, b(10), b(12), b(13), b(14), b(14)-98, b(15)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9)
Precursor origin neutral loss: +

Peptide No.37

AEVEGFEITEIEK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of AEVEGFEITEIEK
Found in AT1G20400.1, myosin heavy chain-related

Match to Query 1738: 1572.698832 from(525.240220,3+)Elution from: 34.385 to 34.385 scan no 3090 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1572.6960
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.04
Matched b ions: b(3), b(5), b(6)++, b(6), b(8), b(8)++, b(9)−98++, b(10)−98++, b(10)++, b(11)−98++, b(12)−98++, b(12)++, b(12)−98++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(5)−98++, y(5)−98, y(5), y(6)−98, y(7)++, y(7)−98++, y(7)−98++, y(8)++, y(8)−98+
Precursor origin neutral loss:

**Peptide No.38**

AEVLFGGEVENASPQK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of AEVLFGGEVENASPQK
Found in AT1G31810.1, actin binding

Match to Query 2477: 1696.768802 from(849.391677,2+)
Elution from: 44.900 to 44.900 scan no 4626 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1696.7708  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 34 Expect: 0.0044  
Matched b ions: b(5), b(7), b(9), b(9)++, b(10), b(11), b(12)−98  
Matched y ions: y(4), y(6), y(8), y(10), y(10)−98++, y(11), y(12)++, y(12), y(13)−98++, y(13)++  
Precursor origin neutral loss: +

Peptide No.39

AEVVVPATESDGDDSVVEK  
Confirmed sites: @S:10  
Ambiguous sites:  

MS/MS Fragmentation of AEVVVPATESDGDDSVVEK  
Found in AT2G45520.1, similar to Os06g0129800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001056684.1); similar to hy  

Match to Query 3850: 2024.881042 from(1013.447797,2+)  
Elution from: 38.054 to 38.054 scan no 3732 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.8826
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 5.3e-008
Matched b ions: b(4), b(5), b(8), b(9), b(10)-98, b(13)++, b(16), b(17), b(17)-98, b(18)
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(13)++, y(13), y(14)++, y(14)-98, y(14), y(14)-98++, y(15)-98++, y(15)++, y(15), y(15)-98, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.40

AEVVVPATESDGDDSVVEK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AEVVVPATESDGDDSVVEK
Found in AT2G45520.1, similar to Os06g0129800 [Oryza sativa (japonica cultivar–group)] (GB:NP_001056684.1); similar to hy

Match to Query 2797: 2024.880876 from(675.967568,3+)
Elution from: 38.144 to 38.144 scan no 3573 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.8826
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(4), b(5)
Matched y ions: y(6), y(6)-98, y(11)++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.41

AFDLGSKPEGTSTPTK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of AFDLGSKPEGTSTPTK
Found in AT5G02240.1, catalytic/ coenzyme binding

Match to Query 2606: 1714.780533 from(572.600787,3+)
Elution from: 29.549 to 29.549 scan no 2585 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1714.7814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00014
Matched b ions: b(2), b(3), b(4), b(11)++, b(12)++
Matched y ions: y(3), y(4), y(5), y(5)−98, y(7), y(9)++, y(9), y(10)−98++, y(11)++, y(12)++, y(13)+, y(14)++, y(14)−98++, y(15)++
Precursor origin neutral loss: +

Peptide No.42

AFDLGSKPEGTSTPTK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of AFDLGSKPEGTSTPTK
Found in AT5G02240.1, catalytic/ coenzyme binding

Match to Query 2829: 1714.778658 from(572.600162,3+)
Elution from: 31.759 to 31.759 scan no 2660 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1714.7814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(3), b(4), b(9)++, b(12)++, b(13)--98++
Matched y ions: y(5), y(6), y(7), y(9)++, y(10)--98++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss:

Peptide No.43

AFDLGSKPEGTSTPTK
Confirmed sites: @T:15
Ambiguous sites:

MS/MS Fragmentation of AFDLGSKPEGTSTPTK
Found in AT5G02240.1, catalytic/ coenzyme binding

Match to Query 2538: 1714.780464 from(572.600764,3+)
Elution from: 29.745 to 29.745 scan no 2609 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1714.7814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 3.3e-005
Matched b ions: b(2), b(3), b(4), b(5), b(11)++
Matched y ions: y(3), y(4)++, y(6), y(9), y(9)++, y(11)++, y(12)+98++, y(13)++, y(14)++, y(14)+98++, y(15)++
Precursor origin neutral loss: +

Peptide No.44

AFFDSADWALLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AFFDSADWALLK
Found in AT4G16146.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69510.2); similar to negatively light–

Match to Query 1760: 1462.652246 from(732.333399,2+)
Elution from: 69.748 to 69.748 scan no 7298 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1462.6533
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.3e-005
Matched b ions: b(7), b(8)–98, b(9)–98, b(11)–98, b(11)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)–98++, y(8), y(8)–98, y(9), y(9)–98, y(10)++, y(10)–98++
Precursor origin neutral loss: +

Peptide No.45

AFGDYDNSDEDGDNDVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AFGDYDNSDEDGDNDVR
Found in AT5G64160.1, similar to Os02g0753200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048144.1)

Match to Query 2991: 1982.678462 from(992.346507,2+)
Elution from: 33.593 to 33.593 scan no 3066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.6803
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 Expect: 1e-008
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(10)+, b(11), b(11)-98, b(12)-98, b(12), b(13), b(14)-98, b(14)-98+, b(14), b(14)+, b(15), b(15)-98, b(15)+, b(16), b(16)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(11)+, y(12), y(12)+, y(13)-98++, y(13)-98, y(13), y(13)+, y(14)-98, y(14)-98++, y(14)+, y(15)+, y(15)-98++, y(15), y(15)-98, y(16)+
Precursor origin neutral loss: +

Peptide No.46

AFGDYDNSDEDGDNDVRR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AFGDYDNSDEDGDNDVRR
Found in AT5G64160.1, similar to Os02g0753200 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001048144.1)

Match to Query 3824: 2138.780736 from(713.934188,3+)
Elution from: 30.012 to 30.012 scan no 2611 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2138.7814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 Expect: 1.6e-008
Matched b ions: b(2), b(3), b(4), b(6), b(9)++, b(11), b(11)++, b(12)−98++, b(12)++, b(13)−98++, b(16)++
Matched y ions: y(2), y(3)++, y(3), y(5)++, y(5), y(7)++, y(7), y(8)++, y(9)++, y(9), y(10)++, y(11)−98++, y(11)++, y(12)++, y(12)−98++, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(15)++, y(15)−98++, y(16)−98++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.47

AFLDEDDPNQLPQSPK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of AFLDEDDPNQLPQSPK
Found in AT2G30530.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01970.1); similar to Os05g0315200 [Oryz]

Match to Query 3396: 1892.816462 from(947.415507,2+)
Elution from: 43.310 to 43.310 scan no 4405 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1892.8193
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 2e-006
Matched b ions: b(6), b(7), b(10), b(11), b(13), b(14)−98
Matched y ions: y(3), y(4), y(5)−98, y(5), y(6), y(6)−98, y(8), y(9), y(10)++, y(10), y(11), y(13), y(13)++
Precursor origin neutral loss:

Peptide No.48
AFNSAIDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of AFNSAIDR
Found in AT5G41870.1, glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
Match to Query 640: 972.409380 from(487.211966,2+)
Elution from: 24.327 to 24.327 scan no 1904 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 972.4066
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.059
Matched b ions: b(2), b(3), b(4)−98, b(6)−98++, b(6)−98, b(7), b(7)++
Matched y ions: y(3), y(6)−98++, y(6)−98, y(6)++, y(7)−98++
Precursor origin neutral loss: +

Peptide No.49

AFSDEQINR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AFSDEQINR
Found in AT1G24300.1, GYF domain-containing protein

Match to Query 825: 1158.470426 from(580.242489,2+) Elution from: 29.884 to 29.884 scan no 2509 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1158.4706
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0047
Matched b ions: b(4)-98, b(5)-98, b(6)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7)-98++, y(7), y(8)-98++
Precursor origin neutral loss: +

Peptide No.50

AFSEGDIQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AFSEGDIQK
Found in AT5G53420.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27900.2); similar to CCT [Medicago truncatula]

Match to Query 623: 1073.442364 from(537.728458,2+)  
Elution from: 29.366 to 29.366 scan no 2558 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1073.4430
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00035
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(4)++, b(4), b(5)−98, b(5), b(6)−98, b(6), b(6)++, b(7)−98, b(7), b(8), b(8)−98, b(8)−98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7)−98++, y(7)−98, y(7), y(7)++, y(8)−98++, y(8)++
Precursor origin neutral loss: +

Peptide No.51

AGDDLSQDEIGVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AGDDLSQDEIGVR
Found in AT5G09390.1, CD2−binding protein−related

Match to Query 1502: 1453.608034 from(727.811293,2+) Elution from: 37.416 to 37.416 scan no 3458 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1453.6086  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 56 Expect: 1.6e-005  
Matched b ions: b(4), b(7)−98, b(9)−98, b(10), b(10)−98  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)−98++, y(8)−98, y(9), y(9)−98++, y(9)−98, y(10)−98++, y(12)++  
Precursor origin neutral loss: +  

Peptide No.52  
AGDMSPDMFK  
Confirmed sites: @S:5  
Ambiguous sites:  

MS/MS Fragmentation of AGDMSPDMFK  
Found in AT5G21990.1, tetratricopeptide repeat (TPR)−containing protein  

Match to Query 1160: 1177.417700 from(589.716126,2+)  
Elution from: 42.013 to 42.013 scan no 4034 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1177.4185
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 5.7e-006
Matched b ions: b(3), b(5)−98, b(6)−98, b(6), b(7)−98, b(8)++, b(8)−98, b(9), b(9)−98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)−98, y(7), y(7)++, y(8)−98++, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.53
AGLPSPMR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AGLPSPMR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 312: 907.398302 from(454.706427,2+)
Elution from: 30.717 to 30.717 scan no 2740 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 907.3987
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.062
Matched b ions: b(3)
Matched y ions: y(4), y(4)++, y(5)++, y(5), y(5)−98++, y(5)−98, y(6)++
Precursor origin neutral loss: +

Peptide No.54
AGSSTTFLSPPSSPR
Confirmed sites: @S:9
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of AGSSTTFLSPPSSPR
Found in AT3G06170.1, TMS membrane family protein / tumour differentially expressed (TDE) family protein

Match to Query 2933: 1650.667864 from(826.341208,2+)
Elution from: 41.557 to 41.557 scan no 4265 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1650.6691
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00019
Matched b ions: b(9)–98
Matched y ions: y(5), y(6)–98, y(6), y(7), y(7)–98, y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.55

AHGTDPSPPMSPILGATR
Confirmed sites: “@S:7,@S:11”
Ambiguous sites:

MS/MS Fragmentation of AHGTDPSPPMSPILGATR
Found in AT3G23920.1, BMY7/TR-BAMY (beta-amylase 7); beta-amylase

Match to Query 3295: 1979.820450 from(660.947426,3+)
Elution from: 34.237 to 34.237 scan no 3214 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1979.8213
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0094
Matched b ions: b(5), b(6), b(7), b(8)-98, b(11)++, b(11), b(11)-196++, b(11)-98++, b(12)-196++, b(13)-98++, b(13)++, b(13)-196++, b(14)+++, b(14)-98++, b(14)-196++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7)+++, y(7), y(8), y(10)+++, y(11)+++, y(11)-98++, y(12)+++, y(13)-98++, y(13)+++, y(16)-196++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.56

AHGTDPSPPMSPILGATR
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of AHGTDPSPPMSPILGATR
Found in AT3G23920.1, BMY7/TR–BAMY (beta–amylase 7); beta–amylase

Match to Query 3643: 1963.823462 from(982.919007,2+)
Elution from: 41.908 to 41.908 scan no 4311 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1963.8264
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.054
Matched b ions: b(5), b(7), b(8)−98
Matched y ions: y(7), y(8)+, y(8), y(11)−98, y(11), y(12), y(13)−98, y(13)
Precursor origin neutral loss: +

Peptide No.57

AHTDDKACKTLMDEDTR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of AHTDDKACKTLMDEDTR
Found in AT1G06910.1, TRFL7 (TRF-LIKE 7); DNA binding / transcription factor

Match to Query 3133: 2085.853818 from(696.291882,3+)
Elution from: 45.513 to 45.513 scan no 4547 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2085.8497
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0069
Matched b ions: b(3), b(4), b(5), b(6)−98, b(8), b(8)++, b(10)−98++, b(12)−98++, b(13)−98++, b(14)++,
b(14)−98++, b(15)++, b(16)−98++
Matched y ions: y(8), y(8)++, y(9), y(9)++, y(12)++, y(13)++, y(14)++, y(16)−98++
Precursor origin neutral loss:

Peptide No.58

AHTDDKACKTLMDEDTR
Confirmed sites: “@T:3,@T:16”
Ambiguous sites:

MS/MS Fragmentation of AHTDDKACKTLMDEDTR
Found in AT1G06910.1, TRFL7 (TRF-LIKE 7); DNA binding / transcription factor

Match to Query 3988: 2165.822076 from(722.947968,3+)
Elution from: 50.539 to 50.539 scan no 5361 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2165.8160
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.035
Matched b ions: b(4), b(5)+, b(5)−98, b(5), b(6)+++, b(8)+, b(8), b(9), b(9)−98++, b(9)+, b(11)−98++, b(11)+++, b(12)+, b(13)−98++, b(14)+, b(16)+, b(16)−98++
Matched y ions: y(5)+, y(5)−98, y(6)−98++, y(6), y(7)+, y(7), y(8)+, y(8)−98, y(9)+, y(9)−98, y(9)−98++, y(10)+++, y(11)+, y(11)−98++, y(12)+, y(13)−98++, y(13)+, y(14)+, y(14)−98++, y(15)+, y(16)−98++, y(16)−196++
Precursor origin neutral loss: +

Peptide No.59
AIAPPELSPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AIAPPELSPR
Found in AT2G16470.1, zinc finger (CCCH-type) family protein / GYF domain-containing protein

Match to Query 771: 1129.551890 from(565.783221,2+)
Elution from: 35.381 to 35.381 scan no 3300 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1129.5532  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 59 Expect: 9.6e-006  
Matched b ions: b(2), b(3), b(4), b(7)  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(7)--98++, y(8), y(8)++, y(8)--98++, y(9)++  
Precursor origin neutral loss:  

Peptide No.60  

AIFSDDSEDDEDQPMNGK  
Confirmed sites: "@S:4,@S:7"  
Ambiguous sites:  

MS/MS Fragmentation of AIFSDDSEDDEDQPMNGK  
Found in AT5G23080.1, TGH (TOUGH); RNA binding  

Match to Query 3820: 2171.725060 from(1086.869806,2+)  
Elution from: 44.717 to 44.717 scan no 4602 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2171.7279
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 3e-005
Matched b ions: b(5), b(6), b(7)-98, b(9), b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(13)-196, b(14)-98, b(15)-98, b(16)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98++, y(14)-98++, y(15), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.61
AIFSDDSEDDDEDQPMNGK
Confirmed sites: "@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of AIFSDDSEDDDEDQPMNGK
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 4017: 2187.719946 from(1094.867249,2+)
Elution from: 40.002 to 40.002 scan no 4005 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2187.7228
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
  M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 28 Expect: 0.0045
Matched b ions: b(4), b(8)=196, b(8)=98, b(9), b(11)=98, b(11), b(12)=196, b(12)=98, b(12), b(13)=196, b(13)=98, b(13), b(14)=196, b(14)=98  
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(15)=98, y(16)++  
Precursor origin neutral loss: +

Peptide No.62

AIFSDDSEDDEDQPMNGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AIFSDDSEDDEDQPMNGK  
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 2945: 2091.758780 from(1046.886666,2+)
Elution from: 40.281 to 40.281 scan no 3819 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2091.7616
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00022
Matched b ions: b(11), b(12), b(13)–98, b(13), b(16)
Matched y ions: y(5), y(7), y(8), y(10), y(12)–98++, y(13), y(14)–98++, y(14), y(15)–
98++, y(16)–98++, y(16)++
Precursor origin neutral loss: +

Peptide No.63
AILNESSEFVGDK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AILNESSEFVGDK
Found in AT3G55440.1, ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-
phosphate isomerase

Match to Query 2113: 1487.654056 from(744.834304,2+)
Elution from: 42.933 to 42.933 scan no 4156 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1487.6544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00028
Matched b ions: b(5), b(6)-98, b(6), b(10)-98, b(10), b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.64
AILSDDEDASR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of AILSDDEDASR
Found in AT1G35220.1, similar to Os05g0355100 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001055287.1); similar to un

Match to Query 1461: 1270.507586 from(636.261069,2+)
Elution from: 30.263 to 30.263 scan no 2572 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1270.5078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 9.7e-007
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98++, y(9), y(9)++, y(9)-98, y(10) ++
Precursor origin neutral loss: +

Peptide No.65
AISMYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AISMYSR
Found in AT2G45980.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G00355.2); similar to conserved hypothet

Match to Query 463: 906.365522 from(454.190037,2+)
Elution from: 28.144 to 28.144 scan no 2407 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 906.3670
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0079
Matched b ions: b(2), b(3)
Matched y ions: y(1), y(2), y(3), y(4), y(5)–98, y(5), y(5)–98++, y(6)++
Precursor origin neutral loss: +

Peptide No.66
ALASFRSNPTN
Confirmed sites: "@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of ALASFRSNPTN
Found in AT2G16850.1, PIP2;8/PIP3B (plasma membrane intrinsic protein 2;8); water channel

Match to Query 2007: 1336.520750 from(669.267651,2+) Elution from: 34.534 to 34.534 scan no 3321 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1336.5213
Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 26 Expect: 0.017
Matched b ions: b(5)-98, b(6), b(7)-196, b(8)-98, b(8), b(8)-196, b(8)-98++, b(9)-98, b(9)-196++, b(10)-196++, b(10)-98++, b(10)++, b(10)-98, b(10)-196
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(9)++, y(9)-98++, y(10)-196++

Precursor origin neutral loss: +

Peptide No.67

ALAVVEKPIEEHTPK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of ALAVVEKPIEEHTPK
Found in AT2G45820.1, DNA-binding protein, putative

Match to Query 3157: 1739.883792 from(580.968540,3+)
Elution from: 28.080 to 28.080 scan no 2441 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1739.8858
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.015
Matched b ions: b(13)—98++, b(13)++, b(14)—98++
Matched y ions: y(3)—98, y(4), y(5)++, y(7)—98++, y(8)—98++, y(8)++, y(9)—98++, y(11)++, y(12)—98++, y(12)++, y(13), y(13)—98++
Precursor origin neutral loss: +

Peptide No.68

ALESQVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ALESQVK
Found in AT5G62050.1, OXA1 (Oxidase assembly 1); protein translocase

Match to Query 233: 853.393896 from(427.704224,2+))
Elution from: 21.007 to 21.007 scan no 1409 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 853.3946
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 25 Expect: 0.035
Matched b ions: b(2), b(3), b(4)-98, b(5)-98
Matched y ions:
Precursor origin neutral loss: +

Peptide No.69
ALGSFRSNATN
Confirmed sites: "@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of ALGSFRSNATN
Found in AT4G35100.1, PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel

Match to Query 1557: 1296.489682 from(649.252117,2+)  
Elution from: 32.019 to 32.019 scan no 2810 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.4900

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 32 Expect: 0.0025

Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)+, b(6)-98, b(7)-98++, b(7)-98, b(7), b(7)-196, b(8)-98, b(8), b(8)+, b(9)-98, b(9), b(9)-98++, b(9)-196, b(9)-196++, b(9)+, b(9)-196++, b(10)-98, b(10)-98++, b(10)-196++, b(10)-196, b(10)-196++

Matched y ions: y(2), y(3), y(4), y(5)+, y(5)-98, y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)-196++, y(8)+, y(8)-196, y(9)-98++, y(9)-98, y(9), y(9)-196, y(9)-196++, y(9)+, y(10)-196++, y(10)-98++, y(10)+, y(10)-196

Precursor origin neutral loss: +

Peptide No. 70

ALGSFRSNATN

Confirmed sites: "@S:4, @S:7, @T:10"

Ambiguous sites:

MS/MS Fragmentation of ALGSFRSNATN

Found in AT4G35100.1, PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel

Match to Query 1969: 1376.455266 from(689.234909,2+)

Elution from: 34.351 to 34.351 scan no 3249 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4564
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0041
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)-196++, b(7)-98, b(8), b(8)-98, b(8)++,
b(9)-98, b(9), b(9)++, b(10), b(10)-98++, b(10)++, b(10)-294++, b(10)-196++
Matched y ions: y(3), y(4), y(5)-196, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-294, y(8), y(8)-98,
y(8)-196++, y(8)-98++, y(9)++, y(9)-196++, y(9), y(9)-98, y(9)-98++, y(9)++, y(9)-294++, y(10)-196++
Precursor origin neutral loss: +

Peptide No.71

ALGSFRSNATN
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ALGSFRSNATN
Found in AT4G35100.1, PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel

Match to Query 1036: 1216.522874 from(609.268713,2+)
Elution from: 27.605 to 27.605 scan no 2285 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1216.5237
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.7e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)–98, b(7), b(7)–98++, b(7)+, b(8), b(8)–98, b(8)+, b(9), b(9)–98, b(9)–98++, b(9)+, b(10), b(10)–98, b(10)+, b(10)–98++
Matched y ions: y(2), y(3), y(4), y(5)–98, y(6), y(7), y(7)–98, y(8), y(8)+, y(8)–98, y(9), y(9)–98++, y(9)–98, y(9)+, y(10)–98++, y(10)+
Precursor origin neutral loss: +

Peptide No.72

ALGSFRSNATN
Confirmed sites: ”@S:7,@T:10”
Ambiguous sites:

MS/MS Fragmentation of ALGSFRSNATN
Found in AT4G35100.1, PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel

Match to Query 1324: 1296.489220 from(649.251886,2+)
Elution from: 30.293 to 30.293 scan no 2682 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1296.4900
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00027
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)−98, b(8), b(8)−98, b(9), b(9)++, b(9)−98, b(9)−98++, b(10)−196++, b(10)−98, b(10)−196, b(10), b(10)−98++, b(10)++
Matched y ions: y(2)−98, y(2), y(3)−98, y(3), y(4), y(5)−98, y(6)−98, y(6)−98++, y(6)−196++, y(6)−98, y(6)−196, y(7)++, y(7), y(7)−98, y(7)−98++, y(8), y(8)−98, y(8)−98++, y(8)++, y(9), y(9)−98, y(9)−98++, y(9)−196++, y(9)−98, y(9)++, y(9)−98++, y(9)−196, y(9)++, y(9)−196++, y(10)++, y(10)−196++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.73

ALIDATSSGSDLEDES GIR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ALIDATSSGSDLEDES GIR
Found in AT5G60160.1, aspartyl aminopeptidase, putative

Match to Query 3536: 2014.869946 from(1008.442249,2+)
Elution from: 46.970 to 46.970 scan no 4897 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2014.8732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 7e−005
Matched b ions: b(5), b(6), b(12)−98, b(13)−98, b(13), b(15), b(18)
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(11)−98, y(11), y(13), y(13)−98, y(14), y(15)
Precursor origin neutral loss: +

Peptide No.74

ALLANYSQTPR
Confirmed sites: ”@S:7,@T:9”
Ambiguous sites:

MS/MS Fragmentation of ALLANYSQTPR
Found in AT1G09770.1, ATCDC5 (Arabidopsis thaliana homolog of cdc5); DNA binding / transcription factor

Match to Query 1925: 1392.582798 from(697.298675,2+) Elution from: 39.436 to 39.436 scan no 3918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1392.5840
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.012
Matched b ions: b(4), b(6), b(7), b(9)–98
Matched y ions: y(2), y(5), y(5)–98, y(6)–98, y(6), y(7)–98, y(7), y(8), y(8)+, y(8)–196, y(9)–98++, y(9)++
Precursor origin neutral loss: +

Peptide No.75

ALLEGGSDDEGASTEAQGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ALLEGGSDDEGASTEAQGR
Found in AT1G64790.1, translational activator family protein

Match to Query 3617: 1941.793612 from(971.904082,2+)
Elution from: 32.692 to 32.692 scan no 3003 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1941.7952
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 1.2e-009
Matched b ions: b(4), b(5), b(6), b(7)–98, b(8)–98, b(9), b(9)–98, b(10), b(11)–98, b(12)–98, b(12), b(13)–98, b(13), b(14)–98, b(14), b(14)–98++, b(15)–98, b(15), b(15)–98++, b(16)–98, b(16), b(17), b(17)–98, b(17)++, b(18), b(18)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)–98, y(10), y(11)++, y(11), y(12), y(13), y(13)–98++, y(13)–98, y(14)–98, y(14)–98++, y(14), y(14)++, y(15)–98, y(15), y(15)–98++, y(15)++, y(16)–98++, y(16)–98, y(16), y(17)++, y(17)–98++, y(18)–98++, y(18)++
Precursor origin neutral loss: +

Peptide No.76

ALLIEDGGGLQSASPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of ALLIEDGGGLQSASPR
Found in AT3G06550.1, similar to O-acetyltransferase [Arabidopsis thaliana] (TAIR:AT2G34410.2); similar to acetyltransfer

Match to Query 2519: 1662.796678 from(832.405615,2+) 
Elution from: 44.251 to 44.251 scan no 4547 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1662.7977
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 Expect: 6.4e-009
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(10), b(11), b(12), b(13), b(14)−98
Matched y ions: y(2), y(3)−98, y(4)−98, y(4), y(5)−98, y(5), y(6)−98, y(7)−98, y(8), y(8)−98, y(9), y(9)−98++, y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)++, y(12)−98, y(13), y(13)−98++, y(13)−98, y(13)++, y(14)−98++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.77

ALPTYTPDSPGDATR
Confirmed sites: @S.9
Ambiguous sites:

MS/MS Fragmentation of ALPTYTPDSPGDATR
Found in AT2G45290.1, transketolase, putative

Match to Query 2309: 1640.708664 from(821.361608,2+)
Elution from: 34.944 to 34.944 scan no 3309 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1640.7083
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0031
Matched b ions: b(6)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(8−98), y(9)−98, y(9), y(10), y(12)++, y(13)++, y(13)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.78

ALPTYTPESPGDATR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ALPTYTPESPGDATR
Found in AT3G60750.1, transketolase, putative

Match to Query 2717: 1654.722320 from(828.368436,2+) Elution from: 36.634 to 36.634 scan no 3530 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1654.7240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 2.6e-006
Matched b ions: b(5), b(6), b(8)
Matched y ions: y(3), y(4), y(6), y(7), y(7)−98, y(8), y(9)−98, y(9), y(10), y(10)−98, y(11), y(12), y(12)++
, y(13)+, y(13)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.79
ALQESMNVGSPPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ALQESMNVGSPPR
Found in AT4G36860.2, LIM domain-containing protein

Match to Query 2056: 1464.641344 from(733.327948,2+)
Elution from: 35.055 to 35.055 scan no 3105 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1464.6432  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 38 Expect: 0.0014  
Matched b ions: b(6), b(7), b(8), b(9), b(10)-98, b(10)  
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)-98, y(11)-98, y(11)-98++, y(11)+  
Precursor origin neutral loss: +  

Peptide No.80  
ALSPTTSVASK  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of ALSPTTSVASK  
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1); similar to hypothetical prote  

Match to Query 815: 1140.542094 from(571.278323,2+)  
Elution from: 24.682 to 24.682 scan no 1890 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1140.5427
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00086
Matched b ions: b(2), b(3)-98, b(3), b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9)-98++, y(9), y(9)+, y(10)+
Precursor origin neutral loss: +

Peptide No.81
ALSPTTSVASKGEK
Confirmed sites: “@S:3,@S:10”
Ambiguous sites:

MS/MS Fragmentation of ALSPTTSVASKGEK
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1);
similar to hypothetical prote

Match to Query 2622: 1534.666886 from(768.340719,2+)
Elution from: 23.343 to 23.343 scan no 1789 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1534.6681
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.034
Matched b ions: b(3), b(7)--98, b(8), b(9)--98, b(12)--196, b(13)
Matched y ions: y(4), y(6)--98, y(7), y(7)--98, y(8), y(9)--98, y(10), y(10)++, y(11)++, y(11)--98, y(11), y(11)--98++, y(12)--98++, y(12)--196++, y(12)++, y(13)--98++, y(13)++
Precursor origin neutral loss: +

Peptide No.82

ALSTSKPDPVVEDQA
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ALSTSKPDPVVEDQA
Found in AT2G41840.1, 40S ribosomal protein S2 (RPS2C)

Match to Query 2576: 1635.738100 from(818.876326,2+)
Elution from: 33.693 to 33.693 scan no 2921 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.7393
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 2.4e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(10), b(10)-98,
   b(11), b(11)-98, b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98, b(13)
   +, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(12)++, y(13)-98, y(13)-98++, y
   (13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.83
ALSTSKPDPVVEDQA
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ALSTSKPDPVVEDQA
Found in AT2G41840.1, 40S ribosomal protein S2 (RPS2C)

Match to Query 2899: 1635.737670 from(818.876111,2+)
Elution from: 31.880 to 31.880 scan no 2938 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.7393
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00023
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(4), y(5), y(7), y(9), y(10), y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.84

AMGTSYTETELNR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AMGTSYTETELNR
Found in AT1G18210.1, calcium-binding protein, putative

Match to Query 2022: 1551.628098 from(776.821325,2+)  
Elution from: 36.060 to 36.060 scan no 3459 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1551.6276
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
 S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 34 Expect: 0.0027
Matched b ions: b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9)-98++, y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.85

AMKSNYTKQEMSNWK
Confirmed sites:
Ambiguous sites: @Y:6orT:7

MS/MS Fragmentation of AMKSNYTKQEMSNWK
Found in AT4G09930.1, avirulence-responsive family protein / avirulence induced gene (AIG1) family protein

Match to Query 3148: 1940.814064 from(486.210792,4+)
Elution from: 25.360 to 25.360 scan no 1982 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1940.8161
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
    M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 Expect: 0.035
Matched b ions: b(7)++, b(8)-98++, b(11)-98++
Matched y ions: y(4)++, y(6)++, y(7)++, y(8)++, y(10)-98++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.86

AMPVAAESPCMEEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AMPVAAESPCMEEK
Found in AT4G35370.1, transducin family protein / WD-40 repeat family protein

Match to Query 2319: 1628.628322 from(815.321437,2+)  
Elution from: 31.828 to 31.828 scan no 2894 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1628.6285
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00039
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(10), b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(3), y(4)++, y(6), y(7)-98, y(8), y(9), y(10)++, y(10), y(10)-98, y(11)-98++, y(11)+, y(11)-98, y(12)++, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.87
ANLQTEDPGSPVSPK
Confirmed sites: “@S:10, @S:13”
Ambiguous sites:

MS/MS Fragmentation of ANLQTEDPGSPVSPK
Found in AT3G09670.1, PWPP domain-containing protein

Match to Query 2448: 1698.688808 from(850.351680,2+)
Elution from: 29.692 to 29.692 scan no 2625 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1698.6903
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0035
Matched b ions: b(7), b(10)-98, b(13)-98
Matched y ions: y(5), y(7), y(8)-98, y(8), y(9), y(11), y(12)+, y(13)-196++
Precursor origin neutral loss: +

Peptide No.88

APDHADYVISPSFGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of APDHADYVISPSFGR
Found in AT4G34860.1, beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase,

Match to Query 2527: 1710.739310 from(856.376931,2+)
Elution from: 41.115 to 41.115 scan no 4132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1710.7403
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.6e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10)−98, b(10), b(12)++, b(14)
Matched y ions: y(3), y(4), y(5), y(6)−98, y(6), y(7)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12)++, y(12)−98++, y(13)−98++, y(13)++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.89

APEDPILGVTVAYNNDPSPVK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of APEDPILGVTVAYNNDPSPVK
Found in AT5G19550.1, ASP2 (ASPARTATE AMINOTRANSFERASE 2)

Match to Query 4149: 2275.075278 from(759.365702,3+)
Elution from: 53.235 to 53.235 scan no 5672 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2275.0773
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00065
Matched b ions: b(3), b(7), b(8), b(9), b(10), b(11), b(11)++, b(12)++, b(12), b(14)++, b(15)++, b(16)++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(13)++, y(14)-98++, y(15)-98++, y(16)-98++
Precursor origin neutral loss:

Peptide No.90
APEEDEEDSGDEDDDRPPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of APEEDEEDSGDEDDDRPPK
Found in AT1G47970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17160.1); similar to conserved hypothet

Match to Query 3469: 2223.795279 from(742.272369,3+)
Elution from: 19.448 to 19.448 scan no 1188 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2223.7964
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 7.7e-008
Matched b ions: b(5), b(7), b(8), b(11)-98, b(12)++, b(14)
Matched y ions: y(3), y(4)++, y(4), y(6)++, y(7)++, y(7), y(8)++, y(8), y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.91
APEEDEDSGDEDDDRPPKR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of APEEDEDSGDEDDDRPPKR
Found in A T1G47970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17160.1); similar to conserved hypothet

Match to Query 4292: 2379.895395 from(794.305741,3+)
Elution from: 18.223 to 18.223 scan no 1082 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2379.8976
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.2e-007
Matched b ions: b(4), b(5), b(6), b(8), b(9)-98, b(9)+, b(11), b(13)+, b(14), b(14)+, b(15), b(18)+, b(19)+, b(19)-98++
Matched y ions: y(4), y(5)+, y(6)+, y(7)+, y(8)+, y(9)+, y(10)+, y(11)+, y(12)-98++, y(12)+, y(13)-98++, y(14)-98++, y(15)-98++, y(15)+, y(16)-98++, y(16)+, y(17)-98++, y(17)+, y(18)-98++, y(18)+, y(19)-98++
Precursor origin neutral loss: +

Peptide No.92
APELHTGGTAGPSSNSAK
Confirmed sites: @S:14
Ambiguous sites:
MS/MS Fragmentation of APELHTGGTAGPSSNSAK
Found in AT5G40930.1, TOM20-4 (TRANSLOCASE OF OUTER MEMBRANE 20-4)

Match to Query 3035: 1760.771865 from(587.931231,3+)
Elution from: 20.796 to 20.796 scan no 1386 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1760.7730
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00099
Matched b ions: b(5), b(8), b(9), b(10), b(11), b(11), b(14)++
Matched y ions: y(4), y(5)−98, y(6), y(6)++, y(6)−98, y(7)+, y(7), y(7)−98, y(7)−98++, y(8)+, y(8), y(8)−98++, y(9)−98, y(9)++, y(10)−98++, y(11)+, y(11)+, y(13)−98++, y(15)+, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.93
APEYALVTQNSDPTSPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of APEYALVTQNSDPTSPR
Found in AT4G08330.1, similar to protein–methionine–S–oxide reductase [Arabidopsis thaliana] (TAIR:AT2G17705.1); similar

Match to Query 3536: 1924.855910 from (963.435231,2+)
Elution from: 39.554 to 39.554 scan no 3819 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1924.8567
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00021
Matched b ions: b(6), b(7), b(10), b(11), b(12), b(12)+, b(14)+, b(14), b(15)−98
Matched y ions: y(4), y(5)−98, y(6), y(7), y(10)−98, y(10), y(11)−98, y(11), y(12), y(13)
Precursor origin neutral loss:

Peptide No.94

APSPVNNPLLGGIPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of APSPVNNPLLGGIPK
Found in AT1G15750.1, TPL/WSIP1 (WUS–INTERACTING PROTEIN 1); protein binding

Match to Query 2324: 1552.799126 from(777.406839,2+)  
Elution from: 52.889 to 52.889 scan no 5401 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1552.8014
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00022
Matched b ions: b(5)++, b(5), b(6), b(7)−98, b(7), b(8)−98, b(10)−98, b(10)++, b(13)−98, b(13), b(14)−98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)++, y(13)−98++, y(13)++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.95

APSPVNNPLLGLSLPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of APSPVNNPLLGLSLPK
Found in AT1G80490.1, TPR1 (TOPLESS-RELATED 1)

Match to Query 2202: 1582.812104 from(792.413328,2+)
Elution from: 52.192 to 52.192 scan no 5545 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.8120
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00088
Matched b ions: b(7), b(7)-98, b(8)-98
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.96

APVCMRDTVMYNAMITGFSHNNDGYSAINLFCKMK
Confirmed sites: “@Y:25,@S:26”
Ambiguous sites: @Y:11orT:8

MS/MS Fragmentation of APVCMRDTVMYNAMITGFSHNNDGYSAINLFCKMK
Found in AT1G25360.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 4505: 4343.720658 from(1448.914162,3+)
Elution from: 60.689 to 60.689 scan no 6220 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 4343.7119
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
- Y11 : Phospho (Y)
- M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
- Y25 : Phospho (Y)
- S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
- M34 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.04
Matched b ions: b(18)++, b(20)++
Matched y ions: y(13)++, y(14)++, y(15)--98++, y(15)++, y(17)++, y(22)++
Precursor origin neutral loss:

Peptide No.97

AQASSDGDEEEAIPLR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AQASSDGDEEEAIPLR
Found in AT5G16150.1, GLT1/PGLCT (GLUCOSE TRANSPORTER 1); carbohydrate transporter/ sugar porter

Match to Query 2410: 1766.733346 from(884.373949,2+)
Elution from: 36.359 to 36.359 scan no 3430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1766.7359
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 9.7e-005
Matched b ions: b(8), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(12), y(14)
Precursor origin neutral loss:

Peptide No.98

AQEVAADSLNSNLVDGQSR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AQEVAADSLNSNLVDGQSR
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 3496: 2053.893202 from(1027.953877,2+)  
Elution from: 43.031 to 43.031 scan no 4382 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2053.8953
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 4.2e-009
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12), b(13), b(13)-98, b(14), b(14)-98, b(15), b(15)-98, b(16)-98, b(17)-98, b(17), b(18)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)+, y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15), y(15)+, y(15)-98, y(16)-98+
Precursor origin neutral loss: +

Peptide No.99

AQEVAADLSNLDVDGQSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AQEVAADLSNLDVDGQSR
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 3915: 2053.892212 from(1027.953382,2+)
Elution from: 42.323 to 42.323 scan no 4272 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2053.8953
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 1.5e-008
Matched b ions: b(5), b(7), b(9)–98, b(9), b(10)–98, b(11), b(11)–98, b(12), b(12), b(13), b(14), b(14)–98, b(15), b(17)–98, b(17), b(18)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(13)–98, y(14), y(14)–98, y(15), y(15)–98, y(16)++
Precursor origin neutral loss: +

Peptide No.100
AQEVAADSLNSLVDGQSR
Confirmed sites: ”@S:8,@S:10”
Ambiguous sites:

MS/MS Fragmentation of AQEVAADSLNSLVDGQSR
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 3817: 2133.859668 from(1067.937110,2+)
Elution from: 45.131 to 45.131 scan no 4624 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2133.8616
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 8.8e−007
Matched b ions: b(4), b(5), b(6), b(7), b(9)−98, b(11)−196, b(12), b(12), b(13), b(13)−98, b(14)−98, b(14)−98, b(14)−196, b(14), b(15), b(15)−98, b(17), b(18)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(12)−98, y(12), y(13)−196++, y(13)−98, y(13), y(13)−196, y(14), y(14)−98, y(15)−98, y(15), y(16)−98, y(17)++
Precursor origin neutral loss: +

Peptide No.101

AQLVSTGGSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of AQLVSTGGSPK
Found in AT3G24870.1, DNA binding

Match to Query 743: 1123.526408 from(562.770480,2+)
Elution from: 21.735 to 21.735 scan no 1534 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.5274
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0037
Matched b ions: b(2), b(3), b(4), b(6)
Matched y ions: y(3)-98, y(5), y(6)+, y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.102
AQPSVESLEVLSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of AQPSVESLEVLSK
Found in AT5G03630.1, monodehydroascorbate reductase, putative

Match to Query 1879: 1465.704100 from(733.859326,2+)
Elution from: 45.015 to 45.015 scan no 4648 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1465.7065
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.019
Matched b ions: b(5)−98, b(6)−98, b(6), b(10)++
Matched y ions: y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11)−98, y(11), y(11)−98++
Precursor origin neutral loss: +

Peptide No.103

AQQLESESEEEMLK
Confirmed sites: "@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of AQQLESESEEEMLK
Found in AT2G25650.1, DNA-binding storekeeper protein–related

Match to Query 2800: 1809.675844 from(905.845198,2+)
Elution from: 39.580 to 39.580 scan no 3929 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1809.6780
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00085
Matched b ions: b(5), b(6)–98, b(7)–98, b(7), b(11)–98, b(12)–98, b(13)–98, b(13)
Matched y ions: y(3), y(5), y(6), y(7), y(7)–98, y(8), y(9)–98, y(9), y(10)–98, y(10), y(11)–98, y(11), y(11)–196, y(12)–98++, y(12)++
Precursor origin neutral loss: +

Peptide No.104
AQQLESESEEEMLK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of AQQLESESEEEMLK
Found in AT2G25650.1, DNA–binding storekeeper protein–related
Match to Query 2960: 1729.712126 from(865.863339,2+)
Elution from: 37.320 to 37.320 scan no 3521 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1729.7117
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00018
Matched b ions: b(4), b(5), b(6), b(9)-98, b(10)-98, b(11), b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(3), y(4), y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.105

AQTGVMTAETGTYR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of AQTGVMTAETGTYR
Found in AT4G38470.1, protein kinase family protein

Match to Query 2132: 1564.660652 from(783.337602,2+)  
Elution from: 31.746 to 31.746 scan no 2883 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1564.6592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 2.7e-005
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(10), y(10)
++, y(11), y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.106
ARDRSPVLDEGSPK
Confirmed sites: "@S:5,@S:13"
Ambiguous sites:

MS/MS Fragmentation of ARDRSPVLDEGSPK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 2887: 1800.743103 from(601.254977,3+)
Elution from: 20.554 to 20.554 scan no 1341 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7444
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 :  Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 :  Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67  Expect: 1.7e-006
Matched b ions: b(3), b(4)++, b(4), b(5)−98++, b(5)+, b(6)−98++, b(6)++, b(7)++, b(7)−98++, b(8)+, b(8)−98++, b(9)−98++, b(9)++, b(10)−98++, b(11)++, b(11)−98++, b(12)++, b(12)−98++, b(13)−196++, b(13)−98++, b(13)++, b(14)−196++, b(14)++, b(14)−98++
Matched y ions: y(2), y(4)−98, y(4), y(5)−98++, y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9)−98, y(9), y(9)++, y(10)+, y(10)−98, y(10), y(10)−98++, y(11)−196++, y(11)++, y(12)++, y(12)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.107

ARLSPDYK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ARLSPDYK
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine.serine-rich splicing factor 41); RNA binding

Match to Query 684: 1028.469236 from(515.241894,2+)
Elution from: 21.561 to 21.561 scan no 1414 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1028.4692
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0098
Matched b ions: b(4)−98, b(5)−98, b(6)−98, b(6), b(7)−98
Matched y ions: y(2)
Precursor origin neutral loss: +

Peptide No.108

ARLSPDYKR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ARLSPDYKR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 1317: 1184.569652 from(593.292102,2+)  
Elution from: 18.604 to 18.604 scan no 1165 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1184.5703
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.016
Matched b ions: b(2), b(3), b(4)–98, b(4), b(5)–98, b(6)–98, b(6)–98, b(7)–98, b(7), b(8)–98, b(8), b(8)++
Matched y ions: y(1), y(3), y(5), y(6), y(6)–98, y(7)–98, y(7)–98++, y(7), y(8)–98++, y(8)++
Precursor origin neutral loss: +

Peptide No.109

ARPSAESLDELVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ARPSAESLDELVK
Found in AT3G52880.1, ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); monodehydroascorbate reductase (NADH)

Match to Query 2281: 1493.712008 from(747.863280,2+)
Elution from: 39.719 to 39.719 scan no 3956 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1493.7126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 51 Expect: 6.5e-005
Matched b ions: b(2), b(4)-98, b(4)+++, b(5)-98, b(6), b(6)-98, b(7)+++, b(7)-98, b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(10)+++, b(11)-98++, b(11)+++, b(11)-98++, b(11), b(12), b(12)-98++, b(12)-98, b(12)+++
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(9), y(10), y(10)-98, y(10)+++, y(11)-98, y(11), y(11)-98++
Precursor origin neutral loss: +

Peptide No. 110

ARSPEYDRYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ARSPEYDRYK
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding

Match to Query 1444: 1363.590843 from(455.537557,3+)
Elution from: 18.695 to 18.695 scan no 1098 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1363.5921
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 29 Expect: 0.0085
Matched b ions: b(3)-98, b(3), b(5), b(7), b(8)+, b(9)-98++, b(9)+
Matched y ions: y(3)+, y(4), y(5), y(5)+, y(6)+, y(7)+, y(8)+
Precursor origin neutral loss: +

Peptide No.111

ARSVDQEEVVVGLEDKA
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ARSVDQEEVVVGLEDKA
Found in AT3G46530.1, RPP13 (RECOGNITION OF PERONOSPORA PARASITICA 13); ATP binding

Match to Query 3475: 2037.924378 from(1019.969465,2+)
Elution from: 43.247 to 43.247 scan no 4411 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2037.9255
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 1.9e-009
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)+, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13), b(13)+, b(13)-98, b(14)-98++, b(14)-98, b(14), b(15), b(15)-98, b(15)-98++, b(16)-98, b(16), b(17), b(17)-98++, b(17)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.112
ASAEAAPASGDSDVNMQDAK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of ASAEAAPASGDSDVNMQDAK
Found in AT1G79920.1, heat shock protein 70, putative / HSP70, putative

Match to Query 3696: 2013.796862 from(1007.905707,2+)
Elution from: 27.320 to 27.320 scan no 2266 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2013.7986
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 69 Expect: 8.9e-007
Matched b ions: b(6), b(8), b(9), b(11)+, b(11), b(14)−98, b(14), b(16), b(16)+, b(17)−98, b(17)−98++, b(18)
Matched y ions: y(6), y(7), y(8), y(9), y(9)−98, y(10), y(11), y(12), y(13)+, y(13), y(14)+, y(14)−98, y(14), y(14)−98++, y(15), y(15)+, y(15)−98++, y(18)+, y(18)−98++, y(19)−98++
Precursor origin neutral loss: +

Peptide No.113
ASAELLGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASAELLGR
Found in AT3G50230.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 269: 895.415612 from(448.715082,2+)
Elution from: 28.106 to 28.106 scan no 2342 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 895.4164
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.012
Matched b ions: b(2), b(5)–98, b(6)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++
Precursor origin neutral loss: +

Peptide No.114

ASAEVLGK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASAEVLGK
Found in AT3G02880.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 237: 853.394160 from(427.704356,2+)
Elution from: 20.968 to 20.968 scan no 1394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 853.3946
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00022
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.115

ASANSLSAPIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ASANSLSAPIK
Found in AT4G10730.1, kinase

Match to Query 1013: 1137.543154 from(569.778853,2+) Elution from: 31.678 to 31.678 scan no 2649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1137.5431
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00049
Matched b ions: b(5), b(6), b(8)-98, b(9), b(10), b(10)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9)++, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.116

ASDMTSAAKEK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of ASDMTSAKE
Found in AT3G17520.1, late embryogenesis abundant domain-containing protein / LEA domain-containing protein

Match to Query 1211: 1233.496209 from(412.172679,3+)
Elution from: 19.520 to 19.520 scan no 1210 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1233.4948
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.02
Matched b ions: b(3), b(5)++, b(6), b(6)++, b(6)−98++, b(7)−98++
Matched y ions: y(1), y(3), y(5)++, y(5), y(6)++, y(7)−98++, y(9)−98++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.117

ASDYSVSSAGDPFR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ASDYSVSSAGDPFR
Found in AT1G08680.1, ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 1633: 1537.605008 from(769.809780,2+) Elution from: 41.104 to 41.104 scan no 4047 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1537.6086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0048
Matched b ions: b(6), b(10)-98++, b(11), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(10)-98, y(13)-98++
Precursor origin neutral loss:

Peptide No.118

ASDYSVSSAGDPFR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ASDYSVSSAGDPFR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 2431: 1537.607234 from(769.810893,2+)
Elution from: 42.316 to 42.316 scan no 4271 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1537.6086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 1.7e-007
Matched b ions: b(5), b(6), b(7), b(9)—98, b(10), b(10)—98, b(11), b(11)—98, b(13)—98, b(13)—98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)—98, y(8)—98++, y(9), y(9)—98, y(10), y(10)—98, y(11), y(11)++, y(12)++
Precursor origin neutral loss:

Peptide No.119
ASEDELHLESMDK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ASEDELHLESMDK
Found in AT5G47690.1, binding

Match to Query 2000: 1697.646680 from(849.830616,2+)
Elution from: 38.536 to 38.536 scan no 3722 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1697.6491
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 Expect: 7e-008
Matched b ions: b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12), b(12)-98, b(13)-98, b(13)
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8)-98++, y(8),
y(9)-98, y(9), y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.120

ASEVGKYATWR
Confirmed sites: “@Y:7,@T:9”
Ambiguous sites:

MS/MS Fragmentation of ASEVGKYATWR
Found in AT2G01500.1, HOS9/PFS2 (HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE 9); transcription factor

Match to Query 1985: 1426.571241 from(476.531023,3+)
Elution from: 20.741 to 20.741 scan no 1313 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1426.5683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7: Phospho (Y)
T9: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 20 Expect: 0.042
Matched b ions: b(5), b(7)++, b(8)++, b(9)++, b(10)++, b(10)-98++
Matched y ions: y(2), y(3)-98, y(4), y(5)++, y(6)-98++
Precursor origin neutral loss: +

Peptide No.121

ASGSPVPVMHSPPRPVTVK
Confirmed sites: @S:12
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of ASGSPVPVMHSPPRPVTVK
Found in AT1G77180.1, chromatin protein family

Match to Query 3962: 2215.025223 from(739.349017,3+)
Elution from: 31.468 to 31.468 scan no 2842 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2215.0261
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.012
Matched b ions: b(7)-98, b(7), b(10), b(11)+++, b(13)-196++, b(16)+++, b(17)-98++
Matched y ions: y(8)+++, y(8), y(9)+++, y(10)-98++, y(12)+++, y(13)+++, y(13)-98++, y(14)-98++, y(14)+++, y(15)+++, y(15)-98++, y(16)+++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.122

ASHGSDDNSSEPMIDTK
Confirmed sites:
Ambiguous sites: @S:2orS:5

MS/MS Fragmentation of ASHGSDDNSSEPMIDTK
Found in AT5G23880.1, CPSF100 (ENHANCED SILENCING PHENOTYPE 5)

Match to Query 3419: 1982.789756 from(992.402154,2+)
Elution from: 31.730 to 31.730 scan no 2844 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.7928
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 7.9e-005
Matched b ions: b(6), b(7), b(7)–98, b(8), b(9), b(11), b(11)–98, b(13), b(14)–98, b(14), b(14)++, b(15), b(16), b(16)–98
Matched y ions: y(3), y(7), y(8), y(9), y(10), y(11), y(13), y(17)++
Precursor origin neutral loss: +

Peptide No.123
ASHGSDDNSESPEMIDTK
Confirmed sites: @S:10
Ambiguous sites: @S:2orS:5

MS/MS Fragmentation of ASHGSDNSSEPMIDTK
Found in AT5G23880.1, CPSF100 (ENHANCED SILENCING PHENOTYPE 5)

Match to Query 3456: 2062.756298 from(1032.385425,2+)
Elution from: 34.485 to 34.485 scan no 3316 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2062.7592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.035
Matched b ions: b(7), b(9)+, b(10)−196, b(11)−98, b(11), b(12)−196, b(14), b(15)−98, b(15), b(16)−98, b(16)
Matched y ions: y(4), y(7), y(9)−98, y(12)
Precursor origin neutral loss: +

Peptide No.124
ASHGSDDNSSEPMIIDTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ASHGSDDNSSEPMIIDTK
Found in AT5G23880.1, CPSF100 (ENHANCED SILENCING PHENOTYPE 5)

Match to Query 3335: 1982.791322 from(992.402937,2+)
Elution from: 30.872 to 30.872 scan no 2778 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.7928
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00028
Matched b ions: b(4), b(7)−98, b(7), b(9)++, b(11)−98, b(11), b(12)−98, b(13), b(14), b(15)−98, b(15), b(16)
Matched y ions: y(4), y(7), y(10), y(11), y(15)−98, y(15), y(16)++
Precursor origin neutral loss: +

Peptide No.125

ASHGSDDNSSEPIMIDTK
Confirmed sites: @S:5orS:9
Ambiguous sites: @S:5orS:9

MS/MS Fragmentation of ASHGSDDNSSEPIMIDTK
Found in AT5G23880.1, CPSF100 (ENHANCED SILENCING PHENOTYP 5)

Match to Query 3303: 1982.792088 from(661.937972,3+)
Elution from: 31.033 to 31.033 scan no 2783 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.7928
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.011
Matched b ions: b(9), b(9)+, b(9)-98++, b(11)-98++, b(11), b(11)+, b(12)-98++, b(13)-98++, b(14)+, b(15)+, b(16)+
Matched y ions: y(2), y(3), y(4), y(5), y(7)+, y(7), y(8), y(9), y(9)+, y(14)+
Precursor origin neutral loss: +

Peptide No.126
ASHGSDDNSSEPMIIDTK
Confirmed sites: "@S:9,@S:10"
Ambiguous sites:

MS/MS Fragmentation of ASHGSDSDNSSEPMIIDTK
Found in AT5G23880.1, CPSF100 (ENHANCED SILENCING PHENOTYPE 5)

Match to Query 2886: 2062.759702 from(1032.387127,2+)
Elution from: 35.911 to 35.911 scan no 3266 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2062.7592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0018
Matched b ions: b(8), b(10), b(11), b(11)-98, b(12)-196, b(14), b(15), b(15)-98, b(16)
Matched y ions: y(7)
Precursor origin neutral loss: +

Peptide No.127

ASLLGELSDESSEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ASLLGELSDESSEK
Found in AT1G34260.1, phosphatidylinositol-4-phosphate 5-kinase family protein

Match to Query 1845: 1543.663546 from(772.839049,2+)  
Elution from: 44.851 to 44.851 scan no 4467 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1543.6654
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0096
Matched b ions: b(4), b(7)
Matched y ions: y(3), y(5), y(6), y(7), y(8)−98, y(8), y(10), y(10)−98, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.128

ASLSLSSAHFSSTSSSSR
Confirmed sites: "@S:2,@S:4"
Ambiguous sites:

MS/MS Fragmentation of ASLSLSSAHFSSTSSSSR
Found in AT5G35170.1, adenylate kinase family protein

Match to Query 3368: 1957.781097 from(653.600975,3+)
Elution from: 49.569 to 49.569 scan no 5219 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1957.7819
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(6)-98, b(6), b(10)++, b(12)-98++, b(13)-196++, b(13)++, b(15)++, b(15)-98++
Matched y ions: y(10)++, y(12)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.129

ASPNIQPANVNR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASPNIQPANVNR
Found in AT5G10470.1, kinesin motor protein–related

Match to Query 1514: 1359.628542 from(680.821547,2+)
Elution from: 25.463 to 25.463 scan no 1995 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1359.6296
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 56 Expect: 2.1e-005
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(11)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(9), y(10)++
Precursor origin neutral loss: +

Peptide No. 130

ASPRPMVERSPSSTSLER
Confirmed sites:
Ambiguous sites: @S:12

MS/MS Fragmentation of ASPRPMVERSPSSTSLER
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to unnamed protein pr

Match to Query 3570: 2081.957208 from(521.496578,4+)
Elution from: 18.344 to 18.344 scan no 1096 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2081.9565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.067
Matched b ions: b(4)++, b(6), b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(9)–98++
Precursor origin neutral loss:

Peptide No.131

ASSFVYSPGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 1065: 1149.485592 from(575.750072,2+) Elution from: 33.670 to 33.670 scan no 2918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1149.4855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0025
Matched b ions: b(4)–98, b(5)–98, b(6), b(6)–98, b(7), b(9)–98++, b(8)++, b(9)–98, b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.132
ASSFVYSPGR
Confirmed sites: "@S:2,@S:7"
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4);
DNA binding

Match to Query 1068: 1229.451994 from(615.733273,2+)
Elution from: 34.563 to 34.563 scan no 3195 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.4519
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.044
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(7)-98
Matched y ions: y(3), y(4), y(4)-98, y(5), y(5)-98, y(5)++, y(6), y(6)-98, y(6)-98++, y(7), y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.133

ASSFVYSPGR
Confirmed sites: "@S:2,@Y:6"
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4);
DNA binding

Match to Query 943: 1229.450974 from(615.732763,2+)
Elution from: 34.442 to 34.442 scan no 3198 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.4519
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 28 Expect: 0.0057
Matched b ions: b(4)−98, b(5), b(5)−98, b(6)−98++, b(7)−98, b(9)−98++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8)++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.134

ASSFVYSPGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 826: 1149.485502 from(575.750027,2+)
Elution from: 32.061 to 32.061 scan no 2921 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1149.4855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0015
Matched b ions: b(4)−98, b(4), b(5)−98, b(6)−98, b(6), b(7), b(9)−98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)−98++, y(8)−98, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.135

ASSFVYSPGR
Confirmed sites: "@S:3,@S:7"
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4);
DNA binding

Match to Query 1057: 1229.450948 from(615.732750,2+)  
Elution from: 34.640 to 34.640 scan no 3272 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.4519
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0018
Matched b ions: b(3), b(4)–98, b(4), b(5)–98, b(5), b(6)–98, b(6), b(7)–98, b(7)–196, b(8)–196
Matched y ions: y(3), y(4), y(4)–98, y(5), y(5)–98, y(5)++, y(6), y(6)–98, y(6)–98++, y(7), y(8)–98++, y(8), y(8)–196++, y(8)++, y(9)–98++
Precursor origin neutral loss: +

Peptide No. 136

ASSFVYSPGR
Confirmed sites: "@S:3,@Y:6"
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP–LIKE ZINC FINGER–CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 1072: 1229.451314 from(615.732933,2+) Elution from: 35.299 to 35.299 scan no 3323 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.4519
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Y6 : Phospho (Y)
Ions Score: 42 Expect: 0.00023
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)-98, b(9)-98++
Matched y ions: y(2), y(3), y(5)++, y(5), y(6), y(6)++, y(7), y(8)-98++, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.137

ASSFVYSPGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ASSFVYSPGR
Found in AT1G08680.1, ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 1054: 1149.485082 from(575.749817,2+)
Elution from: 34.271 to 34.271 scan no 3113 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1149.4855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 42 Expect: 0.0003
Matched b ions: b(5), b(6), b(7)-98, b(9)+
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(8), y(8)+, y(8)-98++, y(9)+
Precursor origin neutral loss: +

Peptide No.138
ASSGDLDNTAIDQILK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ASSGDLDNTAIDQILK
Found in AT5G10540.1, peptidase M3 family protein / thimet oligopeptidase family protein

Match to Query 3340: 1852.877460 from(927.446006,2+)
Elution from: 66.994 to 66.994 scan no 7020 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.8819
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 4.3e-009
Matched b ions: b(5)−98, b(6)−98, b(7)−98, b(9)−98, b(10)−98, b(11)−98, b(12)−98, b(13)−98, b(13)−98++, b(15)−98, b(16)−98
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(11), y(12), y(16)−98++
Precursor origin neutral loss: +

Peptide No.139

ASSGLSYPER

Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ASSGLSYPER
Found in AT5G27630.1, ACBP5 (ACYL-COA BINDING PROTEIN 5, ACYL-COA-BINDING DOMAIN 5); acyl-CoA binding

Match to Query 818: 1145.474760 from(573.744656,2+)
Elution from: 26.239 to 26.239 scan no 2091 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1145.4754
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0005
Matched b ions: b(5), b(5)-98, b(7), b(7)-98, b(8)-98
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(7), y(9)++
Precursor origin neutral loss:

Peptide No.140

ASSGLSYPER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ASSGLSYPER
Found in AT5G27630.1, ACBP5 (ACYL–COA BINDING PROTEIN 5, ACYL–COA–BINDING DOMAIN 5); acyl–CoA binding

Match to Query 1014: 1145.474606 from(573.744579,2+)
Elution from: 27.503 to 27.503 scan no 2291 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1145.4754
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 8.7e-005
Matched b ions: b(3), b(5), b(5)-98, b(6)-98, b(7), b(7)+, b(8)-98, b(8)-98++, b(9)-98++, b(9)+
Matched y ions: y(1), y(3), y(4), y(5)+, y(5), y(6), y(7), y(8)-98, y(8), y(8)-98++, y(8)+, y(9)+
Precursor origin neutral loss:
Peptide No.141
ASSGSADRDVILADLEK
Confirmed sites: @S:2 or S:3
Ambiguous sites: @S:2 or S:3
MS/MS Fragmentation of ASSGSADRDVILADLEK
Found in AT2G45820.1, DNA-binding protein, putative
Match to Query 3268: 1825.845020 from (913.929786,2+)
Elution from: 47.945 to 47.945 scan no 4916 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1825.8458
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0012
Matched b ions: b(9), b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14)-98, b(14), b(16)-98, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(14)++
Precursor origin neutral loss: +

Peptide No.142

ASSGSADRDVILADLEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ASSGSADRDVILADLEK
Found in AT2G45820.1, DNA-binding protein, putative

Match to Query 2943: 1825.845714 from(913.930133,2+) Elution from: 45.868 to 45.868 scan no 4754 polarity:+
Peptide No. 143

ASSPPEGEDEFTDDDGTK

Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ASSPPEGEDEFTDDDGTK
Found in AT5G16260.1, RNA recognition motif (RRM)-containing protein

Match to Query 2871: 1975.720720 from(988.867636,2+)
Elution from: 31.422 to 31.422 scan no 2777 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1975.7208
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 1.4e-009
Matched b ions: b(6)-98, b(6), b(7)-98++, b(8)-98, b(9)-98, b(9), b(10), b(11)-98, b(13), b(14), b(14)-98, b(15), b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15)++, y(17)++
Precursor origin neutral loss:

Peptide No.144

ASSPPEGDEFTDDDGTK
Confirmed sites: @T:12
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ASSPPEGDEFTDDDGTK
Found in AT5G16260.1, RNA recognition motif (RRM)-containing protein

Match to Query 2845: 2055.685026 from(1028.849789,2+)
Elution from: 32.159 to 32.159 scan no 2801 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2055.6871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00042
Matched b ions: b(6)−98, b(6), b(9)−98, b(9), b(10), b(12)−98, b(15), b(17)−98, b(17)−196++
Matched y ions: y(4), y(6), y(7)−98, y(7), y(10), y(12), y(13), y(14)++, y(14), y(15)−98++, y(15)++, y(15)−98, y(15)
Precursor origin neutral loss: +

Peptide No.145

ASSPPEGEDEFTDDDGTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ASSPPEGEDEFTDDDGTK
Found in AT5G16260.1, RNA recognition motif (RRM)−containing protein

Match to Query 3250: 1975.718576 from(988.866564,2+)
Elution from: 31.603 to 31.603 scan no 2819 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1975.7208
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 4.9e-009
Matched b ions: b(6), b(7)–98++, b(9)–98, b(9), b(14), b(14)++, b(15), b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15)++ , y(15), y(16)–98++, y(16)++, y(17)–98++
Precursor origin neutral loss:

Peptide No.146

ASSPPEGEDFDTDDGTK
Confirmed sites: “@S:3,@T:12”
Ambiguous sites:

MS/MS Fragmentation of ASSPPEGEDFDTDDGTK
Found in AT5G16260.1, RNA recognition motif (RRM)–containing protein

Match to Query 2821: 2055.684130 from(1028.849341,2+)
Elution from: 31.680 to 31.680 scan no 2824 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2055.6871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.018
Matched b ions: b(9)−98, b(9), b(13), b(15), b(17)−196++
Matched y ions: y(5), y(7)−98, y(7), y(8), y(10), y(12), y(14)++, y(15)−98++, y(15)++, y(15), y(16)−98++, y(16)−196++, y(16)++
Precursor origin neutral loss: +

Peptide No.147

ASSSVSTLYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ASSSVSTLYK
Found in AT4G03550.1, ATGSL05 (GLUCAN SYNTHASE-LIKE 5; 1,3-beta-glucan synthase/transferase, transferring glycosyl grou

Match to Query 784: 1121.500174 from(561.757363,2+)
Elution from: 27.988 to 27.988 scan no 2370 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1121.5005
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00017
Matched b ions: b(4)-98, b(5)++, b(5)-98, b(5), b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(8)++, y(9)++, y(9)-98++
Precursor origin neutral loss:

Peptide No.148

ASSSVSTLYK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ASSSVSTLYK
Found in AT4G03550.1, ATGSL05 (GLUCAN SYNTHASE-LIKE 5); 1,3-beta-glucan synthase/transferase, transferring glycosyl grou

Match to Query 749: 1121.499802 from(561.757177,2+)  
Elution from: 28.507 to 28.507 scan no 2406 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1121.5005
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0049
Matched b ions: b(5), b(5)-98, b(8)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7)-98++, y(7)-98, y(8)-98++, y(8), y(8)-98, y(8)++, y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.149

ASVNSPTASQMDELDDFSIGR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ASVNSPTASQMDELDDFSIGR
Found in AT4G12770.1, heat shock protein binding

Match to Query 4252: 2318.966832 from(1160.490692,2+)
Elution from: 56.695 to 56.695 scan no 6041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2318.9726
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 5.5e-009
Matched b ions: b(8)-98, b(10)-98, b(14)-98, b(15), b(16)-98, b(16), b(19)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(16)+, y(16), y(17)-98++, y(17)+, y(18)-98++, y(18)+, y(19)-98++, y(19)+
Precursor origin neutral loss: +

Peptide No.150

ASVSDNGHGSEFSFER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ASVSDNGHGSEFSFER
Found in AT3G60600.1, VAP27-1 (VAMP/SYNAPTOBREVIN–ASSOCIATED PROTEIN 27-1); protein binding

Match to Query 3075: 1804.702672 from(903.358612,2+)
Elution from: 36.794 to 36.794 scan no 3338 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.7053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 7.7e-005
Matched b ions: b(5), b(8)−98, b(8), b(11), b(11)−98, b(12), b(13)−98, b(15), b(15)−98
Matched y ions: y(4), y(5), y(8), y(9), y(10), y(11)++, y(11), y(12), y(12)++, y(13)−98++, y(13)++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.151

ASVSDNGNASDFTAAPR
Confirmed sites: 
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of ASVSDNGNASDFTAAPR
Found in AT2G45140.1, vesicle-associated membrane protein, putative / VAMP, putative

Match to Query 2192: 1758.721022 from(880.367787,2+)
Elution from: 32.568 to 32.568 scan no 2830 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1758.7210
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 1.2e-006
Matched b ions: b(5), b(9)-98, b(11), b(14), b(14)-98, b(15)-98
Matched y ions: y(2), y(3), y(4), y(6), y(8), y(9), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.152
ASVSDNGNASDFTAAPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ASVSDNGNASDFTAAPR
Found in AT2G45140.1, vesicle-associated membrane protein, putative / VAMP, putative

Match to Query 3133: 1758.720208 from(880.367380,2+)
Elution from: 32.376 to 32.376 scan no 2960 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1758.7210
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 3.9e-009
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7), b(8)-98, b(8), b(9)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(13), b(14)-98, b(14), b(14)++, b(15)-98, b(15), b(16)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(14)-98++, y(15)-98++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.153

ASYPEIDVQPPSPPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of ASYPEIDVQPPSPPR
Found in AT4G10760.1, EMB1706 (EMBRYO DEFECTIVE 1706); S-adenosylmethionine-dependent methyltransferase

Match to Query 2581: 1731.786008 from(866.900280,2+)
Elution from: 45.803 to 45.803 scan no 4743 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1731.7869
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 62 Expect: 7.8e-006
Matched b ions: b(6), b(8), b(9), b(12)−98, b(12)−98++, b(12)+, b(13)+, b(13)−98++, b(14)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7)−98, y(8), y(9)+, y(9), y(10), y(11)+, y(12)−98++, y(12), y(12)+, y(13)−98++, y(13)+
Precursor origin neutral loss: +

Peptide No.154

ATGAFILTASHNPGGPTEDFGIK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ATGAFILTASHNPGGPTEDFGIK
Found in AT1G23190.1, phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative

Match to Query 4379: 2380.104670 from(1191.059611,2+)
Elution from: 51.631 to 51.631 scan no 5477 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2380.1100
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 3.8e-006
Matched b ions: b(8), b(9), b(11)-98, b(12), b(13)-98, b(14), b(15)-98, b(16)-98, b(19)-98, b(19), b(21)-98++, b(21)++, b(22)++, b(22)-98++
Matched y ions: y(4), y(5), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(15)-98, y(16)-98, y(16), y(17)-98++, y(17), y(17)-98, y(18)-98++, y(19)++, y(20)++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.155
ATGAFILTASHNPGGPTEDFGIK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of ATGAFILTASHNPGGPTEDFGIK
Found in AT1G23190.1, phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative

Match to Query 4464: 2380.104816 from(794.375548,3+)
Elution from: 54.436 to 54.436 scan no 5586 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2380.1100
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 51 Expect: 0.00012
Matched b ions: b(6), b(7), b(12), b(12)++, b(13)−98, b(13)++, b(14)++, b(15)++, b(16)−98++, b(18)++
Matched y ions: y(8)++, y(8), y(9), y(10), y(11)++, y(11), y(14)++, y(16)++, y(17)++, y(17)−98++, y(18)++, y(19)++, y(21)++, y(21)−98++
Precursor origin neutral loss: +

Peptide No.156
ATLWYPSSQSSAANSPPR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of ATLWYPSSQSSAANSPPR
Found in AT1G16520.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56080.1); similar to putative protein [

Match to Query 4056: 2126.941024 from(1064.477788,2+)
Elution from: 44.097 to 44.097 scan no 4414 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2126.9422
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0029
Matched b ions: b(7), b(12), b(13), b(17)−98++
Matched y ions: y(6), y(7), y(8), y(9), y(10)−98, y(14), y(14)++, y(15), y(16)++
Precursor origin neutral loss: +

Peptide No.157

ATSGPAYPER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ATSGPAYPER
Found in AT3G05420.1, ACBP4 (ACYL-COA BINDING PROTEIN 4, ACYL-COA–BINDING DOMAIN 4); acyl–CoA binding

Match to Query 736: 1127.463346 from(564.738949,2+) Elution from: 21.940 to 21.940 scan no 1468 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1127.4648
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.039
Matched b ions:
Matched y ions: y(3), y(6), y(7), y(8), y(8)--98++
Precursor origin neutral loss:

Peptide No.158

ATSPQPDGPSSTGGSLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ATSPQPDGPSSTGGSLK
Found in AT1G59610.1, ADL3 (ARABIDOPSIS DYNAMIN–LIKE 3)

Match to Query 2675: 1665.722948 from(833.868750,2+)
Elution from: 23.272 to 23.272 scan no 1525 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1665.7247
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0075
Matched b ions: b(3), b(5), b(5)−98, b(6)−98++, b(6), b(7)−98, b(7), b(7)−98, b(8)−98, b(10)−98++, b(11)++, b(11)−98++, b(12)−98, b(13)++, b(15)−98++, b(15)++, b(16)
Matched y ions: y(4), y(5), y(6)++, y(7), y(8), y(10), y(12), y(12)++, y(14)++, y(14), y(15)−98++, y(15)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.159

ATSPQPDGPSSTGGSLK
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of ATSPQPDGPSSTGGSLK
Found in AT1G59610.1, ADL3 (ARABIDOPSIS DYNAMIN−LIKE 3)

Match to Query 2220: 1665.723260 from(833.868906,2+)
Elution from: 21.690 to 21.690 scan no 1491 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1665.7247
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.017
Matched b ions: b(3), b(5), b(6)-98++, b(7)-98++, b(7), b(8)-98, b(15), b(15)-98++
Matched y ions: y(6), y(6)++, y(7), y(8), y(10), y(12), y(14)++, y(14)
Precursor origin neutral loss: +

Peptide No.160

ATSPQPDGPTAGGSLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ATSPQPDGPTAGGSLK
Found in AT1G10290.1, ADL6 (DYNAMIN–LIKE PROTEIN 6)

Match to Query 2140: 1562.696018 from(782.355285,2+) Elution from: 24.188 to 24.188 scan no 1823 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1562.6977
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 8.8e-005
Matched b ions: b(3), b(5), b(5)−98, b(7)−98++, b(7)−98, b(8), b(9)−98, b(10)−98++, b(12)−98++, b(14)−98++, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(13), y(13)++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.161
ATTPTPDKEPLLK
Confirmed sites: “@T:2,@T:5”
Ambiguous sites:

MS/MS Fragmentation of ATTPTPDKEPLLK
Found in AT1G15340.1, MBD10 (methyl-CpG-binding domain 10); DNA binding

Match to Query 2065: 1569.708414 from(785.861483,2+)
Elution from: 31.367 to 31.367 scan no 2828 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.7092
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.009
Matched b ions: b(3), b(5)-98, b(6), b(7)-98, b(8), b(8)-98++, b(8)-98, b(9), b(9)-196++, b(9)-98, b(10)+, b(11)-98, b(12), b(12)-196++, b(12)-98++, b(12)+
Matched y ions: y(2), y(4), y(5), y(6), y(8), y(8)+, y(9)+, y(9), y(10), y(10)+, y(10)-98, y(10)-98++, y(11)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.162
ATTPTPDKEPLLK
Confirmed sites: "@T:3,@T:5"
Ambiguous sites:

MS/MS Fragmentation of ATTPTPDKEPLLK
Found in AT1G15340.1, MBD10 (methyl-CpG-binding domain 10); DNA binding

Match to Query 2620: 1569.708531 from(524.243453,3+)
Elution from: 32.058 to 32.058 scan no 2935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.7092
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
T5: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 29 Expect: 0.012
Matched b ions: b(2), b(4), b(8)+, b(9)+196++, b(9)+, b(10)+, b(12)+98++
Matched y ions: y(4), y(5), y(6), y(8)+, y(8), y(9)+, y(10)+, y(10)+98++, y(11)+, y(11)+98++, y(12)+, y(12)+98++, y(12)+196++
Precursor origin neutral loss:

Peptide No.163

AVDAGMLDYDSDDNPIVVDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AVDAGMLDYDSDDNPIVVDK
Found in AT2G47330.1, DEAD/DEAH box helicase, putative

Match to Query 4204: 2246.926198 from(1124.470375,2+) Elution from: 48.446 to 48.446 scan no 4859 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2246.9290
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.9e-007
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(12)++, b(13), b(14)++, b(14), b(14)-98, b(15)-98++, b(15)-98, b(16)-98, b(16), b(17)-98, b(17), b(18), b(18)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(10), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15), y(16)-98++, y(16)+, y(17)+, y(18)+, y(19)-98++
Precursor origin neutral loss: +

Peptide No.164
AVDAGMLDYDSDDNPIVVDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AVDAGMLDYDSDDNPIVVDK
Found in AT2G47330.1, DEAD/DEAH box helicase, putative

Match to Query 4093: 2230.931982 from(1116.473267,2+)
Elution from: 54.531 to 54.531 scan no 5788 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2230.9341
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 1.4e-009
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(12), b(13), b(14), b(14)-98, b(15)-98, b(16)-98, b(16), b(16)+, b(17)+, b(17)-98, b(17), b(17)-98++, b(18)-98++, b(18), b(18)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13)-98, y(13), y(14), y(16), y(17)+, y(18)+, y(18)-98++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.165

AVDAGMLDYDSDDNPIVVDKR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AVDAGMLDYDSDDNPIVVDKR
Found in AT2G47330.1, DEAD/DEAH box helicase, putative

Match to Query 4669: 2387.031106 from(1194.522829,2+)
Elution from: 50.670 to 50.670 scan no 5256 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2387.0352
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.054
Matched b ions: b(13)–98, b(13), b(18)–98
Matched y ions: y(3), y(7), y(8), y(11), y(12)–98, y(13)–98, y(13), y(17)++, y(18)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.166

AVDEMSDGEPLVSFLK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AVDEMSDGEPLVSFLK
Found in AT5G10950.1, cylicin–related

Match to Query 2956: 1831.791298 from(916.902925,2+)  
Elution from: 59.333 to 59.333 scan no 6358 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1831.7950
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5  : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6  : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.001
Matched b ions: b(8)-98, b(9)-98, b(9), b(12)-98, b(12), b(15)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)++, y(11), y(14)-98++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.167

AVELDMNLTDSDQTK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AVELDMNLTDSDQTK
Found in AT5G55210.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22320.1); similar to conserved hypothet

Match to Query 2666: 1758.735686 from(880.375119,2+)
Elution from: 44.474 to 44.474 scan no 4570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1758.7383
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0075
Matched b ions: b(7), b(9), b(12), b(13)–98, b(13)
Matched y ions: y(4), y(6), y(7)–98, y(8), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.168

AVELDMNLTDSDQTK
Confirmed sites:
Ambiguous sites: @S:11orT:14

MS/MS Fragmentation of AVELDMNLTDSDQTK
Found in AT5G55210.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22320.1); similar to conserved hypothet

Match to Query 3055: 1758.737548 from(880.376050,2+)
Elution from: 46.445 to 46.445 scan no 4721 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1758.7383
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.036
Matched b ions: b(6), b(7), b(9)
Matched y ions: y(5), y(6), y(7)-98, y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.169

AVESDSEVSDSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of AVESDSEVSDSK
Found in AT5G26860.1, LON_ARA_ARA (Lon protease homolog gene); ATP binding / ATP-dependent peptidase/ serine-type peptida

Match to Query 1424: 1331.512310 from(666.763431,2+)
Elution from: 19.309 to 19.309 scan no 1181 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1331.5129
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 2.6e-007
Matched b ions: b(4)++, b(5), b(6)--98, b(7)--98, b(8)--98, b(8), b(9), b(9)--98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9)--98, y(9), y(10)++, y(10)--98, y(10), y(10)--98++, y(11)--98++, y(11)--98
Precursor origin neutral loss: +

Peptide No.170
AVGSHCSLSEMDDLDLTR
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase
Match to Query 3992: 2100.847308 from(701.289712,3+)
Elution from: 40.123 to 40.123 scan no 3894 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2100.8493
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 Expect: 0.013
Matched b ions: b(4)-98, b(6)-98, b(6)-98++, b(6), b(8)-, b(8), b(8)-98, b(8), b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(13)++, b(17)++
Matched y ions: y(3), y(4), y(5), y(5), y(6), y(7), y(8), y(8)++, y(10)++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.171
AVGSHCSLSEMDDLDLTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 3498: 2084.852310 from(1043.433431,2+)
Elution from: 46.435 to 46.435 scan no 4836 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2084.8544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 1.3e-007
Matched b ions: b(6)-98, b(7)++, b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14), b(15)-98, b(15), b(16)-98
Matched y ions: y(3), y(5), y(6), y(8), y(10), y(11), y(12), y(13), y(13)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.172
AVGSHCSLSEMDDLDLTR
Confirmed sites: "@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 4010: 2180.812094 from(1091.413323,2+)
Elution from: 42.621 to 42.621 scan no 4352 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2180.8156
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 Expect: 2.6e-006
Matched b ions: b(7)-98, b(8)-196++, b(8)-98, b(8)-196, b(8), b(9), b(9)-98, b(10), b(11), b(12)-98, b(12), b(13), b(15)-98, b(15), b(15)-98++, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98++, y(14)+, y(15)-98++, y(16)-98++, y(16)-196++, y(16)+, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.173

AVGSHCSLSEMDDLDLTR
Confirmed sites: "@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 3874: 2164.816604 from(1083.415578,2+)
Elution from: 50.570 to 50.570 scan no 5345 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2164.8207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.4e-005
Matched b ions: b(6), b(7)-196, b(7)-98, b(8)-196++, b(8)-98, b(8), b(9), b(11)-98, b(11),
      b(12), b(12)-98, b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(15)-98, b(15), b(16)-196++, b(16), b
      (17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14)-98++, y(14)++, y(15)-
      98++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.174

AVGSHCSLSEMDDLDLTR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 3888: 2084.850538 from(1043.432545,2+)
Elution from: 46.781 to 46.781 scan no 4866 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2084.8544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 1.4e-007
Matched b ions: b(5), b(6), b(7)++, b(7)—98, b(8)—98, b(8), b(9)—98, b(9), b(10), b(10)—98, b(11), b(11)—98, b(12), b(12)—98, b(13), b(13)—98, b(14), b(14)++, b(15)—98, b(15), b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)—98, y(13)—98, y(14)++, y(14)—98++, y(15)—98++, y(15)+, y(16)++, y(16)—98++, y(17)—98++, y(17)++
Precursor origin neutral loss: +

Peptide No.175
AVGSHCSLSEMDDLDLTR
Confirmed sites: @S:9
Ambiguous sites:
MS/MS Fragmentation of AVGSHCSLSEMDDLDLTR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta–fructofuranosidase
Match to Query 3995: 2084.853645 from(695.958491,3+)
Elution from: 46.994 to 46.994 scan no 4890 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2084.8544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 5.2e-005
Matched b ions: b(6), b(8)+, b(9), b(10), b(10)–98++, b(10)+, b(11)–98++, b(11)+, b(12)+, b(12)–98++, b(13)+, b(14)+, b(14)–98++, b(15)+, b(16)+, b(17)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9), y(9)+, y(10)+, y(10)–98++, y(11)+
Precursor origin neutral loss: +

Peptide No.176

AVLHSLR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AVLHSLR
Found in AT1G02850.1, glycosyl hydrolase family 1 protein

Match to Query 403: 874.441398 from(438.227975,2+)
Elution from: 29.236 to 29.236 scan no 2600 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 874.4426
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0028
Matched b ions: b(3), b(4), b(5)–98, b(6)–98
Matched y ions: y(1), y(2), y(3)–98, y(3), y(4)–98++, y(4)–98, y(4), y(4)++, y(5)++, y(5), y(5)–98++, y(6)–98++, y(6)–98
Precursor origin neutral loss: +

Peptide No.177

AVQEEDELSPEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of AVQEEDELSPEK
Found in AT5G23540.1, 26S proteasome regulatory subunit, putative

Match to Query 1787: 1452.601324 from(727.307938,2+)
Elution from: 24.976 to 24.976 scan no 1964 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1452.6021
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0014
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)−98, b(9)++, b(9), b(10)−98++, b(10)−98, b(11), b(11)−98, b(11)++
Matched y ions: y(3), y(4), y(4)−98, y(5)−98, y(5), y(6)−98, y(6), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(9)−98++, y(9)++, y(10)++, y(10)−98, y(10)−98++, y(11)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.178

AVSFDDNK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AVSFDDNK
Found in AT5G18760.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 413: 974.373634 from(488.194093,2+)
Elution from: 23.045 to 23.045 scan no 1690 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 974.3746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0021
Matched b ions: b(2), b(3), b(4)-98, b(6)-98, b(6)
Matched y ions: y(2), y(5), y(6)-98, y(6), y(7)+, y(7)-98
Precursor origin neutral loss: +

Peptide No.179

AVSFLQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AVSFLQR
Found in AT4G16690.1, esterase/lipase/thioesterase family protein

Match to Query 432: 899.425522 from(450.720037,2+)
Elution from: 37.865 to 37.865 scan no 3718 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 899.4266
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0028
Matched b ions:
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)--98, y(6)--98, y(6)++
Precursor origin neutral loss: +

Peptide No. 180

AVVDSLSDSEEVGTVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of AVVDSLSDSEEVGTVK
Found in AT1G15280.1, glycine-rich protein

Match to Query 2615: 1741.764878 from(871.889715,2+)
Elution from: 39.566 to 39.566 scan no 3927 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1741.7658
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 2.8e-009
Matched b ions: b(6)–98, b(6), b(7)–98, b(7), b(8)–98, b(9), b(10)–98, b(10), b(11)–98, b(11), b(12)–98, b(12), b(13)–98++, b(14), b(15), b(15)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12)–98, y(12), y(13)++, y(13), y(13)–98, y(13)–98++, y(14)–98++, y(14)+, y(14)–98, y(15)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.181

AVVDSDSLDEEVGTVK
Confirmed sites: ”@S:5,@S:8”
Ambiguous sites:

MS/MS Fragmentation of AVVDSDSLDEEVGTVK
Found in AT1G15280.1, glycine–rich protein

Match to Query 3263: 1821.731128 from(911.872840,2+)
Elution from: 42.341 to 42.341 scan no 4315 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1821.7322
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 2.6e-006
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8)-196, b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-98++, b(11)-196, b(12)-98, b(12), b(12)-196, b(12)-196++, b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(15), b(15)-98, b(15)-196, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)+, y(12)-98, y(12)-98++, y(12)-196, y(13)-98++, y(13)-98, y(13), y(13)+, y(13)-196++, y(13)-196, y(14)-196++, y(14)-98++, y(14)+, y(14), y(14)-98, y(14)-196, y(15)-196++, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.182

AVVDSDLSDDEEVGTVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AVVDSDLSDDEEVGTVK
Found in AT1G15280.1, glycine-rich protein

Match to Query 2101: 1741.764416 from(871.889484,2+) 
Elution from: 37.941 to 37.941 scan no 3646 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1741.7658

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 86 Expect: 2.3e-008

Matched b ions: b(4), b(6), b(7), b(8)-98++, b(9), b(10)-98, b(11)-98, b(12)-98, b(12), b(12)++, b(13)-98, b(13), b(14)-98++, b(14)-98, b(14), b(15), b(15)-98

Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(12)++, y(13)++, y(13), y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(15)-98++

Precursor origin neutral loss: +

Peptide No.183

AVVSEGGNDLVNEK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of AVVSEGGNDLVNEK
Found in AT5G12410.1, THUMP domain-containing protein

Match to Query 1755: 1509.669908 from(755.842230,2+)

Elution from: 32.643 to 32.643 scan no 2938 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1509.6711
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 9.4e-009
Matched b ions: b(5)−98, b(5), b(6), b(6)−98, b(7)++, b(7)−98, b(9), b(10)−98, b(11)−98, b(11), b(12)−98, b(12), b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(11)−98, y(12)−98++, y(12), y(12)−98, y(12)++, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No. 184

AWTLEGESDDEEGHPEEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AWTLEGESDDEEGHPEEK
Found in AT1G20920.1, DEAD box RNA helicase, putative

Match to Query 3710: 2136.813274 from(1069.413913,2+)
Elution from: 35.669 to 35.669 scan no 3406 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2136.8160  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 66 Expect: 1.9e-006  
Matched b ions: b(8), b(8)−98, b(9)−98, b(10), b(11)−98, b(13)−98, b(14)−98, b(14)−98++, b(16)−98, b(16), b(16)−98++, b(16)++, b(17)++, b(17)−98++  
Matched y ions: y(4), y(6), y(7), y(8), y(10), y(11), y(11)−98, y(12)−98, y(13)−98, y(13)−98++, y(13), y(13)++, y(14)−98, y(15)−98++, y(15)++, y(16)++, y(16)−98++  
Precursor origin neutral loss: +  

Peptide No.185  
CGPGKHYETGYVPTDAARASGSGV  
Confirmed sites: “@T:14,@S:20,@S:22”  
Ambiguous sites: @Y:7orT:9  
MS/MS Fragmentation of CGPGKHYETGYVPTDAARASGSGV  
Found in AT1G25275.3, unknown protein  
Match to Query 3895: 2755.973736 from(690.000710,4+)  
Elution from: 26.439 to 26.439 scan no 2024 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2755.9780
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(11)-98++, b(11)++, b(13)++
Matched y ions: y(8)++, y(11)++, y(12)++, y(13)-196++, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.186

CIYDSDDEVDRD
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of CIYDSDDEVDRD
Found in AT4G34450.1, coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative

Match to Query 2233: 1621.606826 from(811.810689,2+)
Elution from: 27.341 to 27.341 scan no 2284 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1621.6079
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.003
Matched b ions: b(7)-98, b(9)-98, b(10)
Matched y ions: y(4), y(5), y(6)+, y(6), y(7), y(8)-98++, y(8)+, y(9)-98++, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.187
CLSLPSSNSAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of CLSLPSSNSAK
Found in AT5G18760.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 1084: 1242.529066 from(622.271809,2+)
Elution from: 31.812 to 31.812 scan no 2888 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1242.5315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.036
Matched b ions: b(2), b(3), b(3)−98, b(4)−98
Matched y ions: y(7), y(8), y(9)−98, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.188
CREKCLTLHNGVGVCSDLYTAPlVPK
Confirmed sites:
Ambiguous sites: @Y:18orT:19

MS/MS Fragmentation of CREKCLTLHNGVGVCSDLYTAPlVPK
Found in AT3G04945.1, LCR18 (Low-molecular-weight cysteine-rich 18)

Match to Query 4298: 2979.414177 from(994.145335,3+)
Elution from: 59.240 to 59.240 scan no 6050 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2979.4169
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.031
Matched b ions: b(8), b(9)+, b(9), b(11), b(15)+, b(20)+, b(21)−98+, b(21)+, b(22)+, b(23)+, b(23)−98+, b(24)+
Matched y ions: y(9)−98, y(10)+, y(10), y(17)+, y(22)−98+
Precursor origin neutral loss: +

Peptide No.189

CSFSGKLVHQMLCR
Confirmed sites: 
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of CSFSGKLVHQMLCR
Found in AT4G04530.1, Ulp1 protease family protein (snoR29)

Match to Query 2609: 1817.772885 from(606.931571,3+)
Elution from: 39.020 to 39.020 scan no 3797 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1817.7776
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.019
Matched b ions: b(4), b(6), b(6)++, b(7), b(8)--98, b(8), b(8)++
Matched y ions: y(4), y(6), y(7), y(7)++, y(8), y(8)++, y(10)++
Precursor origin neutral loss:

Peptide No.190

CVSLNNLSDYEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of CVSLNNLSDYEK
Found in AT1G19000.1, myb family transcription factor

Match to Query 2368: 1520.620642 from(761.317597,2+)
Elution from: 44.572 to 44.572 scan no 4570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1520.6218
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.4e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(5), b(5)+, b(6)-98, b(7)-98, b(7), b(9), b(9)-98, b(10)+, b(10)-98, b(11), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(10)-98, y(10), y(10)-98++, y(11)-98
Precursor origin neutral loss: +

Peptide No.191
DADSPVHSNDAEEEMIR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DADSPVHSNDAEEEMIR
Found in AT4G00752.1, UBX domain-containing protein

Match to Query 2709: 1993.770180 from(997.892366,2+)
Elution from: 33.476 to 33.476 scan no 3070 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1993.7724
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00017
Matched b ions: b(6), b(6)-98, b(7)-98, b(7), b(9)-98, b(10), b(10)-98, b(13), b(16)-98, b(16)
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11)++, y(11), y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.192

DAELIEDDEDSFER
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DAELIEDDEDSFER
Found in AT3G60850.1, similar to Os03g0247100 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001049548.1)

Match to Query 2467: 1761.659748 from(881.837150,2+)
Elution from: 43.486 to 43.486 scan no 4319 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1761.6618
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 8.7e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9), b(10), b(13)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10)−98++, y(10), y(10)−98, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.193

DAESELSVAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DAESELSVAR
Found in AT1G70320.1, UPL2 (UBIQUITIN–PROTEIN LIGASE 2); ubiquitin–protein ligase

Match to Query 759: 1155.479848 from(578.747200,2+)
Elution from: 32.816 to 32.816 scan no 2974 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1155.4808
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 1.6e-005
Matched b ions: b(5)–98, b(5), b(6)–98, b(6), b(7)–98, b(8)–98, b(8), b(9), b(9)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)–98, y(8)–98, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.194

DAGGGVSGEEMPSW
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DAGGGVSGEEMPSW
Found in AT2G38880.1, HAP3A (Heme activator protein (yeast) homolog 3A); transcription factor

Match to Query 1817: 1457.514834 from(729.764693,2+);
Elution from: 56.554 to 56.554 scan no 6025 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1457.5170
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00018
Matched b ions: b(8), b(9), b(10), b(11), b(11)-98, b(12)-98, b(13)
Matched y ions: y(3), y(4), y(5), y(6)++, y(8), y(10)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.195
DAGGGVSGEEMPSW
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of DAGGGVSGEEMPSW
Found in AT2G38880.1, HAP3A (Heme activator protein (yeast) homolog 3A); transcription factor
Match to Query 1441: 1473.509614 from(737.762083,2+)
Elution from: 44.477 to 44.477 scan no 4408 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1473.5119
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 Expect: 0.013
Matched b ions: b(6), b(10), b(11)-98, b(11), b(12)-98, b(13)
Matched y ions: y(3), y(4), y(8)
Precursor origin neutral loss: +

Peptide No.196

DANAALEINPDSAK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DANAALEINPDSAK
Found in AT4G22670.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 1898: 1507.654398 from(754.834475,2+)
Elution from: 36.120 to 36.120 scan no 3467 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 8.1e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(12)−98++, b(12)−98, b(13)−98, b(13), b(13)−98++
Matched y ions: y(4), y(5), y(5)−98, y(6), y(7), y(8), y(9), y(10), y(11)−98++, y(11), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.197

DASLETPIILSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DASLETPIILSPK
Found in AT5G57830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G30830.1); similar to Protein of unknown

Match to Query 1745: 1349.646778 from(675.830665,2+)
Elution from: 45.880 to 45.880 scan no 4647 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1349.6479
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00082
Matched b ions: b(5), b(6), b(9)
Matched y ions: y(3), y(5)−98, y(6), y(7)−98++, y(7), y(8), y(9)+++, y(9), y(11)+
Precursor origin neutral loss: +

Peptide No.198

DASSVSAAASAGSEMDAR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DASSVSAAASAGSEMDAR
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 2784: 1761.686786 from(881.850669,2+)
Elution from: 31.998 to 31.998 scan no 2880 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1761.6876
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.5e-007
Matched b ions: b(4), b(11)-98, b(14), b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(13)-98, y(13), y(14), y(17)++
Precursor origin neutral loss: +

Peptide No.199

DASSVSAASAGSEMDAR
Confirmed sites: "@S:10,@S:13"
Ambiguous sites:

MS/MS Fragmentation of DASSVSAASAGSEMDAR
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 3060: 1841.651406 from(921.832979,2+)
Elution from: 31.682 to 31.682 scan no 2940 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1841.6539
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 7.7e-007
Matched b ions: b(5), b(9), b(10)−98, b(13)−98, b(16)−98, b(17)−98, b(17), b(17)−98++
Matched y ions: y(4), y(6), y(7), y(8)−98, y(9)−98++, y(9)−98, y(9), y(10), y(11), y(12), y(13), y(15), y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.200

DATDILEVSPAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DATDILEVSPAK
Found in AT5G04020.1, calmodulin-binding protein-related (PICBP)

Match to Query 1437: 1337.609252 from(669.811902,2+)
Elution from: 44.767 to 44.767 scan no 4578 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1337.6115
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.7e-006
Matched b ions: b(5), b(6)+, b(6), b(7), b(8), b(8)+, b(9)-98, b(9), b(10)-98, b(11), b(11)+
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(7), y(8)-98, y(8), y(9), y(10), y(11) +
Precursor origin neutral loss: +

Peptide No.201
DATSMGTVEDPK
Confirmed sites: 
Ambiguous sites: @T:3orS:4

MS/MS Fragmentation of DATSMGTVEDPK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 1359: 1329.515164 from(665.764858,2+)
Elution from: 27.423 to 27.423 scan no 2295 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1329.5159
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.013
Matched b ions: b(5)–98++, b(5)–98, b(8)–98, b(9), b(10)
Matched y ions: y(2), y(3), y(4)++, y(4), y(7), y(10)++, y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.202
DAWLDSIEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DAWLDSIEK
Found in AT5G09390.1, CD2–binding protein–related

Match to Query 807: 1155.483302 from(578.748927,2+)
Elution from: 47.983 to 47.983 scan no 4805 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1155.4849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.031
Matched b ions: b(4), b(6)−98, b(8)
Matched y ions: y(4), y(5), y(6), y(7)−98++, y(7)++, y(7)
Precursor origin neutral loss:

Peptide No.203

DDDSRGNGYSPER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DDDSRGNGYSPER
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 2374: 1546.567838 from(774.291195,2+)
Elution from: 18.560 to 18.560 scan no 1041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1546.5685
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.044
Matched b ions: b(9), b(10)-98
Matched y ions: y(10)+, y(10)-98++, y(11)-98++, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.204

DDDSRGNGYSPER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DDDSRGNGYSPER
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 1688: 1546.566310 from(774.290431,2+) Elution from: 18.284 to 18.284 scan no 1034 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1546.5685
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.022
Matched b ions: b(5), b(6), b(10)–98
Matched y ions: y(3), y(5), y(10)–98++, y(10)+, y(11)–98++, y(11)+, y(12)–98++, y(12)+
Precursor origin neutral loss: +

Peptide No.205
DDELGFSSDDEVSANPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DDELGFSSDDEVSANPR
Found in AT1G55040.1, zinc finger (Ran–binding) family protein

Match to Query 3216: 1931.739810 from(966.877181,2+)
Elution from: 43.790 to 43.790 scan no 4485 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1931.7422
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.042
Matched b ions: b(6), b(9)-98, b(11), b(11)-98, b(12)-98, b(12), b(14), b(15), b(15)-98
Matched y ions: y(3), y(5), y(6), y(7)++, y(10)++, y(11), y(12), y(13), y(14)++, y(16)++
Precursor origin neutral loss: +

Peptide No.206
DDELGFSSDDEVSANPR
Confirmed sites: "@S:7,@S:8"
Ambiguous sites:

MS/MS Fragmentation of DDELGFSSDDEVSANPR
Found in AT1G55040.1, zinc finger (Ran-binding) family protein

Match to Query 3789: 2011.705260 from(1006.859906,2+)
Elution from: 48.970 to 48.970 scan no 5146 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2011.7085
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00059
Matched b ions: b(8)-98++, b(11), b(12)-98, b(12), b(12)-196, b(14), b(15)-196++, b(15), b(16)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(11), y(11)-98, y(12)-196++, y(13), y(13)-98++, y(13)-98, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.207

DDLDSSPISIQESTR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DDLDSSPISIQESTR
Found in AT5G27540.1, EMB2473 (EMBRYO DEFECTIVE 2473); GTP binding / calcium ion binding

Match to Query 2726: 1741.738052 from(871.876302,2+) Elution from: 40.735 to 40.735 scan no 4048 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1741.7407
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 3e−005
Matched b ions: b(6)−98, b(8), b(8)−98, b(12)
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(12)++, y(14)++
Precursor ions origin neutral loss: +

Peptide No.208

DDNSAQVADDESLSGQTSHDNDR
Confirmed sites:
Ambiguous sites: @T:17orS:18orS:20

MS/MS Fragmentation of DDNSAQVADDESLSGQTSHDNDR
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unnamed protein pr

Match to Query 3742: 2610.999363 from(871.340397,3+)
Elution from: 27.654 to 27.654 scan no 2184 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2611.0055
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00015
Matched b ions: b(21)-98++
Matched y ions: y(10)++, y(11)++, y(12)++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(20)++, y(22)++
Precursor origin neutral loss:

Peptide No.209

DDSDDETQDMNPSPSR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of DDSDDETQDMNPSPSR
Found in AT3G52115.1, ATGR1 (GAMMA RESPONSE 1)

Match to Query 3178: 2112.791901 from(705.271243,3+)
Elution from: 24.902 to 24.902 scan no 1911 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2112.7943
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.033
Matched b ions: b(6), b(8)−98++, b(8)−98, b(9)−98++, b(9)+, b(10)+, b(11)+, b(11)−98++, b(12)−98++, b(13)−98++, b(14)−98++, b(15)−98++, b(15)+, b(16)−98++, b(16)+
Matched y ions: y(10)+, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.210

DESSDDAGMMGLFD
Confirmed sites: “@S:3,@S:4”
Ambiguous sites:

MS/MS Fragmentation of DESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 2405: 1648.469190 from(825.241871,2+)
Elution from: 89.348 to 89.348 scan no 8438 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1648.4711
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.00043
Matched b ions: b(6), b(7)-98, b(8), b(9), b(10), b(12), b(13)-196++, b(13)++
Matched y ions: y(5), y(7)
Precursor origin neutral loss: +

Peptide No.211

DEVSDDAEATIEQTLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DEVSDDEATIEQTLK
Found in AT1G58200.1, MSL3 (MSCS-LIKE 3)

Match to Query 2230: 1771.737646 from(886.876099,2+)
Elution from: 56.019 to 56.019 scan no 5400 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1771.7401
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 4e-005
Matched b ions: b(5)-98, b(7)-98, b(7), b(8)-98, b(9), b(10)-98++, b(10)-98, b(10), b(12)-98, b(14)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12), y(12)++, y(13)++, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.212

DEWSEGAVSTLLEAYESK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DEWSEGAVSTLLEAYESK
Found in AT3G54390.1, transcription factor

Match to Query 3704: 2092.882826 from(1047.448689,2+)
Elution from: 73.579 to 73.579 scan no 7627 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2092.8877
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 2.6e-005
Matched b ions: b(5)–98, b(7)–98, b(8)–98, b(9)–98, b(11)++, b(13)–98, b(14)–98, b(17)–98++
Matched y ions: y(4), y(6), y(10), y(11), y(13), y(16)++
Precursor origin neutral loss: +

Peptide No.213

DFDSISSEDVDEAEAER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DFDSISSEDVDEAEAEER
Found in AT2G16070.2, PDV2 (PLASTID DIVISION2)

Match to Query 3751: 1992.745730 from(997.380141,2+)
Elution from: 44.067 to 44.067 scan no 4503 polarity:+
Peptide No. 214

DFDSISEDVDEAEAER

Confirmed sites: @S:4
Ambiguous sites: @S:6 or S:7

Monoisotopic mass of neutral peptide Mr(calc): 1992.7473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 86 Expect: 1.3e-008
Matched b ions: b(4)-98, b(5)-98, b(7)-98, b(7), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(11)-98, b(12)-98, b(12), b(12)-98, b(13)-98, b(13), b(13)-98, b(14)-98, b(14), b(14)-98++, b(15), b(15)-98, b(15)-98++, b(15)-98++, b(16)-98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11), y(11), y(14)-98++, y(14)++, y(14), y(15)-98++, y(16)-98++, y(16), y(16)-98++

Precursor origin neutral loss: +

Peptide No. 214

DFDSISEDVDEAEAER

Found in AT2G16070.2, PDV2 (PLASTID DIVISION2)

Match to Query 2852: 2072.710802 from (1037.362677, 2+) Elution from: 50.436 to 50.436 scan no 5043 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1992.7473
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 86 Expect: 1.3e-008
Matched b ions: b(4)-98, b(5)-98, b(7)-98, b(7), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(11)-98, b(12)-98, b(12), b(12)-98, b(13)-98, b(13), b(13)-98, b(14)-98, b(14), b(14)-98++, b(15), b(15)-98, b(15)-98++, b(15)-98++, b(16)-98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11), y(11), y(14)-98++, y(14)++, y(14), y(15)-98++, y(16)-98++, y(16), y(16)-98++

Precursor origin neutral loss: +
Monoisotopic mass of neutral peptide Mr(calc): 2072.7136
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.00063
Matched b ions: b(5)-98, b(9), b(10), b(10)-196, b(13)-98, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(12), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.215
DFDSISSEDVDEAEAER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DFDSISSEDVDEAEAER
Found in AT2G16070.2, PDV2 (PLASTID DIVISION2)

Match to Query 3478: 1992.744674 from(997.379613,2+)
Elution from: 43.119 to 43.119 scan no 4399 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1992.7473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 1.4e-009
Matched b ions: b(4), b(5), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98, b(16)-98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13), y(13)-98++, y(13)-98, y(14)-98++, y(14)+++, y(15)-98++, y(15)+++, y(16)+++
Precursor origin neutral loss: +

Peptide No.216

DFDSISSEDVDEAEAER
Confirmed sites: ”@S:6,@S:7”
Ambiguous sites:

MS/MS Fragmentation of DFDSISSEDVDEAEAER
Found in AT2G16070.2, PDV2 (PLASTID DIVISION2)

Match to Query 3083: 2072.711782 from(1037.363167,2+)
Elution from: 48.413 to 48.413 scan no 4931 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2072.7136
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 1.7e-007
Matched b ions: b(9), b(10)-98, b(10), b(10)-196, b(11), b(13)-98, b(13), b(14), b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(12)-196, y(12), y(14), y(14)-98++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.217

DFDSISSEDVDEAEAER
Confirmed sites:
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of DFDSISSEDVDEAEAER
Found in AT2G16070.2, PDV2 (PLASTID DIVISION2)

Match to Query 3351: 1992.746374 from(997.380463,2+)
Elution from: 43.349 to 43.349 scan no 4419 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1992.7473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 66 Expect: 1.4e-006
Matched b ions: b(8)–98, b(9), b(10)–98, b(10), b(11), b(12)–98, b(13)–98, b(13), b(14)–98, b(14), b(16)–98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)–98, y(14)–98++, y(14)++, y(15)–98++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.218

DFGEETTALSIVNK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DFGEETTALSIVNK
Found in AT1G15930.1, 40S ribosomal protein S12 (RPS12A)

Match to Query 2181: 1602.716098 from(802.365325,2+)
Elution from: 50.882 to 50.882 scan no 5365 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1602.7178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 8.5e-009
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12)-98, b(13), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10)+, y(10), y(12), y(12)+, y(13)++
Precursor origin neutral loss: +

Peptide No.219
DFLSSSSFK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DFLSSSSFK
Found in AT4G08180.1, oxysterol-binding family protein

Match to Query 674: 1096.446898 from(549.230725,2+)
Elution from: 44.687 to 44.687 scan no 4598 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1096.4478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 28 Expect: 0.0081
Matched b ions: b(2), b(3), b(4), b(5)–98
Matched y ions: y(4)++, y(5), y(6), y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.220

DFLSSSSFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DFLSSSSFK
Found in AT4G08180.1, oxysterol–binding family protein

Match to Query 670: 1096.446974 from(549.230763,2+) 
Elution from: 44.745 to 44.745 scan no 4609 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1096.4478  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 28 Expect: 0.0079  
Matched b ions: b(2), b(3), b(4), b(6)  
Matched y ions: y(3), y(4)-98, y(5), y(6), y(7), y(8)++  
Precursor ions origin neutral loss:  

Peptide No.221  
DFMPSDTDFSTK  
Confirmed sites: @T:7  
Ambiguous sites:  

MS/MS Fragmentation of DFMPSDTDFSTK  
Found in AT3G63460.1, EMB2221 (EMBRYO DEFECTIVE 2221)  

Match to Query 1896: 1485.535986 from(743.775269,2+)  
Elution from: 39.154 to 39.154 scan no 3839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1485.5371
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00023
Matched b ions: b(3), b(7)++
Matched y ions: y(3), y(4), y(5), y(7)−98, y(8)−98, y(9)−98, y(9), y(10)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.222

DFMPSDTDFSTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DFMPSDTDFSTK
Found in AT3G63460.1, EMB2221 (EMBRYO DEFECTIVE 2221)

Match to Query 2066: 1469.541690 from(735.778121,2+)
Elution from: 48.454 to 48.454 scan no 4860 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1469.5422
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0031
Matched b ions: b(2), b(3), b(4), b(9)-98
Matched y ions: y(5), y(6)++, y(6), y(8)++, y(8), y(9)-98++, y(9)+, y(9)-98, y(9), y(10), y(10)+, y(10)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.223
DFNGYRSPPR
Confirmed sites: @Y:5
Ambiguous sites:

MS/MS Fragmentation of DFNGYRSPPR
Found in AT4G28990.1, RNA–binding protein–related

Match to Query 1678: 1287.538400 from(644.776476,2+)
Elution from: 26.443 to 26.443 scan no 2174 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1287.5397
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
Ions Score: 19 Expect: 0.066
Matched b ions: b(7)
Matched y ions: y(3), y(4), y(5), y(7)++, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.224

DFPDGSTTASPGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DFPDGSTTASPGR
Found in AT5G38640.1, eukaryotic translation initiation factor 2B family protein / eIF-2B family protein

Match to Query 1342: 1386.543184 from(694.278868,2+)
Elution from: 29.048 to 29.048 scan no 2370 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1386.5453
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00026
Matched b ions: b(6), b(7)
Matched y ions: y(3), y(4), y(7), y(9), y(10)+, y(10), y(11)−98++, y(11)+, y(11), y(12)+
Precursor origin neutral loss: +

Peptide No.225

DFSESRFDDDSEDNLSR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of DFSESRFDDDSEDNLSR
Found in AT5G22120.1, nucleotide binding

Match to Query 3237: 2227.815936 from(743.612588,3+)
Elution from: 39.957 to 39.957 scan no 3778 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2227.8179
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.029
Matched b ions: b(2), b(6), b(8), b(10), b(10)++
Matched y ions: y(7), y(10)++, y(12)−98++, y(14)−98++, y(14)++, y(15)++, y(15)−98++, y(16)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.226

DFSMSILKDLVR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of DFSMSILKDLVR
Found in AT2G22760.1, basic helix–loop–helix (bHLH) family protein

Match to Query 1990: 1598.678367 from(533.900065,3+)
Elution from: 25.537 to 25.537 scan no 1996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1598.6816
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.048
Matched b ions: b(3), b(5), b(6)+, b(6), b(6)−98, b(6)−98++, b(7)+, b(7)−98++, b(8)−98++, b(8)+, b(9)−98++, b(10)−98++
Matched y ions: y(4), y(5), y(6)+, y(6), y(7)+, y(7), y(11)+
Precursor origin neutral loss: +

Peptide No.227

DFSREDSESPMK
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of DFSREDSESPMK
Found in AT5G23680.1, sterile alpha motif (SAM) domain-containing protein

Match to Query 2678: 1586.534256 from(794.274404,2+)
Elution from: 26.490 to 26.490 scan no 2198 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1586.5361
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.043
Matched b ions: b(5), b(6)++, b(7)−98, b(8)−98, b(9)−196, b(9)−98
Matched y ions: y(3), y(8)−196, y(10)++, y(11)−196++, y(11)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.228

DFVASSGSSSPVR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DFVASSGSSSPVR
Found in AT5G55060.1, catalytic

Match to Query 1483: 1374.579862 from(688.297207,2+)
Elution from: 27.990 to 27.990 scan no 2371 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1374.5816
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 8.5e-005
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8), b(9), b(10)-98, b(10), b(11)-98, b(12)
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(7)-98, y(7), y(8), y(9), y(10), y(11), y(11)+, y(11)-98, y(12)+, y(12)-98++
Precursor origin neutral loss:

**Peptide No.229**

DGAELSTRDLQK
Confirmed sites:
Ambiguous sites: @S:6orT:7

MS/MS Fragmentation of DGAELSTRDLQK
Found in AT1G12360.1, KEU (KEULE); protein transporter

Match to Query 1951: 1411.636840 from(706.825696,2+)
Elution from: 55.960 to 55.960 scan no 5991 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6344
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.061
Matched b ions: b(8)−98, b(8), b(9)−98, b(10), b(10)−98, b(11)
Matched y ions: y(2), y(3), y(4), y(7), y(8), y(9)−98++, y(9)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.230

DGALTSNDELESISAR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DGALTSNDELESISAR
Found in AT3G54610.1, GCN5 (Histone acetyltransferase HAT1)

Match to Query 2763: 1756.749890 from(879.382221,2+)
Elution from: 41.900 to 41.900 scan no 4202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1756.7516
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 Expect: 2.3e-007
Matched b ions: b(5), b(8), b(9), b(10), b(11), b(12), b(13), b(14)+, b(14)−98, b(15)
Matched y ions: y(3), y(3)−98, y(4)−98, y(4), y(5)−98, y(6)−98, y(6), y(7)+, y(7)−98, y(7), y(8), y(8)−98, y(9), y(10), y(11), y(11)−98, y(12)−98, y(12), y(13)−98++, y(13)+, y(14)+, y(15)+, y(15)−98++
Precursor origin neutral loss: +

Peptide No.231
DGALTSNDELESIAS
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DGALTSNDELESIAS
Found in AT3G54610.1, GCN5 (Histone acetyltransferase HAT1)

Match to Query 2657: 1756.749716 from(879.382134,2+)
Elution from: 45.296 to 45.296 scan no 4677 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1756.7516
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 67 Expect: 2e-006
Matched b ions: b(4), b(9), b(10), b(11), b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(12)-98, y(13)+, y(15)+
Precursor origin neutral loss:

Peptide No.232

DGDDASMSNGDIASEAVSGELR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DGDDASMSNGDIASEAVSGELR
Found in AT5G04870.1, CPK1 (calcium-dependent protein kinase isoform AK1); calcium- and calmodulin-dependent protein kina

Match to Query 4246: 2361.928714 from(1181.971633,2+)
Elution from: 49.981 to 49.981 scan no 5250 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2361.9267

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 34 Expect: 0.0028

Matched b ions: b(6), b(7)-98, b(10)-98, b(11), b(13)-98, b(14)-98++, b(14)-98, b(15), b(16), b(17)-98, b(18)-98, b(19)-98, b(22)-98++

Matched y ions: y(5), y(6), y(9), y(10), y(11), y(12), y(13), y(16), y(15), y(17)-98, y(17), y(18), y(19)-98++, y(21)-98++, y(22)-98++, y(22)++

Precursor origin neutral loss: +

Peptide No.233

DGDGRLSYGDLK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DGDGRLSYGDLK
Found in AT5G49480.1, ATCP1 (CA2+-BINDING PROTEIN 1); calcium ion binding

Match to Query 1230: 1374.581410 from(688.297981,2+)
Elution from: 33.632 to 33.632 scan no 3082 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1374.5816
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.02
Matched b ions: b(4), b(5), b(6), b(7)–98++, b(8)–98, b(9)++, b(9), b(10)–98, b(10), b(11), b(11)–98, b(11)++
Matched y ions: y(2), y(4), y(5), y(6), y(9)–98++, y(9)++, y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.234

DGDSSSDDEEALAIR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DGDSSSDDEEALAIR
Found in AT1G72440.1, EDA25 (embryo sac development arrest 25)

Match to Query 2354: 1658.630704 from(830.322628,2+)
Elution from: 37.931 to 37.931 scan no 3710 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.6308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0079
Matched b ions: b(3), b(12)-98++, b(12), b(13)
Matched y ions: y(2), y(3), y(5), y(10), y(11), y(12), y(14)++
Precursor origin neutral loss: +

Peptide No.235

DGELGELSPDIR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DGELGELSPDIR
Found in AT3G26935.1, zinc finger (DHHC type) family protein

Match to Query 1840: 1379.595582 from(690.805067,2+)
Elution from: 46.546 to 46.546 scan no 4835 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1379.5969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 6.1e-006
Matched b ions: b(3), b(4), b(6), b(7), b(8)–98, b(8), b(9)–98, b(10), b(10)–98, b(10)++, b(11), b(11)–98
Matched y ions: y(2), y(4), y(5), y(6)–98, y(7), y(8)–98, y(8), y(8)++, y(9), y(9)++, y(9)–98++, y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.236
DGETSEPPEVIPDYENSPR
Confirmed sites:
Ambiguous sites: @Y:14orS:17

MS/MS Fragmentation of DGETSEPPEVIPDYENSPR
Found in AT4G28980.1, CAK1AT (CDK–ACTIVATING KINASE 1AT); kinase/protein serine/threonine kinase
Match to Query 3956: 2209.903026 from(1105.958789,2+)
Elution from: 44.038 to 44.038 scan no 4515 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2209.9052
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 7.1e-007
Matched b ions: b(6), b(10), b(11)
Matched y ions: y(6)++, y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9)−98++, y(9), y(10), y(11), y(12), y(12)++, y(13)++, y(13)−98, y(13), y(13)−98++, y(15)++, y(16)++, y(16)−98++, y(18)−98++, y(18)++
Precursor origin neutral loss: +

Peptide No.237
DGEVLCFGSEEDEIGVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DGEVLCFGSEEDEIGVK
Found in AT5G18570.1, GTP1/OBG family protein

Match to Query 4327: 2219.880758 from(1110.947655,2+)
Elution from: 54.632 to 54.632 scan no 5738 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2219.8816
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.5e-006
Matched b ions: b(6), b(8)–98, b(10), b(11), b(12)–98, b(12), b(14)–98++, b(15)–98, b(16)–98++, b(16)–98, b(16), b(16)++
Matched y ions: y(7), y(8), y(9), y(11), y(12), y(12)–98, y(13), y(13)–98, y(14)–98, y(14), y(15)++, y(15), y(15)–98++, y(16)–98++, y(16), y(16)++, y(18)++
Precursor origin neutral loss: +

Peptide No.238
DGEVSDVEEDEYEAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DGEVSDVEEDEYEAK
Found in AT5G25780.1, EIF3B-2 (eukaryotic translation initiation factor 3B-2); nucleic acid binding / translation initiat

Match to Query 3187: 1792.655030 from(897.334791,2+)
Elution from: 36.637 to 36.637 scan no 3552 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1792.6563
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 6.2e-010
Matched b ions: b(4), b(5), b(6)--98, b(6), b(7)--98, b(7), b(8)--98, b(8), b(9)--98, b(9), b(10)--98, b(10), b(11)--98, b(11), b(12)--98, b(12), b(13)--98, b(13), b(14), b(14)--98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)--98, y(11), y(11)++, y(12)--98++, y(12)--98, y(12), y(12)++, y(13)--98++, y(14)++, y(14)--98++
Precursor origin neutral loss: +

Peptide No.239

DGLLQGNSAAE
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DGLLQGNSAAE
Found in AT1G69840.1, band 7 family protein

Match to Query 837: 1153.465512 from(577.740032,2+)
Elution from: 37.456 to 37.456 scan no 3646 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1153.4652
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 8.4e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)-98, b(9), b(10), b(10)-98
Matched y ions: y(5)++, y(6), y(7), y(8)-98++, y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.240

DGNEVVEPVDGK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DGNEVVEPVDGK
Found in AT2G32910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G61910.3); similar to expressed protein

Match to Query 1603: 1423.584208 from(712.799380,2+)  
Elution from: 25.336 to 25.336 scan no 1980 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1423.5867
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 39 Expect: 0.00066
Matched b ions: b(4), b(5), b(6), b(7), b(9)
Matched y ions: y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(12)++
Precursor origin neutral loss: +

Peptide No. 241

DGNNSEDDEFK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DGNNSEDDEFK
Found in AT3G29075.1, glycine-rich protein

Match to Query 1238: 1348.444892 from(675.229722,2+)  
Elution from: 22.931 to 22.931 scan no 1675 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1348.4456
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00018
Matched b ions: b(3), b(4), b(5), b(6)−98, b(7), b(7)−98, b(8), b(9), b(9)−98, b(10), b(10)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)−98, y(8), y(8)−98, y(9)−98++, y(9)++, y(10)++, y(10)−98++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.242
DGNNSEDDEFKK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DGNNSEDDEFKK
Found in AT3G29075.1, glycine-rich protein

Match to Query 1908: 1476.539354 from(739.276953,2+) Elution from: 19.396 to 19.396 scan no 1219 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1476.5405
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 1.9e-005
Matched b ions: b(4), b(5)–98, b(6)–98, b(7), b(7)–98, b(8)–98, b(8), b(9), b(9)–98, b(10)–98, b(10), b(10)–98++, b(11), b(11)–98, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98, y(8)–98++, y(9)–98++, y(9)++, y(10)–98++, y(10)++, y(11)–98++, y(11)++
Precursor origin neutral loss: +

Peptide No.243
DGQIEETVDTAPASLGSPSR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of DGQIEETVDTAPASLGSPSR
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 3856: 2108.926683 from(703.982837,3+)
Elution from: 43.410 to 43.410 scan no 4220 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2108.9263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 3.6e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)+, b(11), b(11)+, b(12)+, b(13), b(13)+, b(14), b(15)+, b(16)+, b(17)-98++, b(17)+, b(18)-98++
Matched y ions: y(3), y(4)-98, y(4), y(5), y(6)-98, y(7), y(7)+, y(7)-98, y(8)+, y(8)-98, y(8), y(9)+, y(9), y(9)-98++, y(9)-98, y(10), y(10)+, y(11), y(11)+, y(12)-98++, y(12)+, y(13)-98++, y(13)+, y(14)-98++, y(15)+, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.244
DGQIEETVDTAPASLGSPSR
Confirmed sites: S17
Ambiguous sites: @S:17 or S:19

MS/MS Fragmentation of DGQIEETVDTAPASLGSPSR
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 3892: 2108.923058 from(1055.468805,2+)
Elution from: 42.290 to 42.290 scan no 4361 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2108.9263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 4.5e-008
Matched b ions: b(9), b(10), b(11), b(14), b(15), b(19)++
Matched y ions: y(5), y(7), y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(12)-98, y(12), y(13)-98, y(14), y(14)-98, y(15)++, y(17), y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.245
DGQQIYGSPHGVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DGQQIYGSPHGVR
Found in AT1G60110.1, jacalin lectin family protein

Match to Query 1838: 1492.644782 from(747.329667,2+) Elution from: 25.083 to 25.083 scan no 1980 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1492.6460
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 6.4e-005
Matched b ions: b(4), b(5), b(6), b(8)−98, b(10)−98, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)−98, y(8)−98, y(8), y(9), y(9)−98, y(10)−98, y(10)++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.246
DGSDSPIDVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DGSDSPIDVR
Found in AT2G23520.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66950.1); similar to unknown protein [A

Match to Query 786: 1139.448714 from(570.731633,2+)
Elution from: 27.217 to 27.217 scan no 2126 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1139.4496  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 37 Expect: 0.00072  
Matched b ions: b(7), b(8)  
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(7)++, y(8)++, y(9)++  
Precursor origin neutral loss: +

Peptide No.247

DGSSFSMTPK  
Confirmed sites: @T:8  
Ambiguous sites:  

MS/MS Fragmentation of DGSSFSMTPK  
Found in AT1G09770.1, ATCDC5 (Arabidopsis thaliana homolog of cdc5); DNA binding / transcription factor  

Match to Query 752: 1135.423154 from(568.718853,2+)  
Elution from: 32.327 to 32.327 scan no 2918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1135.4257
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.003
Matched b ions:
Matched y ions: y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.248

DGSYDFWTDGEGNLNK
Confirmed sites:
Ambiguous sites: @S:3orY:4

MS/MS Fragmentation of DGSYDFWTDGEGNLNK
Found in AT1G78610.1, mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein

Match to Query 3170: 1896.719140 from(949.366846,2+)
Elution from: 55.836 to 55.836 scan no 5944 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1896.7203
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0046
Matched b ions: b(5)–98, b(6)–98, b(7)–98, b(11)–98
Matched y ions: y(5), y(7), y(8), y(10), y(11), y(12), y(14)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.249

DHRASDDDEEGEIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DHRASDDDEEGEIR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 2615: 1722.646821 from(575.222883,3+)
Elution from: 19.188 to 19.188 scan no 1167 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1722.6482
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 9.5e-007
Matched b ions: b(2), b(3), b(4)+, b(4), b(5)-98++, b(5)++, b(5), b(5)-98, b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98, b(7)++, b(7), b(7)-98++, b(8), b(8)-98++, b(8)-98, b(8)++, b(9)-98, b(9), b(9)++, b(9)-98++, b(10)+, b(11)-98++, b(11)+, b(12)+, b(12)-98++, b(13)+, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9), y(9)+, y(10)+, y(11)-98++, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No. 250

DHRASDDDEEGEIRSER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DHRASDDDEEGEIRSER
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 3758: 2094.822063 from(699.281297,3+)
Elution from: 19.478 to 19.478 scan no 1230 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2094.8239
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 58 Expect: 1.3e-005
Matched b ions: b(4), b(5)-98, b(5), b(6)++, b(6)-98, b(8)-98, b(9)-98, b(13)-98++, b(16)++, b(16)-98++
Matched y ions: y(5)++, y(5), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)-98++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.251
DIDLSFSSPTK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DIDLSFSSPTK
Found in AT2G32240.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05320.3); similar to kinesin, putative

Match to Query 1522: 1288.556828 from(645.285690,2+)
Elution from: 48.443 to 48.443 scan no 4980 polarity:+.
Monoisotopic mass of neutral peptide Mr(calc): 1288.5588
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.5e-005
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6), b(7), b(8)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++
Precursor origin neutral loss:

Peptide No.252

DIDLSFSSPTK
Confirmed sites: T:10 or S:8
Ambiguous sites: @T:10 or S:8

MS/MS Fragmentation of DIDLSFSSPTK
Found in AT2G32240.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05320.3);
similar to kinesin, putative

Match to Query 1240: 1288.557720 from(645.286136,2+)
Elution from: 47.107 to 47.107 scan no 4762 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1288.5588
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0002
Matched b ions: b(3), b(5)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++
Precursor origin neutral loss:

Peptide No.253
DIEQAPTESDSLSPK
Confirmed sites: @S:11 or S:13
Ambiguous sites: @S:11 or S:13

MS/MS Fragmentation of DIEQAPTESDSLSPK
Found in AT3G61480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28350.2); similar to unknown protein [O
Match to Query 1942: 1695.722260 from(848.868406,2+) Elution from: 32.762 to 32.762 scan no 2967 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1695.7240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0082
Matched b ions: b(5), b(8)
Matched y ions: y(6), y(7), y(9), y(10), y(11)-98++, y(11), y(13)++
Precursor origin neutral loss: +

Peptide No.254
DIEQAPTESDSLSPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of DIEQAPTESDSLSPK
Found in AT3G61480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28350.2); similar to unknown protein [O

Match to Query 2033: 1695.722400 from(848.868476,2+)
Elution from: 33.974 to 33.974 scan no 3011 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1695.7240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00025
Matched b ions: b(4), b(5), b(9)++, b(12), b(14)−98++
Matched y ions: y(6), y(7), y(9), y(10), y(10)++, y(11)−98++, y(11), y(11)−98, y(14)++
Precursor origin neutral loss: +

Peptide No.255
DIESEVEVSQEGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DIESEVEVSQEGR
Found in AT3G05420.1, ACBP4 (ACYL-COA BINDING PROTEIN 4, ACYL-COA-BINDING DOMAIN 4); acyl-CoA binding

Match to Query 2111: 1555.639422 from(778.826987,2+)  
Elution from: 40.830 to 40.830 scan no 4098 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1555.6402
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.4e-007
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b (10)-98, b(11), b(11)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11)-98++, y(11)+, y (12)++
Precursor origin neutral loss: +

Peptide No.256
DIESEVEVSQEGR
Confirmed sites: @S:9
Ambiguous sites:
MS/MS Fragmentation of DIESEVEVSQEGR
Found in AT3G05420.1, ACBP4 (ACYL-COA BINDING PROTEIN 4, ACYL-COA-BINDING DOMAIN 4); acyl-CoA binding
Match to Query 1668: 1555.639348 from(778.826950,2+)
Elution from: 35.224 to 35.224 scan no 3297 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1555.6402  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 90 Expect: 7.9e-009  
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)–98, b(10)–98, b(10), b(11), b(11)–98, b(12), b(12)–98  
Matched y ions: y(2), y(3), y(4), y(5)–98, y(5), y(5)++, y(6), y(6)–98, y(7)++, y(7)–98, y(7), y(8), y(8)–98++, y(8)–98, y(9)+, y(9), y(10), y(10)–98, y(10)+, y(11), y(11)–98++, y(11)+, y(12)+  
Precursor origin neutral loss: +  

---

**Peptide No.257**

DIESLSSVSK  
Confirmed sites:  
Ambiguous sites: @S:7orS:9  

MS/MS Fragmentation of DIESLSSVSK  
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra  
Match to Query 772: 1143.504456 from(572.759504,2+)  
Elution from: 34.435 to 34.435 scan no 3197 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1143.5060
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00054
Matched b ions: b(2), b(4), b(5), b(6), b(9)++
Matched y ions: y(4)–98++, y(4), y(5), y(5)–98, y(6), y(7), y(8)++, y(8), y(9)++
Precursor origin neutral loss:

Peptide No.258

DIGSGNFGVAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DIGSGNFGVAR
Found in AT3G50500.1. SPK-2-2 (SNF1-RELATED PROTEIN KINASE 2-2, SNF1-RELATED PROTEIN KINASE 2.2); kinase/ protein kinase

Match to Query 1143: 1171.502376 from(586.758464,2+)
Elution from: 39.494 to 39.494 scan no 3811 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1171.5022
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 9e-005
Matched b ions: b(2), b(3), b(6), b(7)-98, b(7), b(8)++, b(9), b(9)-98, b(9)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(7), y(8)-98, y(8), y(9)-98++, y(9)-98, y(9), y(9)++, y
(10)++
Precursor origin neutral loss: +

Peptide No.259
DIIGLFVSLIK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of DIIGLFVSLIK
Found in AT4G14390.1, ankyrin repeat family protein

Match to Query 1859: 1296.711652 from(649.363102,2+)
Elution from: 50.340 to 50.340 scan no 5369 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.7094
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.028
Matched b ions:
Matched y ions: y(5), y(6), y(7), y(8), y(10)++
Precursor origin neutral loss:

Peptide No.260

DIRSSPGYSDEK
Confirmed sites: "@S:5,@S:9"
Ambiguous sites:

MS/MS Fragmentation of DIRSSPGYSDEK
Found in AT3G23900.1, RNA recognition motif (RRM)–containing protein

Match to Query 2332: 1512.551890 from(757.283221,2+)
Elution from: 21.776 to 21.776 scan no 1540 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1512.5534
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0021
Matched b ions: b(3), b(4), b(5)−98, b(5), b(7)−98, b(8), b(8)−98, b(10)−98, b(10), b(11)
Matched y ions: y(4), y(6), y(7), y(7)−98, y(8)−98++, y(9), y(10)++, y(10)−98++, y(11)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.261
DISPTAAGLGLPVTGGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DISPTAAGLGLPVTGGK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1);
similar to nuclear matrix con

Match to Query 2406: 1632.810970 from(817.412761,2+)
Elution from: 50.804 to 50.804 scan no 5375 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.8123
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 6.2e-008
Matched b ions: b(3), b(6)-98, b(6), b(7)-98, b(8)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13), b(13)-98, b(13)+, b(14), b(14)-98++, b(15)-98, b(16)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)+, y(13), y(14), y(14)+, y(15)-98++, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.262

DISPTAAGLGLPVTGGK
Confirmed sites:
Ambiguous sites: @S:3orT:5

MS/MS Fragmentation of DISPTAAGLGLPVTGGK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 2569: 1632.810898 from(817.412725,2+)
Elution from: 52.562 to 52.562 scan no 5359 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.8123
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0017
Matched b ions: b(6)-98, b(6), b(7)-98, b(9), b(10)-98, b(11), b(11)-98, b(13)-98, b(14)-98++, b(16)
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(15)-98++, y(15)+, y(16)++
Precursor origin neutral loss: +

**Peptide No.263**

DIVGSAYYVAPEVLK
Confirmed sites:
Ambiguous sites: @S:5orY:7

MS/MS Fragmentation of **DIVGSAYYVAPEVLK**
Found in **AT1G50700.1**. CPK33 (calcium-dependent protein kinase 33); calcium- and calmodulin-dependent protein kinase/ kina

Match to Query 2609: 1702.819988 from(852.417270,2+)
Elution from: 59.250 to 59.250 scan no 6320 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1702.8218  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 26 Expect: 0.024  
Matched b ions: b(7)-98, b(8), b(9)-98, b(9), b(10)-98  
Matched y ions: y(5), y(6), y(7), y(8), y(12), y(12)-98++, y(12)++  
Precursor origin neutral loss: +

Peptide No.264

DKDTDTDTIIAEEVTDDQK  
Confirmed sites: @T:4  
Ambiguous sites:  

MS/MS Fragmentation of DKDTDTDTIIAEEVTDDQK  
Found in AT5G24630.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22795.1); similar to unknown protein [O  

Match to Query 3195: 2216.956188 from(739.992672,3+)  
Elution from: 43.120 to 43.120 scan no 4253 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2216.9573
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0044
Matched b ions: b(8), b(10), b(10)++, b(13)++, b(14)--98++, b(14)+, b(15)+, b(16)+, b(17)+, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(14)+, y(18)--98++
Precursor origin neutral loss:

Peptide No.265
DKDTIMEQPSSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DKDTIMEQPSSPR
Found in AT1G30810.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 1692: 1582.668914 from(792.341733,2+)
Elution from: 24.900 to 24.900 scan no 1922 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.6698
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0044
Matched b ions: b(5), b(7), b(8), b(10), b(11)−98
Matched y ions: y(2), y(5), y(6)−98, y(7), y(8), y(9)−98, y(10), y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.266

DKDTIMEQPSSPR
Confirmed sites:
Ambiguous sites: @S:10 or S:11

MS/MS Fragmentation of DKDTIMEQPSSPR
Found in AT1G30810.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 1953: 1582.668276 from(792.341414,2+) Elution from: 24.592 to 24.592 scan no 1870 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.6698
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0061
Matched b ions: b(7), b(8), b(11)−98, b(11)+, b(12)−98++
Matched y ions: y(2), y(4), y(5)−98, y(5), y(6), y(8), y(8)−98, y(9)+, y(12)++
Precursor origin neutral loss: +

Peptide No.267
DKKEEVIEEVASPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DKKEEVIEEVASPK
Found in AT3G57150.1, NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)

Match to Query 2426: 1679.799924 from(560.940584,3+)
Elution from: 31.196 to 31.196 scan no 2805 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1679.8018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00058
Matched b ions: b(2), b(4), b(6), b(6)++, b(7), b(8)++, b(9), b(9)++, b(10)++, b(11)++, b(12)−98++, b(12)++, b(13)−98++
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5), y(5)−98, y(6)−98, y(7), y(7)−98, y(7)++, y(8)−98, y(8), y(8)++, y(9)−98, y(9)−98++, y(10)−98++, y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.268

DLDSQFSSLSLNTK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DLDSQFSSLSLNTK
Found in AT1G58110.1, bZIP family transcription factor

Match to Query 2339: 1633.719834 from(545.580554,3+)
Elution from: 39.121 to 39.121 scan no 3871 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1633.7236
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.039
Matched b ions: b(4), b(8)+, b(10)−98++, b(11)−98++, b(11)+, b(12)−98++, b(13)−98++
Matched y ions: y(8)+, y(10)−98++, y(11)+, y(12)−98++, y(13)−98++
Precursor origin neutral loss:

Peptide No.269

DLFENGSVCMDSESEAER
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DLFENGSVCMDSESEAER
Found in AT2G16640.1, ATTOC132/TOC132 (MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); transmembrane r

Match to Query 3780: 2153.789740 from(1077.902146,2+)
Elution from: 47.782 to 47.782 scan no 4991 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2153.7918
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 94 Expect: 2.7e-009
Matched b ions: b(4), b(8), b(9), b(11), b(14)++, b(15)−98, b(15), b(15)++, b(16)−98++, b(17)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10)−98, y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(15)++, y(16)−98++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.270

DLFENGSCMDSESEAER
Confirmed sites:  
Ambiguous sites: @S:12orS:14

MS/MS Fragmentation of DLFENGSCMDSESEAER
Found in AT2G16640.1, ATTOC132/TOC132 (MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); transmembrane r

Match to Query 3667: 2153.789732 from(1077.902142,2+) 
Elution from: 48.937 to 48.937 scan no 5057 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2153.7918
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0046
Matched b ions: b(8), b(14)+, b(17)
Matched y ions: y(8), y(9), y(10), y(11), y(12), y(13), y(17)+
Precursor origin neutral loss: +

Peptide No.271

DLFGSDNEEYTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DLFGSDNEEYTK
Found in AT4G17620.1, glycine-rich protein

Match to Query 2152: 1496.569420 from(749.291986,2+)
Elution from: 44.612 to 44.612 scan no 4368 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1496.5708
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.2e-007
Matched b ions: b(2), b(3), b(4), b(5)–98, b(6)–98, b(6), b(7)–98, b(8)–98, b(8), b(9)–98, b(9), b(10)–98, b(10), b(10)–98++, b(11)–98, b(11)–98++, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)–98++, y(8), y(8)–98, y(9)–98, y(9), y(9)–98++, y(10), y(10)++, y(10)–98, y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No. 272

DLGSASPPVARPVR
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of DLGSASPPVARPVR
Found in AT4G13350.1, human Rev interacting-like protein-related / hRIP protein-related

Match to Query 2765: 1580.710394 from(791.362473,2+)
Elution from: 32.803 to 32.803 scan no 3063 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1580.7113
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  S6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 25 Expect: 0.022
Matched b ions: b(6)-196, b(6)-98, b(9)-98, b(9), b(10)-++, b(11)-98, b(11), b(12)-196, b(11)-196
Matched y ions: y(3), y(4), y(5), y(8)-++, y(8), y(9), y(9)-98++, y(9)-++, y(10)-++, y(11)-98++, y(11)-196++, y(12)-98++, y(13)-196++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.273
DLGSASPPVARPVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DLGSASPPVARPVR
Found in AT4G13350.1, human Rev interacting-like protein-related / hRIP protein-related

Match to Query 1955: 1500.743652 from(501.255160, 3+)
Elution from: 29.653 to 29.653 scan no 2599 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1500.7449
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0023
Matched b ions: b(2), b(4), b(11)++, b(12)−98++
Matched y ions: y(7)++, y(8)++, y(9)++, y(9)−98++, y(10)++, y(10)−98++, y(11)++, y(12)++, y(12)−98++
Precursor origin neutral loss:

Peptide No.274

DLGSVANSPPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DLGSVANSPPR
Found in AT2G10550.1, uracil DNA N-glycosylase

Match to Query 954: 1191.526694 from(596.770623,2+)
Elution from: 29.340 to 29.340 scan no 2520 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1191.5285
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0003
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(8)--98, b(10)++
Matched y ions: y(3), y(4), y(5), y(5)--98, y(6), y(7), y(7)--98, y(7)++, y(8), y(8)++, y(9)++, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.275

DLHGSPVSDVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DLHGSPVSDVK
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 1329: 1232.542910 from(617.278731,2+) Elution from: 24.027 to 24.027 scan no 1827 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1232.5438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00014
Matched b ions: b(2), b(3), b(4), b(5)−98++, b(5)−98, b(5), b(7)−98, b(7), b(8), b(9), b(9)−98, b(9)++, b(10), b(10)−98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)−98, y(8), y(9)+, y(9)−98++, y(9)−98, y(10)+, y(10)−98++
Precursor origin neutral loss: +

Peptide No.276
DLHGSPVSDVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DLHGSPVSDVK
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 1080: 1232.543236 from(617.278894,2+)
Elution from: 22.615 to 22.615 scan no 1615 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1232.5438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.016
Matched b ions: b(3), b(6), b(9), b(9)++, b(10), b(10)--98
Matched y ions: y(2), y(8), y(8)--98, y(9)++, y(9)--98++, y(10)++, y(10)--98++
Precursor origin neutral loss: +

Peptide No.277

DLIVDTDEEK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of DLIVDTDEEK
Found in AT3G12810.1, PIE1 (PHOTOPERIOD–INDEPENDENT EARLY FLOWERING 1); ATP binding / DNA binding / helicase

Match to Query 1169: 1255.521186 from(628.767869,2+)
Elution from: 34.369 to 34.369 scan no 3199 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1255.5221
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
 T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0002
Matched b ions: b(2), b(3), b(4), b(4)++, b(7), b(7)−98, b(9), b(9)−98
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(6), y(6)−98, y(6)−98++, y(7), y(7)−98, y(8)++, y(8), y(8)−98++, y(9)++
Precursor origin neutral loss:

Peptide No.278

DLLSDGDSVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DLLSDGDSVK
Found in AT3G19440.1, pseudouridine synthase family protein

Match to Query 757: 1127.474604 from(564.744578,2+)
Elution from: 37.815 to 37.815 scan no 3694 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1127.4747
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0003
Matched b ions: b(2), b(3), b(4)−98, b(5)−98, b(7)−98, b(7), b(8)−98, b(8), b(9)−98
Matched y ions: y(3), y(5), y(6), y(7)−98, y(7), y(8)++, y(8), y(8)−98++, y(8)−98, y(9)++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.279

DLLTLDEKSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DLLTLDEKSPR
Found in AT5G15200.1, 40S ribosomal protein S9 (RPS9B)

Match to Query 2042: 1365.653064 from(456.224964,3+)
Elution from: 40.214 to 40.214 scan no 4033 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1365.6541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.018
Matched b ions: b(2)
Matched y ions: y(2), y(3), y(4)++, y(5)++, y(6)++, y(6)--98, y(8)++, y(9)++, y(9)--98++, y(10)++
Precursor origin neutral loss:

Peptide No.280

DLSDGESILR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DLSDGESILR
Found in AT3G17900.1, similar to Os03g0152800 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001048995.1); similar to ex

Match to Query 937: 1183.511108 from(592.762830,2+)
Elution from: 42.947 to 42.947 scan no 4375 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1183.5122

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 68 Expect: 6.7e-007

Matched b ions: b(2), b(3), b(4), b(5), b(6)−98, b(7)−98, b(8)−98, b(9)−98

Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)−98++, y(8), y(8)−98, y(9)++

Precursor origin neutral loss: +

Peptide No.281

DLSEDEEAEIENK

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of DLSEDEEAEIENK

Found in AT5G66540.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to Os12g0133900 [Oryz]

Match to Query 2172: 1599.617620 from(800.816086,2+)

Elution from: 36.698 to 36.698 scan no 3545 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1599.6189

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 91 Expect: 4.4e-009

Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(12)-98++

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98++, y(11)-98, y(11)++, y(12)++, y(12)-98++, y(12)-98++

Precursor origin neutral loss: +

---

**Peptide No. 282**

**DLSEDEEAEIENKGNEK**

Confirmed sites: @S.3

Ambiguous sites:

MS/MS Fragmentation of **DLSEDEEAEIENKGNEK**

Found in **AT5G66540.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to Os12g0133900 [Oryza]

Match to Query 2776: 2027.819872 from(1014.917212,2+)

Elution from: 33.089 to 33.089 scan no 3010 polarity:
Monoisotopic mass of neutral peptide Mr(calc): 2027.8208
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0074
Matched b ions: b(6)-98, b(7), b(9)-98, b(10)-98, b(11)++, b(16)-98++
Matched y ions: y(6), y(7), y(8), y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.283

DLSEDENMEEAEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DLSEDENMEEAEEK
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unnamed protein pr

Match to Query 2667: 1746.616238 from(874.315395,2+)
Elution from: 34.600 to 34.600 scan no 3228 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1746.6179
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 2e-009
Matched b ions: b(4)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12)-98++, b(13)-98, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)-98++, y(12), y(12)-98, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.284
DLSEDENMEEAEEK
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of DLSEDENMEEAEEK
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unnamed protein pr

Match to Query 2398: 1762.608920 from(882.311736,2+)
Elution from: 26.777 to 26.777 scan no 2164 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1762.6128
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 Expect: 0.0024
Matched b ions: b(6), b(7)-98, b(10), b(10)-98, b(13)-98
Matched y ions: y(4), y(5), y(8), y(9), y(10), y(12)-98++, y(12)+, y(13)++
Precursor origin neutral loss: +

Peptide No.285
DLSPISITQPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DLSPISITQPK
Found in AT5G44240.1, haloacid dehalogenase-like hydrolase family protein

Match to Query 1221: 1277.625714 from(639.820133,2+)
Elution from: 43.122 to 43.122 scan no 4398 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1277.6268
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 1.1e-005
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(5), b(6)−98++, b(6)−98, b(7)−98, b(9)−98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)−98++, y(9)++, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.286

DLSRGEATLDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DLSRGEATLDR
Found in AT5G04990.1, sad1/unc-84 protein–related

Match to Query 1913: 1311.581702 from(656.798127,2+) Elution from: 26.510 to 26.510 scan no 2224 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1311.5820
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0059
Matched b ions: b(5), b(6), b(6)−98, b(7), b(10)−98, b(10), b(10)++
Matched y ions: y(3), y(4), y(5), y(7), y(8)++, y(9)−98++, y(9)++, y(10)++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.287

DLSTTLSPTSEEK
Confirmed sites:
Ambiguous sites: @S:10orS:7orT:9

MS/MS Fragmentation of DLSTTLSPTSEEK
Found in AT1G52080.1, AR791; actin binding

Match to Query 1552: 1486.643888 from(744.329220,2+)
Elution from: 35.272 to 35.272 scan no 3182 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.6440
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00019
Matched b ions: b(5), b(6)
Matched y ions: y(2), y(3), y(7), y(7)-98, y(8), y(8)-98, y(9), y(11)++, y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.288
DLSTTLSPTSEEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DLSTTLSPTSEEK
Found in AT1G52080.1, AR791; actin binding

Match to Query 1550: 1486.644404 from(744.329478,2+)
Elution from: 35.159 to 35.159 scan no 3192 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.6440
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.017
Matched b ions: b(6), b(7)++, b(7)−98, b(8)−98++
Matched y ions: y(5), y(6), y(7), y(8), y(8)−98, y(9), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.289

DLTATTGDSSLPLIK
Confirmed sites:
Ambiguous sites: @S:10orS:9

MS/MS Fragmentation of DLTATTGDSSLPLIK
Found in AT3G11900.1, ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); amino acid permease/ amino acid transporter

Match to Query 2201: 1610.777764 from(806.396158,2+)
Elution from: 51.678 to 51.678 scan no 5464 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1610.7804
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0018
Matched b ions: b(6), b(8), b(11), b(11)−98, b(12)−98, b(13)−98, b(14)−98, b(14)
Matched y ions: y(4), y(7)−98, y(9), y(11), y(12), y(14)++
Precursor origin neutral loss: +

Peptide No.290

DLTAVGSPENAPAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DLTAVGSPENAPAK
Found in AT1G12000.1, pyrophosphate—fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dep

Match to Query 1776: 1448.654156 from(725.334354,2+)
Elution from: 30.002 to 30.002 scan no 2647 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1448.6548
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 84 Expect: 3.6e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7)−98, b(8)++, b(9), b(9)−98, b(10)−98, b(10), b(11), b(11)−98, b(11)−98++, b(12)−98, b(13), b(13)−98, b(13)−98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(8)−98, y(8)−98++, y(9), y(9)−98, y(10), y(10)−98, y(10)++, y(11), y(11)++, y(11)−98++, y(11)−98, y(12)++, y(12), y(12)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No. 291
DMDGYVMSPSLSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DMDGYVMSPSLSK
Found in AT2G22300.1, ethylene-responsive calmodulin-binding protein, putative (SR1)

Match to Query 2250: 1508.591676 from(755.303114,2+)
Elution from: 46.215 to 46.215 scan no 4691 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1508.5928
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 2e-008
Matched b ions: b(5), b(6), b(7), b(8)-98, b(10)++, b(10)-98++, b(11), b(11)-98, b(12)
Matched y ions: y(2), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.292

DMMTDLSYPLK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of DMMTDLSYPLK
Found in AT3G02600.1, LPP3 (LIPID PHOSPHATE PHOSPHATASE 3); phosphatidate phosphatase

Match to Query 1761: 1408.562010 from(705.288281,2+)
Elution from: 37.071 to 37.071 scan no 3560 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1408.5655
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(2), b(4), b(5), b(5)−98, b(6), b(7), b(8)−98++, b(9)++, b(9)−98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(9)++, y(10)++
Precursor origin neutral loss:

Peptide No.293
DNDSEPEELLR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DNDSEPEELLR
Found in AT4G27430.1, CIP7 (COP1–INTERACTING PROTEIN 7)

Match to Query 1606: 1395.554346 from(698.784449,2+)
Elution from: 43.466 to 43.466 scan no 4407 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1395.5555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00013
Matched b ions: b(3), b(4)-98, b(4)-98++, b(5)-98, b(5), b(6)+, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98
Matched y ions: y(2), y(3), y(4), y(4)+, y(6), y(7), y(8)-98, y(8), y(8)+, y(9), y(9)-98, y(9)-98++, y(9)+, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.294
DNDVPVSYSGSGGPTK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DNDVPVSYSGSGGPTK
Found in AT1G05150.1, calcium-binding EF hand family protein

Match to Query 2488: 1658.681236 from(830.347894,2+)
Elution from: 31.236 to 31.236 scan no 2810 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 6.4e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)+, b(11), b(12)-98, b(13)-98++, b(13)+, b(13),
b(13)-98, b(14)-98++, b(15), b(15)-98++, b(15)+
Matched y ions: y(3), y(5), y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(11)-98, y(11)+, y(12)+,
y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13)+, y(13), y(13)-98, y(14)+, y(15)+
Precursor origin neutral loss: +

Peptide No.295

DNDVPVSYSGSGGPTK
Confirmed sites:
Ambiguous sites: @S:7orY:8

MS/MS Fragmentation of DNDVPVSYSGSGGPTK
Found in AT1G05150.1, calcium-binding EF hand family protein

Match to Query 1927: 1658.681538 from(830.348045,2+)
Elution from: 32.114 to 32.114 scan no 2795 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 39 Expect: 0.00091
Matched b ions: b(3), b(4), b(5), b(6), b(13)−98++, b(13)++, b(13)−98, b(14)−98++, b(15)
Matched y ions: y(3), y(8)++, y(10), y(10)−98, y(11)−98, y(11), y(12)−98, y(12), y(12)++, y(13)−98++, y(13)++, y(13)−98, y(15)++
Precursor origin neutral loss: +

Peptide No. 296

DNDVPVSYSYGSGGPTK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DNDVPVSYSYGSGGPTK
Found in AT1G05150.1, calcium-binding EF hand family protein

Match to Query 2720: 1658.681582 from(830.348067,2+) Elution from: 32.098 to 32.098 scan no 2821 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 5.3e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)+, b(11), b(13)−98++, b(13), b(13)+, b(13)−98, b(14)−98++, b(15)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(10)−98, y(11)+, y(11)−98, y(11), y(12)−98++, y(12)+, y(12)−98, y(12), y(13)−98++, y(13), y(13)+, y(13)−98, y(15)+
Precursor origin neutral loss: +

Peptide No.297
DNLTLWTSDLNEEGDER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DNLTLWTSDLNEEGDER
Found in AT1G22300.1, GRF10 (GENERAL REGULATORY FACTOR 10); protein phosphorylated amino acid binding

Match to Query 3963: 2085.854658 from(1043.934605,2+)
Elution from: 58.049 to 58.049 scan no 6138 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2085.8528
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.9e-005
Matched b ions: b(10), b(12), b(13)
Matched y ions: y(5), y(6), y(7), y(9)+, y(10), y(11)-98, y(11), y(12), y(13), y(14)+, y(15)+, y(16) ++
Precursor origin neutral loss: +

Peptide No.298

DNLTLWTSDMQDESPEEIK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DNLTLWTSDMQDESPEEIK
Found in AT1G35160.1, GRF4 (GENERAL REGULATORY FACTOR 4); protein phosphorylated amino acid binding

Match to Query 3416: 2345.959220 from(1173.986886,2+)
Elution from: 54.788 to 54.788 scan no 5289 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2345.9610
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 8.4e-007
Matched b ions: b(5), b(6), b(7), b(8), b(11), b(12), b(13), b(14)–98, b(14), b(15)–98, b(16)–98++, b(16), b(18)++
Matched y ions: y(5), y(6), y(7)–98, y(8), y(10), y(11)+, y(12), y(12)–98, y(13), y(13)–98, y(14)–98, y(14)+, y(15), y(15)+, y(17)+, y(17)–98++, y(18)++
Precursor origin neutral loss: +

Peptide No.299

DNLTLWTSMDQDESPEEIK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DNLTLWTSMDQDESPEEIK
Found in AT1G35160.1, GRF4 (GENERAL REGULATORY FACTOR 4); protein phosphorylated amino acid binding

Match to Query 3378: 2329.962748 from(1165.988650,2+)
Elution from: 60.053 to 60.053 scan no 5922 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2329.9661
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 Expect: 1.2e-007
Matched b ions: b(6), b(7), b(11), b(12), b(13), b(14), b(14)−98, b(15)−98
Matched y ions: y(5), y(6), y(8), y(10), y(11), y(12), y(13), y(14), y(15), y(18)++
Precursor origin neutral loss: +

Peptide No.300

DNLTLWTSQMTDEAGDEIK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of DNLTLWTSQMTDEAGDEIK
Found in AT5G38480.1, GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding

Match to Query 3271: 2248.905724 from(1125.460138,2+)
Elution from: 55.586 to 55.586 scan no 5361 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2248.9083
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 8e-006
Matched b ions: b(6), b(12), b(13)-98++, b(13)-98, b(14), b(15), b(17)-98, b(17)++, b(17)-98++
Matched y ions: y(6), y(7), y(8), y(9)-98, y(9), y(10), y(11), y(12), y(12)-98, y(13), y(14), y(14)-98, y(15), y(16), y(16)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.301
DNLTLWTSMDTDEAGDEIK
Confirmed sites: 
Ambiguous sites: @T:7orS:8

MS/MS Fragmentation of DNLTLWTSMDTDEAGDEIK
Found in AT5G38480.1, GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding

Match to Query 3996: 2232.907628 from(1117.461090,2+)
Elution from: 62.174 to 62.174 scan no 6607 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2232.9133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.016
Matched b ions: b(6), b(10)-98, b(17)
Matched y ions: y(6), y(9), y(13), y(14), y(15)
Precursor origin neutral loss: +

Peptide No.302

DNLTLWTSDMTDEAGDEIK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of DNLTLWTSDMTDEAGDEIK
Found in AT5G38480.1, GRF3 (GENERAL REGULAR FACTOR 3); protein phosphorylated amino acid binding

Match to Query 4098: 2232.911344 from(1117.462948,2+) Elution from: 60.019 to 60.019 scan no 6330 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2232.9133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 87 Expect: 2e-008
Matched b ions: b(7), b(12), b(13), b(14)
Matched y ions: y(6), y(7), y(8), y(10), y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(15), y(16), y(18++)
Precursor origin neutral loss:

Peptide No.303
DNNSAKDESITEPPAPVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DNNSAKDESITEPPAPVK
Found in AT3G27390.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40640.1); similar to Steroid nuclear re

Match to Query 2658: 1990.886864 from(996.450708,2+)
Elution from: 30.011 to 30.011 scan no 2603 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1990.8884
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 2.3e-005
Matched b ions: b(3), b(5)->98, b(7), b(8), b(12)->98, b(12), b(13), b(13)++, b(15)->98, b(15)++, b(16)->98++
Matched y ions: y(3), y(6), y(8), y(9), y(10), y(11), y(12), y(14), y(14)++, y(15)->98, y(15)++, y(16)->98++, y(17)++, y(17)->98++
Precursor origin neutral loss: +

Peptide No.304
DNNSAKDESITEPPAPVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DNNSAKDESITEPPAPVK
Found in AT3G27390.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40640.1); similar to Steroid nuclear re

Match to Query 3395: 1990.88848 from(664.636892,3+)
Elution from: 29.950 to 29.950 scan no 2640 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1990.8884
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.024
Matched b ions: b(8), b(9)++, b(10)++, b(10), b(10)−98++, b(11)++, b(12), b(12)++, b(12)−98++, b(13)−98++, b(15)++, b(16)−98++, b(16)++, b(17)++, b(17)−98++
Matched y ions: y(3), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(10)++, y(10)−98++, y(12)−98++, y(15)++
Precursor origin neutral loss:

Peptide No.305

DNNTPSQSISSSTSTMQNLK
Confirmed sites:
Ambiguous sites: "@S:6orS:8, @S:11orS:12"

MS/MS Fragmentation of DNNTPSQSISSSTSTMQNLK
Found in AT1G20200.1, EMB2719 (EMBRYO DEFECTIVE 2719); binding

Match to Query 3424: 2411.990634 from(1207.002593,2+) Elution from: 55.264 to 55.264 scan no 5484 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2411.9917
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0022
Matched b ions: b(10)-98, b(15)-98, b(18)-196++, b(20)-98++, b(20)+, b(20)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(12)-98, y(13)-98, y(16)+, y(17)-98++, y(17), y(17)+, y(18)-98++, y(18)+, y(20)-98++, y(20)+
Precursor origin neutral loss: +

Peptide No.306

DNNVPVSYSNGIPTK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DNNVPVSYSNGIPTK
Found in AT2G32450.1, calcium-binding EF hand family protein

Match to Query 2721: 1740.771402 from(871.392977,2+)
Elution from: 38.520 to 38.520 scan no 3754 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7719
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 47 Expect: 0.00015
Matched b ions: b(3), b(4), b(9), b(13)−98++, b(13)−98, b(13), b(14)−98
Matched y ions: y(3), y(6), y(7)++, y(8), y(9), y(10), y(11), y(12)++, y(12)−98, y(12), y(13)−98++, y(13)−98, y(13), y(15)++
Precursor origin neutral loss: +

Peptide No.307

DNPGLDDDDDSAELESGTFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DNPGLDDDDDSAELESGTFK
Found in AT1G52380.1, Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein

Match to Query 4324: 2218.841894 from(1110.428223,2+) Elution from: 45.229 to 45.229 scan no 4563 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2218.8427
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 Expect: 7.3e-008
Matched b ions: b(9), b(10), b(12)-98, b(13), b(14), b(14)-98, b(15), b(15)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(12), y(14), y(15), y(15)-98, y(17)++, y(17), y(18)-98++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.308

DNPGLDDDDDSAELESGTFKK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DNPGLDDDDDSAELESGTFKK
Found in AT1G52380.1, Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein

Match to Query 4385: 2346.935214 from(1174.474883,2+)
Elution from: 39.478 to 39.478 scan no 3698 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2346.9376
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0038
Matched b ions: b(7), b(10), b(11)-98, b(13)-98, b(14)-98++, b(16)-98
Matched y ions: y(6), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(15), y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.309
DNQPTQSVSVSATSLQNLK
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of DNQPTQSVSVSATSLQNLK
Found in AT1G75990.1, 26S proteasome regulatory subunit S3, putative (RPN3)
Match to Query 4291: 2308.092982 from(1155.053767,2+)
Elution from: 47.731 to 47.731 scan no 4996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2308.0948
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 8.3e-006
Matched b ions: b(10), b(12)−98, b(12), b(13)−98, b(14), b(18)−98, b(19)−98++
Matched y ions: y(7), y(9), y(10), y(11), y(12), y(12)−98, y(13)−98, y(14)−98, y(14), y(15)−98, y(16) ++, y(17)−98++, y(17), y(17)++, y(17)−98, y(18)++, y(19)++, y(20)++
Precursor origin neutral loss: +

Peptide No.310
DNSANFGYSGVNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DNSANFGYSGVNR
Found in AT1G05520.1, transport protein, putative

Match to Query 2097: 1479.577384 from(740.795968,2+)
Elution from: 34.143 to 34.143 scan no 2982 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1479.5779
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 5.6e-007
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.311
DNSVCHEGIITSSSPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of DNSVCHEGIITSSSPR
Found in AT4G35560.1, similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:AT5

Match to Query 2879: 1837.764856 from(919.889704,2+)
Elution from: 28.694 to 28.694 scan no 2467 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1837.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 63 Expect: 3.9e-006
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11)+, b(11), b(12), b(13)-98, b(14)-98, b(14), b(15)-98, b(15)+
Matched y ions: y(2), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(10)-98, y(11), y(12)-98, y(12)+, y(12), y(13)+, y(13)-98++, y(13)-98, y(14)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.312
DNSVCHEGIITSSSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DNSVCHEGIITSSSPR
Found in AT4G35560.1, similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:AT5

Match to Query 3005: 1837.764368 from(919.889460,2+)
Elution from: 29.370 to 29.370 scan no 2524 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1837.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 2e−006
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(10)++, b(11)++, b(11), b(13), b(14)−98, b(14), b(15)−98
Matched y ions: y(2), y(4), y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(8)−98, y(9), y(9)−98, y(10), y(10)++, y(10)−98++, y(10)−98, y(11), y(11)−98, y(12)−98, y(12)++, y(12)−98++, y(12), y(13)−98++, y(13)++, y(14)−98++, y(14)++, y(15)++, y(15)−98++
Precursor origin neutral loss: +

Peptide No.313
DNSVCHEGIITSSSPR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of DNSVCHEGIITSSSPR
Found in AT4G35560.1, similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:AT5)

Match to Query 2967: 1837.765116 from(613.595648,3+)
Elution from: 28.546 to 28.546 scan no 2448 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1837.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0035
Matched b ions: b(2), b(5), b(6)++, b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(10)++, b(10), b(11)−98++, b(11)++, b(12)−98++, b(13)−98++, b(14)++, b(14)−98++, b(15)−98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(5)++, y(6)++, y(6), y(7)++, y(7), y(8)−98, y(9), y(9)−98++, y(9)++, y(10)++, y(10)−98++, y(10), y(11)++, y(12)++, y(13)++, y(13)−98++, y(14)++
Precursor origin neutral loss:

Peptide No.314
DNTSAYLAEVWKEYSKGDSR
Confirmed sites:
Ambiguous sites: "@T:3orS:4orY:6, @T:3orS:4orY:6"

MS/MS Fragmentation of DNTSAYLAEVWKEYSKGDSR
Found in AT1G20050.1, HYD1 (Hydra 1)

Match to Query 4546: 2478.017622 from(827.013150,3+)
Elution from: 57.562 to 57.562 scan no 6136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2478.0141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y6 : Phospho (Y)
Ions Score: 23 Expect: 0.057
Matched b ions: b(6), b(9)+, b(14)+, b(14)−98++, b(15)+, b(15)−98++, b(16)+, b(19)+
Matched y ions: y(5), y(6), y(7)
Precursor origin neutral loss:

Peptide No.315

DPILLGYGSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DPILLGYGSK
Found in AT1G53050.1, protein kinase family protein

Match to Query 1025: 1141.540124 from(571.777338,2+)
Elution from: 47.769 to 47.769 scan no 4991 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1141.5420
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0028
Matched b ions: b(4), b(5)
Matched y ions: y(2), y(5), y(6), y(7), y(9)++
Precursor origin neutral loss: +

Peptide No.316

DPSPPPLSSLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DPSPPPLSSLGK
Found in AT2G34310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29530.1); similar to expressed protein,

Match to Query 1241: 1273.594960 from(637.804756,2+) 
Elution from: 41.208 to 41.208 scan no 4111 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1273.5955
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0033
Matched b ions: b(2), b(3), b(3)−98, b(5), b(7)−98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)−98++, y(10)+, y(11)++
Precursor origin neutral loss: +

Peptide No.317

DPTTKVLDVTAKPKSK
Confirmed sites: "@T:4,@T:10,@S:15"
Ambiguous sites:

MS/MS Fragmentation of DPTTKVLDVTAKPKSK
Found in AT1G16330.1, CYCB3;1 (CYCLIN B3;1); cyclin-dependent protein kinase

Match to Query 3251: 1966.876629 from(656.632819,3+)
Elution from: 34.194 to 34.194 scan no 3208 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1966.8818
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.019
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98++, b(9)++, b(10)++, b(10)-196++, b(11)-196++, b(11)-98++, b(12)-196++, b(13)-196++, b(14)-196++, b(14)-98++
Matched y ions: y(6)-98++, y(6), y(6)-98, y(7)-98++, y(7)-196, y(7)-98, y(8)-196++, y(8)-196, y(9)-196, y(9)-98++, y(10)++, y(10)-196++, y(10)-98++, y(11)-98++, y(11)++, y(11)-196++, y(12)-196++, y(12)++, y(13)-196++, y(13)-98++, y(14)-294++, y(14)-196++, y(14)++, y(15)-294++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.318
DQAVDGLSSDLNGIR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DQAVDGLSSDLNGIR
Found in AT3G63460.1, EMB2221 (EMBRYO DEFECTIVE 2221)

Match to Query 2765: 1638.723658 from(820.369105,2+)
Elution from: 48.697 to 48.697 scan no 5112 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1638.7250
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 2.3e-009
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8)–98, b(9)–98, b(9), b(10)–98, b(10), b(11)–98, b(11), b(12), b(12)–98, b(14)–98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9)–98, y(9), y(10)–98, y(10), y(11), y(11)–98++, y(11)–98, y(12), y(12)–98, y(12)–98++, y(13)++, y(13), y(13)–98++, y(14)++, y(14)–98++
Precursor origin neutral loss: +

Peptide No.319

DQAVDGLSSDLNGIR
Confirmed sites:
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of DQAVDGLSSDLNGIR
Found in AT3G63460.1, EMB2221 (EMBRYO DEFECTIVE 2221)

Match to Query 2364: 1638.725056 from(820.369804,2+)
Elution from: 47.484 to 47.484 scan no 4963 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1638.7250
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 3.7e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(11)−98, b(12)−98, b(12), b(14), b(14)−98
Matched y ions: y(3), y(4), y(6), y(8), y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)−98, y(13)++, y(13), y(13)−98++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.320
DQNGFISAAELR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DQNGFISAAELR
Found in AT1G66410.1, CAM4 (GALMODULIN 4); calcium ion binding

Match to Query 1854: 1399.612530 from(700.813541,2+)
Elution from: 49.984 to 49.984 scan no 5048 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1399.6133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 2.9e-005
Matched b ions: b(5), b(6), b(9)-98, b(10)-98, b(10), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98++, y(7)-98, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.321

DQNGYISASELR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DQNGYISASELR
Found in AT3G22930.1, calmodulin, putative

Match to Query 1415: 1431.601804 from(716.808178,2+)
Elution from: 39.801 to 39.801 scan no 3884 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1431.6031
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.7e-006
Matched b ions: b(2), b(4), b(5), b(6), b(9)−98, b(10)−98
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)−98, y(7)−98, y(7), y(7)++, y(8), y(8)−98, y(9), y(10), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.322
DQPMTESAPESELSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DQPMTESAPESELSPK
Found in AT5G65700.1, BAM1 (big apical meristem 1); ATP binding / kinase/ protein serine/threonine kinase

Match to Query 3000: 1824.747422 from(913.380987,2+)
Elution from: 34.930 to 34.930 scan no 3308 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1824.7488
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0034
Matched b ions: b(8), b(11)-98, b(11), b(14)++, b(14), b(14)-98++, b(15)-98++, b(15)-98, b(15)++
Matched y ions: y(6), y(7)-98, y(8), y(8)-98, y(9), y(10), y(11)-98, y(11), y(12), y(13)++, y(14)++, y(14), y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.323
DQPMTESAPESELSPK
Confirmed sites:
Ambiguous sites: @S:11 or S:14

MS/MS Fragmentation of DQPMTESAPESELSPK
Found in AT5G65700.1, BAM1 (big apical meristem 1); ATP binding / kinase / protein serine/threonine kinase

Match to Query 3263: 1824.746982 from(913.380767,2+)
Elution from: 35.903 to 35.903 scan no 3331 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1824.7488
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00024
Matched b ions: b(8), b(14)++, b(14), b(14)–98++, b(15)–98++
Matched y ions: y(7), y(8), y(8)–98, y(9), y(10), y(11)–98, y(11), y(12), y(13)++, y(14)++, y(14), y
(14)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.324

DQSDEVSADETVPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DQSDEVSADETVPK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2242: 1598.634084 from(800.324318,2+)
Elution from: 27.753 to 27.753 scan no 2340 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1598.6349  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 98 Expect: 1.1e-009  
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(14), b(15)  
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)  
Precursor origin neutral loss: +

Peptide No.325  
DQSPGVLR  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of DQSPGVLR  
Found in AT5G66230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G51230.1); similar to Sugar transporter  

Match to Query 395: 950.421490 from(476.218021,2+)  
Elution from: 24.628 to 24.628 scan no 1788 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 950.4222
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00057
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(5)−98, b(6)−98
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(7)−98++
Precursor origin neutral loss: +

Peptide No.326
DRFPLDESDD
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of DRFPLDESDD
Found in AT4G30760.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G62050.1); similar to Os07g0637200 [Oryz
Match to Query 1226: 1287.464512 from(644.739532,2+)
Elution from: 40.624 to 40.624 scan no 4067 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1287.4656  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 46 Expect: 9.8e-005  
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8)+, b(9)-98++, b(9), b(9)++  
Matched y ions: y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(7), y(8), y(8)-98, y(9)++  
Precursor origin neutral loss: +

Peptide No.327

DRNSPESAISAIADR  
Confirmed sites: @S:4  
Ambiguous sites:  

MS/MS Fragmentation of DRNSPESAISAIADR  
Found in AT5G14540.1, proline–rich family protein  

Match to Query 2944: 1722.791802 from(575.271210,3+)  
Elution from: 54.230 to 54.230 scan no 5696 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1722.7937
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.047
Matched b ions: b(5)++, b(7)-98++, b(8)++, b(9)++, b(9), b(10)++, b(12)++
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss:

Peptide No.328

DRPVVTCLDSSWR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DRPVVTCLDSSWR
Found in AT3G58760.1, ankyrin protein kinase, putative

Match to Query 2542: 1669.727292 from(557.583040,3+)
Elution from: 42.946 to 42.946 scan no 4376 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.7283
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00035
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(7)+, b(8)+, b(9)+, b(12)+
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(6)+, y(7), y(7)+, y(7)-98+
Precursor origin neutral loss: +

Peptide No.329

DRSPLPPPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DRSPLPPPR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 1127: 1113.532836 from(557.773694,2+)
Elution from: 19.005 to 19.005 scan no 1204 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1113.5332
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.044
Matched b ions: b(3), b(3)-98, b(5), b(6)-98, b(7)-98
Matched y ions: y(4), y(6), y(7)-98, y(8)+, y(8)-98++
Precursor origin neutral loss: +

Peptide No.330

DRSPLPPPRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DRSPLPPPRR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 1455: 1269.633102 from(424.218310,3+)
Elution from: 18.068 to 18.068 scan no 1030 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1269.6343
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.03
Matched b ions: b(3)-98, b(3), b(4), b(5), b(5)-98, b(6)-98++, b(9)-98++
Matched y ions: y(1), y(3)++, y(4)++, y(4), y(5)++, y(5), y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No.331

DRSPVLDDEGSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DRSPVLDDEGSPK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1923: 1493.638878 from(747.826715,2+)  
Elution from: 23.436 to 23.436 scan no 1755 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1493.6399
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 5e-008
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11)-98, b(11), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(10)+, y(11), y(11)+, y(11)-98, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.332
DRSPVLDDEGSPK
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of DRSPVLDDEGSPK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1708: 1493.639178 from(747.826865,2+)
Elution from: 21.842 to 21.842 scan no 1503 polarity:+
Peptide No.333

DRSPVLDEGSK
Confirmed sites: "@S:3,@S:11"

Ambiguous sites:

MS/MS Fragmentation of DRSPVLDEGSK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1710: 1573.604558 from(787.809555,2+)
Elution from: 22.946 to 22.946 scan no 1677 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1573.6062  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
S11 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
**Ions Score:** 67 Expect: 9.3e-007  
**Matched b ions:** b(2), b(3)—98, b(3), b(5), b(5)—98, b(6), b(6)—98, b(7), b(7)—98, b(8), b(8)—98, b(9), b(10), b(11)—98, b(11)—196, b(11)—98++, b(12)—196++  
**Matched y ions:** y(2), y(3)—98, y(4), y(4)—98, y(5)—98, y(5), y(6)—98, y(6), y(7), y(7)—98, y(8)—98++, y(8), y(8)—98, y(9)—98, y(9), y(10), y(10)—98, y(11), y(11)—196, y(12)++, y(12)—98++, y(12)—196++  
**Precursor origin neutral loss:** +

**Peptide No. 334**

**DRSPYYMR**  
**Confirmed sites:** @S:3  
**Ambiguous sites:**

**MS/MS Fragmentation of DRSPYYMR**  
Found in AT1G07350.1, transformer serine/arginine-rich ribonucleoprotein, putative

Match to Query 902: 1166.457388 from(584.235970,2+)  
Elution from: 24.508 to 24.508 scan no 1866 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1166.4580
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00046
Matched b ions: b(3)-98, b(3), b(4), b(5), b(6), b(7)
Matched y ions: y(2), y(3), y(5), y(6), y(7)++, y(7)-98++
Precursor origin neutral loss: +

Peptide No.335

DSDDEHPDSDEDPDDLDI
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DSDDEHPDSDEDPDDLDI
Found in AT2G18410.1, similar to Os03g0201700 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001049299.1); similar to Un

Match to Query 3580: 2237.725082 from(1119.869817,2+)
Elution from: 46.589 to 46.589 scan no 4697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2237.7281
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.00037
Matched b ions: b(6), b(8), b(9), b(11)—98, b(11), b(12), b(12)—98, b(13)—98, b(14), b(15), b(15)+, b(16), b(16)+, b(17)—98++, b(17)+, b(18)+, b(18)—98++
Matched y ions: y(7), y(8), y(13), y(14), y(16)—98++, y(18)+
Precursor origin neutral loss: +

Peptide No.336
DSDGGYDGAESPMQK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DSDGGYDGAESPMQK
Found in AT4G25500.1, ATRSP35 (Arabidopsis thaliana arginine-serine-rich splicing factor 35); RNA binding

Match to Query 2284: 1635.574952 from(818.794752,2+);
Elution from: 24.777 to 24.777 scan no 1940 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.5759
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 9.5e-005
Matched b ions: b(7), b(10), b(11)–98, b(14)–98, b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9), y(9)–98, y(10)++, y(11), y(14)++
Precursor origin neutral loss: +

Peptide No.337

DSDIPESEGIDKDGSSPNK
Confirmed sites:
Ambiguous sites: @S:15 or S:16

MS/MS Fragmentation of DSDIPESEGIDKDGSSPNK
Found in AT2G33610.1, ATSWI3B (Arabidopsis thaliana switching protein 3B); DNA binding

Match to Query 2876: 2068.842000 from(1035.428276,2+)
Elution from: 28.933 to 28.933 scan no 2383 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2068.8474
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.019
Matched b ions: b(13)
Matched y ions: y(6), y(7), y(8), y(9)−98, y(14)++, y(15)++, y(15), y(15)−98++, y(16)++, y(16)−98++, y(18)++, y(18)−98++
Precursor origin neutral loss: +

Peptide No.338
DSEAPFVVDDLQPSPK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DSEAPFVVDDLQPSPK
Found in AT3G12980.1, histone acetyltransferase 5 (HAC5)

Match to Query 2847: 1822.798040 from(912.406296,2+)
Elution from: 52.046 to 52.046 scan no 5508 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1822.8026  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 33 Expect: 0.0048  
Matched b ions: b(8), b(12)  
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(12)++, y(12), y(13)++, y(15)++  
Precursor origin neutral loss: +  

Peptide No.339  
DSEDFSDEMGESSGAYIVR  
Confirmed sites: @S:6  
Ambiguous sites:  
MS/MS Fragmentation of DSEDFSDEMGESSGAYIVR  
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/transferase, transferring glyc  
Match to Query 3871: 2172.818164 from(1087.416358,2+)  
Elution from: 50.608 to 50.608 scan no 5329 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2172.8194
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 Expect: 1.2e-008
Matched b ions: b(5), b(6)-98, b(8)-98, b(9)-98, b(11)-98, b(12)-98, b(13)-98, b(15)-98, b(16)-98, b(17)-98, b(17), b(18)-98, b(18)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(15)+, y(15)-98++, y(17)-98++, y(17)+, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.340
DSESDLSELDAPR
Confirmed sites: “@S:4,@S:7”
Ambiguous sites:

MS/MS Fragmentation of DSESDLSELDAPR
Found in AT3G06010.1, homeotic gene regulator, putative

Match to Query 2691: 1592.562276 from(797.288414,2+)
Elution from: 43.768 to 43.768 scan no 4504 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1592.5644
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0019
Matched b ions: b(9)−98, b(10), b(10)−98, b(11)−98, b(11), b(12)−98
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(10), y(11)++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.341

DSLAAAESPDMK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DSLAAAESPDMK
Found in AT3G17850.1, protein kinase, putative

Match to Query 1535: 1370.541776 from(686.278164,2+)
Elution from: 30.302 to 30.302 scan no 2650 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1370.5425
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00029
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)−98, b(8)+, b(9)−98, b(9)−98++, b(10), b(11)+, b(11)−98++, b(12)−98, b(12), b(12)−98++, b(12)+
Matched y ions: y(3), y(5), y(6), y(6)++, y(6)−98, y(7), y(7)−98, y(7)−98++, y(8), y(8)+, y(8)−98, y(9), y(9)−98, y(9)++, y(10)+, y(10)−98, y(11), y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No. 342

DSLAAAESPDMK
Confirmed sites: @S.8
Ambiguous sites:

MS/MS Fragmentation of DSLAAAESPDMK
Found in AT3G17850.1, protein kinase, putative

Match to Query 1579: 1386.535534 from(694.275043,2+)
Elution from: 23.537 to 23.537 scan no 1736 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1386.5374
Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 53 Expect: 2.3e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)−98, b(10), b(12)
Matched y ions: y(5), y(6), y(6)−98++, y(6)−98, y(7), y(7)−98, y(8), y(9), y(9)−98, y(10), y(11)+++, y(12)++

Precursor origin neutral loss: +

Peptide No.343

DSLAGSSEGDFEYSR
Confirmed sites: "@S:7,@S:8"

Ambiguous sites:

MS/MS Fragmentation of DSQLGSSEGDFEYSR
Found in AT1G73450.1, protein kinase, putative

Match to Query 3057: 1835.626718 from(918.820635,2+)
Elution from: 43.057 to 43.057 scan no 4381 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1835.6288
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00016
Matched b ions: b(6), b(9)−196, b(9)−98, b(11)−98, b(11), b(12)−98, b(13)−98, b(13)−196, b(13), b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(9), y(10)−196, y(10), y(11), y(11)−98, y(12), y(13)−98++, y(13)++, y(14)−98++, y(14)++, y(15)−98++, y(15)−196++
Precursor origin neutral loss: +

Peptide No.344

DSLAGGSEGDFEYSR
Confirmed sites:
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of DSLAGGSEGDFEYSR
Found in AT1G73460.1, protein kinase family protein

Match to Query 2151: 1755.660578 from(878.837565,2+)
Elution from: 39.281 to 39.281 scan no 3712 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1755.6624
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0051
Matched b ions: b(6), b(13)
Matched y ions: y(4), y(5), y(6), y(8)++, y(11), y(12)++, y(12), y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.345

DSLAGGSSEGDFEYSR
Confirmed sites: "@S:7,@S:8"
Ambiguous sites:

MS/MS Fragmentation of DSLAGGSSEGDFEYSR
Found in AT1G73450.1, protein kinase, putative

Match to Query 2918: 1835.626718 from(918.820635,2+)
Elution from: 43.877 to 43.877 scan no 4421 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1835.6288
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.01
Matched b ions: b(12)--98, b(13)--196, b(13), b(13)--98
Matched y ions: y(3), y(4), y(5), y(7), y(9), y(11)--98, y(11), y(11)--196, y(12), y(12)--98, y(13)--98++, y(13)++, y(14)++, y(15)++, y(15)--98++
Precursor origin neutral loss: +

Peptide No.346

DSNIAFDTGTYSRP
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DSNIAFDTGTYSRP
Found in AT3G59550.1, SYN3 (Sister chromatid cohesion 1 protein 3)

Match to Query 2536: 1622.660000 from(812.337276,2+)
Elution from: 42.776 to 42.776 scan no 4135 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1622.6613
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.9e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98++, y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.347

DSNVTPDDVSGMRSPSAFFK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of DSNVTPDDVSGMRSPSAFFK
Found in AT3G13300.1, VCS (VARICOSE); nucleotide binding

Match to Query 4354: 2366.970054 from(789.997294,3+)
Elution from: 45.039 to 45.039 scan no 4612 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2366.9726
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0037
Matched b ions: b(3), b(4), b(5), b(17)++
Matched y ions: y(6)++, y(6), y(13)++, y(14)−98++, y(15)++, y(16)−98+, y(16)++, y(17)−
98++, y(18)−98++, y(18)++
Precursor origin neutral loss:

Peptide No.348

DSPLEVVVLNDSGGVK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DSPLEVVVLNDSGGVK
Found in AT1G42970.1, GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B
SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase

Match to Query 2516: 1706.810502 from(854.412527,2+)
Elution from: 55.912 to 55.912 scan no 5946 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1706.8127
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0015
Matched b ions: b(6), b(8), b(9), b(10), b(15)
Matched y ions: y(7), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.349

DSSAGCGVQEPSSPK
Confirmed sites:
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of DSSAGCGVQEPSSPK
Found in AT3G55320.1, PGP20 (P–GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances

Match to Query 1775: 1584.610228 from(793.312390,2+)
Elution from: 21.278 to 21.278 scan no 1356 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.6127
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00024
Matched b ions: b(9), b(10)
Matched y ions: y(5), y(6), y(8), y(9), y(11), y(11)+, y(12)+, y(13)+, y(14)+
Precursor origin neutral loss:

Peptide No.350

DSSSIAGSSSIPATVSTGK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DSSSIAGSSSIPATVSTGK
Found in AT2G38410.1, VHS domain–containing protein / GAT domain–containing protein

Match to Query 3543: 1927.876260 from(964.945406,2+)
Elution from: 36.563 to 36.563 scan no 3419 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1927.8775
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 7e–007
Matched b ions: b(6), b(8), b(9), b(12), b(12)–98, b(14), b(14)+, b(15), b(16)–98, b(16), b(19), b(19)–98++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(11)–98, y(12)–98++, y(12), y(13), y(14), y(15), y(16)+, y(17)+, y(19)+
Precursor origin neutral loss:

Peptide No.351
DSSSYGDQITDSGR
Confirmed sites:
Ambiguous sites: @S:2orS:3orS:4

MS/MS Fragmentation of DSSSYGDQITDSGR
Found in AT5G13950.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G45830.1); similar to unknown protein [O

Match to Query 1691: 1566.585160 from(784.299856,2+) Elution from: 28.818 to 28.818 scan no 2458 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1566.5835
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0014
Matched b ions: b(5)−98, b(9), b(11)++, b(12)++, b(13)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.352

DSSVLVSVSSPMR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DSSVLVSVSSPMR
Found in AT3G22520.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14840.1); similar to CDPK adapter prote

Match to Query 2030: 1442.647344 from(722.330948,2+)
Elution from: 44.971 to 44.971 scan no 4529 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1442.6476
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 3.2e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(10)−98, b(11)+, b(11)−98, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7), y(8), y(8)−98, y(9), y(10), y(10)−98, y(12)+
Precursor origin neutral loss:

Peptide No.353
DSSVLVSVSSPMR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DSSVLVSVSSPMR
Found in AT3G22520.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14840.1);
similar to CDPK adapter prote

Match to Query 2086: 1458.642006 from(730.328279,2+)
Elution from: 37.439 to 37.439 scan no 3537 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1458.6425
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 62 Expect: 5.9e-006
Matched b ions: b(6), b(7), b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7), y(8), y(8)−98, y(9), y(10)++, y(12)++
Precursor origin neutral loss: +

Peptide No.354
DSTPSLSRIESKYLGK
Confirmed sites: “@S:7,@Y:13”
Ambiguous sites:

MS/MS Fragmentation of DSTPSLSRIESKYLGK
Found in AT3G58390.1, eukaryotic release factor 1 family protein / eRF1 family protein

Match to Query 3147: 1939.871214 from(647.631014,3+)
Elution from: 28.404 to 28.404 scan no 2395 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1939.8693
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y13 : Phospho (Y)
Ions Score: 23 Expect: 0.05
Matched b ions: b(6)++, b(7)++, b(10)++, b(11)++, b(14)−98++, b(14)++
Matched y ions: y(11)++, y(12)++, y(13)−98++, y(14)−98++, y(14)++, y(15)++
Precursor origin neutral loss:

Peptide No.355

DSVFSNSMKNSLAKSSSALTTER
Confirmed sites: @S:5 or S:7
Ambiguous sites: @S:5 or S:7

MS/MS Fragmentation of DSVFSNSMKNSLAKSSSALTTER
Found in AT5G64390.1, HEN4 (HUA ENHANCER 4); nucleic acid binding

Match to Query 4630: 2539.167846 from (847.396558, 3+)
Elution from: 63.525 to 63.525 scan no 6768 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2539.1625
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.046
Matched b ions: b(7), b(9), b(16)++, b(17)++, b(18)++, b(19)++, b(21)++, b(22)++
Matched y ions: y(20)++
Precursor origin neutral loss:

Peptide No.356

DSWFMLRPKQTSVACEK
Confirmed sites: @S:2
Ambiguous sites: @T:11orS:12

MS/MS Fragmentation of DSWFMPLRPKQTSVACEK
Found in AT4G17483.1, palmitoyl protein thioesterase family protein

Match to Query 4124: 2257.926656 from(565.488940,4+)
Elution from: 20.220 to 20.220 scan no 1341 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2257.9302
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.059
Matched b ions: b(5)+, b(6)−98++, b(7)−98++, b(8)−98++, b(9)−98++, b(10)−98++
Matched y ions: y(4)+, y(7)−98++, y(7)+, y(8)−98++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.357

DTDFSAESPDLSEDGGGGGGGR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DTDFSAESPDLSEDGGGGGGGR
Found in AT5G28040.1, transcription regulator

Match to Query 3221: 2203.814482 from(1102.914517,2+) Erution from: 37.298 to 37.298 scan no 3567 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2203.8178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 Expect: 1.1e-008
Matched b ions: b(5), b(6), b(7), b(8)–98, b(8), b(9)–98, b(10)–98, b(11)–98, b(11), b(12), b(12)–98, b(13)–98, b(13), b(14), b(17)–98, b(18)++, b(19)
Matched y ions: y(5), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(15)–98, y(16), y(16)–98, y(17), y(18), y(18)++, y(18)–98++, y(19)++, y(19)–98++, y(20)–98++, y(21)++, y(21)–98++
Precursor origin neutral loss: +

Peptide No.358

DTEAAVDAEDESAAEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DTEAAVDAEDESAAEK
Found in AT3G57150.1, NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)

Match to Query 2065: 1729.654774 from(865.834663,2+)
Elution from: 24.804 to 24.804 scan no 1923 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1729.6567
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 1.6e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12)-98, b(13)++, b(13), b(14)-98, b(14), b(15)-98, b(15)
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.359
DTIMEQPSSPR
Confirmed sites:
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of DTIMEQPSSPR
Found in AT1G30810.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 1237: 1339.547840 from(670.781196,2+)
Elution from: 28.316 to 28.316 scan no 2272 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1339.5479
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.012
Matched b ions: b(4), b(5), b(6)
Matched y ions: y(5), y(6), y(6)−98, y(8), y(8)++, y(9)++, y(10)++
Precursor origin neutral loss:

Peptide No.360

DTQSEIADYGYGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DTQSEIADYGYGR
Found in AT3G09070.1, glycine-rich protein

Match to Query 2111: 1553.602316 from(777.808434,2+)
Elution from: 39.782 to 39.782 scan no 3922 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1553.6035  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 63 Expect: 2.8e-006  
Matched b ions: b(6)-98, b(6), b(7)-98, b(7), b(8), b(9)-98, b(9), b(10)-98, b(11)-98, b(11)  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11)+, y(12)++  
Precursor origin neutral loss: +  

Peptide No.361  
DTSAGLDSSVTK  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of DTSAGLDSSVTK  
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein  

Match to Query 1183: 1259.526852 from(630.770702,2+)  
Elution from: 25.470 to 25.470 scan no 1996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.5282
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769 shown in table, 0.0000
Ions Score: 46 Expect: 0.00011
Matched b ions: b(2), b(4)–98, b(5), b(6)–98, b(7), b(11)–98++
Matched y ions: y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(10)–98++, y(10)–98, y(10), y(10)++, y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No. 362
DTSAGLDSSVTK
Confirmed sites: @T:2 or S:3
Ambiguous sites: @T:2 or S:3

MS/MS Fragmentation of DTSAGLDSSVTK
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1117: 1259.526728 from (630.770640, 2+)
Elution from: 24.512 to 24.512 scan no 1859 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.5282
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0047
Matched b ions: b(4)−98, b(6)−98, b(11)−98++
Matched y ions: y(2), y(5), y(7), y(8), y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.363

DTSIPETDEKVSPPEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DTSIPETDEKVSPPEK
Found in AT2G21440.1, RNA recognition motif (RRM)−containing protein

Match to Query 2354: 1850.816793 from(617.946207,3+)
Elution from: 31.641 to 31.641 scan no 2829 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1850.8186
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(4)
Matched y ions: y(8)++, y(10)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss:

Peptide No.364

DTVHSPVLDGQHK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DTVHSPVLDGQHK
Found in AT1G79830.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 2261: 1511.676892 from(756.845722,2+)
Elution from: 21.463 to 21.463 scan no 1402 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1511.6769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.015
Matched b ions: b(5)—98, b(6), b(9)++, b(9), b(10)++, b(12)++
Matched y ions: y(4), y(8), y(9)—98, y(9), y(10)—98++, y(10)++, y(11)—98++, y(12)++
Precursor origin neutral loss: +

Peptide No.365

DTVKEGSSGEEVKTMR
Confirmed sites: @T:16
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of DTVKEGSSGEEVKTMR
Found in AT1G73120.1, unknown protein

Match to Query 3659: 2115.842058 from(706.287962,3+)
Elution from: 41.951 to 41.951 scan no 4241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2115.8432
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 Expect: 0.021
Matched b ions: b(2), b(4), b(6), b(9), b(9)−98++, b(10), b(10)−98++, b(11)++, b(12), b(12)++, b(13)++,
b(14), b(14)−98++, b(15), b(15)++, b(15)−98++
Matched y ions: y(3)−98, y(3), y(4), y(5)−98, y(6)−98, y(8)−98++, y(11)−98++, y(11)++, y(12)−98++,
y(13)−196++, y(14)++, y(15)++, y(15)−196++, y(16)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.366

DVATDDDDAAKE
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of DVATDDDDAAKE
Found in AT3G48890.1, ATMP2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 3); heme binding / tra

Match to Query 1228: 1343.475204 from(672.744878,2+)
Elution from: 20.098 to 20.098 scan no 1307 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1343.4766
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 1.4e-005
Matched b ions: b(6)-98, b(10)-98, b(10), b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(6), y(8), y(9), y(10)+, y(10), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.367

DVFSR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DVFSR
Found in AT2G03890.1, phosphatidylinositol 3- and 4-kinase family protein

Match to Query 176: 799.325670 from(400.670111,2+) Elution from: 31.785 to 31.785 scan no 2753 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 799.3265
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 17 Expect: 0.046
Matched b ions: b(2)
Matched y ions: y(1), y(2), y(3), y(4), y(4)−98, y(4)+, y(5)−98, y(5)−98++, y(5)+
Precursor origin neutral loss:

Peptide No. 368

DVGASPGGNLIVAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DVGASPGGNLIVAK
Found in AT2G32910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G61910.3); similar to expressed protein

Match to Query 1493: 1376.668884 from(689.341718,2+)
Elution from: 37.599 to 37.599 scan no 3665 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.6700
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 2.9e-007
Matched b ions: b(2), b(3), b(4), b(5)–98, b(5), b(6)–98, b(8), b(8)–98, b(9)–98, b(10)–98, b(11)–98, b(11), b(12), b(12)–98, b(13), b(13)–98
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)–98++, y(10), y(11)–98++, y(11), y(11)++, y(12)++, y(12)–98++, y(12), y(12)–98, y(13)–98++, y(13)++, y(13)–98
Precursor origin neutral loss: +

Peptide No.369
DVGLDIVSDEETNGR
Confirmed sites: @S.8
Ambiguous sites:

MS/MS Fragmentation of DVGLDIVSDEETNGR
Found in AT3G21810.1, zinc finger (CCCH-type) family protein

Match to Query 2623: 1697.712864 from(849.863708,2+)
Elution from: 45.880 to 45.880 scan no 4760 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1697.7145
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 5.1e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)–98, b(9)++, b(9), b(10)–98, b(10), b(11)–98, b(11), b(12)–98, b(13), b(13)–98, b(13)–98++, b(13)++, b(14)–98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)–98, y(8), y(9), y(9)–98, y(10)–98, y(10), y(11)–98, y(11), y(12)–98++, y(13)++, y(13)–98++, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.370

DVIVLTPK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of DVIVLTPK
Found in AT5G27970.1, binding

Match to Query 587: 963.501720 from(482.758136,2+)
Elution from: 42.237 to 42.237 scan no 4327 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 963.5042
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 29 Expect: 0.0096
Matched b ions: b(2), b(3), b(4), b(7)++
Matched y ions: y(3)−98, y(3), y(4), y(5), y(5)−98, y(6), y(6)++, y(7)−98++, y(7)−98, y(7)++
Precursor origin neutral loss:

Peptide No.371
DVSDKVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DVSDKVR
Found in AT4G03820.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22270.1); similar to AT3g20300/MQC12_5

Match to Query 302: 897.395020 from(449.704786,2+) Elution from: 28.537 to 28.537 scan no 2406 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 897.3957
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0052
Matched b ions: b(2), b(3), b(5)-98
Matched y ions: y(1), y(3), y(4), y(5)-98, y(5), y(5)+, y(5)-98++, y(6)-98++, y(6)-98, y(6)+
Precursor origin neutral loss: +

Peptide No.372
DVSPGNVMDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DVSPGNVMDK
Found in AT5G35910.1, 3’–5’ exonuclease domain–containing protein / helicase and RNase D C–terminal domain–containing pro

Match to Query 717: 1140.451674 from(571.233113,2+)
Elution from: 30.520 to 30.520 scan no 2670 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1140.4522
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0071
Matched b ions: b(2), b(3), b(3)−98, b(7)−98
Matched y ions: y(2), y(4), y(7), y(8)−98++, y(8), y(9)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.373
DVSPSYESLVDGSGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DVSPSYESLVDGSGR
Found in AT3G06810.1, acyl-CoA dehydrogenase-related

Match to Query 2607: 1646.680610 from(824.347581,2+)
Elution from: 47.088 to 47.088 scan no 4685 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1646.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00055
Matched b ions: b(3), b(7), b(9), b(10), b(13)++, b(13)-98++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(12), y(13)-98++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.374

DVSSEQCILER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DVSSEQCILER
Found in AT1G50890.1, binding

Match to Query 1412: 1414.579126 from(708.296839,2+)  
Elution from: 38.023 to 38.023 scan no 3558 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1414.5799
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.0094
Matched b ions: b(9)
Matched y ions: y(2), y(3), y(5), y(6), y(8)+, y(9)−98++ , y(9)+, y(10)−98++, y(10)+
Precursor origin neutral loss: +

Peptide No.375

DVTQSPISEDMEESPRDK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of DVTQSPISEDMEESPRDK
Found in AT2G26460.1, RED family protein

Match to Query 3063: 2141.880518 from(1071.947535,2+)
Elution from: 34.772 to 34.772 scan no 3238 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2141.8824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00042
Matched b ions: b(7), b(13), b(14)–98, b(16)–98++, b(17)–98++
Matched y ions: y(4), y(5)–98, y(6)–98, y(7), y(8)–98, y(9), y(11)–98++, y(11)–98, y(12), y(13)–98, y(13), y(14)–98++, y(14)++, y(14)–98, y(16)++, y(16)–98++, y(17)++, y(17)–98++
Precursor origin neutral loss: +

Peptide No.376
DVTQSPISEDMEESPRDK
Confirmed sites: “@S:8,@S:14”
Ambiguous sites:

MS/MS Fragmentation of DVTQSPISEDMEESPRDK
Found in AT2G26460.1, RED family protein

Match to Query 3245: 2221.844476 from(1111.929514,2+)
Elution from: 36.225 to 36.225 scan no 3428 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2221.8487
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00076
Matched b ions: b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(17)-196++
Matched y ions: y(4), y(5), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(11), y(11)-98, y(12), y(13)-98, y(13), y(13)-196, y(14)-196++, y(14)+, y(15)-196++, y(16)+, y(16)-98++, y(17)-98++, y(17)+, y(17)-196++
Precursor origin neutral loss: +

Peptide No.377

DVTQSPISEDMEESPRDK
Confirmed sites: @S:14
Ambiguous sites: @T:3orS:5

MS/MS Fragmentation of DVTQSPISEDMEESPRDK
Found in AT2G26460.1, RED family protein

Match to Query 4038: 2221.847954 from(1111.931253,2+)
Elution from: 34.507 to 34.507 scan no 3254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2221.8487
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0086
Matched b ions: b(8)−98, b(10)−98, b(14)−196, b(17)−98++, b(17)−196++
Matched y ions: y(4), y(5), y(6), y(7)−98, y(7), y(8), y(9), y(11), y(13)−98, y(13), y(16)++, y(16)−98++, y(17)−98++, y(17)++, y(17)−196++
Precursor origin neutral loss: +

Peptide No.378
DVVLVESSGEEEA
Confirmed sites:
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of DVVLVESSGEEEA
Found in AT1G31380.1, RECQL2 (Arabidopsis RecQ helicase I2); ATP–dependent helicase/protein binding

Match to Query 1757: 1441.586134 from(721.800343,2+) Elution from: 42.859 to 42.859 scan no 4328 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1441.5861
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.03
Matched b ions: b(5), b(6), b(11), b(12)++
Matched y ions: y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.379
DVVPDVDSYK
Confirmed sites: ”@S:8,@Y:9”
Ambiguous sites:

MS/MS Fragmentation of DVVPDVDSYK
Found in AT4G01400.1, pentatricopeptide (PPR) repeat–containing protein

Match to Query 1418: 1295.470512 from(648.742532,2+)
Elution from: 42.151 to 42.151 scan no 4211 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1295.4723
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y9 : Phospho (Y)
Ions Score: 19 Expect: 0.046
Matched b ions:
Matched y ions: y(3), y(6)++, y(6)−98++, y(7)++, y(7), y(7)−98++, y(8)−98++, y(8)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.380

DYIPNFMEDTQSDRNR
Confirmed sites: @Y:2
Ambiguous sites:

MS/MS Fragmentation of DYIPNFMEDTQSDRNR
Found in AT4G15180.1, SET domain-containing protein

Match to Query 4017: 2095.825257 from(699.615695,3+)
Elution from: 20.083 to 20.083 scan no 1302 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2095.8306
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y2 : Phospho (Y)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.017
Matched b ions: b(7)++, b(8)++, b(9)++, b(10)++, b(11)++, b(15)++
Matched y ions: y(4)++, y(5), y(14)++
Precursor origin neutral loss: +

Peptide No.381
DYNGSSALSTAESEN AK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of DYNGSSALSTAESEN AK
Found in AT4G28600.1, NPGR2 (NO POLLEN GERMINATION RELATED 2); calmodulin binding

Match to Query 2293: 1822.724742 from(912.369647,2+)
Elution from: 31.220 to 31.220 scan no 2773 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1822.7258 
Fixed modifications: Carbamidomethyl (C) 
Variable modifications:  
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 
Ions Score: 52 Expect: 4.1e-005 
Matched b ions: b(4), b(8), b(9), b(12), b(14)−98, b(15)−98++, b(16), b(16)−98++ 
Matched y ions: y(5), y(6)−98, y(7), y(8)−98, y(8), y(9), y(10), y(10)−98, y(11), y(12), y(13), y(14)−98++, y(14), y(15)++, y(16)++ 
Precursor origin neutral loss: + 

Peptide No.382 
DYNSDDDEEEEDDESK 
Confirmed sites: @S:4 
Ambiguous sites:  

MS/MS Fragmentation of DYNSDDDEEEEDDESK 
Found in AT5G48240.1, similar to Os11g0266000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001067664.1); similar to un 

Match to Query 2444: 1883.572780 from(942.793666,2+) 
Elution from: 19.767 to 19.767 scan no 1265 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1883.5742
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.00041
Matched b ions: b(7), b(9)-98, b(10), b(10)-98, b(12)
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(12), y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.383

DYQSGWNSDQDELGCETK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DYQSGWNSDQDELGCETK
Found in AT3G18770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49590.1); similar to IMP dehydrogenase/

Match to Query 3208: 2210.805504 from(1106.410028,2+)
Elution from: 41.435 to 41.435 scan no 3949 polarity:+
Peptide No. 384

DYSPPLAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DYSPPLAR
Found in AT4G28990.1, RNA-binding protein-related

Match to Query 471: 997.426044 from(499.720298,2+)
Elution from: 31.160 to 31.160 scan no 2765 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 997.4270
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0054
Matched b ions: b(2), b(3), b(4)−98
Matched y ions: y(2), y(4), y(5), y(5)++, y(6)−98++, y(6), y(6)−98, y(7)++
Precursor origin neutral loss: +

Peptide No.385

EAAAPAIGDTAQFPSLG
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of EAAAPAIGDTAQFPSLG
Found in AT5G47210.1, nuclear RNA-binding protein, putative

Match to Query 2836: 1694.754788 from(848.384670,2+)
Elution from: 56.876 to 56.876 scan no 6099 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1694.7552
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 4.6e-005
Matched b ions: b(7), b(9), b(11), b(12), b(13), b(16)-98++
Matched y ions: y(4), y(6), y(7), y(9), y(10), y(13)
Precursor origin neutral loss: +

Peptide No.386
EAALAATPSDSPTIFDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EAALAATPSDSPTIFDK
Found in AT3G56490.1, zinc-binding protein, putative / protein kinase C inhibitor, putative

Match to Query 2940: 1812.816646 from(907.415599,2+)  
Elution from: 45.928 to 45.928 scan no 4727 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1812.8182
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 Expect: 5.2e-007
Matched b ions: b(5), b(6), b(7), b(14), b(15), b(16)
Matched y ions: y(3), y(6), y(7), y(9), y(10), y(10)-98, y(11), y(12), y(13), y(14)++
Precursor origin neutral loss:

Peptide No.387

EAALAATPSDSPTIFDK
Confirmed sites: @S:11 or T:13
Ambiguous sites: @S:11 or T:13

MS/MS Fragmentation of EAALAATPSDSPTIFDK
Found in AT3G56490.1, zinc-binding protein, putative / protein kinase C inhibitor, putative

Match to Query 3105: 1812.815234 from(907.414893,2+) Elution from: 46.716 to 46.716 scan no 4638 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1812.8182
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 1.5e-006
Matched b ions: b(5), b(6), b(7), b(14), b(16)
Matched y ions: y(3), y(7), y(9), y(10)-98, y(10), y(11), y(12), y(13), y(14)++, y(15)++
Precursor origin neutral loss:

Peptide No.388
EADDLSDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EADDLSDR
Found in AT5G15160.1, bHLH family protein

Match to Query 744: 999.351926 from(500.683239,2+) Elution from: 24.712 to 24.712 scan no 1940 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 999.3546
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 Expect: 0.054
Matched b ions:
Matched y ions: y(1), y(2), y(3)−98, y(4)−98, y(6)++
Precursor origin neutral loss: +

Peptide No.389

EAEENAETSDNETLGAWK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EAEENAETSDNETLGAWK
Found in AT5G47690.1, binding

Match to Query 3775: 2072.819092 from(1037.416822,2+)
Elution from: 40.800 to 40.800 scan no 3874 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2072.8211
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 3.1e-005
Matched b ions: b(8), b(12)−98, b(14), b(16), b(17)
Matched y ions: y(2), y(4), y(5), y(6), y(10)−98, y(11), y(11)−98, y(12)−98, y(13), y(14), y(15) ++
Precursor origin neutral loss:

Peptide No.390
EAEENAETSDNETLGAWK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of EAEENAETSDNETLGAWK
Found in AT5G47690.1, binding

Match to Query 3533: 2072.819592 from(691.947140,3+) 
Elution from: 39.482 to 39.482 scan no 3916 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2072.8211
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.053
Matched b ions: b(5), b(6), b(7), b(12)++, b(13)++, b(15)++, b(16)--98++, b(17)++
Matched y ions: y(2), y(4), y(5), y(6)--98, y(6), y(10)++, y(10)--98++, y(11)++, y(12)++, y(13)++, y(14) ++
Precursor origin neutral loss: +

Peptide No.391
EAEHDDSDTEGKQENNEMER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EAEHDDSDTEGKQENNEMER
Found in AT5G47690.1, binding

Match to Query 4586: 2441.889432 from(814.970420,3+)
Elution from: 17.886 to 17.886 scan no 1024 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2441.8914
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00037
Matched b ions: b(7)−98, b(12)++, b(14)−98++, b(15)++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)−98++, y(15)−98++, y(15)++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.392
EAILAAGNESDSSDNNSSQSFGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of EAILAAGNESDSSDNNSSQSFGR
Found in AT1G03350.1, BSD domain-containing protein

Match to Query 4393: 2434.985574 from(812.669134,3+)  
Elution from: 37.888 to 37.888 scan no 3704 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2434.9873
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0012
Matched b ions: b(3), b(4), b(5), b(6), b(7)+, b(7), b(9), b(10)+98++, b(11), b(11)+98, b(15)+98++, b(15)+, b(16)+, b(17)+, b(20)+, b(21)+98++, b(21)+
Matched y ions: y(4), y(6), y(7), y(8), y(9)+, y(9), y(12)+, y(14)+98++, y(14)+, y(15)+, y(16)+, y(17)+, y(17)+98++, y(18)+, y(19)+, y(19)+98++, y(20)+, y(20)+98++
Precursor origin neutral loss: +

Peptide No.393

EAISWGQNGSSFSK
Confirmed sites: @S:13
Ambiguous sites:
MS/MS Fragmentation of EAISWGQNGSSFSK
Found in AT4G19180.1, nucleoside phosphatase family protein / GDA1/CD39 family protein
Match to Query 2228: 1576.654114 from(789.334333,2+)
Elution from: 40.560 to 40.560 scan no 4060 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1576.6558
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0059
Matched b ions: b(5), b(7), b(8), b(12)++, b(12)
Matched y ions: y(6), y(7), y(9), y(9)-98, y(10), y(11)++, y(11), y(12)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.394
EALPEFSESK
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of EALPEFSESK
Found in AT2G25270.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G12400.1); similar to H0306F03.12 [Oryza]

Match to Query 1707: 1295.471734 from(648.743143,2+) Elution from: 41.442 to 41.442 scan no 4183 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1295.4723
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.0094
Matched b ions: b(7)-98++, b(8)-98++, b(8)++, b(8)-98, b(8)
Matched y ions: y(3), y(5), y(5)++, y(5)-98, y(6)++, y(6), y(7)-98++, y(7)++, y(7)-98, y(7), y(8)-98++
Precursor origin neutral loss: +

Peptide No.395
EALPEFSES K
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EALPEFSES K
Found in AT2G25270.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G12400.1);
similar to H0306F03.12 [Oryza]

Match to Query 936: 1215.504854 from(608.759703,2+)
Elution from: 38.672 to 38.672 scan no 3639 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1215.5060
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.4e-005
Matched b ions: b(2), b(3), b(8)++, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)−98++, y(7)−98, y(8), y(8)++, y(8)−98++, y(8)−98
Precursor origin neutral loss:

Peptide No.396
EAMTPLSEFEDKL
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EAMTPLSEFEDKL
Found in AT1G56070.1, LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/translation

Match to Query 2218: 1588.671190 from(795.342871,2+)
Elution from: 65.588 to 65.588 scan no 6959 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1588.6731
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(9)-98, b(10), b(11), b(12)-98++
Matched y ions: y(5), y(7), y(8), y(9)++, y(9)-98, y(9), y(10)+, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.397
EANVDGDTASQHEAAWLPGK
Confirmed sites: @S:10
Ambiguous sites:
MS/MS Fragmentation of EANVDGDTASQHEAAWLPGK
Found in AT2G28390.1, SAND family protein
Match to Query 3882: 2174.923422 from(725.981750,3+)  
Elution from: 38.381 to 38.381 scan no 3770 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2174.9269
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.011
Matched b ions: b(4), b(9), b(12)–98++, b(16)++, b(16)–98++
Matched y ions: y(3), y(4), y(5)++, y(11)–98++, y(11)++, y(12)++, y(12)–98++, y(13)++, y(13)–98++, y(14)++, y(15)++, y(16)++, y(16)–98++, y(17)–98++, y(17)++, y(18)++
Precursor origin neutral loss:

Peptide No.398

EASDDDSDDDDAVRDVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EASDDDSDDDDAVRDVK
Found in AT1G15280.1, glycine-rich protein

Match to Query 3314: 1945.705276 from(973.859914,2+)
Elution from: 23.267 to 23.267 scan no 1700 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1945.7062
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0026
Matched b ions: b(6)--98, b(8), b(12)++, b(12)--98, b(13)++, b(13)--98++, b(15)--98++, b(15)--98
Matched y ions: y(4), y(6), y(7), y(8), y(9)++, y(9), y(10), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.399

EASDDDSDDDDAVRDVK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EASDDDSDDDDAVRDVK
Found in AT1G15280.1, glycine-rich protein

Match to Query 3195: 1945.706006 from(973.860279,2+) Elution from: 22.797 to 22.797 scan no 1674 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1945.7062
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.2e-005
Matched b ions: b(4), b(5), b(6), b(8), b(11), b(12)++, b(13), b(13)++, b(13)-98++, b(15)-98, b(15) b(15)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(12)++, y(12)-98++, y(13)++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.400

EASDEEEYDLVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EASDEEEYDLVR
Found in AT1G64790.1, translational activator family protein

Match to Query 1657: 1533.585718 from(767.800135,2+) Elution from: 39.905 to 39.905 scan no 3790 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1533.5872
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00072
Matched b ions: b(5)-98, b(6)-98, b(7)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(10)-98++
Precursor origin neutral loss: +

Peptide No.401
EASFGHAVLEIYNR
Confirmed sites: @Y:12
Ambiguous sites:

MS/MS Fragmentation of EASFGHAVLEIYNR
Found in AT4G36350.1, ATPAP25/PAP25 (purple acid phosphatase 25); acid phosphatase/protein serine/threonine phosphatase

Match to Query 2206: 1684.759521 from(562.593783,3+)
Elution from: 16.981 to 16.981 scan no 890 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1684.7610
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y12 : Phospho (Y)
Ions Score: 22 Expect: 0.058
Matched b ions:
Matched y ions: y(4)++, y(5)++, y(6)++, y(8)++
Precursor origin neutral loss: +

Peptide No.402

EASLEGYQLLNDDVVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EASLEGYQLLNDDVVR
Found in AT5G45275.1, similar to nodulin-related [Arabidopsis thaliana] (TAIR:AT4G19450.1); similar to NFD4 (NUCLEAR FUSI

Match to Query 3069: 1899.860880 from(950.937716,2+)
Elution from: 55.817 to 55.817 scan no 5936 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1899.8615
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00074
Matched b ions: b(7), b(8)-98, b(9), b(10)-98, b(11)++, b(15)
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(14)++
Precursor origin neutral loss: +

Peptide No.403

EATADMSEEFSEGEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/transferase, transferring glyc

Match to Query 2648: 1754.622022 from(878.318287,2+)  
Elution from: 24.991 to 24.991 scan no 1968 polarity:+
Peptide No. 404

EATADMSEEFSEGK
Confirmed sites: @S.7
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycol
Monoisotopic mass of neutral peptide Mr(calc): 1754.6229
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 5.3e-005
Matched b ions: b(7), b(9)--98, b(9), b(12), b(13)--98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10)--98, y(10), y(11), y(11)--98, y(11)--
98++, y(12)+++, y(13)++
Precursor origin neutral loss: +

Peptide No.405

EATADMSEEFSEGEK
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose--phosphate synthase/ transferase, transferring glyc

Match to Query 2965: 1834.587294 from(918.300923,2+)
Elution from: 26.545 to 26.545 scan no 2176 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1834.5893
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M6 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
  S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
  S11 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 47 Expect: 4.5e-005
Matched b ions: b(6), b(7), b(9)++, b(10)−98, b(10), b(12)−98, b(13)−196, b(13)−98++, b(14)−98, b(14)−98++
Matched y ions: y(4), y(5)−98, y(5), y(6)−98, y(6), y(7), y(7)−98, y(8), y(9), y(9)−98, y(10), y(10)++, y(10)−98, y(10)−196, y(11), y(11)−98, y(11)++, y(11)−98++, y(12), y(12)−98++, y(12)++, y(12)−98, y(13)−98++, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.406

EATADMSEEFSEGEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/transferase, transferring glyc

Match to Query 2667: 1738.626286 from(870.320419,2+) Elution from: 33.996 to 33.996 scan no 3186 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1738.6280
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 6.7e-007
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9), b(10), b(12)–98, b(13)–98, b(14)–98, b(14)
Matched y ions: y(3), y(4), y(5)–98, y(6)–98, y(6), y(7)–98, y(8)–98, y(8), y(9)–98, y(9), y(10), y(10)–98, y(10)++, y(11), y(11)–98, y(12), y(12)–98, y(12)–98++, y(12)++, y(13)++, y(13)–98++
Precursor origin neutral loss: +

Peptide No.407
EATADMSEEFSEGEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/ transferase, transferring glyc

Match to Query 3162: 1738.626628 from(870.320590,2+) 
Elution from: 35.737 to 35.737 scan no 3459 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1738.6280
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 5.2e-008
Matched b ions: b(6), b(9)–98, b(9), b(10)–98, b(12), b(14), b(14)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)–98, y(9), y(10), y(10)–98, y(11), y(11)–98, y(11)–98++, y(12)–98++, y(12)–98, y(12), y(12)++, y(13)++, y(13)–98++
Precursor origin neutral loss: +

Peptide No.408

EATADMSEEFSEGEK
Confirmed sites: “@S:7,@S:11”
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/transferase, transferring glyc

Match to Query 2607: 1818.593214 from(910.303883,2+) Elution from: 37.237 to 37.237 scan no 3548 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.5943
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 1.7e-005
Matched b ions: b(5), b(6), b(6)++, b(7)−98, b(7), b(8)−98, b(9), b(9)−98, b(10)−98, b(10), b(11)−98,
           b(12)−98, b(12), b(12)−196, b(12)−98++, b(13)−98, b(13)−196++, b(14)−98, b(14)
Matched y ions: y(3), y(4), y(5)−98, y(5), y(6)−98, y(7)−98, y(8), y(8)−98, y(9)−98, y(9), y(9)++,
y(10), y(10)−98, y(10)−196, y(11), y(11)−98, y(11)−98++, y(11)−196, y(12), y(12)−98, y(12)++,
y(12)−196++, y(12)−98++, y(13)−98++, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.409
EATADMSEEFSEGEK
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glyc

Match to Query 2501: 1754.621658 from(878.318105,2+) Elution from: 25.972 to 25.972 scan no 2066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1754.6229
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 Expect: 0.00057
Matched b ions: b(7), b(10)-98, b(10), b(12)-98, b(13)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.410

EATADMSEEFSEGEK
Confirmed sites: "@T:3,@S:11"
Ambiguous sites:

MS/MS Fragmentation of EATADMSEEFSEGEK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/ transferase, transferring glyc

Match to Query 2288: 1818.592496 from(910.303524,2+)
Elution from: 37.774 to 37.774 scan no 3526 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.5943
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 28 Expect: 0.003
Matched b ions: b(4)−98, b(5)−98, b(6)−98, b(8)−98, b(8), b(9)−98, b(10)−98, b(10), b(12), b(13)−196, b(14)−98, b(14)
Matched y ions: y(3), y(4), y(5)−98, y(5), y(6)−98, y(6), y(7)−98, y(10)−98, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.411
EAVNIFPEKGSYR
Confirmed sites:
Ambiguous sites: @S:11orY:12

MS/MS Fragmentation of EAVNIFPEKGSYR
Found in AT4G30190.1, AHA2 (Arabidopsis H(+)-ATPase 2); ATPase

Match to Query 2441: 1588.729062 from(530.583630,3+)
Elution from: 41.140 to 41.140 scan no 3919 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1588.7286
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.013
Matched b ions:
  Matched y ions: y(4)-98, y(5)-98, y(5), y(6)++, y(6)-98++, y(7)-98++, y(7)++, y(8)-98++, y(9)-98++, y(9)-98++, y(10)++, y(11)-98++, y(11)++
Precursor origin neutral loss:

Peptide No.412

EAVNIFPEKGSYR
Confirmed sites:
Ambiguous sites: @S:11 or Y:12

MS/MS Fragmentation of EAVNIFPEKGSYR
Found in AT4G30190.1, AHA2 (Arabidopsis H(+)-ATPase 2); ATPase

Match to Query 2147: 1588.728477 from(530.583435,3+)
Elution from: 38.764 to 38.764 scan no 3821 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1588.7286
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y12 : Phospho (Y)
Ions Score: 31 Expect: 0.0086
Matched b ions: b(6)++, b(8)++
Matched y ions: y(6)++, y(7)++, y(9)++, y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No.413

ECGPYHPDTLAVYSNLAGTYDAMGR
Confirmed sites: "@Y:5,@T:9,@Y:13,@S:14,@Y:20"
Ambiguous sites:

MS/MS Fragmentation of ECGPYHPDTLAVYSNLAGTYDAMGR
Found in AT3G27960.1, kinesin light chain--related

Match to Query 4785: 3157.043994 from(1053.355274,3+)
Elution from: 27.158 to 27.158 scan no 2273 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3157.0479
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y13 : Phospho (Y)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y20 : Phospho (Y)
Ions Score: 19 Expect: 0.037
Matched b ions: b(8), b(9)+, b(15)−98++, b(16)−98++, b(18)−196++, b(19)−98++, b(19)−196++, b(19)++, b(22)−196++, b(23)−98++, b(23)−196++
Matched y ions: y(6), y(8), y(9), y(10), y(11), y(12), y(17)−196++, y(17)−98++, y(18)−196++, y(17)−98++, y(20)++, y(22)++, y(24)−196++
Precursor origin neutral loss: +

Peptide No.414
ECLYAEPAYFTWDGENK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of ECLYAEPAYFTWDGENK
Found in AT1G35940.1, AT hook motif-containing protein-related

Match to Query 3649: 2284.945416 from(762.655748,3+)
Elution from: 44.819 to 44.819 scan no 4483 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2284.9387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.052
Matched b ions: b(4)++, b(10)++, b(11)++, b(15)++, b(15)−98++, b(16)++, b(16)−98++, b(17)++, b(17)−98++
Matched y ions: y(5)++, y(7)−98, y(16)−98++
Precursor origin neutral loss:

Peptide No.415
EDDNLCNLSGEEDSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EDDNLCNLSGEEDSK
Found in AT1G51745.1, similar to ATP binding / DNA binding [Arabidopsis thaliana]
(TAIR:AT3G21295.1); similar to Os04g059

Match to Query 2905: 1803.648374 from(902.831463,2+)
Elution from: 31.448 to 31.448 scan no 2806 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1803.6506
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 4.4e-006
Matched b ions: b(5), b(6), b(8), b(9)--98, b(11)++, b(11), b(11)--98, b(13)--98, b(13), b(14)--98, b(14) ++
Matched y ions: y(3), y(4), y(5), y(6), y(7)--98, y(7), y(8), y(8)--98, y(9), y(9)--98, y(10)--98, y(10), y (11), y(11)--98, y(12)++, y(13), y(13)--98++
Precursor origin neutral loss: +

Peptide No.416
EDDNLCNLSGEEDESKR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EDDNLCSGLSGEDESKR
Found in AT1G51745.1, similar to ATP binding / DNA binding [Arabidopsis thaliana]
(TAIR:AT3G21295.1); similar to Os04g059

Match to Query 3663: 1959.750318 from(654.257382,3+)
Elution from: 28.686 to 28.686 scan no 2461 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1959.7517
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 5.5e-005
Matched b ions: b(5), b(10)–98++, b(10)++, b(11)–98++, b(12)–98++, b(12)++, b(14)–98++
Matched y ions: y(5)++, y(5), y(6), y(7)++, y(7), y(8)–98++, y(9)–98++, y(9)++, y(10)++, y(10)–98++, y(11)++, y(11)–98++, y(12)++, y(12)–98++, y(13)++, y(13)–98++, y(14)++, y(14)–98++
Precursor origin neutral loss:

Peptide No.417

EDELSGGESSDVADK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EDELSGGESSDVADK
Found in AT1G03140.1, splicing factor Prp18 family protein

Match to Query 2313: 1731.634142 from(866.824347,2+)
Elution from: 26.388 to 26.388 scan no 2111 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1731.6360
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.00086
Matched b ions: b(8)-98, b(14)
Matched y ions: y(5), y(6), y(7), y(8), y(11), y(12), y(12)-98
Precursor origin neutral loss: +

Peptide No.418
EDESSGGLDAESVAESSPK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of EDESSGGLDAESVAESSPK
Found in AT5G42870.1, lipin family protein

Match to Query 2882: 2059.808682 from(1030.911617,2+) 
Elution from: 32.460 to 32.460 scan no 2816 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2059.8106
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 Expect: 9.1e-010
Matched b ions: b(14), b(16), b(17)++
Matched y ions: y(4), y(6)–98, y(6), y(8), y(9), y(10), y(10)–98, y(11)++, y(11), y(12), y(13), y(14), y (14)++, y(15), y(15)–98, y(17), y(17)++
Precursor origin neutral loss:

Peptide No.419

EDGTDDDDDDDVISK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of EDGTDDDDDDDVISK
Found in AT5G55300.1, TOP1BETA (DNA TOPOISOMERASE 1 BETA); DNA topoisomerase type I

Match to Query 2311: 1829.634076 from(915.824314,2+)
Elution from: 29.449 to 29.449 scan no 2451 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1829.6364
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.0094
Matched b ions: b(8), b(10), b(11), b(12)-98, b(12)
Matched y ions: y(4), y(5), y(8)+, y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.420
EDKDMAAPELQSLAATALER
Confirmed sites: "@S:12,@T:16"
Ambiguous sites:

MS/MS Fragmentation of EDKDMAAPELQSLAATALER
Found in AT3G04830.1, binding

Match to Query 3961: 2317.994673 from(773.672167,3+)
Elution from: 60.565 to 60.565 scan no 6329 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2317.9902
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.051
Matched b ions: b(3), b(4)+, b(7), b(16)+, b(18)-98++
Matched y ions: y(4)+, y(6)+, y(16)+, y(17)+, y(18)+
Precursor origin neutral loss:

Peptide No.421

EDLSELYREDLSDVETS
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of EDLSELYREDLSDVETS
Found in AT1G25260.1, acidic ribosomal protein P0–related

Match to Query 3670: 2078.855142 from(1040.434847,2+)
Elution from: 58.592 to 58.592 scan no 6247 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2078.8569
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0043
Matched b ions: b(8), b(9), b(10), b(11), b(12)–98++, b(12)–98, b(12)++, b(13), b(13)++, b(14), b(14)–98++, b(14)–98, b(14)++, b(15), b(15)++, b(15)–98, b(16)++, b(16)–98++
Matched y ions: y(6), y(7)–98, y(9)–98, y(10)–98, y(10), y(11), y(12), y(13)–98++, y(14)–98, y(14)–98++, y(16)++
Precursor origin neutral loss: +

Peptide No.422

EDQLTSPVSDSVDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EDQLTSPVSDSVDR
Found in AT2G43650.1, Sas10/U3 ribonucleoprotein (Utp) family protein

Match to Query 2117: 1626.677392 from(814.345972,2+)
Elution from: 34.890 to 34.890 scan no 3237 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1626.6774
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 1.3e-006
Matched b ions: b(4), b(5), b(6)−98, b(8)+, b(8), b(8)−98, b(9), b(10), b(11)+, b(11), b(11)−98++, b(12), b(12)−98++, b(13)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)+, y(8), y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)++, y(12)++
Precursor origin neutral loss:

Peptide No.423

EDVNIFPEKGSYR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EDVNIFPEKGSYR
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2276: 1632.717447 from(545.246425,3+)
Elution from: 39.177 to 39.177 scan no 3875 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.7184
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0036
Matched b ions: b(3), b(4), b(9)++
Matched y ions: y(2), y(4)−98, y(4), y(5)+, y(5)−98++, y(6)++, y(7)+, y(7)−98++, y(8)+, y(8)−98++, y(9)+, y(10)+, y(10)−98++, y(11)−98++, y(11)++
Precursor origin neutral loss:

Peptide No.424
EDVNIFPEKGSYR
Confirmed sites: @S:11 or Y:12
Ambiguous sites: @S:11 or Y:12

MS/MS Fragmentation of EDVNIFPEKGSYR
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2895: 1632.717591 from(545.246473,3+) Elution from: 39.042 to 39.042 scan no 3929 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.7184
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y12 : Phospho (Y)
Ions Score: 40 Expect: 0.001
Matched b ions: b(3), b(4)
Matched y ions: y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No.425

EDYFTTVDKPLPK
Confirmed sites: "@Y:3,@T:5"
Ambiguous sites:

MS/MS Fragmentation of EDYFTTVDKPLPK
Found in AT4G16080.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45940.1); contains InterPro domain Prot

Match to Query 2904: 1711.716039 from(571.579289,3+)
Elution from: 17.706 to 17.706 scan no 947 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1711.7147
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3: Phospho (Y)
T5: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 27 Expect: 0.015
Matched b ions: b(5)++, b(10)++, b(11)++, b(12)--98++
Matched y ions: y(9)++, y(11)++, y(12)--98++, y(12)++
Precursor origin neutral loss: +

Peptide No.426

EDYFTTVDKPLPK
Confirmed sites: "@Y:3,@T:6"
Ambiguous sites:

MS/MS Fragmentation of EDYFTTVDKPLPK
Found in AT4G16080.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45940.1); contains InterPro domain Prot

Match to Query 2666: 1711.716585 from(571.579471,3+)
Elution from: 17.248 to 17.248 scan no 948 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1711.7147
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y3 : Phospho (Y)
  T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.052
Matched b ions: b(5), b(11)+, b(12)−98++
Matched y ions: y(9)+, y(10)+, y(11)+, y(12)−98++, y(12)+
Precursor origin neutral loss: +

Peptide No.427

EEAASSPVSGAADHQVPASP
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of EEAASSPVSGAADHQVPASP
Found in AT5G55230.1, ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding

Match to Query 3427: 1985.835250 from(993.924901,2+)
Elution from: 32.197 to 32.197 scan no 2907 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.8367
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0003
Matched b ions: b(6), b(7)++, b(8), b(13), b(14), b(15), b(16)++, b(16), b(18)++, b(19)–98++, b(19)++
Matched y ions: y(3), y(4)–98, y(4), y(5)–98, y(7)–98, y(7), y(8)–98, y(9)–98++, y(10), y(11), y(11)–98, y(12)–98, y(12), y(13), y(13)–98, y(14), y(14)–98, y(15)–98, y(15), y(16), y(16)++, y(17)–98++, y(17)++, y(18)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.428

EECCDGWKDGSGEIEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of EECCDGWKDGSGEIEK
Found in AT1G05460.1, SDE3 (SILENCING DEFECTIVE)

Match to Query 3537: 2034.730899 from(679.250909,3+)
Elution from: 28.342 to 28.342 scan no 2421 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2034.7336
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00053
Matched b ions: b(11)+, b(15)−98++, b(15)+, b(16)−98++
Matched y ions: y(2), y(4)+, y(7)+, y(8)+, y(8)−98, y(9), y(9)−98++, y(9)+, y(9)−98, y(10)+, y(10)−98++, y(11)+, y(12)−98++, y(13)+, y(14)+, y(14)−98++, y(15)−98++, y(15)+
Precursor origin neutral loss: +

Peptide No.429

EEDEWSDGWK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EEDEWSDGWK
Found in AT1G05460.1, SDE3 (SILENCING DEFECTIVE)

Match to Query 1542: 1359.464964 from(680.739758,2+)
Elution from: 41.846 to 41.846 scan no 4231 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1359.4656  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 39 Expect: 0.00032  
Matched b ions: b(4), b(6)−98, b(9)−98  
Matched y ions: y(2), y(3), y(4), y(5)−98, y(5), y(6)−98, y(6), y(7)−98, y(7)++, y(8), y(8)−98++, y(8)−98, y(8)++, y(9)++  
Precursor origin neutral loss: +

Peptide No.430

EEFLIGSIEEESQSQPR  
Confirmed sites: @S:16  
Ambiguous sites:

MS/MS Fragmentation of EEFLIGSIEEESQSQPR  
Found in AT1G53590.1, C2 domain-containing protein  
Match to Query 3889: 2143.930728 from(1072.972640,2+)  
Elution from: 54.420 to 54.420 scan no 5812 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2143.9310
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00076
Matched b ions: b(9), b(13), b(15), b(16)-98
Matched y ions: y(5)-98, y(7), y(8), y(9), y(10), y(12), y(13), y(14)+, y(14), y(14)-98++
Precursor origin neutral loss:

Peptide No.431
EEGMSDDGEVYEQFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EEGMSDDGEVYEQFK
Found in AT2G13370.1, CHR5 (chromatin remodeling 5); ATP binding / DNA binding / chromatin binding / helicase

Match to Query 2650: 1970.709600 from(986.362076,2+)
Elution from: 45.092 to 45.092 scan no 4343 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1970.7128
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 1.2e-006
Matched b ions: b(8)++, b(11)–98, b(11), b(12)–98, b(12), b(13)–98, b(14)
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(11)–98, y(12)–98++, y(12)–98, y(13)–98++, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.432

EEIESEDGEILEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EEIESEDGEILEK
Found in AT5G38600.1, proline–rich spliceosome–associated (PSP) family protein / zinc knuckle (CCHC–type) family protein

Match to Query 1798: 1598.659068 from(800.336810,2+)  
Elution from: 39.614 to 39.614 scan no 3754 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1598.6600
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00028
Matched b ions: b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(8), y(9), y(9)-98, y(10)-98, y(11)-98++, y(11), y(11)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.433
EEKEESDDMGFSLFE
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EEKEESDDMGFSLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)

Match to Query 2694: 1985.709652 from(993.862102,2+)
Elution from: 64.861 to 64.861 scan no 6156 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.7125
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 1.6e-005
Matched b ions: b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(12), b(13), b(14), b(14)-98++, b(15)-98++, b(15)++)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98, y(11)
Precursor origin neutral loss: +

Peptide No.434
EEKEESDDMGFSFLFE
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EEKEESDDMGFSFLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)

Match to Query 3299: 2001.704624 from(1001.859588,2+)
Elution from: 57.582 to 57.582 scan no 6035 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2001.7074
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.00041
Matched b ions: b(7), b(8)-98, b(10), b(11), b(12), b(13)++, b(14)-98, b(14)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.435
EELSTLVDKMEISP
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of EELSTLVDKMEISP
Found in AT4G20400.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 2777: 1669.751108 from(835.882830,2+)
Elution from: 59.702 to 59.702 scan no 6415 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.7521
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0043
Matched b ions: b(10), b(11), b(12), b(13)+, b(13)−98++
Matched y ions: y(2), y(3), y(5), y(6)−98, y(6), y(7), y(8)−98, y(9)−98, y(9), y(11)
Precursor origin neutral loss: +

Peptide No.436

EEPEIQVLSDDDSDEEQVK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of EEPEIQVLSDDDSDEEQVK
Found in AT1G47970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17160.1); similar to conserved hypothet

Match to Query 4182: 2282.931477 from(761.984435,3+)
Elution from: 46.066 to 46.066 scan no 4745 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2282.9315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.016
Matched b ions: b(3), b(6), b(7), b(8), b(16)++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(3), y(4), y(6)++, y(7), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(17)++
Precursor origin neutral loss:

**Peptide No.437**

EEPEIQLVLSDDDSDEEQVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EEPEIQLVLSDDDSDEEQVK
Found in AT1G47970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17160.1); similar to conserved hypothet

Match to Query 3926: 2282.929462 from(1142.472007,2+)
Elution from: 44.001 to 44.001 scan no 4437 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2282.9315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 6.9e-005
Matched b ions: b(8), b(9)-98++, b(14), b(18)++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(16)++, y(17)-98++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.438
EESDDDMGFSLFE
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESDDDMGFSLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)
Match to Query 1991: 1599.531028 from(800.772790,2+)
Elution from: 75.491 to 75.491 scan no 7446 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1599.5323
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 Expect: 7.5e-008
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.439

EESDDDMGFSLFE
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESDDDMGFSLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)

Match to Query 2281: 1615.526062 from(808.770307,2+)
Elution from: 67.751 to 67.751 scan no 7167 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1615.5273
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 65 Expect: 5.9e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9)–98, b(9), b(10), b(10)–98, b(11)++, b(11)–98, b(11), b(12) ++, b(12), b(12)–98
Matched y ions: y(2), y(3), y(4), y(6), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.440

EESPQPSGGGSVSPFNSSGK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of EESPQPSGGGSVSPFNSSGK
Found in AT2G38610.1, KH domain-containing protein

Match to Query 3303: 1942.792948 from(972.403750,2+)
Elution from: 32.058 to 32.058 scan no 2888 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.7945
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 3.3e-006
Matched b ions: b(9), b(12), b(13)–98, b(15)–98++, b(15), b(19)++
Matched y ions: y(5), y(6), y(7), y(8), y(8)–98, y(9), y(9)–98, y(11), y(12), y(13), y(13)–98, y(15), y(16)++, y(16), y(16)–98++, y(17)–98++, y(17)++, y(18)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.441
EETSPPSPIASPEEK
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of EETSPPSPIASPEEK
Found in AT3G10480.1, ANAC050; transcription factor

Match to Query 1903: 1676.715864 from(839.365208,2+)
Elution from: 28.513 to 28.513 scan no 2405 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1676.7182
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 4e-005
Matched b ions: b(3), b(4), b(7)-98, b(7), b(8)-98, b(9), b(10), b(11)++, b(11), b(14)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(10)-98, y(11)++, y(11)-98, y(11), y(11)-98++, y(12)++, y(12)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.442

EEVIEEVASPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EEVIEEVASPK
Found in AT3G57150.1, NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)

Match to Query 1465: 1308.584414 from(655.299483,2+)
Elution from: 36.849 to 36.849 scan no 3530 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1308.5850
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 2e-005
Matched b ions: b(4), b(5), b(8), b(10)++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(6), y(7), y(8), y(9), y(9)++
Precursor origin neutral loss:

Peptide No.443
EEVQPETLATPTQSPSR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of EEVQPETLATPTQSPSR
Found in AT1G79280.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 3639: 1948.876296 from(975.445424,2+)
Elution from: 34.326 to 34.326 scan no 3226 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1948.8779
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 1.6e-006
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10), b(13), b(13)++, b(14)++, b(14)--98, b(15)--98++, b(16)--98++
Matched y ions: y(3), y(4), y(4)--98, y(6), y(7), y(7)--98, y(8)--98++, y(8), y(8)--98, y(9)--98, y(9), y(9)++, y(10), y(11), y(11)--98, y(12)++, y(12), y(13)--98++, y(13)--98, y(13), y(13)++, y(14)++, y(14)--98, y(15)--98++
Precursor origin neutral loss: +

Peptide No.444
EEVQPETLATPTQSPSR
Confirmed sites:
Ambiguous sites: @T:12orS:14orS:16

MS/MS Fragmentation of EEVQPETLATPTQSPSR
Found in AT1G79280.1, similar to CIP1 (COP1-INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 2566: 1948.876936 from(975.445744,2+) Elution from: 33.104 to 33.104 scan no 3012 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1948.8779
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 3.1e-005
Matched b ions: b(4), b(7), b(8), b(9), b(10)
Matched y ions: y(6), y(7), y(7)-98, y(8), y(9)-98, y(9), y(10), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.445
EEVQPETLATPTQPSR
Confirmed sites: @T:10,@S:14
Ambiguous sites:

MS/MS Fragmentation of EEVQPETLATPTQPSR
Found in AT1G79280.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 3691: 2028.840708 from(1015.427630,2+)
Elution from: 33.544 to 33.544 scan no 2901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2028.8442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 2e-005
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10)−98, b(11)−98, b(12)−98++, b(13)−98, b(13), b(14)−98, b(14)++, b(15)−196
Matched y ions: y(3), y(4)−98, y(4), y(6), y(7), y(7)−98, y(8)−98++, y(8)−98, y(8), y(8)−196, y(9), y(9)−196, y(10), y(11), y(11)−98, y(12)++, y(13)−98++, y(13)−98, y(13), y(13)++, y(13)−196, y(14)++, y(15)−98++, y(15)++, y(16)−196++, y(16)++
Precursor origin neutral loss: +

Peptide No.446
EEVQPETLATPTQSPSR
Confirmed sites: @T:10
Ambiguous sites: @S:14orS:16

MS/MS Fragmentation of EEVQPETLATPTQSPSR
Found in AT1G79280.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 3560: 2028.841380 from(1015.427966,2+) Elution from: 33.502 to 33.502 scan no 3082 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2028.8442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00081
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10)−98, b(13)−98, b(13)
Matched y ions: y(4), y(4)−98, y(6), y(7), y(7)−98, y(8)−196, y(8)−98++, y(8), y(9), y(9)+, y(9)−196, y(10), y(11), y(11)−98, y(12)+, y(13)−98++, y(13)+, y(13)−98, y(13), y(14)+, y(14)−98++, y(15)−98++, y(15)+, y(15)−196++, y(15)−196++
Precursor origin neutral loss: +

Peptide No.447

EFEPIDSGSELEEDDLK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EFEPIDSGSELEEDDLK
Found in AT1G02870.1, similar to hypothetical protein MtrDRAFT_AC161032g9v1 [Medicago truncatula] (GB:ABE85046.1)

Match to Query 3454: 2030.820948 from(1016.417750,2+)
Elution from: 49.102 to 49.102 scan no 5143 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2030.8245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 3.8e-008
Matched b ions: b(6), b(10), b(11)-98, b(11), b(12), b(12)-98, b(13), b(14), b(14)++, b(15)-98, b(15), b(16)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(13)++, y(13), y(14)-98++, y(14)++, y(14)-98, y(14), y(15)-98, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.448
EFEPIDSGSELEEDDLK
Confirmed sites: ”@S:7,@S:9”
Ambiguous sites:

MS/MS Fragmentation of EFEPIDSGSELEEDDLK
Found in AT1G02870.1, similar to hypothetical protein MtrDRAFT_AC161032g9v1 [Medicago truncatula] (GB:ABE85046.1)

Match to Query 2945: 2110.788738 from(1056.401645,2+)
Elution from: 54.054 to 54.054 scan no 5230 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2110.7908
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00055
Matched b ions: b(3), b(5), b(11)-98, b(11), b(12)-98, b(13)-98, b(14)+, b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(11)-98, y(11), y(12)-98, y(12), y(12)+, y(12)-196, y(13)+, y(13)-98++, y(14)-98++, y(14)+, y(14)-196++, y(15)-98++, y(15)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.449
EFEPIDSGSELEEDDLK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EFEPIDSGSELEEDDLK
Found in AT1G02870.1, similar to hypothetical protein MtrDRAFT_AC161032g9v1 [Medicago truncatula] (GB:ABE85046.1)

Match to Query 3022: 2030.823076 from(1016.418814,2+)
Elution from: 50.104 to 50.104 scan no 5076 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2030.8245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 3.8e-007
Matched b ions: b(7), b(12), b(13), b(13)--98, b(14)--98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)--98, y(10), y(11), y(11)--98, y(12), y(12)--98, y(13) ++, y(14)--98++, y(14)++, y(14), y(14)--98
Precursor origin neutral loss: +

Peptide No.450
EFLTSSDEEEEESVSIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EFLTSSDEEEEESVSIR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB:XP_001055538.1); similar to Os02g0750

Match to Query 2559: 1935.795786 from(968.905169,2+) Elution from: 47.776 to 47.776 scan no 4623 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1935.7986
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 3.4e-008
Matched b ions: b(7), b(11), b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12), y(12)−98, y(13), y(13)++, y(14)−98
Precursor origin neutral loss: +

Peptide No.451

EFLTSSDEEEESVSIR
Confirmed sites: “@S:5,@S:6”
Ambiguous sites:

MS/MS Fragmentation of EFLTSSDEEEESVSIR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB:XP_001055538.1); similar to Os02g0750
Match to Query 3395: 2015.762838 from(1008.888695,2+) Elution from: 50.576 to 50.576 scan no 5325 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2015.7649
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 4.9e-005
Matched b ions: b(7)−196, b(8)−98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(12)−196, y(12), y(13)−196, y(13)
Precursor origin neutral loss: +

Peptide No. 452

EFLTSSDEEEESVSIR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **EFLTSSDEEEESVSIR**
Found in **AT1G36310.1**, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB:XP_001055538.1); similar to Os02g0750

Match to Query 3580: 1935.795804 from(968.905178,2+) Elution from: 45.493 to 45.493 scan no 4771 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1935.7986
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 Expect: 1.3e-007
Matched b ions: b(11), b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(9), y(10), y(11)-98, y(12), y(12)-98, y(13)++, y(14)++, y(14)-98
Precursor origin neutral loss: +

Peptide No.453
EFLTSSDEEEESVISIR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of EFLTSSDEEEESVISIR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB:XP_001055538.1); similar to Os02g0750
Match to Query 2590: 1935.794146 from(968.904349,2+)
Elution from: 47.858 to 47.858 scan no 4615 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1935.7986
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00051
Matched b ions: b(4)-98, b(13)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(10)
Precursor origin neutral loss: +

Peptide No.454

EFLTSSDEEEESVSIR
Confirmed sites: @T:4
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of EFLTSSDEEEESVSIR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB:XP_001055538.1); similar to Os02g0750

Match to Query 3808: 2015.762686 from(1008.888619,2+)
Elution from: 51.573 to 51.573 scan no 5459 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2015.7649
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T4 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
  S6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 33 Expect: 0.0025
Matched b ions: b(7), b(10), b(11), b(13), b(13)−196
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(12), y(13), y(13)−98++, y(14)++, y(14)−98
Precursor origin neutral loss: +

Peptide No.455
EFSFGGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EFSFGGK
Found in AT4G02510.1, TOC159 (translocon outer membrane complex 159)

Match to Query 216: 850.325898 from(426.170225,2+)
Elution from: 35.770 to 35.770 scan no 3352 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 850.3262
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.019
Matched b ions:
  Matched y ions: y(2), y(3), y(4)+, y(4), y(5)
Precursor origin neutral loss:

Peptide No.456

EGDSMQVDSPAAVEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGDSMQVDSPAAVEK
Found in AT2G32730.1, 26S proteasome regulatory subunit, putative

Match to Query 2128: 1657.652546 from(829.833549,2+)
Elution from: 22.922 to 22.922 scan no 1646 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1657.6542
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.3e-006
Matched b ions: b(7), b(8), b(9)−98, b(12), b(12)−98, b(13), b(13)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(11), y(12)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.457
EGDSMQVDSPAAVEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EGDSMQVDSPAAVEK
Found in AT2G32730.1, 26S proteasome regulatory subunit, putative
Match to Query 2096: 1641.658322 from(821.836437,2+)
Elution from: 29.443 to 29.443 scan no 2521 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1641.6593
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.016
Matched b ions: b(5)-98, b(6)-98, b(6), b(7)-98, b(12)-98, b(12), b(12)++, b(13)-98, b(13)-98++, b(14)
Matched y ions: y(3), y(4), y(6), y(8)++, y(13)++
Precursor origin neutral loss: +

Peptide No.458
EGDSMQVDSPAAVEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGDSMQVDSPAAVEK
Found in AT2G32730.1, 26S proteasome regulatory subunit, putative

Match to Query 2771: 1641.657706 from(821.836129,2+)
Elution from: 30.608 to 30.608 scan no 2724 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1641.6593
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.9e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9)–98, b(12), b(12)–98, b(13), b(13)–98, b(14), b(14)–98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)–98, y(9), y(9)–98, y(10)–98, y(11), y(11)++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.459

EGEDVSFSDADSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EGEDVSFSDADSK
Found in AT1G21630.1, calcium-binding EF hand family protein

Match to Query 1846: 1464.529272 from(733.271912,2+)
Elution from: 31.683 to 31.683 scan no 2838 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1464.5293
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00018
Matched b ions: b(5), b(6), b(8)+98, b(11)++, b(11)
Matched y ions: y(2), y(4), y(6), y(6)+98, y(7)+98, y(7), y(8)+98, y(8), y(8)+98++, y(9), y(9)+98, y(10)
Precursor origin neutral loss: +

Peptide No.460

EGELSFDYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EGELSFDYR
Found in AT3G26910.1, hydroxyproline-rich glycoprotein family protein

Match to Query 967: 1194.459250 from(598.236901,2+) Elution from: 43.623 to 43.623 scan no 4428 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1194.4594
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0012
Matched b ions: b(4), b(5)−98, b(6)−98, b(7), b(7)−98, b(7)++, b(8)−98
Matched y ions: y(2), y(3), y(5), y(5)−98, y(5)++, y(6)++, y(6)−98, y(6), y(7)−98, y(7)−98++
Precursor origin neutral loss: +

Peptide No.461

EGFQIMDTSQR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGFQIMDTSQR
Found in AT3G57530.1, CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium- and calmodulin-dependent protein kinase/ kina

Match to Query 1550: 1406.552486 from(704.283519,2+)  
Elution from: 32.808 to 32.808 scan no 2962 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1406.5537
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.017
Matched b ions: b(8)++
Matched y ions: y(3), y(3)–98, y(5), y(6), y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.462
EGFQIMDTSQR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGFQIMDTSQR
Found in AT3G57530.1, CPK32 (CALCIUM–DEPENDENT PROTEIN KINASE 32); calcium– and calmodulin–dependent protein kinase/ kina

Match to Query 1263: 1390.558316 from(696.286434,2+) Elution from: 42.865 to 42.865 scan no 4222 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1390.5588
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00026
Matched b ions: b(3), b(5), b(7), b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)–98, y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.463
EGIESDEEIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EGIESDEEIR
Found in AT5G11260.1, HY5 (ELONGATED HYPOCOTYL 5); DNA binding / transcription factor

Match to Query 1184: 1255.496134 from(628.755343,2+)
Elution from: 30.746 to 30.746 scan no 2744 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1255.4969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0013
Matched b ions: b(2), b(3), b(4), b(5), b(6)–98, b(6)–98++, b(6), b(7)+, b(7)–98, b(7), b(8)–98, b(8), b(9), b(9)–98, b(9)–98++, b(9)+
Matched y ions: y(2), y(3), y(4), y(5), y(6)–98, y(6), y(7)+, y(7)–98, y(7), y(7)–98++, y(8)–98++, y(8)++, y(9)–98++
Precursor origin neutral loss: +

Peptide No.464

EGIESDEEIRR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EGIESDEEIRR
Found in AT5G11260.1, HY5 (ELONGATED HYPOCOTYL 5); DNA binding / transcription factor

Match to Query 1778: 1411.596780 from(471.539536,3+)
Elution from: 26.733 to 26.733 scan no 2162 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.5980
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 48 Expect: 9.1e-005
Matched b ions: b(6), b(6)-98, b(7)-98++, b(8)-98++, b(9)-98++
Matched y ions: y(3)++, y(3), y(4)++, y(5)++, y(6)++, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)++, y(10)++
Precursor origin neutral loss:

Peptide No.465
EGSLQLEGEN
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EGSLQLEGEN
Found in AT5G19450.1, CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); calcium- and calmodulin-dependent protein kinase/kin

Match to Query 814: 1154.449000 from(578.231776, 2+)
Elution from: 35.000 to 35.000 scan no 3171 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1154.4492
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00062
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8)++, b(9)-98, b(9), b(9)++
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.466

EGTKGSSGNLVDAAR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EGTKGSSGNLVDAAR
Found in AT5G64813.1, GTP–binding protein–related

Match to Query 2115: 1540.687864 from(771.351208,2+)
Elution from: 22.580 to 22.580 scan no 1640 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.6882
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.012
Matched b ions: b(6), b(7)–98, b(10)–98, b(11), b(12), b(12)–98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(11)–98++, y(11), y(11)–98, y(12)++, y(13)++, y(13)–98++, y(14), y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.467

EGVDVTEDEMDIQVLK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of EGVDVTEDEMDIQVLK
Found in AT2G16485.1, zinc ion binding

Match to Query 3335: 1898.817832 from(950.416192,2+)
Elution from: 56.863 to 56.863 scan no 5873 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1898.8220
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.052
Matched b ions: b(8)
Matched y ions: y(6), y(9), y(11)−98, y(11), y(12), y(13)−98
Precursor origin neutral loss: +

Peptide No.468

EHSDEMIADQ
Confirmed sites: @S:3orT:5
Ambiguous sites: @S:3orT:5

MS/MS Fragmentation of EHSDEMIADQ
Found in AT2G24640.1, ubiquitin carboxyl-terminal hydrolase family protein / zinc finger (MYND type) family protein

Match to Query 1269: 1354.474758 from(678.244655,2+)  
Elution from: 28.070 to 28.070 scan no 2268 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1354.4748
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0018
Matched b ions: b(6), b(7), b(8), b(9), b(10)++, b(10)
Matched y ions: y(3), y(5)
Precursor origin neutral loss:

Peptide No.469
EIAEAFLGSPVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EIAEAFLGSPVK
Found in AT3G12580.1, HSP70 (heat shock protein 70); ATP binding

Match to Query 1441: 1339.642418 from(670.828485,2+)
Elution from: 49.125 to 49.125 scan no 5136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1339.6424
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 4.3e-006
Matched b ions: b(7), b(8)
Matched y ions: y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)
Precursor origin neutral loss: +

Peptide No.470

EIAEEVQSESK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of EIAEEVQSESK
Found in AT3G15980.1, coatamer protein complex, subunit beta 2 (beta prime), putative

Match to Query 1141: 1327.553602 from(664.784077,2+)
Elution from: 24.282 to 24.282 scan no 1840 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1327.5544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00051
Matched b ions: b(7)++, b(8), b(9), b(9)++
Matched y ions: y(4), y(5)++, y(5)-98, y(6), y(6)-98++, y(7), y(8), y(8)++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.471
EIAEEVQSESK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of EIAEEVQSESK
Found in AT3G15980.1, coatomer protein complex, subunit beta 2 (beta prime), putative

Match to Query 1350: 1327.553398 from(664.783975,2+)
Elution from: 24.294 to 24.294 scan no 1875 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1327.5544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0021
Matched b ions: b(5), b(7)+, b(7), b(8)−98, b(8)+, b(9)−98
Matched y ions: y(2), y(4), y(4)−98, y(5)+, y(5)−98, y(6), y(6)−98++, y(7), y(8)+, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.472

EIAEGVTQIVQMLETEEE
Confirmed sites: @T:15
Ambiguous sites:

MS/MS Fragmentation of EIAEGVTQIVQMLETEEE
Found in AT5G62390.1, ATBAG7 (ARABIDOPSIS THALIANA BCL–2–ASSOCIATED ATHANOGENE 7); calmodulin binding

Match to Query 3725: 2142.923272 from(1072.468912,2+)  
Elution from: 71.525 to 71.525 scan no 7444 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2142.9279
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
 M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
 T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
 Ions Score: 50 Expect: 9.1e−005
Matched b ions: b(8), b(9), b(10), b(11), b(14), b(16), b(17)+
Matched y ions: y(8), y(10), y(15)
Precursor origin neutral loss: +

Peptide No.473
EIAEGVTQIVQMLETEEE
Confirmed sites: @T:15
Ambiguous sites:
MS/MS Fragmentation of EIAEGVTQIVQMLETEEE
Found in AT5G62390.1, ATBAG7 (ARABIDOPSIS THALIANA BCL–2–ASSOCIATED ATHANOGENE 7); calmodulin binding

Match to Query 3992: 2126.931624 from(1064.473088,2+)
Elution from: 79.150 to 79.150 scan no 8088 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2126.9330
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 8e−005
Matched b ions: b(6), b(9), b(10), b(11), b(12), b(14), b(16), b(16)+, b(17)+, b(17)−98++
Matched y ions: y(7), y(8)−98, y(8), y(9), y(9)−98, y(10), y(12)
Precursor origin neutral loss: +

Peptide No.474

EIASEGSCEVK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EIASEGSCEVK
Found in AT5G12410.1, THUMP domain-containing protein

Match to Query 1289: 1287.505032 from(644.759792,2+)
Elution from: 21.351 to 21.351 scan no 1476 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1287.5053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0024
Matched b ions: b(6), b(10), b(10)−98
Matched y ions: y(5), y(6), y(6)−98, y(7), y(8), y(8)++, y(9)−98++, y(9), y(9)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.475
EIASEGVNDQVNEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EIASEGVNDQVNEK
Found in AT5G12410.1, THUMP domain-containing protein

Match to Query 2668: 1610.681416 from(806.347984,2+)
Elution from: 28.369 to 28.369 scan no 2418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1610.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.4e-006
Matched b ions: b(3), b(5)–98, b(6), b(7)–98, b(8)–98, b(9), b(10)–98, b(11)–98, b(11), b(12)++, b(12), b(13)–98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)–98, y(11)++, y(11), y(11)–98++, y(12)–98++, y(12), y(12)–98, y(12)++
Precursor origin neutral loss: +

Peptide No.476

EIDENDSQIEAVEER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EIDENDSQIEAVEER
Found in AT5G25070.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16730.1); similar to Os08g0516000 [Oryz

Match to Query 2370: 1854.749308 from(928.381930,2+)
Elution from: 37.470 to 37.470 scan no 3585 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1854.7520
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.032
Matched b ions: b(9)-98, b(10), b(12)–98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(12)++
Precursor origin neutral loss: +

Peptide No.477

EIDGSGSQNQHPVGSPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of EIDGSGSQNQHPVGSPR
Found in AT5G15030.1, paired amphipathic helix repeat-containing protein

Match to Query 3017: 1843.783494 from(615.601774,3+)
Elution from: 19.852 to 19.852 scan no 1249 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1843.7850
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00024
Matched b ions: b(3), b(4), b(15)--98++
Matched y ions: y(2), y(3), y(6), y(7)++, y(8)++, y(8)--98, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)--98++, y(15)++
Precursor origin neutral loss:

Peptide No.478
EIEDDIAGYSEESSEER
Confirmed sites: @S:10
Ambiguous sites: @S:13 or S:14

MS/MS Fragmentation of EIEDDIAGYSEESSEER
Found in AT2G46020.1, ATBRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA); ATP binding / DNA binding / helicase/ transcription regul

Match to Query 3557: 2116.739542 from(1059.377047,2+)
Elution from: 41.099 to 41.099 scan no 4139 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2116.7398

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S14 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 23 Expect: 0.016

Matched b ions: b(7), b(9), b(14)–196

Matched y ions: y(7), y(8), y(8)–98, y(9)–98, y(9), y(10)–98, y(10), y(11)–98, y(11), y(12), y(13)–98, y(14)–98++, y(16)–98++

Precursor origin neutral loss: +

Peptide No. 479

EIEVADYESSDEDRHFK

Confirmed sites: ”@S:9,@S:10”

Ambiguous sites:

MS/MS Fragmentation of EIEVADYESSDEDRHFK

Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1); similar to hypothetical prote

Match to Query 3723: 2227.833660 from(743.618496,3+)

Elution from: 35.990 to 35.990 scan no 3470 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2227.8347
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00013
Matched b ions: b(6), b(10)–98, b(11)++, b(14)–196++, b(15)–196++, b(16)++
Matched y ions: y(2), y(3), y(4)++, y(6)++, y(8)++, y(8)–98++, y(9)++, y(10)++, y(10)–98++, y(11)++, y(11)–196++, y(12)++, y(12)–98++, y(13)++, y(13)–98++, y(13)–196++, y(14)–98++, y(14)++, y(14)–196++, y(15)++, y(15)–98++
Precursor origin neutral loss:

Peptide No.480

EIEVADYESSDEDRHFK
Confirmed sites: "@Y:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of EIEVADYESSDEDRHFK
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1); similar to hypothetical prote

Match to Query 3565: 2227.832310 from(1114.923431,2+)
Elution from: 36.219 to 36.219 scan no 3415 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2227.8347
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.022
Matched b ions: b(8), b(16)−98++
Matched y ions: y(4), y(6), y(7), y(8), y(11)++, y(11)−98, y(11), y(13)++, y(13)−98++, y(14)−98++, y(14)++, y(15)−98++, y(15)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.481
EIGANVFDKPSHPNSPTVYDWMYSNETR
Confirmed sites:
Ambiguous sites: "@Y:23orS:24orT:27, @Y:23orS:24orT:27"

MS/MS Fragmentation of EIGANVFDKPSHPNSPTVYDWMYSNETR
Found in AT5G44300.1, dormancy/auxin associated family protein

Match to Query 5440: 3429.402999 from(1144.141609,3+)
Elution from: 53.400 to 53.400 scan no 5598 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3429.4050
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M22 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
  Y23 : Phospho (Y)
  T27 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.04
Matched b ions: b(8), b(10), b(12), b(13), b(14), b(15), b(16)+, b(17)+, b(18)+, b(19)+, b(20)+
Matched y ions: y(7), y(7)-98, y(10)-98, y(10), y(11)-98, y(14)+, y(14)-98++, y(15)-98++, y(15)+, y(16)+, y(16)-98++, y(20)-98++, y(20)+, y(22)-98+
Precursor origin neutral loss: +

Peptide No.482
EIITLDPSSPK
Confirmed sites:
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of EIITLDPSSPK
Found in AT1G67950.1, RNA recognition motif (RRM)-containing protein

Match to Query 1212: 1278.610612 from(640.312582,2+)
Elution from: 41.194 to 41.194 scan no 4033 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1278.6108
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00011
Matched b ions: b(5), b(9)++
Matched y ions: y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9)
Precursor origin neutral loss:

Peptide No.483

EILSDVDADNDGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EILSDVDADNDGR
Found in AT1G50700.1. CPK33 (calcium-dependent protein kinase 33); calcium- and calmodulin-dependent protein kinase/ kina

Match to Query 1552: 1497.602442 from(749.808497,2+)
Elution from: 40.923 to 40.923 scan no 4024 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1497.5984
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.049
Matched b ions: b(4), b(6)−98, b(8)++, b(10)++, b(11)−98++, b(12)−98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(10)−98++, y(10)++, y(11), y(11)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.484

EISDDEDEDEPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISDDEDEDEPK
Found in AT5G52640.1, HSP81−1 (HEAT SHOCK PROTEIN 81−1); ATP binding / unfolded protein binding

Match to Query 2241: 1499.518496 from(750.766524,2+) Elution from: 22.280 to 22.280 scan no 1584 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1499.5188
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0031
Matched b ions: b(9), b(10)–98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(8)++, y(8), y(10), y(10)–98++
Precursor origin neutral loss: +

Peptide No.485
EISDDEDEDEPKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISDDEDEDEPKK
Found in AT5G52640.1, HSP81-1 (HEAT SHOCK PROTEIN 81-1); ATP binding / unfolded protein binding

Match to Query 2632: 1627.613094 from(814.813823,2+)
Elution from: 19.119 to 19.119 scan no 1166 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1627.6138
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0001
Matched b ions: 
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)+, y(9), y(10), y(10)+, y(11)−98++, y(11)+
Precursor origin neutral loss: +

Peptide No.486

EISDDEEEEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISDDEEEEEK
Found in AT5G56030.1, HSP81–2 (EARLY–RESPONSIVE TO DEHYDRATION 8); ATP binding

Match to Query 1722: 1430.496082 from(716.255317,2+)
Elution from: 20.206 to 20.206 scan no 1296 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1430.4973
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 6.4e-005
Matched b ions: b(3), b(5), b(6), b(8), b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)–98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.487
EISDDEEEEEEKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISDDEEEEEEKK
Found in AT5G56030.1, HSP81–2 (EARLY–RESPONSIVE TO DEHYDRATION 8); ATP binding

Match to Query 1709: 1558.591658 from(780.303105,2+)  
Elution from: 18.732 to 18.732 scan no 1045 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1558.5923
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.019
Matched b ions:
Matched y ions: y(2), y(3), y(5), y(7), y(9)++, y(10)++, y(10)--98++, y(11)++
Precursor origin neutral loss: +

Peptide No.488
EISDDEEEEEEKKDEEGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISDDEEEEEEKKDEEGK
Found in AT5G56030.1, HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding

Match to Query 3772: 2116.819736 from(1059.417144,2+)
Elution from: 20.145 to 20.145 scan no 1288 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2116.8208
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.2e-005
Matched b ions: b(8)-98, b(10)-98, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)+, y(13), y(14)+, y(15)+, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.489
EISPGDIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EISPGDIR
Found in AT5G13020.1, emsy N terminus domain-containing protein / ENT domain-containing protein

Match to Query 495: 965.420694 from(483.717623,2+)
Elution from: 31.584 to 31.584 scan no 2751 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 965.4219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0013
Matched b ions: b(2), b(5)−98, b(5), b(6)
Matched y ions: y(1), y(2), y(4), y(5), y(5)++, y(6), y(6)++, y(6)−98++
Precursor origin neutral loss: +

Peptide No.490
EKPLVQVLSDDDSEVK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of EKPLVQVLSDDDSEVK
Found in AT3G17160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47970.1); similar to hypothetical protet

Match to Query 3469: 1879.880536 from(940.947544,2+)  
Elution from: 42.207 to 42.207 scan no 4350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1879.8815
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00086
Matched b ions:
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)+, y(11), y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.491

EKPLVQVLSDDDSEVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EKPLVQVLSDDDSEVK
Found in AT3G17160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47970.1); similar to hypothetical prote

Match to Query 3286: 1879.879347 from(627.633725,3+)
Elution from: 42.146 to 42.146 scan no 4052 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1879.8815
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 7.9e-007
Matched b ions: b(2), b(4), b(5), b(6), b(7)++, b(7), b(8), b(8)++, b(9)–98, b(9)–98++, b(9)++, b(10)++, b(10)–98++, b(11)++, b(12)–98++, b(14)++, b(14)–98++, b(15)++, b(15)–98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98++, y(8)–98, y(8)++, y(9), y(9)–98++, y(9)–98, y(9)++, y(10), y(10)–98, y(10)++, y(10)–98++, y(11)++, y(11)–98++, y(12)–98++, y(12)++, y(13)++, y(14)++, y(14)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.492

EKPLVQVLSDDDSEVK
Confirmed sites: "@S:9,@S:13"
Ambiguous sites:

MS/MS Fragmentation of EKPLVQVLSDDDSEVK
Found in AT3G17160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47970.1); similar to hypothetical prote

Match to Query 3346: 1959.845559 from(654.289129,3+) Elution from: 44.331 to 44.331 scan no 4521 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1959.8479
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00044
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(9)−98++, b(9)++, b(10)++, b(12)++, b(13)++, b(13)−196++, b(14)++, b(14)−98++, b(14)−196++, b(15)−98++, b(15)−196++, b(15)++
Matched y ions: y(4), y(5)−98, y(6)++, y(6), y(7), y(8)−98++, y(8)−98, y(8), y(8)−196, y(8)++, y(9)−98++, y(9), y(9)++, y(9)−196++, y(10)−98, y(10), y(10)−196++, y(10)−98++, y(10)−196, y(10)++, y(11)++, y(11)−196++, y(12)−98++, y(12)++, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(14)−196++
Precursor origin neutral loss: +

Peptide No.493
EKSLEIEPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EKSLEIEPK
Found in AT2G16940.1, RNA recognition motif (RRM)−containing protein

Match to Query 871: 1151.547280 from(576.780916,2+)
Elution from: 24.190 to 24.190 scan no 1856 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1151.5475
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0014
Matched b ions: b(2), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7), y(7)-98, y(8)+, y(8)-98++
Precursor origin neutral loss: +

Peptide No.494

ELAELYLSLQMYK
Confirmed sites: “@S:8,@Y:12”
Ambiguous sites:

MS/MS Fragmentation of ELAELYLSLQMYK
Found in AT5G28220.1, binding

Match to Query 2197: 1759.757310 from(587.593046,3+)
Elution from: 27.277 to 27.277 scan no 2134 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1759.7544

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y12 : Phospho (Y)

Ions Score: 31 Expect: 0.0062

Matched b ions: b(4), b(5), b(7)++, b(7), b(8)++, b(9)++, b(11)++
Matched y ions: y(2), y(3), y(4)++, y(5)++, y(7)−98++, y(7)++, y(11)−98++, y(12)−98++, y(12)++

Precursor origin neutral loss: +

Peptide No.495

ELFASEDDEAGK

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of ELFASEDDEAGK

Found in AT2G25170.1, PKL/SSL2 (PICKLE, SUPPRESSOR OF SLR2)

Match to Query 1446: 1389.533510 from(695.774031,2+)

Elution from: 34.320 to 34.320 scan no 3161 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1389.5337
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0042
Matched b ions: b(2), b(11)-98, b(11), b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)-98++, y(10)-98++, y(10)+, y(10)
Precursor origin neutral loss:

Peptide No.496

ELGWSDDEDK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ELGWSDDEDK
Found in AT1G61690.1, binding / zinc ion binding

Match to Query 1046: 1272.453898 from(637.234225,2+)
Elution from: 35.755 to 35.755 scan no 3366 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1272.4547
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 3.6e-005
Matched b ions: b(2), b(4)++, b(7), b(8)++, b(8)−98, b(8), b(9)−98
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)−98, y(7), y(7)++, y(7)−98, y(8), y(8)−98, y(8)++
Matched y ions: y(8)−98++
Precursor origin neutral loss: +

Peptide No.497
ELISEDSVSPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ELISEDSVSPR
Found in AT5G19320.1, RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator

Match to Query 1161: 1310.575252 from(656.294902,2+) Elution from: 32.443 to 32.443 scan no 2933 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1310.5755
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00094
Matched b ions: b(2), b(3), b(4), b(5), b(7)-98, b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(5), y(6), y(6)-98, y(8), y(8)+, y(8)-98, y(9), y(9)+
Precursor origin neutral loss: +

Peptide No.498

ELISEDSVSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ELISEDSVSPR
Found in AT5G19320.1, RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator

Match to Query 1107: 1310.574822 from(656.294687,2+)  
Elution from: 32.393 to 32.393 scan no 2918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1310.5755
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1e-005
Matched b ions: b(2), b(3), b(4), b(8), b(9), b(10)–98
Matched y ions: y(2), y(3)–98, y(4)–98, y(5)–98, y(6), y(7), y(8), y(8)–98, y(9), y(9) ++, y(10)++
Precursor origin neutral loss: +

Peptide No.499
ELKFDDGDSDDAK
Confirmed sites: “@S:8,@S:10”
Ambiguous sites:
MS/MS Fragmentation of ELKFDDGDSDDAK
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2451: 1700.584314 from(851.299433,2+) Elution from: 31.965 to 31.965 scan no 2931 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1700.5855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0013
Matched b ions: b(7), b(13)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.500

ELKWKDQSGK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ELKWKDQSGK
Found in AT3G16110.1, ATPDIL1–6 (PDI–LIKE 1–6); thiol–disulfide exchange intermediate

Match to Query 1227: 1297.60677 from(433.542635,3+)
Elution from: 17.954 to 17.954 scan no 996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1297.6067
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.036
Matched b ions: b(5)++, b(6)++, b(7)++, b(9)−98++
Matched y ions: y(4)−98, y(7)−98++, y(7)++, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.501
ELLESGSGDEDLSVGFEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ELLESGSGDEDLSVGFEK
Found in AT5G21970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G63090.1); similar to Os03g0181400 [Oryz]

Match to Query 3584: 1989.845362 from(995.929957,2+)
Elution from: 53.827 to 53.827 scan no 5517 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1989.8455
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0066
Matched b ions: b(9), b(12)−98, b(14)−98, b(14), b(15)
Matched y ions: y(4), y(5), y(6), y(8), y(12), y(14)−98, y(14), y(15)−98++, y(15)++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.502

ELLPEPFNSPQR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ELLPEPFNSPQR
Found in AT3G54710.1, ATCDT1B/CDT1/CDT1B (ARABIDOPSIS HOMOLOG OF YEAST CDT1 B); cyclin-dependent protein kinase

Match to Query 2334: 1505.690452 from(753.852502,2+)
Elution from: 51.055 to 51.055 scan no 5392 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1505.6915
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0023
Matched b ions: b(5), b(8)
Matched y ions: y(4), y(5), y(5)-98, y(7)-98, y(7), y(7)++, y(8), y(8)++, y(9)-98, y(9), y(9)-98++, y(10)++, y(10)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.503
ELQSPTAESLPAEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ELQSPTAESLPAEK
Found in AT5G61970.1, signal recognition particle–related / SRP–related

Match to Query 1759: 1578.717732 from(790.366142,2+) Elution from: 33.182 to 33.182 scan no 2910 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1578.7178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.011
Matched b ions: b(9), b(10)−98, b(10), b(11)−98
Matched y ions: y(4), y(6), y(8), y(10), y(11), y(11)−98, y(12)++
Precursor origin neutral loss: +

Peptide No.504
ELQSPTAESLPAEK
Confirmed sites: @S:4orT:6
Ambiguous sites: 

MS/MS Fragmentation of ELQSPTAESLPAEK
Found in AT5G61970.1, signal recognition particle−related / SRP−related

Match to Query 2181: 1578.717702 from(790.366127,2+)  
Elution from: 31.999 to 31.999 scan no 2917 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1578.7178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.024
Matched b ions: b(7)−98, b(10), b(11)−98
Matched y ions: y(4), y(5), y(6), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.505
ELSLTSPEVVTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of ELSLTSPEVVTK
Found in AT3G51800.1, ATG2 (G2p-related protein); metalloexopeptidase

Match to Query 1815: 1381.673980 from(691.844266,2+)
Elution from: 44.679 to 44.679 scan no 4377 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1381.6741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1.9e-005
Matched b ions: b(5), b(8)–98, b(8), b(9), b(9)–98, b(10), b(10)–98, b(11)
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11)++
Precursor origin neutral loss:

Peptide No.506

ELSLTSPEVVTK
Confirmed sites:
Ambiguous sites: @T:5

MS/MS Fragmentation of ELSLTSPEVVTK
Found in AT3G51800.1, ATG2 (G2p–related protein); metalloexopeptidase

Match to Query 1892: 1381.672892 from(691.843722,2+)
Elution from: 43.963 to 43.963 scan no 4489 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1381.6741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0027
Matched b ions: b(2), b(5)--98, b(5), b(8)--98, b(9), b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9)++, y(9), y(10), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.507
ELSNDFER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ELSNDFER
Found in AT1G35720.1, ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding
Match to Query 651: 1088.416610 from(545.215581,2+)
Elution from: 30.952 to 30.952 scan no 2737 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1088.4175
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0012
Matched b ions: b(2), b(4), b(5)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)−98++
Precursor origin neutral loss: +

Peptide No.508

ELSPTGLDSSPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ELSPTGLDSSPR
Found in AT3G51950.1, zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein

Match to Query 1382: 1337.585842 from(669.800197,2+)
Elution from: 33.137 to 33.137 scan no 3066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1337.5864
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1e-005
Matched b ions: b(2), b(3), b(4)–98, b(4), b(6)–98, b(7)–98, b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(9)+, y(10), y(10)–98++, y(10)+
Precursor origin neutral loss: +

Peptide No.509

EMMEAYTEMLTYIKSAVTR
Confirmed sites: "@T:11,@Y:12"
Ambiguous sites: @Y:6orT:7

MS/MS Fragmentation of EMMEAYTEMLTYIKSAVTR
Found in AT2G26990.1, FUS12 (FUSCA 12); binding

Match to Query 3942: 2521.957518 from(841.659782,3+)
Elution from: 43.086 to 43.086 scan no 4254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2521.9622
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y12 : Phospho (Y)
Ions Score: 22 Expect: 0.052
Matched b ions: b(9)-98, b(16)-98++, b(16)+, b(17)+, b(17)-98++, b(18)-98++
Matched y ions: y(7)+, y(12)+, y(12)-98++, y(14)+, y(14)-98++, y(16)+, y(16)-196++, y(17)+, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.510
EMSFAHTAKASDK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of EMSFAHTAKASDK
Found in AT3G03300.1, DCL2 (DICER-LIKE 2); ATP-dependent helicase/ribonuclease III

Match to Query 2307: 1501.626444 from(501.549424,3+)
Elution from: 24.524 to 24.524 scan no 1963 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1501.6272
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.024
Matched b ions: b(3)++, b(6)++, b(7)++, b(7)-98++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(3)++, y(8)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.511

EMVEYDSSDDEDRHK
Confirmed sites: ”@S:7,@S:8”
Ambiguous sites:

MS/MS Fragmentation of EMVEYDSSDDEDRHK
Found in AT4G17410.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47430.1); similar to hypothetical prote

Match to Query 3072: 2160.737385 from(721.253071,3+)
Elution from: 31.649 to 31.649 scan no 2820 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2160.7384
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0043
Matched b ions: b(10)−196++, b(12)++, b(14)−196++
Matched y ions: y(2), y(4)++, y(7)++, y(9)++, y(10)++, y(11)++, y(11)−196++, y(11)−98++, y(12)++, y(12)−98++, y(13)++, y(13)−98++, y(14)−98++, y(14)++, y(14)−196++
Precursor origin neutral loss:

Peptide No.512

ENIFCSQASNLSTEMAR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of ENIFCSQASNLSTEMAR
Found in AT3G13290.1, transducin family protein / WD-40 repeat family protein

Match to Query 3543: 2036.831796 from(1019.423174,2+)
Elution from: 47.998 to 47.998 scan no 5028 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2036.8332
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00066
Matched b ions: b(8), b(16)++
Matched y ions: y(5), y(6), y(8)−98, y(8), y(9), y(9)−98, y(10), y(12), y(14)
Precursor origin neutral loss: +

Peptide No.513
ENIIASASSPMK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ENIIASASSPMK
Found in AT5G06460.1, ATUBA2 (Arabidopsis thaliana ubiquitin activating enzyme 2); ubiquitin activating enzyme

Match to Query 1651: 1326.588698 from(664.301625,2+) Elution from: 37.807 to 37.807 scan no 3475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1326.5890
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 1.7e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(11)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No.514

ENIIASASSPMKK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ENIIASASSPMKK
Found in AT5G06460.1, ATUBA2 (Arabidopsis thaliana ubiquitin activating enzyme 2); ubiquitin activating enzyme

Match to Query 2384: 1454.682876 from(728.348714,2+)
Elution from: 30.489 to 30.489 scan no 2771 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6840
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00015
Matched b ions: b(7), b(12)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9), y(10), y(10)++, y(11)–98
Precursor origin neutral loss: +

Peptide No. 515
ENILDDSDSGEVK
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of ENILDDSDSGEVK
Found in AT3G48060.1, bromo-adjacent homology (BAH) domain-containing protein
Match to Query 1731: 1499.602064 from (750.808308, 2+)
Elution from: 34.583 to 34.583 scan no 3196 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1499.6028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00011
Matched b ions: b(3), b(10)+, b(10), b(11), b(12)−98++
Matched y ions: y(2), y(5), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)+, y(10)−98, y(11), y(11)++)
Precursor origin neutral loss: +

Peptide No.516
ENILDDSDSGEVK
Confirmed sites: “@S:7, @S:9”
Ambiguous sites:

MS/MS Fragmentation of ENILDDSDSGEVK
Found in AT3G48060.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1760: 1579.567738 from(790.791145,2+)
Elution from: 40.295 to 40.295 scan no 3821 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1579.5691
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0019
Matched b ions: b(3), b(4), b(7)-98, b(10), b(12), b(12)-98++
Matched y ions: y(2), y(6)+, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)+, y(10), y(10)-98++, y(10)-98, y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.517
ENILDDSNGEVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ENILDDSNGEVK
Found in AT3G48060.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 2168: 1499.601774 from(750.808163,2+)
Elution from: 36.150 to 36.150 scan no 3252 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1499.6028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 4.7e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8)++, b(10)–98++, b(10)–98, b(11)–98, b(11), b(12), b(12)–98
Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(7), y(7)–98, y(8), y(8)–98, y(8)–98++, y(9)–98, y(9), y(10)++, y(10), y(10)–98, y(11), y(11)++
Precursor origin neutral loss: +

Peptide No. 518
ENLGVMLSFNTALKSNLLISTSK
Confirmed sites: “@S:8,@T:11,@S:15”
Ambiguous sites: @S:20orT:21orS:22

MS/MS Fragmentation of ENLGVMLSFNTALKSNLLISTSK
Found in AT5G52545.1, nucleotide binding

Match to Query 4272: 2799.209028 from(700.809533,4+)
Elution from: 37.885 to 37.885 scan no 3632 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2799.2008
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
- T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
- S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
- S22 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.028
Matched b ions: b(6)++, b(6), b(10)−98++, b(11)++, b(12)++, b(12)−98++, b(13)++, b(13)−98++, b(13)−196++, b(15)−294++, b(16)−294++, b(16)−196++, b(16)++, b(17)−294++, b(18)−294++, b(18)−196++, b(19)−294++, b(20)−294++, b(22)−392++
Matched y ions: y(4), y(5)−98, y(5), y(7), y(7)−98, y(8), y(8)−98++, y(8), y(10)−98++, y(10)++, y(11)++, y(12)−98++, y(12)++, y(13)−294++, y(13)−196++, y(14)−294++, y(14)−196++, y(15)−98++, y(17)−98++, y(17)−392++, y(17)−196++, y(18)−196++, y(19)−392++, y(19)−294++, y(20)−196++, y(21)−294++
Precursor origin neutral loss:
Peptide No.519
ENNIGDEVGWSK
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of ENNIGDEVGWSK
Found in AT3G62580.1, similar to late embryogenesis abundant domain-containing protein / LEA domain-containing protein [A
Match to Query 1711: 1426.575482 from(714.295017,2+)  
Elution from: 39.299 to 39.299 scan no 3858 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1426.5765
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.051
Matched b ions: b(10)++, b(11)−98++
Matched y ions: y(3), y(4), y(5), y(8)−98, y(8), y(9), y(10)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.520

ENNIIDAGDSEK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **ENNIIDAGDSEK**
Found in **AT4G39680.1**, SAP domain–containing protein

Match to Query 1578: 1383.554148 from(692.784350,2+)
Elution from: 27.529 to 27.529 scan no 2310 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1383.5555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 1.8e-005
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(9)++, b(10)-98, b(11)
Matched y ions: y(2), y(3), y(5), y(6)-98, y(7), y(8), y(8)-98, y(9), y(10)
Precursor origin neutral loss: +

Peptide No.521

ENSGFGFLLLTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ENSGFGFLLLTR
Found in AT5G20490.1, XIK (Myosin-like protein XIK); motor/ protein binding

Match to Query 1366: 1319.591068 from(660.802810,2+)
Elution from: 59.149 to 59.149 scan no 6340 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1319.5910
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00039
Matched b ions: b(3), b(6)--98, b(7), b(8)--98, b(8), b(9)--98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.522
ENSLRHEEETGVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ENSLRHEEETGVK
Found in AT4G39150.1, DNAJ heat shock N-terminal domain-containing protein

Match to Query 2571: 1606.697714 from(804.356133,2+)
Elution from: 18.852 to 18.852 scan no 1198 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1606.6988
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 26 Expect: 0.021
Matched b ions: b(8)–98, b(9)–98, b(11)++, b(12)–98++, b(12)++
Matched y ions: y(4), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)–98++
Precursor origin neutral loss: +

Peptide No.523
ENSPGPSGSVSPFNSNAMK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ENSPGPSGSVSPFNSNAMK
Found in AT3G08620.1, KH domain-containing protein

Match to Query 3426: 1985.815748 from (993.915150, 2+)
Elution from: 39.797 to 39.797 scan no 3924 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.8189
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0024
Matched b ions: b(9)-98, b(10)-98, b(11), b(16)-98++, b(17)++, b(18)
Matched y ions: y(6), y(8), y(10), y(11), y(12), y(14), y(16)+, y(17)-98++
Precursor origin neutral loss: +

Peptide No.524
ENTKPLAETNTKSR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of ENTKPLAETNTKSR
Found in AT1G65030.1, transducin family protein / WD-40 repeat family protein

Match to Query 2231: 1667.789664 from(556.937164,3+)
Elution from: 34.480 to 34.480 scan no 3184 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1667.7879
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.038
Matched b ions: b(4), b(9)++, b(10)++, b(11)++, b(12)++, b(13)++
Matched y ions: y(4), y(5), y(12)++
Precursor origin neutral loss:

Peptide No.525

EPFSGGSDNANYETALK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EPFSGGSDNANYETALK
Found in AT2G19470.1, CKL5 (Casein Kinase I-like 5); casein kinase I/ kinase

Match to Query 3279: 1878.766206 from(940.390379,2+)
Elution from: 42.977 to 42.977 scan no 4162 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1878.7672  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
**Ions Score:** 49 **Expect:** 7.2e-005  
**Matched b ions:** b(9)-98, b(13)++, b(15)-98++  
**Matched y ions:** y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98, y(12)-98, y(13), y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)-98, y(16)-98++  
**Precursor origin neutral loss:** +

---

**Peptide No.526**

**EPLTIEDAVLK**  
**Confirmed sites:** @T:4  
**Ambiguous sites:**

---

**MS/MS Fragmentation of EPLTIEDAVLK**  
Found in **AT5G35750.1, AHK2 (ARABIDOPSIS HISTIDINE KINASE 2)**

**Match to Query 1466:** 1306.644123 from(436.555317,3+)  
**Elution from:** 22.535 to 22.535 scan no 1599 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1306.6421
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0059
Matched b ions: b(3)++, b(6)−98++, b(6)++, b(7)−98++, b(8)−98++, b(10)−98++
Matched y ions: y(7)++
Precursor origin neutral loss:

Peptide No.527

EPWHDLHSKIDGPAAYDVLTNFEERWLK
Confirmed sites: “@S:8,@Y:16,@T:20”
Ambiguous sites:

MS/MS Fragmentation of EPWHDLHSKIDGPAAYDVLTNFEERWLK
Found in AT2G42010.1, PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D

Match to Query 5278: 3605.554468 from(902.395893,4+)
Elution from: 63.634 to 63.634 scan no 6819 polarity:+
Peptide No. 528

EQAVWALGNVAGDSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of EQAVWALGNVAGDSPR
Found in AT3G06720.1, AT-IMP (Arabidopsis thaliana importin alpha); protein transporter

Match to Query 2122: 1748.785182 from(875.399867,2+)
Elution from: 50.310 to 50.310 scan no 5040 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1748.7882

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S14: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 69  **Expect:** 1.5e-006

**Matched b ions:** b(7), b(10), b(12), b(13)

**Matched y ions:** y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(12), y(13)-98

**Precursor origin neutral loss:** +

---

**Peptide No.529**

EQGNGQGESSDDEFDSR

**Confirmed sites:** @S:10

**Ambiguous sites:**

MS/MS Fragmentation of **EQGNGQGESSDDEFDSR**

Found in **AT1G65440.1, GTB1 (GLOBAL TRANSCRIPTION FACTOR GROUP B1); RNA binding / hydrolase, acting on ester bonds**

Match to Query 2775: 1935.673634 from(968.844093,2+)

Elution from: 22.839 to 22.839 scan no 1635 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1935.6755
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00034
Matched b ions: b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)−98, y(9), y(9)−98, y(11), y(13), y(15)++
Precursor origin neutral loss:

Peptide No.530

EQGNGQGEFFDDEFDSR
Confirmed sites: ”@S:9,@S:10”
Ambiguous sites:

MS/MS Fragmentation of EQGNGQGEFFDDEFDSR
Found in AT1G65440.1, GTB1 (GLOBAL TRANSCRIPTION FACTOR GROUP B1); RNA binding / hydrolase, acting on ester bonds

Match to Query 3742: 2015.639910 from(1008.827231,2+)  
Elution from: 25.874 to 25.874 scan no 2136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2015.6418
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00037
Matched b ions: b(9), b(15)
Matched y ions: y(4), y(5), y(8), y(9), y(9)−196, y(10), y(11)−98++, y(11)−98, y(11), y(13), y(15)−196++, y(15), y(15)+, y(16)−98++
Precursor origin neutral loss: +

Peptide No.531

ERDRSPLPPPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ERDRSPLPPPR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 1622: 1398.676659 from(467.232829.3+)
Elution from: 17.864 to 17.864 scan no 1015 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1398.6769
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.057
Matched b ions: b(4)++, b(5)--98++, b(5)--98, b(5), b(5)++, b(6)--98, b(6)--98++, b(7)--98++, b(8)++, b(9)--98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(6), y(6)++, y(8)++, y(8)--98++
Precursor origin neutral loss: +

Peptide No.532

ERGSPDYGR
Confirmed sites: @S:4  
Ambiguous sites:

MS/MS Fragmentation of ERGSPDYGR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 970: 1115.438816 from(558.726684,2+)
Elution from: 15.787 to 15.787 scan no 822 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1115.4397
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.003
Matched b ions: b(4), b(5), b(5)−98, b(6)
Matched y ions: y(3), y(4), y(5)
Precursor origin neutral loss: +

Peptide No.533

ERTSPDYGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ERTSPDYGR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 1098: 1159.465272 from(580.739912,2+) Elution from: 17.017 to 17.017 scan no 879 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1159.4659
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.015
Matched b ions: b(3), b(4)--98, b(4), b(5)--98, b(6), b(6)--98
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(7)+
Precursor origin neutral loss: +

Peptide No.534

ERTSPDYGR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of ERTSPDYGR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 852: 1159.464980 from(580.739766,2+)
Elution from: 17.048 to 17.048 scan no 869 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1159.4659
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0039
Matched b ions: b(3), b(4)−98, b(4), b(5)−98
Matched y ions: y(2), y(3), y(4), y(5), y(8)−98++
Precursor origin neutral loss: +

Peptide No.535

ERVASPENGAVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ERVASPENGAVR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 1520: 1363.623856 from(682.819204,2+)
Elution from: 18.705 to 18.705 scan no 1125 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1363.6245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:  
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 3.7e-005
Matched b ions: b(2), b(3), b(4), b(5)-98, b(7), b(8), b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.536
ESEVLSSVSPTESR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESEVLSSVSPTESR
Found in AT3G16620.1, ATTOC120 (Arabidopsis thaliana translocon outer complex protein 120); GTP binding / protein translo

Match to Query 2233: 1585.687092 from(793.850822,2+) Elution from: 32.310 to 32.310 scan no 2922 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1585.6872
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 2.1e-006
Matched b ions: b(4), b(5), b(6), b(8), b(9)-98, b(12), b(13)-98++
Matched y ions: y(2), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y (11)-98
Precursor origin neutral loss: +

Peptide No.537
ESEVLSSVSPTESR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of ESEVLSSVSPTESR
Found in AT3G16620.1, ATTOC120 (Arabidopsis thaliana translocon outer complex protein 120); GTP binding / protein translo

Match to Query 2505: 1585.686402 from(793.850477,2+) Elution from: 32.655 to 32.655 scan no 2896 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1585.6872
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.8e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(12)−98++, b(13)−98++
Matched y ions: y(2), y(3), y(4), y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)++, y(11), y(11)−98, y(11)−98++
Precursor origin neutral loss: +

Peptide No.538

ESLAAALALVHEHEESPKEK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of ESLAAALALVHEHEESPKEK
Found in AT5G25520.2, transcription elongation factor-related

Match to Query 4133: 2267.080521 from(756.700783,3+)
Elution from: 44.012 to 44.012 scan no 4514 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2267.0834
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.046
Matched b ions: b(13)++, b(18)-98++, b(19)++
Matched y ions: y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.539

ESLGASGSSSGNSFVAPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ESLGASGSSSGNSFVAPR
Found in AT5G21990.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 3032: 1788.766678 from(895.390615,2+)
Elution from: 35.270 to 35.270 scan no 3134 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1788.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 5.3e-006
Matched b ions: b(10)-98, b(15), b(15)-98, b(16), b(16)-98
Matched y ions: y(2), y(3), y(4), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(14), y(15)++, y(16) ++
Precursor origin neutral loss: +

Peptide No.540
ESLGASGSSGNSFVAPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ESLGASGSSGNSFVAPR
Found in AT5G21990.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 3031: 1788.766676 from(895.390614,2+)
Elution from: 37.163 to 37.163 scan no 3388 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1788.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 Expect: 2.7e-008
Matched b ions: b(6)++, b(13)−98, b(14)−98, b(14), b(15), b(15)−98, b(16), b(16)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)−98, y(12), y(13), y(13)−98, y(14), y(15)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.541
ESLGASGSSGNSFVAPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESLGASGSSGNSFVAPR
Found in AT5G21990.1, tetratricopeptide repeat (TPR)−containing protein

Match to Query 3210: 1788.766536 from(895.390544,2+)  
Elution from: 36.575 to 36.575 scan no 3531 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1788.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 2.1e-007
Matched b ions: b(6), b(8)++, b(9), b(10)−98, b(13)++, b(14), b(15), b(15)−98, b(16)−98, b(16)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11)−98++, y(11), y(12)−98, y(12), y(13)−98, y(13), y(14), y(15)++, y(15)−98++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.542

ESNIVDGSGSPGVK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ESNIVDGSGSPGVK
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 1981: 1424.617686 from(713.316119,2+)  
Elution from: 27.095 to 27.095 scan no 2145 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1424.6184
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9), b(10)-98, b(13)-98, b(13)++
Matched y ions: y(4), y(5), y(6)-98, y(6)++, y(6), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.543
ESNIVDGSGSPGVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of ESNIVDGSGSPGVK
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 1803: 1424.616834 from(713.315693,2+) Elution from: 26.690 to 26.690 scan no 2162 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1424.6184
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00019
Matched b ions: b(3), b(4), b(5), b(6), b(8)-98, b(8), b(9)-98, b(10)-98, b(13), b(13)++
Matched y ions: y(4), y(7)-98, y(8), y(8)-98, y(9)-98, y(10), y(10)-98, y(11), y(11)++, y(12)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.544
ESQSVSPSSILQK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of ESQSVSPSSILQK
Found in AT5G63640.1, VHS domain-containing protein / GAT domain-containing protein

Match to Query 2065: 1468.679600 from(735.347076,2+)
Elution from: 40.253 to 40.253 scan no 3802 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1468.6810

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 46 Expect: 0.00022

Matched b ions: b(5), b(6)-98, b(6), b(9)+, b(10)-98, b(11), b(11)-98, b(12), b(12)-98

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)+, y(8), y(9), y(9)-98, y(10), y(10)-98, y(10)+, y(11)+, y(11)-98++, y(12)+

Precursor origin neutral loss: +

Peptide No.545

ESQSVSPSSILQK

Confirmed sites: @S:9

Ambiguous sites:

MS/MS Fragmentation of ESQSVSPSSILQK

Found in AT5G63640.1, VHS domain-containing protein / GAT domain-containing protein

Match to Query 1856: 1468.680338 from(735.347445,2+)

Elution from: 39.140 to 39.140 scan no 3837 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1468.6810
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.015
Matched b ions: b(10)−98, b(12), b(12)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.546

ESSDEALVSMLASR
Confirmed sites: @S:2orS:3
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ESSDEALVSMLASR
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra
Match to Query 2444: 1573.669328 from(787.841940,2+) Elution from: 57.722 to 57.722 scan no 6105 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1573.6694
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1.4e-005
Matched b ions: b(5), b(7)-98, b(8), b(9), b(10)++, b(10), b(11), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.547

ESSDEALVSMLASR
Confirmed sites: @S:2 or S:3
Ambiguous sites: @S:2 or S:3

MS/MS Fragmentation of ESSDEALVSMLASR
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to erythrocyte membra

Match to Query 2148: 1589.662756 from(795.838654,2+)
Elution from: 46.781 to 46.781 scan no 4866 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1589.6644
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 Expect: 0.00046
Matched b ions: b(5), b(8), b(9), b(12)
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.548

ESSDEALVSMLASR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ESSDEALVSMLASR
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2630: 1573.667732 from(787.841142,2+)
Elution from: 57.325 to 57.325 scan no 6062 polarity:+

...
Monoisotopic mass of neutral peptide Mr(calc): 1573.6694
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 1.4e-007
Matched b ions: b(8), b(8)-98, b(10)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss:

Peptide No.549

ESSDEALVSMLASR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of ESSDEALVSMLASR
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2523: 1589.662164 from(795.838358,2+)
Elution from: 48.738 to 48.738 scan no 5120 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1589.6644
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.00065
Matched b ions:
Matched y ions: y(3), y(6), y(7), y(8), y(9)
Precursor origin neutral loss:

**Peptide No.550**

ESVTSPDRETPLTKD
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ESVTSPDRETPLTKD
Found in AT1G06070.1, bZIP transcription factor, putative (bZIP69)

Match to Query 2375: 1753.776060 from(585.599296,3+)
Elution from: 28.404 to 28.404 scan no 2382 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1753.7771  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 40 Expect: 0.001  
Matched b ions: b(7)++, b(9)++, b(10)−98++  
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(8)++, y(11)−98++, y(11)++, y(12)++, y(12)−98++, y(13)−98++, y(13)++, y(14)++  
Precursor origin neutral loss:  

Peptide No.551  
ETQSVGDELLNTLK  
Confirmed sites: @S:4  
Ambiguous sites:  

MS/MS Fragmentation of ETQSVGDELLNTLK  
Found in AT3G51740.1, IMK2 (INFLORESCENCE MERISTEM RECEPTOR–LIKE KINASE 2); ATP binding / kinase/ protein serine/threonin  

Match to Query 2310: 1625.752332 from(813.883442,2+)  
Elution from: 54.666 to 54.666 scan no 5842 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1625.7549
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0068
Matched b ions: b(6)++, b(7), b(8)−98
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(10), y(12)−98++
Precursor origin neutral loss: +

Peptide No.552

ETSDDEELAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ETSDDEELAR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 933: 1243.459626 from(622.737089,2+)  
Elution from: 21.254 to 21.254 scan no 1441 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.4605
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0049
Matched b ions:
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.553
ETSDDEELAR
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of ETSDDEELAR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 1086: 1243.459472 from(622.737012,2+)
Elution from: 21.296 to 21.296 scan no 1476 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.4605
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.044
Matched b ions:
Matched y ions: y(2), y(3), y(4), y(6), y(7)
Precursor origin neutral loss:

Peptide No.554

EVDFLVKSPKEDCLEVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EVDFLVKSPKEDCLEVK
Found in AT3G58110.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42370.1);
similar to Os06g0538200 [Oryz

Match to Query 3868: 2113.998645 from(705.673491,3+)
Elution from: 44.216 to 44.216 scan no 4552 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2114.0006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0017
Matched b ions: b(4)++, b(5), b(12)−98++, b(13)++, b(14)−98++, b(15)−98++, b(15)++, b(16)−98++
Matched y ions: y(2), y(5), y(6), y(7), y(8)++, y(9)++, y(9), y(10)−98++, y(10)++, y(11)−98++, y(12)++
, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(15)++, y(15)−98++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.555

EVDSDEEFYMISGETK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EVDSDEEFYMISGETK
Found in AT1G63210.1, RNA binding / hydrolase, acting on ester bonds

Match to Query 3484: 1957.751758 from(979.883155,2+) 
Elution from: 52.678 to 52.678 scan no 5374 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1957.7540
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.2e-006
Matched b ions: b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12), b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(13), y(14), y(14)-98++, y(14)+, y(15)−98++, y(15)+
Precursor origin neutral loss: +

Peptide No.556

EVDSDEEFYMISGETK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EVDSDEEFYMISGETK
Found in AT1G63210.1, RNA binding / hydrolase, acting on ester bonds

Match to Query 2698: 1973.743850 from(987.879201,2+)
Elution from: 46.239 to 46.239 scan no 4440 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1973.7489
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(13)-98++, b(14), b(14)-98++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.557
EVEVTNVNSDGDQSDINSK
Confirmed sites: @S:9
Ambiguous sites:
MS/MS Fragmentation of EVEVTNVNSDGDQSDINSK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con
Match to Query 3222: 2128.877286 from(1065.445919,2+) Elution from: 29.072 to 29.072 scan no 2472 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2128.8797
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 94 Expect: 2.8e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9–98), b(10), b(12), b(13), b(13)–98, b(14), b(14)–98, b(15)–98, b(15)–98++, b(16), b(16)–98, b(17), b(17)–98, b(18), b(18)–98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(11)–98, y(11), y(12)–98, y(12), y(13), y(13)–98, y(14), y(14)–98, y(14)++, y(15), y(15)++, y(15)–98++, y(15)–98, y(16)++, y(16)–98++, y(16), y(16)–98, y(17)–98++, y(17)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.558

EVEVTNVNSDGQSDINSK
Confirmed sites: “@S:9,@S:14”
Ambiguous sites:

MS/MS Fragmentation of EVEVTNVNSDGQSDINSK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 3687: 2208.843336 from(1105.428944,2+)
Elution from: 31.192 to 31.192 scan no 2874 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2208.8460
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 3.7e-007
Matched b ions: b(6), b(7), b(8), b(9)−98, b(10), b(10)−98, b(12), b(13), b(14)−196, b(14)−98, b(14), b(15), b(16), b(16)−98, b(17), b(17)++, b(18)−196++, b(18)−98++
Matched y ions: y(3), y(4), y(5), y(6)−98, y(6), y(7)−98, y(7), y(8), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12)−98, y(12), y(12)−196, y(13), y(13)−98, y(13)−196++, y(14), y(14)−98, y(15)++, y(15), y(15)−98, y(16)−98++, y(16)++, y(16)−98, y(17)++, y(17)−98++, y(18)−98++, y(18)−196++
Precursor origin neutral loss: +

Peptide No.559

EVLSDVDSDNDGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EVLSDVDSDNDGR
Found in AT3G20410.1, CPK9 (CALMODULIN–DOMAIN PROTEIN KINASE 9); calcium- and calmodulin–dependent protein kinase/kinase

Match to Query 1870: 1499.576222 from(750.795387,2+)
Elution from: 33.792 to 33.792 scan no 3154 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1499.5777
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 6.9e-010
Matched b ions: b(5)-98, b(6)-98, b(6), b(7), b(8)-98, b(8), b(9), b(11), b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(11), y(11)-98, y(11)++, y(12)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.560

EVPSFIQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of EVPSFIQR
Found in AT3G08510.1, ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C

Match to Query 596: 1054.484324 from(528.249438,2+)
Elution from: 38.902 to 38.902 scan no 3839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1054.4848
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00051
Matched b ions: b(2)
Matched y ions: y(1), y(2), y(3), y(4), y(5)+, y(5), y(6)−98++, y(6)+, y(6)−98, y(6), y(7)−98++, y(7)−98, y(7)+
Precursor origin neutral loss: +

Peptide No.561
EVQLNGITFK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of EVQLNGITFK
Found in AT3G26935.1, zinc finger (DHHC type) family protein

Match to Query 1029: 1227.589538 from(614.802045,2+)
Elution from: 48.128 to 48.128 scan no 5033 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc): 1227.5900**

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

**Ions Score:** 21  **Expect:** 0.064

**Matched b ions:** b(3), b(8)-98++

**Matched y ions:** y(3), y(5), y(6), y(7), y(8)+, y(8)-98++, y(9)-98++

**Precursor origin neutral loss:**

---

**Peptide No. 562**

**EVSPDSGEFGSSR**

**Confirmed sites:** @S:3

**Ambiguous sites:**

**MS/MS Fragmentation of EVSPDSGEFGSSR**

Found in **AT2G27285.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27280.1); similar to PREDICTED: similar

Match to Query 1662: 1432.549394 from(717.281973,2+)

Elution from: 27.250 to 27.250 scan no 2272 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1432.5507
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 9.5e-007
Matched b ions: b(3), b(5)−98, b(7)−98, b(8)−98++, b(8)−98, b(9)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)−98++, y(11) +++, y(12)−98, y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.563
EVSPDSGEGFSSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EVSPDSGEGFSSR
Found in AT2G27285.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27280.1); similar to PREDICTED: similar

Match to Query 2103: 1432.546710 from(717.280631,2+) Elution from: 27.283 to 27.283 scan no 2339 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1432.5507
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 21 Expect: 0.029
Matched b ions: b(12)–98
Matched y ions: y(4), y(5), y(7), y(8), y(8)–98, y(10), y(10)++, y(11)++, y(11)–98++, y(11), y(12)–98++
Precursor origin neutral loss: +

Peptide No.564

EVSTLSDPGSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of EVSTLSDPGSPR
Found in AT4G05150.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 1193: 1323.570564 from(662.792558,2+)
Elution from: 25.130 to 25.130 scan no 1966 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1323.5707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 2.5e-005
Matched b ions: b(5), b(7), b(10), b(11)–98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(10)++, y(10), y(11)–98++
Precursor origin neutral loss: +

Peptide No.565

EVTAEMSEDFSEGEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 2241: 1782.652526 from(892.333539,2+) Elution from: 29.215 to 29.215 scan no 2392 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1782.6542
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 1.7e-005
Matched b ions: b(6), b(7)++, b(7), b(9), b(10), b(11)−98, b(12)−98++, b(12)−98, b(13)++, b(14)−98, b(14)
Matched y ions: y(3), y(4), y(5)−98, y(5), y(6)−98, y(6), y(7)−98, y(8)−98++, y(9)−98, y(9), y(10)−98, y(10), y(11)−98, y(11), y(12), y(12)−98++, y(12)−98, y(12)++, y(13)++, y(13)−98++, y(13)−98, y(14)−98++
Precursor origin neutral loss: +

Peptide No.566
EVTAEMSEDFSEGEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose−phosphate synthase

Match to Query 2186: 1782.652464 from(892.333508,2+) Elution from: 28.120 to 28.120 scan no 2364 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1782.6542
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6: Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
S7: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 60 Expect: 3.8e-006
Matched b ions: b(5), b(6), b(7)–98, b(8)–98, b(9)–98, b(10)–98, b(12), b(12)–98++, b(13)++, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)–98, y(9), y(10)–98, y(10), y(10)++, y(11), y(11)–98, y(11)–98++, y(11)++, y(12), y(12)++, y(12)–98++, y(13)–98++, y(13)++, y(13), y(14)–98++
Precursor origin neutral loss: +

Peptide No.567

EVTAEMSEDFSEGEK
Confirmed sites: “@S:7, @S:11”
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 3243: 1862.619718 from(932.317135,2+) 
Elution from: 30.497 to 30.497 scan no 2488 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1862.6206
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0011
Matched b ions: b(5), b(8)-98, b(9), b(10)-98, b(10), b(12)-98, b(12), b(14)
Matched y ions: y(4), y(5)-98, y(5), y(6)-98, y(8)-98++, y(9), y(9)-98, y(10), y(10)-196, y(12)-98++, y(12), y(13)-98++, y(14)-196++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.568
EVTAEMSEDFSEGEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2211: 1766.658150 from(884.336351,2+)
Elution from: 38.012 to 38.012 scan no 3534 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1766.6593
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 5.3e-010
Matched b ions: b(5), b(6), b(7), b(9), b(10), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(13)+, b(14)-98, b(14), b(14)-98++
Matched y ions: y(3), y(4), y(5)-98, y(6)-98, y(6), y(7)-98, y(7), y(8)-98++, y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)-98++, y(13), y(13)+, y(13)-98, y(14)-98++, y(14)-98
Precursor origin neutral loss: +

Peptide No.569
EVTAEMSEDFSEGEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2749: 1766.657962 from(884.336257,2+)
Elution from: 38.917 to 38.917 scan no 3799 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1766.6593
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 3.7e-005
Matched b ions: b(5), b(8)-98, b(10)-98, b(11)-98, b(12)-98, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(12)-98++, y(13)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.570

EVTAEMSEDSEGKEK
Confirmed sites: “@S:7, @S:11”
Ambiguous sites:

MS/MS Fragmentation of EVTAEMSEDSEGKEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 2395: 1846.623558 from(924.319055,2+)
Elution from: 39.699 to 39.699 scan no 3745 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1846.6256
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 3.2e-005
Matched b ions: b(5), b(6), b(7)–98++, b(7)–98, b(8), b(8)–98, b(9)–98, b(9), b(10)–98, b(10), b(11)–98, b(11)–196, b(12)–98, b(12)–196, b(13), b(13)–98, b(14)–98, b(14), b(14)–196++
Matched y ions: y(3), y(4), y(5)–98, y(5), y(5)++, y(6)–98, y(6), y(7)–98, y(7), y(8)–98++, y(8), y(9)–98, y(9), y(9)–196, y(10)–98, y(10), y(10)–196, y(10)–98++, y(11)–98, y(11), y(11)–98++, y(11)–196, y(12), y(12)–98, y(12)–196++, y(12)++, y(12)–98++, y(12)–196, y(13)–98++, y(13)–98, y(13), y(13)–196++, y(13)++, y(14)–98++, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.571
EVTAEMSEDFSEGEK
Confirmed sites: @T:3
Ambiguous sites:
MS/MS Fragmentation of EVTAEMSEDFSEGEK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 2203: 1782.652594 from(892.333573,2+)
Elution from: 29.163 to 29.163 scan no 2413 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1782.6542

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- T3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- M6 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983

**Ions Score:** 35 **Expect:** 0.0015

**Matched b ions:** b(3)-98, b(4)-98, b(5)-98, b(6)-98, b(8)-98, b(9), b(10)-98, b(11)-98, b(12)-98++, b(13)+++, b(14)-98, b(14), b(14)-98++

**Matched y ions:** y(3), y(5), y(6), y(7), y(10)+++, y(13)+++, y(13)-98++, y(13)-98, y(13), y(14)-98++, y(14)+

**Precursor origin neutral loss:** +

---

**Peptide No.572**

**EVTAEMSEDFSEGEK**

**Confirmed sites:** "@T:3,@S:11"

**Ambiguous sites:**

**MS/MS Fragmentation of EVTAEMSEDFSEGEK**

Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 2939: 1846.624786 from(924.319669,2+)

Elution from: 39.680 to 39.680 scan no 3900 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1846.6256
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
    S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.046
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(8)-98, b(10)-98, b(10)
Matched y ions: y(3), y(5)-98, y(5), y(6)-98, y(7)-98, y(7), y(8), y(13)-98++, y(13)-196++, y(13)+, y(14)-196++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.573
EYAQITALPRGSR
Confirmed sites: @Y:2
Ambiguous sites:

MS/MS Fragmentation of EYAQITALPRGSR
Found in AT5G39870.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28980.1); contains InterPro domain Prot

Match to Query 2645: 1540.739181 from(514.587003,3+)
Elution from: 33.586 to 33.586 scan no 3169 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.7399
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
Ions Score: 48 Expect: 0.00015
Matched b ions: b(3)++, b(3), b(4), b(4)++, b(5), b(5)++, b(6), b(6)++, b(7), b(7)++, b(8)++, b(8), b(12)
++
Matched y ions: y(5), y(5)++, y(6), y(6)++, y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++
Precursor origin neutral loss:

Peptide No.574
FADELIANAAYIGTPGK
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of FADELIANAAYIGTPGK
Found in AT3G52930.1, fructose-bisphosphate aldolase, putative

Match to Query 2863: 1829.856420 from(915.935486,2+)
Elution from: 54.258 to 54.258 scan no 5762 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1829.8600
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 1.6e-005
Matched b ions: b(8), b(11), b(12), b(13), b(14), b(15)-98
Matched y ions: y(4), y(5), y(8), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.575

FAQVSSDEEDDVPITR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of FAQVSSDEEDDVPITR
Found in AT4G11560.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 3106: 1886.792310 from(944.403431,2+)
Elution from: 39.695 to 39.695 scan no 3947 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1886.7935
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 1.8e-006
Matched b ions: b(6), b(7), b(8)–98, b(9), b(9)–98, b(10)–98, b(10), b(11), b(11)–98, b(12)–98, b(12), b(13)–98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(12)–98, y(13), y(13)–98, y(14)–98++
Precursor origin neutral loss: +

Peptide No. 576

FAQVSSDEEDDVPITR
Confirmed sites: “@S:5, @S:6”
Ambiguous sites:

MS/MS Fragmentation of FAQVSSDEEDDVPITR
Found in AT4G11560.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 3515: 1966.756786 from(984.385669,2+)
Elution from: 45.131 to 45.131 scan no 4437 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1966.7598
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00025
Matched b ions: b(8)-98, b(9), b(10)-98++, b(10), b(11)-98, b(12)-196, b(12)-98, b(12), b(13)-196,
  b(13)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(11), y(12), y(13)-98
Precursor origin neutral loss: +

Peptide No.577
FAQVSSDEEDDVPI TR
Confirmed sites:
Ambiguous sites: @S:5 or S:6

MS/MS Fragmentation of FAQVSSDEEDDVPI TR
Found in AT4G11560.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 3151: 1886.791150 from(944.402851,2+)
Elution from: 40.592 to 40.592 scan no 4029 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1886.7935
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 2e–007
Matched b ions: b(3), b(4), b(6), b(7)–98, b(7), b(8)–98, b(9)–98, b(9), b(10), b(10)–98, b(11), b(12)–98, b(12), b(13)–98++, b(13)–98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(12), y(12)–98, y(13), y(13)–98
Precursor origin neutral loss: +

Peptide No.578
FCFWENTPSPPR
Confirmed sites: ”@T:7,@S:9”
Ambiguous sites:

MS/MS Fragmentation of FCFWENTPSPPR
Found in AT4G02720.1, similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:AT1G20920.1); similar to Os

Match to Query 2959: 1696.613332 from(849.313942,2+) Elution from: 61.738 to 61.738 scan no 6498 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1696.6146
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 32 Expect: 0.002
Matched b ions: b(6), b(7)–98
Matched y ions: y(3), y(4), y(5)–98, y(5), y(6), y(7), y(7)–98, y(8), y(9)
Precursor origin neutral loss: +

Peptide No.579
FDDDSEDNDLSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of FDDDSEDNDLSR
Found in AT5G22120.1, nucleotide binding

Match to Query 1749: 1506.513904 from(754.264228,2+)
Elution from: 27.122 to 27.122 scan no 2210 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1506.5148
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 2.1e-009
Matched b ions: b(2), b(4), b(6)–98, b(7), b(7)–98, b(8)–98, b(8), b(9)–98, b(9), b(10)–98, b(10), b(10)–98++, b(10)++, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)–98, y(8), y(8)–98++, y(9)–98, y(9), y(9)–98++, y(10), y(10)–98, y(10)++, y(11)–98, y(11)–98++
Precursor origin neutral loss: +

Peptide No.580

FDDESDSDDIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of FDDESDSDDIR
Found in AT5G47490.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47480.1); similar to hypothetical prote

Match to Query 1351: 1392.471088 from(697.242820,2+)
Elution from: 27.895 to 27.895 scan no 2244 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1392.4718
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 6.2e-006
Matched b ions: b(2), b(3), b(4), b(5)−98++, b(6), b(9)−98, b(9), b(10)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98, y(7), y(8)−98, y(8), y(9)−98++, y(9), y(9)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.581
FDDEYDSDEITEDVPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of FDDEYDSDEITEDVPR
Found in AT4G25070.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G48860.2); similar to expressed protein

Match to Query 3579: 2023.754350 from(1012.884451,2+)
Elution from: 46.598 to 46.598 scan no 4849 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2023.7572
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.002
Matched b ions: b(6), b(9)−98, b(10)−98, b(10), b(13)++, b(13), b(14)−98
Matched y ions: y(4), y(5), y(6), y(11)−98, y(12), y(12)−98
Precursor origin neutral loss: +

Peptide No.582
FDDYDRDSESEEDNLGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of FDDYDRDSESEEDNLGR
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19710.1); similar to MAPK activating pr

Match to Query 3017: 2140.782382 from(1071.398467,2+)
Elution from: 32.974 to 32.974 scan no 2907 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2140.7858
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00018
Matched b ions: b(7), b(8), b(9), b(10), b(11)–98, b(12)–98, b(13)–98, b(13), b(16)++
Matched y ions: y(4), y(6), y(7), y(9), y(10)–98, y(12)–98++, y(13)–98++, y(14)–98++, y(14)++, y(15)–98++, y(15)++, y(16)–98++
Precursor origin neutral loss: +

Peptide No.583
FDDYDRDSESEEDNLGR
Confirmed sites: “@Y:4,@S:10”
Ambiguous sites:

MS/MS Fragmentation of FDDYDRDSESEEDNLGR
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19710.1); similar to MAPK activating pr

Match to Query 3816: 2220.750306 from(1111.382429,2+)
Elution from: 34.971 to 34.971 scan no 3271 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2220.7521
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y4 : Phospho (Y)
  S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00043
Matched b ions: b(7), b(8), b(9), b(10)-98, b(11)-98, b(12), b(12)+, b(13)-98, b(13), b(13)+, b(15)-98, b(15), b(15)+, b(16)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(14)-98++, y(14)+, y(15)-98++, y(15)+
Precursor origin neutral loss: 

Peptide No.584
FDELYRSSWAMDHCVNEGEVTKLK
Confirmed sites: “@Y:5,@S:8”
Ambiguous sites:

MS/MS Fragmentation of FDELYRSSWAMDHCVNEGEVTKLK
Found in AT4G03210.1, XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds

Match to Query 4034: 3089.266059 from(1030.762629,3+)
Elution from: 33.508 to 33.508 scan no 2952 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3089.2701
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.028
Matched b ions: b(7), b(9), b(10)++, b(12)++, b(14)++, b(15)−98++, b(18)−98++, b(22)−98++, b(23)−98++, b(23)++
Matched y ions: y(5), y(6), y(7)++, y(7), y(8), y(11), y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.585
FDFLHGIDSPASSPR
Confirmed sites: ”@S:9,@S:12”
Ambiguous sites:

MS/MS Fragmentation of FDFLHGIDSPASSPR
Found in AT4G11270.1, transducin family protein / WD-40 repeat family protein

Match to Query 3297: 1804.719732 from(903.367142,2+)
Elution from: 57.925 to 57.925 scan no 6173 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.7222

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- **S9**: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- **S12**: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 25 Expect: 0.019

Matched b ions: b(3), b(5), b(7), b(8), b(9)−98, b(9), b(11)−98, b(11), b(12)++, b(12)−98, b(13)−98, b(13)−196, b(14)−196

Matched y ions: y(2), y(5), y(6), y(6)−98, y(7)−98, y(7), y(8)−98, y(9)−98, y(9)−98, y(10), y(10)−98, y(11), y(13)−98++, y(13)++, y(14)++

Precursor origin neutral loss: +

---

**Peptide No. 586**

FDFLHGIDSPASSPR

Confirmed sites: "@S:9,@S:13"

Ambiguous sites:

MS/MS Fragmentation of FDFLHGIDSPASSPR

Found in AT4G11270.1, transducin family protein / WD-40 repeat family protein

Match to Query 2909: 1804.720934 from (903.367743, 2+)

Elution from: 58.894 to 58.894 scan no 6284 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.7222
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00077
Matched b ions: b(3), b(5), b(7), b(8), b(9)–98, b(9), b(11), b(11)–98, b(13)–196, b(13)–98, b(14)–196
Matched y ions: y(2), y(3), y(4), y(5), y(6)–98, y(6), y(7)–98, y(7), y(8)–98++, y(8), y(8)–98, y(10), y(10)–98, y(11)–98, y(11)++, y(11)–98++, y(12)–98++, y(13)–98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.587

FDGEESSPPDFDEDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of FDGEESSPPDFDEDR
Found in AT5G53310.1, myosin heavy chain-related

Match to Query 3322: 1830.660810 from(916.337681,2+)
Elution from: 38.847 to 38.847 scan no 3839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1830.6621
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 4.2e-005
Matched b ions: b(6)—98, b(7)—98, b(8)—98, b(10), b(10)—98, b(12), b(14)—98, b(14)
Matched y ions: y(3), y(4), y(5), y(8), y(9), y(10)—98, y(10), y(11)—98, y(13)++, y(13)—98++, y(14)++
Precursor origin neutral loss: +

Peptide No.588
FDLSSADSPPSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of FDLSSADSPPSK
Found in AT1G71860.1, PTP1 (PROTEIN TYROSINE PHOSPHATASE 1)

Match to Query 1405: 1329.548734 from(665.781643,2+)
Elution from: 34.943 to 34.943 scan no 3313 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1329.5490
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 5.9e-006
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8)–98, b(8), b(9)–98, b(11)–98
Matched y ions: y(3), y(4), y(5)–98, y(6), y(6)–98, y(7), y(7)–98, y(8), y(9), y(9)–98++, y(9)–98, y(10)+, y(10), y(11)–98
Precursor origin neutral loss: +

Peptide No.589
FDNYGPNSESDGDQPIDK
Confirmed sites: “@S:8,@S:10”
Ambiguous sites:

MS/MS Fragmentation of FDNYGPNSESDGDQPIDK
Found in AT2G19710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29440.1); similar to MAPK activating pr

Match to Query 3605: 2156.759888 from(1079.387220,2+)
Elution from: 36.711 to 36.711 scan no 3567 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2156.7612
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.024
Matched b ions: b(11), b(13), b(14), b(14)-98, b(15)-98, b(15)-196, b(16)-98++, b(16)-98, b(16)++
Matched y ions: y(4), y(5), y(7), y(9), y(13)-98, y(13), y(14)-98++, y(14), y(14)-196, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.590

FDQIGDDDSGFEPVSDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of FDQIGDDDSGFEPVSDK
Found in AT4G02510.1, TOC159 (translocon outer membrane complex 159)

Match to Query 3555: 2078.795612 from(1040.405082,2+)
Elution from: 44.931 to 44.931 scan no 4630 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2078.7993
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 5.2e-008
Matched b ions: b(3), b(4), b(6), b(8), b(9)-98, b(10), b(11)-98, b(12)-98, b(13)-98, b(13), b(14)-98, b(15), b(15)-98, b(16)-98++, b(16), b(17)
Matched y ions: y(3), y(5), y(6), y(7), y(9)+, y(9), y(10)-98, y(10), y(11)-98, y(12)-98, y(12), y(13), y(14), y(14)-98, y(15), y(16)-98++, y(16)++, y(17)
Precursor origin neutral loss: +

Peptide No.591

FDSEANGWHSDNELDSK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of FDSEANGWHSDNELDSK
Found in AT2G15900.1, phox (PX) domain-containing protein

Match to Query 3750: 2029.766790 from(1015.890671,2+)
Elution from: 34.279 to 34.279 scan no 3235 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2029.7690
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 4.3e-005
Matched b ions: b(8), b(9), b(10)-98, b(11)-98, b(11), b(12), b(13), b(13)-98, b(14), b(14)+, b(14)-98, b(15)-98, b(15), b(15)+, b(15)-98++, b(16)
Matched y ions: y(3), y(4), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)-98, y(12), y(12)-98++, y(12)-98, y(12)+, y(13)-98++, y(13), y(13)+, y(14)+, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.592

FDSEANGWHSDNELDSK
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of FDSEANGWHSDNELDSK
Found in AT2G15900.1, phox (PX) domain-containing protein

Match to Query 3041: 2029.765188 from(1015.889870,2+)
Elution from: 34.142 to 34.142 scan no 3219 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2029.7690
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0093
Matched b ions: b(7), b(8)−98, b(9)−98, b(11), b(13), b(14), b(15)−98, b(15), b(15)++, b(16)++
Matched y ions: y(6), y(7), y(8), y(9), y(14)++, y(14), y(15)++, y(15)−98++
Precursor origin neutral loss: +

Peptide No.593

FDSIGSTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FDSIGSTR
Found in AT1G21630.1, calcium–binding EF hand family protein

Match to Query 367: 961.390648 from(481.702600,2+)
Elution from: 24.863 to 24.863 scan no 1917 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 961.3906
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.01
Matched b ions: b(2), b(4)−98
Matched y ions: y(3), y(4), y(5), y(6)−98
Precursor origin neutral loss: +

Peptide No.594
FDWDHPLHLQPMSPTTVK
Confirmed sites:
Ambiguous sites: @T:15 or T:16

MS/MS Fragmentation of FDWDHPLHLQPMSPTTVK
Found in AT3G29360.1, UDP-glucose 6-dehydrogenase, putative

Match to Query 3588: 2244.006348 from(749.009392,3+)
Elution from: 48.988 to 48.988 scan no 4965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2244.0075
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.028
Matched b ions: b(5), b(7), b(8)++, b(8), b(10)++, b(10), b(14)++, b(17)++
Matched y ions: y(6), y(7), y(8), y(8)++, y(8)–98, y(10), y(10)++, y(12)++, y(13)–98++, y(14)++, y(14)–98++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.595

FDWDHPLHLQPMSPTTVK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of FDWDHPLHLQPMSPTTVK
Found in AT5G15490.1, UDP-glucose 6-dehydrogenase, putative

Match to Query 4095: 2228.010066 from(743.677298,3+)
Elution from: 53.476 to 53.476 scan no 5729 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2228.0126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.029
Matched b ions: b(5), b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(13)–98++, b(13)++, b(14)–98++, b(14)++, b(15)++, b(15)–98++
Matched y ions: y(5), y(6), y(7), y(8)++, y(8), y(8)–98, y(12)++, y(13)–98++, y(14)++, y(14)–98++, y(15)–98++, y(15)++, y(16)–98++, y(16)++
Precursor origin neutral loss: +

Peptide No.596

FEDQPGSPESLATR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of FEDQPGSPESLATR
Found in AT1G27460.1, NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding

Match to Query 2305: 1612.676562 from(807.345557,2+)
Elution from: 35.807 to 35.807 scan no 3391 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1612.6770
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 69 Expect: 8.8e-007
Matched b ions: b(2), b(3), b(4), b(7)-98, b(9)-98, b(11), b(12), b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(10)++, y(11)++, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.597
FEDQPGSPESLATR
Confirmed sites: “@S:7, @S:10”
Ambiguous sites:

MS/MS Fragmentation of FEDQPGSPESLATR
Found in AT1G27460.1, NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding

Match to Query 2386: 1692.641624 from(847.328088,2+)
Elution from: 39.173 to 39.173 scan no 3817 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1692.6433
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.022
Matched b ions: b(2), b(3), b(4), b(7)−98, b(9)−98, b(10)−196++, b(12)++, b(12)−98
Matched y ions: y(2), y(3), y(8), y(9), y(10)−98, y(10), y(12)++, y(12)−98
Precursor origin neutral loss: +

Peptide No.598
FEELTSSTGSNK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **FEELTSSTGSNK**
Found in **AT1G19870.1**, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 1495: 1378.565312 from(690.289932,2+)
Elution from: 27.160 to 27.160 scan no 2260 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1378.5653
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00043
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)
Matched y ions: y(4), y(4)–98, y(5), y(6)–98, y(7), y(7)–98, y(8), y(8)–98, y(9), y(10)–98, y(10)
Precursor origin neutral loss: +

Peptide No.599
FEELTSSTGSNK
Confirmed sites:
Ambiguous sites: @S:7orT:8

MS/MS Fragmentation of FEELTSSTGSNK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 1596: 1378.565478 from(690.290015,2+)
Elution from: 27.290 to 27.290 scan no 2276 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1378.5653
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.0089
Matched b ions: b(2), b(3), b(4), b(5), b(8)–98, b(9)–98
Matched y ions: y(6)–98, y(6), y(7)–98, y(8), y(8)–98, y(9), y(9)–98, y(10)
Precursor origin neutral loss: +

Peptide No.600

FENMTQVMGGSSR
Confirmed sites:
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of FENMTQVMGGSSR
Found in AT3G55005.1, TON1B (TONNEAU 1B)

Match to Query 2223: 1522.593656 from(762.304104,2+) Elution from: 42.517 to 42.517 scan no 4101 polarity:+

Elution from: 42.517 to 42.517 scan no 4101 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1522.5945
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.06
Matched b ions: b(7), b(8), b(12)++
Matched y ions: y(5)--98, y(5), y(6), y(7)--98, y(8), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.601
FENVFSSISSSPTK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of FENVFSSISSSPTK
Found in AT4G12770.1, heat shock protein binding

Match to Query 2266: 1608.706630 from(805.360591,2+)
Elution from: 49.450 to 49.450 scan no 5204 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1608.7072
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 1.6e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8)+, b(8), b(9), b(13)+
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(8)-98, y(8), y(9), y(10), y(10)-98++, y(11), y(11)-98, y(11)+, y(12), y(13)+
Precursor origin neutral loss:

Peptide No.602
FENVFSSISSSPTK
Confirmed sites: @S:11orT:13
Ambiguous sites: @S:11orT:13

MS/MS Fragmentation of FENVFSSISSSPTK
Found in AT4G12770.1, heat shock protein binding

Match to Query 2334: 1608.705578 from(805.360065,2+)+
Elution from: 49.419 to 49.419 scan no 5202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1608.7072
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 1.5e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(6), b(8)++, b(8), b(9), b(10)
Matched y ions: y(4), y(5), y(5)−98, y(6), y(7)−98, y(8)−98, y(8), y(9), y(10)−98++, y(10), y(11), y(11)−98, y(12)
Precursor origin neutral loss:

Peptide No.603

FFRQESTDSLAVGSPPK
Confirmed sites: @S:14
Ambiguous sites: @T:7

MS/MS Fragmentation of FFRQESTDSLAVGSPPK
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty-ac

Match to Query 3717: 2024.865258 from(675.962362,3+) Elution from: 42.817 to 42.817 scan no 4384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.8645
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.053
Matched b ions: b(6), b(9)++, b(10)++, b(10)−98++, b(11)−98++, b(11)++, b(12)−98++, b(12)++, b(12)−98++, b(12)−196++, b(14)−196++, b(15)−196++
Matched y ions: y(3), y(4), y(5)−98, y(6), y(6)−98, y(7)−98, y(7), y(9)++, y(12)−98++, y(12)++, y(13)−196++, y(15)++
Precursor origin neutral loss: +

Peptide No.604
FGAADTFKIPDEVDISQLS
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of FGAADTFKIPDEVDISQLS
Found in AT2G20900.2, diacylglycerol kinase, putative

Match to Query 3864: 2131.970148 from(1066.992350,2+)
Elution from: 65.197 to 65.197 scan no 6941 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2131.9714
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00084
Matched b ions: b(7)-98, b(8), b(9), b(14), b(15), b(16), b(17)+, b(17)-98++, b(18)-98++, b(18)+
Matched y ions: y(7), y(9), y(10), y(11), y(12), y(15), y(17)+
Precursor origin neutral loss: +

Peptide No.605
FGLGSSPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of FGLGSSPK
Found in AT3G10980.1, SAG20 (WOUND-INDUCED PROTEIN 12)

Match to Query 266: 871.382944 from(436.698748,2+)
Elution from: 29.553 to 29.553 scan no 2571 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 871.3840
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.012
Matched b ions: b(2), b(3), b(7)
Matched y ions: y(3), y(4), y(4)-98, y(5), y(6), y(6)+, y(7)
Precursor origin neutral loss:

Peptide No.606
FGMSPSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of FGMSPSK
Found in AT3G09840.1, CDC48 (CELL DIVISION CYCLE 48); ATPase

Match to Query 299: 832.316982 from(417.165767,2+)
Elution from: 24.632 to 24.632 scan no 1929 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 832.3190
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.015
Matched b ions: b(2), b(4), b(4)−98, b(5)−98, b(6)−98, b(6)
Matched y ions: y(3), y(4), y(4)−98, y(5), y(5)−98++, y(5)++, y(6), y(6)−98
Precursor origin neutral loss: +

Peptide No.607
FGQVSISNASR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of FGQVSISNASR
Found in AT3G58750.1, CSY2 (CITRATE SYNTHASE 2); citrate (SI)−synthase

Match to Query 1093: 1244.553698 from(623.284125,2+)
Elution from: 31.109 to 31.109 scan no 2793 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1244.5550
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 51 Expect: 6e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)
Matched y ions: y(2)-98, y(3)-98, y(4)-98, y(4), y(5)-98, y(5), y(6)-98++, y(6), y(6)-98, y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(8)-98++, y(9)-98++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.608

FGQVSISNASR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of FGQVSISNASR
Found in AT3G58750.1, CSY2 (CITRATE SYNTHASE 2); citrate (SI)- synthase

Match to Query 1364: 1244.554402 from(623.284477,2+) Elution from: 32.127 to 32.127 scan no 2917 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1244.5550
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.023
Matched b ions: b(3), b(4), b(5), b(6), b(7)−98, b(8), b(8)−98
Matched y ions: y(3), y(5)−98, y(5), y(6), y(6)−98, y(7)−98, y(7), y(7)−98++, y(8), y(8)−98
Precursor origin neutral loss: +

Peptide No.609

FGSSFLSSGLIR
Confirmed sites: “@S:3,@S:4”
Ambiguous sites:

MS/MS Fragmentation of FGSSFLSSGLIR
Found in AT2G39130.1, amino acid transporter family protein

Match to Query 2300: 1429.603392 from(715.808972,2+)
Elution from: 71.318 to 71.318 scan no 7228 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1429.6043
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0034
Matched b ions: b(5)-98, b(6)-98, b(6)-196, b(9)++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10)-196++
Precursor origin neutral loss: +

Peptide No.610

FGSWPDGLDSTVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FGSWPDGLDSTVK
Found in AT3G12050.1, Aha1 domain-containing protein

Match to Query 2473: 1487.631958 from(744.823255,2+)
Elution from: 52.502 to 52.502 scan no 5628 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1487.6333
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0029
Matched b ions: b(4)-98, b(9)-98, b(11)++, b(12)-98, b(12)-98++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)++, y(10)++, y(11)-98++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.611

FNDEFGCEEDTDDCDGEK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of FNDEFGCEEDTDDCDGEK
Found in AT1G17690.1, similar to zinc finger protein–related [Arabidopsis thaliana] (TAIR:AT5G63740.1); similar to Os05g0

Match to Query 3215: 2260.704298 from(1131.359425,2+)
Elution from: 37.108 to 37.108 scan no 3441 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2260.7086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 4.9e-007
Matched b ions: b(5), b(10), b(12), b(12)-98, b(13), b(15), b(16)-98
Matched y ions: y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(10)-98, y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)+++, y(14)-98++, y(14)-98, y(15)+++, y(16)+++
Precursor origin neutral loss: +

Peptide No.612

FNFDLSDEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of FNFDLSDEK
Found in AT4G27910.1, PHD finger protein-related / SET domain-containing protein (TX4)

Match to Query 1497: 1280.495046 from(641.254799,2+)
Elution from: 48.674 to 48.674 scan no 4889 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1280.4962
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 5.8e-006
Matched b ions: b(2), b(3), b(4)++, b(9), b(9)++
Matched y ions: y(3), y(4), y(5)--98, y(6)--98, y(7)--98, y(7), y(8), y(8)--98, y(9)--98, y(9)++
Precursor origin neutral loss: +

Peptide No.613
FNFDLSDESK
Confirmed sites: @S:6 or S:8
Ambiguous sites: @S:6 or S:8

MS/MS Fragmentation of FNFDLSDESK
Found in AT4G27910.1, PHD finger protein–related / SET domain–containing protein (TX4)

Match to Query 1099: 1280.494122 from(641.254337,2+) Elution from: 48.443 to 48.443 scan no 4677 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1280.4962
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.0071
Matched b ions: b(2), b(3), b(4)++, b(9)
Matched y ions: y(5)-98, y(6)-98, y(7)-98, y(7), y(8)++, y(8), y(8)-98, y(9)
Precursor origin neutral loss: +

Peptide No.614

FNVTIWYNSSYK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of FNVTIWYNSSYK
Found in AT3G47750.1, ATATH3 (ABC2 homolog 3); ATPase, coupled to transmembrane movement of substances

Match to Query 2643: 1600.696926 from(534.572918,3+)
Elution from: 24.828 to 24.828 scan no 1935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1600.6963
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0017
Matched b ions: b(4)++, b(4)−98, b(6)++, b(7)+, b(8)++, b(10)++, b(11)++, b(11)−98++
Matched y ions: y(7)++, y(10)++, y(11)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.615

FQEVDIEAEIAEVRGTERVMK
Confirmed sites: @T:16
Ambiguous sites:

MS/MS Fragmentation of FQEVDIEAEIAEVRGTERVMK
Found in AT2G26750.1, epoxide hydrolase, putative

Match to Query 4379: 2429.125038 from(810.715622,3+)
Elution from: 50.930 to 50.930 scan no 5371 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2429.1184
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.059
Matched b ions: b(6), b(7), b(8), b(12)+, b(14)+, b(16)+, b(16)-98+, b(17)+, b(20)-98++, b(20)++
Matched y ions: y(5)+, y(5), y(7)+, y(8)-98++, y(8)-98, y(8)-98++, y(9)-98, y(10)+, y(11)-98++, y(11)+, y(13)-98++, y(13)+, y(14)-98++, y(19)-98++, y(20)-98++, y(20)+
Precursor origin neutral loss: +

Peptide No.616
FREGDAKVSPLK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of FREGDAKVSPLK
Found in AT1G67820.1, protein phosphatase 2C, putative / PP2C, putative

Match to Query 2206: 1425.700698 from(476.240842,3+)
Elution from: 25.549 to 25.549 scan no 2053 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1425.7017
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.017
Matched b ions: b(5), b(6), b(9)–98++, b(9)++, b(10)–98++, b(11)–98++
Matched y ions: y(3), y(4)–98, y(5), y(5)–98, y(6)++, y(7)++, y(7)–98++, y(9)–98++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.617
FRESGDSDDDGEDDRK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of FRESGDSDDDGEDDRK
Found in AT5G44200.1, CBP20 (CAP–BINDING PROTEIN 20); RNA binding

Match to Query 3208: 1921.695150 from(641.572326,3+)
Elution from: 16.697 to 16.697 scan no 877 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1921.6963
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 29 Expect: 0.0057
Matched b ions: b(5)++, b(7)−98, b(8)−98, b(9), b(9)−98++, b(9)++, b(10)−98, b(10), b(10)++
Matched y ions: y(2), y(3), y(4), y(6)++, y(7)++, y(8)++, y(9)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.618
FRESGDSDDGEGDRK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of FRESGDSDDGEGDRK
Found in AT5G44200.1, CBP20 (CAP-BINDING PROTEIN 20); RNA binding

Match to Query 2741: 1921.694217 from(641.572015,3+) 
Elution from: 16.542 to 16.542 scan no 839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1921.6963
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 1.6e-006
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(9)++, b(10)-98, b(10), b(10)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(13)-98++, y(13)++, y(14)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.619
FRSFKGDTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FRSFKGDTR
Found in AT5G62890.1, permease, putative

Match to Query 1344: 1192.538301 from(398.520043,3+)
Elution from: 19.190 to 19.190 scan no 1193 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1192.5390
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.059
Matched b ions: b(2), b(3)−98, b(4)−98, b(5)−98++, b(5)−98, b(5)++, b(7)++, b(7)−98++
Matched y ions: y(2), y(4), y(6)++
Precursor origin neutral loss: +

Peptide No.620
FRSLDFGER
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of FRSLDFGER
Found in AT2G18020.1, EMB2296 (EMBRYO DEFECTIVE 2296); structural constituent of ribosome

Match to Query 1506: 1205.522190 from(603.768371,2+)  
Elution from: 36.343 to 36.343 scan no 3566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1205.5230
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.01
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(4), b(5), b(6), b(8)
Matched y ions: y(2), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.621
FSDQPVMLDVYSPDR
Confirmed sites: @Y:11orS:12
Ambiguous sites: @Y:11orS:12

MS/MS Fragmentation of FSDQPVMLDVYSPDR
Found in AT5G10020.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 3322: 1847.777170 from(924.895861,2+)
Elution from: 55.163 to 55.163 scan no 5804 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1847.7801
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.056
Matched b ions: b(4), b(10)
Matched y ions: y(5), y(6), y(7)-98, y(8), y(9), y(11), y(12)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.622

FSDSSVQSDMK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of FSDSSVQSDMK
Found in AT5G02500.1, HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding

Match to Query 1180: 1309.488348 from(655.751450,2+)
Elution from: 33.050 to 33.050 scan no 2917 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1309.4897
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00046
Matched b ions: b(7)-98, b(9)-98, b(9), b(10), b(10)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.623

FSDSSVQSDMK
Confirmed sites: @S:4orS:5
Ambiguous sites: @S:4orS:5

MS/MS Fragmentation of FSDSSVQSDMK
Found in AT5G02500.1, HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding

Match to Query 1182: 1309.488648 from(655.751600,2+)
Elution from: 33.113 to 33.113 scan no 2901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1309.4897
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0047
Matched b ions: b(7), b(9), b(10)++
Matched y ions: y(2), y(4), y(5), y(6), y(8)−98, y(9)−98, y(9)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.624

FSFGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of FSFGR
Found in AT2G31800.1, ankyrin protein kinase, putative

Match to Query 111: 692.267534 from(347.141043,2+)
Elution from: 34.903 to 34.903 scan no 3319 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 692.2683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 17 Expect: 0.023
Matched b ions: b(2), b(2)-98, b(2)++, b(3)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)-98
Precursor origin neutral loss: +

Peptide No.625
FSGGAATAIDDEASSDSDK
Confirmed sites:
Ambiguous sites: @S:14orS:15

MS/MS Fragmentation of FSGGAATAIDDEASSDSDK
Found in AT2G39340.1, SAC3/GANP family protein

Match to Query 3530: 1922.740244 from(962.377398,2+)
Elution from: 33.393 to 33.393 scan no 2995 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1922.7418
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00023
Matched b ions: b(9), b(16)
Matched y ions: y(6)−98, y(7), y(9), y(10), y(10)++, y(11), y(12), y(13), y(14), y(15), y(17)++, y(17)−98
Precursor origin neutral loss: +

Peptide No.626
FSGSPVSTGTPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of FSGSPVSTGTPK
Found in AT2G26570.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42880.1); similar to unknown protein [A

Match to Query 1147: 1243.546986 from(622.780769,2+)
Elution from: 24.695 to 24.695 scan no 1925 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.5485
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00051
Matched b ions: b(4)−98, b(4), b(5)−98, b(5), b(6)−98, b(9)−98++, b(10)−98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10)−98++, y(10), y(10)−98
Precursor origin neutral loss: +

Peptide No.627
FSGSPVSTGTPK
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of FSGSPVSTGTPK
Found in AT2G26570.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42880.1); similar to unknown protein [A

Match to Query 1361: 1243.547362 from(622.780957,2+) Elution from: 25.549 to 25.549 scan no 2025 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.5485
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.01
Matched b ions: b(2), b(6), b(10)-98, b(10)+, b(10), b(11)-98++
Matched y ions: y(2), y(4)-98, y(5), y(7), y(8)-98++, y(8)-98, y(9)-98, y(10)-98++, y(10), y(10)-98, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.628

FSKKSPKPETAGTDEPGPYK
Confirmed sites: “@S:5,@Y:19”
Ambiguous sites:

MS/MS Fragmentation of FSKKSPKPETAGTDEPGPYK
Found in AT5G01590.1, similar to RNA binding protein [Bigelowiella natans] (GB:ABA27214.1); contains domain GYF domain (S

Match to Query 4534: 2323.017810 from(775.346546,3+)  
Elution from: 42.233 to 42.233 scan no 4260 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2323.0174
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y19 : Phospho (Y)
Ions Score: 27 Expect: 0.025
Matched b ions: b(4), b(6)−98, b(6), b(7)−98, b(7), b(8)++, b(8)−98, b(8), b(9)−98++, b(11)−98, b(13)−98, b(13)−98++, b(15)++, b(16)++, b(16)−98++, b(19)−98++
Matched y ions: y(4), y(7), y(8)++, y(12), y(12)++, y(13)++, y(14)++, y(15)++, y(17)++, y(19)−98++
Precursor origin neutral loss:

Peptide No.629

FSNYDSDDWETLSDDLRL
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of FSNYDSDDWETLSDDLRL
Found in AT5G05040.1, cysteine protease inhibitor

Match to Query 3894: 2156.821160 from(1079.417856,2+)
Elution from: 57.295 to 57.295 scan no 6103 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2156.8212
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0033
Matched b ions: b(5), b(7), b(8), b(10), b(12), b(14)−98, b(14), b(14)−98++
Matched y ions: y(5)−98, y(5), y(6)−98, y(7)−98, y(7), y(8), y(9)−98, y(9), y(10)−98, y(11), y(12), y (12)−98
Precursor origin neutral loss: +

Peptide No.630

FSNYDSDDWETLSDDL
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of FSNYDSDDWETLSDDL
Found in AT5G05040.1, cysteine protease inhibitor

Match to Query 4193: 2156.817226 from(1079.415889,2+)
Elution from: 62.259 to 62.259 scan no 6700 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2156.8212
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00011
Matched b ions: b(5), b(7), b(9)+, b(9)−98, b(9), b(10)−98, b(11)−98, b(11), b(12), b(12)−98, b(15)−98, b(15)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(13), y(13)−98, y(14)−98++, y(14)+, y(15)−98++, y(15)++
Precursor origin neutral loss: +

Peptide No.631

FSNYDSDDWETLSDDLR
Confirmed sites: @S:13
Ambiguous sites: @Y:4orS:6

MS/MS Fragmentation of FSNYDSDDWETLSDDLR
Found in AT5G05040.1, cysteine protease inhibitor

Match to Query 3300: 2236.783912 from(1119.399232,2+)
Elution from: 63.074 to 63.074 scan no 6132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2236.7875
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y4 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0014
Matched b ions: b(7), b(8), b(9), b(10), b(12), b(13)−98, b(15)−98
Matched y ions: y(5), y(5)−98, y(6)−98, y(7)−98, y(7), y(8)−98, y(8), y(9), y(10), y(11), y(15)−98++
Precursor origin neutral loss: +

Peptide No.632

FSPIGSGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of FSPIGSGR
Found in AT4G26650.1, RNA recognition motif (RRM)−containing protein

Match to Query 423: 899.389496 from(450.702024,2+)  
Elution from: 28.882 to 28.882 scan no 2525 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 899.3902
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.04
Matched b ions: b(2), b(3), b(5)−98++, b(7)−98++
Matched y ions: y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.633

FSQTLASYSGSD
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of FSQTLASYSGSD
Found in AT4G16770.1, oxidoreductase, 2OG-Fe(II) oxygenase family protein

Match to Query 1479: 1341.511890 from(671.763221,2+)
Elution from: 39.539 to 39.539 scan no 3923 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.5126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 4.5e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(6)+, y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.634

FSQTLASYSGSD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of FSQTLASYSGSD
Found in AT4G16770.1, oxidoreductase, 2OG-Fe(II) oxygenase family protein

Match to Query 1689: 1341.512328 from(671.763440,2+)
Elution from: 39.981 to 39.981 scan no 3766 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.5126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.00082
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)++
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.635

FSSLASSLGYR
Confirmed sites: "@S:7,@Y:10"
Ambiguous sites:

MS/MS Fragmentation of FSSLASSLGYR
Found in AT2G01490.1, phytanoyl–CoA dioxygenase (PhyH) family protein

Match to Query 1889: 1346.534676 from(674.274614,2+) Elution from: 32.441 to 32.441 scan no 2991 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1346.5308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y10: Phospho (Y)
Ions Score: 19 Expect: 0.061
Matched b ions: b(5)
Matched y ions: y(5)−98, y(6)−98, y(7)−98, y(9)++, y(10)−98
Precursor origin neutral loss: +

Peptide No.636
FSSLSLLPSQTSPK
Confirmed sites: @T:11orS:12orS:9
Ambiguous sites: @T:11orS:12orS:9

MS/MS Fragmentation of FSSLSLLPSQTSPK
Found in AT3G55270.1, MKP1 (MKP1); MAP kinase phosphatase

Match to Query 2206: 1570.762208 from(786.388380,2+)
Elution from: 51.330 to 51.330 scan no 5341 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1570.7644
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.02
Matched b ions: b(7)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(13)+
Precursor origin neutral loss:

Peptide No.637

FSTVGDSDEYNPTLPKPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of FSTVGDSDEYNPTLPKPR
Found in AT1G17745.1, PGDH (3-PHOSPHOGLYCERATE DEHYDROGENASE); phosphoglycerate dehydrogenase

Match to Query 4055: 2188.965084 from(730.662304,3+)
Elution from: 38.744 to 38.744 scan no 3866 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2188.9677
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00087
Matched b ions: b(9)-98, b(12)++, b(12)-98++
Matched y ions: y(4), y(5), y(7)+, y(10)+, y(12)-98++, y(13)+, y(14)+, y(15)-98++, y(15)+, y(16)-98++, y(16)+, y(17)-98++, y(17)+, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.638

FSVDERSARGGHSSLVMR
Confirmed sites: "@S:2,@S:13"
Ambiguous sites:

MS/MS Fragmentation of FSVDERSARGGHSSLVMR
Found in AT4G15755.1, C2 domain-containing protein

Match to Query 3935: 2149.912200 from(717.644676,3+)
Elution from: 29.430 to 29.430 scan no 2565 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2149.9129
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.022
Matched b ions: b(3)-98, b(4), b(4)-98, b(7)-98, b(12)-98++, b(12)++
Matched y ions: y(5), y(7)-98, y(7), y(8)-98, y(9)-98, y(10)-98++, y(12)++, y(12)-98++, y(14)++, y(14)-98, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.639

FSVSPVVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of FSVSPVVR
Found in AT1G56070.1, LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation

Match to Query 631: 969.469470 from(485.742011,2+)
Elution from: 39.259 to 39.259 scan no 3914 polarity:+
Peptide No.640

FSYNSYPDSAESSPR

Confirmed sites:
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of FSYNSYPDSAESSPR
Found in AT5G09620.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 2519: 1785.687024 from(893.850788,2+)
Elution from: 35.233 to 35.233 scan no 3283 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1785.6883
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00012
Matched b ions: b(3), b(5), b(6), b(8), b(9), b(10), b(11), b(13), b(13)−98, b(13)−98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)−98++, y(8), y(9), y(9)−98, y(9)++, y(10)−98, y(10), y(10)−98++, y(11), y(12), y(12)−98, y(13)−98++, y(13)++
Precursor origin neutral loss:

**Peptide No.641**

**FSYNSYPDSAESSPR**

Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **FSYNSYPDSAESSPR**
Found in **AT5G09620.1**, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 2877: 1785.686814 from(893.850683,2+)
Elution from: 35.219 to 35.219 scan no 3347 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1785.6883

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S13 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 75 Expect: 1.6e-007

Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)-98, b(13)-98++

Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)+, y(6)-98, y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)+, y(11), y(11)-98, y(12), y(13), y(13)-98++, y(13)+, y(14)+

Precursor origin neutral loss:

Peptide No.642

FSYNSYPDSAESSPR

Confirmed sites: ”@S:9,@S:13”

Ambiguous sites:

MS/MS Fragmentation of FSYNSYPDSAESSPR

Found in AT5G09620.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 3427: 1865.653614 from(933.834083,2+)

Elution from: 38.780 to 38.780 scan no 3830 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1865.6546
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 6.4e-007
Matched b ions: b(4), b(6), b(7), b(9)–98++, b(11), b(11)–98
Matched y ions: y(2), y(3), y(4)–98, y(4), y(5), y(6), y(7), y(7)–98, y(8), y(8)–98, y(9)++, y(9)–98, y(9), y(10), y(11), y(11)–196++, y(12), y(12)–196++, y(13)++, y(14)–196++, y(14)++
Precursor origin neutral loss: +

Peptide No.643

FSYNSYPDSTDSSPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of FSYNSYPDSTDSSPR
Found in AT5G64430.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 2926: 1801.682406 from(901.848479,2+)
Elution from: 34.976 to 34.976 scan no 3314 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1801.6832
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00038
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(10), b(10)++, b(11), b(12), b(13)−98, b(13)−98++
Matched y ions: y(2), y(3), y(4)−98, y(4), y(5)−98++, y(5), y(5)−98, y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)−98++, y(11)−98, y(12), y(12)−98++, y(12)++, y(13), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.644
FTFLGDVVPR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of FTFLGDVVPR
Found in AT5G50470.1, CCAAT-box binding transcription factor Hap5a, putative

Match to Query 1220: 1229.585907 from(410.869245,3+)
Elution from: 18.641 to 18.641 scan no 1092 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.5845
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.027
Matched b ions: b(3)−98, b(6)+++, b(6)−98++, b(7)−98++, b(7)+++, b(8)+++, b(8)−98++, b(9)−98++, b(9) +++,
Matched y ions: y(1), y(3), y(7)+
Precursor origin neutral loss: +

Peptide No.645
FTNPSPCNSPVLQR
Confirmed sites: “@S:5,@S:9”
Ambiguous sites:

MS/MS Fragmentation of FTNPSPCNSPVLQR
Found in AT1G09730.1, Ulp1 protease family protein

Match to Query 3153: 1775.709448 from(888.862000,2+)
Elution from: 35.012 to 35.012 scan no 3347 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1775.7103
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0032
Matched b ions: b(11), b(12)–98
Matched y ions: y(2), y(5), y(6), y(8), y(9)–98, y(9), y(10)++, y(10)–98++, y(11)–98++, y(11)+, y(11)–98, y(11), y(11)–196++, y(12)++
Precursor origin neutral loss: +

Peptide No.646

FTQGGYVDTGSPTVGSGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of FTQGGYVDTGSPTVGSGR
Found in AT2G45200.1, GOS12 (GOLGI SNARE 12); SNARE binding

Match to Query 3335: 1864.797240 from(933.405896,2+)
Elution from: 33.747 to 33.747 scan no 3138 polarity:+
**Peptide No.647**

FTQGGYVDTSPTVGSGR  
Confirmed sites: @T:13  
Ambiguous sites: 

MS/MS Fragmentation of FTQGGYVDTSPTVGSGR  
Found in AT2G45200.1, GOS12 (GOLGI SNARE 12); SNARE binding  

Match to Query 3253: 1864.797692 from(933.406122,2+)  
Elution from: 34.167 to 34.167 scan no 2985 polarity:+

---

**Monoisotopic mass of neutral peptide Mr(calc):** 1864.7992  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
**Ions Score:** 89 Expect: 9.2e-009  
**Matched b ions:** b(3), b(4), b(6), b(7)+, b(7)+, b(8)+, b(8), b(9), b(10), b(11)−98, b(11), b(12)−98, b(13)−98, b(13), b(14)−98, b(14), b(15), b(15)−98, b(16)−98, b(16)−98++  
**Matched y ions:** y(4), y(5), y(7), y(8), y(8)−98, y(9)−98, y(9), y(10), y(10)−98, y(11), y(11)−98+, y(11)−98, y(12), y(12)−98, y(13), y(14), y(14)+, y(15)−98, y(15), y(16)+, y(16)−98++  
**Precursor origin neutral loss:** +
Monoisotopic mass of neutral peptide Mr(calc): 1864.7992
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 6.5e-007
Matched b ions: b(3), b(6), b(7)++, b(7), b(8), b(9), b(10), b(11), b(13), b(13)−98, b(14)−98, b(14), b(15), b(16)−98, b(17)−98++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8), y(9)−98, y(9), y(10), y(10)−98, y(11)−98, y(11), y(12), y(12)−98, y(12)++, y(13), y(13)−98, y(14)−98, y(14), y(14)++, y(15), y(15)−98, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.648

FTQGYVDTGSPTVGSGR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of FTQGYVDTGSPTVGSGR
Found in AT2G45200.1, GOS12 (GOLGI SNARE 12); SNARE binding

Match to Query 2996: 1864.796958 from(933.405755,2+)
Elution from: 33.726 to 33.726 scan no 3104 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1864.7992  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 72 Expect: 4.5e-007  
Matched b ions: b(6), b(7), b(8), b(11)-98, b(13), b(14), b(14)-98  
Matched y ions: y(4), y(5), y(7), y(8), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(14), y(15), y(15)-98, y(16)-98++, y(16)++  
Precursor origin neutral loss: +  

Peptide No.649  
FTSDEDNADPEVVR  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of FTSDEDNADPEVVR  
Found in AT5G08610.1, DEAD box RNA helicase (RH26)  

Match to Query 2247: 1672.661598 from(837.338075,2+)  
Elution from: 31.362 to 31.362 scan no 2771 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1672.6617
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 7.6e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8), b(9), b(9)-98, b(10)+, b(12), b(12)-98, b(13), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++, y(12)-98, y(12), y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.650
FTSDEDNADPEVVR
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of FTSDEDNADPEVVR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2785: 1672.660844 from(837.337698,2+)
Elution from: 32.446 to 32.446 scan no 2960 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1672.6617
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 5.4e-007
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6), b(8), b(9), b(10)-98, b(11), b(11)+, b(12), b(13), b(13)-98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11), y(13)-98++
Precursor origin neutral loss:

Peptide No.651

FTSDEDNADPEVVRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FTSDEDNADPEVVRR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2949: 1828.762350 from(915.388451,2+)
Elution from: 27.701 to 27.701 scan no 2333 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1828.7628

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 35 Expect: 0.0028

Matched b ions: b(5), b(7)−98, b(8), b(9), b(9)−98, b(10)−98, b(10)++, b(11)++

Matched y ions: y(6)++, y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)−98++, y(13)++

Precursor origin neutral loss: +

Peptide No.652

FTSEDVMQNVD
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FTSEDVMQNVD
Found in AT3G49910.1, 60S ribosomal protein L26 (RPL26A)

Match to Query 1300: 1363.498864 from(682.756708,2+)
Elution from: 45.534 to 45.534 scan no 4364 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1363.5003
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 2.2e-005
Matched b ions: b(4), b(5), b(6), b(6)−98, b(7), b(7)−98, b(8), b(8)−98, b(9), b(9)++, b(9)−98, b(10)++, b(10)−98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(9)++, y(9)−98
Precursor origin neutral loss: +

Peptide No.653
FVASGGANVGDSPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of FVASGGANVGDSPR
Found in AT4G35240.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17110.1);
similar to Os09g0547300 [Oryz

Match to Query 1724: 1412.606918 from(707.310735,2+)
Elution from: 25.608 to 25.608 scan no 2048 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1412.6085
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2e-007
Matched b ions: b(2), b(9), b(10), b(11), b(12)−98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(6)−98, y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13)−98++, y(13)−98
Precursor origin neutral loss: +

Peptide No.654

FVYDSEDEEIVEAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of FVYDSEDEEIVEAK
Found in AT5G66230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G51230.1); similar to Sugar transporter

Match to Query 3032: 1751.717802 from(876.866177,2+)
Elution from: 46.162 to 46.162 scan no 4684 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1751.7178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 9.8e-009
Matched b ions: b(5)++, b(6)-98, b(7), b(8)-98, b(9)-98, b(10)-98, b(11), b(11)-98, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)-98++, y(12), y(12)++, y(12)-98, y(13)-98++, y(13)-98
Precursor origin neutral loss: +

Peptide No.655
FYMEPETSDGSMASGSMAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of FYMEPETSDGSMASGSMAR
Found in AT1G48410.1, AGO1 (ARGONAUTE 1)

Match to Query 3967: 2219.818044 from(1110.916298,2+)
Elution from: 43.963 to 43.963 scan no 4505 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2219.8210
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 2.6e-008
Matched b ions: b(4), b(7), b(14), b(14)++, b(15), b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(12), y(13)–98, y(13), y(14), y(14)–98, y(15), y(15)++, y(16)+, y(16)+, y(16)–98, y(16), y(16)–98++, y(17)–98++, y(18)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.656
FYVIYSFFFVR
Confirmed sites: “@Y:2.@S:6”
Ambiguous sites:
MS/MS Fragmentation of FYVIYSFFFVR
Found in AT4G16590.1, ATCSLA01 (Cellulose synthase-like A1); glucosyltransferase/transferase, transferring glycosyl grou

Match to Query 2820: 1646.695404 from(824.354978,2+)
Elution from: 27.915 to 27.915 scan no 2376 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1646.6975
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.047
Matched b ions: b(3), b(4), b(5)
Matched y ions:
Precursor origin neutral loss: +

Peptide No.657

GALLQDSEEEDG
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GALLQDSEEEDG
Found in AT5G64010.1, unknown protein

Match to Query 1242: 1341.496986 from(671.755769,2+)
Elution from: 36.161 to 36.161 scan no 3320 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.4973
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0067
Matched b ions: b(4), b(7), b(8), b(9), b(10), b(10)+, b(11)+
Matched y ions: y(7), y(8)
Precursor origin neutral loss: +

Peptide No.658
GANSDTNSDTESIASDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GANSDTNSDTESIASDR
Found in AT5G47910.1, RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)

Match to Query 2924: 1818.689108 from(910.351830,2+)
Elution from: 24.133 to 24.133 scan no 1850 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.6905
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 5.3e-009
Matched b ions: b(5)–98, b(7)–98, b(8)–98, b(8), b(9)–98, b(10)–98, b(13)–98, b(14)–98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)
Precursor origin neutral loss: +

Peptide No.659

GANSDTNSDTESIASDR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GANSDTNSDTESIASDR
Found in AT5G47910.1, RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)

Match to Query 2292: 1818.688520 from(910.351536,2+)
Elution from: 23.930 to 23.930 scan no 1726 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.6905
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 6.9e-009
Matched b ions: b(5), b(8), b(9)−98, b(10), b(11)−98, b(12), b(13)−98, b(14), b(14)−98, b(15), b(16)−98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)−98, y(13), y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No. 660
GASDIDSEDEFYDVER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GASDIDSEDEFYDVER
Found in AT3G55020.1, RabGAP/TBC domain-containing protein

Match to Query 2527: 1925.719234 from(963.866893,2+)
Elution from: 47.445 to 47.445 scan no 4751 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1925.7204
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 4.4e-008
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(12), b(12)-98, b(13), b(14), b(14)-98, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.661

GASDIDSEDEFYDVER
Confirmed sites: "@S:3,@S:7"
Ambiguous sites:

MS/MS Fragmentation of GASDIDSEDEFYDVER
Found in AT3G55020.1, RabGAP/TBC domain-containing protein

Match to Query 2738: 2005.685130 from(1003.849841,2+)
Elution from: 51.069 to 51.069 scan no 5127 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2005.6867
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 6.8e-007
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7)+, b(8)-196, b(8)-98, b(9), b(9)-98, b(10)-98++, b(10)-98, b(10)-196, b(11)-196, b(11)-98, b(11), b(12)-98, b(12), b(12)-196, b(13), b(13)-98, b(14)-98, b(14), b(15)-98, b(15), b(15)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(13), y(13)+, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.662
GASDIDSEDEFYDVER
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of GASDIDSEDEFYDVER
Found in AT3G55020.1, RabGAP/TBC domain-containing protein

Match to Query 2503: 1925.719106 from(963.866829,2+)
Elution from: 45.431 to 45.431 scan no 4517 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1925.7204
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 3.8e-009
Matched b ions: b(4), b(5), b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)+, b(9), b(10)-98, b(10), b
(10)-98++, b(11)-98, b(11), b(11)+++, b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98, b(15)-98++,
b(15), b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10)-98, y(10), y(10)+, y(11)-98, y(11), y(11)
++, y(11)-98++, y(12)-98++, y(12)-98, y(12)+++, y(13)+++, y(13), y(13)-98++, y(13)-98, y(14)-98++,
y(14)+++, y(15)+++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.663
GASPVAAYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GASPVAAYR
Found in AT4G25500.1, ATRSP35 (Arabidopsis thaliana arginine/serine–rich splicing factor 35); RNA binding

Match to Query 394: 970.427028 from(486.220790,2+)
Elution from: 23.135 to 23.135 scan no 1719 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc): 970.4273**

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 43  **Expect:** 0.00016

**Matched b ions:** b(3), b(6)-98, b(7)-98
**Matched y ions:** y(2), y(3), y(4), y(5), y(5)+, y(6), y(6)+, y(7)-98++, y(7)+, y(8)-98++

**Precursor origin neutral loss:** +

---

**Peptide No.664**

GATSGPLDPPAGEISR

**Confirmed sites:** @S:4

**Ambiguous sites:**

**MS/MS Fragmentation of GATSGPLDPPAGEISR**

Found in AT2G35350.1, PLL1 (POLTERGEIST LIKE 1); protein phosphatase type 2C

**Match to Query 2280:** 1603.722488 from(802.868520,2+)

**Elution from:** 37.890 to 37.890 scan no 3670 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1603.7243
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.002
Matched b ions: b(5)-98, b(7)-98, b(7), b(8), b(8)-98, b(11), b(13)-98++, b(14)-98, b(15)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(12)++, y(13)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.665

GAYTDITRKSIDATTSSK
Confirmed sites: "@S:10,@T:15,@S:16"
Ambiguous sites: @Y:3orT:4

MS/MS Fragmentation of GAYTDITRKSIDATTSSK
Found in AT2G35880.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32330.1); similar to putative BRI1-KD

Match to Query 3027: 2146.798185 from(716.606671,3+)
Elution from: 52.578 to 52.578 scan no 5092 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2146.8027
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.046
Matched b ions: b(5)++, b(7)−98, b(11)++, b(13)−196++, b(14)++, b(14)−98++, b(15)++, b(15)−196++, b(15)−98++, b(16)++, b(16)−98++
Matched y ions: y(6)−98, y(7)−196
Precursor origin neutral loss: +

Peptide No.666

GAYTDITRKSIDATTSK
Confirmed sites: "@T:7,@S:10,@T:15,@S:16"
Ambiguous sites:

MS/MS Fragmentation of GAYTDITRKSIDATTSK
Found in AT2G35880.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32330.1); similar to putative BRI1−KD i

Match to Query 3065: 2146.798650 from(716.606826,3+)
Elution from: 52.546 to 52.546 scan no 5080 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2146.8027
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.036
Matched b ions: b(11)++, b(14)++, b(15)++, b(16)++, b(16)−98++
Matched y ions: y(6)−98, y(13)++
Precursor origin neutral loss: +

Peptide No.667

GCDPNSPEFDVQAGVNPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GCDPNSPEFDVQAGVNPR
Found in AT5G18420.1, similar to expressed protein [Oryza sativa (japonica cultivar−group)] (GB:ABA96658.1); similar to O

Match to Query 3628: 2037.825082 from(1019.919817,2+) Elution from: 39.718 to 39.718 scan no 3947 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2037.8251
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00057
Matched b ions: b(6)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(12)-98, b(15)-98, b(16), b(17)-98
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(12), y(15)+, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.668

GCFDISEDEDNATTPDWK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GCFDISEDEDNATTPDWK
Found in AT5G14720.1, protein kinase family protein

Match to Query 3994: 2178.804330 from(1090.409441,2+)
Elution from: 50.063 to 50.063 scan no 5237 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2178.8089
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 78 Expect: 1e-007
Matched b ions: b(5), b(7)–98, b(10)–98, b(11), b(12)–98, b(13)–98, b(14), b(14)–98, b(14)++,
b(15)–98, b(15)–98++, b(16), b(16)–98++, b(16)–98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(12), y(13), y(15), y(16)–98++
Precursor origin neutral loss: +

Peptide No.669

GCFSCFDSSDDEK
Confirmed sites: @S:8 or S:9
Ambiguous sites: @S:8 or S:9

MS/MS Fragmentation of GCFSCFDSSDDEK
Found in AT5G13160.1, PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase

Match to Query 2563: 1632.510180 from (817.262366, 2+)
Elution from: 37.178 to 37.178 scan no 3390 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.5109
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 1.3e-007
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(10), b(11), b(12), b(12)–98
Matched y ions: y(2), y(3), y(4), y(6), y(6)–98, y(7), y(7)–98, y(8), y(8)–98, y(9), y(9)–98, y(9)++, y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.670
GCFSCFDSSDDEK
Confirmed sites: ”@S:8,@S:9”
Ambiguous sites:

MS/MS Fragmentation of GCFSCFDSSDDEK
Found in AT5G13160.1, PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase

Match to Query 3103: 1712.478058 from(857.246305,2+) 
Elution from: 39.500 to 39.500 scan no 3965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1712.4772
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.0053
Matched b ions: b(4), b(6), b(11), b(11)-98
Matched y ions: y(6)-196, y(6)-98, y(6), y(7), y(7)-196, y(8), y(9), y(10), y(10)-196, y(11)-196++
Precursor origin neutral loss: +

Peptide No.671
GCFSCFDSSDDEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GCFSCFDSSDDEK
Found in AT5G13160.1, PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase

Match to Query 2737: 1632.510014 from(817.262283,2+) 
Elution from: 36.891 to 36.891 scan no 3574 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.5109
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 2.2e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)−98, b(10), b(11), b(12), b(12)−98
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(11)++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.672
GDFVAKEEDEWSDGWK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of GDFVAKEEDEWSDGWK
Found in AT1G05460.1, SDE3 (SILENCING DEFECTIVE)

Match to Query 2972: 1976.780200 from(989.397376,2+)
Elution from: 46.938 to 46.938 scan no 4740 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1976.7829
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 3.4e-008
Matched b ions: b(5), b(7), b(8), b(10), b(11), b(12)-98, b(13)-98, b(15)-98, b(15)-
98++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(9)-98, y(10)-98, y (11)-98, y(12)-98++, y(12)-98, y(12)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.673
GDLTPEELK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of GDLTPEELK
Found in AT1G62740.1, stress-inducible protein, putative

Match to Query 648: 1080.473202 from(541.243877,2+)
Elution from: 33.449 to 33.449 scan no 3075 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1080.4740
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 34 Expect: 0.0016
Matched b ions: b(3), b(4)−98, b(4), b(5)+, b(5)−98, b(6)−98, b(7)−98, b(7), b(8)−98
Matched y ions: y(2), y(3), y(4)+, y(5), y(6), y(7)+, y(7), y(7)−98++
Precursor origin neutral loss: +

Peptide No. 674

GDPSSPHVPEESVKK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GDPSSPHVPEESVKK
Found in AT1G76510.1, ARID/BRIGHT DNA-binding domain-containing protein

Match to Query 2549: 1671.749331 from (558.257053, 3+)
Elution from: 21.208 to 21.208 scan no 1457 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1671.7505  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 24 Expect: 0.03  
Matched b ions: b(2), b(4), b(8)–98, b(10)–98++, b(12)++  
Matched y ions: y(7)++, y(8)++, y(9)++, y(10)++, y(12)++, y(13)++, y(13)–98++, y(14)–98++  
Precursor origin neutral loss: +

Peptide No.675

GEANISYICSR  
Confirmed sites: @Y:7  
Ambiguous sites:  

MS/MS Fragmentation of GEANISYICSR  
Found in AT2G30980.1, shaggy-related protein kinase delta / ASK-delta / ASK-dzeta (ASK4)  

Match to Query 1599: 1348.547428 from(675.280990,2+)  
Elution from: 32.453 to 32.453 scan no 2934 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1348.5482
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 72 Expect: 2.9e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)+, y(7), y(8), y(8)+, y(9)+, y(9)
Precursor origin neutral loss:

Peptide No.676
GEATLDRSQGQDLGPVTR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GEATLDRSQGQDLGPVTR
Found in AT5G04990.1, sad1/unc-84 protein–related

Match to Query 3405: 1978.909686 from(660.643838,3+)
Elution from: 31.615 to 31.615 scan no 2829 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1978.9109
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00052
Matched b ions: b(5), b(8)-98, b(11)-98++, b(11)+, b(12)-98++, b(13)-98++, b(13)+, b(14)+, b(14)-98++, b(15)-98++, b(15)+, b(16)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)+, y(9)+, y(12)-98++, y(12)+, y(13)+, y(13)-98++, y(14)+, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No. 677
GELLLVSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GELLLVSK
Found in AT3G45330.1, lectin protein kinase family protein

Match to Query 555: 937.485680 from(469.750116,2+), 352.485680 from(286.38058+2+)
Elution from: 29.945 to 29.945 scan no 2697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 937.4885
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0021
Matched b ions: b(2), b(3), b(4), b(5)
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.678

GELSDEEGEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GELSDEEGEEK
Found in AT4G18260.1, cytochrome B561-related

Match to Query 1161: 1300.469122 from(651.241837,2+)
Elution from: 23.036 to 23.036 scan no 1580 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1300.4707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0014
Matched b ions: b(7)-98, b(9)-98, b(9), b(10)-98, b(10)++
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9)++, y(9), y(9)-98++, y(9)-98
Precursor origin neutral loss: +

Peptide No.679

GEPNISYICSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of GEPNISYICSR
Found in AT1G06390.1, GSK1 (GSK3/SHAGGY-LIKE PROTEIN KINASE 1); kinase

Match to Query 1658: 1374.563210 from(688.288881,2+) Elution from: 37.286 to 37.286 scan no 3589 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1374.5639
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 69 Expect: 6.1e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(9)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9)++, y(9)
Precursor origin neutral loss:

Peptide No.680

GEPNVSYICSR
Confirmed sites:
Ambiguous sites: @S:10orY:7

MS/MS Fragmentation of GEPNVSYICSR
Found in AT1G09840.1, shaggy-related protein kinase kappa / ASK-kappa (ASK10)

Match to Query 1759: 1360.547766 from(681.281159,2+)
Elution from: 32.867 to 32.867 scan no 2810 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1360.5482
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0085
Matched b ions: b(4), b(5), b(6)
Matched y ions: y(5), y(6), y(7), y(7)-98, y(9)++, y(9)
Precursor origin neutral loss: +

Peptide No.681

GEPNVSYICSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GEPNVSYICSR
Found in AT1G09840.1, shaggy-related protein kinase kappa / ASK-kappa (ASK10)

Match to Query 1510: 1360.547714 from(681.281133,2+)
Elution from: 31.606 to 31.606 scan no 2864 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1360.5482
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0025
Matched b ions: b(5), b(6), b(7), b(8)++, b(10)++
Matched y ions: y(2), y(4), y(6), y(6)−98, y(7), y(7)−98, y(9)++, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.682

GEPNVSYICSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of GEPNVSYICSR
Found in AT1G09840.1, shaggy–related protein kinase kappa / ASK–kappa (ASK10)

Match to Query 1516: 1360.546964 from(681.280758,2+)
Elution from: 32.146 to 32.146 scan no 2900 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1360.5482
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 42 Expect: 0.00035
Matched b ions: b(5), b(6), b(7), b(8)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9)
Precursor origin neutral loss: +

Peptide No.683

GERPAFTPQSGNFR
Confirmed sites: "@T:7,@S:10"
Ambiguous sites:

MS/MS Fragmentation of GERPAFTPQSGNFR
Found in AT1G48920.1, nucleolin, putative

Match to Query 2675: 1722.690558 from(862.352555,2+)
Elution from: 34.732 to 34.732 scan no 3248 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1722.6916
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.028
Matched b ions: b(3), b(6), b(7)−98, b(7), b(9), b(9)+, b(10)−196, b(10)−98
Matched y ions: y(4), y(5), y(6), y(7), y(7)−98, y(8)+, y(10), y(11)−98, y(11), y(12)−196++
Precursor origin neutral loss: +

Peptide No.684
GESEPIAAAAAVAGPSSPQSR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of GESEPIAAAAAVAGPSSPQSR
Found in AT4G35890.1, La domain-containing protein

Match to Query 3769: 2031.923208 from(1016.968880,2+)
Elution from: 40.085 to 40.085 scan no 3996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2031.9262
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 6.4e-008
Matched b ions: b(9), b(11), b(12), b(13), b(14), b(17)−98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(12), y(13), y(14), y(15), y(17)++
Precursor origin neutral loss: +

Peptide No.685

GESEPIAAAAAVAGPSSPQSR
Confirmed sites: 
Ambiguous sites: @S:17orS:20

MS/MS Fragmentation of GESEPIAAAAAVAGPSSPQSR
Found in AT4G35890.1, La domain-containing protein

Match to Query 3701: 2031.922768 from(1016.968660,2+) 
Elution from: 40.656 to 40.656 scan no 3855 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2031.9262
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 8.8e-005
Matched b ions: b(8), b(11), b(12), b(13), b(14), b(16)
Matched y ions: y(5), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(12), y(13), y(14), y(18)−98++
Precursor origin neutral loss:

Peptide No.686

GESSLEPDSTPSSPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GESSLEPDSTPSSPK
Found in AT4G20400.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 2304: 1596.656604 from(799.335578,2+)
Elution from: 25.187 to 25.187 scan no 1953 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1596.6556
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0047
Matched b ions: b(5), b(6), b(9), b(10), b(13)−98
Matched y ions: y(3), y(4)−98, y(5), y(6), y(7), y(8)−98++, y(9), y(9)−98, y(10), y(11), y(12), y(14)++
Precursor origin neutral loss: +

Peptide No.687

GESELLEPDSTPSSPK
Confirmed sites: "@S:9,@S:13"
Ambiguous sites:

MS/MS Fragmentation of GESELLEPDSTPSSPK
Found in AT4G20400.1, transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein

Match to Query 3012: 1676.620218 from(839.317385,2+) Elution from: 26.336 to 26.336 scan no 2178 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1676.6219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0046
Matched b ions: b(6), b(8), b(10)−98, b(12), b(12)−98++, b(14)++
Matched y ions: y(5), y(6), y(7)−98, y(8)−98, y(8), y(9)−98, y(9), y(9)−196, y(10), y(10)++, y(11), y(12)−196++
Precursor origin neutral loss:

Peptide No.688
GETQLYATIDLQK
Confirmed sites:
Ambiguous sites: @T:3 or Y:6

MS/MS Fragmentation of GETQLYATIDLQK
Found in AT3G15730.1, PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D

Match to Query 1887: 1558.725414 from(780.369983,2+)
Elution from: 43.385 to 43.385 scan no 4293 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1558.7280
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.058
Matched b ions: b(6)–98, b(7)–98, b(10)–98, b(11)–98, b(12)–98
Matched y ions: y(6)
Precursor origin neutral loss: +

Peptide No.689
GEVVSQSCAVSPR
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of GEVVSQSCAVSPR
Found in AT5G37190.1, CIP4 (COP1–interacting protein 4)
Match to Query 1728: 1454.619726 from(728.317139,2+) Elution from: 23.814 to 23.814 scan no 1810 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6224  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 52 Expect: 2.4e-005  
Matched b ions: b(4), b(9), b(10)  
Matched y ions: y(2), y(3), y(3)--98, y(5), y(6)+, y(6), y(7), y(9), y(10), y(10)+, y(11)--98++  
Precursor origin neutral loss: +

Peptide No.690

GFAVDAKGNVYVADK  
Confirmed sites: @Y:11  
Ambiguous sites:  

MS/MS Fragmentation of GFAVDAKGNVYVADK  
Found in AT1G23890.1, NHL repeat-containing protein  

Match to Query 2655: 1632.759330 from(545.260386,3+)  
Elution from: 38.759 to 38.759 scan no 3818 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1632.7548
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y11 : Phospho (Y)
Ions Score: 28 Expect: 0.014
Matched b ions: b(4), b(5)++, b(8)++, b(9), b(10)++, b(11)++, b(13)++, b(14)++
Matched y ions: y(4), y(5), y(6), y(6)++, y(7)++, y(8)++, y(11)++
Precursor origin neutral loss:

Peptide No.691

GFDASLSEDDIK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GFDASLSEDDIK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1231: 1375.553112 from(688.783832,2+)  
Elution from: 40.216 to 40.216 scan no 3924 polarity:+
Peptide No.692

GFDASLSEDDIK
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of GFDASLSEDDIK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1938: 1455.519028 from(728.766790,2+)
Elution from: 45.183 to 45.183 scan no 4585 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1455.5207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0003
Matched b ions: b(3), b(6)−98, b(6), b(8)−196, b(11)−98
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(9)−98++, y(10), y(10)−98++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.693

GFDASLSEDDIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GFDASLSEDDIK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1667: 1375.553456 from(688.784004,2+)
Elution from: 42.634 to 42.634 scan no 4261 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1375.5544
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 1.3e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)−98, b(8)−98, b(9)++, b(9), b(9)−98, b(10)−98, b(10), b(11)−98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)−98++, y(7), y(7)−98, y(7)++, y(7), y(8)−98, y(8)−98++, y(8)++, y(8)−98++, y(9), y(9)−98, y(9)++, y(10)++, y(10), y(10)−98++, y(10)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.694
GFGHVEFASSEEAQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of GFGHVEFASSEEAQK
Found in AT1G48920.1, nucleolin, putative

Match to Query 2790: 1701.701502 from(568.241110,3+)
Elution from: 35.864 to 35.864 scan no 3214 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1701.7035

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 52 Expect: 2.5e-005

Matched b ions: b(5), b(6), b(7), b(7)++, b(8), b(8)++, b(9), b(9)++, b(10)++, b(11)++, b(12)++, b(12)−98++, b(13)++, b(14)++, b(14)−98++

Matched y ions: y(3), y(4), y(5), y(6)−98++, y(6)−98, y(6), y(7)−98++, y(7)++, y(7), y(7)−98, y(8)++, y(8), y(9)++, y(11)−98++, y(11)++, y(12)++, y(13)++, y(13)−98++, y(14)−98++

Precursor origin neutral loss:

Peptide No. 695

GFGHVEFASSEEAQK

Confirmed sites: @S:9

Ambiguous sites:

MS/MS Fragmentation of GFGHVEFASSEEAQK

Found in AT1G48920.1, nucleolin, putative

Match to Query 2640: 1701.702548 from(851.858550,2+)
Elution from: 33.646 to 33.646 scan no 3135 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1701.7035
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 1.7e-005
Matched b ions: b(4), b(5), b(6), b(7), b(9)–98, b(10)–98, b(11)–98, b(12)–98, b(12), b(13), b(14), b(14)–98, b(14)–98++, b(14)++
Matched y ions: y(3), y(4), y(6)++, y(6), y(7)–98, y(8)–98, y(9), y(9)–98, y(10)–98, y(10), y(11), y(11)–98, y(12)++, y(12)–98++, y(13)++, y(14)–98++
Precursor origin neutral loss: +

Peptide No.696
GFGVEDSDAESPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GFGVEDSDAESPR
Found in AT5G12150.1, pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein

Match to Query 1590: 1444.549342 from(723.281947,2+)
Elution from: 31.580 to 31.580 scan no 2798 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1444.5507
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 5.7e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8), b(8)-98, b(10)-98, b(10), b(11), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9)-98++, y(9), y(10)-98, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.697
GFQEPSSPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GFQEPSSPK
Found in AT2G39480.1, PGP6; ATPase, coupled to transmembrane movement of substances

Match to Query 617: 1055.432708 from(528.723630,2+)
Elution from: 21.608 to 21.608 scan no 1480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1055.4324
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.0055
Matched b ions: b(2), b(3), b(4)
Matched y ions: y(3), y(5)++, y(5), y(6), y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No.698
GFSDSDTNVNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GFSDSDTNVNR
Found in AT2G01190.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 1131: 1290.488138 from(646.251345,2+) Elution from: 25.080 to 25.080 scan no 1873 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1290.4877
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 8.9e-006
Matched b ions: b(2), b(4)-98, b(4), b(6)-98, b(7), b(8)-98, b(9)-98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9), y(10)++
Precursor origin neutral loss: +

**Peptide No.699**

**GFVADDSDIESPR**
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **GFVADDSDIESPR**
Found in **AT5G19390.1**, pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein

Match to Query 1549: 1486.597364 from(744.305958,2+)
Elution from: 39.034 to 39.034 scan no 3681 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.5977
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00027
Matched b ions: b(7)–98, b(9)–98, b(10)–98, b(10), b(11), b(11)–98, b(12)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(10)++, y(10)–98, y(10)–98++, y(11)++, y(11)–98
Precursor origin neutral loss: +

Peptide No.700
GFVPFVPGSPTER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GFVPFVPGSPTER
Found in AT3G05030.1, NHX2 (sodium proton exchanger 2); sodium:hydrogen antiporter
Match to Query 2321: 1468.673534 from(735.344043,2+)
Elution from: 54.998 to 54.998 scan no 5820 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1468.6751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(3), b(5), b(6), b(11)−98++, b(11)+, b(11)−98, b(11), b(12)++
Matched y ions: y(2), y(4), y(5), y(7), y(7)−98, y(8), y(8)−98, y(9)+, y(9), y(9)−98, y(10)−98++, y(10)++,
y(10)−98, y(10), y(11)−98++, y(11)+, y(11)−98, y(12)++
Precursor origin neutral loss:

Peptide No.701

GFVPFVPGSPTER
Confirmed sites:
Ambiguous sites: @T:11orS:9

MS/MS Fragmentation of GFVPFVPGSPTER
Found in AT3G05030.1, NHX2 (sodium proton exchanger 2); sodium:hydrogen antiporter

Match to Query 2064: 1468.673516 from(735.344034,2+)
Elution from: 56.163 to 56.163 scan no 5790 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1468.6751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:

T11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00093
Matched b ions: b(5), b(6), b(8), b(11)-98++, b(11)+, b(11), b(12)+
Matched y ions: y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)+, y(9), y(10)-98++, y(10)+, y(10), y(11)-98++, y(11)-98, y(11)+, y(12)+
Precursor origin neutral loss:

Peptide No.702

GFVTESAAKPEGTNSPPEK
Confirmed sites:
Ambiguous sites: @T:13orS:15

MS/MS Fragmentation of GFVTESAAKPEGTNSPPEK
Found in AT1G77680.1, ribonuclease II family protein

Match to Query 3546: 2024.907603 from(675.976477,3+)
Elution from: 27.742 to 27.742 scan no 2304 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.9091
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0036
Matched b ions: b(5), b(9), b(18)-98++
Matched y ions: y(8)-98, y(10)++, y(11)++, y(12)-98++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss:

Peptide No.703
GGDLGSFGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GGDLGSFGR
Found in AT2G18040.1, PIN1AT (parvulin 1At)

Match to Query 350: 944.374000 from(473.194276,2+)
Elution from: 31.550 to 31.550 scan no 2817 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 944.3752
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0017
Matched b ions: b(3), b(4), b(5), b(7)−98
Matched y ions: y(2), y(3), y(4), y(4)++, y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No.704

GGGLQAQPVESNSL
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GGGLQAQPVESNSL
Found in AT3G19895.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G12940.1);
similar to Os02g0829600 [Oryz]

Match to Query 1746: 1435.633464 from(718.824008,2+)
Elution from: 38.484 to 38.484 scan no 3749 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1435.6344
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 3.3e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(11)++
Matched y ions: y(3), y(4), y(5), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(12)−98++
Precursor origin neutral loss: +

Peptide No.705

GGISDEFSR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GGISDEFSR
Found in AT2G37050.1, kinase

Match to Query 577: 1046.406288 from(524.210420,2+)
Elution from: 34.402 to 34.402 scan no 3240 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1046.4070
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 2.5e-005
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(7)+, b(8)-98, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)-98++, y(7)+, y(7)-98++, y(8)-98++, y(8)+
Precursor origin neutral loss: +

Peptide No.706

GGMTSHAAVVAR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of GGMTSHAAVVAR
Found in AT4G15530.1, PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE); kinase/ pyruvate, phosphate dikinase

Match to Query 1684: 1251.542452 from(626.778502,2+) Elution from: 16.904 to 16.904 scan no 932 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1251.5431
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00089
Matched b ions: b(4)−98, b(4)++, b(6)−98, b(7)++, b(8), b(9)−98, b(9), b(10), b(10)−98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.707

GGMTSHAAVVAR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GGMTSHAAVVAR
Found in AT4G15530.1, PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE); kinase/ pyruvate, phosphate dikinase

Match to Query 1502: 1235.546265 from(412.856031,3+)
Elution from: 20.898 to 20.898 scan no 1422 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1235.5481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00021
Matched b ions: b(3), b(5), b(6)+, b(7)-98++, b(7)+, b(8), b(8)-98++, b(8)+, b(9)+, b(9)-98++, b(10)-98++, b(10)+, b(11)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)+, y(7)+, y(7)-98, y(8)-98++, y(8)+, y(8)-98++, y(9)-98++, y(9)+, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.708
GGMTSHAAVVAR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of GGMTSHAAVVAR
Found in AT4G15530.1, PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE); kinase/ pyruvate, phosphate dikinase

Match to Query 1089: 1235.546718 from(618.780635,2+)
Elution from: 20.959 to 20.959 scan no 1423 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1235.5481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 84 Expect: 2.4e-008
Matched b ions: b(3), b(4)—98, b(5)—98, b(6)—98, b(6), b(7), b(8), b(8)—98, b(9), b(9)—98, b(10)—98++, b(10), b(10)—98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)—98++, y(9), y(9)—98, y(10)++, y(10)—98++
Precursor origin neutral loss: +

Peptide No.709
GGPAVTPAGSFGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of GGPAVTPAGSFGR
Found in AT3G63000.1, NPL4 family protein

Match to Query 1390: 1252.559196 from(627.286874,2+)
Elution from: 32.948 to 32.948 scan no 2935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1252.5601
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 6.1e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)++, b(9), b(10), b(10)++, b(11)−98, b(12)−98, b(12)++
Matched y ions: y(2), y(3), y(5)−98, y(5), y(6), y(6)++, y(6)−98, y(7)−98, y(7), y(7)−98++, y(8), y(8)−98, y(9), y(9)−98, y(10)++, y(11)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.710
GGSDDETRDANFMR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GGSDDETRDANFMR
Found in AT1G78650.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22795.1); similar to Os01g0204000 [Oryz]

Match to Query 2174: 1649.612750 from(825.813651,2+)
Elution from: 29.026 to 29.026 scan no 2475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1649.6141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0018
Matched b ions: b(9)−98
Matched y ions: y(5), y(6), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.711
GGSEEPNVEEDSVAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GGSEEPNVEEDSVAR
Found in AT3G20550.1. DDL (DAWDLE)

Match to Query 2440: 1653.650698 from(827.832625,2+)
Elution from: 28.425 to 28.425 scan no 2395 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1653.6519
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 6.4e-009
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(8), b(8)+, b(9), b(9)-98, b(10)-98, b(10), b(11), b(13)-98, b(14)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(10), y(10)+, y(11), y(11)+, y(12), y(12)+, y(13)-98+, y(13)+
Precursor origin neutral loss: +

Peptide No.712

GGSFLAGNLSFNR
Confirmed sites: "@S:3,@S:10"
Ambiguous sites:

MS/MS Fragmentation of GGSFLAGNLSFNR
Found in AT3G05090.1, transducin family protein / WD-40 repeat family protein

Match to Query 2525: 1498.598934 from(750.306743,2+)
Elution from: 56.805 to 56.805 scan no 6063 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1498.6006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 4.9e-006
Matched b ions: b(4)−98, b(5)−98, b(6)−98, b(6), b(7)−98, b(8)−98, b(9)−98, b(10)−98, b(12)−98, b(12)
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5), y(5)−98, y(6)++, y(6)−98, y(6), y(7)++, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10)++, y(11)++, y(11)−98++, y(11)−196++
Precursor origin neutral loss: +

Peptide No.713
GGSWELSSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GGSWELSSR**
Found in **AT3G48760.1**, zinc finger (DHHC type) family protein

Match to Query 614: 1057.423124 from(529.718838,2+)
Elution from: 33.568 to 33.568 scan no 2985 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1057.4229
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0018
Matched b ions: b(4)–98, b(5)–98, b(6)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(7)–98++
Precursor origin neutral loss: +

Peptide No.714

GGYADVYQGILPEGKLIAVK
Confirmed sites: ”@Y:3,@Y:7”
Ambiguous sites:

MS/MS Fragmentation of GGYADVYQGILPEGKLIAVK
Found in AT3G05140.1, protein kinase family protein

Match to Query 3752: 2250.069537 from(751.030455,3+)
Elution from: 50.170 to 50.170 scan no 5216 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2250.0737
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
Y7 : Phospho (Y)
Ions Score: 27 Expect: 0.029
Matched b ions: b(4), b(5), b(6), b(7), b(12)++, b(16)++, b(19)++
Matched y ions: y(11), y(13)++, y(14)++, y(16)++, y(16)
Precursor origin neutral loss:

**Peptide No.715**

GHLSVSDLDDYISSDPDTK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of GHLSVSDLDDYISSDPDTK
Found in AT1G15290.1, binding

Match to Query 3833: 2140.955088 from(1071.484820,2+)
Elution from: 62.517 to 62.517 scan no 6646 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2140.9565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00026
Matched b ions: b(7), b(9), b(10), b(12), b(15), b(15)-98
Matched y ions: y(4), y(6), y(7), y(9), y(9)-98, y(10), y(14)
Precursor origin neutral loss: +

Peptide No.716

GHSNVWNSHPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GHSNVWNSHPK
Found in AT3G43980.1, 40S ribosomal protein S29 (RPS29A)

Match to Query 1850: 1341.560208 from(671.787380,2+)
Elution from: 19.024 to 19.024 scan no 1221 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.5615
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 7.8e-007
Matched b ions: b(2), b(3)−98, b(4), b(5)−98, b(4), b(4)−98, b(5), b(6)++, b(6), b(6)−98++, b(8), b(8)−98, b(9), b(9)−98, b(9)++, b(10)−98++, b(10)++
Matched y ions: y(2), y(3), y(4)++, y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9)−98, y(9), y(9)−98++
Precursor origin neutral loss: +

Peptide No.717
GIALDSNVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GIALDSNVK
Found in AT1G61730.1, DNA–binding storekeeper protein–related

Match to Query 469: 995.468086 from(498.741319,2+)
Elution from: 30.851 to 30.851 scan no 2725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 995.4688
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00069
Matched b ions: b(2), b(3), b(4), b(5), b(6)–98, b(7)–98++, b(7)–98, b(8), b(8)–98
Matched y ions: y(3), y(4), y(4)–98, y(5), y(5)–98, y(6)–98, y(6), y(7)+, y(7), y(7)–98, y(8)+, y(8)–98++
Precursor origin neutral loss: +

Peptide No.718
GIAYLEFSEGK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GIAYLEFSEGK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1272: 1292.567570 from(647.291061,2+) Elution from: 49.421 to 49.421 scan no 5200 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1292.5689
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 4.8e-005
Matched b ions: b(3), b(4), b(5), b(7), b(8)–98, b(9)–98
Matched y ions: y(3), y(4)–98, y(4), y(5)–98, y(6)–98, y(6), y(7), y(7)–98, y(8), y(8)–98, y(8)++, y(9), y(9)–98, y(9)++, y(9)–98++, y(10)++
Precursor origin neutral loss: +

Peptide No.719
GIEMSDEFDGK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GIEMSDEFDGK
Found in AT1G67120.1, midasin–related

Match to Query 1363: 1306.477700 from(654.246126,2+)
Elution from: 39.353 to 39.353 scan no 3898 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1306.4788
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00018
Matched b ions: b(3), b(5)+, b(5)−98, b(6)−98, b(7)−98, b(7), b(8), b(8)−98, b(9), b(9)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)−98++, y(7)−98, y(8)−98, y(8), y(9)+, y(9), y(9)−98, y(9)−98++
Precursor origin neutral loss: +

Peptide No.720

GIESDEEESPPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GIESDEEESPPR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 1333: 1423.549816 from(712.782184,2+)  
Elution from: 26.749 to 26.749 scan no 2169 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1423.5504
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.034
Matched b ions: b(4)–98, b(7)–98, b(8)–98, b(8), b(9), b(9)–98
Matched y ions: y(3), y(4), y(5), y(8), y(10)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.721

GIESDEEESPPR
Confirmed sites: ”@S:4,@S:9”
Ambiguous sites:

MS/MS Fragmentation of GIESDEEESPPR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 2312: 1503.515266 from(752.764909,2+)
Elution from: 28.495 to 28.495 scan no 2454 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1503.5167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0014
Matched b ions: b(4)-98, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)-196, b(11)-196++, b(11)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.722
GIESDEEESPPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GIESDEEESPPR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 1602: 1423.550270 from(712.782411,2+)
Elution from: 23.539 to 23.539 scan no 1739 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1423.5504
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 9e-005
Matched b ions: b(6), b(8), b(9)–98
Matched y ions: y(3), y(4), y(4)–98, y(5), y(6), y(6)–98, y(7), y(8), y(9), y(10), y(10)–98, y(10)++, y (10)–98++
Precursor origin neutral loss: +

**Peptide No.723**

GIESDEEESPPRK
Confirmed sites: “@S:4,@S:9”
Ambiguous sites:

MS/MS Fragmentation of GIESDEEESPPRK
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 2365: 1631.610694 from(816.812623,2+) Elution from: 23.798 to 23.798 scan no 1773 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1631.6117
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0072
Matched b ions: b(4)—98, b(5), b(6)—98, b(7), b(7)—98, b(8)—98, b(9)—196, b(9)—98, b(10)—196, b(10)++
Matched y ions: y(4), y(5), y(6), y(6)—98, y(7), y(8)—98, y(10)—98++, y(11)—196, y(11)—98++, y(12)++
Precursor origin neutral loss: +

Peptide No.724

GIESDEEESPPRK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GIESDEEESPPRK
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 1664: 1551.643888 from(776.829220,2+)
Elution from: 19.781 to 19.781 scan no 1267 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1551.6453
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.064
Matched b ions: b(7), b(8), b(9)–98
Matched y ions: y(4), y(5), y(10)–98, y(10)++
Precursor origin neutral loss: +

Peptide No. 725

GILAADESTGTIGK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGTIGK
Found in AT3G52930.1, fructose–bisphosphate aldolase, putative

Match to Query 1571: 1411.658482 from(706.836517,2+)
Elution from: 36.957 to 36.957 scan no 3511 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 2.2e-007
Matched b ions: b(4), b(5), b(6), b(7), b(11)-98++, b(11)-98, b(12), b(12)-98, b(13), b(13)-98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)+, y(11)-98, y(12)-98++, y(12)+, y(12)
Precursor origin neutral loss: +

Peptide No.726
GILAADESTGTIGK
Confirmed sites: @T:11
Ambiguous sites:
MS/MS Fragmentation of GILAADESTGTIGK
Found in AT3G52930.1, fructose-bisphosphate aldolase, putative

Match to Query 1666: 1411.658956 from(706.836754,2+)
Elution from: 36.021 to 36.021 scan no 3420 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 Expect: 5.7e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)+, b(11)-98, b(11), b(11)+, b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(2), y(3), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)+, y(11), y(11)-98++, y(11)+, y(11)-98, y(12), y(12)+, y(12)-98++, y(12)-98
Precursor origin neutral loss: +

Peptide No.727
GILAADESTGTIGK
Confirmed sites:
Ambiguous sites: @S:8orT:9

MS/MS Fragmentation of GILAADESTGTIGK
Found in AT2G36460.1, fructose-bisphosphate aldolase, putative

Match to Query 1313: 1411.658866 from(706.836709,2+)
Elution from: 36.928 to 36.928 scan no 3511 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0014
Matched b ions: b(4), b(5), b(7), b(9)-98, b(11), b(12), b(12)-98, b(12)++
Matched y ions: y(5), y(7), y(7)-98, y(8), y(9), y(10), y(11)-98++, y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.728
GILAADESTGTIGK
Confirmed sites: ”@T:9,@T:11”
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGTIGK
Found in AT2G36460.1, fructose–bisphosphate aldolase, putative

Match to Query 1565: 1491.624188 from(746.819370,2+)
Elution from: 38.918 to 38.918 scan no 3666 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1491.6259
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0059
Matched b ions: b(5), b(10)++, b(11)−98, b(12)−98
Matched y ions: y(3), y(4), y(5)−98, y(6), y(7), y(7)−98, y(9)−98, y(9), y(10), y(10)−98, y(11), y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.729

GIQGFGSFNHK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GIQGFGSFNHK
Found in AT3G46540.1, epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related

Match to Query 1703: 1270.549044 from(636.281798,2+)
Elution from: 36.235 to 36.235 scan no 3498 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1270.5495
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.022
Matched b ions: b(3), b(8)-98, b(9)++
Matched y ions: y(5), y(5)-98, y(6)-98, y(7)-98, y(8)-98, y(8), y(9)-98++
Precursor origin neutral loss: +

Peptide No.730

GISINAAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GISINAAR
Found in AT3G58730.1, (VACUOLAR ATP SYNTHASE SUBUNIT D); hydrogen ion transporting ATP synthase, rotational mechanism / h

Match to Query 393: 880.416084 from(441.215318,2+)
Elution from: 28.496 to 28.496 scan no 2471 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 880.4167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.8e-005
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(5)−98, b(5), b(6)−98, b(6), b(6)++, b(7)−98, b(7), b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)−98++, y(6)−98, y(6), y(6)++
Precursor origin neutral loss: +

Peptide No.731
GIVIDYESNN
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GIVIDYESNN
Found in AT5G61730.1, ATATH11 (ABC2 homolog 11); ATPase, coupled to transmembrane movement of substances

Match to Query 896: 1202.484176 from(602.249364,2+)
Elution from: 43.348 to 43.348 scan no 4289 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1202.4856
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00012
Matched b ions: b(3), b(4), b(6), b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.732

GKFTSDEDNADPEVVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GKFTSDEDNADPEVVR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2702: 1857.776838 from(929.895695,2+)
Elution from: 29.714 to 29.714 scan no 2568 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1857.7781
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 6.9e-008
Matched b ions: b(3), b(5)-98, b(6), b(7)-98++, b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)-98++, b(12)-98, b(12), b(13)-98++, b(13), b(13)-98, b(14)-98++, b(14), b(14)++, b(15)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++, y(12)-98, y(13)-98++, y(13), y(13)-98, y(14)-98++, y(14), y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.733
GKFTSDEDNADPEVVR
Confirmed sites:
Ambiguous sites: @T:4 or S:5

MS/MS Fragmentation of GKFTSDEDNADPEVVR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 3059: 1857.778460 from(929.896506,2+)
Elution from: 30.585 to 30.585 scan no 2689 polarity:+

---

Peptide No.733
GKFTSDEDNADPEVVR
Confirmed sites:
Ambiguous sites: @T:4 or S:5

MS/MS Fragmentation of GKFTSDEDNADPEVVR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 3059: 1857.778460 from(929.896506,2+)
Elution from: 30.585 to 30.585 scan no 2689 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1857.7781
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0013
Matched b ions: b(5), b(6), b(6)–98, b(7)–98++, b(8), b(8)–98, b(10)–98, b(10), b(11)–98, b(11), b (15)
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10), y(13)–98++
Precursor origin neutral loss: +

Peptide No.734

GKFTSDEDNADPEVVR
Confirmed sites: “@T:4,@S:5”
Ambiguous sites:

MS/MS Fragmentation of GKFTSDEDNADPEVVR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 3526: 1937.742686 from(969.878619,2+)
Elution from: 34.976 to 34.976 scan no 3342 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1937.7445
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.3e-006
Matched b ions: b(4)-98, b(5)-98, b(6)-196, b(6), b(7)-196, b(7), b(8)-196, b(8)-98, b(9), b(10)-196, b(10)-98, b(10), b(11)-196, b(11)-98, b(11), b(12)-196, b(12), b(13), b(14), b(15)-98, b(15)
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13)-196, y(14)-98++
Precursor origin neutral loss: +

Peptide No.735

GKFTSDEDNADPEVVRR
Confirmed sites: @S.5
Ambiguous sites:

MS/MS Fragmentation of GKFTSDEDNADPEVVRR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 3643: 2013.878184 from(672.300004,3+)
Elution from: 28.846 to 28.846 scan no 2264 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2013.8792
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00025
Matched b ions: b(3), b(6)-98, b(7), b(8), b(8)-98, b(10), b(10)+++, b(11), b(11)-98, b(11)-98++, b(11)+++, b(12)-98++, b(14)+++, b(15)-98++
Matched y ions: y(3), y(4), y(6)+++, y(6), y(7)+++, y(9)+++, y(10)+++, y(11)+++, y(12)+++, y(13)-98++, y(13)+++, y(14)-98++, y(15)-98++, y(15)+++, y(15)+
Precursor origin neutral loss: +

Peptide No.736

GKFTSDEDNADPEVVRR
Confirmed sites: "@T:4,@S:5"
Ambiguous sites:

MS/MS Fragmentation of GKFTSDEDNADPEVVRR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2947: 2093.842266 from(698.954698,3+)
Elution from: 31.932 to 31.932 scan no 2747 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2093.8456
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0035
Matched b ions: b(3), b(4)−98, b(5), b(6)−196, b(7), b(8), b(8)−98, b(8)−196, b(9)−98++, b(11)−196, b(11), b(11)−98, b(11)−196++, b(11)−98++, b(11)−196++, b(11)−98++, b(13)++, b(14)−98++, b(15)−196++
Matched y ions: y(4), y(4)++, y(6)++, y(6), y(9)++, y(10)++, y(11)++, y(13)−98++, y(13)++, y(14)−196++, y(14)++, y(15)−98++, y(15)++, y(15)−196++
Precursor origin neutral loss: +

Peptide No.737

GKSLTDEDLDELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GKSLTDEDLDELK
Found in AT3G50350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G33985.1); similar to Os04g0282200 [Oryz]

Match to Query 1675: 1541.685394 from(771.849973,2+)
Elution from: 37.703 to 37.703 scan no 3495 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6862
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0021
Matched b ions: b(6)−98, b(6), b(7)−98, b(10)−98, b(11)−98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11)−98
Precursor origin neutral loss: +

Peptide No.738

GLAYDTSDDQQDITR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of GLAYDTSDDQQDITR
Found in AT2G39730.1, RCA (RUBISCO ACTIVASE)

Match to Query 2198: 1776.720706 from(889.367629,2+)
Elution from: 34.657 to 34.657 scan no 3126 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1776.7203
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00025
Matched b ions: b(8)−98, b(11)++, b(13)−98, b(14)++
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(11)−98++, y(11)−98, y(12)++, y(12)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.739

GLDIDTAGHHYTV
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of GLDIDTAGHHYTV
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2089: 1477.622260 from(739.818406,2+)
Elution from: 42.268 to 42.268 scan no 4068 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1477.6238
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0089
Matched b ions: b(3), b(5), b(6), b(7), b(9), b(10), b(11), b(11)++, b(12)−98++, b(12)++
Matched y ions: y(3)−98, y(3), y(4)−98, y(4), y(6)−98, y(6), y(7)−98, y(8)−98++, y(8), y(8)−98, y(9)−98, y(9), y(10)−98++, y(10), y(10)++, y(11)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.740

GLDIDTAGHHYTV
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of GLDIDTAGHHYTV
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2141: 1477.621104 from(493.547644,3+)
Elution from: 41.894 to 41.894 scan no 4128 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1477.6238
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.054
Matched b ions: b(2), b(3)++, b(6)−98
Matched y ions: y(5), y(8)++, y(9)++, y(10)++, y(11)−98++, y(11)++
Precursor origin neutral loss:

Peptide No.741

GLDIETPSHYTV
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of GLDIETPSHYTV
Found in AT4G30190.1, AHA2 (Arabidopsis H(+)−ATPase 2); ATPase

Match to Query 1937: 1410.605612 from(706.310082,2+)
Elution from: 48.298 to 48.298 scan no 4961 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1410.6068
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00067
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(9), b(10), b(11)++, b(11)-98++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(6)-98, y(7), y(7)-98, y(8), y(9), y(9)-98++, y(9)+, y(10), y(10)-98++, y(10)-98, y(10)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.742

GLESDEEGDDDEEYMH
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GLESDEEGDDDEEYMH
Found in AT1G15440.1, transducin family protein / WD-40 repeat family protein

Match to Query 3809: 2219.745972 from(740.922600,3+)
Elution from: 35.074 to 35.074 scan no 3291 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2219.7474
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 1e-005
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7), b(9), b(10)-98, b(11)+, b(12)+, b(13)-98++, b(15)-98++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(7)+, y(7), y(8), y(8)+, y(9)+, y(9), y(10)+, y(11), y(11)+, y(12)+, y(13)+, y(14)+, y(15)+, y(15)-98++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.743

GLESDEEGDDDDEEYMHR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GLESDEEGDDDDEEYMHR
Found in AT1G15440.1, transducin family protein / WD-40 repeat family protein

Match to Query 3278: 2235.739746 from(1118.877149,2+)
Elution from: 28.268 to 28.268 scan no 2384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2235.7423
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 78 Expect: 4.4e-008
Matched b ions: b(6)-98, b(7)-98, b(9), b(9)-98, b(10)-98, b(11)-98, b(11), b(12), b(12), b(13)++, b(13)-98, b(14)-98, b(15)-98, b(16)-98++, b(17)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(9)++, y(11), y(11)++, y(13)++, y(13), y(14)++, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.744
GLGFCDDSDATPSGSLSIPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GLGFCDDSDATPSGSLSIPK
Found in AT3G09850.1, D111/G-patch domain-containing protein

Match to Query 3689: 2102.884044 from(1052.449298,2+)
Elution from: 51.867 to 51.867 scan no 5505 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2102.8867
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0096
Matched b ions: b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(18)-98, b(18), b(19)-98
Matched y ions: y(9), y(10), y(12), y(13)-98, y(14), y(19)-98++
Precursor origin neutral loss: +

Peptide No.745

GLGTIDLEPMLDGATSASPTR
Confirmed sites:
Ambiguous sites: @S:16orS:18

MS/MS Fragmentation of GLGTIDLEPMLDGATSASPTR
Found in AT5G14270.1, ATBET9 (ARABIDOPSIS THALIANA BROMODOMAIN AND EXTRATERMINAL DOMAIN PROTEIN 9); DNA binding

Match to Query 3896: 2180.998434 from(1091.506493,2+) 
Elution from: 61.408 to 61.408 scan no 6527 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2181.0024
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 5.1e-006
Matched b ions: b(8), b(12), b(14), b(18)–98
Matched y ions: y(3), y(6), y(7)–98, y(8)–98, y(9), y(10), y(13)–98, y(13), y(14), y(15), y(16), y(17)++
Precursor origin neutral loss: +

Peptide No.746

GLLNDDSPTGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GLLNDDSPTGK
Found in AT4G09580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71940.1); similar to conserved hypothet

Match to Query 896: 1195.510276 from(598.762414,2+) Elution from: 30.850 to 30.850 scan no 2635 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1195.5122
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 4.9e-005
Matched b ions: b(5), b(7)-98
Matched y ions: y(2), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9)++, y(9), y(9)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.747

GLLNDDSPTGKR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GLLNDDSPTGKR
Found in AT4G09580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71940.1); similar to conserved hypothet

Match to Query 1429: 1351.613460 from(676.814006,2+)
Elution from: 25.091 to 25.091 scan no 1981 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1351.6133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.051
Matched b ions: b(5), b(6), b(7)−98, b(8), b(10)++, b(11), b(11)−98++
Matched y ions: y(3), y(5), y(6)−98, y(6), y(7), y(7)−98, y(8)++, y(8)−98, y(8), y(9)−98, y(9), y(9)++, y(9)−98++, y(10)++, y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.748
GLLNDDSPTGKR
Confirmed sites: @T:9
Ambiguous sites:
MS/MS Fragmentation of GLLNDDSPTGKR
Found in AT4G09580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71940.1); similar to conserved hypothet

Match to Query 1427: 1351.611915 from(451.544581,3+)
Elution from: 25.166 to 25.166 scan no 1991 polarity:+
**Peptide No.749**

GLLNQHTPSPSAR
Confirmed sites: "@T:7, @S:11"
Ambiguous sites:

MS/MS Fragmentation of GLLNQHTPSPSAR
Found in AT1G27750.1, nucleotide binding

Match to Query 2625: 1536.647554 from(769.331053,2+)
Elution from: 29.280 to 29.280 scan no 2606 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1536.6487
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.036
Matched b ions: b(5), b(6), b(7), b(7)−98, b(8)−98, b(9), b(11)−98++, b(11)++, b(12)
Matched y ions: y(2), y(3), y(4)−98, y(5), y(6)−98, y(6), y(7), y(7)−98, y(8)−98, y(8), y(10)−98++, y(10)++, y(11)−98++, y(11)−196++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.750

GLLNQHTPSPSAR
Confirmed sites:”@T:7,@S:9”
Ambiguous sites:

MS/MS Fragmentation of GLLNQHTPSPSAR
Found in AT1G27750.1, nucleotide binding

Match to Query 2626: 1536.648123 from(513.223317,3+)
Elution from: 29.150 to 29.150 scan no 2588 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1536.6487
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.053
Matched b ions: b(2), b(4), b(7), b(9)-196++, b(10)-196++, b(11)-98++, b(12)-98++
Matched y ions: y(4)++, y(4), y(5), y(6)+, y(6)-98, y(6)-98++, y(8)-98++, y(8)-196++, y(9)+, y(9)-98++, y(10)++, y(10)-98++, y(11)+, y(11)-98++, y(11)-196++
Precursor origin neutral loss: +

Peptide No.751
GLQVAEEEDSPGEAQEDFYK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of GLQVAEEEDSPGEAQEDFYK
Found in AT3G16940.1, calmodulin-binding protein

Match to Query 3873: 2261.930978 from(1131.972765,2+)
Elution from: 45.158 to 45.158 scan no 4599 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2261.9365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00061
Matched b ions: b(13), b(15)−98, b(18)
Matched y ions: y(5), y(7), y(10), y(11), y(12), y(12)−98, y(16)++, y(16), y(17)−98++
Precursor origin neutral loss: +

Peptide No.752

GLSEEELKPIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GLSEEELKPIK
Found in AT3G09070.1, glycine-rich protein

Match to Query 1823: 1321.652312 from(661.833432,2+) Elution from: 34.452 to 34.452 scan no 3263 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1321.6530
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0011
Matched b ions: b(3)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(10), b(10)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.753

GLSLEEEDSSDDDENR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of GLSLEEEDSSDDDENR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2454: 1888.683120 from(945.348836,2+)
Elution from: 32.595 to 32.595 scan no 2953 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1888.6847
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 1.7e-007
Matched b ions: b(5), b(6), b(7), b(8), b(10), b(10)−98, b(11)−98, b(12), b(13), b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)−98, y(12)++, y(13)+, y(13)−98++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.754

GLSLEEEDSSDDDENR
Confirmed sites: “@S:9,@S:10”
Ambiguous sites:

MS/MS Fragmentation of GLSLEEEDSSDDDENR
Found in AT5G08610.1, DEAD box RNA helicase (RH26)

Match to Query 2867: 1968.646904 from(985.330728,2+)
Elution from: 38.700 to 38.700 scan no 3756 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1968.6510
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0002
Matched b ions: b(5), b(11), b(13), b(14), b(15)−196
Matched y ions: y(3), y(4), y(5), y(8)−98++, y(8), y(8)−196, y(8)−98, y(9)−98, y(9), y(9)−196, y(11), y(12), y(13)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.755

GLTIEELPSDEEVEER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GLTIEELPSDEEVEER
Found in AT2G45380.1, similar to calcium ion binding [Arabidopsis thaliana] (TAIR:AT4G34070.1); similar to Os08g0117900 [

Match to Query 2522: 1923.831766 from(962.923159,2+)  
Elution from: 46.743 to 46.743 scan no 4666 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1923.8350
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.015
Matched b ions: b(5), b(7), b(12)–98, b(12), b(13)–98, b(14), b(15)
Matched y ions: y(7), y(8), y(9)–98, y(9), y(10), y(15)++
Precursor origin neutral loss: +

Peptide No.756

GMSFVHETSPYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GMSFVHETSPYK
Found in AT2G37790.1, aldo/keto reductase family protein

Match to Query 2423: 1461.598760 from(731.806656,2+)
Elution from: 36.876 to 36.876 scan no 3614 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1461.5999
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.1e-005
Matched b ions: b(3)-98, b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(11), b(11)-98
Matched y ions: y(3), y(4), y(5), y(7), y(7)+, y(8), y(9)+, y(9), y(10)-98++, y(10)+, y(11)+
Precursor origin neutral loss: +

Peptide No.757

GMSTNEGSGDNMGQPDLTTELYVSTYEAAAK
Confirmed sites: “@T:4,@Y:28”
Ambiguous sites: @Y:24

MS/MS Fragmentation of GMSTNEGSGDNMGQPDLTTELYVSTYEAAAK
Found in AT2G45260.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G34080.1); similar to expressed protein

Match to Query 4213: 3737.414631 from(1246.812153,3+)
Elution from: 45.437 to 45.437 scan no 4518 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3737.4228
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y24 : Phospho (Y)
Y28 : Phospho (Y)
Ions Score: 25 Expect: 0.029
Matched b ions: b(9), b(10), b(10)−98, b(11)−98, b(11), b(12), b(13)−98, b(14)−98, b(14), b(15), b(16)++, b(16), b(17)−98, b(17)−98++, b(18)−98++, b(18)+++, b(19)−98++, b(19)+++, b(20)−98++, b(22)++, b(27)−98++, b(28)−98++, b(28)++, b(28)−98++, b(29)++, b(32)+, b(32)−98++
Matched y ions: y(9), y(13)+, y(14), y(14)+, y(15), y(15)+, y(16)+, y(17)+, y(19)+, y(20)+, y(24)+, y(25)+, y(27)+, y(28)+, y(29)+, y(30)−98++, y(30)+
Precursor origin neutral loss: +

Peptide No.758

GNEDDDWSVESDEDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of GNEDDDWSVESDEDK
Found in AT3G13780.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02720.1); similar to SMAD/FHA [Medicago

Match to Query 2281: 1818.607348 from(910.310950,2+)
Elution from: 33.377 to 33.377 scan no 3057 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.011
Matched b ions: b(6), b(7), b(9), b(10), b(12)−98
Matched y ions: y(5), y(6)−98, y(6), y(7)−98, y(8), y(8)−98, y(9), y(10), y(10)−98, y(11)++ , y(14)−98++
Precursor origin neutral loss: +

Peptide No.759

GNLGTDSAETTNYPGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GNLGTDSAETTNYPGK
Found in AT2G17280.1, phosphoglycerate/bisphosphoglycerate mutase family protein

Match to Query 2576: 1703.702614 from(852.858583,2+) Elution from: 28.094 to 28.094 scan no 2387 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1703.7039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.015
Matched b ions: b(9)−98, b(10), b(11)−98, b(12), b(13), b(14)−98, b(15)++
Matched y ions: y(3), y(5), y(7), y(10)
Precursor origin neutral loss: +

Peptide No.760

GNNGDVHSPTASVSAQSVSSAR
Confirmed sites: @T:10orS:12
Ambiguous sites: @T:10orS:12

MS/MS Fragmentation of GNNGDVHSPTASVSAQSVSSAR
Found in AT5G49830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10385.1); similar to expressed protein

Match to Query 3528: 2206.960041 from(736.660623,3+)
Elution from: 25.751 to 25.751 scan no 2036 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2206.9603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00031
Matched b ions: b(6), b(12), b(12)+, b(13)−98+, b(13)+, b(14)+, b(16)+, b(17)+, b(18)+, b(18)−98+, b(19)+
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10)+, y(10), y(14)+, y(17)−98+
Precursor origin neutral loss:

Peptide No.761

GNNGDVHSPTASVSAQSVSSAR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of GNNGDVHSPTASVSAQSVSSAR
Found in AT5G49830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10385.1); similar to expressed protein

Match to Query 4214: 2206.958343 from(736.660057,3+)
Elution from: 27.072 to 27.072 scan no 2232 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2206.9603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.001
Matched b ions: b(6), b(7), b(9), b(10)+, b(11), b(11)+, b(12)−98++, b(12)+, b(13)+, b(13)−98++, b(14)−98++, b(14)+, b(15)−98++, b(16)+, b(17)+, b(18)+, b(18)−98++, b(19)+, b(20)+
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(8)+, y(9), y(10), y(11), y(13)+, y(14)−98++, y(17)−98++, y(17)+
Precursor origin neutral loss:

Peptide No.762
GNNGVSIGTFSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of GNNGVSIGTFSPK
Found in AT3G48440.1, zinc finger (CCCH-type) family protein

Match to Query 1439: 1356.606540 from(679.310546,2+)
Elution from: 38.134 to 38.134 scan no 3737 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1356.6074
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 5.9e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(11)-98, b(11), b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-98++, y(9), y(9)-98, y(9)++, y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.763
GNNGVSIGTFSPK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of GNNGVSIGTFSPK
Found in AT3G48440.1, zinc finger (CCCH-type) family protein

Match to Query 2079: 1356.606772 from(679.310662,2+)  
Elution from: 38.219 to 38.219 scan no 3819 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1356.6074
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(5), b(7), b(10)–98
Matched y ions: y(5), y(6), y(7), y(8), y(8)–98++, y(9), y(9)–98, y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.764

GNSSNDHELGLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GNSSNDHELGLR
Found in AT5G47910.1, RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)

Match to Query 2395: 1490.650520 from(746.332536,2+)
Elution from: 34.991 to 34.991 scan no 3331 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1490.6514
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 5.3e-007
Matched b ions: b(3)-98, b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(11)-98, b(11), b(11)+, b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)+, y(11)-98++, y(11)-98, y(11)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.765

GNSSQNLQL
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GNSSQNLQL
Found in AT3G21250.1, ATMRP6 (Arabidopsis thaliana multidrug resistance-associated protein 6)

Match to Query 520: 1039.432826 from(520.723689,2+)
Elution from: 37.659 to 37.659 scan no 3605 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1039.4335
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0051
Matched b ions: b(5), b(5)-98, b(6), b(7), b(7)-98++, b(7)-98, b(7)++, b(8), b(8)+, b(8)-98, b(8)-98++
Matched y ions: y(2), y(3), y(4), y(6)-98++, y(6)+
Precursor origin neutral loss:

Peptide No.766
GPGNYSFNK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GPGNYSFNK
Found in AT1G68060.1, ATMAP70-1 (MICROTUBULE-ASSOCIATED PROTEINS 70-1); microtubule binding

Match to Query 626: 1062.416480 from(532.215516,2+);
Elution from: 27.781 to 27.781 scan no 2309 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1062.4171
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00086
Matched b ions: \( b(4), b(5), b(6)-98, b(8)-98 \)
Matched y ions: \( y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(7)-98, y(7), y(7)+, y(7)-98++, y(8)-98++, y(8)-98++ \)
Precursor origin neutral loss: +

Peptide No. 767

GPPDPAVIAATRTTETSK
Confirmed sites: "@T:11,@T:16,@S:17"
Ambiguous sites: @T:13 or T:14

MS/MS Fragmentation of GPPDPAVIAATRTTETSK
Found in AT5G06210.1, RNA-binding protein, putative

Match to Query 3770: 2130.804666 from(711.275498,3+) 
Elution from: 53.640 to 53.640 scan no 5725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2130.8078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- T11 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- T14 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- T16 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S17 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 27 Expect: 0.013
Matched b ions: b(9), b(12)++, b(14)−196++, b(15)+, b(15)−98++, b(16)++, b(17)++
Matched y ions: y(8)++., y(9)++, y(10)++, y(10)−392
Precursor origin neutral loss:

Peptide No.768

GPPDPAVIAATTTETSK
Confirmed sites: "@T:13, @T:14, @T:16, @S:17"
Ambiguous sites:

MS/MS Fragmentation of GPPDPAVIAATTTETSK
Found in AT5G06210.1, RNA-binding protein, putative

Match to Query 4072: 2130.803718 from(711.275182,3+)
Elution from: 56.483 to 56.483 scan no 5965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2130.8078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(7)++, b(9), b(11)++, b(14)-196++, b(15)-98++, b(15)++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(3), y(4), y(10)-294++, y(10)++, y(10)-392
Precursor origin neutral loss:

Peptide No.769

GPSGSPWYGSDR
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of GPSGSPWYGSDR
Found in AT1G29910.1, CAB3 (CHLOROPHYLL A/B BINDING PROTEIN 3); chlorophyll binding

Match to Query 1584: 1344.512412 from(673.263482,2+)
Elution from: 32.874 to 32.874 scan no 2990 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1344.5135
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.0094
Matched b ions: b(5)--98, b(7)--98, b(8)--98
Matched y ions: y(4), y(5), y(6), y(7), y(10)++, y(11)--98++
Precursor origin neutral loss: +

Peptide No.770

GPSGSPWYGSDR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GPSGSPWYGSDR
Found in AT1G29910.1, CAB3 (CHLOROPHYLL A/B BINDING PROTEIN 3); chlorophyll binding

Match to Query 1450: 1344.512830 from(673.263691,2+)
Elution from: 31.948 to 31.948 scan no 2910 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1344.5135

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 66 Expect: 1.2e-006
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(8), b(8)++, b(9)-98, b(11), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8)-98++, y(8), y(9)-98, y(9), y(9)-98++, y(9)++, y(10), y(10)-98, y(10)++, y(10)-98++, y(11)-98++

Precursor origin neutral loss: +

Peptide No.771

GPVIEEIDSDEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GPVIEEIDSDEK
Found in AT4G22740.1, glycine-rich protein

Match to Query 2026: 1524.622680 from(763.318616,2+)
Elution from: 36.261 to 36.261 scan no 3452 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1524.6232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 2.4e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)−98++, b(10)−98, b(11)++, b(11), b(12), b(12)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)−98, y(5), y(6), y(6)−98, y(7), y(7)−98, y(8)−98, y(8), y(9), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12)−98
Precursor origin neutral loss: +

Peptide No.772

GPVIEEIDSDDEKEGEGDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GPVIEEIDSDDEKEGEGDK
Found in AT4G22740.1, glycine-rich protein

Match to Query 3015: 2139.869680 from(1070.942116,2+)
Elution from: 33.005 to 33.005 scan no 2999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2139.8732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 4.3e-005
Matched b ions: b(6), b(7), b(8), b(10)–98, b(11)+, b(11), b(11)–98, b(12)–98, b(12), b(14)–98++, b(16)–98, b(17)–98++, b(17)+, b(18)–98++, b(18)+
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)–98, y(11), y(12)–98, y(12), y(13)–98, y(14)–98, y(14), y(16)+, y(16)–98++, y(17)–98++, y(17)+, y(18)+, y(18)–98++
Precursor origin neutral loss: +

Peptide No.773

GQTPLFPR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of GQTPLFPR
Found in AT1G77120.1, ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase

Match to Query 760: 994.462656 from(498.238604,2+)
Elution from: 34.800 to 34.800 scan no 3357 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 994.4637
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00085
Matched b ions: b(2), b(3), b(3)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)-98++, y(6)-98, y(7)-98++
Precursor origin neutral loss: +

Peptide No.774
GRDQSLSPDRK
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of GRDQSLSPDRK
Found in AT3G53500.1, RSZ32; nucleic acid binding

Match to Query 1960: 1417.574312 from(709.794432,2+)  
Elution from: 16.472 to 16.472 scan no 836 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1417.5752
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.041
Matched b ions: b(3), b(5)−98, b(6), b(6)−98, b(7)−98, b(8)−196, b(9)−98, b(9), b(10)++
Matched y ions: y(2), y(4), y(7), y(8)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.775

GREPSPEPLL
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GREPSPEPLL
Found in AT5G10540.1, peptidase M3 family protein / thimet oligopeptidase family protein

Match to Query 1407: 1329.643202 from(665.828877,2+)
Elution from: 28.846 to 28.846 scan no 2489 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1329.6442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 33 Expect: 0.005
Matched b ions: b(2), b(3), b(5)−98, b(5), b(6)−98, b(7), b(7)−98, b(9)++, b(10)−98
Matched y ions: y(4), y(6), y(7), y(8)−98, y(8), y(9)−98++
Precursor origin neutral loss: +

Peptide No.776

GRGESRSPPPYEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GRGESRSPPPYEK
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 2631: 1538.686275 from(513.902701,3+) Elution from: 16.793 to 16.793 scan no 918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1538.6878  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 30 Expect: 0.0083  
Matched b ions: b(5)—98, b(7)—98++, b(7)++, b(7)—98, b(8)—98++, b(9)++, b(10)—98++, b(11)++, b(11)—98++, b(12)—98++, b(12)++  
Matched y ions: y(5), y(6), y(6)++, y(8)++  
Precursor origin neutral loss: +  

Peptide No. 777  
GRGESRSPPPYEK  
Confirmed sites: @S:7  
Ambiguous sites:  

MS/MS Fragmentation of GRGESRSPPPYEK  
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding  
Match to Query 2276: 1538.684388 from (513.902072, 3+)  
Elution from: 17.633 to 17.633 scan no 924 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1538.6878
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.007
Matched b ions: b(4), b(6)++, b(7)−98++, b(7)+, b(7)−98, b(8)−98++, b(9)+, b(10)−98++, b(11)+, b(11)−98++, b(12)−98++, b(12)++
Matched y ions: y(4), y(5), y(6)+, y(6)++, y(7)−98, y(7)−98++, y(9)+, y(9)−98++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.778
GRLELSAVPSSYSSGQLDPK
Confirmed sites:
Ambiguous sites: @S:13orS:14

MS/MS Fragmentation of GRLELSAVPSSYSSGQLDPK
Found in AT5G57330.1, aldose 1-epimerase family protein

Match to Query 4213: 2170.027836 from(1086.021194,2+)
Elution from: 43.979 to 43.979 scan no 4491 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2170.0307
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 9e-006
Matched b ions: b(4), b(6), b(7), b(8), b(10), b(12), b(14)-98, b(15)-98, b(16)-98, b(16)-98++, b(17), b(18)-98, b(18), b(18)+++, b(19)-98, b(19)-98++
Matched y ions: y(6), y(8)+++, y(10)-98, y(11), y(12)-98, y(12), y(13), y(14)-98, y(15), y(16), y(17)-98++, y(19)+
Precursor origin neutral loss: +

Peptide No.779

GRRSPSPYK
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of GRRSPSPYK
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 1030: 1206.493737 from(403.171855,3+)
Elution from: 14.605 to 14.605 scan no 709 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1206.4947
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.05
Matched b ions: b(3), b(4)−98++, b(4)++, b(5)−98++, b(6)−98++, b(6)−196++, b(7)−196++, b(8)−196++, b(8)++, b(8)−98++
Matched y ions: y'(5), y(5)++, y(6)−98++, y(6)++
Precursor origin neutral loss: +

Peptide No.780
GRRSPSPYK
Confirmed sites: ”@S:4,@Y:8”
Ambiguous sites:

MS/MS Fragmentation of GRRSPSPYK
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 918: 1206.493467 from(403.171765,3+)  
Elution from: 14.840 to 14.840 scan no 732 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1206.4947
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4  : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y8   : Phospho (Y)
Ions Score: 22 Expect: 0.044
Matched b ions: b(3), b(3)++, b(4)--98++, b(4)++, b(5)--98++, b(6)++, b(6)--98++, b(7)--98++, b(8)--98++, b(8)++
Matched y ions: y(5)++, y(6)--98++
Precursor origin neutral loss: +

Peptide No.781
GRSPPP PPPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GRSPPP PPPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 1053: 1136.548569 from(379.856799,3+)
Elution from: 16.878 to 16.878 scan no 935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1136.5492
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.011
Matched b ions: b(4)++, b(5)++, b(5)−98++, b(6)−98++, b(6)++, b(7)−98++, b(7)++, b(8)++, b(9)−98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++
Precursor origin neutral loss: +

Peptide No.782
GRSPVDLDISFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GRSPVDLDISFK
Found in AT1G21580.1, hydroxyproline–rich glycoprotein family protein

Match to Query 2151: 1412.669620 from(707.342086,2+) Elution from: 44.559 to 44.559 scan no 4606 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1412.6700
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 39 Expect: 0.0011
Matched b ions: b(3), b(3)−98, b(6), b(8), b(8)−98, b(9), b(9)−98, b(10), b(11)−98++
Matched y ions: y(3), y(4), y(6), y(7), y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.783

GRSVLDTPLSSAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GRSVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2238: 1437.695258 from(719.854905,2+)  
Elution from: 34.604 to 34.604 scan no 3279 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1437.6977
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 7.4e-005
Matched b ions: b(3)-98, b(4)-98, b(6), b(6)-98, b(7), b(7)-98, b(9), b(9)-98
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.784

GRSVLDTTPLSSAR
Confirmed sites: "@S:3,@S:10"
Ambiguous sites:

MS/MS Fragmentation of GRSVLDTTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2474: 1517.662778 from(759.838665,2+)
Elution from: 36.562 to 36.562 scan no 3542 polarity:+
Monoisotopic mass of neutral peptide \( \text{Mr}(\text{calc}) \): 1517.6640

Fixed modifications: Carbamidomethyl (C)

Variable modifications:

S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 37 Expect: 0.0016

Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6)-98, b(6), b(6)+, b(7)-98, b(7), b(7)-98++, b(9), b(10)+++, b(10)-98, b(12)

Matched y ions: y(3), y(4), y(4)-98, y(4)+, y(5), y(6), y(6)-98, y(6)+, y(7), y(7)-98, y(7)-98++, y(8)-98++, y(8)-98, y(8), y(9)-98, y(10), y(10)-98, y(11), y(11)+

Precursor origin neutral loss: +

**Peptide No. 785**

GRSVLDTPLSSAR

Confirmed sites: "@S:3,@S:11"

Ambiguous sites:

MS/MS Fragmentation of **GRSVLDTPLSSAR**

Found in **AT1G35580.1**, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2011: 1517.662928 from(759.838740,2+)

Elution from: 36.431 to 36.431 scan no 3475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1517.6640
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0017
Matched b ions: b(3)-98, b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(7)-98++, b(9), b(10)-98++, b(12)++
Matched y ions: y(4)++, y(4), y(5), y(6)-98, y(6), y(6)++, y(7), y(7)-98, y(8), y(8)-98++, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.786
GRSVLDTPPLSSAR
Confirmed sites: ”@S:3,@T:7”
Ambiguous sites:
MS/MS Fragmentation of GRSVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase
Match to Query 2362: 1517.663054 from(759.838803,2+)
Elution from: 33.131 to 33.131 scan no 3063 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1517.6640

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 43 Expect: 0.00039

Matched b ions: b(3)−98, b(3), b(4)−98, b(5)−98, b(5), b(6)−98, b(6), b(6)++, b(7)−98, b(7), b(7)−196, b(9), b(9)−98, b(10)−196++, b(10)++, b(10)−98, b(12)++

Matched y ions: y(3), y(4), y(5), y(5)++, y(6), y(7), y(7)−98, y(8), y(8)−98, y(8)−98++, y(9), y(9)−98, y(10)−98, y(10), y(11)−98, y(11), y(11)−196, y(11)++, y(12)++

Precursor origin neutral loss: +

Peptide No.787

GRSVLDTPLSSAR

Confirmed sites: "@S:3,@T:7,@S:10"

Ambiguous sites:

MS/MS Fragmentation of GRSVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2549: 1597.629084 from(799.821818,2+)

Elution from: 34.358 to 34.358 scan no 3250 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1597.6303
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00036
Matched b ions: b(3)−98, b(3), b(4)−98, b(5)−98, b(5), b(6)−98, b(6), b(7), b(7)−196, b(9)−98, b(9), b(10)−98, b(12)
Matched y ions: y(3), y(4)−98, y(4), y(5), y(6)−98, y(6), y(7), y(7)−196, y(8), y(9), y(9)−98, y(10), y(10)++, y(10)−98, y(11)−98, y(11)−196, y(11), y(11)+, y(11)−98++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.788

GRSVLDTPLSSAR
Confirmed sites: ”@S:3,@T:7,@S:11”
Ambiguous sites:

MS/MS Fragmentation of GRSVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2245: 1597.629186 from(799.821869,2+)
Elution from: 35.227 to 35.227 scan no 3360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1597.6303
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00022
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(6)-98, b(6)++, b(6), b(7), b(7)-196, b(9)-98, b(9), b(10)++, b(11)-294, b(12)++
Matched y ions: y(4)-98, y(4), y(5), y(6)-98, y(6), y(7), y(7)-196, y(8), y(8)-98, y(9), y(9)-98, y(9)-196, y(10), y(10)++, y(10)-98, y(10)-196, y(11)-98, y(11), y(11)++, y(11)-196++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.789
GRSYSRSPPPYR
Confirmed sites: ”@S:3,@S:5,@S:7”
Ambiguous sites:

MS/MS Fragmentation of GRSYSRSPPPYR
Found in AT4G31580.1, SRZ-22 (serine/arginine-rich 22)

Match to Query 2692: 1661.614240 from(831.814396,2+)
Elution from: 22.233 to 22.233 scan no 1602 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6153
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.014
Matched b ions: b(3), b(3)−98, b(4)−98, b(5)−196, b(5)−98, b(6)−98, b(7)−98, b(7)−196, b(7), b(8)−98, b(8), b(10)−98++, b(10)++, b(11)−98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)−98, y(8), y(9), y(10)−98, y(10), y(10)++, y(11)−98++
Precursor origin neutral loss: +

Peptide No.790

GRSYSRSPPPYR
Confirmed sites: "@S:3,@S:7"
Ambiguous sites: @Y:4orS:5

MS/MS Fragmentation of GRSYSRSPPPYR
Found in AT4G31580.1, SRZ-22 (serine/arginine-rich 22)

Match to Query 1906: 1661.613969 from(554.878599,3+)
Elution from: 21.934 to 21.934 scan no 1544 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6153
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y4 : Phospho (Y)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.034
Matched b ions: b(3)−98, b(3), b(5)−98, b(6)−98++, b(6)+, b(7)−196++, b(7)−98, b(7), b(7)−98++, b(7)+, b(8)−98, b(8)−196++, b(8)−98++, b(9)−196++, b(9)−98++, b(11)−98++, b(11)−196++
Matched y ions: y(3), y(4)+, y(4), y(5)+, y(5), y(6), y(6)−98, y(7)−98++, y(7)+, y(9)−98++, y(9)+, y(10)−98++, y(10)+, y(10)−196++
Precursor origin neutral loss: +

Peptide No.791

GRSYSRSPPPYR
Confirmed sites: "@S:3,@Y:11"
Ambiguous sites: @Y:4orS:5

MS/MS Fragmentation of GRSYSRSPPPYR
Found in AT4G31580.1, SRZ-22 (serine/arginine-rich 22)

Match to Query 2865: 1661.614052 from(831.814302,2+)
Elution from: 22.463 to 22.463 scan no 1633 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6153
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Y4 : Phospho (Y)
  Y11 : Phospho (Y)
Ions Score: 26 Expect: 0.012
Matched b ions: b(5)-98, b(6), b(6)-98, b(7)-98, b(8)-98, b(11), b(11)-98
Matched y ions: y(3), y(4), y(6), y(7), y(9), y(10)-98, y(10), y(10)+, y(10)-98++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.792

GRSYTPSPPR
Confirmed sites: "@S:3,@Y:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of GRSYTPSPPR
Found in AT1G55310.1, SR33 (SC35-like splicing factor 33); RNA binding

Match to Query 1717: 1356.465258 from(679.239905,2+)
Elution from: 23.100 to 23.100 scan no 1742 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1356.4666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y4 : Phospho (Y)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.063
Matched b ions: b(2), b(3), b(5)−98, b(5), b(6), b(7)−98++, b(7)−196, b(7)−98, b(7), b(8)−196++, b(9)
Matched y ions: y(3), y(4), y(5)−98, y(5), y(6), y(7), y(8)−98, y(8)−196, y(8)++
Precursor origin neutral loss: +

Peptide No. 793

GRSYTPSPPR
Confirmed sites: "@S:3,@T:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of GRSYTPSPPR
Found in AT3G13570.1, SCL30a (SC35-like splicing factor 30a); RNA binding

Match to Query 2001: 1356.464832 from(453.162220,3+)
Elution from: 23.037 to 23.037 scan no 1710 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1356.4666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.021
Matched b ions: b(4)-98, b(5)-196++, b(5)-98, b(5), b(5)-98++, b(6)-196++, b(6)+, b(7)-196++,
 b(7)-294++, b(7)-98++, b(8)-294++, b(8)-196++, b(9)-294++, b(9)-196++
Matched y ions: y(1), y(3), y(4)-98, y(5)+, y(5), y(6)-196, y(6)-98++, y(6)-196++, y(7)-98++, y(9)-
294++
Precursor origin neutral loss: +

Peptide No.794
GSADLVDDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSADLVDDR
Found in AT3G12640.1, RNA binding / nucleic acid binding

Match to Query 564: 1026.400886 from(514.207719,2+)
Elution from: 24.621 to 24.621 scan no 1787 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1026.4019
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00063
Matched b ions: b(4)-98, b(6)-98, b(7)-98
Matched y ions: y(2), y(3), y(4), y(6)
Precursor origin neutral loss: +

Peptide No. 795
GSASVISELSAADADVLLLKGYK
Confirmed sites: ”@S:2,@S:4”
Ambiguous sites: @T:23orY:24

MS/MS Fragmentation of GSASVISELSAADADVLLLKGYK
Found in AT1G55860.1, UPL1 (UBIQUITIN–PROTEIN LIGASE 1); ubiquitin–protein ligase

Match to Query 5003: 2776.227596 from(695.064175,4+)
Elution from: 49.092 to 49.092 scan no 5165 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2776.2261
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y24 : Phospho (Y)
Ions Score: 28 Expect: 0.021
Matched b ions: b(6)++, b(6), b(7), b(9), b(10)−98, b(10)++, b(12)++, b(13)−196++, b(13)++, b(13)−98++, b(14)−98++, b(15)++, b(17)++, b(18)++, b(19)++, b(21)−98++
Matched y ions: y(4), y(5), y(6)++, y(6), y(13)++, y(19)++

Peptide origin neutral loss:

Peptide No.796

GSDDGYSSDSVLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSDDGYSSDSVLR
Found in AT1G12360.1, KEU (KEULE); protein transporter

Match to Query 1433: 1436.544216 from(719.279384,2+)
Elution from: 32.848 to 32.848 scan no 2987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1436.5456
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00063
Matched b ions: b(6)-98++, b(6)-98, b(6), b(7)-98, b(10)-98
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(12)++
Precursor origin neutral loss: +

Peptide No.797
GSDDGYSSDSVLR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GSDDGYSSDSVLR
Found in AT1G12360.1, KEU (KEULE); protein transporter

Match to Query 1434: 1436.545250 from(719.279901,2+)
Elution from: 31.288 to 31.288 scan no 2782 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1436.5456
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 5.2e-007
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(10), b(11)-98, b(11), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9), y(9)++, y(10)++, y(10), y(11), y(11)++
Precursor origin neutral loss:

Peptide No.798

GSDEEDFVFHGTPIER
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSDEEDFVFHGTPIER
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 3534: 1913.780510 from(957.897531,2+)  
Elution from: 47.026 to 47.026 scan no 4938 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1913.7832
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 8.4e-007
Matched b ions: b(6)–98, b(8)–98, b(9)–98, b(10)–98, b(10), b(11)–98, b(12)–98, b(15)–98
Matched y ions: y(4), y(5), y(6), y(7), y(10), y(11), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.799

GSDSVEDVETQHQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GSDSVEDVETQHQR
Found in AT5G15020.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G01320.1); similar to paired amphipathic

Match to Query 2113: 1764.730365 from(589.250731,3+)
Elution from: 28.608 to 28.608 scan no 2418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1764.7315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.041
Matched b ions: b(5)-98, b(6)-98, b(11)-98++
Matched y ions: y(3), y(7)++, y(8)++, y(9)++, y(10)++, y(12)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.800

GSESPGVDGNTNALDYTTK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSESPGVDGNTNALDYTTK
Found in AT1G51690.1, ATB ALPHA (protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform); nucleotide binding

Match to Query 3427: 2004.828310 from(1003.421431,2+)
Elution from: 35.544 to 35.544 scan no 3394 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2004.8313

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**

S2 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 71  **Expect:** 7.9e-007

**Matched b ions:** b(7)-98, b(8)-98, b(8), b(9), b(10)-98, b(10), b(13)-98, b(13)-98++, b(14), b(14)-98, b(15), b(15)-98, b(16)-98, b(17)-98

**Matched y ions:** y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(15)++, y(15), y(16)++, y(18)-98++

**Precursor origin neutral loss:** +

---

**Peptide No. 801**

**GSESPGVDGNTNALDYTTK**

**Confirmed sites:** @S:4

**Ambiguous sites:**

**MS/MS Fragmentation of GSESPGVDGNTNALDYTTK**

Found in **AT1G51690.1**, ATB ALPHA (protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform); nucleotide binding

Match to Query 3360: 2004.828452 from(1003.421502,2+)  
Elution from: 35.499 to 35.499 scan no 3383 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2004.8313
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 4.3e-007
Matched b ions: b(7)-98, b(7), b(8)-98, b(8), b(9), b(10)-98, b(11)-98, b(12), b(14)-98, b(14), b(15), b(15)-98, b(16)-98, b(17), b(18)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(15)++, y(15), y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.802

GSFGYLDPEYFR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSFGYLDPEYFR
Found in AT5G59700.1, protein kinase, putative

Match to Query 2495: 1529.621216 from(765.817884,2+)
Elution from: 60.226 to 60.226 scan no 6365 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1529.6227
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0079
Matched b ions: b(6)−98, b(7)−98
Matched y ions: y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No. 803
GSGGSDDEDEVNSV
Confirmed sites:
Ambiguous sites: @S:2 or S:5

MS/MS Fragmentation of GSGGSDDEDEVNSV
Found in AT1G71080.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G38050.1); similar to hypothetical prote

Match to Query 1476: 1445.482226 from(723.748389,2+)
Elution from: 29.230 to 29.230 scan no 2394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1445.4831
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.00092
Matched b ions: b(7), b(8), b(10), b(11), b(12), b(13)++
Matched y ions: y(3), y(13)−98++
Precursor origin neutral loss: +

Peptide No.804

GSLEGSTGAVLK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GSLEGSTGAVLK
Found in AT4G32650.1, transcription factor

Match to Query 1185: 1197.561846 from(400.194558,3+)
Elution from: 16.312 to 16.312 scan no 835 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5642
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0047
Matched b ions: b(3)++, b(6)++, b(7)++, b(8)++, b(9)++, b(10)++, b(10)-98++, b(11)++
Matched y ions: y(1), y(2)++, y(6)++, y(10)++
Precursor origin neutral loss:

**Peptide No.805**

GSLEGSTGAVLK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of GSLEGSTGAVLK
Found in AT4G32605.1, transcription factor

Match to Query 990: 1197.560742 from(400.194190,3+)
Elution from: 15.818 to 15.818 scan no 779 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5642
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.049
Matched b ions: b(3)++, b(6), b(7)++, b(8)++, b(9)++, b(10)++, b(10)-98++, b(11)++
Matched y ions: y(6)++, y(6)-98++, y(10)++, y(10)-98++
Precursor origin neutral loss:

Peptide No.806

GSLGSPEKGENGDLKK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GSLGSPEKGENGDLKK
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 2540: 1694.785821 from(565.935883,3+)
Elution from: 19.541 to 19.541 scan no 1235 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1694.7876
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.015
Matched b ions: b(8)-98++, b(8), b(9)++, b(10)++, b(11)-98++, b(12)-98++, b(13)-98++, b(14)-98++
Matched y ions: y(4), y(6), y(7)++, y(7), y(8)++, y(9)++, y(11)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.807

GSNSPGSIDSSMDMHAE
Confirmed sites:
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of GSNSPGSIDSSMDMHAE
Found in AT4G09830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64780.1); similar to conserved hypothet

Match to Query 2280: 1800.630182 from(901.322367,2+)
Elution from: 37.650 to 37.650 scan no 3488 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.6331
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0046
Matched b ions: b(4)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(10)-98, b(15)-98++, b(16)-98++
Matched y ions: y(4), y(7), y(9), y(10), y(13)
Precursor origin neutral loss: +

Peptide No.808
GSPNNYFR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSPNNYFR
Found in AT3G02180.1, SP1L3 (SPIRAL 1–LIKE3)

Match to Query 836: 1033.401304 from(517.707928,2+)
Elution from: 29.875 to 29.875 scan no 2660 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1033.4018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.00077
Matched b ions: b(3), b(5)−98, b(6), b(6)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6)
Precursor origin neutral loss: +

Peptide No.809
GSSGISDDMESSSPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GSSGISDDMESSSPR
Found in AT4G36630.1, EMB2754 (EMBRYO DEFECTIVE 2754); small GTPase regulator

Match to Query 1974: 1590.586348 from(796.300450,2+)
Elution from: 25.492 to 25.492 scan no 1990 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1590.5869
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 5.2e-007
Matched b ions: b(5), b(6), b(10), b(12)
Matched y ions: y(2), y(3)-98, y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)+, y(13)+, y(14)+
Precursor origin neutral loss:

Peptide No.810

GSSGISDDMESSSPR
Confirmed sites:
Ambiguous sites: "@S:2orS:3, @S:11orS:12orS:13"

MS/MS Fragmentation of GSSGISDDMESSSPR
Found in AT4G36630.1, EMB2754 (EMBRYO DEFECTIVE 2754); small GTPase regulator

Match to Query 2901: 1670.551234 from(836.282893,2+) Elution from: 30.228 to 30.228 scan no 2708 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1670.5532
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0029
Matched b ions: b(6), b(8)
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.811

GSSGISDDMESSSPR
Confirmed sites: “@S:6,@S:11”
Ambiguous sites:

MS/MS Fragmentation of GSSGISDDMESSSPR
Found in AT4G36630.1, EMB2754 (EMBRYO DEFECTIVE 2754); small GTPase regulator

Match to Query 1965: 1670.552510 from(836.283531,2+)  
Elution from: 29.716 to 29.716 scan no 2486 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1670.5532
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.022
Matched b ions: b(8)-98, b(8), b(10)-98, b(10), b(11)++, b(12)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(12)++, y(12)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.812

GSSVGGLDQLESASPEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of GSSVGGLDQLESASPEK
Found in AT5G14270.1, ATBET9 (ARABIDOPSIS THALIANA BROMODOMAIN AND EXTRATERMINAL DOMAIN PROTEIN 9); DNA binding

Match to Query 3074: 1739.760686 from(870.887619,2+)
Elution from: 39.565 to 39.565 scan no 3935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1739.7614
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 4.4e-008
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(11)++, b(12), b(13), b(14)−98, b(14), b(15)−98, b (16)−98
Matched y ions: y(3), y(4), y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y (10), y(10)−98, y(11), y(11)−98++, y(12), y(12)−98, y(13), y(13)−98++, y(13)−98, y(13)++, y(14)−98, y (14), y(14)++, y(14)−98++, y(15)++, y(15)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No. 813

GSSVGLDQLESASPEK
Confirmed sites: @S:14
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of GSSVGLDQLESASPEK
Found in AT5G14270.1, ATBET9 (ARABIDOPSIS THALIANA BROMODOMAIN AND EXTRATERMINAL DOMAIN PROTEIN 9); DNA binding

Match to Query 2660: 1819.727506 from(910.871029,2+)
Elution from: 44.001 to 44.001 scan no 4456 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1819.7277
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0032
Matched b ions: b(7)-98, b(8), b(11)-98, b(13)-98
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(13), y(13)-98, y(14)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.814

GSTPTDLPGEDVADNR
Confirmed sites:
Ambiguous sites: @S:2orT:3

MS/MS Fragmentation of GSTPTDLPGEDVADNR
Found in AT5G11670.1, ATNADP-ME2 (NADP-MALIC ENZYME 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ mali

Match to Query 2011: 1722.708862 from(862.361707,2+)
Elution from: 34.737 to 34.737 scan no 3225 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1722.7097
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 3.2e-005
Matched b ions: b(6), b(7), b(7)-98, b(9)-98++, b(10), b(11), b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(9), y(10), y(11), y(13), y(13)++
Precursor origin neutral loss:

Peptide No.815
GSVSPQLQDVQTLR
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of GSVSPQLQDVQTLR
Found in AT2G39810.1, HOS1 (High expression of osmotically responsive genes 1)
Match to Query 2558: 1606.772194 from(804.393373,2+)
Elution from: 42.375 to 42.375 scan no 4192 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1606.7716
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 2.2e−005
Matched b ions: b(5), b(7)−98, b(8)−98++, b(8), b(9), b(10)−98, b(13)−98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)−98++, y(12)−98++, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.816

GSYRELSEIAEQAK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSYRELSEIAEQAK
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2962: 1659.746442 from(554.256090,3+)
Elution from: 40.124 to 40.124 scan no 4049 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1659.7505
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0027
Matched b ions: b(3), b(4), b(6)--98++, b(6)--98, b(7)--98++, b(7)--98, b(8)--98, b(8)--98++, b(9)--98++, b(10)--98++, b(10)+++, b(13)--98++, b(13)+++
Matched y ions: y(3), y(4), y(5), y(6), y(6)+++, y(7), y(8)+++, y(9)+++, y(12)+++
Precursor origin neutral loss: +

Peptide No.817

GSYRELSEIAEQAK
Confirmed sites: @Y:3
Ambiguous sites:

MS/MS Fragmentation of GSYRELSEIAEQAK
Found in AT2G18960.1, AHA1 (PLASMA MEMBRANE PROTON ATPASE); ATPase

Match to Query 2649: 1659.750405 from(554.257411,3+)
Elution from: 42.413 to 42.413 scan no 4087 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1659.7505
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3: Phospho (Y)
Ions Score: 32 Expect: 0.0073
Matched b ions: b(3), b(4), b(6), b(8), b(8)++, b(10)++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(9)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.818

GTMEGMIDKYMKCTGGGR
Confirmed sites: "@Y:10,@T:14"
Ambiguous sites:

MS/MS Fragmentation of GTMEGMIDKYMKCTGGGR
Found in AT1G71692.1, AGL12 (AGAMOUS-LIKE 12); transcription factor

Match to Query 3599: 2150.808624 from(717.943484,3+)
Elution from: 28.014 to 28.014 scan no 2388 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2150.8059
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y10 : Phospho (Y)
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.017
Matched b ions: b(3), b(7)+, b(10)+, b(11)+, b(12)+, b(15)+, b(15)-98+), b(16)+, b(16)-98+, b(17)+
Matched y ions: y(2), y(3), y(6)-98, y(6), y(7)-98+, y(8)-98, y(9)+, y(10)+, y(12)+, y(12)-98+, y(13)+, y(13)-98+, y(14)+, y(15)+, y(15)-98+, y(17)+, y(17)-98+
Precursor origin neutral loss:

Peptide No.819

GTNSETEQESLNVNVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of GTNSETEQESLNVNVR
Found in AT1G32750.1, HAF01 (Histone acetyltransferase TAFII250 family); DNA binding

Match to Query 3254: 1942.825284 from(972.419918,2+)
Elution from: 35.668 to 35.668 scan no 3411 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.8269
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 5.7e-007
Matched b ions: b(5), b(8)-98, b(8), b(9), b(11)-98, b(11), b(12), b(13)-98, b(13), b(14)-98, b(14), b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.820

GTNSETEQESLNVVNSR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of GTNSETEQESLNVVNSR
Found in AT1G32750.1, HAF01 (Histone acetyltransferase TAFII250 family); DNA binding

Match to Query 3458: 1942.824592 from(972.419572,2+)
Elution from: 37.036 to 37.036 scan no 3371 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.8269
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 9.7e-009
Matched b ions: b(6), b(7)-98, b(8), b(9), b(9)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(14)
Precursor origin neutral loss: +

Peptide No.821

GVCENDSEDEFYDAER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GVCENDSEDEFYDAER
Found in AT2G39280.1, RabGAP/TBC domain-containing protein

Match to Query 3385: 2013.691644 from(1007.853098,2+)
Elution from: 37.501 to 37.501 scan no 3652 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2013.6935

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 77 Expect: 5e-008

Matched b ions: b(6)++, b(8)—98, b(9), b(10)—98, b(10), b(11)—98, b(11), b(12)—98, b(13),
        b(13)—98, b(14), b(14)++, b(15)—98, b(15), b(15)++, b(15)—98++

Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)—98, y(11)—98, y(11), y(12), y(12)—
        98, y(13)—98++, y(14)++, y(14)—98++, y(15)—98++

Precursor origin neutral loss: +

Peptide No. 822

GVDSDELTAEK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of GVDSDELTAEK
Found in AT1G54090.1, ATEXO70D2 (exocyst subunit EXO70 family protein D2); protein binding

Match to Query 1006: 1242.501046 from (622.257799, 2+)
Elution from: 34.094 to 34.094 scan no 3027 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 1242.5016
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.1e-007
Matched b ions: b(5), b(6)–98, b(6), b(7)–98, b(7), b(8), b(8)++, b(8)–98, b(9), b(9)–98, b(10), b(10)–98, b(10)–98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)–98++, y(9)–98, y(9), y(9)++, y(10)–98++, y(10)–98
Precursor origin neutral loss: +

Peptide No.823
GVEFDDDLETEKSDGTIGER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GVEFDDDLETEKSDGTIGER
Found in AT1G42550.1, PMI1 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 4261: 2290.946180 from(1146.480366,2+)
Elution from: 41.206 to 41.206 scan no 4146 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2290.9478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 7.5e-007
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)−98, b(14), b(14)−98, b(16)−98++, b(17)−98, b(17), b(18), b(18)++, b(18)−98++, b(19)−98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)−98, y(8), y(9)−98, y(9), y(10)−98, y(11)−98, y(11), y(12)−98, y(12), y(13), y(13)−98++, y(13)−98, y(14)−98, y(14), y(14)++, y(14)−98++, y(15)−98++, y(15), y(15)++, y(15)−98, y(16)++, y(16)−98++, y(17)−98++, y(17)++, y(18)−98++, y(18)++, y(19)−98++
Precursor origin neutral loss: +

Peptide No.824

GVEFDDLETTEKSDGTIGER
Confirmed sites: "@S:13,@T:16"
Ambiguous sites:

MS/MS Fragmentation of GVEFDDLETTEKSDGTIGER
Found in AT1G42550.1, PMI1 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 4627: 2370.910714 from(1186.462633,2+)
Elution from: 44.308 to 44.308 scan no 4535 polarity:+

Peptide No.824

GVEFDDLETTEKSDGTIGER
Confirmed sites: "@S:13,@T:16"
Ambiguous sites:

MS/MS Fragmentation of GVEFDDLETTEKSDGTIGER
Found in AT1G42550.1, PMI1 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 4627: 2370.910714 from(1186.462633,2+)
Elution from: 44.308 to 44.308 scan no 4535 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2370.9141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S13 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- T16 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 40 Expect: 0.00073
Matched b ions: b(6), b(7), b(9), b(10), b(11), b(12), b(13)–98, b(14)–98, b(16)–98, b(17)–98, b(18)–98++, b(19)–196++, b(19)–196
Matched y ions: y(3), y(4), y(6)–98, y(6), y(7)–98, y(8)–98, y(8)–196, y(8), y(9)–98, y(9), y(10)–196, y(11), y(11)–98, y(13)–98, y(13)++, y(13)–196, y(13), y(14), y(14)–98, y(14)–98++, y(15)–98++, y(15)++, y(16)–196, y(16)–196++, y(17)–98++, y(17)+, y(18)–98++, y(19)–196++
Precursor origin neutral loss: +

Peptide No. 825
GVPFSKSPSPEISK
Confirmed sites: ”@S:7,@S:9”
Ambiguous sites:

MS/MS Fragmentation of GVPFSKSPSPEISK
Found in AT5G12080.1, mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein

Match to Query 2749: 1618.703248 from(810.358900,2+)
Elution from: 35.133 to 35.133 scan no 3350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1618.7044
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.029
Matched b ions: b(5), b(6), b(7)−98, b(7), b(9)−98, b(10)++, b(13)−98++
Matched y ions: y(5), y(6), y(7)−98, y(7)−98, y(8), y(9), y(10), y(10)−98++, y(11), y(11)++, y(11)−98++, y(12)++, y(12)−98, y(12)−98++, y(12)−196++, y(13)−98++, y(13)−196, y(13)−196++
Precursor origin neutral loss: +

Peptide No.826

GVSDLYLFTDFSDEDTEEDGGYRLPQEMFVSR
Confirmed sites: "@S:3,@Y:6,@T:9,@S:12"
Ambiguous sites:

MS/MS Fragmentation of GVSDLYLFTDFSDEDTEEDGGYRLPQEMFVSR
Found in AT3G58940.1, F-box family protein

Match to Query 4311: 4036.506096 from(1346.509308,3+)
Elution from: 28.641 to 28.641 scan no 2434 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 4036.5116
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Y6 : Phospho (Y)
T9 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 22 Expect: 0.068
Matched b ions: b(6)-98, b(8)-98, b(13)+, b(19)-98++, b(20)+, b(21)+, b(22)-196++, b(23)-294++, b(24)+, b(25)+, b(25)-98++, b(26)-294++, b(30)-294++
Matched y ions: y(13)++, y(15)++, y(15), y(16)++, y(18)++, y(20)+, y(24)-98++, y(26)-196++, y(26)-98++, y(27)-98++, y(27)+, y(28)-196++, y(28)-98++, y(29)-196++
Precursor origin neutral loss: +

Peptide No.827
GVSDSELLELSQLEEQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GVSDSELLELSQLEEQK
Found in AT4G31590.1, ATCSLC05 (Cellulose synthase-like C5); transferase, transferring glycosyl groups

Match to Query 3695: 1982.906938 from(992.460745,2+)
Elution from: 60.952 to 60.952 scan no 6453 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.9085
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 1.1e-006
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98, b(12)+, b(13)-98, b(13), b(14)-98, b(14)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.828

GVSDSELLELSQLEEQK
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of GVSDSELLELSQLEEQK
Found in AT4G31590.1, ATCSLC05 (Cellulose synthase–like C5); transferase, transferring glycosyl groups

Match to Query 3729: 1982.907206 from(992.460879,2+)
Elution from: 60.685 to 60.685 scan no 6530 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1982.9085
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 1.1e-005
Matched b ions: b(6)-98, b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-98++, b(11), b(13), b(14)-98, b(14)
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.829
GVTFGSFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GVTFGSFK
Found in AT1G08640.1, heat shock protein binding

Match to Query 363: 921.398634 from(461.706593,2+) Elution from: 41.280 to 41.280 scan no 4132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 921.3997
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00036
Matched b ions: b(2), b(3), b(4), b(7)-98
Matched y ions: y(2), y(3)-98, y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98++, y(6)-98, y(6)+, y(7)-98, y(7)-98++, y(7)++
Precursor origin neutral loss: +

Peptide No.830

GWSESSSPNVR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GWSESSSPNVR
Found in AT1G62020.1, coatamer protein complex, subunit alpha, putative

Match to Query 1658: 1284.512334 from(643.263443,2+);
Elution from: 25.725 to 25.725 scan no 2126 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1284.5135
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00039
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(7)–98, b(7), b(8)–98, b(9)++, b(10), b(10)–98
Matched y ions: y(2), y(4), y(5)–98, y(6), y(7), y(7)–98, y(8), y(9), y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.831

GYDGADSPIR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 800: 1129.444304 from(565.729428,2+) 
Elution from: 23.227 to 23.227 scan no 1697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1129.4441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.000033
Matched b ions: b(2), b(3), b(5)
Matched y ions: y(1), y(3), y(4), y(5), y(7), y(7)-98, y(8)+, y(8)
Precursor origin neutral loss: +

Peptide No.832

GYDGADSPIRESPSR
Confirmed sites:
Ambiguous sites: @S:12orS:14orS:7

MS/MS Fragmentation of GYDGADSPIRESPSR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 2750: 1685.703627 from(562.908485,3+) Elution from: 25.972 to 25.972 scan no 2160 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1685.7046
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.026
Matched b ions:
Matched y ions: y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.833
GYDGADSPIRESPSR
Confirmed sites: "@S:7,@S:12"
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIRESPSR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 2983: 1765.669950 from(589.563926,3+)
Elution from: 26.550 to 26.550 scan no 1959 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1765.6709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 3.2e-005
Matched b ions: b(2), b(3), b(5), b(10)+, b(11)−98++
Matched y ions: y(3), y(4)+, y(4), y(5)−98, y(6)−98++, y(6)+, y(7)+, y(7)−98++, y(8)+, y(9)+, y(9)−98++, y(9)−196++, y(10)+, y(10)−98++, y(11)+, y(11)−98++, y(12)+, y(12)−98++, y(13)+, y(13)−98++, y(13)−196++
Precursor origin neutral loss: +

Peptide No.834
GYDGADSPIRESPSR
Confirmed sites: “@S:7,@S:14”
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIRESPSR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 2209: 1765.670049 from(589.563959,3+)
Elution from: 26.199 to 26.199 scan no 1992 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1765.6709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00017
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(10)++
Matched y ions: y(3)++, y(5)-98, y(5)+, y(6)-98++, y(7)++, y(8), y(8)-98++, y(8)+, y(9)-196++, y(9)-98++, y(10)+, y(10)-98++, y(11)+, y(11)-98++, y(12)++, y(12)-98++, y(13)+, y(13)-98++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.835
GYDGADSPIRESPSR
Confirmed sites: "@Y:2,@S:12"
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIRESPSR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 3082: 1765.669730 from(883.842141,2+)
Elution from: 26.204 to 26.204 scan no 2026 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1765.6709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y2 : Phospho (Y)
  S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.018
Matched b ions: b(10), b(11), b(12)–98
Matched y ions: y(3), y(4), y(6), y(7)++, y(7), y(7)–98, y(8)–98++, y(8)–98, y(8), y(12)–98++
Precursor origin neutral loss: +

Peptide No.836

GYDGADSPIRESPSR
Confirmed sites: “@Y:2,@S:14”
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIRESPSR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 3231: 1765.669566 from(883.842059,2+)
Elution from: 25.181 to 25.181 scan no 2018 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1765.6709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0089
Matched b ions: b(6), b(9), b(10), b(10)+, b(11), b(13)+, b(14), b(14)+
Matched y ions: y(2), y(3)-98, y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(7)+, y(7)-98, y(7), y(8),
y(8)-98+, y(8)-98, y(9)-98++, y(9), y(10), y(11)+, y(12)+, y(12)-98++, y(13)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.837
GYDGADSPIRESPSRSPPAEE
Confirmed sites: "@S:12,@S:16"
Ambiguous sites:

MS/MS Fragmentation of GYDGADSPIRESPSRSPPAEE
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 3391: 2375.928784 from(1188.971668,2+)
Elution from: 33.456 to 33.456 scan no 2970 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2375.9308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0047
Matched b ions: b(11), b(12), b(12)–98, b(13)–98, b(14), b(15), b(15)–98++, b(16)–196, b(16)–98, b(16), b(19)–98++, b(20)+, b(20)–98++
Matched y ions: y(5), y(6), y(6)–98, y(7), y(9)–98, y(9), y(10)–98, y(11)–196, y(13)–196++, y(13)+, y(14)–98++, y(15)–98++, y(15)–196++, y(15)+, y(15), y(16)++, y(16)–196++, y(18)–98++, y(18)+, y(18)–196++, y(19)–98++, y(20)++
Precursor origin neutral loss: +

Peptide No.838
GYDGADSPIRESSPSR
Confirmed sites: ”@S:13,@S:15”
Ambiguous sites:
MS/MS Fragmentation of GYDGADSPIRESSPSR
Found in AT5G52040.2, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 2366: 1852.702041 from(618.574623,3+)
Elution from: 25.996 to 25.996 scan no 1994 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.7029
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.04
Matched b ions: b(2), b(6)
Matched y ions: y(4), y(8)++, y(9)−98++, y(9)++, y(10)++, y(11)++, y(12)++, y(12)−196++, y(13)++, y(13)−98++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.839
GYDGADSPIRESSPSR
Confirmed sites: @S:7
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of GYDGADSPIRESSPSR
Found in AT5G52040.2, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 2408: 1852.700928 from(618.574252,3+)  
Elution from: 26.114 to 26.114 scan no 1981 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.7029
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 22 Expect: 0.04  
Matched b ions: b(3), b(6)  
Matched y ions: y(3), y(7)++, y(9)++, y(10)++, y(11)++, y(11)—98++, y(12)++, y(13)++, y(13)—98++, y(14)++, y(14)—98++  
Precursor origin neutral loss: +

Peptide No.840

HAETDDELLEK
Confirmed sites: @T:4  
Ambiguous sites:

MS/MS Fragmentation of HAETDDELLEK
Found in AT3G18240.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21460.1); similar to Os08g0513300 [Oryz]

Match to Query 1494: 1378.563866 from(690.289209,2+)  
Elution from: 25.629 to 25.629 scan no 2053 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1378.5653
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 5.8e-008
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)++, b(7)-98++, b(8), b(8)-98, b(8)++, b(9)-98, b(9), b(10)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98++, y (10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.841
HAETDDELMEK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of HAETDDELMEK
Found in AT4G21460.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2); similar to Os08g0513300 [Oryz

Match to Query 1469: 1396.520432 from(699.267492,2+)
Elution from: 22.463 to 22.463 scan no 1586 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1396.5217
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 6.9e-008
Matched b ions: b(2), b(3), b(4)−98, b(4), b(4)+, b(5)−98, b(5), b(6)−98, b(6), b(7), b(7)−98, b(8), b(8)−98, b(9)−98, b(9), b(9)−98++, b(10), b(10)−98
Matched y ions: y(2), y(3), y(4), y(4)+, y(5), y(6), y(7), y(8)−98, y(8), y(9)−98, y(9), y(10)−98, y(10), y(10)−98++, y(10)+
Precursor origin neutral loss: +

Peptide No.842

HAETDDELMEK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of HAETDDELMEK
Found in AT4G21460.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2); similar to Os08g0513300 [Oryz]

Match to Query 1955: 1412.515874 from(707.265213,2+)
Elution from: 19.071 to 19.071 scan no 1160 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1412.5167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 50 Expect: 3.4e-005
Matched b ions: b(4)-98, b(5)-98, b(7)-98, b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(9)-98, y(9)-98++
Precursor origin neutral loss: +

Peptide No.843

HDDSDDEVMDVVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HDDSDDEVMDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 2494: 1610.590038 from(806.302295,2+)
Elution from: 39.021 to 39.021 scan no 3637 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1610.5919
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 1.3e-009
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)-98, b(10)-98++, b(11)-98++, b(11)-98, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.844
HDDSDDEVMDVVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HDDSDDEVMDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 1864: 1626.586558 from(814.300555,2+);
Elution from: 29.395 to 29.395 scan no 2416 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1626.5869
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 89 Expect: 4.9e-009
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9), b(10), b(11), b(12), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)+, y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98++, y(12)-98
Precursor origin neutral loss: +

Peptide No.845

HDGIHDSPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of HDGIHDSPR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1045: 1112.439010 from(557.226781,2+)
Elution from: 14.286 to 14.286 scan no 671 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1112.4400
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00081
Matched b ions: b(2), b(4), b(6), b(7)−98
Matched y ions: y(1), y(2), y(3), y(4)−98, y(5), y(7), y(7)−98, y(8)−98++, y(8)
Precursor origin neutral loss: +

Peptide No.846

HELEEGELSPTASR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of HELEEGELSPTASR
Found in AT1G10450.1, paired amphipathic helix repeat-containing protein

Match to Query 2337: 1633.697162 from(817.855857,2+)
Elution from: 26.836 to 26.836 scan no 2216 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1633.6984
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 8.3e-007
Matched b ions: b(2), b(4), b(5), b(6), b(8), b(9)−98, b(9), b(10)++, b(12)−98++, b(12)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6)−98, y(6), y(7)−98, y(8)−98, y(9)−98, y(9), y(10)−98, y(10), y(11), y(12)−98, y(12), y(13)−98, y(13)−98++, y(13)+
Precursor origin neutral loss: +

Peptide No.847
HELEEGELSPTASR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of HELEEGELSPTASR
Found in AT1G10450.1, paired amphipathic helix repeat-containing protein

Match to Query 1883: 1633.697307 from(545.573045,3+)
Elution from: 28.353 to 28.353 scan no 2277 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1633.6984
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.017
Matched b ions: b(4), b(5), b(7), b(7)++, b(9)++, b(10)++, b(12)−98++, b(12)++
Matched y ions: y(4), y(5)−98, y(6), y(6)++, y(7)++, y(7)−98++, y(7), y(8)++, y(10)++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.848

HEVPFDSDQDED
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of HEVPFDSDQDED
Found in AT2G03390.1, uvrB/uvrC motif-containing protein

Match to Query 1616: 1396.478906 from(699.246729.2+) Elution from: 32.006 to 32.006 scan no 2918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1396.4820
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00033
Matched b ions: b(2), b(3), b(5), b(6), b(8)–98, b(8), b(9), b(9)++, b(9)–98++, b(10)–98++, b(10)++ b(10)
Matched y ions: y(3), y(5)–98, y(5), y(6), y(6)–98, y(7), y(8), y(8)–98, y(9)–98
Precursor origin neutral loss: +

Peptide No.849
HFSFGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of HFSFGSR
Found in AT2G21500.1, protein binding / zinc ion binding

Match to Query 474: 916.358350 from(459.186451,2+)
Elution from: 28.027 to 28.027 scan no 2407 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 916.3592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 Expect: 0.05
Matched b ions: b(2), b(3)−98
Matched y ions: y(4), y(5)−98, y(5), y(6)−98
Precursor origin neutral loss: +

Peptide No.850
HGGFAYMYFDDDESHK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of HGGFAYMYFDDDESHK
Found in AT4G13510.1, AMT1;1 (AMMONIUM TRANSPORT 1); ammonium transporter

Match to Query 3716: 1997.728962 from(999.871757,2+) Elution from: 44.706 to 44.706 scan no 4645 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1997.7291
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00037
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(11), b(12), b(14)--98, b(15)++
Matched y ions: y(8), y(8)--98, y(9), y(10)--98, y(11)++
Precursor origin neutral loss: +

Peptide No.851
HHTEDTDENTQAAEIER
Confirmed sites:
Ambiguous sites: @T:3orT:6

MS/MS Fragmentation of HHTEDTDENTQAAEIER
Found in AT2G26300.1, GPA1 (G PROTEIN ALPHA SUBUNIT 1); signal transducer

Match to Query 3782: 2074.824090 from(692.615306,3+)
Elution from: 21.652 to 21.652 scan no 1338 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2074.8229
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 31 Expect: 0.0052
Matched b ions: b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(15)++
Matched y ions: y(4), y(5), y(7), y(8), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.852
HKSFDDDDSTMR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of HKSFDDDDSTMR
Found in AT3G14350.1, leucine-rich repeat transmembrane protein kinase, putative
Match to Query 2093: 1532.559388 from(767.286970,2+)
Elution from: 19.063 to 19.063 scan no 1205 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.5603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00011
Matched b ions: b(5), b(8)
Matched y ions: y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(10)−98, y(10), y(11)−98++
Precursor origin neutral loss: +

Peptide No.853
HLNQQPSESVSDSQSPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of HLNQQPSESVSDSQSPR
Found in AT5G65910.1, BSD domain-containing protein

Match to Query 3701: 1974.842637 from(659.288155,3+)
Elution from: 20.727 to 20.727 scan no 1387 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1974.8432
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 1.5e-006
Matched b ions: b(5), b(6)++, b(7)++, b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(11)++, b(13)++, b(14)++, b(15)−98++, b(15)++, b(16)−98++
Matched y ions: y(2), y(3), y(3)−98, y(4)−98, y(5)−98, y(6), y(7), y(7)++, y(8), y(8)−98, y(8)−98++, y(9), y(10)−98++, y(10)++, y(11)++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.854
HLQEIPRSPSASP-DNGIAK
Confirmed sites: ”@S:8,@S:12”
Ambiguous sites:

MS/MS Fragmentation of HLQEIPRSPSASP-DNGIAK
Found in AT5G13530.1, KEG (KEEP ON GOING); protein binding / protein kinase/ ubiquitin−protein ligase

Match to Query 4239: 2175.965163 from(726.328997,3+)
Elution from: 31.264 to 31.264 scan no 2708 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2175.9715
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(2), b(3), b(4), b(5), b(7)+, b(8)+, b(8)-98++, b(8)-98, b(9)-98++, b(9)-98++, b(11)-98++, b(11)+, b(12)-98++, b(12)-196++, b(13)-196++, b(14)-98++, b(14)+, b(16)+, b(16)-98++, b(17)+, b(17)-98++, b(17)-196++, b(18)-98++, b(18)+, b(18)-196++
Matched y ions: y(2), y(5)+, y(5), y(6), y(7), y(8)-98, y(8), y(9), y(10), y(11)-98, y(11), y(11)+, y(12)-196++, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(14)-196++, y(15)-98++, y(15)+, y(16)-196++, y(16)-98++, y(16)+, y(17)-196++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.855
HLSDDGYFSDSVLGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of HLSDDGYFSDSVLGR
Found in AT4G12120.1, SEC1B; protein transporter

Match to Query 3186: 1746.724286 from(874.369419,2+)
Elution from: 46.896 to 46.896 scan no 4921 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1746.7250
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00013
Matched b ions: b(2), b(4)–98, b(5), b(5)–98, b(7)–98, b(8), b(9), b(13)
Matched y ions: y(5), y(7), y(10), y(10)+, y(11), y(12), y(13)–98, y(13)
Precursor origin neutral loss: +

Peptide No.856

HLSWSVNEISTQLSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of HLSWSVNEISTQLSR
Found in AT2G15900.1, phox (PX) domain-containing protein

Match to Query 3372: 1835.853124 from(918.933838,2+)
Elution from: 52.455 to 52.455 scan no 5576 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1835.8567
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0008
Matched b ions: b(3)−98, b(4)++, b(5), b(8), b(9)−98, b(9), b(10)
Matched y ions: y(5)++, y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13)−98, y(14)−98++
Precursor origin neutral loss: +

Peptide No.857
HPWLSYPYEPISA
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of HPWLSYPYEPISA
Found in AT1G73450.1, protein kinase, putative

Match to Query 2586: 1638.709438 from(820.361995,2+)
Elution from: 59.747 to 59.747 scan no 6183 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1638.7119
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 9.6e-005
Matched b ions: b(4), b(6), b(8), b(9), b(11)
Matched y ions: y(3), y(4), y(4)-98, y(5), y(7)-98, y(7), y(8), y(11)
Precursor origin neutral loss: +

Peptide No.858

HRDYSPPLAR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of HRDYSPPLAR
Found in AT4G28990.1, RNA-binding protein-related

Match to Query 1305: 1290.583659 from(431.201829,3+)
Elution from: 22.087 to 22.087 scan no 1574 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1290.5870
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.024
Matched b ions: b(3), b(5)−98++, b(5), b(5)−98, b(5)++, b(6)−98, b(6)−98++, b(8)++, b(8)−98++, b(9)−98++
Matched y ions: y(2), y(4), y(5), y(5)++, y(6)++, y(7)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.859

HRLSSQGLLSPISR
Confirmed sites: “@S:4,@S:5”
Ambiguous sites:

MS/MS Fragmentation of HRLSSQGLLSPISR
Found in AT2G39130.1, amino acid transporter family protein

Match to Query 3225: 1806.851943 from(603.291257,3+) Elution from: 42.275 to 42.275 scan no 4306 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1806.8542
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0092
Matched b ions: b(6)-98++, b(7)++, b(7), b(7)-98++, b(8), b(8)-98++, b(8)++, b(9)++, b(9), b(9)-196++, b(9)-98++, b(10)++, b(10)-98++, b(10)-196++, b(11)-98++, b(11)-196++, b(12)++, b(13)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(9)++, y(11)-98++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.860

HSLSVDGSSTLESIEAK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HSLSVDGSSTLESIEAK
Found in AT2G40620.1, bZIP transcription factor family protein

Match to Query 3031: 1838.827754 from(920.421153,2+)
Elution from: 42.420 to 42.420 scan no 4306 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1838.8298
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 6.3e-006
Matched b ions: b(5)–98, b(6), b(8), b(12)–98++, b(13)++, b(15)–98
Matched y ions: y(3), y(5), y(6), y(7), y(11), y(12), y(13), y(14)–98, y(14), y(15)–98, y(16)–98++
Precursor origin neutral loss: +

Peptide No.861

HSQHKNTLYSSHDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of HSQHKNTLYSSHDK
Found in AT1G70620.1, cyclin-related

Match to Query 2748: 1760.760663 from(587.927497,3+)
Elution from: 25.828 to 25.828 scan no 2079 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1760.7631
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.051
Matched b ions: b(4), b(7)++, b(7), b(8)++, b(9)+, b(12)−98++, b(12)++, b(13)−98++, b(13)++
Matched y ions: y(4), y(5)−98, y(5), y(6), y(6)+, y(6)−98, y(7)−98++, y(7)−98, y(7)+, y(8)−98, y(9)−98++, y(9)+, y(12)+
Precursor origin neutral loss: +

Peptide No.862

HSYSENDLLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HSYSENDLLK
Found in AT5G52580.1, similar to Os02g0709800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047892.1); similar to Ra

Match to Query 1218: 1284.537826 from(643.276189,2+)
Elution from: 30.291 to 30.291 scan no 2683 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1284.5387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.5e-005
Matched b ions: b(2), b(4)–98, b(5)–98, b(6), b(7)+, b(7), b(7)–98, b(8), b(9), b(9)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)–98, y(8)–98, y(8), y(9)–98, y(9), y(9)–98++
Precursor origin neutral loss: +

Peptide No.863
HVESMSQLPSGAGK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HVESMSQLPSGAGK
Found in AT5G36880.1, acetyl-CoA synthetase, putative / acetate-CoA ligase, putative

Match to Query 1895: 1506.652396 from(754.333474,2+)
Elution from: 27.505 to 27.505 scan no 2306 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1506.6537
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0027
Matched b ions: b(5)–98, b(7), b(8)–98, b(8), b(12)++
Matched y ions: y(6), y(7), y(9), y(10), y(11)–98, y(12)–98
Precursor origin neutral loss: +

Peptide No.864

HYESEDEEVDQTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HYESEDEEVDQTR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 2039: 1715.630840 from(858.822696,2+)
Elution from: 21.369 to 21.369 scan no 1470 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.6312
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 3.7e-005
Matched b ions: b(3), b(4)-98, b(6), b(9)-98, b(9), b(10), b(11)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(11)-98
Precursor origin neutral loss: +

Peptide No.865
IALESESPAK
Confirmed sites: @S:5
Ambiguous sites:
MS/MS Fragmentation of IALESESPAK
Found in AT3G61260.1, DNA-binding family protein / remorin family protein

Match to Query 748: 1123.515214 from(562.764883,2+) Elution from: 26.957 to 26.957 scan no 2091 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.5162
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2e−005
Matched b ions: b(2), b(3), b(4), b(5)++, b(5)−98, b(6)−98, b(7)−98, b(7), b(8)−98, b(9)−98
Matched y ions: y(3), y(6), y(6)−98, y(7), y(7)−98, y(8)++, y(8), y(8)−98, y(8)−98++, y(9), y(9)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.866
IALESESPAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IALESESPAK
Found in AT3G61260.1, DNA-binding family protein / remorin family protein

Match to Query 748: 1123.515560 from(562.765056,2+)
Elution from: 25.658 to 25.658 scan no 2056 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.5162
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.8e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8)-98, b(9), b(9)-98
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)+, y(8), y(8)-98, y(8)-98++, y(9), y(9)+
Precursor origin neutral loss: +

Peptide No.867
IAQENESGEEMLK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IAQENESGEEMLK
Found in AT2G25650.1, DNA-binding storekeeper protein-related

Match to Query 2401: 1556.642158 from(779.328355,2+)
Elution from: 31.168 to 31.168 scan no 2695 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1556.6429
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0016
Matched b ions: b(5), b(6), b(9)**, b(9)-98, b(10), b(11), b(11)-98, b(11)**, b(12), b(12)-98, b(12)**
Matched y ions: y(3), y(4), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(11)-98**, y(11)**
  y(11)-98, y(12)**, y(12)-98**
Precursor origin neutral loss: +

Peptide No.868

IAQGSQSADPNPAMASQTASVK
Confirmed sites: @S:7
Ambiguous sites: @T:18orS:20

MS/MS Fragmentation of IIAQGSQSADPNPAMASQTASVK
Found in AT3G43300.1, ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding

Match to Query 4444: 2333.957622 from(778.993150,3+)
Elution from: 32.638 to 32.638 scan no 2987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2333.9600
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  M14 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
  S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.046
Matched b ions: b(3), b(6), b(11)+, b(11)−98++, b(12)−98++, b(13)+, b(14)−98++, b(15)+
Matched y ions: y(5), y(7)−98, y(9), y(12)+, y(13)−98++, y(14)−98++, y(19)−196++
Precursor origin neutral loss: +

Peptide No.869

ICCVTYSVSRLSLMLSPIPAVALTR
Confirmed sites: @T:5,@Y:6,@S:7,@T:24
Ambiguous sites:

MS/MS Fragmentation of ICCVTYSVSRLSLMLSPIPAVALTR
Found in AT4G00400.1, phospholipid/glycerol acyltransferase family protein

Match to Query 4750: 3142.348941 from(1048.456923,3+)
Elution from: 59.556 to 59.556 scan no 6321 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3142.3509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y6 : Phospho (Y)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T24 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.049
Matched b ions: b(7), b(8)−98, b(9), b(12)−196
Matched y ions: y(6), y(7)−98, y(16)+++, y(17)+++, y(17), y(18)−98++, y(18)+++, y(19)+++, y(22)+++, y(24)++
Precursor origin neutral loss:

Peptide No.870
ICSSKGTILIAR
Confirmed sites: "@S:3,@S:4,@T:7"
Ambiguous sites:

MS/MS Fragmentation of ICSSKGTILIAR
Found in AT1G73480.1, hydrolase, alpha/beta fold family protein

Match to Query 2179: 1557.643544 from(779.829048,2+)
Elution from: 33.597 to 33.597 scan no 3093 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1557.6428
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.046
Matched b ions: b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(11)++
Matched y ions: y(3), y(4), y(5), y(9)-196++
Precursor origin neutral loss: +

Peptide No.871
IDDTATSENEVTEIEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IDDTATSENEVTEIEK
Found in AT5G01400.1, ESP4 (ENHANCED SILENCING PHENOTYPE 4); binding

Match to Query 2410: 1872.785660 from(937.400106,2+)
Elution from: 35.762 to 35.762 scan no 3367 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1872.7877
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 86 Expect: 2e-008
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(10), b(11), b(11)-98, b(12), b(13), b(14), b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(10)-98, y(11), y(12), y(13)+, y(13), y(14)++
Precursor origin neutral loss: +

Peptide No.872
IDGVSVSSSLSSEASSPK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of IDGVSVSSSLSSEASSPK
Found in AT5G26740.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05940.1);
similar to Protein of unknown
Match to Query 3197: 1815.813310 from(908.913931,2+)
Elution from: 40.182 to 40.182 scan no 4009 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1815.8139
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 93 Expect: 4.4e-009
Matched b ions: b(6), b(9), b(10), b(11), b(12), b(13), b(14), b(15), b(16)-98, b(17)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13)-98, y(13), y(14), y(14)+, y(15)-98, y(15)-98++, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.873

IDIDESLFSN
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IDIDESLFSN
Found in AT2G38140.1, PSRP4 (PLASTID–SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome

Match to Query 1044: 1231.499632 from(616.757092,2+)
Elution from: 59.625 to 59.625 scan no 6349 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1231.5009
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00027
Matched b ions: b(5), b(6), b(7), b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)−98, y(9)++
Precursor origin neutral loss: +

Peptide No.874

IDSEGVLCGASFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IDSEGVLCGASFK
Found in AT3G15450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1); similar to unknown [Glycine m

Match to Query 2297: 1461.619286 from(731.816919,2+)  
Elution from: 45.458 to 45.458 scan no 4718 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1461.6210
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 9.3e-008
Matched b ions: b(5)–98, b(6)–98, b(7)–98, b(8)–98, b(10)–98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11)–98++, y(12)–98, y(12)–98++
Precursor origin neutral loss: +

Peptide No.875

IDSFNGEQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IDSFNGEQR
Found in AT5G22035.1, ubiquitin−specific protease−related

Match to Query 1176: 1144.454162 from(573.234357,2+)
Elution from: 23.192 to 23.192 scan no 1783 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1144.4550
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.031
Matched b ions: b(4)-98, b(5), b(7)-98
Matched y ions: y(3), y(4), y(5)
Precursor origin neutral loss: +

Peptide No.876

IDTLTPQDSPQRV
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IDTLTPQDSPQRV
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 2399: 1548.717538 from(775.366045,2+) 
Elution from: 34.972 to 34.972 scan no 3305 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1548.7185
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.001
Matched b ions: b(3), b(5), b(8), b(9)++, b(10)−98++, b(11)++, b(12)++, b(12)−98++
Matched y ions: y(2), y(4), y(5), y(6)−98, y(7), y(8)−98, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.877

IDTLTPQDSPQRV
Confirmed sites: @S:9
Ambiguous sites: @T:3orT:5

MS/MS Fragmentation of IDTLTPQDSPQRV
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 1871: 1628.683736 from(815.349144,2+) Elution from: 36.624 to 36.624 scan no 3380 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1628.6848
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.014
Matched b ions: b(5)-98, b(8), b(9)-98, b(9)-196, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(11)-98++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.878
IDVYFNEASGGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IDVYFNEASGGK
Found in AT5G44340.1, TUB4 (tubulin beta-4 chain)

Match to Query 1556: 1378.579448 from(690.297000,2+)
Elution from: 41.787 to 41.787 scan no 4187 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1378.5805
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0012
Matched b ions: b(3), b(5), b(6), b(11)--98++
Matched y ions: y(4)--98, y(5)--98, y(5), y(6), y(7), y(7)--98, y(8), y(8)++, y(8)--98, y(9)++, y(9)--98, y(9), y(10)--98++, y(10), y(10)--98, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.879
IEDEPRSPTSPQLR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IEDEPRSPTSPQLR
Found in AT3G55600.1, similar to cation exchanger, putative (CAX10) [Arabidopsis thaliana] (TAIR:AT1G54110.1); similar to

Match to Query 2577: 1703.786205 from(568.936011,3+) 
Elution from: 26.107 to 26.107 scan no 2117 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1703.7879
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.057
Matched b ions: b(2), b(4), b(7)-98, b(9)-98++
Matched y ions: y(4), y(6), y(7)+, y(7), y(10)+, y(10)-98++, y(11)+, y(12)-98++, y(12)+, y(13)++
Precursor origin neutral loss:

Peptide No.880

IEEDVTSEVEMASK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IEEDVTSEVEMASK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 1833: 1645.676848 from(823.845700,2+)
Elution from: 40.975 to 40.975 scan no 4017 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1645.6793
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 7.5e-007
Matched b ions: b(5), b(8), b(9), b(9)-98, b(10)-98, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(9)-98, y(10), y(11), y(13)++
Precursor origin neutral loss:

Peptide No.881
IEEDVTSEVEMASK
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of IEEDVTSEVEMASK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding
Match to Query 2506: 1661.675814 from(831.845183,2+)
Elution from: 39.101 to 39.101 scan no 3865 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6743
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 Expect: 0.0066
Matched b ions: b(5), b(6), b(10), b(11)++, b(13)
Matched y ions: y(3), y(5), y(6), y(8)−98++, y(8), y(9)−98, y(9), y(10), y(10)−98, y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.882

IEEDVTSEVEMASK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of IEEDVTSEVEMASK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 2688: 1645.678288 from(823.846420,2+)
Elution from: 42.081 to 42.081 scan no 4241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1645.6793
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1.2e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)–98, b(7)–98, b(8)–98, b(9), b(10)–98, b(10), b(11), b(12), b(12)–98, b(13), b(13)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)–98, y(10), y(10)–98, y(11), y(11)–98, y(12)++, y(12), y(13)++
Precursor origin neutral loss:

Peptide No.883
IELGLSSDEDEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IELGLSSDEDEK
Found in AT1G06210.1, VHS domain-containing protein / GAT domain-containing protein

Match to Query 1316: 1413.590176 from(707.802364,2+)
Elution from: 38.206 to 38.206 scan no 3676 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1413.5912
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 7.7e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6)−98, b(7)+, b(7)−98, b(8), b(8)−98, b(9), b(9)−98, b(10), b(10)−98, b(10)−98++, b(11), b(11)−98, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98, y(7), y(8), y(8)−98, y(9)−98++, y(9)−98, y(9), y(10)+, y(10), y(10)−98++, y(10)−98, y(11)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.884
IELGLSSDEDEK
Confirmed sites: "@S:6,@S:7"
Ambiguous sites:

MS/MS Fragmentation of IELGLSSDEDEK
Found in AT1G06210.1, VHS domain-containing protein / GAT domain-containing protein

Match to Query 1578: 1493.556532 from(747.785542,2+)
Elution from: 43.591 to 43.591 scan no 4160 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1493.5575  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
S7: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
Ions Score: 44 Expect: 0.00015  
Matched b ions: b(2), b(3), b(4), b(5), b(8), b(9)-98, b(10)-98, b(10), b(10)-196, b(11), b(11)-98  
Matched y ions: y(2), y(3), y(4), y(6), y(7)-98, y(7), y(7)-196, y(8)-98, y(9)-98, y(9), y(9)-196, y(10)-98++, y(10), y(10)-196, y(10)-98, y(10)+, y(11)+  
Precursor origin neutral loss: +  

Peptide No. 885  
IELGLSSDEDEK  
Confirmed sites: @S:7  
Ambiguous sites:  

MS/MS Fragmentation of IELGLSSDEDEK  
Found in AT1G06210.1, VHS domain-containing protein / GAT domain-containing protein  
Match to Query 1727: 1413.590088 from(707.802320,2+)  
Elution from: 38.340 to 38.340 scan no 3764 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1413.5912
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 3.7e-006
Matched b ions: b(2), b(3), b(4), b(5), b(7)++, b(7)–98, b(8), b(8)–98, b(9), b(9), b(10), b(10)–98, b(10)–98++, b(11), b(11)++, b(11)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)–98++, y(7)–98, y(7), y(8)–98, y(8), y(8)++, y(8)–98++, y(9)–98, y(9), y(9)–98++, y(10), y(10)–98++, y(10)–98, y(11), y(11)++, y(11)–98, y(11)–98++
Precursor origin neutral loss: +

Peptide No.886
IELQSQSWPMQQSFSPEK
Confirmed sites:
Ambiguous sites: @S:13orS:15

MS/MS Fragmentation of IELQSQSWPMQQSFSPEK
Found in AT4G38470.1, protein kinase family protein

Match to Query 4139: 2228.980314 from(1115.497433,2+)
Elution from: 52.768 to 52.768 scan no 5618 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2228.9813
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0067
Matched b ions: b(6), b(8), b(10)
Matched y ions: y(6), y(10)–98, y(10), y(11), y(12), y(14)
Precursor origin neutral loss: +

Peptide No.887

IEMTSPVVTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of IEMTSPVVTK
Found in AT2G37970.1, SOUL heme-binding family protein

Match to Query 977: 1199.550188 from(600.782370,2+)
Elution from: 21.575 to 21.575 scan no 1506 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1199.5509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 59 Expect: 8.5e-006
Matched b ions: b(2), b(3), b(4), b(5)-98, b(7), b(7)-98, b(8)-98, b(8), b(8)++
Matched y ions: y(2), y(3), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.888

IENVPEMPLVVSDSAEAVEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of IENVPEMPLVVSDSAEAVEK
Found in AT3G09630.1, 60S ribosomal protein L4/L1 (RPL4A)

Match to Query 3491: 2235.032742 from(1118.523647,2+)
Elution from: 54.707 to 54.707 scan no 5598 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2235.0381  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 47 Expect: 0.00026  
Matched b ions: b(7), b(9), b(11), b(13)  
Matched y ions: y(7), y(9), y(12), y(13)-98, y(13), y(14), y(15)++, y(16)+, y(16)-98, y(16), y(16)-98++, y(17)-98++, y(17)  
Precursor origin neutral loss: +

Peptide No.889  
IESLASDVEKSSARVFQQEK  
Confirmed sites: “@S:6,@S:11,@S:12”  
Ambiguous sites:  
MS/MS Fragmentation of IESLASDVEKSSARVFQQEK  
Found in AT3G08780.1, similar to hypothetical protein [Medicago sativa] (GB:AAL15647.1)  
Match to Query 4562: 2490.047265 from(831.023031,3+)  
Elution from: 30.689 to 30.689 scan no 2703 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2490.0481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0038
Matched b ions: b(3), b(7)−98, b(8), b(9), b(12)++, b(14)++, b(15)+, b(15)−98++, b(16)+, b(17)−196++, b(18)−98++, b(19)−98++, b(19)−196++
Matched y ions: y(5), y(6), y(8), y(9), y(10)+, y(11)+, y(11)−196++, y(11)−98++, y(12)+, y(12)−98++, y(13)−196++, y(13)−98++, y(14)+, y(16)+, y(17)+, y(17)−196++, y(18)+, y(18)−98++, y(19)++
Precursor origin neutral loss: +

Peptide No.890
IEVDSDGDGER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **IEVDSDGDGER**
Found in **AT1G80930.1**, MIF4G domain−containing protein / MA3 domain−containing protein

Match to Query 1071: 1270.470536 from(636.242544,2+)
Elution from: 22.282 to 22.282 scan no 1482 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1270.4714
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 1.6e-006
Matched b ions: b(2), b(3), b(5), b(6), b(8), b(10)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)+, y(8)-98, y(8), y(9)-98++, y(9)-98, y(9), y (9)+, y(10)-98, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.891
IFVGLSPEVTDRDLER
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of IFVGLSPEVTDRDLER
Found in AT5G04280.1, glycine–rich RNA–binding protein

Match to Query 3368: 1981.948593 from(661.656807,3+)
Elution from: 48.309 to 48.309 scan no 5068 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1981.9509

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 31 Expect: 0.0083

Matched b ions: b(9)++, b(10)−98++, b(14)++
Matched y ions: y(6), y(9)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)−98++, y(15)++, y(16)++

Precursor origin neutral loss: +

Peptide No.892

IGIWQYGDIESDDEDTGPAR

Confirmed sites: @S:11

Ambiguous sites:

MS/MS Fragmentation of IGIWQYGDIESDDEDTGPAR
Found in AT5G07350.1, tudor domain-containing protein / nuclease family protein

Match to Query 3955: 2315.955492 from(1158.985022,2+) (1158.985022,2+)

Elution from: 57.245 to 57.245 scan no 6000 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2315.9583
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 2.5e-008
Matched b ions: b(6), b(8), b(9), b(12)−98, b(12), b(13), b(15)−98++, b(15)−98, b(16)−98
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(10)−98, y(11)−98, y(12)−98, y(12), y(13)−98, y(14)−98, y(14), y(15)++, y(15)−98, y(15), y(16)−98, y(17)−98++, y(17)++, y(19)++
Precursor origin neutral loss: +

Peptide No.893
IGNSDVEDEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of IGNSDVEDEK
Found in AT1G26300.1, BSD domain-containing protein

Match to Query 878: 1184.458298 from(593.236425,2+) Elution from: 21.389 to 21.389 scan no 1399 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1184.4598
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 53 Expect: 2.1e-005
Matched b ions: b(3), b(5)–98, b(5), b(6)–98, b(6)–98++, b(8)–98, b(8), b(9)++, b(9)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)–98, y(8)–98++, y(8)–98, y(8)++, y(9)–98, y(9), y(9)–98++, y(9)++
Precursor origin neutral loss: +

Peptide No.894

IGNSDVEEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of IGNSDVEEEK
Found in AT1G69030.1, similar to BSD domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G26300.1); similar to Os04

Match to Query 950: 1198.474558 from(600.244555,2+) Elution from: 20.999 to 20.999 scan no 1437 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1198.4754
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 4.3e-007
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6)-98++, b(6), b(7)-98, b(7), b(7)+, b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)+, y(8)-98, y(8)-98++, y(8), y(8)+, y(9)-98, y(9), y(9)+, y(9)-98++
Precursor origin neutral loss: +

Peptide No.895

IGSMFHR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IGSMFHR
Found in AT1G53590.1, C2 domain-containing protein

Match to Query 494: 926.382758 from(464.198655,2+)
Elution from: 32.046 to 32.046 scan no 2949 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 926.3833
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00013
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(6)-98
Matched y ions: y(1), y(2), y(4), y(4)++, y(5)-98++, y(5)-98, y(5)++, y(6)-98, y(6), y(6)-98++, y(6)++
Precursor origin neutral loss: +

Peptide No.896

IGSSEMLIEGEDVR
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of IGSSEMLIEGEDVR
Found in AT4G01290.1, similar to unknown [Oryza sativa] (GB:AAF00138.1); similar to Os06g0105900 [Oryza sativa (japonica

Match to Query 2590: 1613.699678 from(807.857115,2+)
Elution from: 47.554 to 47.554 scan no 4966 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1613.7007
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.4e-005
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(8)-98, b(8)-98, b(9)-98, b(9), b(12), b(12)+, b(13)-98
Matched y ions: y(2), y(3), y(5), y(6), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.897

IGSYIYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IGSYIYR
Found in AT5G42870.1, lipin family protein

Match to Query 570: 950.425356 from(476.219954,2+)
Elution from: 37.924 to 37.924 scan no 3735 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 950.4262

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 41  **Expect:** 0.00037

**Matched b ions:** b(2), b(3), b(4)+98, b(5), b(5)+98, b(6)+98

**Matched y ions:** y(1), y(2), y(3), y(4), y(5)+98++, y(5)+98, y(5), y(6)+98, y(6), y(6)+98++, y(6)++

**Precursor origin neutral loss:** +

---

**Peptide No.898**

**IHEESGSDDLELTLGNSSTR**

**Confirmed sites:** @S:5

**Ambiguous sites:** "@S:17orS:18orT:19, @S:17orS:18orT:19"

**MS/MS Fragmentation of** IHEESGSDDLELTLGNSSTR

**Found in AT1G78700.1, brassinosteroid signalling positive regulator-related**

**Match to Query 3836:** 2398.899423 from(800.640417,3+)

**Elution from:** 48.765 to 48.765 scan no 4946 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2398.8968
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.044
Matched b ions: b(5), b(6), b(8)−98, b(8), b(9), b(9)−98, b(10), b(10)+, b(10)−98, b(10)−98++, b(13) ++
Matched y ions: y(8), y(10)++, y(10), y(10)−98, y(11)+, y(12)+, y(19)−294++
Precursor origin neutral loss: +

Peptide No. 899

IHGHGDSSSLSDSDDDKK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of IHGHGDSSSLSDSDDDKK
Found in AT5G41600.1, BTI3 (VIRB2−INTERACTING PROTEIN 3)

Match to Query 3355: 1978.788189 from(660.603339,3+)
Elution from: 15.649 to 15.649 scan no 776 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1978.7905

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 22 Expect: 0.04

Matched b ions: b(2), b(5)++, b(6), b(8), b(9), b(11)–98++, b(12)++, b(12)–98++, b(14)++, b(14)–98++, b(15)++, b(16)–98++

Matched y ions: y(2), y(6), y(7), y(8), y(8)–98, y(11)–98++, y(12)–98++, y(16)–98++, y(16)++

Precursor origin neutral loss: +

Peptide No.900

IHGHGDSSLSDSDDDKK

Confirmed sites: "@S:11,@S:13"

Ambiguous sites:

MS/MS Fragmentation of IHGHGDSSLSDSDDDKK

Found in AT5G41600.1, BTI3 (VIRB2–INTERACTING PROTEIN 3)

Match to Query 3069: 2058.754302 from(687.258710,3+) 

Elution from: 16.151 to 16.151 scan no 861 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2058.7569  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 22 Expect: 0.021  
Matched b ions: b(2), b(4), b(5)++, b(6), b(8), b(8)++, b(9)++, b(9), b(10)++, b(10), b(11), b(11)-98++, b(12)++, b(12)-98++, y(2), y(4), y(5), y(6), y(6)++, y(6)-98++, y(6)-196++, y(7)-98++, y(8)-98++, y(8)-196++, y(9)-98++, y(10)-98++, y(10)-196++, y(12), y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)-196++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)++, y(17)-98++, y(17)-196++  
Matched y ions: y(2), y(4), y(5), y(6), y(6)++, y(6)-98++, y(6)-196++, y(7)-98++, y(8)-98++, y(8)-196++, y(9)-98++, y(10)-98++, y(12), y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)-196++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)++, y(17)-98++, y(17)-196++  
Precursor origin neutral loss: +

Peptide No.901
IHGHGDSSLSDSDDDKK  
Confirmed sites: @S:13  
Ambiguous sites:

MS/MS Fragmentation of IHGHGDSSLSDSDDDKK  
Found in AT5G41600.1, BTI3 (VIRB2-INTERACTING PROTEIN 3)

Match to Query 3325: 1978.788636 from(660.603488,3+)  
Elution from: 15.661 to 15.661 scan no 775 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1978.7905
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.06
Matched b ions: b(2), b(5)+, b(6), b(10)+, b(11)+, b(12)+, b(13)+, b(15)+, b(16)−98++, b(16)+
Matched y ions: y(3), y(6)−98++, y(6), y(7)−98, y(8), y(8)−98, y(15)−98++, y(16)−98++, y(16)+
Precursor origin neutral loss: +

Peptide No.902

IHGHGDSSLSDSDDDKK
Confirmed sites: ”@S:7,@S:13”
Ambiguous sites:

MS/MS Fragmentation of IHGHGDSSLSDSDDDKK
Found in AT5G41600.1, BTI3 (VIRB2–INTERACTING PROTEIN 3)

Match to Query 2828: 2058.753849 from(687.258559,3+)
Elution from: 15.943 to 15.943 scan no 817 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2058.7569

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 23 Expect: 0.017

Matched b ions: b(2), b(4), b(5)+, b(6), b(7)−98++ , b(9)−98++, b(10)−98++, b(11)−98++, b(12)+, b(12)−98++, b(13)−98++, b(14)+, b(15)−98++, b(16)−98++, b(16)−196++, b(16)+, b(17)+
Matched y ions: y(4), y(6), y(6)−98++, y(8)−98++, y(15)−196++, y(16)+, y(16)+, y(16)−98++, y(16)−196++

Precursor origin neutral loss: +

Peptide No.903

IHGHGDSSLSDSLSDDKK

Confirmed sites: 
Ambiguous sites: @S:8

MS/MS Fragmentation of IHGHGDSSLSDSLSDDKK
Found in AT5G41600.1, BTI3 (VIRB2-INTERACTING PROTEIN 3)

Match to Query 3715: 1978.788666 from(660.603498,3+)
Elution from: 16.019 to 16.019 scan no 809 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1978.7905
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.016
Matched b ions: b(2), b(5)+, b(6), b(8)-98++, b(9)-98++, b(12)-98++, b(14)-98++, b(15)+, b(16)-98++, b(16)+
Matched y ions: y(11)-98++, y(12)-98++, y(14)-98++, y(15)-98++, y(16)+, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.904
IHHPPSPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IHHPPSPR
Found in AT5G54430.1, universal stress protein (USP) family protein

Match to Query 492: 1019.468406 from(510.741479,2+)
Elution from: 14.486 to 14.486 scan no 731 polarity:+

---

Monoisotopic mass of neutral peptide Mr(calc): 1978.7905
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.016
Matched b ions: b(2), b(5)+, b(6), b(8)-98++, b(9)-98++, b(12)-98++, b(14)-98++, b(15)+, b(16)-98++, b(16)+
Matched y ions: y(11)-98++, y(12)-98++, y(14)-98++, y(15)-98++, y(16)+, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.904
IHHPPSPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IHHPPSPR
Found in AT5G54430.1, universal stress protein (USP) family protein

Match to Query 492: 1019.468406 from(510.741479,2+)
Elution from: 14.486 to 14.486 scan no 731 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1019.4702
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.014
Matched b ions: b(2), b(3)
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6)+, y(6)
Precursor origin neutral loss: +

Peptide No.905

IHHSDDEEDDTFYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of IHHSDDEEDDTFYR
Found in AT3G10400.1, RNA recognition motif (RRM)—containing protein

Match to Query 3394: 2020.744866 from(1011.379709,2+)
Elution from: 30.530 to 30.530 scan no 2784 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2020.7476
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 8e-007
Matched b ions: b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(13)
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10), y(11), y(12)-98, y(13)-98++, y(13)-98, y(13), y(13)+++, y(14)++, y(14)-98+++  
Precursor origin neutral loss: +

Peptide No.906

IIAGKPDDTEYEIEGESESALAAGTSPWMNSSTLK
Confirmed sites: "@T:9,@S:18,@S:20,@T:26,@S:27"
Ambiguous sites:

MS/MS Fragmentation of IIAGKPDDTEYEIEGESESALAAGTSPWMNSSTLK
Found in AT4G32250.1, protein kinase family protein

Match to Query 5099: 4209.641109 from(1404.220979,3+)
Elution from: 49.886 to 49.886 scan no 5238 polarity:+
Monoisotopic mass of neutral peptide \( \text{Mr(calc)} \): 4209.6508

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- T9: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S18: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S20: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- T26: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S27: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 24 Expect: 0.059

Matched b ions: b(10), b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(15)-98, b(16), b(21)+, b(23)-98++, b(24)+, b(24)-98++, b(24)-196++, b(26)+, b(26)-98++, b(26)-294++, b(27)-294++, b(27)-392++, b(28)-392++, b(28)-490++, b(29)+, b(29)-98++, b(30)+, b(30)-98++, b(31)+, b(31)-98++, b(33)+, b(33)-98++, b(34)+, b(34)-392++, b(34)-392++, b(34)-196++, b(35)-490++

Matched y ions: y(7), y(9), y(10)+, y(12)-98++, y(12)-98, y(12)-98, y(13)-98, y(13)-196, y(15), y(16), y(17)-294, y(19)-392++, y(20)-294++, y(20)+, y(22)-294++, y(23)+, y(25)-294++, y(26)+, y(26)-392++, y(29)-98++, y(30)-392++, y(30)-294++, y(31)-490++, y(31)-392++, y(32)-294++, y(32)-392++, y(33)+, y(35)-392++, y(35)-490++, y(35)-196++

Precursor origin neutral loss: +

**Peptide No. 907**

\( \text{IIDGSPPPSPK} \)

Confirmed sites: "@S:5,@S:9"

Ambiguous sites:

MS/MS Fragmentation of **IIDGSPPPSPK**

Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1332: 1266.528842 from(634.271697,2+) Elution from: 27.093 to 27.093 scan no 2210 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1266.5298
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0001
Matched b ions: b(2), b(3), b(4)+, b(4), b(5)−98, b(5), b(6)−98, b(7)−98, b(8)−98, b(9)−98, b(9)−98++, b(9), b(9)−196++, b(9)++, b(10)−196, b(10)−98, b(10)−196++, b(10)−98++
Matched y ions: y(2), y(3), y(4)−98, y(4), y(5), y(6)−98, y(6), y(6)+, y(6), y(7), y(7)−98++, y(7)−196++, y(8)−98, y(8), y(8)+, y(8)−98++, y(9)−98, y(9), y(9)−98++, y(9)+, y(9)−196, y(10), y(10)+, y(10)−98++
Precursor origin neutral loss: +

Peptide No.908

IIGVDFNSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of IIGVDFNSK
Found in AT1G77120.1, ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase

Match to Query 619: 1071.499526 from(536.757039,2+)
Elution from: 41.182 to 41.182 scan no 4145 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1071.5001
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0018
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)−98++, b(8)−98
Matched y ions: y(3)−98, y(3), y(4)−98, y(5), y(5)−98, y(5)−98++, y(6)−98, y(6), y(6)++, y(7)−98, y(7), y(8), y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.909
IIQGEDSDSDYSEPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IIQGEDSDSDYSEPK
Found in AT1G20920.1, DEAD box RNA helicase, putative

Match to Query 2468: 1761.697822 from(881.856187,2+)
Elution from: 27.045 to 27.045 scan no 2210 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1761.6982
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00017
Matched b ions: b(7), b(10), b(12)+, b(13), b(13)-98++, b(13)+, b(14)--98++
Matched y ions: y(3), y(4), y(5), y(7), y(9), y(10), y(12)--98, y(12), y(13)+, y(13)--98++, y(14)+
Precursor origin neutral loss: +

Peptide No.910
IIQLPQSSPDESPNASTK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of IIQLPQSSPDESPNASTK
Found in AT4G29860.1, EMB2757/TAN (EMBRYO DEFECTIVE 2757); nucleotide binding

Match to Query 3474: 1990.922396 from(996.468474,2+)
Elution from: 37.109 to 37.109 scan no 3601 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1990.9248
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 1.2e-006
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9), b(10), b(11), b(12)–98, b(14)–98, b(15), b(15)–98++, b(15)++, b(17)–98++
Matched y ions: y(3), y(6), y(7), y(9), y(10), y(10)–98, y(11), y(12), y(13)++, y(14)++, y(14)–98, y(14), y(14)–98++, y(15)–98, y(15), y(15)++, y(15)–98++, y(16)++, y(17)++
Precursor origin neutral loss: +

**Peptide No.911**

IKIDIDESLFSN
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of IKIDIDESLFSN
Found in AT2G38140.1, PSRP4 (PLASTID–SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome

Match to Query 2200: 1472.679736 from(737.347144,2+)
Elution from: 60.199 to 60.199 scan no 6486 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1472.6799
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 7.9e-005
Matched b ions: b(4), b(5), b(6)+, b(6), b(7), b(8), b(9), b(10), b(11)-98++
Matched y ions: y(3)-98, y(4), y(5), y(7), y(8), y(9)+, y(11)+
Precursor origin neutral loss: +

Peptide No.912
IKPSATAAAPPAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IKPSATAAAPPAK
Found in AT1G61730.1, DNA-binding storekeeper protein-related

Match to Query 1952: 1489.753476 from(745.884014,2+)
Elution from: 19.653 to 19.653 scan no 1253 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1489.7541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 1.4e-006
Matched b ions: b(3)=98, b(3), b(6)=98++, b(10)=98, b(10), b(11)=98, b(11), b(12)=98
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13)=98, y(13), y(13)=98++, y(14)=98++, y(14)
Precursor origin neutral loss: +

Peptide No.913
IKPSATTAAAPPAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of IKPSATTAAAPPAK
Found in AT1G61730.1, DNA-binding storekeeper protein-related

Match to Query 1698: 1489.753431 from(497.591753,3+)
Elution from: 19.463 to 19.463 scan no 1190 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1489.7541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 23 Expect: 0.03
Matched b ions: b(4), b(6)--98++, b(7), b(7)++, b(9)--98++, b(9)++, b(10)--98++, b(11)++, b(12)--98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)++, y(11)--98++, y(13)++
Precursor origin neutral loss:

Peptide No.914
IKSPSATTAAPPAK
Confirmed sites:
Ambiguous sites: @S:5 or T:7

MS/MS Fragmentation of IKSPSATTAAPPAK
Found in AT1G61730.1, DNA-binding storekeeper protein-related

Match to Query 2002: 1489.753776 from (497.591868, 3+)
Elution from: 19.784 to 19.784 scan no 1300 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1489.7541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.013
Matched b ions: b(2), b(7)−98++, b(7)+, b(8), b(8)+, b(8)−98++, b(9), b(9)−98++, b(9)+, b(10)−98++, b(10)+, b(11)+, b(12)−98++
Matched y ions: y(4), y(5)+, y(5), y(6), y(7), y(7)+, y(8), y(8)+, y(11)−98++, y(13)+
Precursor origin neutral loss:

Peptide No. 915
IKSPSATTAAAPPAK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of IKSPSATTAAAPPAK
Found in AT1G61730.1, DNA-binding storekeeper protein-related

Match to Query 2482: 1489.753014 from(497.591614,3+)
Elution from: 19.385 to 19.385 scan no 1254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1489.7541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.003
Matched b ions: b(2), b(5), b(8), b(8)-98, b(8)+, b(9)-98++, b(9)+, b(10)-98++, b(10)+, b(11)+, b(12)-98++, b(14)-98++
Matched y ions: y(4), y(5)+, y(5), y(6), y(7)+, y(7), y(8), y(9)-98, y(11)-98++, y(12)-98++, y(13)+, y(14)+
Precursor origin neutral loss:

Peptide No.916
ILEISLNNVSSDDLNR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ILEISLNNVSSDDLNR
Found in AT2G26890.1, GRV2 (KATAMARI2); binding / heat shock protein binding

Match to Query 3291: 1880.884698 from(941.449625,2+)
Elution from: 54.347 to 54.347 scan no 5575 polarity:+
Peptide No.917

ILEISLNNVSSDDLNR
Confirmed sites:
Ambiguous sites: @S:10orS:11

MS/MS Fragmentation of ILEISLNNVSSDDLNR
Found in AT2G26890.1, GRV2 (KATAMARI2); binding / heat shock protein binding

Match to Query 3018: 1880.885228 from(941.449890,2+)
Elution from: 52.443 to 52.443 scan no 5555 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1880.8880
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0012
Matched b ions: b(9), b(13)
Matched y ions: y(3), y(4), y(7), y(8)−98, y(9), y(10)−98, y(10), y(11), y(12), y(12)−98, y(15)++
Precursor origin neutral loss: +

Peptide No.918

ILNDSDSGELK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ILNDSDSGELK
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1667: 1269.548384 from(635.781468,2+)
Elution from: 29.440 to 29.440 scan no 2601 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1269.5489
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.021
Matched b ions: b(2), b(4), b(9)−98, b(10)−98++, b(10)−98
Matched y ions: y(2), y(6), y(7), y(8)−98, y(8), y(9)++, y(9), y(9)−98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.919

ILNDSDSGELK
Confirmed sites: “@S:5,@S:7”
Ambiguous sites:

MS/MS Fragmentation of ILNDSDSGELK
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1877: 1349.514370 from(675.764461,2+)
Elution from: 34.336 to 34.336 scan no 3296 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1349.5153
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00038
Matched b ions: b(2), b(3), b(4), b(6), b(6)-98, b(7)-98, b(8)-98, b(8)-196, b(9)-196, b(9)-98, b(9), b(9)+, b(10), b(10)-98, b(10)-196++, b(10)-196, b(10)-98++
Matched y ions: y(2), y(4), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(7)-196, y(8)-98++, y(8)-98, y(8), y(8)+, y(8)-196, y(9)-98++, y(9)-98, y(9), y(9)-196++, y(9)+, y(9)-196, y(10)+, y(10), y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.920

ILNDSDSGELK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ILNDSDSGELK
Found in AT3G48050.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1237: 1269.548010 from(635.781281,2+)
Elution from: 28.740 to 28.740 scan no 2471 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1269.5489
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 5.1e-006
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6), b(7)-98, b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(9)-98++, y(9)++, y(10), y(10)++, y(10)-98
Precursor origin neutral loss: +

Peptide No.921

ILSHSQEVSPR
Confirmed sites: "@S:3,@S:9"
Ambiguous sites:

MS/MS Fragmentation of ILSHSQEVSPR
Found in AT4G14740.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22810.1); similar to Protein of unknown

Match to Query 1940: 1411.588432 from(706.801492,2+) Elution from: 23.205 to 23.205 scan no 1628 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.5898
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.037
Matched b ions: b(4)-98, b(5), b(5)-98, b(6)-98, b(7), b(7)-98, b(8)-98++, b(8), b(8)-98, b(9)-196, b(9)-98
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5), y(5)-98++, y(9)-98, y(9)-196++, y(9)-98, y(9)-196, y(9)-196
Precursor origin neutral loss: +

Peptide No.922
ILSHSQEVSPR
Confirmed sites: ”@S:5,@S:9”
Ambiguous sites:

MS/MS Fragmentation of ILSHSQEVSPR
Found in AT4G14740.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22810.1); similar to Protein of unknown

Match to Query 1895: 1411.587250 from(706.800901,2+)
Elution from: 23.335 to 23.335 scan no 1533 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.5898
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.001
Matched b ions: b(4), b(5)−98, b(5), b(6)−98, b(7), b(7)−98, b(8)−98++, b(8)−98, b(8), b(9)−196, b(9)−98, b(10)−196
Matched y ions: y(2), y(3), y(3)−98, y(6)−98, y(7)−98, y(7), y(8)++, y(8)−98++, y(9)−98, y(9), y(9)−98++, y(9)++, y(10)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.923

ILSQSQEVSPR
Confirmed sites: “@S:5,@S:9”
Ambiguous sites:

MS/MS Fragmentation of ILSQSQEVSPPR
Found in AT3G22810.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14740.2); similar to Protein of unknown

Match to Query 1481: 1402.587820 from(702.301186,2+)
Elution from: 27.442 to 27.442 scan no 2253 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1402.5894
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 28 Expect: 0.0083
Matched b ions: b(5), b(7), b(8)−98, b(8), b(9)−98
Matched y ions: y(2), y(3), y(3)−98, y(4), y(5), y(7), y(7)−98, y(9)−98++, y(9)−98, y(9), y(9)++, y(10)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.924

ILSQSQEVSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ILSQSQEVSPR
Found in AT3G22810.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14740.2); similar to Protein of unknown

Match to Query 1398: 1322.622966 from(662.318759,2+) Elution from: 24.622 to 24.622 scan no 1882 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1322.6231
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 31 Expect: 0.0039
Matched b ions: b(8), b(9), b(9)−98, b(10)−98
Matched y ions: y(2), y(3), y(4)−98, y(4), y(6), y(7), y(8), y(8)++, y(9), y(9)−98, y(9)++, y(9)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.925

INIPSPSPPSSPR
Confirmed sites: @S:11
Ambiguous sites: @S:10 or S:7

MS/MS Fragmentation of INIPSPSPPSSPR
Found in AT1G35510.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01480.1); similar to Growth regulator p

Match to Query 1981: 1507.645626 from(754.830089,2+) Elution from: 40.770 to 40.770 scan no 4053 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00042
Matched b ions: b(2), b(3), b(5), b(10), b(10)++
Matched y ions: y(3)−98, y(7), y(8), y(8)++, y(9), y(9)++, y(10)+, y(10)−98, y(10), y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.926

INIPSPSPSSPR
Confirmed sites: "@S:7,@S:10"
Ambiguous sites:

MS/MS Fragmentation of INIPSPSPSSPR
Found in AT1G35510.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01480.1); similar to Growth regulator p

Match to Query 2191: 1507.646900 from(754.830726,2+)
Elution from: 41.212 to 41.212 scan no 3928 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.005
Matched b ions: b(3), b(5), b(6), b(7), b(8)−98, b(9)++, b(10)++, b(10)
Matched y ions: y(5)−98, y(5), y(6)−98, y(7)−98, y(8)++, y(8), y(8)−196, y(9), y(9)++, y(10)++, y(10), y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.927

INIPSPSPPSSPR
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of INIPSPSPPSSPR
Found in AT1G35510.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01480.1); similar to Growth regulator p

Match to Query 2440: 1507.645842 from(754.830197,2+)  
Elution from: 40.859 to 40.859 scan no 4125 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6473
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0014
Matched b ions: b(3), b(5), b(7)−98, b(8), b(9)−98, b(10)++, b(10)
Matched y ions: y(2), y(3)−98, y(4), y(5)−98, y(6), y(7)−196, y(8)−98, y(8), y(9)++, y(9), y(10)++, y
  (10), y(10)−98++, y(10)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.928

INNTPGSGEALLR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of INNTPGSGEALLR
Found in AT5G66230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G51230.1); similar to Sugar transporter

Match to Query 1693: 1420.671140 from(711.342846,2+)
Elution from: 36.141 to 36.141 scan no 3436 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1420.6711
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.004
Matched b ions: b(4), b(7)−98, b(12)
Matched y ions: y(2), y(6), y(8), y(8)−98, y(9)−98, y(9), y(10)++, y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.929

INSAESMELWASQQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/transferase, transferring glyc

Match to Query 3239: 1800.773552 from(901.394052,2+) Elution from: 48.001 to 48.001 scan no 5021 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7753
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 Expect: 1.7e-008
Matched b ions: b(4)-98, b(5), b(5)-98, b(6)-98, b(7), b(7)-98, b(8), b(8)+, b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)+, y(9), y(10), y(11), y(12), y(13), y(13)-98++, y(13)-98, y(13)+, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.930
INSAESMELWASQQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/ transferase, transferring glyc

Match to Query 2855: 1816.769014 from(909.391783,2+)
Elution from: 39.090 to 39.090 scan no 3830 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1816.7702
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 98 Expect: 1.8e-009
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14), b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(12)++, y(13)-98++, y(13)-98, y(13)++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.931
INSAESMELWASQQK
Confirmed sites: "@S:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glyc

Match to Query 2712: 1880.738306 from(941.376429,2+)
Elution from: 51.699 to 51.699 scan no 5165 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1880.7416
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)+, b(9), b(10)-98, b(10), b(11)-196, b(11)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)+, y(9), y(10), y(11)-98, y(12), y(13)-196++
Precursor origin neutral loss: +

Peptide No.932

INSAESMELWASQQK
Confirmed sites: "@S:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glyc

Match to Query 3501: 1896.735492 from(949.375022,2+)
Elution from: 41.353 to 41.353 scan no 4142 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1896.7366
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 1.5e-005
Matched b ions: b(4)-98, b(5), b(5)-98, b(7)-196, b(7)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-196, b(10)-98, b(10)-196, b(10), b(11)-98, b(11), b(11)-196, b(11)++, b(12), b(13), b(13)-98, b(13)-196++, b(14), b(14)-98++, b(14)-196
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12), y(13)-196++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.933

INSAESMELWASQQK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/transferase, transferring glyc

Match to Query 3301: 1800.773649 from(601.265159,3+)
Elution from: 46.773 to 46.773 scan no 4905 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7753
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 9.4e-005
Matched b ions: b(4), b(5)+, b(6), b(6)–98, b(7), b(7)–98, b(8), b(8)–98, b(8)+, b(8)–98++, b(9), b(9)–98, b(9)+, b(10), b(10)+, b(10)–98++, b(11)+, b(11), b(11)–98++, b(12)+, b(13)+, b(13)–98++, b(13)+, b(14)+
Matched y ions: y(2), y(3)+, y(3), y(4), y(5), y(5)+, y(6)+, y(6), y(7)+, y(7), y(8)+, y(9)+, y(14)+, y(14)–98++
Precursor origin neutral loss:

Peptide No.934

INSAESMELWASQQK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of INSAESMELWASQQK
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose–phosphate synthase/ transferase, transferring glyc

Match to Query 2952: 1816.769241 from(606.597023,3+)
Elution from: 38.923 to 38.923 scan no 3808 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1816.7702
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58 Expect: 1.5e-005
Matched b ions: b(4), b(5)++, b(6)−98, b(6), b(7)−98, b(7), b(7)−98++, b(8), b(8)−98, b(8), b(8)++, b(8)−98++, b(9), b(9)++, b(9)−98, b(9)−98++, b(10), b(10)−98, b(10)−98++, b(11)++, b(11), b(11)−98++, b(12)++, b(13)++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(9)++, y(11)−98++, y(13)−98++, y(13)++, y(14)−98++
Precursor origin neutral loss:

Peptide No.935
IPNNGSSSEGEISPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of IPNNGSSSEGEISPR
Found in AT3G45190.1, SIT4 phosphatase-associated family protein

Match to Query 1714: 1595.682398 from(798.848475,2+)
Elution from: 24.936 to 24.936 scan no 1926 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1595.6828
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(11), b(12), b(13)−98, b(13)++
Matched y ions: y(2), y(3), y(3)−98, y(4)−98, y(5)++, y(5), y(6)−98, y(6), y(7)−98, y(8), y(9), y(9)−98, y(10)−98, y(12)−98, y(13)−98, y(13), y(13)++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.936
IPSTGLSSPEAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IPSTGLSSPEAR
Found in AT3G33530.1, transducin family protein / WD−40 repeat family protein

Match to Query 1319: 1293.595484 from(647.805018,2+)
Elution from: 28.522 to 28.522 scan no 2442 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1293.5966
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0081
Matched b ions: b(5), b(6), b(7)−98, b(8)−98, b(10), b(10)++, b(10)−98++, b(11)−98
Matched y ions: y(2), y(4), y(6), y(6)−98, y(7)−98, y(8), y(8)−98, y(9)++, y(10), y(10)++, y(11)++, y(11)−98, y(11)−98++
Precursor origin neutral loss: +

Peptide No.937
IPSTGLSSPEAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of IPSTGLSSPEAR
Found in AT3G33530.1, transducin family protein / WD-40 repeat family protein

Match to Query 1275: 1293.595338 from(647.804945,2+) Elution from: 28.321 to 28.321 scan no 2418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1293.5966
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0031
Matched b ions: b(6), b(8)-98, b(10)
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(8), y(8)-98, y(10), y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.938
IQEGPEGSLQSEMK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of IQEGPEGSLQSEMK
Found in AT1G68790.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67230.1); similar to nuclear matrix con

Match to Query 2574: 1611.683880 from(806.849216,2+)
Elution from: 35.479 to 35.479 scan no 3275 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1611.6851
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.8e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(11) ++, b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98++, y(9), y(9)+, y(10)-98, y(10), y(10)-98++, y(11)-98, y(11), y(11)+, y(12)-98++, y(12)+, y(12)-98, y(12), y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.939
IQHLTPNIGTVYSMGPDFRVLVR
Confirmed sites: @T:5
Ambiguous sites: @Y:12orS:13

MS/MS Fragmentation of IQHLTPNIGTVYSMGPDFRVLVR
Found in AT1G79210.1, 20S proteasome alpha subunit B, putative

Match to Query 4867: 2845.342809 from(949.454879,3+)
Elution from: 56.248 to 56.248 scan no 5979 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2845.3387

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y12 : Phospho (Y)
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 27 Expect: 0.028
Matched b ions: b(8)-98, b(9), b(10)+, b(10)-98++, b(11)-98++, b(11)-98, b(11), b(15)-98, b(15)-98++, b(19)-98++, b(22)-98++
Matched y ions: y(7), y(8)+, y(8)+, y(9)+, y(10), y(13), y(13)+, y(14), y(14)+, y(15)+, y(16)+, y(21)+, y(22)+, y(22)-98++, y(23)+

Precursor origin neutral loss: +

Peptide No.940

IRPSTSPESL

Confirmed sites: ”@S:6,@S:9”

Ambiguous sites:

MS/MS Fragmentation of IRPSTSPESL

Found in AT2G34750.1, RNA polymerase I specific transcription initiation factor RRN3 family protein

Match to Query 1610: 1245.503700 from(623.759126,2+)

Elution from: 34.889 to 34.889 scan no 3317 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1245.5043
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.00099
Matched b ions: b(2), b(4), b(5), b(6), b(7)−98, b(8)++, b(8), b(9)−98, b(9)−98++, b(9)++
Matched y ions: y(2)−98, y(2), y(3), y(4)−98, y(4), y(5), y(5)−196, y(5)−98, y(6), y(6)−196++, y(6)−98, y(6)−196, y(7), y(8)−98, y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.941
IRSEMQIWSEDDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of IRSEMQIWSEDDK
Found in AT4G10120.1, ATSPS4F; sucrose-phosphate synthase/transferase, transferring glycosyl groups

Match to Query 2610: 1715.718268 from(858.866410,2+)
Elution from: 40.679 to 40.679 scan no 4078 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.7226
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.019
Matched b ions: b(5), b(6), b(7), b(7)-98, b(8)-98, b(8), b(11), b(12)
Matched y ions: y(5), y(6), y(7), y(10), y(11)-98
Precursor origin neutral loss: +

Peptide No.942

ISEGQVVPSDSLEDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of ISEGQVVPSDSLEDK
Found in AT1G15940.1, similar to binding [Arabidopsis thaliana] (TAIR:AT1G80810.1); similar to Tudor [Medicago truncatula]

Match to Query 2899: 1681.744822 from(841.879687,2+)
Elution from: 36.832 to 36.832 scan no 3566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1681.7447
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0038
Matched b ions: b(5), b(6), b(7), b(8), b(10), b(11), b(12)–98++, b(14)
Matched y ions: y(5), y(7), y(8)–98, y(8), y(9), y(9)–98, y(10), y(10)–98, y(10)++, y(11)–98++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.943
ISETKPPTSPLRK
Confirmed sites: 
Ambiguous sites: @T:8orS:9

MS/MS Fragmentation of ISETKPPTSPLRK
Found in AT5G06910.1, ATJ6 (ARABIDOPSIS J-DOMAIN PROTEIN 6); heat shock protein binding / unfolded protein binding

Match to Query 2509: 1532.792427 from(511.938085,3+)
Elution from: 21.679 to 21.679 scan no 1549 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.7963
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(9)−98++, b(11)++, b(12)−98++, b(12)++
Matched y ions: y(7)++, y(8)−98++, y(8)++, y(9)++, y(10)++, y(11)++, y(11)−98++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.944

ISEVVVDKSVE
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ISEVVVDKSVE
Found in AT3G57490.1, 40S ribosomal protein S2 (RPS2D)

Match to Query 1517: 1282.605086 from(642.309819,2+)
Elution from: 33.642 to 33.642 scan no 3132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1282.6057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 4.3e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)++, b(9)−98, b(9)−98++, b(10)−98++, b(10)−98, b(10)
Matched y ions: y(4), y(5)−98, y(6)−98, y(6)−98++, y(6), y(7), y(7)−98, y(8)−98++, y(9)++, y(10)−98, y(10)++
Precursor origin neutral loss: +

Peptide No.945
ISNSAPVTPPVSSPTSR
Confirmed sites:
Ambiguous sites: "@S:2orS:4, @S:12orS:13orT:15orS:16"

MS/MS Fragmentation of **ISNSAPVTPPVSSPTSR**
Found in **AT1G19350.1**, BES1 (BRI1–EMS–SUPPRESSOR 1); transcription regulator

Match to Query 3050: 1855.811312 from(928.912932,2+)
Elution from: 34.135 to 34.135 scan no 3168 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1855.8118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.023
Matched b ions: b(8)−98
Matched y ions: y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(12)
Precursor origin neutral loss: +

Peptide No.946

ISSEDEMAGMDMTR
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of ISSEDEMAGMDMTR
Found in AT4G13510.1, AMT1;1 (AMMONIUM TRANSPORT 1); ammonium transporter

Match to Query 2331: 1651.590866 from(826.802709,2+)
Elution from: 38.949 to 38.949 scan no 3845 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1651.5929
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 8e-006
Matched b ions: b(5), b(7), b(8), b(10), b(11), b(12)++
Matched y ions: y(3), y(3)−98, y(4)−98, y(4), y(5), y(6)−98, y(7), y(7)−98, y(8), y(9), y(10), y(12), y(12)−98++, y(12)++, y(13)+, y(13)−98++
Precursor origin neutral loss: +

Peptide No. 947

ISSVDVFENWFAQHK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ISSVDVFENWFAQHK
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose−phosphate synthase

Match to Query 3148: 1885.837947 from(629.619925,3+)
Elution from: 61.621 to 61.621 scan no 6557 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1885.8400
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 9.2e-006
Matched b ions: b(2), b(3), b(4)–98, b(5), b(6), b(6)–98, b(7)++, b(11)–98++, b(11)++, b(14)–98++, b(14)++
Matched y ions: y(2), y(4), y(7)++, y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)–98++, y(13)++,
y(14)–98++, y(14)++
Precursor origin neutral loss:

Peptide No.948

ISTELATPDSKP
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ISTELATPDSKP
Found in AT1G72380.1, similar to Conserved hypothetical protein [Oryza sativa (japonica cultivar–group)] (GB:AAK52107.1)

Match to Query 1426: 1337.611008 from(669.812780,2+)
Elution from: 30.253 to 30.253 scan no 2681 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1337.6116
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 3.8e-006
Matched b ions: b(4), b(5), b(6), b(11)++
Matched y ions: y(4), y(4)-98, y(5), y(6)++, y(6)-98, y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)-98++
Precursor origin neutral loss:

Peptide No.949

ISTPSSPSLPPVR
Confirmed sites: “@S:5,@S:10”
Ambiguous sites:

MS/MS Fragmentation of ISTPSSPSLPPVR
Found in AT1G73350.1, similar to Os02g0637900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047530.1); similar to co

Match to Query 2428: 1583.697572 from(792.856062,2+)
Elution from: 41.623 to 41.623 scan no 3983 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1583.6997
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.011
Matched b ions: b(5)-98, b(10)-98
Matched y ions: y(4), y(5), y(8), y(9), y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.950

ITFDNSDDED
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of ITFDNSDDED
Found in AT1G31970.1, DEAD/DEAH box helicase, putative

Match to Query 1102: 1249.402212 from(625.708382,2+)
Elution from: 34.554 to 34.554 scan no 3256 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1249.4024  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 36 Expect: 0.00026  
Matched b ions: b(4), b(5), b(5)++, b(6)−98, b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(9)−98, b(9)−98++  
Matched y ions: y(2), y(3), y(5), y(5)−98, y(6), y(7)  
Precursor origin neutral loss: +

Peptide No.951

ITFDNSDDED  
Confirmed sites: @T:2  
Ambiguous sites:

MS/MS Fragmentation of ITFDNSDDED  
Found in AT1G31970.1, DEAD/DEAH box helicase, putative

Match to Query 1545: 1249.402320 from(625.708436,2+)  
Elution from: 34.652 to 34.652 scan no 3290 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1249.4024  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 33 Expect: 0.00056  
Matched b ions: b(2), b(3)++, b(6), b(7), b(8), b(9), b(9)++  
Matched y ions: y(9)++  
Precursor origin neutral loss: +  

Peptide No.952  
ITPHDIDSDTDQIFLR  
Confirmed sites: @S:8  
Ambiguous sites:  

MS/MS Fragmentation of ITPHDIDSDTDQIFLR  
Found in AT2G46040.1, ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein  

Match to Query 3247: 1964.886018 from(983.450285,2+)  
Elution from: 51.222 to 51.222 scan no 5406 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1964.8881
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 3.9e-006
Matched b ions: b(4), b(6), b(7), b(8)−98, b(10)−98, b(11)−98, b(11), b(13), b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(12)−98, y(12), y(13)++, y(13)−98++, y(14)−98++, y(14)+, y(15)++
Precursor origin neutral loss: +

Peptide No.953
ITPHIDSDTDQIFLR
Confirm sites: T:10orS:8
Ambiguous sites: @T:10orS:8

MS/MS Fragmentation of ITPHDSDTDQIFLR
Found in AT2G46040.1, ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein

Match to Query 3572: 1964.883282 from(655.968370,3+)
Elution from: 52.714 to 52.714 scan no 5600 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1964.8881
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.033
Matched b ions: b(7), b(10)-98, b(10)++, b(12)++, b(13)-98++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(9)+, y(10)+, y(12)-98++, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.954

IVDSLKAESVESGEK
Confirmed sites: "@S:9,@S:12"
Ambiguous sites:

MS/MS Fragmentation of IVDSLKAESVESGEK
Found in AT1G17210.1, zinc ion binding

Match to Query 2497: 1749.745742 from(875.880147,2+)
Elution from: 31.271 to 31.271 scan no 2784 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1749.7474
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 5.8e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9)–98, b(10)–98, b(10)–98++, b(11)–98, b(11), b(12)–196, b(12)–196++, b(13)++, b(14)–196, b(14), b(14)–98
Matched y ions: y(3), y(4)–98, y(4), y(5)–98, y(6)–98, y(6), y(7)–98, y(8), y(8)++, y(8)–98, y(8)–196, y(9)–98, y(9), y(10)–98, y(10), y(11)++, y(12)–98++, y(13)–196++, y(13)++, y(14)–196++, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.955

IVEEEFKDDQSSDEVA
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of IVEEEFKDDQSSDEVA
Found in AT4G05440.1, EDA35 (embryo sac development arrest 35)

Match to Query 3055: 2046.825122 from(1024.419837,2+)
Elution from: 35.419 to 35.419 scan no 3305 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2046.8306
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.009
Matched b ions: b(7), b(8), b(9), b(11), b(12), b(13)-98, b(14)++, b(15)++, b(15)-98++, b(16)++
Matched y ions: y(8), y(8)-98, y(10), y(12), y(16)++
Precursor origin neutral loss: +

Peptide No.956
IVGTADVTVSQSPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of IVGTADVTVSQSPK
Found in AT4G19600.1, cyclin family protein

Match to Query 1890: 1480.716720 from(741.365636,2+) Elution from: 30.813 to 30.813 scan no 2720 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1480.7174
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 4.5e-007
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(11)
Matched y ions: y(3), y(3)-98, y(4), y(5), y(5)+, y(5)-98, y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(9)+, y(9)-98, y(10), y(11)-98++, y(11)+, y(12), y(12)+, y(12)-98++, y(13)-98++, y(13)-98, y(13)+
Precursor origin neutral loss: +

Peptide No.957

IVSDLESPTNR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IVSDLESPTNR
Found in AT5G55060.1, catalytic

Match to Query 1296: 1309.590482 from(655.802517,2+) Elution from: 27.955 to 27.955 scan no 2366 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1309.5915
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 3.1e-005
Matched b ions: b(2), b(3), b(4), b(5), b(7–98), b(8–98), b(9)
Matched y ions: y(2), y(3), y(4), y(5–98), y(6), y(6–98), y(7), y(7–98), y(7)++, y(8), y(8–98), y(9), y(9–98++), y(9)–98, y(9)+++, y(10–98), y(10–98++), y(10)++
Precursor origin neutral loss: +

Peptide No.958
IVVHPDSPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IVVHPDSPR
Found in AT4G29220.1, phosphofructokinase family protein

Match to Query 1046: 1098.521250 from(550.267901,2+) Elution from: 20.206 to 20.206 scan no 1335 polarity:+

Peptide No.958
IVVHPDSPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IVVHPDSPR
Found in AT4G29220.1, phosphofructokinase family protein

Match to Query 1046: 1098.521250 from(550.267901,2+) Elution from: 20.206 to 20.206 scan no 1335 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1098.5223
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.007
Matched b ions: b(2), b(4), b(6), b(7−98), b(8)++
Matched y ions: y(1), y(2), y(3), y(4)−98, y(5), y(6)++, y(6), y(7)−98++, y(7), y(7)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.959

KADSDEEAEFDVEGR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KADSDEEAEFDVEGR
Found in AT2G34357.1, binding

Match to Query 2178: 1775.686020 from(888.850286,2+)
Elution from: 32.251 to 32.251 scan no 2908 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1775.6886
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 1e-009
Matched b ions: b(3), b(4)–98, b(5)–98, b(5), b(6)–98++, b(6)–98, b(6), b(7)–98, b(7), b(8), b(8)–98,
b(9), b(9)–98, b(10)–98, b(10), b(11)–98, b(11), b(12)–98, b(12), b(13), b(13)–98
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(11), y(12), y(12)–98, y(13)–
98++, y(13), y(13)–98, y(14)–98, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.960

KADVLSEDSPGEGRK
Confirmed sites: @S.9
Ambiguous sites:

MS/MS Fragmentation of KADVLSEDSPGEGRK
Found in AT3G54760.1, dentin sialophosphoprotein-related

Match to Query 1882: 1666.754436 from(556.592088,3+)
Elution from: 19.410 to 19.410 scan no 1202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1666.7563
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00032
Matched b ions: b(4), b(9)+, b(9)−98, b(10)−98++, b(14)−98++, b(14)+
Matched y ions: y(5), y(6)+, y(6), y(7)−98++, y(7)−98, y(8)−98++, y(9)−98++, y(11)+, y(11)−98++, y(12)−98++, y(14)+, y(14)−98++
Precursor origin neutral loss: +

Peptide No.961

KAELVELLGSDSS
Confirmed sites: @S:10orS:12
Ambiguous sites: @S:10orS:12

MS/MS Fragmentation of KAELVELLGSDSS
Found in AT1G06190.1, ATP binding / ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism

Match to Query 1713: 1426.655714 from(714.335133,2+)
Elution from: 53.311 to 53.311 scan no 5647 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1426.6592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(Shown in table), 97.9769
Ions Score: 28 Expect: 0.01
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(12)++
Matched y ions: y(5)–98, y(5), y(6), y(7), y(8), y(10)
Precursor origin neutral loss: +

Peptide No.962

KAELVELLGSDSS
Confirmed sites:
Ambiguous sites: @S:12 or S:13

MS/MS Fragmentation of KAELVELLGSDSS
Found in AT1G06190.1, ATP binding / ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism

Match to Query 1646: 1426.658318 from(714.336435,2+)
Elution from: 53.771 to 53.771 scan no 5708 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1426.6592

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S13 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 75  **Expect:** 1.8e-007

**Matched b ions:** b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)

**Matched y ions:** y(3), y(3)-98, y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(10), y(11)++

**Precursor origin neutral loss:** +

---

**Peptide No.963**

**KAESISDLENK**

**Confirmed sites:** @S:4

**Ambiguous sites:**

**MS/MS Fragmentation of KAESISDLENK**

Found in **AT3G19770.1**, vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein

**Match to Query 1606:** 1312.590086 from(657.302319,2+)

**Elution from:** 27.035 to 27.035 scan no 2227 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1312.5911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.9e-007
Matched b ions: b(3), b(4)−98, b(5), b(5)−98, b(6), b(6)−98, b(7), b(7)−98, b(8)−98, b(8), b(9)−98, b(9), b(10), b(10)++, b(10)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)−98, y(8), y(8)++, y(9)−98, y(10)−98, y(10), y(10)−98++
Precursor origin neutral loss: +

Peptide No.964

KAEVVVPATESDGDDSVVEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KAEVVVPATESDGDDSVVEK
Found in AT2G45520.1, similar to Os06g0129800 [Oryza sativa (japonica cultivar–group)] (GB:NP_001056684.1); similar to hy

Match to Query 3886: 2152.975284 from(718.665704,3+)
Elution from: 33.069 to 33.069 scan no 3024 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2152.9776
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 5.4e-006
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(10), b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(14)++,
+ b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98++, y(10)++, y(11)++, y(11), y(12)++, y(12)-98, y(12)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.965
KASGNYEVLGPEYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KASGNYEVLGPEYK
Found in AT1G17210.1, zinc ion binding

Match to Query 2793: 1633.736304 from(817.875428,2+)
Elution from: 33.735 to 33.735 scan no 3162 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1633.7388
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00011
Matched b ions: b(8), b(9), b(9)--98, b(10), b(11)--98, b(12)--98
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(13)--98++
Precursor origin neutral loss: +

Peptide No.966

KASLPNYER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KASLPNYER
Found in AT5G18760.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 1282: 1156.527772 from(579.271162,2+)
Elution from: 24.168 to 24.168 scan no 1865 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1156.5277
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.045
Matched b ions: b(2), b(4)-98
Matched y ions: y(5), y(6), y(7)-98, y(8)-98, y(8)++
Precursor origin neutral loss: +

Peptide No.967

KASSGSADRDVILADLEK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of KASSGSADRDVILADLEK
Found in AT2G45820.1, DNA-binding protein, putative

Match to Query 3360: 1953.939495 from(652.320441,3+)
Elution from: 40.396 to 40.396 scan no 4038 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1953.9408
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0025
Matched b ions: b(4)-98, b(5), b(6), b(7), b(8), b(9)+, b(10)+, b(10)-98++, b(11), b(11)-98++, b(11)+, b(11)+, b(12)+, b(12)-98++, b(13)+, b(13)-98++, b(14)+, b(14)-98++, b(15)+, b(15)+, b(16)+, b(17)-98++, b(17)+
Matched y ions: y(3), y(4), y(5), y(6), y(7)+, y(7), y(8), y(10)+, y(12)+, y(14)+, y(16)-98++, y(16)+, y(17)-98++, y(17)+
Precursor origin neutral loss: +

Peptide No.968
KASSGSADRDVILADLEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KASSGSADRDVILADLEK
Found in AT2G45820.1, DNA−binding protein, putative

Match to Query 3649: 1953.939708 from(652.320512,3+)
Elution from: 41.865 to 41.865 scan no 4211 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1953.9408
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.038
Matched b ions: b(4)-98, b(6), b(7)-98, b(7), b(8), b(8)+, b(9)+, b(9)-98, b(10)+, b(11), b(11)+, b(11)-98++, b(12)+, b(12)-98++, b(13)-98++, b(13)+, b(14)+, b(15)+, b(15)-98++, b(16)-98++, b(16)+, b(16)-98++, b(17)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)+, y(12)+, y(13)+, y(14)+, y(15)-98++, y(15)+, y(16)-98++, y(17)-98++, y(17)+
Precursor origin neutral loss: +

Peptide No.969
KDDEEEVEEEQPLSPAAR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of KDDEEEVEEEQPLSPAAR
Found in AT3G49210.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49200.1); similar to condensation domai

Match to Query 3051: 2149.903660 from(1075.959106,2+)
Elution from: 30.307 to 30.307 scan no 2642 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2149.9052
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 4.7e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(13), b(14)–98, b(17)
Matched y ions: y(4), y(6), y(7)–98, y(7), y(8)–98, y(9)–98, y(10), y(10)–98, y(15), y(16)–98
Precursor origin neutral loss: +

Peptide No.970

KDEDLSEEDLELK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **KDEDLSEEDLELK**
Found in **AT2G20580.1**, AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A); binding

Match to Query 2162: 1641.700200 from(821.857376,2+)
Elution from: 36.242 to 36.242 scan no 3418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1641.7022
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.4e-005
Matched b ions: b(4), b(5), b(8)--98, b(9)--98, b(10)--98, b(11)--98, b(11), b(12)--98++, b(12)++, b(12)--98
Matched y ions: y(2), y(5), y(8), y(9)--98, y(9), y(11)++, y(11), y(12)--98++, y(12)--98
Precursor origin neutral loss: +

Peptide No.971

KDEPAEESDGDLGFGLFD
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of KDEPAEESDGDLGFGLFD
Found in AT1G01100.1, 60S acidic ribosomal protein P1 (RPP1A)

Match to Query 3822: 2019.795604 from(1010.905078,2+)
Elution from: 72.316 to 72.316 scan no 7623 polarity:+
**Peptide No.972**

KDLSEDENMEEAEEK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of **KDLSEDENMEEAEEK**

Found in **AT5G53440.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unnamed protein pr

Match to Query 2741: 1874.710924 from(938.362738,2+)

Elution from: 26.401 to 26.401 scan no 2123 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1874.7128
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 95 Expect: 2.5e-009
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(8), b(9)-98, b(10)-98, b(10), b(11)-98, b(12)-98++, b(13)-98, b(13), b(14)-98, b(14)+++, b(14)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)+++, y(9), y(10), y(11), y(12)-98++, y(12)-98, y(12), y(13)-98, y(13)-98++, y(13)+++, y(14)-98++, y(14)-98
Precursor origin neutral loss: +

Peptide No.973
KDPLESMDSGILVTEK
Confirmed sites: "@S:9,@T:14"
Ambiguous sites:

MS/MS Fragmentation of KDPLESMDSGILVTEK
Found in AT5G45930.1, CHLI2; magnesium chelatase

Match to Query 3436: 1936.816248 from(646.612692,3+)
Elution from: 43.946 to 43.946 scan no 4285 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1936.8141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.02
Matched b ions: b(2), b(6)++, b(6), b(8)++, b(10)−98++, b(11)++, b(11), b(11)−98++, b(12)++, b(13)−98++, b(14)++, b(14)−98++, b(15)−98++
Matched y ions: y(4)++, y(4), y(5), y(5)++, y(6), y(7), y(8)++, y(10)++, y(10), y(10)−98++, y(11)−98++, y(12)++, y(14)++
Precursor origin neutral loss: +

Peptide No.974
KDPLESMDSGILVTEK
Confirmed sites: "@S:6,@T:14"
Ambiguous sites:

MS/MS Fragmentation of KDPLESMDSGILVTEK
Found in AT5G45930.1, CHLI2; magnesium chelatase

Match to Query 3162: 1936.817442 from(646.613090,3+)
Elution from: 42.347 to 42.347 scan no 4292 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1936.8141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.036
Matched b ions: b(2), b(5), b(11)++, b(12), b(12)++, b(13)−98++, b(14)++, b(14)−98++, b(15)−98++, b(15)++
Matched y ions: y(4)++, y(4), y(5), y(6), y(7), y(10)++, y(14)++
Precursor origin neutral loss:

Peptide No.975
KDQSDEDEEEEMKILVEGFV
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KDQSDEDEEEEMKILVEGFV
Found in AT1G15230.1, similar to Os09g0344700 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001062932.1)

Match to Query 4463: 2545.078161 from(849.366663,3+)
Elution from: 60.173 to 60.173 scan no 6345 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2545.0818
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.012
Matched b ions: b(13)++, b(14)−98++, b(16)++, b(17)++, b(17)−98++, b(18)++, b(19)++, b(20)++
Matched y ions:
  Precursor origin neutral loss: +

Peptide No.976

KEEFLIGSIEEESQSQSPR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of KEEFLIGSIEEESQSQSPR
Found in AT1G53590.1, C2 domain-containing protein

Match to Query 4331: 2272.021214 from(1137.017883,2+)
Elution from: 48.306 to 48.306 scan no 5064 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2272.0260
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.0001
Matched b ions: b(6), b(7), b(8), b(9), b(12), b(14), b(16), b(17)-98
Matched y ions: y(7), y(7)-98, y(8)-98, y(10), y(10)-98, y(11)-98, y(12)-98, y(12), y(13)-98, y(13), y(16)
Precursor origin neutral loss: +

Peptide No.977

KEEKEESDDDMGFSLFE
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEEKEESDDDMGFSLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)

Match to Query 2983: 2113.804758 from(1057.909655,2+) Elution from: 56.514 to 56.514 scan no 5674 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2113.8074
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 1.6e-006
Matched b ions: b(4), b(6), b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(10)++, b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(15)+, b(15)-98++, b(16)-98++, b(16)+
Matched y ions: y(5), y(6), y(7), y(8), y(11), y(14), y(15), y(16)-98++
Precursor origin neutral loss: +

Peptide No.978
KEEKEESDDDMGFSLFE
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEEKEESDDDMGFSLFE
Found in AT2G27710.1, 60S acidic ribosomal protein P2 (RPP2B)

Match to Query 3314: 2129.799932 from(1065.907242,2+)
Elution from: 49.138 to 49.138 scan no 4984 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2129.8024

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- M11 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983

**Ions Score:** 80 **Expect:** 6.1e-008

**Matched b ions:** b(3), b(4), b(5), b(6)+, b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(10)++, b(11)-98, b(11), b(11)-98++, b(11)+, b(12), b(12)-98, b(12)-98++, b(12)+, b(13)-98, b(13), b(13)-98++, b(13)+, b(14), b(14)-98++, b(14)-98, b(14)+, b(15)-98, b(15)-98++, b(15), b(15)+, b(16)-98++, b(16)+

**Matched y ions:** y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)-98, y(13), y(14), y(14)-98, y(14)-98++, y(14)+, y(15)-98, y(15), y(15)-98++, y(16)-98, y(16)-98++, y(16)+

**Precursor origin neutral loss:** +

---

**Peptide No.979**

**KEESDEEDYEGGFGLFDEE**

**Confirmed sites:** @S:4

**Ambiguous sites:**

**MS/MS Fragmentation of KEESDEEDYEGGFGLFDEE**

Found in **AT3G11250.1**, 60S acidic ribosomal protein P0 (RPP0C)

Match to Query 4115: 2302.826500 from(1152.420526,2+)

Elution from: 61.522 to 61.522 scan no 6480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2302.8314
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 5.5e-009
Matched b ions: b(5), b(6)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(14), b(15), b(16), b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(3), y(4), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(16), y(18)++
Precursor origin neutral loss: +

Peptide No.980
KEESEEEEGDFGFDLFG
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KEESEEEEGDFGFDLFG
Found in AT4G25890.1, 60S acidic ribosomal protein P3 (RPP3A)

Match to Query 3010: 2042.765706 from(1022.390129,2+)
Elution from: 70.354 to 70.354 scan no 6592 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2042.7669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00054
Matched b ions: b(6), b(7), b(8), b(10), b(11), b(14)++, b(15), b(15)−98++, b(15)++, b(16)−98++, b (16)++
Matched y ions: y(7), y(9), y(12)
Precursor origin neutral loss: +

Peptide No.981

KELESSGVVISQDLALKVLR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KELESSGVVISQDLALKVLR
Found in AT5G15980.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 4137: 2263.222443 from(755.414757,3+)
Elution from: 49.192 to 49.192 scan no 5228 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2263.2188
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.0077
Matched b ions: b(3), b(11)++, b(12)++, b(13)−98++, b(13)++, b(14)++, b(15)++, b(16)−98++, b(16)++,
b(17)++, b(18)−98++, b(19)−98++
Matched y ions: y(8)++, y(9), y(11)++, y(12)−98++, y(14)++, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss:

Peptide No.982
KETSDDEELAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KETSDDEELAR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 1477: 1371.553824 from(686.784188,2+)
Elution from: 18.803 to 18.803 scan no 1155 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1371.5555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 8.1e-005
Matched b ions: b(3), b(4)-98, b(5), b(6), b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(9)-98, y(10)-98
Precursor origin neutral loss: +

Peptide No.983

KETSDDEELAR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of KETSDDEELAR
Found in AT1G80930.1. MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 1779: 1371.553844 from(686.784198,2+)
Elution from: 19.777 to 19.777 scan no 1136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1371.5555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.027
Matched b ions: b(3)−98, b(4)−98, b(6), b(8)−98, b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)−98, y(10)−98, y(10)++
Precursor origin neutral loss: +

Peptide No.984
KFSEQNIGAPPSYEEAVSDSR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of KFSEQNIGAPPSYEEAVSDSR
Found in AT2G43160.1, epsin N-terminal homology (ENTH) domain-containing protein

Match to Query 3449: 2390.040615 from(797.687481,3+)
Elution from: 41.801 to 41.801 scan no 4197 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2390.0427
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00014
Matched b ions: b(3), b(5), b(6)+, b(7), b(7)+, b(7)-98, b(8)-98++, b(9), b(9)+, b(9)-98++, b(9)-98, b(10)-98++, b(12)+, b(12), b(14)-98++, b(15)+, b(15)-98++, b(16)+, b(16)-98++, b(17)+, b(17)-98++, b(19)+
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)+, y(11), y(12)+, y(12), y(13)+, y(14)+
Precursor origin neutral loss:

Peptide No.985

KFSPIVWDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KFSPIVWDR**
Found in **AT1G67580.1**, protein kinase family protein

Match to Query 1522: 1226.583518 from(614.299035,2+)
Elution from: 43.623 to 43.623 scan no 4475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1226.5849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.036
Matched b ions: b(2), b(3)--98, b(3), b(4)++, b(5)--98, b(6), b(6)--98++
Matched y ions: y(3), y(4), y(5)++, y(6), y(6)++, y(7)++, y(7)--98, y(7)--98++, y(8), y(8)--98++, y(8)--98
Precursor origin neutral loss: +

Peptide No.986
KFSPIVWDRDDHER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KFSPIVWDRDDHER
Found in AT1G67580.1, protein kinase family protein

Match to Query 2760: 1878.838712 from(470.716954,4+) Elution from: 35.741 to 35.741 scan no 3428 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1878.8414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0073
Matched b ions: b(2), b(3)+, b(4)+98, b(4)+98++, b(5)+98, b(5), b(6)+, b(6)+98, b(9)+98++, b(9)+++, b(10)+98++, b(10)+++, b(11)+
Matched y ions: y(1), y(2), y(3)+, y(4)+, y(4), y(6)+, y(8)+, y(9)+, y(11)+
Precursor origin neutral loss: +

Peptide No.987
KGGSDDETRDANFMR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KGGSDDETRDANFMR
Found in AT1G78650.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22795.1); similar to Os01g0204000 [Oryz

Match to Query 3157: 1777.707270 from(593.576366,3+)
Elution from: 25.195 to 25.195 scan no 2022 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1777.7090

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 32 Expect: 0.0043

Matched b ions: b(4), b(4)−98, b(5)−98, b(5), b(6), b(6)−98, b(7)−98, b(7), b(9)+, b(10)+, b(10)−98+, b(11)−98++, b(14)−98++

Matched y ions: y(4)+, y(4), y(5), y(6), y(8)+, y(9)+, y(10)+, y(11)+, y(12)+, y(13)−98++, y (14)−98++, y(14)+

Precursor origin neutral loss: +

Peptide No. 988

KGRFGITYATNVTDR

Confirmed sites: “@Y:8,@T:10”

Ambiguous sites:

MS/MS Fragmentation of KGRFGITYATNVTDR

Found in AT2G21710.1, EMB2219 (EMBRYO DEFECTIVE 2219); transferase

Match to Query 3081: 1857.812740 from(929.913646,2+)

Elution from: 42.488 to 42.488 scan no 4315 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1857.8175
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y8 : Phospho (Y)
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0036
Matched b ions: b(4), b(6), b(7), b(11)−98, b(12)−98, b(13)−98, b(14)−98, b(14)++
Matched y ions: y(4), y(11), y(11)−98
Precursor origin neutral loss: +

Peptide No.989

KGSGLSGDQYAVMVSCR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KGSGLSGDQYAVMVSCR
Found in AT3G17900.1, similar to Os03g0152800 [Oryza sativa (japonica cultivar−group)] (GB:NP_001048995.1); similar to ex

Match to Query 3430: 1893.808862 from(947.911707,2+)
Elution from: 39.034 to 39.034 scan no 3884 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1893.8114
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 1.5e-009
Matched b ions: b(5)-98, b(8), b(8)-98, b(10), b(11), b(12)-98, b(12), b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(16)-98, y(16)+, y (16)-98++
Precursor origin neutral loss: +

Peptide No.990

KGSGLSGDQYAVMVSCR
Confirmed sites: @Y:10
Ambiguous sites:

MS/MS Fragmentation of KGSGLSGDQYAVMVSCR
Found in AT3G17900.1, similar to Os03g0152800 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001048995.1); similar to ex

Match to Query 3398: 1893.810951 from(632.277593,3+)
Elution from: 39.436 to 39.436 scan no 3909 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1893.8114
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y10 : Phospho (Y)
Ions Score: 29 Expect: 0.014
Matched b ions: b(11)+, b(13)+, b(14)+, b(15)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(9)+
Precursor origin neutral loss:

Peptide No.991
KHSWPTEEFSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KHSWPTEEFSR
Found in AT3G24180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G49900.1);
similar to unknown protein [A

Match to Query 2695: 1595.711208 from(532.911012,3+)
Elution from: 38.781 to 38.781 scan no 3850 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1595.7133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0028
Matched b ions: b(3)-98, b(4)-98, b(4)+, b(5)-98++, b(5)-98, b(6)-98++, b(7)+, b(7)-98++, b(8)-98++, b(9)+, b(10)-98++
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7), y(8)+, y(9)+, y(10)-98++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.992
KIDTLTPQDSPQRV
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of KIDTLTPQDSPQRV
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 2417: 1676.811320 from(839.412936,2+)
Elution from: 30.077 to 30.077 scan no 2654 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1676.8134
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.5e-007
Matched b ions: b(3), b(5), b(6), b(7), b(9), b(10)–98, b(10), b(12)–98++, b(13)++, b(13)–98++
Matched y ions: y(3), y(4), y(5), y(5)–98, y(6), y(7), y(7)–98, y(8)–98, y(8), y(9), y(9)–98, y(10)–98, y(11), y(12), y(12)–98, y(13)–98
Precursor origin neutral loss: +

Peptide No.993

KIDTLTPQDSPQRV
Confirmed sites: ”@T:6,@S:10”
Ambiguous sites:

MS/MS Fragmentation of KIDTLTPQDSPQRV
Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 3213: 1756.779290 from(879.396921,2+)
Elution from: 31.991 to 31.991 scan no 2953 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1756.7798

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- T6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 43 **Expect:** 0.00043

**Matched b ions:** b(3), b(5), b(6)-98, b(9), b(9)-98, b(10)-98, b(13)+, b(13)-98++

**Matched y ions:** y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10)+, y(11)

**Precursor origin neutral loss:** +

---

**Peptide No.994**

KIDTLTPQDSPQRV

**Confirmed sites:** "@T:6, @S:10"

**Ambiguous sites:**

MS/MS Fragmentation of KIDTLTPQDSPQRV

Found in AT5G67220.1, nitrogen regulation family protein

Match to Query 2141: 1756.776976 from(879.395764,2+)  
Elution from: 32.102 to 32.102 scan no 2889 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1756.7798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 3.9e-005
Matched b ions: b(5), b(6)-98, b(8), b(9), b(9)-98, b(10)-98, b(13)-98++, b(13)++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(11)-98, y(11)
Precursor origin neutral loss: +

Peptide No.995

KISGILDDGSVGFR
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of KISGILDDGSVGFR
Found in AT5G49890.1, CLC-C (chloride channel C); anion channel/ voltage-gated chloride channel

Match to Query 2077: 1542.742496 from(772.378524,2+)  
Elution from: 47.939 to 47.939 scan no 4803 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1542.7442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 5.6e-007
Matched b ions: b(3)-98, b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(12)
Matched y ions: y(3), y(6)+++, y(6), y(7)+++, y(7), y(8), y(9), y(11), y(12), y(12)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.996

KISGPLDYSGSMK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KISGPLDYSGSMK
Found in AT1G78880.1, balbiani ring 1-related / BR1-related

Match to Query 2405: 1461.656094 from(731.835323,2+)
Elution from: 36.039 to 36.039 scan no 3524 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1461.6574
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0076
Matched b ions: b(3)–98, b(7)–98, b(7), b(8)–98, b(10)++
Matched y ions: y(6), y(9), y(10), y(11)–98, y(11), y(12)–98, y(12)–98++
Precursor origin neutral loss: +

Peptide No.997
KKDEPAEESDGDGLGFGLFD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KKDEPAEESDGDGLGFGLFD
Found in AT1G01100.1, 60S acidic ribosomal protein P1 (RPP1A)

Match to Query 3589: 2147.890616 from(1074.952584,2+)
Elution from: 57.383 to 57.383 scan no 5916 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2147.8935

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S9: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 72 Expect: 6e-007

Matched b ions: b(4), b(5), b(7), b(8), b(9)−98, b(10)−98, b(10), b(12)−98++, b(12)−98, b(12), b(13), b(13)−98, b(14), b(14)−98, b(15)−98, b(15), b(15)−98++, b(15)++, b(16)++, b(16)−98++, b(17)−98++, b(17)++, b(18)−98++

Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(11)−98, y(12), y(13), y(13)−98, y(14), y(14)−98, y(15)−98, y(15), y(16), y(17), y(17)−98, y(18)++

Precursor origin neutral loss: +

Peptide No.998

KKDSVEMVDAEQK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of KKDSVEMVDAEQK

Found in AT3G18610.1, ATRANGAP1 (RAN GTPASE-ACTIVATING PROTEIN 1); nucleic acid binding

Match to Query 2452: 1700.731422 from(567.917750,3+)

Elution from: 21.007 to 21.007 scan no 1462 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1700.7328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 2.3e-006
Matched b ions: b(2), b(4)-98, b(5)+, b(5)-98, b(5), b(6)-98++, b(6)+, b(6), b(7)+, b(7)-98++, b(8), b(8)+, b(8)-98++, b(9)+, b(9)-98++, b(10)+, b(11)+, b(11)-98++, b(12)+, b(12)-98++, b(13)+
Matched y ions: y(3), y(4), y(5), y(6), y(6)+, y(7), y(7)+, y(7), y(8), y(8)+, y(11)+
Precursor origin neutral loss: +

Peptide No.999

KKEESEEEGDFGFDLFG
Confirmed sites: @S.5
Ambiguous sites:

MS/MS Fragmentation of KKEESEEEGDFGFDLFG
Found in AT4G25890.1, 60S acidic ribosomal protein P3 (RPP3A)

Match to Query 3703: 2170.859418 from(1086.436985,2+)
Elution from: 67.317 to 67.317 scan no 6929 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2170.8619
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 8.6e-007
Matched b ions: b(4), b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98++, b(14)-98++, b(14)+++, b(15)-98++, b(15)-98, b(15)+++, b(16)-98++, b(16)+++, b(17)-98++, b(17)+++
Matched y ions: y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1000

KKPEVAESSKSGDEAEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KKPEVAESSKSGDEAEK
Found in AT5G61790.1, calnexin 1 (CNX1)

Match to Query 2490: 1897.864719 from(633.628849,3+)
Elution from: 14.530 to 14.530 scan no 714 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.8669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00017
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(9), b(9)++, b(10)++, b(11)–98++, b(12)++, b(13)–98++, b(13)++, b(14)–98++, b(14)++, b(15)–98++, b(15)++, b(16)++, b(16)–98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)–98, y(7), y(8), y(8)++, y(8)–98++, y(9)–98++, y(10)++, y(10)–98++, y(12)++, y(12)–98++, y(13)–98++, y(13)++, y(14)++, y(15)–98++, y(15)++, y(16)–98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1001

KKPEVAESSKSGDEAEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of KKPEVAESSKSGDEAEK
Found in AT5G61790.1, calnexin 1 (CNX1)

Match to Query 2733: 1897.864887 from(633.628905,3+)
Elution from: 14.437 to 14.437 scan no 691 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.8669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.013
Matched b ions: b(10)++, b(11)−98++, b(13)++, b(14)−98++, b(15)−98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(9)++, y(10)++, y(14)++, y(15)−98++, y(15)+++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1002

KKSSDVEMVDAEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KKSSDVEMVDAEK
Found in AT1G48920.1, nucleolin, putative

Match to Query 2413: 1544.677668 from(773.346110,2+)
Elution from: 19.209 to 19.209 scan no 1246 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1544.6793
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 75 Expect: 2.1e-007
Matched b ions: b(2), b(3), b(5), b(5)–98, b(6)–98, b(6), b(7)–98, b(7), b(8)–98++, b(8), b(8)–98, b(9), b(9)–98, b(9)++, b(10)–98, b(10), b(11)–98, b(11), b(11)++, b(11)–98++, b(12), b(12)–98, b(12)–98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7), y(8), y(9), y(10)++, y(10), y(11)–98, y(11), y(11)++, y(12)–98, y(12), y(12)++, y(12)–98++
Precursor origin neutral loss: +

Peptide No. 1003

KKSSDVEMVDAEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KKSSDVEMVDAEK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1648: 1544.678360 from (773.346456, 2+)
Elution from: 19.509 to 19.509 scan no 1231 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 1544.6793
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 6.9e-008
Matched b ions: b(2), b(4), b(4)+, b(5), b(5)–98, b(6), b(6)–98, b(7), b(7)–98, b(8), b(8)–98, b(8)+, b(8)–98++, b(9)–98, b(9), b(9)–98++, b(9)+, b(10), b(10)–98, b(11), b(11)–98++, b(11)–98, b(11)+, b(12), b(12)–98, b(12)–98++, b(12)+
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(8), y(9), y(10), y(10)–98, y(11), y(11)–98, y(11)+, y(12)–98, y(12)–98++, y(12)+
Precursor origin neutral loss: +

Peptide No.1004

KLADSNSTTNGNK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of KLADSNSTTNGNK
Found in AT3G49140.1, binding

Match to Query 1809: 1428.625848 from(477.215892,3+)
Elution from: 23.090 to 23.090 scan no 1679 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1428.6246
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.046
Matched b ions: b(5), b(10)++, b(11)++, b(12)++
Matched y ions: y(5)−98, y(6)−98, y(8)++, y(10)++, y(10)−98++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.1005

KLDDEVLSDDDDQVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of KLDDEVLSDDDDQVR
Found in AT4G18950.1, ankyrin protein kinase, putative

Match to Query 2101: 1725.745940 from(863.880246,2+)
Elution from: 35.319 to 35.319 scan no 3188 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1725.7458
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0019
Matched b ions: b(6), b(7), b(8)-98, b(11)-98
Matched y ions: y(4), y(5), y(6), y(7)-98, y(8)-98, y(10)-98, y(11)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1006

KLDDEVLSDDDQVRK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of KLDDEVLSDDDQVRK
Found in AT4G18950.1, ankyrin protein kinase, putative

Match to Query 3213: 1853.838816 from(618.953548,3+)
Elution from: 31.070 to 31.070 scan no 2566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1853.8408
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.004
Matched b ions: b(5), b(6), b(9)++, b(9)–98, b(9), b(12)–98++, b(13)–98++
Matched y ions: y(4)++, y(4), y(5)++, y(6)++, y(7)++, y(9)–98++, y(10)–98++, y(10)++, y(11)–98, y(11)–98++, y(11)++, y(12)–98++, y(13)–98++, y(13)++, y(14)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1007

KLDHFVCAECSSDDDVKK
Confirmed sites: “@S:11,@S:12”
Ambiguous sites:

MS/MS Fragmentation of KLDHFVCAECSSDDDVKK
Found in AT4G22140.1, DNA binding

Match to Query 4235: 2311.887344 from(578.979112,4+)
Elution from: 29.531 to 29.531 scan no 2546 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2311.8891
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.012
Matched b ions: b(4), b(6)++, b(7)++, b(8), b(8)++, b(9)++, b(10)++, b(11)++, b(14)−196++, b(15)++, b(15)−98++, b(15)−196++, b(16)−98++, b(16)−196++
Matched y ions: y(5)++, y(7)−98++, y(8)++, y(9)−98++, y(11)−98++, y(12)++, y(12)−196++, y(12)−98++, y(13)−98++, y(13)++, y(13)−196++, y(14)−196++
Precursor origin neutral loss: +

Peptide No.1008
KLEEGPKDEEESDK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of KLEEGPKDEEESDK
Found in AT1G20693.1, HMGB2 (HIGH MOBILITY GROUP B 2); transcription factor

Match to Query 2032: 1711.717284 from(571.579704,3+)
Elution from: 17.049 to 17.049 scan no 935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1711.7189
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.013
Matched b ions: b(3), b(4), b(9)++, b(13)--98++, b(13)++
Matched y ions: y(4), y(5), y(6)--98++, y(10)++, y(10)--98++, y(11)--98++, y(12)++, y(12)--98++, y(13)--98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1009
KLESSLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KLESSLK
Found in AT1G31330.1, PSAF (photosystem I subunit F)

Match to Query 392: 883.441236 from(442.727894,2+)
Elution from: 20.052 to 20.052 scan no 1360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 883.4416

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 44 Expect: 0.00023

Matched b ions: b(1), b(3), b(4)–98++, b(5)–98, b(6)–98, b(6)
Matched y ions: y(1), y(2), y(3), y(4), y(4)–98, y(5)–98, y(5), y(6)–98, y(6)

Peptide origin neutral loss: +

Peptide No.1010

KLETLDETSEGEEAK

Confirmed sites: @S:9

Ambiguous sites:

MS/MS Fragmentation of KLETLDETSEGEEAK
Found in AT2G19385.1, nucleic acid binding / zinc ion binding

Match to Query 2767: 1757.759134 from(879.886843,2+)
Elution from: 26.064 to 26.064 scan no 2076 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1757.7608
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 84 Expect: 3.4e-008
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9)-98, b(10), b(10)-98, b(12), b(13)-98, b(13), b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(14), y(14)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1011
KLETLDSEGEAK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of KLETLDSEGEAK
Found in AT2G19385.1, nucleic acid binding / zinc ion binding

Match to Query 2098: 1757.760231 from(586.927353,3+)
Elution from: 25.483 to 25.483 scan no 1999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1757.7608
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 3.3e-005
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(7)+, b(8)-98, b(8)-98++, b(9)+, b(9)-98++, b(10)-98++, b(10)+, b(11)+, b(12)+, b(12)-98++, b(13)+, b(14)+, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)+, y(8), y(8)-98++, y(8)-98, y(9)+, y(10)-98++, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1012
KLLSPIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KLLSPIK
Found in AT2G25660.1, EMB2410 (EMBRYO DEFECTIVE 2410)

Match to Query 393: 877.503250 from(439.758901,2+)
Elution from: 29.883 to 29.883 scan no 2643 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 877.5038
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.048
Matched b ions: b(1), b(2), b(3), b(4)-98, b(5)-98, b(6), b(6)-98
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5)
Precursor origin neutral loss: +

Peptide No.1013
KLSELSDDEDFDEQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KLSELSDDEDFDEQK
Found in AT3G48500.1, PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding

Match to Query 3446: 1876.760235 from(626.594021,3+)
Elution from: 36.338 to 36.338 scan no 3499 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1876.7615
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00018
Matched b ions: b(2), b(3)−98, b(4)−98++, b(5)++, b(5)−98, b(6), b(6)++, b(6)−98, b(7), b(7)−98++, b(7)++, b(8), b(8)−98++, b(8)++, b(8)−98, b(9)−98++, b(9), b(9)−98, b(9)++, b(10), b(10)−98, b(10)++, b(10)−98++, b(10)++, b(11)++, b(11)−98, b(11)−98++, b(12)++, b(12)−98++, b(13)++, b(13)−98++, b(14)++, b(14)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(13)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1014
KLSELSDDEDDEQK
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of KLSELSDDEDDEQK
Found in AT3G48500.1, PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding

Match to Query 3417: 1876.759724 from(939.387138,2+)
Elution from: 36.641 to 36.641 scan no 3430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1876.7615
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 9.1e-010
Matched b ions: b(4), b(5), b(6)−98, b(6), b(7)−98, b(7), b(8)−98, b(8), b(9)−98, b(9), b(10)−98, b(10), b(11), b(11)−98, b(12)−98, b(12)++, b(12), b(13)−98, b(13), b(13)−98++, b(14), b(14)−98, b(14)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)−98, y(11)−98, y(11), y(11)−98++, y(12)−98, y(13), y(13)−98, y(13)−98++, y(14)−98++, y(14), y(14)−98, y(14)++
Precursor origin neutral loss: +

Peptide No.1015
KLSFFSEPQEEK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of KLSFFSEPQEEK
Found in ATCG01130.1. Identical to Putative membrane protein ycf1 (ycf1-B) [Arabidopsis Thaliana] (GB:P56785); similar to

Match to Query 2909: 1675.748714 from(838.881633,2+)
Elution from: 40.969 to 40.969 scan no 4140 polarity:+


**Peptide No.1016**

KLSSALSAASSACDHIR

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of KLSSALSAASSACDHIR

Found in **AT1G04410.1**, malate dehydrogenase, cytosolic, putative

Match to Query 3326: 1852.846677 from(618.622835,3+)

Elution from: 37.379 to 37.379 scan no 3652 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.8502
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0027
Matched b ions: b(4), b(6), b(8)-98++, b(8), b(9)+, b(14)+, b(15)+, b(16)-98++, b(16)+
Matched y ions: y(2), y(4), y(5), y(7)+, y(7), y(8)+, y(8), y(9), y(13)+, y(14)+, y(15)-98++, y(15)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1017

KLSSLEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KLSSLEK
Found in AT1G79350.1, EMB1135 (EMBRYO DEFECTIVE 1135); DNA binding

Match to Query 412: 883.441170 from(442.727861,2+)
Elution from: 20.118 to 20.118 scan no 1327 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 883.4416
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.003
Matched b ions: b(1), b(3)–98, b(3), b(4)–98, b(5)–98, b(6)–98, b(6)
Matched y ions: y(3), y(5)–98, y(6)–98, y(6)
Precursor origin neutral loss: +

Peptide No.1018
KLSSLGTR
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of KLSSLGTR
Found in AT4G01990.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 339: 940.473600 from(471.244076,2+) Elution from: 20.978 to 20.978 scan no 1396 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 940.4743
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.018
Matched b ions: b(2), b(6)++
Matched y ions: y(3), y(4), y(5)−98, y(6)−98, y(7)−98
Precursor origin neutral loss: +

Peptide No.1019

KMRGSIATPTVPK
Confirmed sites: ”@S:5,@T:8”
Ambiguous sites:

MS/MS Fragmentation of KMRGSIATPTVPK
Found in AT2G01930.1, ATBPC1/BBR/BPC1/BPC1 (BASIC PENTACYSTEINE1); DNA binding / specific transcriptional repressor/ tran

Match to Query 2386: 1544.719014 from(515.913614,3+) 
Elution from: 19.617 to 19.617 scan no 1231 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1544.7187
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.047
Matched b ions: b(8)++, b(9)++, b(9)−98++, b(10)++, b(10)−196++, b(11)++, b(12)−196++, b(12)−98++
Matched y ions: y(9)−98++
Precursor origin neutral loss:

Peptide No.1020

KMSSNSLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KMSSNSLR
Found in AT5G36880.2, AMP binding / acetate-CoA ligase / catalytic

Match to Query 643: 1001.435868 from(501.725210,2+)
Elution from: 17.128 to 17.128 scan no 966 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1001.4365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.003
Matched b ions: b(3)-98, b(6)-98, b(6)
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7)
Precursor origin neutral loss: +

Peptide No.1021

KNSDDDSDDDDFLASR
Confirmed sites: ”@S:3,@S:8”
Ambiguous sites:

MS/MS Fragmentation of KNSDDDSDDDDFLASR
Found in AT1G19990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11600.1); similar to conserved hypothet

Match to Query 2659: 1973.654906 from(987.834729,2+) 
Elution from: 37.672 to 37.672 scan no 3513 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1973.6565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 1.3e-008
Matched b ions: b(4)-98, b(6), b(7), b(8)-98, b(9)-98, b(10), b(11)-196++, b(11)-98, b(11), b(12)-98, b(13), b(14)-196, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(12), y(12)-98, y(13), y(14)
Precursor origin neutral loss: +

Peptide No.1022
KNSLRVPEHVQNGIIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KNSLRVPEHVQNGIIK**
Found in **AT4G30890.1**, UBP24 (UBIQUITIN–SPECIFIC PROTEASE 24); ubiquitin–specific protease

Match to Query 3670: 2010.075108 from(503.526053,4+)
Elution from: 35.289 to 35.289 scan no 3384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2010.0775
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.025
Matched b ions: b(4), b(5)-98++, b(5)++, b(6)-98++, b(7)++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(14)-98++, b(14)++, b(15)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1023
KNSVDFDFEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KNSVDFDFEK
Found in AT3G22190.1, IQD5 (IQ-domain 5); calmodulin binding

Match to Query 1745: 1307.542328 from(654.778440,2+)
Elution from: 35.690 to 35.690 scan no 3477 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1307.5434
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.4e-007
Matched b ions: b(4)--98, b(5)--98, b(6), b(7), b(7)--98, b(7)--98++, b(8), b(9), b(9)--98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)--98, y(8), y(9)--98, y(9), y(9)--98++
Precursor origin neutral loss: +

Peptide No.1024

KNVYRQGSR
Confirmed sites: ”@Y:4,@S:8”
Ambiguous sites:

MS/MS Fragmentation of KNVYRQGSR
Found in AT4G19510.1, disease resistance protein (TIR-NBS-LRR class), putative

Match to Query 1756: 1266.529076 from(634.271814,2+).
Elution from: 25.345 to 25.345 scan no 2041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1266.5271
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y4 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.018
Matched b ions: b(3), b(4), b(6), b(7)
Matched y ions: y(2), y(5)−98, y(5)++, y(6)−98, y(6), y(7)−98, y(8)−98, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1025

KPEVAESSKSGDEAEKK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KPEVAESSKSGDEAEKK
Found in AT5G61790.1, calnexin 1 (CNX1)

Match to Query 2700: 1897.864893 from(633.628907,3+)
Elution from: 13.489 to 13.489 scan no 649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.8669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0074
Matched b ions: b(7), b(11)++, b(13)++, b(15)++, b(16)++, b(16)−98++
Matched y ions: y(14)++, y(15)++, y(16)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1026
KPHLMPSSPEHVDGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KPHLMPSSPEHVDGK
Found in AT2G43650.1, Sas10/U3 ribonucleoprotein (Utp) family protein

Match to Query 2666: 1737.789279 from(580.270369,3+)
Elution from: 22.100 to 22.100 scan no 1576 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1737.7909
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00032
Matched b ions: b(2), b(4), b(5), b(6)+, b(8)-98, b(8)+, b(9)-98++, b(10)-98++, b(11)+, b(12)-98++, b(12)+, b(13)+, b(13)-98++, b(14)+, b(14)-98++
Matched y ions: y(2), y(4)+, y(5), y(7)+, y(8)+, y(9)+, y(10)-98++, y(11), y(11)+, y(12)+, y(13)+, y(13)-98++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1027
KPHLMPSSPEHVDGK
Confirmed sites:
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of KPHLMPSSPEHVDGK
Found in AT2G43650.1, Sas10/U3 ribonucleoprotein (Utp) family protein

Match to Query 2731: 1737.789609 from(580.270479,3+)
Elution from: 22.368 to 22.368 scan no 1612 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1737.7909
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.023
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8)−98, b(12)++, b(13)++, b(13)−98++, b(14)++, b(14)−98++
Matched y ions: y(2), y(4)++, y(7)++, y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(13)−98++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1028
KPIEEEYSYGSGSDIPTMRMVK
Confirmed sites: "@S:7,@Y:8,@S:11"
Ambiguous sites:

MS/MS Fragmentation of KPIEEEYSYGSGSDIPTMRMVK
Found in AT5G01620.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38320.1);
similar to Os03g0817900 [Oryz]

Match to Query 4212: 2795.097201 from(932.706343,3+)
Elution from: 27.253 to 27.253 scan no 2227 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2795.1025
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  Y8 : Phospho (Y)
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 Expect: 0.039
Matched b ions: b(7)−98, b(8)++, b(8), b(9)++, b(9), b(10)−98, b(11)++, b(11), b(11)−98++, b(12), b(12)++, b(13)++, b(15)++, b(17)++, b(17)−98++, b(21)++
Matched y ions: y(10), y(11), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(18)−98++, y(18)−196++, y(19)++
Precursor origin neutral loss:

Peptide No.1029

KPISDEVNDSDEEYK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of KPISDEVNDSDEEYK
Found in AT3G12480.1, transcription factor, putative

Match to Query 2307: 1846.749086 from(924.381819,2+)  
Elution from: 26.326 to 26.326 scan no 2112 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1846.7509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0017
Matched b ions: b(7), b(9), b(13)−98++, b(13)++, b(14)−98
Matched y ions: y(5), y(6), y(7)−98, y(8)−98, y(8), y(9), y(9)−98, y(12), y(13)++, y(13), y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1030
KPISDEVNDSDEEYKK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of KPISDEVNDSDEEYKK
Found in AT3G12480.1, transcription factor, putative

Match to Query 2663: 1974.844071 from(659.288633,3+) Elution from: 23.409 to 23.409 scan no 1657 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1974.8459
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.6e-005
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(10)+, b(11)+, b(13)--98++, b(13)+, b(15)++
Matched y ions: y(5)+, y(6)+, y(7)--98++, y(8)--98, y(8)--98++, y(8)+, y(9)--98, y(9)+, y(9)--98++,
y(10)--98++, y(11)--98++, y(12)--98++, y(13)+, y(13)--98++, y(14)--98++, y(14)+, y(15)--98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1031

KPVLSNNNDASTLK
Confirmed sites: @S.5
Ambiguous sites:

MS/MS Fragmentation of KPVLSNNNDASTLK
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1);
similar to hypothetical prote

Match to Query 2474: 1579.759018 from(790.886785,2+)
Elution from: 25.093 to 25.093 scan no 1878 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1579.7607
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 44 Expect: 0.0003
Matched b ions: b(4), b(5)−98, b(8)−98, b(8), b(9), b(9)−98, b(11)−98++, b(12)++, b(13), b(13)−98, b(13)−98++, b(13)++
Matched y ions: y(3), y(5), y(8), y(9), y(9)++, y(10)−98, y(10), y(11)−98, y(11), y(11)−98++, y(11)++, y(12), y(12)−98, y(12)++, y(12)−98++, y(13)−98, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No. 1032

KPVYNLDDSDDDFVPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KPVYNLDDSDDDFVPK
Found in AT2G25170.1, PKL/SSL2 (PICKLE, SUPPRESSOR OF SLR2)

Match to Query 3508: 2060.859910 from (1031.437231, 2+)
Elution from: 44.159 to 44.159 scan no 4530 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2060.8616
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 1.3e-005
Matched b ions: b(6), b(7), b(8), b(9)-98, b(11), b(12)-98, b(13), b(14), b(15), b(15)-98, b(16)-98
Matched y ions: y(5), y(9), y(9)-98, y(10), y(13), y(14), y(15)-98, y(15), y(16)-98
Precursor origin neutral loss: +

Peptide No.1033

KPVSNLDDSDDDDFVPKK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KPVSNLDDSDDDDFVPKK
Found in AT2G25170.1, PKL/SSL2 (PICKLE, SUPPRESSOR OF SLR2)

Match to Query 4018: 2188.954485 from(730.658771,3+)
Elution from: 39.331 to 39.331 scan no 3862 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2188.9565  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 55 Expect: 3.6e-005  
Matched b ions: b(2), b(3), b(6), b(7), b(8), b(10), b(11)-98++, b(11)-98, b(11)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++  
Matched y ions: y(3), y(4), y(5), y(6)++, y(8)++, y(10)++, y(10), y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++  
Precursor origin neutral loss: +  

Peptide No.1034  
KPVYNLDDSDDDFVPKK  
Confirmed sites: @Y:4  
Ambiguous sites:

MS/MS Fragmentation of KPVYNLDDSDDDFVPKK  
Found in AT2G25170.1, PKL/SSL2 (PICKLE, SUPPRESSOR OF SLR2)  

Match to Query 3159: 2188.955811 from(730.659213,3+)  
Elution from: 38.535 to 38.535 scan no 3716 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2188.9565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y4 : Phospho (Y)
Ions Score: 47 Expect: 0.00021
Matched b ions: b(7), b(11), b(13)++, b(14)++, b(15)++, b(17)++
Matched y ions: y(3), y(5), y(7)++, y(8)++, y(12)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1035
KQETSEGDDFAGLSGDESYED
Confirmed sites: @S:18 or Y:19
Ambiguous sites: 
MS/MS Fragmentation of KQETSEGDDFAGLSGDESYED
Found in AT5G48240.1, similar to Os11g0266000 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001067664.1); similar to un
Match to Query 3435: 2357.866526 from(1179.940539,2+)
Elution from: 44.152 to 44.152 scan no 4211 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2357.8696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y19 : Phospho (Y)
Ions Score: 62 Expect: 3.3e-006
Matched b ions: b(8), b(10), b(11), b(12), b(13), b(14), b(15), b(16), b(17)++, b(20)++
Matched y ions: y(7), y(8), y(10), y(11), y(12), y(13), y(15), y(17)
Precursor origin neutral loss: +

Peptide No.1036

KQPEEENGELSESEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KQPEEENGELSESEK
Found in **AT5G16730.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02930.1); similar to Protein kinase PKN

Match to Query 2219: 1811.745162 from(906.879857,2+) Elution from: 19.571 to 19.571 scan no 1223 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1811.7462
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00075
Matched b ions: b(5), b(6), b(9), b(10), b(11)–98++, b(12)–98, b(14)–98, b(14)–98++, b(14)++
Matched y ions: y(5)–98, y(5), y(6)–98, y(8), y(8)–98, y(9)–98, y(10), y(12), y(12)++, y(13)–98, y(13), y(13)–98++, y(13)++, y(14)–98, y(14)–98++
Precursor origin neutral loss: +

Peptide No.1037
KQPEEENGELSESEK
Confirmed sites:
Ambiguous sites: @S:11 or S:13

MS/MS Fragmentation of KQPEEENGELSESEK
Found in AT5G16730.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02930.1); similar to Protein kinase PKN

Match to Query 2840: 1811.745502 from(906.880027,2+)
Elution from: 20.061 to 20.061 scan no 1280 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1811.7462
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0071
Matched b ions: b(5), b(6), b(9), b(10), b(14)−98++
Matched y ions: y(8), y(9), y(12), y(12)+, y(13)−98, y(13), y(13)−98++, y(13)+++, y(14)−98
Precursor origin neutral loss: +

Peptide No.1038

KQSFSHDALPQSTQR
Confirmed sites:
Ambiguous sites: @S:12orT:13

MS/MS Fragmentation of KQSFSHDALPQSTQR
Found in AT4G31160.1, transducin family protein / WD-40 repeat family protein

Match to Query 3323: 1808.818371 from(603.946733,3+)
Elution from: 23.421 to 23.421 scan no 1777 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1808.8206
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0095
Matched b ions: b(4), b(5), b(6)++, b(7), b(7)++, b(8), b(11)++
Matched y ions: y(4), y(5)++, y(5), y(6)−98++, y(7)−98++, y(8)++, y(9)++, y(9)−98++, y(9), y(10)−98++, y(11)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1039
KRSFDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KRSFDER
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 549: 1016.442548 from(509.228550,2+)
Elution from: 15.407 to 15.407 scan no 746 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1016.4440
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.026
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98
Matched y ions: y(1), y(2), y(5)-98, y(5), y(6), y(6)++, y(6)-98++
Precursor origin neutral loss: +

Peptide No.1040
KSEEIDEMWK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of KSEEIDEMWK
Found in AT1G32130.1, similar to IWS1 C-terminus family protein [Arabidopsis thaliana] (TAIR:AT4G19000.1); similar to Os0

Match to Query 2053: 1373.556436 from(687.785494,2+)
Elution from: 39.337 to 39.337 scan no 3917 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1373.5574
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Ions Score: 25 Expect: 0.014
  Matched b ions: b(3)−98, b(6)−98++, b(9), b(9)−98
  Matched y ions: y(4), y(6), y(7), y(8), y(9)−98
Precursor origin neutral loss: +

Peptide No.1041

KSMSGGMSGSEEGMSGSEGGMSGGGGKSK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of KSMSGGMSGSEEGMSGSEGGMSGGGGKSK
Found in AT5G07530.1, GRP17 (Glycine rich protein 17)

Match to Query 4561: 2838.040956 from(947.020928,3+)
Elution from: 25.317 to 25.317 scan no 1976 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2838.0448
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M14 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M21 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 27 Expect: 0.014
Matched b ions: b(5), b(9), b(12), b(17)-98++, b(17)++, b(18)++, b(19)-98++, b(24)++, b(24)-98++, b(25)-98++, b(25)++, b(27)-98++, b(28)-98++, b(29)-98++
Matched y ions: y(7)++, y(9)++, y(15)-98, y(18)-98++, y(19)-98++, y(19)++, y(23)-98++, y(23)++, y(24)-98++, y(27)-98++, y(28)-98++
Precursor origin neutral loss: +

Peptide No.1042

KSPARPEILNDWR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of KSPARPEILNDWR
Found in AT4G13350.1, human Rev interacting–like protein–related / hRIP protein–related

Match to Query 2968: 1660.807377 from(554.609735,3+)
Elution from: 37.135 to 37.135 scan no 3649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1660.8086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0054
Matched b ions: b(2)−98, b(2), b(5)−98, b(5)−98++, b(5)++, b(5), b(7), b(7)++, b(7)−98, b(8)−98++, b(8), b(8)++, b(8)−98, b(9)++, b(9)−98++, b(9)++, b(9)−98++, b(10)++, b(11)++, b(11)−98++, b(12)−98++, b(12)++
Matched y ions: y(2), y(2)++, y(4)++, y(4), y(5), y(6), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1043
KSSDVEMVDAEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KSSDVEMVDAEK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1579: 1416.583360 from(709.298956,2+)
Elution from: 22.206 to 22.206 scan no 1560 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1416.5843
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 Expect: 2.2e-008
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)+, b(7), b(8), b(9), b(9)-98, b(10), b(11), b(11)-98, b(11)-98+
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(11)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.1044
KTEIVKPESCSNEGDVK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KTEIVKPESCSNEGDVK
Found in AT4G19150.1, ankyrin repeat family protein

Match to Query 2723: 1998.895659 from(667.305829,3+)
Elution from: 20.292 to 20.292 scan no 1332 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1998.8969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0042
Matched b ions: b(5), b(6), b(10)++, b(11)−98++, b(12)++, b(13)−98++, b(14)++, b(15)−98++, b(15)++, b(16)−98++, b(16)++
Matched y ions: y(2), y(7), y(10)++, y(11), y(11)++, y(11)−98++, y(12)++, y(13), y(13)−98++, y(13)++, y(14)++, y(15)−98++, y(15)++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1045
KTEIVKPESCSNEGDKV
Confirmed sites: @S.9
Ambiguous sites:

MS/MS Fragmentation of KTEIVKPESCSNEGDKV
Found in AT4G19150.1, ankyrin repeat family protein

Match to Query 3462: 1998.894996 from(667.305608,3+)
Elution from: 20.756 to 20.756 scan no 1368 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1998.8969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.04
Matched b ions: b(2), b(5), b(6), b(7), b(8), b(9)++, b(11)−98++, b(12)++, b(13)++, b(14)++, b(15)++,
b(15)−98++, b(16)−98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(9)−98, y(10), y(10)−98++, y(10)++, y(11), y(11)−98, y(11)++,
y(11)−98++, y(12)++, y(13)++, y(13)−98++, y(14)++, y(15)++, y(15)−98++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1046
KTEIVKPESCSNEGDK
Confirmed sites: "@S:9,@S:11"
Ambiguous sites:

MS/MS Fragmentation of KTEIVKPESCSNEGDK
Found in AT4G19150.1, ankyrin repeat family protein

Match to Query 2876: 2078.861418 from(693.961082,3+)
Elution from: 22.231 to 22.231 scan no 1570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2078.8632
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0042
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(10)-98, b(11)-98++, b(11)-196++, b(12)-98++, b(12)-98++, b(13)-98++, b(13)-98++, b(14)-98++, b(14)-98++, b(15)-98++, b(15)-98++, b(15)-196++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10), y(10)++, y(11), y(11)-98++, y(11)-98, y(12)++, y(12)-98++, y(12)-196++, y(13)-98++, y(13)+, y(13)-196++, y(14)-98++, y(14)+, y(15)-196++, y(15)-98++, y(15)+, y(16)-98++, y(16)+, y(16)-196++
Precursor origin neutral loss: +

Peptide No.1047

KVCVEVPLESSS
Confirned sites: @S:10orS:11orS:12

MS/MS Fragmentation of KVCVEVPLESSS
Found in AT5G47680.1, RNA binding / tRNA methyltransferase

Match to Query 1671: 1412.623874 from(707.319213,2+)
Elution from: 42.491 to 42.491 scan no 4280 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1412.6258
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0059
Matched b ions: b(4), b(5), b(6), b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(6)−98, y(7), y(8), y(9)−98, y(11)++
Precursor origin neutral loss: +

Peptide No. 1048

KVDAASRSQSPYAAE
Confirmed sites: "@S:6,@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of KVDAASRSQSPYAAE
Found in AT5G64200.1, ATSC35 (""Arabidopsis thaliana arginine-serine-rich splicing factor 35, 35 kDa protein""); RNA bindin

Match to Query 2331: 1818.661516 from(910.338034,2+) Elution from: 23.403 to 23.403 scan no 1628 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1818.6627
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00054
Matched b ions: b(3), b(5), b(6)-98, b(7)-98, b(7), b(8)-196, b(9)-98, b(9), b(10)-196, b(10)-98, b(10), b(10)-294, b(10)-98++, b(11)-196++, b(11)-98, b(12)-294, b(12)-98++, b(12)-196++, b(12)++, b(13)-196++, b(13)++, b(13)-98++, b(13)-294++, b(14)-196, b(14)-98++, b(14)++, b(14)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(10)++, y(11)++, y(11)-98, y(11), y(11)-98++, y(12)-98, y(12), y(12)++, y(13), y(13)-98, y(13)-294, y(13)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No. 1049

KVEEVKDESSDDAGMMGLFD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 3923: 2280.913737 from(761.311855,3+)
Elution from: 52.896 to 52.896 scan no 5511 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2280.9167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.028
Matched b ions: b(9), b(11)++, b(12)++, b(13)−98++, b(15)++, b(15)−98++, b(16)++, b(16)−98++, b(17)++, b(18)++, b(18)−98++, b(19)++, b(19)−98++
Matched y ions: y(2), y(5), y(12)++, y(16)++
Precursor origin neutral loss:

Peptide No.1050

KVEEVKDESSDDAGMMGLFD
Confirmed sites:  
Ambiguous sites: @S:10orS:9

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4187: 2296.910220 from(766.644016,3+)
Elution from: 42.147 to 42.147 scan no 4272 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2296.9116
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 Expect: 0.015
Matched b ions: b(5), b(6), b(7), b(8)+, b(10), b(11)-98++, b(12)+, b(12)-98++, b(13)-98++, b(14)+, b(15)+, b(16)+, b(17)+, b(17)-98++, b(18)+, b(18)-98++, b(19)+
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(12)-98++, y(15)+, y(15)-98++, y(16)-98++, y(16)+, y(17)-98++
Precursor origin neutral loss:

Peptide No.1051

KVEEVKDESSDDAGMMGLFD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4266: 2296.908662 from(1149.461607,2+)
Elution from: 43.961 to 43.961 scan no 4510 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2296.9116  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 46 Expect: 0.00021  
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(11)−98, b(12), b(13)−98, b(13), b(14)−98, b(15)−98, b(16)+, b(18)−98++, b(18)+, b(19)+, b(19)−98++  
Matched y ions: y(8), y(9), y(12), y(12)−98, y(15)+, y(15), y(16), y(19)+  
Precursor origin neutral loss: +  

Peptide No.1052  
KVEEVKDESSDDAGMMGLFD  
Confirmed sites: @S:9  
Ambiguous sites:  

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD  
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)  
Match to Query 4440: 2280.911392 from(1141.462972,2+)  
Elution from: 53.463 to 53.463 scan no 5606 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2280.9167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.9e-006
Matched b ions: b(5), b(6), b(8), b(9)-98, b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14)-98, b(14), b(15)-98, b(15), b(16)+, b(17)-98, b(17)-98++, b(18)-98++, b(18)+, b(19)+, b(19)-98++
Matched y ions: y(5), y(6), y(8), y(9), y(12), y(13), y(13)-98, y(14)-98, y(14), y(15), y(16)-98, y(16), y(18)-98++
Precursor origin neutral loss: +

Peptide No.1053
KVEEVKDESSDAGMMGLFD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KVEEVKDESSDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4216: 2312.903196 from(1157.458874,2+)
Elution from: 35.470 to 35.470 scan no 3384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2312.9065
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 Expect: 0.01
Matched b ions: b(6), b(8), b(9)−98, b(11), b(12)−98, b(12), b(13)−98, b(13), b(15)−98++, b(16)−98++, b(16)++, b(18)−98++, b(18)++, b(19)++, b(19)−98++
Matched y ions: y(8), y(9), y(14), y(18)++, y(19)−98++
Precursor origin neutral loss: +

Peptide No.1054

KVVEVKDESSDDAGMMGLFD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KVVEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4102: 2296.907554 from(1149.461053,2+) 
Elution from: 43.918 to 43.918 scan no 4499 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2296.9116
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.024
Matched b ions: b(5), b(8), b(9)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(5), y(8), y(9), y(12), y(15)++, y(15), y(16)-98++, y(16), y(19)-98++
Precursor origin neutral loss: +

Peptide No.1055

KVEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:9,@S:10"
Ambiguous sites:

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4042: 2360.879478 from(1181.447015,2+)
Elution from: 58.656 to 58.656 scan no 6143 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2360.8830
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 70 Expect: 6.9e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(14)-196, b(15)-98++, b(15), b(15)-98, b(16)-98++, b(16)-98, b(16)-98++, b(16)-196++, b(16), b(16)-98, b(17), b(17)-98++, b(17)-196++, b(18)-196++, b(18)-98++, b(18)-98++, b(19)-98++, b(19)-98, b(19)-98++, b(19)-196++, b(19), b(19)-98++, b(19)-196++
Matched y ions: y(6), y(8), y(9), y(11), y(12)-98, y(12), y(13)-98, y(13), y(14), y(14)-98, y(14)-98, y(15), y(15)-98, y(16)-196++, y(16), y(16)-98, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1056
KVEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:9,@S:10"
Ambiguous sites:
MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4113: 2392.873260 from(798.631696,3+)
Elution from: 40.783 to 40.783 scan no 4026 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2392.8728
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 Expect: 0.0012
Matched b ions: b(3), b(5), b(6)++, b(6), b(8)+, b(9)-98, b(10)-196, b(11)-196++, b(11)+, b(12)+, b(12)-196++, b(12)-98++, b(13)-98++, b(13)-196++, b(14)+, b(14)-196++, b(15)-98++, b(15)+, b(16)+, b(16)-98++, b(17)+, b(17)-98++, b(18)-196++, b(18)+, b(18)-98++, b(19)+, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(11)+, y(13)+, y(14)+, y(15)+, y(16)-98++, y(16)+, y(18)+, y(19)-98++, y(19)+
Precursor origin neutral loss: +

Peptide No.1057

KVEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:9, @S:10"
Ambiguous sites:

MS/MS Fragmentation of KVEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 3393: 2376.874768 from(1189.444660,2+)
Elution from: 50.240 to 50.240 scan no 4875 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2376.8779  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 48 Expect: 8.8e-005  
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)–98, b(9), b(10)–196, b(11), b(11)–98, b(12)–196, b(12)–98, b(12), b(13), b(13)–98, b(13)–196, b(14), b(15), b(15)–98, b(16)++, b(16)–196++, b(16)–98++, b(17), b(17)–98++, b(17)–196++, b(18)–196++, b(18)–98++, b(18)++, b(19)–98++, b(19)–196++, b(19)++  
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(11)–98, y(12), y(13), y(14)–98, y(15), y(15)–98, y(16)–98, y(16), y(16)–196, y(18)–98++, y(18)–196++, y(18)++, y(19)–98++, y(19)++  
Precursor origin neutral loss: +  

Peptide No.1058  
KVSNPSFIAAQSK  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of KVSNPSFIAAQSK  
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding  
Match to Query 2412: 1455.711964 from(728.863258,2+)  
Elution from: 27.610 to 27.610 scan no 2353 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1455.7122
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.6e-007
Matched b ions: b(2), b(3)−98, b(3), b(4)−98, b(4), b(6), b(6)−98, b(7)−98, b(7), b(8)−98, b(8), b(9)−98, b(9), b(10), b(10)−98, b(11), b(11)−98, b(12)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11)−98, y(11), y(12)−98++, y(12)−98, y(12)
Precursor origin neutral loss: +

Peptide No.1059
KVSNPSFIAAQSK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of KVSNPSFIAAQSK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 2411: 1455.711135 from(486.244321,3+)
Elution from: 27.617 to 27.617 scan no 2354 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1455.7122
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0076
Matched b ions: b(3), b(6)++, b(6), b(7), b(7)−98++, b(7)++, b(8), b(8)++, b(9)−98++, b(9)++,
  b(10)++, b(10)−98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8)++, y(9)−98++, y(11)−98++
Precursor origin neutral loss:

Peptide No.1060
KVSYFSDESDDDED
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KVSYFSDESDDDED
Found in AT3G10400.1, RNA recognition motif (RRM)−containing protein

Match to Query 1827: 1614.558306 from(808.286429,2+)
Elution from: 35.18 to 35.18 scan no 3195 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1614.5610
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 8.7e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)+, b(8), b(10), b(11), b(11)−98++, b(11)+, b(12)−98++, b(12)+
Matched y ions: y(7), y(8)−98, y(9), y(9)−98, y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1061
KWDHDLFDEANKSPAK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of KWDHDLFDEANKSPAK
Found in AT3G19650.1, cyclin-related

Match to Query 3364: 1979.876592 from(660.966140,3+)
Elution from: 33.764 to 33.764 scan no 3155 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1979.8778
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 1e-006
Matched b ions: b(2), b(3), b(4), b(5), b(5)+, b(6), b(6)+, b(7), b(7)+, b(8)+, b(8), b(9), b(9)+, b(10)+, b(10), b(11)+, b(12)+, b(13)-98+, b(13)+, b(14)-98+, b(15)+, b(15)-98+
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(7), y(7)+, y(7)-98, y(8)-98+, y(9)-98, y(9), y(9)-98, y(9)+, y(9)-98+, y(10), y(10)+, y(10)-98+, y(11)+, y(11)-98+, y(12)+, y(13)+, y(13)-98+, y(14)-98+, y(14)+, y(15)+, y(15)-98+
Precursor origin neutral loss: +

Peptide No.1062

KYVEDLESGFSSDVESK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of KYVEDLESGFSSDVESK
Found in AT3G18480.1, CCAAT displacement protein-related / CDP-related

Match to Query 3490: 1997.848068 from(999.931310,2+)
Elution from: 42.191 to 42.191 scan no 4276 polarity:+
Peptide No. 1063

LAAPSSPFDDDSDDVDEQPLVR
Confirmed sites: @S:12
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of LAAPSSPFDDDSDDVDEQPLVR
Found in AT4G11740.1, SAY1

Match to Query 4639: 2547.003760 from(1274.509156, 2+)
Elution from: 53.251 to 53.251 scan no 5674 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2547.0091
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.06
Matched b ions: b(6)-98, b(9)+, b(10)-98, b(10)-98++, b(11)-98, b(11), b(12)-196, b(13), b(14)+, b(14), b(15), b(17), b(18)-98, b(18)-196++, b(19)-196++, b(20)-196++, b(20)-98++, b(21)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(11), y(12)-98, y(12), y(13), y(14), y(16)-98, y(16), y(18)+, y(18)-98++, y(19)+, y(19)-98++, y(20)-98++, y(20)+
Precursor origin neutral loss: +

Peptide No.1064
LAAPSSPFDDDSDDVDEQPLVR
Confirmed sites: "@S:6,@S:12"
Ambiguous sites:

MS/MS Fragmentation of LAAPSSPFDDDSDDVDEQPLVR
Found in AT4G11740.1, SAY1

Match to Query 4640: 2547.008220 from(1274.511386,2+)
Elution from: 54.341 to 54.341 scan no 5764 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2547.0091

Fixed modifications: Carbamidomethyl (C)

Variable modifications:

S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 27 Expect: 0.018

Matched b ions: b(6), b(6)-98, b(9), b(10), b(11)-98, b(12)-196, b(13), b(14)-196++, b(14)-98++, b(14), b(15)-196++, b(15), b(16), b(17)-98, b(18)-98, b(19)++, b(19)-196++, b(19)-196++, b(19), b(19)-196++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++

Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(12)++, y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(16), y(17)-98++, y(18)++, y(18)-196++, y(18)-196, y(18)-98++, y(19)-98++, y(19)-196++, y(19)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)+, y(20)-98++, y(21)++

Precursor origin neutral loss: +

Peptide No.1065

LADETTVAEDCSEEEK

Confirmed sites: @S:12

Ambiguous sites:

MS/MS Fragmentation of LADETTVAEDCSEEEK

Found in AT5G05920.1, DHS (DHS)

Match to Query 2508: 1904.720302 from(953.367427,2+) Elution from: 27.923 to 27.923 scan no 2248 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1904.7234
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0048
Matched b ions: b(7), b(9), b(10), b(15)
Matched y ions: y(6)–98, y(7), y(8)–98, y(8), y(9)–98, y(9), y(10), y(10)–98, y(11), y(12)
Precursor origin neutral loss: +

Peptide No.1066

LASDLALASPDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of LASDLALASPDK
Found in AT1G71770.1, PAB5 (POLY(A)–BINDING PROTEIN); RNA binding

Match to Query 1488: 1279.605442 from(640.809997,2+)
Elution from: 37.177 to 37.177 scan no 3604 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1279.6061
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 Expect: 5.7e-008
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)–98, b(9), b(11), b(11)++
Matched y ions: y(2), y(3), y(4)–98, y(4), y(5)–98, y(5), y(6), y(6)–98, y(7), y(7)–98++, y(7)–98, y(8), y(8)–98, y(8)++, y(9), y(10), y(10)–98++, y(10)–98, y(10)++, y(11), y(11)++, y(11)–98, y(11)–98++
Precursor origin neutral loss: +

Peptide No.1067
LASDLALASPDKHPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of LASDLALASPDKHPR
Found in AT1G71770.1, PAB5 (POLY(A)–BINDING PROTEIN); RNA binding

Match to Query 2989: 1669.817484 from(557.613104,3+)
Elution from: 28.363 to 28.363 scan no 2480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.8188
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 1.4e-006
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8), b(9)−98++, b(11)−98++, b(11), b(13)++, b(13)−98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6)++, y(7)−98++, y(7)++, y(8)−98++, y(8)++, y(9)−98++, y(10)++, y(10)−98++, y(11)++, y(11)−98++, y(12)++, y(12)−98++, y(13)++, y(13)−98++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1068
LASIDSFDSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LASIDSFDSR
Found in AT3G10540.1, 3-phosphoinositide-dependent protein kinase, putative

Match to Query 948: 1189.501366 from(595.757959,2+)
Elution from: 40.756 to 40.756 scan no 4051 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1189.5016
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.6e-005
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(6)-98, b(8), b(8)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(9)-
98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1069
LASINVENVESNR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of LASINVENVESNR
Found in AT2G36460.1, fructose-bisphosphate aldolase, putative
Match to Query 2290: 1523.696390 from(762.855471,2+)
Elution from: 42.082 to 42.082 scan no 4153 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1523.6980
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00035
Matched b ions: b(4)–98, b(6)–98, b(7)–98, b(9)–98, b(10)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)–98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1070
LASINVENETNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LASINVENETNR
Found in AT3G52930.1, fructose-bisphosphate aldolase, putative

Match to Query 2336: 1537.712910 from(769.863731,2+) Elution from: 42.332 to 42.332 scan no 4186 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1537.7137
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 9.2e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(9)-98, b(10), b(12)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(9), y(10), y(11)-98++, y(11)++, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1071

LASKVDAIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LASKVDAIK
Found in AT1G55490.1, CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding

Match to Query 862: 1023.535792 from(512.775172,2+) Elution from: 27.486 to 27.486 scan no 2336 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1023.5365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.032
Matched b ions: b(3)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7), b(8)-98, b(8)
Matched y ions: y(3), y(5), y(6), y(7)-98++, y(7)++, y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1072
LCAEMFNTSDETDEEDENK
Confirmed sites:
Ambiguous sites: @T:12orS:9

MS/MS Fragmentation of LCAEMFNTSDETDEEDENK
Found in AT2G47980.1, SCC3 (sister-chromatide cohesion protein 3); binding

Match to Query 4358: 2371.834408 from(1186.924480,2+)
Elution from: 35.835 to 35.835 scan no 3395 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2371.8345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0011
Matched b ions: b(6), b(7), b(8), b(16)
Matched y ions: y(11), y(12), y(13), y(14), y(15)
Precursor origin neutral loss: +

Peptide No.1073

LCAEMFNTSDETDEEDENK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of LCAEMFNTSDETDEEDENK
Found in AT2G47980.1, SCC3 (sister−chromatide cohesion protein 3); binding

Match to Query 4230: 2355.837408 from(1178.925980,2+)
Elution from: 41.690 to 41.690 scan no 4207 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2355.8396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 2.9e-007
Matched b ions: b(6), b(7), b(8), b(9), b(12)–98, b(13), b(13)–98, b(14)–98, b(14), b(15), b(15)–98++, b(16), b(16)–98, b(17)–98
Matched y ions: y(4), y(6), y(7), y(8)–98, y(8), y(9)–98, y(9), y(10)–98, y(10), y(11)–98, y(12), y(12)–98, y(13), y(13)–98, y(14), y(14)–98, y(15), y(15)++, y(16)–98, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No. 1074
LCQQTVGLDTLLEKTWESLR
Confirmed sites: "@T:11,@T:15,@S:18"
Ambiguous sites:

MS/MS Fragmentation of LCQQTVGLDTLLEKTWESLR
Found in AT5G47250.1, disease resistance protein (CC-NBS-LRR class), putative

Match to Query 4987: 2617.101141 from(873.374323,3+)
Elution from: 49.086 to 49.086 scan no 5061 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2617.0937

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 24 Expect: 0.04

Matched b ions: b(4), b(7), b(9), b(10), b(14)++, b(15)++, b(16)++, b(18)−98++, b(18)++, b(18)−294++, b(19)++

Matched y ions: y(6), y(6)−98, y(9)−98, y(10)++, y(11)++, y(12)−196++, y(13)++, y(14)−294++, y(16)++,
y(17)++

Precursor origin neutral loss:

Peptide No.1075

LDADNYETDEDLK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of LDADNYETDEDLK
Found in AT4G14710.1, ATARD2; acireductone dioxygenase (Fe2+-requiring)/ metal ion binding

Match to Query 2223: 1619.622946 from(810.818749,2+)
Elution from: 33.094 to 33.094 scan no 3060 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1619.6240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 8.2e-007
Matched b ions: b(3), b(4), b(5), b(6), b(8)−98, b(9), b(9)−98, b(10), b(10)−98, b(11), b(11)−98, b(12), b(12)−98, b(12)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)−98, y(6)++, y(6), y(7), y(7)−98++, y(7)−98, y(8)−98, y(8), y(9), y(9)−98, y(9)++, y(10), y(10)−98, y(10)++, y(11)−98++, y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No. 1076
LDADNYETDEDLKK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of LDADNYETDEDLKK
Found in AT4G14710.1, ATARD2; acireductone dioxygenase (Fe2+−requiring)/ metal ion binding

Match to Query 2353: 1747.717458 from(583.579762,3+)
Elution from: 27.802 to 27.802 scan no 2301 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1747.7189
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0031
Matched b ions: b(2), b(4), b(5), b(8)-98, b(11)-98++, b(13)-98++
Matched y ions: y(5), y(6)++, y(7)-98++, y(7)+, y(8)++, y(9)+, y(10)++, y(10)-98++, y(11)+, y(12)+, y(12)-98++, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1077
LDEITSDDDQFYK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LDEITSDDDQFYK
Found in AT5G64813.1, GTP–binding protein–related

Match to Query 1957: 1667.659092 from(834.836822,2+)  
Elution from: 44.429 to 44.429 scan no 4268 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1667.6604
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 9.1e-006
Matched b ions: b(3), b(4), b(5), b(6)-98, b(8), b(9), b(10), b(10)-98, b(11), b(11)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)++, y(10)-98, y(11)++, y(11), y(11)-98++, y(12)++
Precursor origin neutral loss:

Peptide No.1078
LDGLLSSPSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LDGLLSSPSK
Found in AT3G27190.1, uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative

Match to Query 710: 1095.519618 from(548.767085,2+)
Elution from: 35.442 to 35.442 scan no 3377 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1095.5213
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0011
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(8)++
Matched y ions: y(3), y(4)-98++, y(4), y(5), y(5)-98, y(6), y(6)-98, y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1079
LDGLLSSPSK
Confirmed sites:
Ambiguous sites: @S:7orS:9

MS/MS Fragmentation of LDGLLSSPSK
Found in AT3G27190.1, uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative

Match to Query 671: 1095.519908 from(548.767230,2+)
Elution from: 35.454 to 35.454 scan no 3377 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1095.5213
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.024
Matched b ions: b(2), b(3), b(4), b(5)
Matched y ions: y(4), y(5), y(5)−98, y(6), y(6)−98, y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1080

LDSESEDISDQENLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LDSESEDISDQENLK
Found in AT5G61330.1, rRNA processing protein–related

Match to Query 2224: 1800.729134 from(901.371843,2+)
Elution from: 33.539 to 33.539 scan no 3078 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7302
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0082
Matched b ions: b(6)–98, b(7), b(8)–98
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(13)–98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1081
LDSESEDISDQENLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LDSESEDISDQENLK
Found in AT5G61330.1, rRNA processing protein–related

Match to Query 3056: 1800.728584 from(901.371568,2+)
Elution from: 32.752 to 32.752 scan no 2794 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7302
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 6.8e-005
Matched b ions: b(4), b(5)–98, b(6)–98, b(7)–98, b(8)–98, b(10)–98, b(10), b(11)–98, b(12)–98, b(14)–98, b(14)
Matched y ions: y(4), y(5), y(6), y(11)–98, y(11), y(13)–98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1082
LDSESEDISDQENLK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of LDSESEDISDQENLK
Found in AT5G61330.1, rRNA processing protein-related

Match to Query 2282: 1800.727838 from(901.371195,2+) Elution from: 32.453 to 32.453 scan no 2815 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1800.7302
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 1.2e-007
Matched b ions: b(4), b(5), b(6)++, b(6), b(7), b(8)++, b(8), b(9)−98, b(10), b(11)−98, b(11), b(12), b(12)−98, b(13)−98, b(14)−98, b(14), b(14)−98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)−98, y(7), y(8), y(8)−98, y(9)−98, y(9), y(10)−98, y(10), y(11)−98, y(11), y(11)−98++, y(13)−98++, y(13)++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1083
LDSNGNTIEARQDGIGATK
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of LDSNGNTIEARQDGIGATK
Found in AT1G38050.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22200.1); similar to Serolo (GB:ABF9566)

Match to Query 3478: 2038.926921 from(680.649583,3+) Elution from: 43.187 to 43.187 scan no 4403 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2038.9320
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.034
Matched b ions: b(3)++, b(6)--98, b(8)++, b(8)--98, b(10)---98++, b(10), b(10)+, b(11)+, b(11)--98++, b(12)+, b(12)--98++, b(13)+, b(13)--98++, b(17)+, b(17)--98++, b(18)+, b(18)--98++
Matched y ions: y(5), y(7), y(9), y(9)++
Precursor origin neutral loss:

Peptide No.1084
LDTASDSGAAIASPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of LDTASDSGAAIASPK
Found in AT3G27700.1, RNA recognition motif (RRM)-containing protein

Match to Query 1890: 1482.659784 from(742.337168,2+)
Elution from: 26.329 to 26.329 scan no 2147 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1482.6603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
\( S13 \) : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 2.8e-005
Matched \( b \) ions: \( b(6) \), \( b(11) \), \( b(12) \)
Matched \( y \) ions: \( y(3) \), \( y(4)\)-98, \( y(4) \), \( y(5) \), \( y(6) \), \( y(8) \), \( y(9) \), \( y(10) \), \( y(11) \), \( y(13)\)++
Precursor origin neutral loss: +

Peptide No.1085

LDVVAMDVDQPGSDLK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of LDVVAMDVDQPGSDLK
Found in AT1G51450.1, SPla/Ryanodine receptor (SPRY) domain-containing protein

Match to Query 2800: 1780.794274 from(891.404413,2+)  
Elution from: 49.624 to 49.624 scan no 5226 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1780.7954
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0015
Matched b ions: b(6), b(8), b(9), b(10)
Matched y ions: y(5), y(6), y(6)-98, y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.1086
LDVYESAVGDSNTK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LDVYESAVGDSNTK
Found in AT5G61970.1, signal recognition particle-related / SRP-related

Match to Query 2185: 1576.664096 from(789.339324,2+)
Elution from: 36.050 to 36.050 scan no 3424 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1576.6657
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.003
Matched b ions: b(4), b(6), b(7), b(8), b(9)+, b(9), b(10), b(12)–98, b(12)++, b(13)
Matched y ions: y(4), y(5)–98, y(6)–98, y(6), y(7)–98, y(8)–98, y(8), y(9), y(9)–98, y(10), y(10)++, y(11), y(12)–98, y(13)–98++
Precursor origin neutral loss: +

Peptide No.1087
LDVYESAVGDSNTK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of LDVYESAVGDSNTK
Found in AT5G61970.1, signal recognition particle–related / SRP–related

Match to Query 2456: 1576.664216 from(789.339384,2+)
Elution from: 36.375 to 36.375 scan no 3394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1576.6657
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 8.9e-005
Matched b ions: b(5), b(7), b(8), b(10), b(12), b(12)++
Matched y ions: y(4), y(5), y(5)−98, y(6)−98, y(6), y(7)−98, y(8), y(9), y(9)−98, y(10)−98, y(10), y(11)−98, y(11), y(11)++, y(12)−98, y(12)−98++, y(12)++, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1088

LEDCQMDSDEDDYGK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LEDCQMDSDEDDYGK
Found in AT1G27750.1, nucleotide binding

Match to Query 2479: 1914.616294 from(958.315423,2+)
Elution from: 23.312 to 23.312 scan no 1712 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1914.6172
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.0059
Matched b ions: b(7), b(10), b(12)--98++, b(12), b(13)++, b(13)
Matched y ions: y(3), y(6), y(8)--98, y(9)--98, y(10), y(11)+, y(12)++, y(13)--98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1089
LEDCQMDSDEDDYGK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of LEDCQMDSDEDDYGK
Found in AT1G27750.1, nucleotide binding

Match to Query 3205: 1898.621200 from(950.317876,2+)
Elution from: 29.340 to 29.340 scan no 2553 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1898.6223
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 3.8e-007
Matched b ions: b(5), b(6), b(7), b(9), b(10), b(10)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)+, y(12)-98++, y(12)-98, y(13)-98++, y(13)+, y(13), y(13)-98, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1090

LEEISDGESGNI
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LEEISDGESGNI
Found in AT5G13020.1, emsy N terminus domain-containing protein / ENT domain-containing protein

Match to Query 1332: 1341.532630 from(671.773591,2+)
Elution from: 40.846 to 40.846 scan no 3969 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.5337
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
\([\text{S5}]: \text{Phospho (ST)}\), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 61 Expect: 2.3e-006
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)--98, b(6), b(8), b(8)--98, b(9), b(10), b(11), b(11)++, b(11)--98, b(11)--98++
Matched y ions: y(4), y(6), y(8), y(9)--98, y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.1091

LEEVSEMGYDPLGENPAGEICIR
Confirmed sites: "@S:5,@Y:9"
Ambiguous sites:

MS/MS Fragmentation of LEEVSEMGYDPLGENPAGEICIR
Found in AT2G47240.1, long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein

Match to Query 4768: 2753.103988 from(1377.559270,2+)
Elution from: 45.972 to 45.972 scan no 4765 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2753.1002
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y9 : Phospho (Y)
Ions Score: 27 Expect: 0.023
Matched b ions: b(6), b(7)−98, b(7), b(8)−98, b(9)−98, b(9), b(10), b(10)−98, b(11)−98, b(11), b(12)−
98, b(12), b(14)−98, b(14), b(15), b(15)−98, b(16)++, b(17)−98, b(22)−98++, b(22)++
Matched y ions: y(6), y(9), y(11), y(12), y(13), y(14), y(16), y(19)++, y(20)−98++, y(21)++, y(22)−
98++, y(22)++
Precursor origin neutral loss: +

Peptide No.1092

LEGASEESSLSQGLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LEGASEESSLSQGLK
Found in AT2G15860.1, similar to unknown protein [Oryza sativa (japonica cultivar−group)]] (GB:AAP03423.1)

Match to Query 2440: 1639.769530 from(820.892041,2+) Elution from: 49.403 to 49.403 scan no 5200 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1639.7705
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 6.7e-005
Matched b ions: b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(14)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(12)-98++, y(13)-98, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1093

LEGAVTSDIEAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LEGAVTSDIEAR
Found in AT1G04860.1, UBP2 (UBIQUITIN–SPECIFIC PROTEASE 2); ubiquitin–specific protease

Match to Query 1238: 1339.601980 from(670.808266,2+)
Elution from: 34.817 to 34.817 scan no 3122 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1339.6020
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(5), b(8)–98, b(8)
Matched y ions: y(4), y(5), y(6), y(7)–98, y(7), y(8), y(10)
Precursor origin neutral loss:

Peptide No. 1094

LELSAVPSSYSSGQLDPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of LELSAVPSSYSSGQLDPK
Found in AT5G57330.1, aldose 1–epimerase family protein

Match to Query 3191: 1956.906364 from(979.460458,2+)
Elution from: 48.046 to 48.046 scan no 4955 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1956.9081
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0063
Matched b ions: b(6), b(10), b(11)++, b(12)−98, b(15), b(16), b(17)−98
Matched y ions: y(9), y(10), y(12)−98, y(12), y(13), y(13)−98, y(15)++, y(16)
Precursor origin neutral loss: +

Peptide No.1095
LENSVQQGSSPR
Confirmed sites: @S:10
ambiguous sites:

MS/MS Fragmentation of LENSVQQGSSPR
Found in AT2G15860.1, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP03423.1)
Match to Query 1312: 1380.601800 from(691.308176,2+)
Elution from: 18.759 to 18.759 scan no 1136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1380.6034
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 6.8e-009
Matched b ions: b(2), b(3), b(4), b(5)++, b(6), b(7), b(8), b(8)++, b(9), b(10)–98, b(10), b(10)–98++, b(11)–98
Matched y ions: y(2), y(3), y(3)–98, y(4), y(4)–98, y(5), y(5)–98++, y(5)–98, y(6), y(6)–98, y(7), y(8), y(8)–98++, y(8)–98, y(8)++, y(9), y(9)++, y(9)–98, y(10), y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No. 1096

LEQLSEGEDDVEVNPGLTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LEQLSEGEDDVEVNPGLTR
Found in AT1G03910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G53800.1); similar to unknown protein [O

Match to Query 3995: 2178.963836 from(1090.489194,2+)
Elution from: 45.990 to 45.990 scan no 4735 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2178.9681
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 2.4e-008
Matched b ions: b(5)-98, b(7)-98, b(8)-98, b(9)-98, b(10), b(11)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15)+, b(17)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(15), y(15)-98, y(16)-98, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1097
LESNENSDGGVVASPPLPTK
Confirmed sites: "@S:7,@S:13"
Ambiguous sites:

MS/MS Fragmentation of LESNENSDGAVASPLPTK
Found in AT3G48060.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 3846: 2112.898084 from(1057.456318,2+)
Elution from: 41.544 to 41.544 scan no 4216 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2112.9017
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.012
Matched b ions: b(6), b(10), b(10)−98, b(11)−98, b(11), b(12)−98, b(13)−98, b(14)−196
Matched y ions: y(6), y(7), y(8), y(9)−98, y(9), y(10), y(10)−98, y(13)−98, y(17)−98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1098
LESPSEVSEETSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LESPSEVSEETSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to erythrocyte membra

Match to Query 1602: 1500.624034 from(751.319293,2+)
Elution from: 27.945 to 27.945 scan no 2222 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1500.6232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 9e-005
Matched b ions: b(3), b(5), b(6)--98, b(6), b(7)--98, b(9), b(10)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)--98++, y(11), y(12)--98++
Precursor origin neutral loss: +

Peptide No.1099

LETLDETSEGEEAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LE TLDETSEGEEAK
Found in AT2G19385.1, nucleic acid binding / zinc ion binding

Match to Query 2389: 1629.664786 from(815.839669,2+)
Elution from: 28.660 to 28.660 scan no 2460 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1629.6658
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 3.4e-005
Matched b ions: b(3), b(5), b(6), b(7), b(9)-98, b(11)-98, b(12), b(12)-98, b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.1100

LETLDETSEGEEAK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of LETLDETSEGEEAK
Found in AT2G19385.1, nucleic acid binding / zinc ion binding

Match to Query 1872: 1629.664774 from(815.839663,2+)
Elution from: 29.616 to 29.616 scan no 2473 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1629.6658
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 2.3e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)–98, b(8)–98, b(9)–98, b(10)–98, b(10)++, b(11), b(11)–98, b(12), b(12)–98, b(12)++, b(13), b(13)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9)–98, y(9), y(10)–98, y(10), y(11), y(11)++, y(12)++, y(12), y(12)–98, y(12)–98++, y(13)++
Precursor origin neutral loss:

Peptide No.1101
LGAGLVQSPPLDR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LGAGLVQSPPLDR
Found in AT5G3420.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27900.2);
similar to CCT [Medicago trun

Match to Query 1620: 1304.648570 from(653.331561,2+)
Elution from: 42.006 to 42.006 scan no 4230 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1304.6489
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 6.1e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8)–98, b(10), b(10)–98, b(11)–98, b(11)
Matched y ions: y(2), y(4), y(5), y(5)–98, y(6)+++, y(6)–98, y(6), y(7), y(7)–98++, y(7)–98, y(7)+++, y(8), y(9), y(9)–98++, y(9)–98, y(9)+++, y(10)–98++, y(10)++, y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.1102
LGDISDGENEGAFR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LGDISDGENEGAFR
Found in AT2G44440.1, emsy N terminus domain-containing protein / ENT domain-containing protein

Match to Query 1712: 1558.628152 from(780.321352,2+)
Elution from: 39.922 to 39.922 scan no 3792 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1558.6300
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 2.3e-007
Matched b ions: b(3), b(6)−98, b(6), b(7)−98, b(8)−98, b(9), b(9)−98, b(10)−98, b(10), b(12)−98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(10)++, y(10)−98, y(11), y(11)−98, y(11)−98++, y(11)++, y(12)−98++, y(13)−98, y(13)++
Precursor origin neutral loss: +

Peptide No.1103
LGDISDGENEGAFRR
Confirmed sites: @S.5
Ambiguous sites:
MS/MS Fragmentation of LGDISDGENEGAFRR
Found in AT2G44440.1, emsy N terminus domain-containing protein / ENT domain-containing protein
Match to Query 2279: 1714.730778 from(858.372665,2+)
Elution from: 33.470 to 33.470 scan no 3048 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1714.7311
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0077
Matched b ions: b(6)−98, b(11)++
Matched y ions: y(5), y(8), y(9), y(10)++, y(11)++, y(12)−98++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.1104

LGGDGASASPTASTVR
Confirmed sites: "@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of LGGDGASASPTASTVR
Found in AT2G17480.1, MLO8 (MILDEW RESISTANCE LOCUS O 8); calmodulin binding

Match to Query 2104: 1534.604284 from(768.309418,2+)  
Elution from: 26.000 to 26.000 scan no 2130 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1534.6065
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0012
Matched b ions: b(4), b(7)=98, b(8)=196, b(10)=98, b(11)=98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(8)=98, y(9), y(11)=98, y(11)=98++, y(12)=98++, y(13)=98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1105
LGGDGSASPTASTVR
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of LGGDGSASPTASTVR
Found in AT2G17480.1, MLO8 (MILDEW RESISTANCE LOCUS O 8); calmodulin binding

Match to Query 1730: 1454.639660 from(728.327106,2+)
Elution from: 23.181 to 23.181 scan no 1725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6402
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 2.6e-005
Matched b ions: b(4), b(8)–98, b(10)+, b(11)–98, b(13)+, b(14)–98+
Matched y ions: y(3), y(4), y(5), y(6), y(8)–98, y(9), y(9)–98, y(10)–98, y(11), y(11)–98, y(13)–98+, y(13)+, y(14)–98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1106

LGGDGSASPTASTVR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of LGGDGSASPTASTVR
Found in AT2G17480.1, MLO8 (MILDEW RESISTANCE LOCUS O 8); calmodulin binding

Match to Query 2026: 1454.638446 from(728.326499,2+)
Elution from: 24.451 to 24.451 scan no 1678 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6402
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00073
Matched b ions: b(4), b(7), b(10)++, b(10)−98, b(11)−98
Matched y ions: y(2), y(4), y(5), y(6), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(11), y(11)−98++, y(11)−98, y(12)−98++, y(12)++, y(13)−98++, y(13)++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1107

LGLHSLR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LGLHSLR
Found in AT1G10630.1, ADP−ribosylation factor, putative

Match to Query 381: 874.441756 from(438.228154,2+)
Elution from: 30.100 to 30.100 scan no 2691 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 874.4426
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 9.3e-005
Matched b ions: b(4), b(5)-98, b(6), b(6)-98
Matched y ions: y(1), y(2), y(3), y(3)-98, y(4)-98++, y(4)-98, y(4), y(4)+, y(5)+, y(5), y(5)-98++, y(5)-98, y(6)+, y(6)-98, y(6), y(6)-98++
Precursor origin neutral loss: +

Peptide No.1108
LGPQRSPIR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LGPQRSPIR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1046: 1102.564341 from(368.528723,3+) Elution from: 20.357 to 20.357 scan no 1374 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1102.5648
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0036
Matched b ions: b(2), b(5), b(5)++, b(6)−98++, b(6)−98, b(6), b(6)++, b(7), b(7)−98++, b(8)++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(4)++, y(4)−98, y(5), y(5)++, y(5)−98++, y(6)++, y(7)−98++, y(7)++, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1109
LGRLSLDER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LGRLSLDER
Found in AT4G32330.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25480.1);
similar to putative BRI1−KD i

Match to Query 1249: 1137.553772 from(569.784162,2+)
Elution from: 30.336 to 30.336 scan no 2726 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1137.5543
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.014
Matched b ions: b(3), b(4), b(5)+, b(5), b(5)−98, b(6)−98, b(7)−98, b(7), b(8)−98, b(8)+
Matched y ions: y(1), y(2), y(3), y(4), y(8)+
Precursor origin neutral loss: +

Peptide No.1110

LGSFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSFR
Found in AT1G24220.1, paired amphipathic helix repeat-containing protein

Match to Query 66: 658.283464 from(330.149008,2+)
Elution from: 25.552 to 25.552 scan no 2069 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 658.2839
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0017
Matched b ions: b(2), b(3)−98, b(3), b(4)−98
Matched y ions: y(1), y(2), y(2)++, y(3)−98, y(3), y(3)−98++, y(4)−98, y(4), y(4)++, y(4)−98++
Precursor origin neutral loss: +

Peptide No.1111

LGSKPEENATEEESS
Confirmed sites:
Ambiguous sites: @S:14orS:15

MS/MS Fragmentation of LGSKPEENATEEESS
Found in AT3G59820.1, calcium-binding mitochondrial protein–related

Match to Query 2011: 1685.665496 from(843.840024,2+)
Elution from: 20.617 to 20.617 scan no 1273 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1685.6669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.015
Matched b ions: b(7), b(9), b(10), b(11), b(12)
Matched y ions: y(6), y(7)-98, y(11)
Precursor origin neutral loss: +

Peptide No.1112
LGSLQPLK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of LGSLQPLK
Found in AT3G55160.1, similar to putative death receptor interacting protein [Oryza sativa (japonica cultivar-group)] (GB

Match to Query 413: 934.486548 from(468.250550,2+)
Elution from: 27.957 to 27.957 scan no 2143 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 934.4888
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.027
Matched b ions: b(3), b(4), b(5), b(6)++, b(6)
Matched y ions: y(3)
Precursor origin neutral loss:

Peptide No.1113

LGSSEGYLQDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSSEGYLQDR
Found in AT4G12640.1, RNA recognition motif (RRM)-containing protein

Match to Query 1613: 1303.543866 from(652.779209,2+)
Elution from: 34.903 to 34.903 scan no 3304 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1303.5445
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1.5e-005
Matched b ions: b(3), b(5)+98, b(6)+98, b(7)+98++, b(7)+98, b(8)+98, b(9)+98, b(10), b(10)+98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)+98, y(9)+98++, y(9), y(10)+98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1114
LHEDLENGEISPVK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LHEDLENGEISPVK
Found in AT4G15180.1, SET domain–containing protein

Match to Query 2198: 1658.753794 from(830.384173,2+) Elution from: 32.990 to 32.990 scan no 2986 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.7552
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00021
Matched b ions: b(2), b(5), b(6), b(9), b(10), b(11)–98, b(13), b(13)–98++
Matched y ions: y(4), y(5)–98, y(5), y(7), y(8), y(9), y(10), y(11), y(12)–98, y(12), y(13)–98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1115

LHGCAEEPTDDEGGDK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of LHGCAEEPTDDEGGDK
Found in AT3G11450.1, DNAJ heat shock N-terminal domain-containing protein / cell division protein-related

Match to Query 2249: 1808.654920 from(905.334736,2+)
Elution from: 18.530 to 18.530 scan no 1107 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1808.6560
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0059
Matched b ions: b(5), b(6), b(7), b(10), b(12)−98++, b(15), b(15)−98++
Matched y ions: y(5), y(6), y(9)−98, y(9), y(14)−98, y(14), y(15)−98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1116

LHGCAEEPTDDEGGDKK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of LHGCAEEPTDDEGGDKK
Found in AT3G11450.1, DNAJ heat shock N-terminal domain-containing protein / cell division protein-related

Match to Query 3137: 1936.751844 from(646.591224,3+)
Elution from: 17.580 to 17.580 scan no 967 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1936.7509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0071
Matched b ions: b(6), b(7), b(12)−98++, b(15)++
Matched y ions: y(7)++, y(9)++, y(10)++, y(10)−98++, y(11)++, y(15)++, y(15)−98++
Precursor origin neutral loss: +

Peptide No.1117

LHVPDEIDESP
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LHVPDEIDESP
Found in AT2G20000.1, HBT (HOBBIT); binding

Match to Query 1361: 1329.548600 from(665.781576,2+)
Elution from: 40.935 to 40.935 scan no 4108 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1329.5490
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.7e-005
Matched b ions: b(2), b(3), b(5), b(6), b(7), b(8), b(9), b(10)−98, b(10), b(10)++, b(10)−98++
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5), y(7), y(7)−98++, y(8)−98, y(8), y(9)−98
Precursor origin neutral loss: +

Peptide No.1118

LIDEFALSGSK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LIDEFALSGSK
Found in AT2G22560.1, kinase interacting protein-related

Match to Query 1420: 1258.583526 from(630.299039,2+)  
Elution from: 48.392 to 48.392 scan no 4973 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1258.5846
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 9.1e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)+, b(10)-98
Matched y ions: y(3)-98, y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98++, y(6)-98, y(7), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)-98
Precursor origin neutral loss: +

Peptide No.1119
LIDEFALSGSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LIDEFALSGSK
Found in AT2G22560.1, kinase interacting protein-related

Match to Query 1135: 1258.584908 from(630.299730,2+)
Elution from: 46.601 to 46.601 scan no 4845 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1258.5846
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00031
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8)–98, b(10)++
Matched y ions: y(4), y(4)–98, y(5), y(6)–98++, y(6), y(6)–98, y(7), y(8), y(9)–98, y(9)
Precursor origin neutral loss: +

Peptide No.1120

LIEEVSHSSGSPNPVSD
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LIEEVSHSSGSPNPVSD
Found in AT3G02880.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 2562: 1832.781792 from(917.398172,2+)  
Elution from: 32.568 to 32.568 scan no 2928 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1832.7829
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 62 Expect: 5.9e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)–98, b(11), b(12)–98, b(13)–98, b(13), b(13)++, b(14)++, b(14)–98++, b(15)–98++, b(15)++, b(16)–98++, b(16)++
Matched y ions: y(4), y(6), y(7), y(8), y(8)–98, y(9)–98, y(9), y(10), y(11), y(12), y(12)–98, y(13), y(13)–98, y(14)–98++, y(14)++, y(15)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No. 1121
LIEEVSHSSGSPNPVSD
Confirmed sites: ”@S:11,@S:16”
Ambiguous sites:
MS/MS Fragmentation of LIEEVSHSSGSPNPVSD
Found in AT3G02880.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 2823: 1912.747674 from(957.381113,2+)
Elution from: 34.497 to 34.497 scan no 3186 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1912.7492
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 6.4e-005
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11)--98, b(11), b(12)--98, b(13), b(13)--98, b(14)+, b(14)--98, b(14)--98++, b(15)--98++, b(15), b(15)+, b(16)--196++, b(16)+, b(16)--98++
Matched y ions: y(4), y(4)--98, y(5), y(6)--98, y(6), y(7)--98, y(7), y(8), y(8)--98, y(9), y(9)--98, y(10)--98, y(10), y(10)--196, y(12)--98, y(12), y(13), y(14), y(14)--98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1122
LIEEVSHSSGSPNVPVSD
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of LIEEVSHSSGSPNVPVSD
Found in AT3G02880.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 3155: 1832.783008 from(917.398780,2+)
Elution from: 34.796 to 34.796 scan no 3070 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1832.7829
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0011
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(13), b(15), b(15)++, b(16)++
Matched y ions: y(3), y(4), y(4)–98, y(5)–98, y(5), y(6)–98, y(6), y(7), y(8), y(8)–98, y(9)–98, y(10)++,
  y(11), y(12), y(12)–98, y(15)++
Precursor origin neutral loss: +

Peptide No. 1123
LIHPLPPAITSPETSPER
Confirmed sites: @S:15
Ambiguous sites: @T:10 or S:11

MS/MS Fragmentation of LIHPLPPAITSPETSPER
Found in AT2G27210.1, kelch repeat–containing serine/threonine phosphoesterase family protein

Match to Query 3868: 2113.981574 from (1057.998063, 2+)
Elution from: 48.461 to 48.461 scan no 4861 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2113.9850

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S11 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- S15 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 28 Expect: 0.018

Matched b ions: b(3), b(5), b(9), b(11)−98, b(12)−98, b(13), b(15)−98, b(16)−196
Matched y ions: y(3), y(4)−98, y(4), y(5)−98, y(7)−98, y(7), y(11), y(13), y(13)−98, y(15)−98, y(15), y(15)++, y(16)−98++, y(16)++, y(17)++, y(17)−98++

Precursor origin neutral loss: +

Peptide No. 1124

LKDLSEDEEEAEIENK

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of LKDLSEDEEEAEIENK

Found in AT5G66540.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to Os12g0133900 [Oryz

Match to Query 2928: 1840.795768 from(921.405160,2+) Elution from: 35.295 to 35.295 scan no 3314 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1840.7979
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 1.7e-009
Matched b ions: b(3), b(6)−98, b(6), b(7)−98, b(7), b(9)−98++, b(9), b(10)−98, b(10), b(11)−98, b(11), b(11)−98++, b(12)−98, b(12), b(12)−98++, b(13), b(13)−98, b(14), b(14)−98, b(14)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)−98, y(11), y(12)−98, y(12)++, y(12), y(13)−98, y(13), y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1125
LKLSDSDEEEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of LKLSDSDEEEEK
Found in AT5G62190.1, PRH75 (plant RNA helicase 75); ATP-dependent helicase

Match to Query 2286: 1587.652876 from(794.833714,2+) Elution from: 24.554 to 24.554 scan no 1868 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1587.6552
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00015
Matched b ions: b(6)++, b(6)−98, b(6), b(9), b(10)−98, b(10), b(11)−98++, b(12)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10)−98, y(10), y(11)−98, y(11), y(12)++, y(12)−98++
Precursor origin neutral loss: +

**Peptide No.1126**

LKLSDSDEESEK
Confirmed sites: “@S:4,@S:6”
Ambiguous sites:

MS/MS Fragmentation of LKLSDSDEESEK
Found in AT5G62190.1, PRH75 (plant RNA helicase 75); ATP-dependent helicase

Match to Query 2530: 1667.620902 from(834.817727,2+)
Elution from: 26.027 to 26.027 scan no 2104 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1667.6216
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0068
Matched b ions: b(3), b(5), b(5)−98, b(7)−98, b(9)−196++, b(9)−196, b(10)−196, b(10)−98, b(10), b(12)−98, b(12)−196, b(12)++
Matched y ions: y(3), y(4), y(6), y(7), y(8)−98, y(8), y(8)++, y(9), y(10), y(11)−98, y(11), y(11)−196++, y(12)++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.1127
LKLSDSDEEESEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LKLSDSDEEESEK
Found in AT5G62190.1, PRH75 (plant RNA helicase 75); ATP−dependent helicase

Match to Query 1756: 1587.653686 from(794.834119,2+)
Elution from: 23.520 to 23.520 scan no 1753 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1587.6552
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.3e-005
Matched b ions: b(2), b(3), b(5), b(6)++, b(7)--98, b(8), b(9), b(9)--98, b(10)--98, b(12), b(12)--98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)--98, y(8), y(9)--98, y(10), y(10)--98, y(11)--98, y(11), y(12)++, y(12)--98++
Precursor origin neutral loss: +

Peptide No. 1128

LKLSDSDEEESEKK
Confirmed sites: “@S:4,@S:6”
Ambiguous sites:

MS/MS Fragmentation of LKLSDSDEEESEKK
Found in AT5G62190.1, PRH75 (plant RNA helicase 75); ATP-dependent helicase

Match to Query 2181: 1795.714500 from(599.578776,3+)
Elution from: 22.308 to 22.308 scan no 1580 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1795.7165

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 23 Expect: 0.037

Matched b ions: b(2), b(3), b(4), b(5)+98++, b(5), b(6), b(8), b(9)+196, b(9)+98++, b(9)+196++, b(10)+196++, b(11)+++, b(12)+++, b(12)+196++, b(13)+196++

Matched y ions: y(4), y(5), y(6)+++, y(7)+++, y(8)+++, y(9)+98++, y(9)+196++, y(10)+++, y(11)+98++, y(11)+++, y(11)+196++, y(12)+98++, y(12)+++, y(12)+196++, y(13)+

Precursor origin neutral loss: +

Peptide No.1129

LLDGVSASSAHTGPR

Confirmed sites: "@S:10,@T:14"

Ambiguous sites:

MS/MS Fragmentation of LLDGVASSAHTGPR
Found in AT1G29220.1, transcriptional regulator family protein

Match to Query 2921: 1683.699738 from(562.240522,3+)
Elution from: 30.964 to 30.964 scan no 2788 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1683.7018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00012
Matched b ions: b(2), b(3), b(5), b(7), b(9)+, b(14)−98++, b(15)−196++
Matched y ions: y(2), y(3)+, y(5)−98, y(5)+, y(7)−98, y(8)+, y(8)−196, y(9)+, y(11)+, y(11)−98, y(11)−98++, y(12)−98++, y(12)−196++, y(12)−196, y(12)+, y(13)+, y(13)−98++, y(14)+, y(14)−98++, y(15)+, y(15)−98++
Precursor origin neutral loss: +

Peptide No.1130

LLDGVASSSAHGTPR
Confirmed sites: "@S:8,@T:14"
Ambiguous sites:

MS/MS Fragmentation of LLDGVASSSAHGTPR
Found in AT1G29220.1, transcriptional regulator family protein

Match to Query 2922: 1683.700244 from(842.857398,2+)
Elution from: 30.949 to 30.949 scan no 2786 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1683.7018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00061
Matched b ions: b(5), b(7), b(8), b(8)−98, b(11)−98++, b(12)−98, b(12), b(13)−98++, b(13), b(14)−98, b(14), b(14)−196, b(15)−98
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5), y(6), y(7), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12)−98, y(13)+, y(13)−98++, y(13)−196++, y(14)+, y(14)−98++, y(15)+
Precursor origin neutral loss: +

Peptide No. 1131

LLTFNISGSPFSPR
Confirmed sites: ‘@T:3,@S:7,@S:9,@S:12’
Ambiguous sites:

MS/MS Fragmentation of LLTFNISGSPFSPR
Found in AT2G46495.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 3044: 1854.674982 from(619.232270,3+)
Elution from: 24.015 to 24.015 scan no 1800 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1854.6796
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.049
Matched b ions: b(5)−98, b(7)−196, b(9)++, b(9)−196++, b(10)−98++, b(10)−294++, b(11)−294++, b(11)++
Matched y ions: y(2), y(3), y(4), y(6)−98, y(8)−196++, y(8)−98++, y(9)++, y(12)−98++, y(13)−98++, y(13)−294++
Precursor origin neutral loss: +

Peptide No.1132
LMDVHGDYSAEDVGVK
Confirmed sites: @S:9
Ambiguous sites: 

MS/MS Fragmentation of LMDVHGDYSAEDVGVK
Found in AT3G04840.1, 40S ribosomal protein S3A (RPS3aA)

Match to Query 3222: 1813.759108 from(907.886830,2+)
Elution from: 38.979 to 38.979 scan no 3742 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1813.7593

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 79 Expect: 9.6e-008

Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(13), b(15), b(15)-98++, b(15)-98

Matched y ions: y(3), y(4), y(5), y(8)-98, y(9)-98, y(9), y(10)-98, y(11)-98, y(11), y(12)-98++, y(12)++, y(12)-98, y(12), y(13)-98++, y(13)++, y(13)-98, y(14), y(14)++, y(15)++

Precursor origin neutral loss: +

Peptide No. 1133

LMYAASDNEEDVMQDVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LMYAASDNEEDVMQDVK
Found in AT1G80680.1, PRE (PRECOZ, SUPPRESSOR OF AUXIN RESISTANCE3)

Match to Query 2875: 2068.797906 from (1035.406229, 2+)
Elution from: 35.987 to 35.987 scan no 3298 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2068.8006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 Expect: 0.0012
Matched b ions: b(3), b(7)+, b(10)−98, b(11), b(12)−98, b(12), b(15)−98, b(16)−98
Matched y ions: y(5), y(7), y(8), y(10), y(12), y(13)−98, y(14)−98, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.1134
LMYAASDNEEDVMQDVK
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of LMYAASDNEEDVMQDVK
Found in AT1G80680.1, PRE (PRECOZ, SUPPRESSOR OF AUXIN RESISTANCE3)
Match to Query 3708: 2036.808300 from(1019.411426,2+)
Elution from: 48.697 to 48.697 scan no 4892 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2036.8108
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 3.1e-007
Matched b ions: b(4), b(5), b(6)--98, b(7)--98, b(8), b(9)--98++, b(9)--98, b(9), b(10)--98, b(10), b(11), b(11)--98, b(12)--98, b(12), b(13)--98, b(13), b(13)++, b(14) --98, b(14), b(14)++, b(15)--98++, b(15)++, b(15), b(16)--98, b(16), b(16)--98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)--98, y(13)--98, y(13)--98++, y(13), y(13)++, y(14), y(14)--98++, y(14)--98, y(15)--98++, y(15)--98, y(15), y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1135
LMYAASDNEEDVMQDVK
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of LMYAASDNEEDVMQDVK
Found in AT1G80680.1, PRE (PRECOZ, SUPPRESSOR OF AUXIN RESISTANCE3)

Match to Query 3572: 2052.804170 from(1027.409361,2+)
Elution from: 38.546 to 38.546 scan no 3795 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2052.8057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 Expect: 0.0011
Matched b ions: b(9)−98, b(10)−98, b(11), b(12)−98, b(14), b(14)++, b(15)−98++, b(15)++, b(15), b(16)−98++, b(16)−98
Matched y ions: y(3), y(5), y(6), y(8), y(10), y(12)−98, y(12), y(14)++, y(15)−98++, y(15)++, y(15), y(16)++
Precursor origin neutral loss: +

Peptide No.1136

LNIDTDSSSPQNIISPK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of LNIDTDSSSPQNIISPK
Found in AT3G53180.1, glutamate-ammonia ligase

Match to Query 3536: 1907.886094 from(954.950323,2+)
Elution from: 45.446 to 45.446 scan no 4685 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1907.8877
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 Expect: 8.7e-008
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(11), b(12)++, b(13), b(14), b(14)++, b(15)−98, b(16)−98++
Matched y ions: y(3), y(4)−98, y(5), y(6), y(7), y(8), y(8)−98++, y(8)−98, y(9), y(9)−98, y(10), y(11), y(12), y(13), y(14), y(16)++
Precursor origin neutral loss: +

Peptide No.1137
LNIDTDSSSPQNIISPK
Confirmed sites: "@S:9,@S:15"
Ambiguous sites:
MS/MS Fragmentation of LNIDTDSSSPQNIISPK
Found in AT3G53180.1, glutamate-ammonia ligase

Match to Query 3643: 1987.848518 from(994.931535,2+)  
Elution from: 48.266 to 48.266 scan no 5054 polarity:+

---


---

---
Monoisotopic mass of neutral peptide Mr(calc): 1987.8540
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 3.9e-007
Matched b ions: b(5), b(6), b(12), b(13), b(14), b(15)-98, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)-98, y(8), y(9), y(9)-196, y(10), y(11), y(12), y(13)++, y(13), y(14), y(15)++, y(15)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1138

LNLDRSSGDESMEDEPETK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LNLDRSSGDESMEDEPETK
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 4351: 2230.887687 from(744.636505,3+)
Elution from: 32.886 to 32.886 scan no 2927 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2230.8936
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00013
Matched b ions: b(4), b(9)++, b(9), b(10), b(11)++, b(12)−98++, b(12)++, b(13)++, b(14)++, b(14)−98++, b(15)++, b(15)−98++, b(17)++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(13)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.1139

LNLDRSSGDESMEDPETK
Confirmed sites: S6
Ambiguous sites: @S:6 or S:7

MS/MS Fragmentation of LNLDRSSGDESMEDPETK
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 3223: 2230.893896 from(1116.454224,2+)
Elution from: 31.575 to 31.575 scan no 2810 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2230.8936
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.017
Matched b ions: b(7)-98, b(9)-98, b(9), b(10)-98, b(13)-98, b(14)-98, b(15)-98, b(16)-98++, b(18)++
Matched y ions: y(4), y(5), y(9), y(10), y(12), y(15)++, y(18)++
Precursor origin neutral loss: +

Peptide No.1140

LNLDRSSGDESMEDEPETK
Confirmed sites: @S:11
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of LNLDRSSGDESMEDEPETK
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 3345: 2310.855372 from(1156.434962,2+)
Elution from: 33.210 to 33.210 scan no 3026 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2310.8600
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00011
Matched b ions: b(4), b(7)-98, b(8)-98, b(9)-98, b(10), b(11)-98, b(12)-98, b(13)-98, b(14)-196, b(14)-98, b(15), b(15)-98, b(16)-98++, b(15)-196, b(16)-196++, b(17)-98, b(18)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)-98, y(10), y(10)-98, y(11), y(12)-98, y(12), y(15)-98++, y(15)-196, y(16)+, y(17)-98++, y(17)+, y(18)+
Precursor origin neutral loss: +

Peptide No.1141

LNLDRESSGDESMEDEPETK
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of LNLDRESSGDESMEDEPETK
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 4159: 2326.855983 from(776.625937, 3+)
Elution from: 29.341 to 29.341 scan no 2570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2326.8549
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 Expect: 0.037
Matched b ions: b(5), b(6), b(9), b(11)-196++, b(12)-98++, b(13)-98++, b(13)+, b(14)+, b(14)-196++, b(15)-98++, b(15)+, b(15)-196++, b(16)-98, b(16)-196++, b(16)+, b(17)+, b(17)-98++, b(18)-196++, b(18)-98++
Matched y ions: y(2), y(4), y(5), y(6)+, y(6), y(7), y(9), y(12)+, y(13)-98++, y(13)+, y(15)+, y(17)-98++, y(17)+
Precursor origin neutral loss: +

Peptide No.1142
LNPSLNSADSESK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of LNPSLNSADSESK
Found in AT1G12830.1, similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:AT3G50690.1); similar to

Match to Query 1790: 1440.612392 from(721.313472,2+)
Elution from: 25.804 to 25.804 scan no 2074 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1440.6133

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S12 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 41  **Expect:** 0.00051

**Matched b ions:** b(11), b(11)++, b(12)−98++

**Matched y ions:** y(4), y(5), y(7), y(7)−98, y(8), y(9), y(10)++, y(10), y(11)−98++, y(11)++, y(11), y(11)−98, y(12)++

**Precursor origin neutral loss:** +

---

**Peptide No.1143**

**LPDESGVEPTENSPK**

**Confirmed sites:** @S:13

**Ambiguous sites:**

MS/MS Fragmentation of **LPDESGVEPTENSPK**

Found in **AT1G30470.1**, SIT4 phosphatase–associated family protein

Match to Query 2261: 1677.711716 from(839.863134,2+)

Elution from: 28.263 to 28.263 scan no 2372 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1677.7134
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0098
Matched b ions: b(5), b(7), b(8), b(13)–98
Matched y ions: y(3), y(4)–98, y(6), y(7)++, y(7)–98, y(7), y(8), y(9), y(10)–98, y(10), y(11), y(13), y(13)–98++, y(14)++
Precursor origin neutral loss: +

Peptide No. 1144

LPKPQGQTVGSFR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of LPKPQGQTVGSFR
Found in AT4G01690.1, PPOX (PROTOPORPHYRINOGEN OXIDASE); protoporphyrinogen oxidase

Match to Query 2144: 1493.737884 from(498.919904,3+)
Elution from: 18.941 to 18.941 scan no 1039 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1493.7391
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.058
Matched b ions: b(3), b(4), b(5), b(6), b(9)-98++, b(12)++
Matched y ions: y(4), y(5), y(6)-98, y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1145
LPLDIDSPTK
Confirmed sites:
Ambiguous sites: @S:7orT:9

MS/MS Fragmentation of LPLDIDSPTK
Found in AT5G55530.1, C2 domain-containing protein

Match to Query 901: 1177.562408 from(589.788480,2+)
Elution from: 41.673 to 41.673 scan no 4205 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1177.5632
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.022
Matched b ions:
Matched y ions: y(5), y(5)−98, y(6), y(7), y(8), y(8)++, y(9)++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.1146
LPSFTAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LPSFTAK
Found in AT3G11330.1, leucine-rich repeat family protein

Match to Query 214: 842.392748 from(422.203650,2+ )
Elution from: 34.863 to 34.863 scan no 3290 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 842.3939
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 3.8e-006
Matched b ions: b(2), b(3), b(5), b(6)−98, b(6)
Matched y ions: y(1), y(2), y(3), y(4), y(5)−98, y(5)−98++, y(5), y(5)++, y(6)++, y(6)−98, y(6), y(6)−98++
Precursor origin neutral loss: +

Peptide No.1147

LPSPPPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LPSPPPR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 196: 842.405122 from(422.209837,2+) Elution from: 23.628 to 23.628 scan no 1781 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 842.4051  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 36 Expect: 0.0018  
Matched b ions: b(2), b(3), b(3)--98  
Matched y ions: y(2), y(3), y(4), y(5)--98++, y(5)--98, y(5), y(6)++, y(6)  
Precursor origin neutral loss: +

Peptide No.1148

LPSPPVAQR  
Confirmed sites: @S:3  
Ambiguous sites:

MS/MS Fragmentation of LPSPPVAQR  
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 569: 1043.515778 from(522.765165,2+)  
Elution from: 30.159 to 30.159 scan no 2631 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1043.5165
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0016
Matched b ions: b(2), b(3), b(3)−98, b(5)−98, b(6), b(6)−98, b(7)−98, b(7), b(8)−98
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)−98++, y(7)−98, y(7), y(7)++, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1149
LPSPSIEQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LPSPSIEQR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 704: 1105.516428 from(553.765490,2+)
Elution from: 29.454 to 29.454 scan no 2572 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1105.5169
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.1e-006
Matched b ions: b(2), b(3)−98, b(3), b(5)−98, b(6)−98, b(7), b(7)−98, b(7)++, b(8), b(8)−98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)−98++, y(7), y(7)−98, y(7)++, y(8)++, y(8), y(8)−98++, y(8)−98
Precursor origin neutral loss: +

Peptide No.1150
LPVILDQYTPDMR
Confirmed sites: "@Y:8,@T:9"
Ambiguous sites:

MS/MS Fragmentation of LPVILDQYTPDMR
Found in AT4G09140.1, ATMLH1 (Arabidopsis thaliana MutL−homologue 1)

Match to Query 3054: 1834.762518 from(612.594782,3+)
Elution from: 19.971 to 19.971 scan no 1297 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1834.7613
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y8 : Phospho (Y)
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.03
Matched b ions: b(4)++, b(5)++, b(5), b(9)-98++, b(10)-98++, b(10)++, b(13)−98++, b(13)++
Matched y ions: y(4)++, y(4), y(6)−98++, y(7)−98++, y(9)−98++, y(9)++, y(11)++, y(11)−98++, y(12)−98++, y(12)++, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1151
LQEIWDEVGESDDERDK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LQEIWDEVGESDDERDK
Found in AT5G55230.1, ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1);
microtubule binding

Match to Query 3883: 2141.876586 from(1071.945569,2+)
Elution from: 44.299 to 44.299 scan no 4553 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2141.8790
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 1.4e-006
Matched b ions: b(6), b(8), b(10), b(11)-98, b(12)-98, b(13)-98, b(16)-98, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7)-98, y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(12), y(13)-98, y(13)++, y(13)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1152
LQPHTTDFLDISNPK
Confirmed sites: @S:12
Ambiguous sites:
MS/MS Fragmentation of LQPHTTDFLDISNPK
Found in AT2G21270.1, ubiquitin fusion degradation UFD1 family protein
Match to Query 2878: 1804.837018 from(903.425785,2+) Elution from: 43.534 to 43.534 scan no 4452 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.8397
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 7.6e-005
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(12)++
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(6), y(7), y(8), y(10), y(11), y(11)-98, y(12)++, y(12), y (12)-98++, y(13)-98++, y(13)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.1153
LQVVSEWMRPDSIVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LQVVSEWMRPDSIVK
Found in AT1G55350.1, DEK1 (DEFECTIVE KERNEL 1); calpain/ cysteine-type endopeptidase

Match to Query 3442: 1865.910201 from(622.977343,3+)
Elution from: 26.885 to 26.885 scan no 2276 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1865.9110
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.064
Matched b ions: b(9)−98++, b(9)++, b(10)−98++, b(12)−98++, b(13)++, b(13)−98++, b(14)−98++
Matched y ions: y(2), y(7), y(9)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1154

LRMEPDLDLNASP
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of LRMEPDLDLNASP
Found in AT1G03800.1, ATERF10/ERF10 (ERF domain protein 10); DNA binding / transcription factor / transcriptional repressor

Match to Query 2384: 1549.683898 from(775.849225,2+)
Elution from: 52.618 to 52.618 scan no 5501 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1549.6847
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 7.9e-005
Matched b ions: b(4), b(7), b(8), b(9), b(10), b(11)++, b(11), b(12)−98, b(12), b(12)−98++, b(12)++
Matched y ions: y(4), y(6), y(9), y(12)++
Precursor origin neutral loss: +

Peptide No.1155

LRPKSPSSSLDDVEAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LRPKSPSSSLDDVEAK
Found in AT4G33400.1, dem protein–related / defective embryo and meristems protein–related

Match to Query 3233: 1807.870329 from(603.630719,3+)
Elution from: 26.159 to 26.159 scan no 2153 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1807.8717
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0017
Matched b ions: b(4), b(5)+98, b(12)+, b(13)+98, b(14)+, b(14)+98
Matched y ions: y(2), y(4), y(6), y(8), y(9), y(11)+, y(12)+98, y(14)+
Precursor origin neutral loss: +

Peptide No.1156

LRSLDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LRSLDER
Found in AT4G34860.1, beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase,

Match to Query 622: 967.447634 from(484.731093,2+)
Elution from: 19.482 to 19.482 scan no 1260 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.4488
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0022
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(6)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)-98
Precursor origin neutral loss: +

Peptide No.1157
LSELSDDEDFDEQK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LSELSDDEDFDEQK
Found in AT3G48500.1, PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding

Match to Query 2887: 1748.665704 from(875.340128,2+)
Elution from: 38.584 to 38.584 scan no 3813 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1748.6665
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 5.8e-009
Matched b ions: b(4), b(6)−98, b(6), b(7)−98, b(7), b(8), b(9), b(9)−98, b(10), b(10)−98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)−98, y(11), y(11)−98++, y(11)−98, y(12)−98++, y(13)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1158
LSFAEDFENGSDDEDDGENK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LSFAEDFENGSDDEDDGENK
Found in AT2G21150.1, XAP5 family protein

Match to Query 3772: 2196.798408 from(1099.406480,2+)
Elution from: 48.415 to 48.415 scan no 5002 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2196.8008
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 Expect: 9.4e-010
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(11)−98, b(12)−98, b(12), b(13)−98, b(13), b(14)−98, b(15)+, b(15), b(15)−98, b(17)−98, b(17), b(18)−98, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12)−98++, y(12)−98, y(12), y(13)−98, y(13), y(14), y(14)−98, y(15)−98, y(15)−98++, y(16)−98, y(16)+, y(17)+, y(17)−98++, y(18)−98++, y(18)+
Precursor origin neutral loss: +

Peptide No.1159
LSFDDSDQSSPPAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LSFDDSDQSSPPAK
Found in AT4G37630.1, CYCD5;1 (CYCLIN D5;1); cyclin-dependent protein kinase

Match to Query 2169: 1572.632748 from(787.323650,2+)
Elution from: 33.176 to 33.176 scan no 3038 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1572.6345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0015
Matched b ions: b(3), b(4), b(5), b(8), b(9), b(10)-98++, b(10)-98, b(11)+++, b(12)-98++, b(12)+++, b(13)
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7)-98++, y(8), y(9), y(10), y(11), y(12)+++, y(13)+
Precursor origin neutral loss:

Peptide No.1160

LSFDSDQSSPPAK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LSFDDSDQSSPPAK
Found in AT4G37630.1, CYCD5;1 (CYCLIN D5;1), cyclin-dependent protein kinase

Match to Query 2073: 1572.633446 from(787.323999,2+)
Elution from: 32.561 to 32.561 scan no 2988 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1572.6345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0028
Matched b ions: b(3), b(4), b(5), b(6)–98, b(7)–98, b(8)–98, b(10)–98, b(10)–98++, b(11)++, b(12)–98, b(12)–98++, b(12)++, b(13)–98
Matched y ions: y(4), y(9), y(10), y(11), y(12)++, y(13)++
Precursor origin neutral loss:

Peptide No.1161

LSGKHDDSDDEVMDVVR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of LSGKHDDSDDEVMDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 3356: 1995.822930 from(666.281586,3+) 
Elution from: 33.060 to 33.060 scan no 3075 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1995.8244
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.8e-005
Matched b ions: b(5)-98, b(6), b(6)-98, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98, b(11), b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)++, y(14)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1162

LSGHDDSDDEVDVVR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of LSGHDDSDDEVDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 3629: 2011.818105 from(671.613311,3+)
Elution from: 27.867 to 27.867 scan no 2131 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2011.8194
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 Expect: 0.0015
Matched b ions: b(6)+++, b(7)-98, b(8), b(9)-98++, b(9)+, b(9)-98++, b(10)-98++, b(11)-98++, b(11)+, b(11)-98++, b(12), b(12)+++, b(12)-98++, b(13)+, b(14)+, b(15)-98++, b(16)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)+, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1163

LSGKHDDSDDEVMDVVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LSGKHDDSDDEVMDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 3600: 1995.822608 from(998.918580,2+)
Elution from: 35.418 to 35.418 scan no 3154 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1995.8244
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 5.8e-008
Matched b ions: b(6), b(7), b(9), b(9)--98, b(10)--98, b(10), b(12)--98, b(14), b(14)--98, b(15)--98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)--98, y(11)--98, y(11), y(12), y(12)--98, y(13)--98, y(13), y(13)--98++, y(15)++, y(15)--98++
Precursor origin neutral loss: +

Peptide No.1164
LSGHDDSDDEVMDVVR
Confirmed sites: @S.8
Ambiguous sites:

MS/MS Fragmentation of LSGKHDDSDDEVMDVVR
Found in AT1G73770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18240.2)

Match to Query 3519: 2011.818027 from(671.613285,3+)
Elution from: 25.828 to 25.828 scan no 2077 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2011.8194

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 50 Expect: 7.6e-005

Matched b ions: b(6), b(7)+, b(7), b(8), b(8)+, b(8)-, b(8)-98++, b(8)-98+, b(9), b(9)+, b(10)-98++, b(10)-98+, b(10)-, b(11)+, b(11)+, b(11)-98++, b(12)-98++, b(12)+, b(13)+, b(13)-98++, b(14)+, b(14)-98++, b(15)+, b(15)-98++, b(16)-98++, b(16)+

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)+, y(7), y(7)+, y(8), y(8)+, y(9), y(10)-98++, y(10)+, y(11)-98++, y(12)-98++, y(13)+, y(15)+, y(15)-98++, y(16)-98++, y(16)+

Precursor origin neutral loss: +

Peptide No.1165

LSLDDDTVSSPK

Confirmed sites: @S:10

Ambiguous sites:

MS/MS Fragmentation of LSLDDDTVSSPK

Found in AT1G73980.1, phosphoribulokinase/uridine kinase family protein

Match to Query 1760: 1355.584232 from(678.799392,2+)

Elution from: 35.812 to 35.812 scan no 3319 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1355.5857
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0001
Matched b ions: b(4), b(5), b(8)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11)
Precursor origin neutral loss:

Peptide No.1166

LSLDEDLVSSSSSPK
Confirmed sites:
Ambiguous sites: "@S:10orS:11orS:12, @S:10orS:11orS:12"

MS/MS Fragmentation of LSLDEDLVSSSSSPK
Found in AT1G26190.1, phosphoribulokinase/uridine kinase family protein

Match to Query 2898: 1635.664242 from(818.839397,2+) Elution from: 49.094 to 49.094 scan no 5185 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.6681
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00026
Matched b ions: b(7), b(8)
Matched y ions: y(5), y(6), y(6)-98, y(7)-196, y(7), y(8), y(8)-98, y(8)-196, y(9), y(11), y(13)
Precursor origin neutral loss:

Peptide No.1167

LSLDEDLVSSSSPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of LSLDEDLVSSSSPK
Found in AT1G26190.1, phosphoribulokinase/uridine kinase family protein

Match to Query 2416: 1555.700356 from(778.857454,2+) Elution from: 46.044 to 46.044 scan no 4768 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1555.7018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 3e−007
Matched b ions: b(4), b(6), b(8), b(9), b(11)++, b(11), b(12)−98
Matched y ions: y(3), y(3)−98, y(4), y(5), y(6), y(6)−98, y(7)−98, y(8), y(9), y(10), y(11), y(11)−98, y(12), y(12)++, y(12)−98++, y(13)−98++, y(13)++
Precursor origin neutral loss:

Peptide No. 1168
LSLDSPA
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LSLDSA
Found in AT3G13460.1, ECT2; protein binding

Match to Query 293: 909.419664 from(455.717108,2+)
Elution from: 28.683 to 28.683 scan no 2430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 909.4208  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 40 Expect: 0.00066  
Matched b ions: b(2)  
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(7)  
Precursor origin neutral loss: +  

Peptide No.1169

LSNSGDAKVR  
Confirmed sites: @S:4  
Ambiguous sites:

MS/MS Fragmentation of LSNSGDAKVR  
Found in AT1G03740.1, protein kinase family protein

Match to Query 943: 1125.521238 from(563.767895,2+)  
Elution from: 28.714 to 28.714 scan no 2456 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1125.5179
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.053
Matched b ions: b(2), b(4), b(5)++, b(5), b(9)−98, b(9)
Matched y ions: y(1), y(3)++, y(5)++, y(6)++, y(7)++, y(8)−98++, y(8)++, y(8)−98
Precursor origin neutral loss: +

Peptide No.1170

LSPDETLAAK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of LSPDETLAAK
Found in AT3G25545.1, similar to Os01g0219000 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001042416.1)

Match to Query 788: 1123.516458 from(375.512762,3+) Elution from: 24.961 to 24.961 scan no 1961 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.5162
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.023
Matched b ions: b(2), b(4), b(7)++, b(8)++, b(9)++
Matched y ions: y(3), y(4)++, y(6)++, y(7)++, y(8)++, y(8)−98++, y(9)++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.1171
LSSEDDDVLSSEEEK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LSSEDDDVLSSEEEK
Found in AT5G15120.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39890.1); similar to unknown protein [O

Match to Query 2149: 1760.682672 from(881.348612,2+)
Elution from: 33.056 to 33.056 scan no 3014 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1760.6877
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 Expect: 4.5e-008
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(13)++, b(14)-98, b(14)++
Matched y ions: y(2), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(12)-98, y(13)-98++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1172
LSSLDMSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LSSLDMSR
Found in AT3G48195.1, phox (PX) domain-containing protein

Match to Query 449: 987.409212 from(494.711882,2+)
Elution from: 29.953 to 29.953 scan no 2603 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 987.4096
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.044
Matched b ions: b(2), b(4)-98, b(5), b(5)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98++, y(6)-98, y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.1173
LSSPTGEAEEMEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LSSPTGEAEEMEK
Found in AT1G09730.1, Ulp1 protease family protein

Match to Query 2178: 1486.588418 from(744.301485,2+)
Elution from: 32.363 to 32.363 scan no 2949 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.5898
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 7.5e-006
Matched b ions: b(3), b(6)–98, b(7)–98, b(8), b(8)–98, b(9), b(10)–98, b(10), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(8), y(9), y(10), y(10)+, y(11)–98++, y(11)–98, y(11)+, y(12)–98++, y(12)+
Precursor origin neutral loss:

Peptide No. 1174
LSSPTGEAEEMEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LSSPTGEAEEMEK
Found in AT1G09730.1, Ulp1 protease family protein

Match to Query 1808: 1502.582786 from(752.298669,2+)
Elution from: 21.705 to 21.705 scan no 1493 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1502.5847  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 27 Expect: 0.0098  
Matched b ions:  
Matched y ions: y(4), y(5), y(7), y(8), y(10), y(10)++, y(11)−98++, y(12)−98++, y(12)++  
Precursor origin neutral loss:  

Peptide No.1175  

LSSPTGEAEEMEK  
Confirmed sites: @T:5  
Ambiguous sites:  

MS/MS Fragmentation of LSSPTGEAEEMEK  
Found in AT1G09730.1, Ulp1 protease family protein  

Match to Query 1972: 1486.588888 from(744.301720,2+)  
Elution from: 32.169 to 32.169 scan no 2901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.5898
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 40 Expect: 0.00078
Matched b ions: b(7)-98, b(8)-98, b(9), b(10)-98, b(11)-98++, b(12)-98, b(12)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9)++, y(9)-98, y(10)-98, y(10)-98++, y(10) ++, y(11)-98++, y(11), y(11)++, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1176
LSSSPQCTLSGSSPPVGSLPK
Confirmed sites: “@S:13,@S:18”
Ambiguous sites:

MS/MS Fragmentation of LSSSPQCTLSGSSPPVGSLPK
Found in AT5G21160.1, La domain-containing protein / proline-rich family protein

Match to Query 4286: 2244.969416 from(1123.491984,2+)
Elution from: 45.099 to 45.099 scan no 4642 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2244.9738
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.01
Matched b ions: b(6), b(9), b(10), b(12), b(13)−98, b(13), b(14)−98, b(16), b(18)++, b(19)−98, b(20)−196
Matched y ions: y(5)−98, y(7), y(8)−98, y(8), y(9)−98, y(9), y(11)−98, y(11), y(11)−196, y(12)−98, y(12), y(13), y(14), y(15), y(16)++, y(17)−98++, y(17)++, y(18)−98++, y(18)++, y(19)−98++, y(19)++, y(20)++
Precursor origin neutral loss: +

Peptide No.1177
LSVDSSENQSPQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LSVDSSENQSPQK
Found in AT1G04950.1, TAFII59 (TATA box associated factor II 59); transcription initiation factor

Match to Query 1591: 1497.633706 from(749.824129,2+)
Elution from: 21.904 to 21.904 scan no 1463 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1497.6348
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 2.9e-006
Matched b ions: b(5), b(9), b(10), b(12)–98
Matched y ions: y(3), y(4)–98, y(4), y(5)–98, y(5), y(6)–98, y(7), y(8), y(9)–98, y(10), y(10)–98, y(11)++, y(11), y(11)–98, y(11)–98++
Precursor origin neutral loss: +

Peptide No.1178
LSVDSSENNQSPQK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LSVDSSENQSPQK
Found in AT1G04950.1, TAFII59 (TATA box associated factor II 59); transcription initiation factor

Match to Query 2033: 1497.633750 from(749.824151,2+)
Elution from: 21.789 to 21.789 scan no 1500 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1497.6348
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.021
Matched b ions: b(7)-98, b(10)-98
Matched y ions: y(6), y(8), y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(11)-98, y(11)-98, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1179

LSWGRSPNK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LSWGRSPNK
Found in AT1G49600.1, ATRBP47A (ARABIDOPSIS THALIANA RNA–BINDING PROTEIN 47A); RNA binding

Match to Query 1115: 1123.516704 from(562.765628,2+) 
Elution from: 25.335 to 25.335 scan no 2041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.5175
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.014
Matched b ions: b(2), b(5), b(6)−98, b(6), b(8), b(8)−98, b(8)−98++, b(8)++
Matched y ions: y(2), y(3), y(4)−98, y(4), y(5)++, y(5), y(5)−98, y(6), y(6)++, y(6)−98, y(7)+, y(7)−98++, y(7), y(8)++, y(8)−98, y(8)−98++
Precursor origin neutral loss: +

Peptide No. 1180

LTSDLGASSSGGANNGK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of LTSDLGASSSGGANNGK
Found in AT1G15690.1, AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase

Match to Query 2580: 1614.688282 from(808.351417,2+)
Elution from: 23.294 to 23.294 scan no 1640 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1614.6886
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 3.6e-005
Matched b ions: b(7), b(8), b(9), b(10), b(11)–98, b(13)–98, b(13)++, b(14)–98++, b(15)–98++, b(15)
Matched y ions: y(4), y(7), y(9), y(10), y(11), y(12), y(13), y(14)++, y(15)++, y(15), y(15)–98++, y(16)
++
Precursor origin neutral loss: +

Peptide No.1181

LTSDLGASSSGGANNGK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LTSDLGASSSGGANNGK
Found in AT1G15690.1, AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase

Match to Query 2207: 1614.688520 from(808.351536,2+)  
Elution from: 22.240 to 22.240 scan no 1601 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1614.6886
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00014
Matched b ions: b(4), b(6), b(7), b(8)−98, b(11)−98, b(13)−98, b(14)−98++, b(15)−98++
Matched y ions: y(3), y(5), y(7), y(9), y(10), y(10)−98, y(11), y(12), y(12)−98, y(13), y(13)+, y(13)−98++, y(14)+, y(15)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1182
LTSDLGASSSGGANNGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of LTSDLGASSSGGANNGK
Found in AT1G15690.1, AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase

Match to Query 2673: 1614.688066 from(808.351309,2+)
Elution from: 23.064 to 23.064 scan no 1698 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1614.6886
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 9.6e-005
Matched b ions: b(4), b(5), b(7), b(8), b(9), b(11)–98, b(12), b(13)–98, b(14), b(14)–98, b(14)–98++, b(15)–98++, b(15), b(15)++
Matched y ions: y(4), y(6), y(7), y(9), y(9)–98, y(10), y(11), y(12)–98, y(12), y(13), y(13)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1183
LVDDSYTPTASSSAK
Confirmed sites:
Ambiguous sites: @S:11 or S:12 or S:13

MS/MS Fragmentation of LVDDSYTPTASSSAK
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2326: 1620.691478 from(811.353015,2+)
Elution from: 29.553 to 29.553 scan no 2549 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1620.6920
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 9e-005
Matched b ions: b(4), b(6), b(7), b(10)
Matched y ions: y(5), y(6), y(7), y(8), y(8)–98, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(13), y(14)–98, y(14)++
Precursor origin neutral loss: +

Peptide No.1184
LVDDSYTPTASSSAK
Confirmed sites:
Ambiguous sites: @S:11orS:12orS:13

MS/MS Fragmentation of LVDDSYTPTASSSAK
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2699: 1620.692894 from(811.353723,2+)  
Elution from: 29.823 to 29.823 scan no 2617 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1620.6920
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00012
Matched b ions: b(6), b(7), b(9)
Matched y ions: y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14)++
Precursor origin neutral loss: +

**Peptide No.1185**

LVELSDDEETPVER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **LVELSDDEETPVER**
Found in **AT1G79950.1**, helicase-related

Match to Query 2343: 1709.738876 from(855.876714,2+)
Elution from: 38.564 to 38.564 scan no 3721 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1709.7396  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 66 Expect: 1.7e-006  
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(13)-98  
Matched y ions: y(2), y(4), y(5), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98++, y(12)++, y(13)-98++  
Precursor origin neutral loss: +

Peptide No.1186  
LVNEPETEPSSPQR  
Confirmed sites: @S:10  
Ambiguous sites:  
MS/MS Fragmentation of LVNEPETEPSSPQR  
Found in AT2G46020.1, ATBRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA); ATP binding / DNA binding / helicase/ transcription regul  
Match to Query 2740: 1661.727178 from(831.870865,2+)  
Elution from: 25.281 to 25.281 scan no 1903 polarity:+
Peptide No.1187

LVNEPETEPSSPQR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LVNEPETEPSSPQR
Found in AT2G46020.1, ATBRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA); ATP binding / DNA binding / helicase / transcription regul

Match to Query 2838: 1661.727756 from(831.871154,2+)
Elution from: 24.993 to 24.993 scan no 1958 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.7298
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00066
Matched b ions: b(4), b(6), b(7), b(8), b(8)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7)−98, y(7), y(8), y(10), y(10)++, y(10)−98, y(11)++, y(12)−98++, y(12)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.1188
LVPIESNVSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of LVPIESNVSPK
Found in AT3G19210.1, ATRAD54/CHR25 (ARABIDOPSIS HOMOLOG OF RAD54); ATP binding / DNA binding / helicase

Match to Query 1660: 1261.629171 from(421.550333,3+) Elution from: 19.663 to 19.663 scan no 1265 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1261.6319
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0033
Matched b ions: b(5)++, b(6)++, b(7)++, b(8)++, b(9)++, b(9)-98++, b(10)-98++
Matched y ions: y(2), y(3)−98, y(3), y(4), y(4)−98, y(5)−98++, y(5), y(5)++, y(5)−98, y(7)−98++, y(9)++,
y(10)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1189
LVVLFQSNKD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LVVLFQSNKD
Found in AT2G02220.1, ATPSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor / protein serine/threonine kinase

Match to Query 1362: 1241.605134 from(621.809843,2+)
Elution from: 47.574 to 47.574 scan no 4868 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1241.6057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0026
Matched b ions: b(2), b(4)++, b(4), b(5), b(6), b(8)++, b(9)++
Matched y ions: y(5)--98, y(6)--98, y(6), y(7), y(8), y(8)++, y(8)--98, y(9)--98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1190
LYEQPGEVDSLDPSK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of LYEQPGEVDSLDPSK
Found in AT4G25770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10040.1);
similar to Os03g0726800 [Oryz

Match to Query 3039: 1842.791982 from(922.403267,2+)
Elution from: 36.665 to 36.665 scan no 3542 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1842.7924
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 2.3e-005
Matched b ions: b(2), b(3), b(4), b(7), b(9), b(11), b(12), b(13)−98++
Matched y ions: y(4), y(7), y(8)−98, y(9), y(11), y(12)+, y(12)−98, y(12), y(13)+, y(14), y(14) ++, y(15)+, y(15)−98++
Precursor origin neutral loss: +

Peptide No.1191
LYEQPGEVDSDLPSK
Confirmed sites:
Ambiguous sites: @S:13orS:15

MS/MS Fragmentation of LYEQPGEVDSDLPSK
Found in AT4G25770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10040.1);
similar to Os03g0726800 [Oryz]
Match to Query 3352: 1842.791584 from(922.403068,2+)
Elution from: 37.743 to 37.743 scan no 3690 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1842.7924
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00075
Matched b ions: b(4), b(7), b(9), b(12)
Matched y ions: y(4), y(5), y(5)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(11), y(12), y(12)++, y(12)-98, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No. 1192
MAEASLTIVSHEEALMK
Confirmed sites: “@S:5, @T:7, @S:10”
Ambiguous sites:

MS/MS Fragmentation of MAEASLTIVSHEEALMK
Found in AT1G24460.1, myosin-related

Match to Query 3570: 2130.804375 from(711.275401,3+)  
Elution from: 48.220 to 48.220 scan no 5032 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 2130.8056
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 Expect: 0.012
Matched b ions: b(6), b(6)-98, b(7)-196, b(8), b(9)++, b(10)++, b(11)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(5), y(9)++, y(14)-294++, y(16)++, y(16)-98++
Precursor origin neutral loss:

Peptide No.1193
MAIDNV SPEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MAIDNV SPEK
Found in AT3G23980.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT5G41790.1); similar to

Match to Query 925: 1182.498804 from(592.256678,2+)
Elution from: 28.786 to 28.786 scan no 2434 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1182.4991
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.5e-005
Matched b ions: b(2), b(3), b(5), b(6), b(7−98), b(9)
Matched y ions: y(3), y(4), y(4−98), y(5), y(5−98), y(6), y(7), y(7−98), y(8)++, y(8), y(8−98++), y(8)−98, y(9)
Precursor origin neutral loss: +

Peptide No.1194

MASDSSLGNTNDGPPSPGENVSSPIENTYSSPAALHR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of MASDSSLGNTNDGPPSPGENVSSPIENTYSSPAALHR
Found in AT2G16440.1, DNA replication licensing factor, putative

Match to Query 5281: 3835.666041 from(1279.562623,3+)
Elution from: 48.294 to 48.294 scan no 5066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3835.6632
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.003
Matched b ions: b(25)−98++
Matched y ions: y(6), y(8), y(10), y(11), y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(21)++
+, y(22)++, y(23)−98++, y(32)++
Precursor origin neutral loss:

Peptide No.1195
MASIDAQLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MASIDAQLR
Found in AT2G42600.1, ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2);
phosphoenolpyruvate carboxylase

Match to Query 677: 1099.472676 from(550.743614,2+) Elution from: 29.432 to 29.432 scan no 2569 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1099.4733
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 5.4e-005
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(4), b(5), b(5)–98, b(6), b(6)–98, b(7)–98, b(7), b(8)–98, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(7)–98, y(7), y(7)–98++, y(7)++, y(8)
Precursor origin neutral loss: +

Peptide No.1196

MASIDAQLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MASIDAQLR
Found in AT3G14940.1, ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase

Match to Query 1020: 1083.477138 from(542.745845,2+) Elution from: 35.404 to 35.404 scan no 3438 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1083.4784
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 4.8e-007
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(5), b(5)–98, b(6)–98, b(6)–98++, b(7)–98, b(7)+, b(8)–98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)–98++, y(7)–98, y(7), y(7)+, y(8)–98, y(8)+, y(8), y(8)–98++
Precursor origin neutral loss: +

Peptide No.1197

MASIDVHLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MASIDVHLR
Found in AT1G53310.1, ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); phosphoenolpyruvate carboxylase

Match to Query 821: 1136.503990 from(569.259271,2+)
Elution from: 31.237 to 31.237 scan no 2754 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1136.5049
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 3.6e-005
Matched b ions: b(2), b(3)−98, b(4)−98, b(4), b(5), b(5)−98++, b(5)−98, b(6)−98, b(6), b(7)−98, b(7)++, b(8), b(8)−98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)−98++, y(7)−98, y(7), y(7)++, y(8)−98, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1198
MASIDVHLR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of MASIDVHLR
Found in AT1G53310.1, ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1);
phosphoenolpyruvate carboxylase

Match to Query 888: 1120.509312 from(561.261932,2+)
Elution from: 37.876 to 37.876 scan no 3660 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1120.5100
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 74 Expect: 2.3e-007
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(6)-98, b(7)-98, b(7), b(7)+, b(8)-98++, b(8)-98, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(4)+, y(5), y(6), y(6)+, y(7)-98++, y(7)-98, y(7), y(7)+, y(8), y(8)-98, y(8)-98++, y(8)+
Precursor origin neutral loss: +

Peptide No.1199

MASMVNVTSIIVTR
Confirmed sites: "@S:9,@T:13"
Ambiguous sites:

MS/MS Fragmentation of MASMVNVTSIIVTR
Found in AT5G41470.1, similar to nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana] (TAIR:AT1G71480).

Match to Query 2537: 1696.737330 from(566.586386,3+)
Elution from: 27.438 to 27.438 scan no 2264 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1696.7330
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.06
Matched b ions: b(2), b(5)+, b(5), b(7), b(7)+, b(8)+, b(8), b(9)-98, b(9)+, b(12)-98+, b(13)-98++, b(13)-196++
Matched y ions: y(6), y(7)-98++, y(7), y(7)-196++, y(7)+, y(8)-196++, y(8)-98++, y(8)+, y(9)-98++, y(9)-196++, y(10)-196++, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.1200

MDDSLSPR
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of MDDSLSPR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1060: 1095.334112 from(548.674332,2+)
Elution from: 20.382 to 20.382 scan no 1387 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1095.3345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.00099
Matched b ions: b(2), b(3), b(4)+, b(4)−98, b(5)−98, b(6)−98, b(6)−196, b(7)−196, b(7)+
Matched y ions: y(2), y(3)−98, y(3), y(4)−98, y(5)−98, y(5)+, y(5), y(5)−196, y(6), y(6)−98
Precursor origin neutral loss: +

Peptide No.1201

MDDSLSPR
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of MDDSLSPR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 635: 1079.339040 from(540.676796,2+)
Elution from: 25.625 to 25.625 scan no 1945 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1079.3396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00017
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98++, b(6)-196, b(6)-98, b(7)++
Matched y ions: y(1), y(2), y(3)-98, y(4)-98, y(4), y(5)-98, y(5)-196, y(5), y(6), y(6)-98, y(6)-196, y(6)-98++, y(6)++, y(7), y(7)-98, y(7)-196, y(7)-98++, y(7)++
Precursor origin neutral loss: +

Peptide No.1202
MDDSLSPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MDDSLSPR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 441: 999.372304 from(500.693428,2+)  
Elution from: 24.070 to 24.070 scan no 1812 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 999.3732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00024
Matched b ions: b(2), b(5), b(6)–98
Matched y ions: y(2), y(3), y(3)–98, y(4), y(5), y(6)–98, y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.1203

MDGRFSPVGAGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MDGRFSPVGAGR
Found in AT3G07810.1, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative

Match to Query 1924: 1328.568742 from(665.291647,2+)
Elution from: 28.492 to 28.492 scan no 2454 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1328.5696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0014
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)−98, b(6), b(7)−98, b(8), b(10), b(11)
Matched y ions: y(3), y(4), y(6), y(7), y(7)−98, y(8), y(8)−98, y(10)−98++, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.1204

MDPDCESEDEDEKEEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MDPDCESEDEDEKEEK
Found in AT2G16470.1, zinc finger (CCCH-type) family protein / GYF domain-containing protein

Match to Query 3177: 2063.683550 from(1032.849051,2+)
Elution from: 19.152 to 19.152 scan no 1158 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2063.6860
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 27 Expect: 0.0041
Matched b ions: b(6), b(8)-98, b(9), b(10)-98, b(10)++, b(13), b(14)-98, b(14), b(15)-98, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(10), y(11), y(12)-98++, y(12)-98, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No. 1205

MEPDLDLNASP
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of MEPDLDLNASP
Found in AT1G03800.1, ATERF10/ERF10 (ERF domain protein 10); DNA binding / transcription factor / transcriptional repressors

Match to Query 1514: 1280.498194 from (641.256373,2+)
Elution from: 50.274 to 50.274 scan no 5291 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1280.4996
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 2.3e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)
Matched y ions: y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No. 1206

MGAVSSKESGSSTSDNR
Confirmed sites:
Ambiguous sites: @S:13 or T:14

MS/MS Fragmentation of MGAVSSKESGSSTSDNR
Found in AT2G29580.1, zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein

Match to Query 3161: 1881.743334 from(628.255054,3+)
Elution from: 50.953 to 50.953 scan no 5394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1881.7411
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0069
Matched b ions: b(4), b(5), b(6)+, b(9), b(10)+, b(11), b(12)+, b(14)+, b(14)-98++, b(15)+, b(15)-98++, b(16)-98++
Matched y ions: y(3), y(4), y(6)-98, y(7)-98++, y(7)-98, y(8)-98++, y(9)-98, y(10)-98, y(10)-98++, y(10), y(13)-98++, y(14)+, y(15)-98++, y(17)+, y(17)-98++
Precursor origin neutral loss:

Peptide No.1207

MGGDSDDDEEMNLSLVPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of MGGDSDDDEEMNLSLVPK
Found in AT3G03050.1, CSLD3 (CELLULOSE SYNTHASE-LIKE 3); cellulose synthase/transferase, transferring glycosyl groups

Match to Query 3724: 2046.777220 from(1024.395886,2+)
Elution from: 52.028 to 52.028 scan no 5292 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2046.7799
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 5.3e-005
Matched b ions: b(7)-98, b(10), b(11), b(13)-98, b(13), b(15), b(16)-98, b(16), b(17)-98++, b(17)-98
Matched y ions: y(7), y(8), y(11), y(12), y(13), y(15), y(15)-98, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1208
MGGDSDDDEEMNLVSLPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of MGGDSDDDEEMNLVSLPK
Found in AT3G03050.1, CSLD3 (CELLULOSE SYNTHASE–LIKE 3); cellulose synthase/transferase, transferring glycosyl groups

Match to Query 3942: 2062.777166 from(1032.395859,2+)
Elution from: 44.276 to 44.276 scan no 4531 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2062.7748
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 Expect: 0.00012
Matched b ions: b(5), b(7), b(8), b(9)–98, b(13)–98, b(15), b(16), b(16)–98
Matched y ions: y(3), y(5), y(8), y(10), y(11), y(12), y(13), y(14)++, y(15)–98, y(15)
Precursor origin neutral loss: +

Peptide No.1209
MGGDSDDDEEMNLSLVPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of MGGDSDDDEEMNLSLVPK
Found in AT3G03050.1, CSLD3 (CELLULOSE SYNTHASE–LIKE 3); cellulose synthase/transferase, transferring glycosyl groups

Match to Query 3110: 2030.781228 from(1016.397890,2+)
Elution from: 52.488 to 52.488 scan no 5383 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2030.7849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 6.6e-006
Matched b ions: b(7), b(8), b(10), b(10)-98, b(11), b(15)-98, b(16), b(16)-98, b(17)-98
Matched y ions: y(5), y(7), y(8), y(11), y(12), y(14), y(14)-98, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1210

MGHASVAVGGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of MGHAGAIVSGGK
Found in AT5G08300.1, succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthase, a

Match to Query 1085: 1163.515194 from(582.764873,2+) Elution from: 24.568 to 24.568 scan no 1891 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1163.5158
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.021
Matched b ions: b(3), b(4), b(6), b(7), b(8)
Matched y ions: y(5)−98, y(6)−98, y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1211
MGKEDSESEDEGDTVPLK
Confirmed sites: "@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of MGKEDSESEDEGDTVPLK
Found in AT3G19510.1, homeobox protein (HAT 3.1)

Match to Query 2972: 2124.781548 from(1063.398050,2+)
Elution from: 30.821 to 30.821 scan no 2710 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2124.7847
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00033
Matched b ions: b(5), b(7)–98, b(7), b(8)–98, b(9), b(9)–196, b(10)–98, b(10), b(11), b(11)–98, b(13)–196, b(13), b(14), b(15)–98, b(15), b(15)–196, b(16)–196, b(17)–98++
Matched y ions: y(3), y(5), y(7), y(8), y(9), y(10), y(11), y(11)–98, y(12), y(13)–98, y(13), y(14)++, y(16)–98++, y(16)++, y(16)–196++, y(17)++
Precursor origin neutral loss: +

Peptide No.1212
MGLVNESDSEDSSEHDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MGLVNESDSEDSSEHDK
Found in AT4G10750.1, HpcH/Hpal aldolase family protein

Match to Query 2864: 1973.718867 from(658.913565,3+)
Elution from: 21.353 to 21.353 scan no 1438 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1973.7197
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.035
Matched b ions: b(2), b(3), b(11)++, b(12)−98++, b(16)++
Matched y ions: y(5), y(9)++, y(11)−98++, y(13)++, y(13)−98++, y(14)−98++, y(14)++, y(15)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1213

MGLVNESDSEDSEHDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MGLVNESDSEDSEHDK
Found in AT4G10750.1, HpCH/Hpal aldolase family protein

Match to Query 2919: 1957.723842 from(979.869197,2+)
Elution from: 25.937 to 25.937 scan no 2061 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1957.7248
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 3.5e-009
Matched b ions: b(3), b(4), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(11), b(11)-98, b(14)++, b(14)-98++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)-98, y(13), y(13)++, y(13)-98++, y(14)-98++, y(14)-98, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1214

MGLVNESDSEDSSEHDK
Confirmed sites: "@S:7,@S:12"
Ambiguous sites:

MS/MS Fragmentation of MGLVNESDSEDSSEHDK
Found in AT4G10750.1, HpcH/HpaI aldolase family protein

Match to Query 2799: 2037.688776 from(680.236868,3+)
Elution from: 28.895 to 28.895 scan no 2457 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2037.6911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 28 Expect: 0.0034
Matched b ions: b(3), b(6), b(7)-98, b(7), b(8), b(12)-196++, b(12)+, b(14)-98++, b(14)+, b(14)-196++, b(15)-98++, b(16)-98++
Matched y ions: y(5), y(7), y(9), y(10)+, y(11)-98++, y(12)+, y(12)-98++, y(13)-98++, y(13)+, y(13)-196++, y(14)-196++, y(14)-98++, y(14)+, y(15)+, y(15)-98++, y(16)+
Precursor origin neutral loss: +

Peptide No.1215

MGLVNESDSEDSSEHDK
Confirmed sites: @S:7
Ambiguous sites: @S:12 or S:13

MS/MS Fragmentation of MGLVNESDSEDSSEHDK
Found in AT4G10750.1, HpcH/HpaI aldolase family protein

Match to Query 3053: 2037.690432 from(680.237420,3+) 
Elution from: 29.534 to 29.534 scan no 2604 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2037.6911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.025
Matched b ions: b(3), b(4), b(7), b(8), b(11)-98++, b(13)-196++, b(14)++, b(14)-196++, b(16)-98++
Matched y ions: y(6), y(7), y(10)++, y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(13)-196++, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1216

MGLVNESDSEDSSEHDK
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of MGLVNESDSEDSSEHDK
Found in AT4G10750.1, HpcH/Hpal aldolase family protein

Match to Query 2825: 2037.689280 from(680.237036,3+)
Elution from: 30.080 to 30.080 scan no 2535 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2037.6911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 6.5e-005
Matched b ions: b(3), b(4), b(6), b(7), b(7)−98, b(8), b(8)−98, b(9)−98++, b(9)−196, b(11)−98, b(11)−98++, b(11)++, b(12)−196++, b(12)++, b(12)−98++, b(14)−98++, b(14)++, b(14)−196++, b(16)−98++, b(16)++
Matched y ions: y(5), y(6)++, y(7)++, y(8)++, y(8), y(9)−98++, y(9)++, y(10)−98, y(10)++, y(11)−196++, y(11)−98++, y(12)++, y(12)−98++, y(13)−98++, y(13)++, y(13)−196++, y(14)−196++, y(14)−98++, y(14)++, y(15)++, y(15)−196++, y(15)−98++, y(16)++, y(16)−98++, y(16)−196++
Precursor origin neutral loss: +

Peptide No.1217

MGLVNESDSEDSEHDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of MGLVNESDSEDSEHDK
Found in AT4G10750.1, HpcH/HpaI aldolase family protein

Match to Query 3193: 1957.723653 from(653.581827,3+)
Elution from: 27.044 to 27.044 scan no 2210 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1957.7248
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00017
Matched b ions: b(3), b(4), b(6), b(7), b(9)–98, b(10), b(11)–98++, b(14)–98++, b(14)+, b(16)+, b(16)–98++
Matched y ions: y(2), y(5), y(6), y(7)+, y(7), y(8), y(10)+, y(11)–98++, y(12)+, y(12)–98++, y(13)–98++, y(13)+, y(14)–98++, y(14)+, y(15)+, y(15)–98++, y(16)+, y(16)–98++
Precursor origin neutral loss: +

Peptide No.1218

MGSGGSSVVLDPENGLETESRK
Confirmed sites: ”@S:3,@T:18,@S:20”
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of MGSGGSSVVLDPENGLETESRK
Found in AT1G66840.1, RAV2 (REGULATOR OF THE ATPASE OF THE VACUOLAR MEMBRANE); DNA binding / transcription factor

Match to Query 4653: 2567.934495 from(856.985441,3+)
Elution from: 28.738 to 28.738 scan no 2438 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2567.9293
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.038
Matched b ions: b(9)−98, b(10)−196, b(12)−196, b(16)++, b(18)++, b(18)−294++, b(19)++, b(20)−294++, b(20)++
Matched y ions: y(9)++, y(13)++, y(14)−98++, y(17)++, y(20)++
Precursor origin neutral loss: +

Peptide No.1219
MISPDQNGVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MISPDQNGVK
Found in AT5G06000.1, EIF3G2 (eukaryotic translation initiation factor 3G2); RNA binding / translation initiation factor

Match to Query 884: 1167.498936 from(584.756744,2+)
Elution from: 36.415 to 36.415 scan no 3511 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1167.4995
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.022
Matched b ions: b(2), b(3)–98, b(5)–98, b(7)–98++, b(8)–98++, b(9)–98, b(9)–98++, b(9)++
Matched y ions: y(6), y(7), y(8)–98++, y(8), y(8)–98, y(8)++, y(9)–98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1220

MKDTDSEEELK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MKDTDSEEELK
Found in AT1G66410.1, CAM4 (CALMODULIN 4); calcium ion binding

Match to Query 1742: 1403.552462 from(702.783507,2+)
Elution from: 20.223 to 20.223 scan no 1301 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1403.5527
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 5.9e-006
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8), b(8)−98, b(9)−98, b(9), b(9)−98++, b(10), b(10)−98
Matched y ions: y(2), y(4)++, y(4), y(5), y(6), y(6)−98++, y(6)−98, y(7)−98, y(7), y(8)−98, y(8), y(9)−98, y(9), y(9)−98++, y(10)−98++, y(10)++, y(10)−98
Precursor origin neutral loss: +

Peptide No.1221

MKTDSEELK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of MKTDSEEELK
Found in AT1G66410.1, CAM4 (CALMODULIN 4); calcium ion binding

Match to Query 2222: 1403.551916 from(702.783234,2+) Elution from: 19.764 to 19.764 scan no 1305 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1403.5527
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 6.1e-006
Matched b ions: b(2), b(3), b(4)–98, b(4), b(5), b(7), b(8)–98, b(9)–98, b(9), b(10), b(10)–98
Matched y ions: y(2), y(4)++, y(4), y(6), y(7), y(8)–98, y(8), y(9)–98, y(9), y(10)–98++, y(10)++, y(10)–98
Precursor origin neutral loss: +

Peptide No.1222
MLDTLSKSRNVGDAQK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of MLDTLSKSRNVGDAQK
Found in AT1G71060.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 3260: 1841.871876 from(461.475245,4+)
Elution from: 32.031 to 32.031 scan no 2904 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1841.8706
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.044
Matched b ions: b(10)--98++, b(12)++, b(13)++
Matched y ions: y(3)++, y(8)++, y(10)--98++, y(11)--98++, y(11)++, y(12)++, y(13)--98++
Precursor origin neutral loss:

Peptide No.1223

MMVGTRR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of MMVGTRR
Found in AT3G59110.1, protein kinase family protein

Match to Query 576: 961.389240 from(481.701896,2+)
Elution from: 24.857 to 24.857 scan no 1958 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 961.3874
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.047
Matched b ions: b(2), b(3), b(4), b(5)—98, b(6)++
Matched y ions: y(3)—98
Precursor origin neutral loss: +

Peptide No.1224

MNSYVSGKEVENMNYLKAVIK
Confirmed sites: ”@S:3,@Y:4,@Y:15”
Ambiguous sites:

MS/MS Fragmentation of MNSYVSGKEVENMNYLKAVIK
Found in AT5G42590.1, CYP71A16 (cytochrome P450, family 71, subfamily A, polypeptide 16); oxygen binding

Match to Query 4154: 2672.098974 from(891.706934,3+)
Elution from: 47.910 to 47.910 scan no 4966 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2672.1068
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y4 : Phospho (Y)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y15 : Phospho (Y)
Ions Score: 23 Expect: 0.052
Matched b ions: b(5)-98, b(6)-98, b(6), b(7)-98, b(9)-98, b(10)-98, b(16)++, b(18)++, b(19)-98++
Matched y ions:
Precursor origin neutral loss: +

Peptide No.1225

MNTVANYDSDTAAAAAEVPGVASSGKDMEK
Confirmed sites: "@Y:7,@T:11"
Ambiguous sites:

MS/MS Fragmentation of MNTVANYDSDTAAAAAEVPGVASSGKDMEK
Found in AT5G64420.1, DNA polymerase V family

Match to Query 3808: 3159.271983 from(1054.097937,3+)
Elution from: 26.530 to 26.530 scan no 2142 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3159.2814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.044
Matched b ions: b(8), b(9), b(11), b(11)-98, b(12)-98++, b(12)++, b(13)-98++, b(14)-98, b(15)-98++, b(16)-98++, b(17)+, b(17)-98++, b(18)+, b(18)-98++, b(19)-98++, b(19)+, b(24)-98++, b(25)-98++, b(26)+
Matched y ions: y(8), y(9), y(11), y(12), y(15), y(16)+, y(21)-98++, y(22)-98++, y(25)-98++, y(26)-98++
Precursor origin neutral loss: +

Peptide No.1226
MPVSASSEDEEEVER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MPVSASSEDEEEVER
Found in AT2G19710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29440.1); similar to MAPK activating pr

Match to Query 2135: 1772.678374 from(887.346463,2+)
Elution from: 30.437 to 30.437 scan no 2659 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1772.6811
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 2.6e-005
Matched b ions: b(3), b(5), b(8), b(10)-98, b(11)
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(12), y(12)-98, y(13)-98, y(13)+, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1227

MQETEELSDGDEEIGGEESTK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of MQETEELSDGDEEIGGEESTK
Found in AT1G69070.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unknown protein [O

Match to Query 4542: 2391.911602 from(1196.963077,2+)
Elution from: 37.029 to 37.029 scan no 3584 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2391.9148
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 89 Expect: 8.4e-009
Matched b ions: b(6), b(7), b(9), b(11)–98, b(12)–98, b(13)–98, b(14), b(15)–98, b(20)–98++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(12), y(13), y(14)–98, y(14), y(15)–98, y(15), y(17)–98, y(18)–98, y(19)–98++, y(19)++, y(20)++
Precursor origin neutral loss: +

Peptide No. 1228

MQSFQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MQSFQR
Found in AT5G64220.1, calmodulin-binding protein

Match to Query 262: 875.335304 from(438.674928,2+)
Elution from: 21.140 to 21.140 scan no 1426 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 875.3361
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.00065
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98++, b(5)
Matched y ions: y(1), y(2), y(3), y(4)-98++, y(4)-98, y(4), y(5)-98, y(5), y(5)++
Precursor origin neutral loss: +

Peptide No.1229
MQVGPSECVYR
Confirmed sites:
Ambiguous sites: @Y:10orS:6

MS/MS Fragmentation of MQVGPSECVYR
Found in AT1G35435.1. Encodes a defensin-like (DEFL) family protein.

Match to Query 1380: 1404.556818 from(469.192882,3+)
Elution from: 20.230 to 20.230 scan no 1263 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1404.5567
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y10 : Phospho (Y)
Ions Score: 20 Expect: 0.067
Matched b ions: b(2), b(3), b(4)
Matched y ions: y(6)++, y(8)++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1230

MSDDGERGEYLFK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of MSDDGERGEYLFK
Found in AT2G43130.1. ARA4 (Arabidopsis Rab GTPase homolog A5c); GTP binding

Match to Query 2641: 1812.689988 from(605.237272,3+)
Elution from: 41.816 to 41.816 scan no 4199 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1812.6913
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2  : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0067
Matched b ions: b(5), b(5)−98, b(10)−98++, b(13)−98++
Matched y ions: y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.1231
MSITCELLNLTSK
Confirmed sites: @S:2
Ambiguous sites:
MS/MS Fragmentation of MSITCELLNLTSK
Found in AT5G35750.1, AHK2 (ARABIDOPSIS HISTIDINE KINASE 2)
Match to Query 2239: 1588.727625 from(530.583151,3+)
Elution from: 39.587 to 39.587 scan no 3896 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1588.7242
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.016
Matched b ions: b(4), b(6)−98++, b(7)−98++, b(7)++, b(8)−98++
Matched y ions: y(5)++, y(8)++, y(9)++, y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No. 1232

MSPSVACVQTVGDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of MSPSVACVQTVGDR
Found in AT3G63070.1, PWWP domain-containing protein

Match to Query 2674: 1585.661954 from(793.838253,2+)
Elution from: 37.037 to 37.037 scan no 3618 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1585.6629

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 73 Expect: 3.7e-007

Matched b ions: b(5)--98, b(6)--98, b(7)--98, b(7++)--98++, b(8)--98, b(8)--98++, b(9)--98, b(9), b(11)--98, b(11), b(13)--98++

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(12), y(13)++

Precursor origin neutral loss: +

Peptide No.1233

MSQLELQELSSP
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of MSQLELQELSSP
Found in AT3G14120.1, similar to Nuclear pore complex, rNup107 component (sc Nup84) (ISS) [Ostreococcus tauri] (GB:CAL505)

Match to Query 2135: 1585.656340 from(793.835446,2+)
Elution from: 49.005 to 49.005 scan no 5130 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1585.6582
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- M1: Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
- S12: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 36 Expect: 0.0013
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(11)++, b(12), b(12)-98, b(12)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(8), y(9), y(10)++
Precursor origin neutral loss:

Peptide No.1234

MSQLELQEELSSP
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of MSQLELQEELSSP
Found in AT3G14120.1, similar to Nuclear pore complex, rNup107 component (sc Nup84) (ISS)
[Ostreococcus tauri] (GB:CAL505)

Match to Query 2161: 1569.662222 from(785.838387,2+)
Elution from: 52.882 to 52.882 scan no 5593 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.6633
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0042
Matched b ions: b(5), b(6), b(7), b(9), b(11)++, b(12)++
Matched y ions: y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1235
MSQLELQEELSSP
Confirmed sites: @S:12
Ambiguous sites:
MS/MS Fragmentation of MSQLELQEELSSP
Found in AT3G14120.1, similar to Nuclear pore complex, rNup107 component (sc Nup84) (ISS)
[Ostreococcus tauri] (GB:CAL505)
Match to Query 2530: 1569.662582 from(785.838567,2+)
Elution from: 53.153 to 53.153 scan no 5664 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.6633
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.6e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(10)+, b(11), b(12)-98, b(12), b(12)+
Matched y ions: y(3)-98, y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)+
Precursor origin neutral loss:

Peptide No.1236

MSSPERWEAK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of MSSPERWEAK
Found in AT3G26560.1, ATP–dependent RNA helicase, putative

Match to Query 1721: 1299.531000 from(650.772776,2+)
Elution from: 24.907 to 24.907 scan no 2015 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1299.5318
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0042
Matched b ions: b(3), b(4)−98, b(4), b(5), b(6), b(7), b(8)−98++, b(8), b(8)+++, b(8)−98, b(9), b(9)++
Matched y ions: y(2), y(4), y(5), y(6)+++, y(7), y(7)+++, y(9)+++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.1237
MSSPERWEAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MSSPERWEAK
Found in AT3G26560.1, ATP−dependent RNA helicase, putative

Match to Query 1733: 1299.531196 from(650.772874,2+)
Elution from: 24.992 to 24.992 scan no 1976 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1299.5318
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0084
Matched b ions: b(3), b(3)−98, b(5), b(6), b(8)−98++, b(8)−98, b(8), b(8)++, b(9), b(9)−98, b(9)++
Matched y ions: y(2), y(4), y(5), y(7), y(7)++, y(8)−98++, y(8)−98, y(8)++, y(9)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1238

MSSRENPSGICK
Confirmed sites: @S:8
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of MSSRENPSGICK
Found in AT1G18480.1, calcineurin–like phosphoesterase family protein

Match to Query 1635: 1524.553971 from(509.191933,3+)  
Elution from: 20.676 to 20.676 scan no 1316 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1524.5503
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.05
Matched b ions: b(4)-98, b(5)-98, b(5), b(7)-98, b(8)-98++
Matched y ions: y(4), y(6)++, y(7)-98++, y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1239

MTAIDSDDDGVVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MTAIDSDDDGVVR
Found in AT1G70770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23170.1); similar to Os01g0128400 [Oryza

Match to Query 1756: 1488.579092 from(745.296822,2+)
Elution from: 29.553 to 29.553 scan no 2546 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1488.5803
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.1e-007
Matched b ions: b(3), b(4), b(5)++, b(5), b(7), b(11), b(12)–98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)–98, y(8), y(9)–98, y(10)–98, y(11), y(11)–98
Precursor origin neutral loss: +

Peptide No.1240
MTAIDSDDDGVVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MTAIDSDDDGVVR
Found in AT1G70770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23170.1);
similar to Os01g0128400 [Oryz

Match to Query 1893: 1472.584486 from(737.299519,2+)
Elution from: 33.625 to 33.625 scan no 3132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1472.5854
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.3e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6)−98, b(6)−98++, b(6), b(7), b(7)−98, b(8)−98, b(8), b(9), b(9)−98, b(10), b(11), b(11)−98, b(11)++, b(12)−98, b(12), b(12)−98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8)−98, y(8), y(9)−98, y(9), y(9)−98++, y(9)+, y(10), y(10)−98, y(10)++, y(10)−98++, y(11)−98++, y(11), y(11)++, y(11)−98, y(12), y(12)+, y(12)−98, y(12)−98++
Precursor origin neutral loss: +

Peptide No.1241
MTAIDSDDGTVRSK
Confirmed sites: “@S:6,@S:14”
Ambiguous sites:

MS/MS Fragmentation of MTAIDSDDGTVRSK
Found in AT1G70770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23170.1);
similar to Os01g0128400 [Oryz]

Match to Query 2571: 1767.675738 from(590.232522,3+)
Elution from: 31.728 to 31.728 scan no 2899 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1767.6787
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.039
Matched b ions: b(2), b(10)++, b(11)−98++
Matched y ions: y(2), y(4), y(5)−98++, y(5)−98, y(6)++, y(6)−98++, y(6)−98, y(10)++, y(10)−98++, y(11)++, y(11)−98++, y(12)−98++, y(12)++, y(13)−98++, y(13)++, y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1242

MTYLSPYLDSLSPNFK
Confirmed sites: @S:10
Ambiguous sites: "@T:2orY:3, @S:5"

MS/MS Fragmentation of MTYLSPYLDSLSPNFK
Found in AT3G62280.1, carboxylic ester hydrolase

Match to Query 3604: 2130.804057 from(711.275295,3+)
Elution from: 50.675 to 50.675 scan no 5247 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2130.8063
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y3 : Phospho (Y)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.057
Matched b ions: b(5)++, b(6)--98, b(6), b(7)--98, b(11)++, b(13)++, b(14)++, b(14)--98++, b(15)++, b (15)--98++
Matched y ions: y(7)--98++, y(13)--98++, y(15)++, y(15)--98++
Precursor origin neutral loss:

Peptide No.1243

MTYLSPYLDSLSPNFK
Confirmed sites: "@S:10,@S:12"
Ambiguous sites: @T:2orY:3

MS/MS Fragmentation of MTYLSPYLDSLSPNFK
Found in AT3G62280.1, carboxylic ester hydrolase

Match to Query 3652: 2114.808177 from(705.943335,3+)
Elution from: 56.093 to 56.093 scan no 5963 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2114.8114
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y3: Phospho (Y)
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.046
Matched b ions: b(4)++, b(13)++, b(14)++, b(15)++
Matched y ions: y(7)−98, y(9)−196
Precursor origin neutral loss:

Peptide No.1244

MTYLSPYLDSLSPNFK
Confirmed sites: @S:10
Ambiguous sites: "@T:2orY:3, @S:5orY:7"

MS/MS Fragmentation of MTYLSPYLDSLSPNFK
Found in AT3G62280.1, carboxylic ester hydrolase

Match to Query 3549: 2114.807895 from(705.943241,3+)
Elution from: 54.870 to 54.870 scan no 5701 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2114.8114
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
Y7 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0038
Matched b ions: b(4)++, b(8)++, b(10)--98++, b(11)++, b(13)++, b(14)++, b(15)++, b(15)--98++
Matched y ions:
Precursor origin neutral loss:

Peptide No.1245

MTYLSPYLDSLSPNFK
Confirmed sites: "@T:2,@Y:7,@S:10"
Ambiguous sites:

MS/MS Fragmentation of MTYLSPYLDSLSPNFK
Found in AT3G62280.1, carboxylic ester hydrolase

Match to Query 3288: 2114.808993 from(705.943607,3+)
Elution from: 54.843 to 54.843 scan no 5629 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2114.8114
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y7 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.022
Matched b ions: b(4)++, b(6)++, b(10)−98++, b(10)−196++, b(11)++, b(13)++, b(14)++, b(14)−98++, b(15)++, b(15)−98++
Matched y ions: y(5)++, y(7)−98++, y(14)++, y(14)−98++
Precursor origin neutral loss:

Peptide No.1246

MVGEYDSAENSLEER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MVGEYDSAENSLEER
Found in AT3G48430.1, REF6 (RELATIVE OF EARLY FLOWERING 6); transcription factor

Match to Query 2263: 1807.695848 from(904.855200,2+)
Elution from: 38.602 to 38.602 scan no 3630 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1807.6971
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 3.8e-006
Matched b ions: b(6), b(9)-98, b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)-98++, y(13)-98++, y(13), y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1247

MVGEYDSAENSLEER
Confirmed sites: “@S:7,@S:11”
Ambiguous sites:

MS/MS Fragmentation of MVGEYDSAENSLEER
Found in AT3G48430.1, REF6 (RELATIVE OF EARLY FLOWERING 6); transcription factor

Match to Query 3049: 1887.661820 from(944.838186,2+)
Elution from: 38.371 to 38.371 scan no 3726 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1887.6634
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 6.1e-005
Matched b ions: b(6), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(12)+, b(12)-196, b(12)-98, b(13), b(13)-196++, b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(8)-98, y(9), y(9)-196++, y(9)-98, y(10)-98, y(10), y(10)-196, y(11)-98, y(11), y(11)-196, y(13)-98++, y(13)-196, y(13)-196++, y(13)+, y(14)-196++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1248
MVGEYDAENSLEER
Confirmed sites: "@Y:5,@S:11"
Ambiguous sites:

MS/MS Fragmentation of MVGEYDAENSLEER
Found in AT3G48430.1, REF6 (RELATIVE OF EARLY FLOWERING 6); transcription factor

Match to Query 2721: 1887.660428 from(944.837490,2+)
Elution from: 38.384 to 38.384 scan no 3715 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1887.6634
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 6.2e-005
Matched b ions: b(4), b(9), b(10), b(11)−98, b(12)++, b(12)−98, b(13), b(13)−98, b(14)−98
Matched y ions: y(2), y(3), y(4), y(5)−98, y(5), y(6)−98, y(6), y(7)−98, y(8)−98, y(8), y(10)++, y(10), y(11)−98, y(11), y(11)−98++, y(11)++, y(12)−98++, y(13)−98++, y(13)−98, y(13)++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No. 1249
MVKSPDPLEEQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of MVKSPDPLEEQR
Found in AT1G67580.1, protein kinase family protein

Match to Query 2248: 1507.673560 from(754.844056,2+)
Elution from: 28.070 to 28.070 scan no 2277 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 4.6e-005
Matched b ions: b(3), b(4)-98, b(6)-98, b(7), b(10), b(10)++
Matched y ions: y(2), y(3), y(6), y(7), y(8), y(9)-98, y(10)-98++, y(10)++, y(10)-98, y(10), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1250

MVLFPKSPSPVNK
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of MVLFPKSPSPVNK
Found in AT1G43690.1, ubiquitin interaction motif-containing protein

Match to Query 2321: 1602.726066 from(802.370309,2+)
Elution from: 42.811 to 42.811 scan no 4358 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1602.7281
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00051
Matched b ions: b(3), b(4), b(7), b(7)-98, b(8)+, b(8)-98, b(9)-98, b(10)+, b(11)-98++, b(12)-196++, b(12)-196, b(12)-98++
Matched y ions: y(2), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9)-98, y(9), y(9)+, y(10)+, y(10), y(10)-98++, y(11)-98++, y(11)+, y(12)-196++, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.1251

MVRSHLLRATPEASPLKPASSPSNCR
Confirmed sites: "@S:4, @S:14"
Ambiguous sites:

MS/MS Fragmentation of MVRSHLLRATPEASPLKPASSPSNCR
Found in AT4G03480.1, ankyrin repeat family protein

Match to Query 4359: 3037.406949 from(1013.476259, 3+)
Elution from: 57.052 to 57.052 scan no 5854 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3037.4028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.042
Matched b ions: b(8)++, b(8), b(15)++, b(16)++, b(19)++, b(21)++, b(21)-98++, b(22)-196++, b(23)++,
b(23)-196++, b(23)-98++, b(24)-196++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(5), y(9), y(13)++, y(16)++, y(17)-98++, y(18)++, y(21)-98++, y(24)++, y(25)-98++,
y(25)++
Precursor origin neutral loss: +

Peptide No.1252

MVTVTVSDSITK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of MVTVTVSDSITK
Found in AT5G17210.2, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61065.1);
similar to unknown protein [S]

Match to Query 1457: 1359.637908 from(680.826230,2+)
Elution from: 28.810 to 28.810 scan no 2483 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1359.6357  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
**Ions Score:** 39 **Expect:** 0.00053  
**Matched b ions:** b(6), b(8), b(10)  
**Matched y ions:** y(2)–98, y(4)–98, y(5), y(6)++, y(6)–98, y(7)–98++, y(8), y(8)–98, y(9)–98, y(10)–98, y(10), y(11)–98, y(11)++  
**Precursor origin neutral loss:** +

---

**Peptide No.1253**

**MYGVGGSSTAGFAEAYAMRK**  
**Confirmed sites:** @Y:2  
**Ambiguous sites:**

**MS/MS Fragmentation of MYGVGGSSTAGFAEAYAMRK**  
Found in **AT4G08555.1**, unknown protein

Match to Query 3387: 2148.894825 from(717.305551,3+)  
Elution from: 62.292 to 62.292 scan no 6362 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2148.9009
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
M18 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 Expect: 0.035
Matched b ions: b(6)++, b(7)++, b(8)++, b(10)++, b(13)++, b(14)++, b(17)++
Matched y ions: y(5), y(19)++
Precursor origin neutral loss:

Peptide No.1254

NAELTVDTSSEDQTKPLEK
Confirmed sites:
Ambiguous sites: @S:11orT:15orS:9

MS/MS Fragmentation of NAELTVDTSSEDQTKPLEK
Found in AT1G54710.1, AtATG18h (Arabidopsis thaliana homolog of yeast autophagy 18 (ATG18) h)

Match to Query 3590: 2299.007952 from(767.343260,3+)
Elution from: 32.930 to 32.930 scan no 2976 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2299.0104
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0058
Matched b ions:
Matched y ions: y(12)++, y(14)++, y(15)−98++, y(15)++, y(16)++, y(16)−98++, y(17)++, y(17)−98++, y(18)++
Precursor origin neutral loss:

Peptide No.1255

NAPSSDDEDDEDRMEK
Confirmed sites: “@S:4,@S:5”
Ambiguous sites:

MS/MS Fragmentation of NAPSSDDEDDEDRMEK
Found in AT2G18220.1, Identical to Nucleolar complex protein 2 homolog (Protein NOC2 homolog) [Arabidopsis Thaliana] (GB):

Match to Query 2774: 2011.637128 from(1006.825840,2+)
Elution from: 21.974 to 21.974 scan no 1443 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2011.6391
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.002
Matched b ions: b(15)++, b(15)-98++
Matched y ions: y(6), y(9), y(10), y(12)++, y(13)++, y(13), y(13)-98++, y(14)-98++, y(14)-98, y(14)-196++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1256

NASAASDISSISSR
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of NASAASDISSISSR
Found in AT5G52882.1, ATP binding / nucleoside-triphosphatase / nucleotide binding

Match to Query 1989: 1444.618898 from(723.316725,2+)
Elution from: 34.811 to 34.811 scan no 3072 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1444.6195
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 1.1e-008
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)+, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(11)+, b(11)-98, b(11), b(13)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.1257

NASFLWR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NASFLWR
Found in AT3G05200.1, ATL6 (Arabidopsis T?xicos en Levadura 6); protein binding / zinc ion binding

Match to Query 642: 972.421506 from(487.218029,2+)
Elution from: 48.205 to 48.205 scan no 5054 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 972.4218
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0027
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(5)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(5)-98++, y(6)+, y(6)-98++
Precursor origin neutral loss: +

Peptide No.1258
NASSVSSPGLDSDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NASSVSSPGLDSDK
Found in AT5G49110.1, similar to PREDICTED: similar to KIAA1794 protein isoform 3 [Pan troglodytes] (GB:XP_001166926.1);

Match to Query 2029: 1442.592876 from(722.303714,2+)
Elution from: 23.524 to 23.524 scan no 1670 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1442.5926
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 3.7e-005
Matched b ions: b(5), b(10)-98++, b(12)-98
Matched y ions: y(3), y(4), y(8), y(9), y(10), y(10)-98, y(11), y(12), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1259

NATEVPSPDYSQGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NATEVPSPDYSQGK
Found in AT1G20760.1, calcium–binding EF hand family protein

Match to Query 1917: 1571.651790 from(786.833171,2+) Elution from: 27.347 to 27.347 scan no 2240 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6504
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0005
Matched b ions: b(4), b(5), b(6), b(12)++
Matched y ions: y(4), y(6), y(7)++, y(8)++, y(9)−98, y(9), y(9)−98++, y(9)++, y(10), y(10)−98, y(10)−98++, y(11), y(12)++, y(12)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1260

NATEVPSPDYSQGK
Confirmed sites: @Y:10
Ambiguous sites:

MS/MS Fragmentation of NATEVPSPDYSQGK
Found in AT1G20760.1, calcium-binding EF hand family protein

Match to Query 1735: 1571.648870 from(786.831711,2+) Elution from: 28.354 to 28.354 scan no 2306 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6504
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y10 : Phospho (Y)
Ions Score: 32 Expect: 0.0035
Matched b ions: b(4), b(5), b(8)++, b(10), b(12)
Matched y ions: y(4), y(8), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.1261
NDAEEDLLSELEGEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NDAEEDLLSELEGEK
Found in AT4G10120.1, ATSPS4F; sucrose-phosphate synthase/ transferase, transferring glycosyl groups

Match to Query 3012: 1856.754160 from(929.384356,2+)
Elution from: 55.840 to 55.840 scan no 5979 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1856.7564
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 5.7e-005
Matched b ions: b(6), b(8), b(9), b(10), b(11), b(12)–98, b(13)–98, b(14)–98++, b(15)
Matched y ions: y(5), y(6)–98, y(6), y(7), y(8), y(8)–98, y(9), y(9)–98, y(10), y(11), y(14)–98++, y(15) ++
Precursor origin neutral loss: +

Peptide No.1262

NDAEEDLLSESEGEEK
Confirmed sites: ”@S:9,@S:12”
Ambiguous sites:

MS/MS Fragmentation of NDAEEDLLSESEGEEK
Found in AT4G10120.1, ATSPS4F; sucrose-phosphate synthase/ transferase, transferring glycosyl groups

Match to Query 3233: 1936.718922 from(969.366737,2+)
Elution from: 59.401 to 59.401 scan no 6076 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1936.7227
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 7.1e-005
Matched b ions: b(6), b(8), b(9), b(10)–98, b(10), b(11)–98, b(12)–98, b(12)–196, b(13)–98, b(15)
Matched y ions: y(3), y(4), y(5)–98, y(5), y(6), y(7), y(8)–98, y(8), y(9)–196, y(9)–98, y(9), y(10)–98, y(11), y(11)–98, y(12), y(13)–98++, y(14)–98++, y(14)–196, y(14)++, y(15)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1263
NDDGGGSGSKFDLEGSEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NDDGGGSGSKFDLEGSEK
Found in AT5G13160.1, PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase

Match to Query 2752: 1877.729210 from(939.871881,2+)
Elution from: 28.567 to 28.567 scan no 2413 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1877.7316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.024
Matched b ions: b(12)-98
Matched y ions: y(6), y(7), y(11), y(15)-98++, y(15)+, y(16)-98++, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.1264

NDEQVDEGSLDGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NDEQVDEGSLDGR
Found in AT1G70320.1, UPL2 (UBIQUITIN-PROTEIN LIGASE 2); ubiquitin–protein ligase

Match to Query 1618: 1512.571658 from(757.293105,2+) Elution from: 24.967 to 24.967 scan no 1832 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1512.5729
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 Expect: 2.2e-008
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(9)–98, b(10)–98, b(10)+, b(11)
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6)–98, y(6)+, y(6), y(7), y(7)–98++, y(7)–98, y(8), y(8)–98, y(9), y(9)–98, y(10)–98, y(10), y(11), y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.1265
NDEQVEEGSLDGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NDEQVEEGSLDGR
Found in AT1G55860.1, UPL1 (UBIQUITIN–PROTEIN LIGASE 1); ubiquitin–protein ligase

Match to Query 1642: 1526.587688 from(764.301120,2+);
Elution from: 25.182 to 25.182 scan no 1858 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1526.5885
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0015
Matched b ions: b(5), b(6), b(7), b(10)-98
Matched y ions: y(3), y(5), y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1266

NDLNQSSDDEQPFGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NDLNQSSDDEQPFGK
Found in AT3G19520.1, similar to ATP binding / aminoacyl-tRNA ligase [Arabidopsis thaliana] (TAIR:AT1G28500.1); contains

Match to Query 2702: 1772.686260 from(887.350406,2+)
Elution from: 32.915 to 32.915 scan no 3036 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1772.6890
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0048
Matched b ions: b(5), b(6), b(7), b(9)–98++, b(9), b(10), b(11), b(12)–98
Matched y ions: y(4), y(7), y(9), y(10), y(12), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1267
NDTADGYAMSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NDTADGYAMSPR
Found in AT5G06560.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11850.2); similar to expressed protein

Match to Query 1550: 1376.504968 from(689.259760,2+) Elution from: 27.255 to 27.255 scan no 2237 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.5068
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 Expect: 2.4e-009
Matched b ions: b(2), b(5), b(6), b(8), b(9)
Matched y ions: y(2), y(3), y(4), y(5)-98++, y(5), y(6), y(7), y(8)-98++, y(8), y(9), y(9)-98++, y(9)++, y(10), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.1268
NDTASEISLFNVVSPPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of NDTASEISLFNVVSPPR
Found in AT2G16900.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35110.3); similar to pPEARLI 4 gene prod

Match to Query 3248: 1924.890650 from(963.452601,2+)
Elution from: 60.918 to 60.918 scan no 6483 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1924.8931
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00033
Matched b ions: b(12), b(13), b(14)−98
Matched y ions: y(3), y(4), y(4)−98, y(5)−98, y(5), y(6)−98, y(7), y(8), y(10), y(11), y(14)−98++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1269
NEDIQESLGTCDSFDK
Confirmed sites: @S:13
Ambiguous sites:
MS/MS Fragmentation of NEDIQESLGTCDSFDK
Found in AT1G48090.1, C2 domain-containing protein
Match to Query 3432: 1936.738870 from(969.376711,2+)
Elution from: 42.753 to 42.753 scan no 4132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1936.7397
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.2e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(10), b(12), b(13)-98, b(14)-98++, b(14)+, b(15)
Matched y ions: y(4)-98, y(5)-98, y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(10), y(11), y(13), y(13)+, y(14), y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1270

NEEDVSPSLEGTLTEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NEEDVSPSLEGTLTEK
Found in AT2G24940.1, ATMAPR2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 2); heme binding / t

Match to Query 2954: 1725.733904 from(863.874228,2+)
Elution from: 43.897 to 43.897 scan no 4388 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1725.7345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.056
Matched b ions: b(4), b(5), b(6)-98, b(13)-98++, b(14)-98++
Matched y ions: y(6), y(9), y(10), y(11)-98, y(12), y(13)+, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1271
NELVETPPSPVSVK
Confirmed sites:
Ambiguous sites: @S:12orS:9

MS/MS Fragmentation of NELVETPPSPVSVK
Found in AT4G23800.1, high mobility group (HMG1/2) family protein

Match to Query 2551: 1574.758688 from(788.386620,2+)
Elution from: 39.660 to 39.660 scan no 3948 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1574.7592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0023
Matched b ions: b(3), b(4), b(5), b(6), b(13)−98++
Matched y ions: y(8), y(9), y(10), y(11), y(11)−98, y(12)++
Precursor origin neutral loss:

Peptide No.1272
NELVETPPSPVSVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NELVETPPSPVSVK
Found in AT4G23800.1, high mobility group (HMG1/2) family protein

Match to Query 2083: 1574.758282 from(788.386417,2+)
Elution from: 38.427 to 38.427 scan no 3776 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1574.7592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 8.5e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(9)−98, b(11)−98, b(11)++, b(13)−98++
Matched y ions: y(3), y(5), y(6), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.1273
NELVETPPSPVSVK
Confirmed sites: “@S:9,@S:12”
Ambiguous sites:

MS/MS Fragmentation of NELVETPPSPVSVK
Found in AT4G23800.1, high mobility group (HMG1/2) family protein

Match to Query 2674: 1654.723248 from(828.368900,2+)
Elution from: 41.502 to 41.502 scan no 4191 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1654.7256
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.037
Matched b ions: b(3), b(5), b(6), b(7)
Matched y ions: y(8)−98, y(8), y(9), y(11), y(13)++
Precursor origin neutral loss: +

Peptide No.1274

NELVETPPSPVSVK
Confirmed sites: @T:6
Ambiguous sites: @S:12orS:9

MS/MS Fragmentation of NELVETPPSPVSVK
Found in AT4G23800.1, high mobility group (HMG1/2) family protein

Match to Query 2716: 1654.721738 from(828.368145,2+)
Elution from: 45.074 to 45.074 scan no 4639 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1654.7256
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.04
Matched b ions: b(6)−98
Matched y ions: y(6), y(7), y(8), y(8)−98, y(9), y(10)++, y(11), y(11)−98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1275

NELVETPPSPVSVK
Confirmed sites: “@T:6,@S:9”
Ambiguous sites:

MS/MS Fragmentation of NELVETPPSPVSVK
Found in AT4G23800.1, high mobility group (HMG1/2) family protein

Match to Query 2673: 1654.722776 from(828.368664,2+)  
Elution from: 44.253 to 44.253 scan no 4524 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1654.7256

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- **T6:** Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- **S9:** Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 30  **Expect:** 0.0088

**Matched b ions:** b(3), b(6)−98, b(10)−98, b(13), b(13)−98++, b(13)++

**Matched y ions:** y(5), y(7), y(8), y(8)−98, y(9), y(10), y(11), y(11)−98, y(12)++, y(12)−98++, y(13)++

**Precursor origin neutral loss:** +

---

**Peptide No. 1276**

**NENATASTPTPGASPD SER**

**Confirmed sites:** @S:14

**Ambiguous sites:**

*MS/MS Fragmentation of NENATASTPTPGASPD SER*

Found in **AT3G12010.1**, similar to Colon cancer–associated protein Mic1–like containing protein, expressed [Oryza sativa (j

Match to Query 3555: 1980.801972 from(991.408262,2+)

Elution from: 23.662 to 23.662 scan no 1575 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1980.8062
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0088
Matched b ions:
Matched y ions: y(5), y(8), y(9)-98, y(11), y(12), y(13)
Precursor origin neutral loss: +

Peptide No.1277
NEVTPYLVSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NEVTPYLVSR
Found in AT3G25840.1, protein kinase family protein

Match to Query 1708: 1256.579798 from(629.297175,2+)
Elution from: 34.184 to 34.184 scan no 3274 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1256.5802
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0019
Matched b ions: b(2), b(3), b(4), b(8), b(8)++
Matched y ions: y(2)-98, y(3)-98, y(5), y(5)-98, y(6), y(6)++, y(7), y(7)++, y(8), y(8)-98, y(8)-98++, y(8)++
Precursor origin neutral loss:

Peptide No.1278
NEVTPYLVSР
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of NEVTPYLVSР
Found in AT3G25840.1, protein kinase family protein

Match to Query 1291: 1256.579232 from(629.296892,2+)
Elution from: 35.230 to 35.230 scan no 3312 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1256.5802
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
Y6 : Phospho (Y)
Ions Score: 36 Expect: 0.0017
Matched b ions: b(2), b(3), b(4), b(7), b(8)+, b(8), b(9)
Matched y ions: y(2), y(4)+, y(6), y(6)+, y(7), y(7)+, y(8), y(8)+
Precursor origin neutral loss:

Peptide No.1279

NEVVDTSCEDADATQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NEVVDTSCEDADATQK
Found in AT2G45460.1, forkhead-associated domain-containing protein / FHA domain-containing protein

Match to Query 2351: 1860.707020 from(931.360786,2+)
Elution from: 25.580 to 25.580 scan no 2012 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1860.7084  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
**Ions Score:** 65  
**Expect:** 1.4e-006  
**Matched b ions:** b(3), b(4), b(5), b(6), b(9)+, b(10), b(12)-98++, b(12), b(13), b(15)-98++, b(15)-98  
**Matched y ions:** y(4), y(5), y(6), y(7), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(13)+, y(14)+, y(14)-98++, y(15)+  
**Precursor origin neutral loss:** +

**Peptide No. 1280**

**NEWSDGWNSNGGGTK**  
**Confirmed sites:** @S:4  
**Ambiguous sites:**

**MS/MS Fragmentation of** **NEWSDGWNSNGGGTK**  
**Found in** **AT1G05460.1**, **SDE3** (SILENCING DEFECTIVE)

**Match to Query 2016:** 1687.625130 from (844.819841, 2+)  
**Elution from:** 39.205 to 39.205 scan no 3683 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 7.9e-007
Matched b ions: b(2), b(3), b(4)-98, b(5), b(6)-98, b(7)–98, b(8)–98, b(8), b(10)–98, b(14)–98++, b (14)–98
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(12)–98, y(13)++, y(13)–98, y(13), y(13)– 98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1281

NEWSDGWNSNGGGTK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NEWSDGWNSNGGGTK
Found in AT1G05460.1, SDE3 (SILENCING DEFECTIVE)

Match to Query 1970: 1687.625744 from(844.820148,2+)
Elution from: 36.624 to 36.624 scan no 3480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.3e-005
Matched b ions: b(3), b(5), b(9)-98, b(10)-98, b(14)-98++
Matched y ions: y(3), y(7), y(8), y(8)-98, y(9), y(10)-98, y(10), y(11)-98, y(12), y(13)-98, y(13), y(13)+, y(14)++
Precursor origin neutral loss: +

Peptide No.1282

NEWSDGWNSNGGGTK
Confirmed sites:
Ambiguous sites: @T:14orS:9

MS/MS Fragmentation of NEWSDGWNSNGGGTK
Found in AT1G05460.1, SDE3 (SILENCING DEFECTIVE)

Match to Query 1925: 1687.630044 from(844.822298,2+)
Elution from: 36.595 to 36.595 scan no 3468 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6263
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 5.6e-005
Matched b ions: b(3), b(5), b(14)−98++, b(14)−98, b(14)++
Matched y ions: y(7), y(8)−98, y(8), y(10), y(11), y(12), y(13)++, y(13), y(14)++
Precursor origin neutral loss: +

Peptide No.1283

NFANSFGR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NFANSFGR
Found in AT1G42550.1, PMI1 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 547: 991.390960 from(496.702756,2+)
Elution from: 33.490 to 33.490 scan no 3079 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 991.3912
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00096
Matched b ions: b(2), b(3), b(4), b(5)−98
Matched y ions: y(1), y(2), y(3), y(4)−98, y(4), y(5), y(5)−98, y(6), y(6)−98, y(7)++
Precursor origin neutral loss: +

Peptide No. 1284

NFGSDSEKLEIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NFGSDSEKLEIK
Found in AT5G16720.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70750.1);
similar to Os03g0708700 [Oryza]

Match to Query 2045: 1558.726222 from(780.370387,2+)
Elution from: 43.438 to 43.438 scan no 4436 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1558.7279
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 7.8e-005
Matched b ions: b(5)-98, b(5), b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(11)-98, b(12), b(12)-98, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10)++, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1285

NFIRSFSSGR
Confirmed sites: "@S:5,@S:7"

Ambiguous sites:

MS/MS Fragmentation of NFIRSFSSGR
Found in AT5G25240.1, similar to NHL repeat-containing protein [Arabidopsis thaliana] (TAIR:AT5G14890.1); similar to cons

Match to Query 1415: 1329.526300 from(665.770426,2+)
Elution from: 39.102 to 39.102 scan no 3832 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1329.5267
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.017
Matched b ions: b(4), b(5)–98, b(6)–98, b(7)–98, b(7)++, b(7)–196
Matched y ions: y(3), y(4), y(5)–98, y(6)–98, y(6), y(6)–196, y(7), y(8)–98++, y(8)–98, y(8), y(8)–196, y(8)++, y(9)++, y(9)–98++
Precursor origin neutral loss: +

Peptide No.1286
NFLVFQGDVESIASKNPK
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of NFLVFQGDVESIASKNPK
Found in AT3G54670.1, TTN8 (TITAN8); ATP binding
Match to Query 3826: 2072.001216 from(691.674348,3+)
Elution from: 24.910 to 24.910 scan no 2004 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2071.9979
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.058
Matched b ions: b(5), b(11)++, b(15)++, b(16)++, b(17)++
Matched y ions:
Precursor origin neutral loss: +

Peptide No.1287

NFSPGDVSDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1114: 1172.449602 from(587.232077,2+)
Elution from: 32.053 to 32.053 scan no 2907 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1172.4499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 2.7e-005
Matched b ions: b(2), b(3)−98, b(3), b(4)++, b(5)−98, b(6), b(7)−98
Matched y ions: y(1), y(2), y(3), y(4), y(6), y(7), y(7)++, y(8)−98++, y(8)−98, y(8), y(8)++, y(9)++, y (9)−98++
Precursor origin neutral loss: +

Peptide No.1288

NFSPGDVSDR
Confirmed sites: “@S:3,@S:8”
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1688: 1252.415482 from(627.215017,2+)
Elution from: 31.324 to 31.324 scan no 2886 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1252.4162
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0009
Matched b ions: b(2), b(3)–98, b(3), b(4), b(6), b(6)–98, b(7)–98, b(7)
Matched y ions: y(2), y(3), y(4), y(4)–98, y(5), y(6), y(6)+, y(7)–98, y(7), y(7)–98++, y(8)–98, y(8), y(8)–98++, y(8)–196, y(8)+, y(9)+, y(9)–98++, y(9)–196++
Precursor origin neutral loss: +

Peptide No.1289
NFSPGDVSDR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 857: 1172.448510 from(587.231531,2+)
Elution from: 28.309 to 28.309 scan no 2300 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1172.4499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 56 Expect: 7.1e-006
Matched b ions: b(2), b(3), b(3)++, b(6), b(7)
Matched y ions: y(1), y(2), y(3), y(4)−98, y(4), y(5), y(6), y(6)++, y(7)−98, y(7), y(7)++, y(7)−98++, y(8)++, y(8), y(8)−98, y(8)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1290

NFSPGDVSDREAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDREAK
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 2175: 1500.624429 from(501.215419,3+)
Elution from: 29.914 to 29.914 scan no 2408 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1500.6245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0063
Matched b ions: b(2), b(3)-98, b(3), b(4)+, b(7)-98, b(8)-98, b(10)-98+, b(11)-98++, b(12)-98++
Matched y ions: y(2), y(7)+, y(9)+, y(10)+, y(11)+, y(11)-98++, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.1291

NFSPGDVSDREAK
Confirmed sites: "@S:3, @S:8"
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDREAK
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 2243: 1580.589904 from(791.302228,2+)
Elution from: 28.927 to 28.927 scan no 2465 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1580.5909
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.00087
Matched b ions: b(2), b(3)-98, b(3), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8)-196, b(8), b(9)-98, b(9)-196, b(9), b(10), b(10)-196++, b(10)-98, b(10)-98++, b(11)-98, b(11), b(11)++, b(12), b(12)-98, b(12)-196++, b(12)-98++, b(12)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(7), y(8), y(8)-98, y(9)++, y(9), y(9)-98++, y(9)-98, y(10)-98++, y(10)++, y(10)-98, y(10), y(11)-98++, y(11), y(11)-196++, y(11)-196, y(11)-98, y(11)++, y(12)++, y(12)-98++, y(12)-196++, y(12)-98
Precursor origin neutral loss: +

Peptide No.1292
NFSPGDVSDREAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NFSPGDVSDREAK
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 2228: 1500.623188 from(751.318870,2+) Elution from: 25.973 to 25.973 scan no 1995 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1500.6245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 78 Expect: 8.3e-008
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9), b(9)-98, b(10)-98++, b(10)+, b(10)-98++, b(11), b(11)-98, b(12), b(12)-98++
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9)+, y(9), y(9)-98++, y(10)-98++, y(10)+, y(10)-98, y(10), y(11)+, y(11)-98++, y(11)-98, y(11), y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1293

NFTPLDEFDGK
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of NFTPLDEFDGK
Found in AT3G07790.1, DGC14-related

Match to Query 1461: 1361.553222 from(681.783887,2+)
Elution from: 50.968 to 50.968 scan no 5376 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1361.5540
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0026
Matched b ions: b(2), b(3)-98, b(3), b(5)+, b(5), b(6), b(9), b(9)+
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)-98++, y(9), y(10)+
Precursor origin neutral loss: +

Peptide No.1294

NGLNLTSVDSLEGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NGLNLTSVDSLEGR
Found in AT2G20190.1, CLIP-associating protein (CLASP) –related

Match to Query 2391: 1553.706824 from(777.860688,2+)
Elution from: 49.906 to 49.906 scan no 5165 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1553.7086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 3.4e-006
Matched b ions: b(3), b(5), b(6), b(9), b(12)−98++, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7), y(7)−98, y(8)−98, y(8), y(9), y(9)−98, y(10), y(10)++
, y(11), y(11)−98, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1295

NGNSNQTGSPTLP Serg
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NGNSNQTGSPTLP Serg
Found in AT3G62800.1, DRB4 (double-stranded RNA-binding domain (DsRBD)-containing protein 4); double-stranded RNA binding

Match to Query 2707: 1737.730208 from(869.872380,2+) from(869.872380,2+)
Elution from: 24.725 to 24.725 scan no 1896 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1737.7319
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.021
Matched b ions: b(7), b(9)−98, b(12)−98, b(12)
Matched y ions: y(4), y(7), y(9), y(10), y(11), y(15)++
Precursor origin neutral loss: +

Peptide No.1296
NGSVKVER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NGSVKVER
Found in AT3G55870.1, anthranilate synthase, alpha subunit, putative

Match to Query 436: 967.448128 from(484.731340,2+) Elution from: 20.207 to 20.207 scan no 1224 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.4487
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.011
Matched b ions: b(3), b(4), b(5)-98, b(6)-98, b(6), b(7), b(7)-98
Matched y ions: y(1), y(2), y(4), y(5), y(6)-98, y(7)++, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1297

NGSVSGTELVEDDHER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NGSVSGTELVEDDHER
Found in AT5G16260.1, RNA recognition motif (RRM)–containing protein

Match to Query 2341: 1822.735926 from(912.375239,2+)
Elution from: 29.815 to 29.815 scan no 2472 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1822.7370
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 Expect: 1.4e-008
Matched b ions: b(8), b(9–98, b(10–98, b(15–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12–98, y(13–98, y(14)++, y (14–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1298
NGSVSGTELVEDDHER
Confirmed sites: @T:7
Ambiguous sites:
MS/MS Fragmentation of NGSVSGTELVEDDHER
Found in AT5G16260.1, RNA recognition motif (RRM)-containing protein

Match to Query 2974: 1822.736808 from(608.586212,3+)
Elution from: 29.143 to 29.143 scan no 2493 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1822.7370
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0055
Matched b ions: b(3), b(6), b(8), b(9)-98
Matched y ions: y(3)++, y(4)++, y(6)++, y(6), y(9)+, y(11)-98++, y(12)-98++, y(12)+, y(12)-98++, y(13)+, y(13)-98++, y(13)++, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1299

NGVEEVLGLPLSDLFEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of NGVEEVLGLPLSDLFEK
Found in AT1G53240.1, malate dehydrogenase (NAD), mitochondrial

Match to Query 3613: 1939.880384 from(970.947468,2+)
Elution from: 70.606 to 70.606 scan no 7481 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1939.8815
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.028
Matched b ions: b(6), b(7), b(8), b(10), b(16)
Matched y ions: y(7), y(8)-98, y(9), y(16)++
Precursor origin neutral loss: +

Peptide No.1300

NGVGEVESPIER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NGVGEVESPIER
Found in AT4G25500.1, ATRSP35 (Arabidopsis thaliana arginine-serine-rich splicing factor 35); RNA binding

Match to Query 1525: 1364.596468 from(683.305510,2+)  
Elution from: 30.392 to 30.392 scan no 2662 polarity:+
**Peptide No.1301**

**NIDSGNEEEDIR**

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of **NIDSGNEEEDIR**

Found in **AT2G46020.1, ATBRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA); ATP binding / DNA binding / helicase/ transcription regul**

Match to Query 1949: 1526.588484 from(764.301518,2+)

Elution from: 27.013 to 27.013 scan no 2240 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1526.5885
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 3.6e-007
Matched b ions: b(6)-98, b(7)-98, b(8), b(9), b(10), b(11), b(11)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98++, y(11)-98, y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.1302
NISGSMQSPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NISGSMQSPR
Found in AT5G06140.1, phox (PX) domain-containing protein

Match to Query 1074: 1155.473690 from(578.744121,2+)
Elution from: 22.256 to 22.256 scan no 1502 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1155.4743
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.038
Matched b ions: b(2), b(7), b(8), b(8), b(9)++
Matched y ions: y(2), y(3), y(6), y(7), y(8), y(8), y(8), y(8), y(8), y(9)++, y(9)++
Precursor origin neutral loss: +

Peptide No.1303

NKGDIGSASQEF
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NKGDIGSASQEF
Found in AT1G08880.1, histone H2A, putative

Match to Query 1149: 1331.539000 from(666.776776,2+)
Elution from: 31.995 to 31.995 scan no 2865 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1331.5394
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0006
Matched b ions: b(2), b(4), b(5), b(6), b(7)–98, b(8)–98, b(9)–98, b(10)–98, b(10), b(10)–98++, b(11)–98++, b(11)++
Matched y ions: y(6), y(6)–98, y(7), y(7)–98, y(8), y(8)–98, y(10)–98, y(10), y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.1304

NKGDIGSASQEF
Confirmed sites: “@S:7,@S:9”
Ambiguous sites:

MS/MS Fragmentation of NKGDIGSASQEF
Found in AT1G08880.1, histone H2A, putative

Match to Query 1837: 1411.504580 from(706.759566,2+)
Elution from: 37.917 to 37.917 scan no 3714 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1411.5057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.019
Matched b ions: b(4), b(5), b(6), b(8), b(8)−98, b(9), b(10), b(11)−98++, b(11)+, b(11)−196++
Matched y ions: y(5), y(6)−98, y(6)+, y(7)−98, y(7), y(7)−196, y(10)−98, y(10), y(10)+, y(11)+, y(11)−98++
Precursor origin neutral loss: +

Peptide No.1305

NKGDIGSASQEF
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NKGDIGSASQEF
Found in AT1G08880.1, histone H2A, putative

Match to Query 1206: 1331.538384 from(666.776468,2+)
Elution from: 31.928 to 31.928 scan no 2866 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1331.5394
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0047
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)++, b(10), b(10)–98, b(11)–98++, b(11)++, b(11)
Matched y ions: y(4)–98, y(4), y(5)–98, y(6), y(6)–98, y(7), y(7)–98, y(8), y(8)–98, y(9)++, y(10), y (11)++
Precursor origin neutral loss: +

Peptide No.1306

NLCELQSSNQSPSR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NLCELQSSNQSPSR
Found in AT1G27500.1, kinesin light chain–related

Match to Query 2782: 1698.702386 from(850.358469,2+)
Elution from: 28.678 to 28.678 scan no 2241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1698.7032
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 7.1e-007
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9), b(10), b(11)-98, b(11), b(11)++, b(12)-98, b(12)-98++, b(13)
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(6), y(6)-98, y(7)+, y(7)-98, y(7), y(8), y(9), y(9)-98, y(9)++, y(10), y(10)-98, y(11), y(11)++, y(12), y(12)++, y(12)-98++, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1307

NLCELQSSNQSPSR
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of NLCELQSSNQSPSR
Found in AT1G27500.1, kinesin light chain-related

Match to Query 3110: 1778.668846 from(890.341699,2+)
Elution from: 31.183 to 31.183 scan no 2697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1778.6696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.035
Matched b ions: b(4), b(5), b(6), b(7), b(9)−98
Matched y ions: y(3), y(4)−98, y(6), y(7)++, y(7)−98, y(8), y(8)−98, y(10), y(12)−98++, y(12)++, y(13) ++
Precursor origin neutral loss: +

Peptide No.1308

NLCELQSSNQSPSR
Confirmed sites: @S:8
Ambiguous sites: @S:11 or S:13

MS/MS Fragmentation of NLCELQSSNQSPSR
Found in AT1G27500.1, kinesin light chain-related

Match to Query 2585: 1778.667778 from(890.341165,2+) 
Elution from: 31.242 to 31.242 scan no 2833 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1778.6696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0035
Matched b ions: b(4), b(5), b(6)
Matched y ions: y(4), y(6), y(7), y(8), y(8)-98, y(9)-98++, y(10), y(11), y(12)+, y(12)-98++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1309

NLDVSSVEEISR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NLDVSSVEEISR
Found in AT3G13300.1. VCS (VARICOSE); nucleotide binding

Match to Query 1936: 1426.633310 from(714.323931,2+)
Elution from: 42.609 to 42.609 scan no 4113 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1426.6340
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0003
Matched b ions: b(2), b(3), b(4), b(6), b(7)–98, b(8)–98, b(9), b(10), b(10)–98
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(8)–98, y(9), y(9)–98, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.1310
NLEGIQDSSDQITTSLGK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of NLEGIQDSSDQITTSLGK
Found in AT1G04400.1, CRY2 (CRYPTOCHROME 2)

Match to Query 3307: 1984.897830 from(993.456191,2+)
Elution from: 43.315 to 43.315 scan no 4420 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1984.8990
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 5e-005
Matched b ions: b(9), b(10), b(11), b(12), b(13), b(14)
Matched y ions: y(6), y(7), y(8), y(9)-98, y(11), y(12), y(15), y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.1311

NLFGAYSNGGESANK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NLFGAYSNGGESANK
Found in AT1G14850.1, NUP155 (Nucleoporin 155)

Match to Query 2486: 1607.659678 from(804.837115,2+)
Elution from: 41.868 to 41.868 scan no 4015 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1607.6616
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0003
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(11), b(13)++, b(13)−98, b(14), b(14)−98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(12), y(12)−98, y(13)++, y(13), y(13)−98++, y(13)−98, y(14)++
Precursor origin neutral loss:

Peptide No.1312

NLFKSPSPK
Confirmed sites: “@S:5, @S:7”
Ambiguous sites:

MS/MS Fragmentation of NLFKSPSPK
Found in AT1G48950.1, zinc ion binding

Match to Query 1159: 1176.495696 from(589.255124,2+)  
Elution from: 29.681 to 29.681 scan no 2570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1176.4981
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0007
Matched b ions: b(3), b(4), b(5)—98, b(7)—98, b(7), b(8)—196
Matched y ions: y(2), y(3), y(4)—98, y(4), y(5), y(5)—98, y(6), y(7), y(7)—98, y(8)+, y(8)—98++
Precursor origin neutral loss: +

Peptide No.1313

NLGVSGCCDDDSSEEDECVK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of NLGVSGCCDDDSSEEDECVK
Found in AT3G21820.1, SET domain-containing protein

Match to Query 4390: 2353.796492 from(1177.905522,2+)
Elution from: 30.997 to 30.997 scan no 2778 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2353.8021
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 2.1e-008
Matched b ions: b(9), b(10), b(11), b(14)−98, b(15)−98, b(15), b(16), b(18)−98++, b(18)++, b(19)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)−98, y(9)−98, y(9), y(10), y(11), y(12), y(14), y(15), y(15)++, y(16)++, y(16)−98++, y(17)−98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1314
NLNFNIADAFGVDGEKSDD
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of NLNFNIADAFGVDGEKSDD
Found in AT1G35670.1, ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2); calcium- and calmodulin-dependent protein kinase/kin

Match to Query 3669: 2119.871670 from(1060.943111,2+)
Elution from: 68.588 to 68.588 scan no 7203 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2119.8735

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**

S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

**Ions Score:** 61 **Expect:** 6.2e−006

**Matched b ions:** b(6), b(8), b(10), b(12), b(13), b(18)−98++, b(18)++

**Matched y ions:** y(6)−98, y(6), y(7), y(7)−98, y(8), y(9), y(9)−98, y(10), y(11), y(11)−98, y(12), y(12)−98, y(13), y(13)−98, y(13)−98++, y(15), y(16), y(16)−98, y(16)++, y(17)++, y(17)−98++, y(18)++

**Precursor origin neutral loss:** +

---

**Peptide No.1315**

**NLSDLSTLDDSK**

**Confirmed sites:** @S:3

**Ambiguous sites:**

**MS/MS Fragmentation of** NLSDLSTLDDSK

**Found in** AT1G72410.1, COP1–interacting protein–related

**Match to Query 1859:** 1386.590458 from(694.302505,2+)

**Elution from:** 46.051 to 46.051 scan no 4769 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1386.5916
Fixed modifications: Carbamidomethyl (C)
Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 1.1e-008
Matched b ions: b(2), b(3), b(3)–98, b(4), b(4)–98, b(5)–98, b(5), b(6)–98, b(7)–98, b(7), b(8)–98, b(8), b(10)–98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)–98, y(10), y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.1316

NLSESLSDEELNK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NLSESLSDEELNK
Found in AT1G49760.1, PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor

Match to Query 1621: 1556.658112 from(779.336332,2+)
Elution from: 35.771 to 35.771 scan no 3360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1556.6607
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 4.7e-005
Matched b ions: b(5), b(7)-98, b(9), b(10), b(11)-98, b(12)-98++, b(12)
Matched y ions: y(2), y(3), y(4), y(6)++, y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)-98, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1317

NLSGKAETMSTNVER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NLSGKAETMSTNVER
Found in AT5G41950.1, binding

Match to Query 3001: 1715.753022 from(858.883787,2+)
Elution from: 27.985 to 27.985 scan no 2385 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.7549
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 9.8e-006
Matched b ions: b(3)–98, b(6)–98, b(7)–98, b(9), b(13), b(14)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)+, y(13)–98++, y(13)+, y(13)–98, y(14)+, y(14)–98++
Precursor origin neutral loss: +

Peptide No.1318
NLSTPPPVVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NLSTPPPVVR
Found in AT4G30160.1, VLN4 (ARABIDOPSIS THALIANA VILLIN 4); actin binding

Match to Query 1096: 1158.579176 from(580.296864,2+)
Elution from: 33.842 to 33.842 scan no 3055 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1158.5798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.011
Matched b ions: b(2), b(3)-98, b(4)-98, b(4)-98++, b(5)++, b(6)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1319

NLSYRER
Confirmed sites:
Ambiguous sites: @S:3 or Y:4

MS/MS Fragmentation of NLSYRER
Found in AT1G12300.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 532: 1016.443100 from(509.228826,2+)  
Elution from: 14.549 to 14.549 scan no 697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1016.4440
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0094
Matched b ions: b(4)–98, b(5)–98, b(5)
Matched y ions: y(1), y(2), y(3)
Precursor origin neutral loss: +

Peptide No.1320

NMDLLDSQLSDDDGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NMDLLDSQLSDDDGR
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2–LIKE PROTEIN 5); RNA binding

Match to Query 2993: 1772.689398 from(887.351975,2+)
Elution from: 50.459 to 50.459 scan no 5107 polarity:+
Peptide No.1321

NMDLLDSQLSDDDRER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NMDLLDSQLSDDDRER
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2–LIKE PROTEIN 5); RNA binding

Match to Query 3861: 2073.829587 from(692.283805,3+)
Elution from: 37.749 to 37.749 scan no 3682 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2073.8310
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 8.7e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6)+, b(6), b(9)+, b(11)+, b(12)+
Matched y ions: y(4), y(5)+, y(5), y(6)+, y(7)+, y(8)+, y(8)+, y(8)+, y(9)+, y(9)+, y(10)+, y(11)+, y(11)+, y(12)+, y(13)+, y(13)+, y(13)+, y(14)+, y(14)+, y(14)+, y(15)+, y(15)+, y(16)+, y(16)+
Precursor origin neutral loss: +

Peptide No.1322
NMDLLDSQLSDDDGRER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NMDLLDSQLSDDDGRER
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2–LIKE PROTEIN 5); RNA binding

Match to Query 3653: 2073.827882 from(1037.921217,2+)
Elution from: 37.378 to 37.378 scan no 3602 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2073.8310
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.012
Matched b ions: b(5), b(6), b(8)--98, b(11)--98, b(11), b(12)
Matched y ions: y(4), y(5), y(6), y(8), y(11++)--98, y(11)--98, y(11), y(11)--98++, y(14)--98++, y(14)++, y (15)--98++, y(15)++, y(16)++, y(16)--98++
Precursor origin neutral loss: +

Peptide No.1323

NMDLLDSQLSDDDGRER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NMDLLDSQLSDDDGRER
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RNA binding

Match to Query 3665: 2057.834130 from(686.951986,3+)
Elution from: 43.576 to 43.576 scan no 4459 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2057.8361
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00091
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8), b(9), b(9)+, b(11)+
Matched y ions: y(4)+, y(4), y(5), y(6)+, y(6), y(7)+, y(8), y(8)+, y(8)-98++, y(9)-98++, y(9)+, y(10)-98++, y(10)+, y(11)-98++, y(12)+, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(15)+, y(15)-98++, y(16)+, y(16)-98++
Precursor origin neutral loss:

Peptide No.1324
NMDLLDSQLSDDDGRER
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of NMDLLDSQLSDDDGRER
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RNA binding
Match to Query 3580: 2057.833664 from(1029.924108,2+)
Elution from: 43.571 to 43.571 scan no 4457 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2057.8361
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 2.4e-005
Matched b ions: b(3), b(5), b(6), b(8)−98, b(9)−98, b(10)−98, b(11)−98, b(11), b(12)−98, b(12), b(13)−98, b(13), b(14)+, b(14)−98, b(14)−98++, b(16)
Matched y ions: y(4), y(5), y(6), y(7), y(10)+++, y(11)−98++, y(11)−98, y(11), y(11)+, y(12), y(14)−98++, y(14)+, y(15)−98++, y(15)+, y(16)++
Precursor origin neutral loss: +

Peptide No. 1325
NMGGDEIAEPTSPK
Confirmed sites:
Ambiguous sites: @T:11 or S:12

MS/MS Fragmentation of NMGGDEIAEPTSPK
Found in AT1G78110.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22230.1); similar to Os09g0370000 [Oryz]

Match to Query 2230: 1524.616214 from(763.315383,2+) Elution from: 30.431 to 30.431 scan no 2479 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1524.6167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 1.1e-006
Matched b ions: b(5), b(7), b(9), b(13)–98
Matched y ions: y(4), y(5), y(5)–98, y(6), y(6)–98, y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13) ++
Precursor origin neutral loss: +

Peptide No.1326

NMGGDEIAEPTSPK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of NMGGDEIAEPTSPK
Found in AT1G78110.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22230.1); similar to Os09g0370000 [Oryz]

Match to Query 2292: 1524.615220 from(763.314886,2+) Elution from: 30.137 to 30.137 scan no 2556 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1524.6167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 4.6e-007
Matched b ions: b(2), b(5), b(6), b(7), b(9), b(12)−98, b(13)−98++, b(13)−98, b(13)++
Matched y ions: y(3), y(5), y(6), y(6)−98, y(7), y(8), y(9), y(11), y(12), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1327

NMNHKLEDSEEEDSE
Confirmed sites: ”@S:10,@S:15”
Ambiguous sites:

MS/MS Fragmentation of NMNHKLEDSEEEDSE
Found in AT5G10070.1, RNase L inhibitor protein–related

Match to Query 3511: 2093.716156 from(1047.865354,2+)
Elution from: 27.308 to 27.308 scan no 2292 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2093.7173
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0035
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(11), b(11)−98, b(13)++, b(13), b(13)−98++, b(14)++, b(14)−98++, b(15)−98++, b(15)−196++
Matched y ions: y(7)−196, y(7), y(7)−98, y(10)−98, y(10), y(14), y(14)++, y(15)−98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1328

NMNHKLEDSEEEDSE
Confirmed sites: "@S:10,@S:15"
Ambiguous sites:

MS/MS Fragmentation of NMNHKLEDSEEEDSE
Found in AT5G10070.1, RNase L inhibitor protein−related

Match to Query 2899: 2077.720076 from(1039.867314,2+)
Elution from: 33.585 to 33.585 scan no 2987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2077.7224
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 9.8e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)-98++, b(11), b(11)-98++, b(11)+, b(12), b(12)-98++, b(13), b(13)+, b(13)-98++, b(14)-98++, b(14)+, b(15)-98++, b(15)-196++, b(15)+
Matched y ions: y(5), y(6), y(7)-98, y(7), y(8)-196, y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(10)-196, y(11), y(11)-98++, y(12), y(13)-196++, y(14)+, y(14)-98++, y(15)+, y(15)-98
Precursor origin neutral loss: +

Peptide No.1329

NMQQLNQSPDIDGELSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NMQQLNQSPDIDGELSK
Found in AT2G38770.1, similar to LBA1/UPF1 (LOW-LEVEL BETA-AMYLASE 1), RNA helicase [Arabidopsis thaliana] (TAIR:AT5G4701)

Match to Query 3767: 2011.854792 from(1006.934672,2+) Elution from: 36.976 to 36.976 scan no 3475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2011.8558
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 2.9e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)−98, b(9)−98, b(10)−98, b(10), b(11), b(11)−98, b(12)−98, b(12), b(13)−98, b(14), b(14)−98, b(14)++, b(15)−98, b(15), b(15)−98++, b(16), b(16)−98, b(16)−98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)−98, y(11)−98, y(11), y(12), y(12)−98, y(13), y(13)−98, y(14)−98, y(14)++, y(14)−98++, y(15)−98++, y(15), y(15)++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1330

NMQLNLNSSPAREDGELSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NMQLNLNSSPAREDGELSK
Found in AT2G38770.1, similar to LBA1/UPF1 (LOW-LEVEL BETA-AMYLASE 1), RNA helicase [Arabidopsis thaliana] (TAIR:AT5G4701)

Match to Query 3287: 1995.858536 from(998.936544,2+)
Elution from: 41.229 to 41.229 scan no 4088 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1995.8608  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S8 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
**Ions Score:** 99 Expect: 1.2e-009  
**Matched b ions:** b(3), b(4), b(5), b(6), b(7), b(8)−98, b(8), b(9), b(9)−98, b(10), b(10)−98, b(11)−98, b(11), b(12), b(13)++, b(14), b(15), b(15)++, b(16)−98++, b(16)−98, b(16)++  
**Matched y ions:** y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)−98, y(11), y(12), y(12)−98, y(13), y(15)++, y(15)−98++, y(16)++, y(16)−98++  
**Precursor origin neutral loss:** +

---

**Peptide No.1331**

**NNDSCVVSGDETIEK**  
**Confirmed sites:** @S.8  
**Ambiguous sites:**

MS/MS Fragmentation of **NNDSCVVSGDETIEK**  
Found in **AT3G29760.1**, NLI interacting factor (NIF) family protein

Match to Query 2159: 1745.680154 from(873.847353,2+)  
Elution from: 29.567 to 29.567 scan no 2439 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1745.6815
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 6.9e-007
Matched b ions: b(4), b(6), b(7), b(8)-98, b(9)-98, b(9), b(10), b(11)-98, b(11), b(13)-98, b(13), b(14)-98, b(14)++
Matched y ions: y(3), y(4), y(5), y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13), y(14)++
Precursor origin neutral loss: +

Peptide No.1332

NNFTSASLPSEFCNLNK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NNFTSASLPSEFCNLNK
Found in AT2G33020.1, leucine-rich repeat family protein

Match to Query 3574: 2021.853816 from(506.470730,4+)
Elution from: 23.119 to 23.119 scan no 1712 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2021.8553
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 23 Expect: 0.055
Matched b ions: b(5)++, b(7)++, b(9)-98++
Matched y ions: y(3)++, y(3), y(4), y(7)+, y(9)++, y(10)++, y(11)-98++
Precursor origin neutral loss:

Peptide No. 1333

NNITSGPVLVYPMNRNK
Confirmed sites: "@S:5, @Y:11"
Ambiguous sites:

MS/MS Fragmentation of NNITSGPVLVYPMNRNK
Found in AT5G56970.1, CKX3 (CYTOKININ OXIDASE 3); cytokinin dehydrogenase

Match to Query 3834: 2091.922152 from(698.314660, 3+)
Elution from: 49.281 to 49.281 scan no 5175 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2091.9213
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y11 : Phospho (Y)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 Expect: 0.036
Matched b ions: b(2), b(4), b(6), b(7)-98, b(9)-98++, b(10)-98++, b(10)+, b(11)+, b(12)-98++, b(13)-98++, b(15)-98++, b(16)-98++
Matched y ions: y(5), y(7), y(10)+, y(14)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1334

NNSLSLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NNSLSLR
Found in AT4G16720.1, 60S ribosomal protein L15 (RPL15A)

Match to Query 274: 882.395630 from(442.205091,2+)
Elution from: 25.356 to 25.356 scan no 1996 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 882.3960
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(2), b(3)–98, b(4)–98, b(5)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)–98++, y(6)++
Precursor origin neutral loss: +

Peptide No.1335
NPLSPNSGQANLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NPLSPNSGQANLK
Found in AT3G50370.1, similar to cupin family protein [Arabidopsis thaliana] (TAIR:AT2G18540.1); similar to Unknown prote

Match to Query 1918: 1418.655438 from(710.334995,2+)
Elution from: 31.500 to 31.500 scan no 2625 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1418.6555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 4.2e-006
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(6)-98, b(7), b(7)+, b(7)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(9)+, y(10), y(10)-98++, y(10)-98, y(10)+, y(11)+, y(11)-98++, y(11), y(11)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1336
NPMDDLFGEDSDNDSR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NPMDDLFGEDSDNDSR
Found in AT4G17620.1, glycine-rich protein

Match to Query 3350: 1905.669356 from(953.841954,2+)
Elution from: 57.127 to 57.127 scan no 5906 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1905.6724
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 4.8e-005
Matched b ions: b(6), b(7), b(11)-98
Matched y ions: y(4), y(7), y(9), y(9)-98, y(10)-98, y(10), y(11), y(12), y(13), y(13)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.1337

NPMDDLFGEDSDNDSR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of NPMDDLFGEDSDNDSR
Found in AT4G17620.1, glycine-rich protein

Match to Query 3081: 1905.669708 from(953.842130,2+) Elution from: 56.185 to 56.185 scan no 5971 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1905.6724
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.017
Matched b ions: b(7), b(9), b(10), b(11)
Matched y ions: y(7), y(9), y(9)-98, y(10)-98, y(10), y(13), y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1338

NPSNLNLNLQLQDQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NPSNLNLNLQDQR
Found in AT1G62740.1, stress-inducible protein, putative

Match to Query 2479: 1653.749258 from(827.881905,2+)
Elution from: 44.173 to 44.173 scan no 4537 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1653.7512
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 2e-005
Matched b ions: b(5)++, b(5), b(6), b(6)-98, b(7)-98, b(8), b(10), b(11), b(11)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(7), y(8), y(9), y(10), y(12)++
Precursor origin neutral loss: +

Peptide No.1339
NPTRPVVSP
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NPTRPVVSP
Found in AT5G20350.1, TIP1 (TIP GROWTH DEFECTIVE 1)

Match to Query 547: 1045.494722 from(523.754637,2+)
Elution from: 24.512 to 24.512 scan no 1904 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1045.4957
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.012
Matched b ions: b(4), b(5)++, b(6), b(7), b(7)++, b(8)++, b(8)−98, b(8)−98++
Matched y ions: y(2), y(3), y(3)−98, y(5), y(6), y(7)++, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1340

NPVSYESEDNGVYQQSGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NPVSYESEDNGVYQQSGR
Found in AT3G48430.1, REF6 (RELATIVE OF EARLY FLOWERING 6); transcription factor

Match to Query 4004: 2107.842986 from(1054.928769,2+)
Elution from: 32.991 to 32.991 scan no 2941 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2107.8483
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00019
Matched b ions: b(9)-98, b(11), b(12)-98, b(13)-98, b(16)-98++
Matched y ions: y(4), y(6), y(8)++, y(8), y(9), y(10), y(12), y(15), y(16)-98
Precursor origin neutral loss: +

Peptide No.1341
NQLESIGHSPEGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NQLESIGHSPEGK
Found in AT5G42570.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48660.1);
similar to unknown protein [O

Match to Query 2206: 1474.644038 from(738.329295,2+)
Elution from: 24.986 to 24.986 scan no 1957 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1474.6453
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.4e-005
Matched b ions: b(2), b(3), b(4)++, b(4), b(5), b(6), b(8), b(9)−98, b(9), b(10)−98, b(10)++, b(11)−98, b(11), b(11)++, b(12), b(12)−98
Matched y ions: y(4), y(5), y(5)−98, y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10)−98, y(11)++, y(11)−98, y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.1342

NQLESIGHSPEGKK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NQLESIGHSPEGKK
Found in AT5G42570.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48660.1); similar to unknown protein [O

Match to Query 2322: 1602.738874 from(802.376713,2+) Elution from: 20.878 to 20.878 scan no 1413 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1602.7402
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0011
Matched b ions: b(3), b(4), b(8), b(9), b(9)-98, b(10)-98, b(11), b(12), b(13), b(13)+, b(13)-98++
Matched y ions: y(5), y(6), y(7)-98, y(7), y(8), y(10), y(10)-98, y(11)-98, y(12)-98++, y(12)+, y(13)++
Precursor origin neutral loss: +

Peptide No.1343
NQSTFLPSAYDSDKVSDGK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of NQSTFLPSAYDSDKVSDGK
Found in AT4G37280.1, MRG family protein

Match to Query 4216: 2251.002978 from(751.341602,3+)
Elution from: 47.817 to 47.817 scan no 4779 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2251.0045
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0084
Matched b ions: b(13)++
Matched y ions: y(6), y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(16)++, y(17)++, y(18)++,
y(18)-98++
Precursor origin neutral loss:

Peptide No.1344

NQTQLSPPDVSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NQTQLSPPDVSR
Found in AT3G26730.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 1975: 1507.666232 from(754.840392,2+)  
Elution from: 30.519 to 30.519 scan no 2717 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1507.6668
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 5e-006
Matched b ions: b(6), b(7)-98, b(8)-98, b(10), b(10)-98, b(11)-98, b(12), b(12)-98++
Matched y ions: y(2), y(3), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No. 1345

NRSLVDVQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NRSLVDVQR
Found in AT5G58350.1, WNK4 (Arabidopsis WNK kinase 4); kinase

Match to Query 1255: 1165.559804 from(583.787178,2+)
Elution from: 22.316 to 22.316 scan no 1664 polarity:+
Monoisotopic mass of neutral peptide \( \text{Mr(calc)} \): 1165.5604

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 46 Expect: 0.00017

Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(4), b(5), b(5)–98, b(6), b(6)–98, b(7), b(7)–98, b(8), b(8)–98

Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8)++

Precursor origin neutral loss: +

Peptide No.1346

NRSPSPLYR

Confirmed sites: “@S:3,@S:5”

Ambiguous sites:

MS/MS Fragmentation of NRSPSPLYR

Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 1386: 1248.504744 from(625.259648,2+) 

Elution from: 24.102 to 24.102 scan no 1837 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1248.5053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.029
Matched b ions: b(2), b(3)−98, b(3), b(4)−98, b(5)−196, b(5)−98, b(5)−196++, b(6)−196, b(7)−98, b(7), b(8)−98, b(8), b(8)−196, b(8)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(6)−98, y(6), y(7), y(7)−196, y(7)++, y(7)−98, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1347

NRSPSPLYR
Confirmed sites: “@S:3,@Y:8”
Ambiguous sites:

MS/MS Fragmentation of NRSPSPLYR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 1085: 1248.504248 from(625.259400,2+) Elution from: 22.893 to 22.893 scan no 1642 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1248.5053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Y8 : Phospho (Y)
Ions Score: 21 Expect: 0.052
Matched b ions: b(2), b(3)-98, b(3), b(5)-98, b(7)-98, b(8)-98, b(8)
Matched y ions: y(3), y(5), y(5)+, y(6), y(7), y(7)-98, y(8)+, y(8)-98++
Precursor origin neutral loss: +

Peptide No.1348
NRWDETPTPGR
Confirmed sites: “@T:6,@T:8”
Ambiguous sites:

MS/MS Fragmentation of NRWDETPTPGR
Found in AT5G64270.1, splicing factor, putative

Match to Query 1937: 1487.558614 from(744.786583,2+)
Elution from: 25.599 to 25.599 scan no 2016 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1487.5595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.04
Matched b ions: b(3), b(4), b(5), b(6)-98, b(8)-98, b(8)-196, b(10)-98++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6), y(7), y(8), y(9)++, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1349
NSASPEESLGK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NSASPEESLGK
Found in AT4G11560.1, bromo-adjacent homology (BAH) domain-containing protein

Match to Query 1206: 1197.489724 from(599.752138,2+)
Elution from: 22.884 to 22.884 scan no 1477 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.4914
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.039
Matched b ions: b(4)–98, b(9)–98
Matched y ions: y(4), y(7), y(8), y(9)–98++, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.1350

NSASPIVGGESPVGLNGQDR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NSASPIVGGESPVGLNGQDR
Found in AT3G53500.1, RSZ32; nucleic acid binding

Match to Query 2937: 2089.940434 from(1045.977493,2+)
Elution from: 37.971 to 37.971 scan no 3650 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2089.9429
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 2.7e-005
Matched b ions: b(17)-98++, b(19)++, b(20)-98, b(20)-98++
Matched y ions: y(7), y(8), y(9), y(10), y(12), y(13), y(14), y(15)-98, y(16)++, y(17)-98++, y(17)+, y(18), y(18)++, y(19)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.1351

NSASPIVGGESPVGLNGQDR
Confirmed sites: @S:12
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of NSASPIVGGESPVGLNGQDR
Found in AT3G53500.1, RSZ32; nucleic acid binding

Match to Query 3130: 2169.907060 from(1085.960806,2+)
Elution from: 39.486 to 39.486 scan no 3844 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2169.9092
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 2.1e-007
Matched b ions: b(4)-98, b(6)-98, b(7)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)-196, b(13)-98, b(14)-196, b(14)-98, b(14), b(15), b(16), b(16)-98, b(19)-98++, b(20), b(20)-196++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(10)-98, y(12), y(13), y(13)-98++, y(14), y(14)-98, y(15), y(15)-98, y(16)+++, y(17)+++, y(17), y(17)-98++, y(20)+++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.1352

NSASPIVGGESPVGLNGQDR
Confirmed sites: "@S:4,@S:12"
Ambiguous sites:

MS/MS Fragmentation of NSASPIVGGESPVGLNGQDR
Found in AT3G53500.1, RSZ32; nucleic acid binding

Match to Query 4104: 2169.906940 from(1085.960746,2+)
Elution from: 40.395 to 40.395 scan no 4038 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2169.9092

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S4: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
- S12: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 97  **Expect:** 2.7e-009

**Matched b ions:** b(4)-98, b(4), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)-196, b(14)-196, b(14)-98, b(14), b(15), b(15)-98, b(16)-98, b(16), b(16)-98++, b(17), b(17)-98, b(19)-98, b(19), b(19)+++, b(19)-98++, b(20), b(20)-196++, b(20)-98, b(20)-98++

**Matched y ions:** y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98++, y(13), y(13)-98, y(14), y(14)-98, y(15), y(15)-98, y(16)+++, y(16), y(17)+++, y(17)-98, y(17), y(17)-98++, y(18)-98++, y(18), y(18)+++, y(19)-98++, y(19)+++, y(20)+++, y(20)-98++

**Precursor origin neutral loss:** +

---

**Peptide No.1353**

**NSDSEEMFDSDGEDEEEDK**

**Confirmed sites:** @S:10

**Ambiguous sites:**

**MS/MS Fragmentation of NSDSEEMFDSDGEDEEEDK**

Found in [AT4G08310.1](https://www.arabidopsis.org), similar to unknown protein [Arabidopsis thaliana](https://www.arabidopsis.org) (TAIR:AT1G44780.2); similar to hypothetical prote

**Match to Query 3263:** 2285.728974 from(1143.871763,2+)

**Elution from:** 34.636 to 34.636 scan no 3123 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2285.7314
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 Expect: 4.5e-009
Matched b ions: b(6), b(7), b(8), b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98++, b(13), b(14), b(14)-98, b(15), b(16), b(17)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(13)-98, y(13), y(13)-98++, y(14)+, y(14)-98, y(14), y(15)-98++, y(16)+, y(16)-98++, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1354

NSEDSGVTVDGSPSAK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NSEDSGVTVDGSPSAK
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 1867: 1628.655144 from(815.334848,2+)
Elution from: 22.512 to 22.512 scan no 1541 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1628.6566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 4.3e-007
Matched b ions: b(7), b(8), b(9), b(10), b(12)–98, b(15)++
Matched y ions: y(4), y(5), y(6), y(7), y(7)–98, y(8)–98, y(9), y(9)–98, y(10), y(10)–98, y(11), y(12), y(13), y(15)++, y(15)–98++
Precursor origin neutral loss: +

Peptide No.1355
NSEDSGVTVDGSPSAK
Confirmed sites:
Ambiguous sites: @S:12orS:14

MS/MS Fragmentation of NSEDSGVTVDGSPSAK
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase
Match to Query 2549: 1628.654278 from(815.334415,2+) Elution from: 22.962 to 22.962 scan no 1487 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1628.6566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00031
Matched b ions: b(4), b(5), b(7), b(9), b(10), b(15)++
Matched y ions: y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(10), y(11), y(12), y(15)++
Precursor origin neutral loss: +

Peptide No.1356

NSESAFEESHSSEEVR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NSESAFEESHSSEEVR
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1);
similar to Os06g0206100 [Oryz]

Match to Query 3064: 1902.725178 from(952.369865,2+)
Elution from: 25.673 to 25.673 scan no 2025 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1902.7268
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0013
Matched b ions: b(8), b(14), b(15)
Matched y ions: y(4), y(5), y(6)−98, y(6), y(7)−98, y(8), y(8)−98, y(9)−98, y(10)−98, y(10), y(12)−98++, y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1357
NSESAFEESHSSEEVR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NSESAFEESHSSEEVR
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 2460: 1902.725223 from(635.249017,3+)
Elution from: 24.744 to 24.744 scan no 1901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1902.7268
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00059
Matched b ions: b(2), b(3), b(7), b(11)++, b(13)++, b(14)++, b(15)−98++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(5)−98, y(7)++, y(7)−98, y(8)++, y(9)++, y(10)−98++, y(11)++, y(12)++, y(12)−98++, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(15)++, y(15)−98++
Precursor origin neutral loss:

Peptide No.1358

NSESAFEESHSSEEVR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NSESAFEESHSSEEVR
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 3218: 1902.725712 from(635.249180,3+)
Elution from: 24.887 to 24.887 scan no 1951 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1902.7268
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00033
Matched b ions: b(2), b(3), b(8)
Matched y ions: y(2), y(3)++, y(3), y(7), y(8)++, y(9)++, y(10)−98++, y(11)++, y(11)−98++, y(12)++, y(12)−98++, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(15)++, y(15)−98++
Precursor origin neutral loss:

Peptide No.1359

NSESGLELLSK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of NSESGLELLSK
Found in AT3G28180.1, ATCSLC04 (Cellulose synthase-like C4); transferase, transferring glycosyl groups

Match to Query 1127: 1255.568262 from(628.791407,2+)
Elution from: 42.818 to 42.818 scan no 4354 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1255.5697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 2.4e-007
Matched b ions: b(2), b(3)-98, b(4), b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(9)+, b(9), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)+, y(10)-98, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1360

NSFTSPVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NSFTSPVK
Found in AT3G12280.1, RBR1 (RETINOBLASTOMA–RELATED 1)

Match to Query 398: 958.415128 from(480.214840,2+)
Elution from: 27.806 to 27.806 scan no 2232 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 958.4161
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0031
Matched b ions: b(2), b(3), b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(6)--98++, y(7), y(7)++
Precursor origin neutral loss:

Peptide No.1361

NSFTSPVK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of NSFTSPVK
Found in AT3G12280.1, RBR1 (RETINOBLASTOMA-RELATED 1)

Match to Query 372: 958.415444 from(480.214998,2+)
Elution from: 27.365 to 27.365 scan no 2252 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 958.4161
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0081
Matched b ions: b(2), b(3), b(4)−98, b(7)
Matched y ions: y(3), y(4), y(5), y(5)−98, y(6), y(6)−98++, y(7)++, y(7)
Precursor origin neutral loss: +

Peptide No.1362

NSLESGNGSPEANSLVGNDENVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NSLESGNGSPEANSLVGNDENVK
Found in AT5G38600.1, proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein

Match to Query 4438: 2410.027077 from(804.349635,3+)
Elution from: 36.465 to 36.465 scan no 3518 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2410.0284
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0021
Matched b ions: b(4), b(7), b(8), b(9), b(9)–98, b(10)–98, b(12), b(12)–98++, b(14)–98++, b(14), b(15)++, b(16)++, b(16)–98++, b(18)++, b(18)–98++, b(19)–98++, b(22)++
Matched y ions: y(6), y(7), y(8)++, y(8), y(9), y(14)++, y(15)++, y(16)++, y(17)++, y(19)++, y(20)++
Precursor origin neutral loss: +

Peptide No.1363

NSLNISMR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of NSLNISMR
Found in AT2G17290.1, CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); anion channel/calcium- and calmodulin-dependent protein

Match to Query 824: 1013.435724 from(507.725138,2+)
Elution from: 33.719 to 33.719 scan no 3187 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1013.4365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00019
Matched b ions: b(2)-98, b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98++, b(6), b(6)-98, b(7)-
98
Matched y ions: y(1), y(2), y(3), y(5), y(6), y(7)++, y(7)-98, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1364
NSLNISMR
Confirmed sites: “@S:2, @S:6”
Ambiguous sites:

MS/MS Fragmentation of NSLNISMR
Found in AT4G35310.1, CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); calcium- and calmodulin-dependent protein kinase/ kinase

Match to Query 658: 1093.401592 from(547.708072,2+)
Elution from: 37.539 to 37.539 scan no 3594 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1093.4028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 25 Expect: 0.0083
Matched b ions: b(3)−98, b(4), b(5), b(5)−98, b(6)−196++, b(6)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++
Precursor origin neutral loss: +

Peptide No.1365

NSLNISMRS
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NSLNISMRS
Found in AT4G35310.1, CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); calcium− and calmodulin−dependent protein kinase/kinase

Match to Query 502: 1013.435836 from(507.725194,2+)
Elution from: 34.066 to 34.066 scan no 3148 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1013.4365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00057
Matched b ions: b(2), b(3), b(4), b(5), b(6)−98++, b(6)−98
Matched y ions: y(1), y(2), y(3)−98, y(4), y(4)−98, y(5)−98, y(5), y(6), y(6)−98, y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No.1366

NSLNISMR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NSLNISMR
Found in AT4G35310.1. CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); calcium- and calmodulin-dependent protein kinase/ kinase

Match to Query 666: 1029.430870 from(515.722711,2+)
Elution from: 25.270 to 25.270 scan no 1986 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1029.4314
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 Expect: 0.00011
Matched b ions: b(2), b(3), b(4), b(5), b(6−98, b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)−98, y(5)−98, y(5), y(6), y(6)++, y(7)++, y(7)−98++
Precursor origin neutral loss: +

Peptide No.1367

NSLNISMRDA
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NSLNISMRDA
Found in AT4G35310.1, CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); calcium- and calmodulin-dependent protein kinase/ kinase

Match to Query 976: 1199.500370 from(600.757461,2+)
Elution from: 37.848 to 37.848 scan no 3702 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1199.5005

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 43  **Expect:** 0.0002

**Matched b ions:** b(3), b(5), b(7)--98, b(8), b(8)++, b(9)--98++, b(9)++

**Matched y ions:** y(2), y(3), y(4), y(5), y(5)--98, y(6), y(6)--98, y(7), y(7)--98, y(7)++, y(8)++, y(8)--98, y(8), y(9)++, y(9)--98++

**Precursor origin neutral loss:** +

---

**Peptide No.1368**

**NSLNISMRDV**

**Confirmed sites:** @S:6

**Ambiguous sites:**

**MS/MS Fragmentation of NSLNISMRDV**

Found in **AT2G17290.1**, CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); anion channel/calmodulin-dependent protein

**Match to Query 1028:** 1227.530956 from(614.772754,2+)

**Elution from:** 44.634 to 44.634 scan no 4591 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1227.5318
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0015
Matched b ions: b(2), b(3), b(4), b(5), b(5)+, b(6)+, b(7)-98, b(7), b(8), b(9), b(9)+, b(9)-98+
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(6)+, y(7)-98, y(7), y(8), y(8)-98, y(8)+, y(9)+, y(9)-98+
Precursor origin neutral loss: +

Peptide No.1369

NSLNISMRDV
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NSLNISMRDV
Found in AT2G17290.1, CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); anion channel/calcium- and calmodulin-dependent protein

Match to Query 1129: 1243.525772 from(622.770162,2+) Elution from: 34.114 to 34.114 scan no 3165 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.5268
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.016
Matched b ions: b(3), b(4), b(5), b(7)++, b(9)++
Matched y ions: y(5)−98, y(5), y(6), y(6)−98, y(7), y(7)−98, y(8)−98, y(8)−98++, y(8)++, y(9)++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.1370

NSMMATVSSGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NSMMATVSSGK
Found in AT3G46450.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 953: 1191.465546 from(596.740049,2+)
Elution from: 26.255 to 26.255 scan no 2102 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1191.4665
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0091
Matched b ions: b(3), b(5)++, b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1371

NSMSPSLATTDG
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NSMSPSLATTDG
Found in AT2G36570.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 1421: 1259.473036 from(630.743794,2+)
Elution from: 34.181 to 34.181 scan no 2987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.4741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00015
Matched b ions: b(4), b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(9), b(10), b(11)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.1372
NSMSPSLATTDG
Confirmed sites:
Ambiguous sites: @S:4orS:6

MS/MS Fragmentation of NSMSPSLATTDG
Found in AT2G36570.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 969: 1259.474460 from(630.744506,2+)
Elution from: 33.225 to 33.225 scan no 3028 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.4741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.026
Matched b ions: b(7), b(7)-98, b(8), b(8)-98, b(9), b(10)
Matched y ions: y(4), y(5), y(6), y(9)+
Precursor origin neutral loss: +

Peptide No.1373

NSNSDEAFSSEEEEER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of NSNSDEAFSSEEEEER
Found in AT3G06400.1, CHR11 (CHROMATIN-REMODELING PROTEIN 11); DNA-dependent ATPase

Match to Query 3437: 1937.678198 from(969.846375,2+)
Elution from: 28.385 to 28.385 scan no 2201 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1937.6799
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 3.4e-005
Matched b ions: b(8)++, b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(8), y(8)—98, y(9)—98++, y(9), y(9)—98, y(10), y(12), y(13), y(15)++
Precursor origin neutral loss: +

Peptide No.1374

NSPDPPDASAVTLDSYR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of NSPDPPDASAVTLDSYR
Found in AT2G32910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G61910.3); similar to expressed protein

Match to Query 2939: 1812.755264 from(907.384908,2+)
Elution from: 40.981 to 40.981 scan no 4081 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1812.7567
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.2e-007
Matched b ions: b(4), b(4)-98, b(8)-98++, b(8), b(9)-98, b(10)-98, b(10), b(12), b(15)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)+, y(12), y(14)+, y(15)+
Precursor origin neutral loss: +

Peptide No.1375
NSSFDYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NSSFDYR
Found in AT3G02750.1, protein phosphatase 2C family protein / PP2C family protein
Match to Query 399: 967.343356 from(484.678954,2+)
Elution from: 25.977 to 25.977 scan no 2064 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.3436
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0019
Matched b ions: b(3), b(4), b(4)−98, b(5), b(6)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)−98, y(5)+, y(6)+, y(6)−98++
Precursor origin neutral loss: +

Peptide No.1376

NSSFDYRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NSSFDYRR
Found in AT3G02750.1, protein phosphatase 2C family protein / PP2C family protein

Match to Query 721: 1123.442962 from(562.728757,2+)
Elution from: 21.348 to 21.348 scan no 1467 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1123.4447
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.029
Matched b ions: b(4), b(5)−98, b(7)++
Matched y ions: y(3), y(5)++, y(6)++, y(6)−98++, y(7)++
Precursor origin neutral loss: +

Peptide No.1377

NSSSSSFGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of NSSSSSFGR
Found in AT5G44530.1, subtilase family protein

Match to Query 515: 1007.373906 from(504.694229,2+)
Elution from: 23.178 to 23.178 scan no 1690 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1007.3709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.026
Matched b ions: b(2), b(4), b(5), b(5)-98, b(6), b(7)-98++, b(8)++
Matched y ions: y(4), y(8)++
Precursor origin neutral loss: +

Peptide No.1378
NSTSISPVSSPALNR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NSTSISPVSSPALNR
Found in AT5G20900.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43440.1); similar to ZIM motif family p

Match to Query 2193: 1608.748892 from(805.381722,2+) Elution from: 34.052 to 34.052 scan no 3189 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1608.7508
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.9e-006
Matched b ions: b(6)−98, b(7), b(8), b(8)−98, b(10), b(12)++
Matched y ions: y(2), y(3), y(5), y(6), y(7)++, y(7), y(9), y(10), y(10)++, y(10)−98, y(11), y(12), y(12)++,
y(12)−98++, y(13)−98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1379

NSTSISPVSSPALNR
Confirmed sites: “@S:6,@S:10”
Ambiguous sites:

MS/MS Fragmentation of NSTSISPVSSPALNR
Found in AT5G20900.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43440.1);
similar to ZIM motif family p

Match to Query 2934: 1688.714228 from(845.364390,2+)
Elution from: 35.365 to 35.365 scan no 3381 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1688.7171
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 1.2e-005
Matched b ions: b(8), b(9), b(10), b(10)-98, b(11), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)
Precursor origin neutral loss: +

Peptide No.1380

NSVSSPIMTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NSVSSPIMTR
Found in AT2G36910.1, ATGP1 (ARABIDOPSIS THALIANA P GLYCOPROTEIN1); calmodulin binding

Match to Query 919: 1186.504652 from(594.259602,2+)
Elution from: 23.016 to 23.016 scan no 1703 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1186.5053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48 Expect: 9.6e-005
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)+, b(8)+
Matched y ions: y(2), y(3), y(4)+, y(5), y(6)-98++, y(6)-98, y(7), y(7)-98, y(7)-98++, y(7)+, y(8)+, y(8)-98, y(8)-98+, y(9)+
Precursor origin neutral loss:

Peptide No.1381

NSVVSPVVGAGGDSSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVGAGGDSSK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 2103: 1538.696704 from(770.355628,2+)
Elution from: 31.159 to 31.159 scan no 2800 polarity:+

---
Monoisotopic mass of neutral peptide Mr(calc): 1538.6977
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 3.7e-009
Matched b ions: b(3), b(4), b(5)–98, b(5)++, b(6)–98++, b(6)–98, b(7)–98, b(8), b(9)–98, b(9), b(10)–98, b(10), b(11)–98, b(13), b(13)–98, b(14), b(14)–98, b(15), b(15)–98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(12)–98++, y(12)–98, y(13)++, y(13), y(13)–98++, y(13)–98, y(14)–98++, y(14), y(14)–98, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1382

NSVVSPVVGAGGDSSK
Confirmed sites: @S:5
Ambiguous sites: @S:14 or S:15

MS/MS Fragmentation of NSVVSPVVGAGGDSSK
Found in AT2G37340.1, RSZ33 (Arginine/serine–rich Zinc knuckle–containing protein 33); nucleic acid binding / nucleotide

Match to Query 2855: 1618.662336 from(810.338444,2+)
Elution from: 34.743 to 34.743 scan no 3349 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1618.6640
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 5.9e-007
Matched b ions: b(3), b(4), b(5)−98, b(5)+, b(6)−98++, b(7)−98, b(8)−98, b(10)−98, b(10), b(11)−98, b(13), b(13)−98
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(12)−98, y(12), y(12)−98++, y(13), y(13)−196++, y(13)+, y(13)−98, y(13)−98++, y(14)−98, y(14)−98++, y(14)−196, y(14)+, y(15)+, y(15)−196++, y(15)−98++
Precursor origin neutral loss: +

Peptide No.1383
NSVVSPVVAGGDSSKEDR
Confirmed sites: @S:14
Ambiguous sites:
MS/MS Fragmentation of NSVVSPVVAGGDSSKEDR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 3168: 1938.867094 from(970.440823,2+)  
Elution from: 27.401 to 27.401 scan no 2292 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1938.8683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00032
Matched b ions: b(10), b(13), b(16), b(18)-98, b(18)
Matched y ions: y(5), y(6)-98, y(6), y(9), y(11)-98, y(11), y(12), y(12)-98, y(13)-98, y(13), y(13)++, y(14), y(14)-98, y(14)-98++, y(15)-98++, y(15)++, y(15), y(15)-98, y(16)-98++, y(16)-98, y(16)++, y(17)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1384

NSVVSPVVGAGGDSSKEDR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVGAGGDSSKEDR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 3501: 1938.867081 from(647.296303,3+)  
Elution from: 28.565 to 28.565 scan no 2436 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1938.8683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 3.8e-006
Matched b ions: b(3), b(4), b(5), b(14)++
Matched y ions: y(6)++, y(8)++, y(11)−98, y(11)++, y(12)−98, y(12)++, y(12)−98++, y(13)−98++, y(13)++, y(14)++, y(14)−98++, y(15)−98++, y(15)++, y(16)++, y(16)−98++, y(17)−98++, y(17)++, y(17)−98++, y(18)++
Precursor origin neutral loss:

Peptide No.1385

NSVVSPVVGAGGDSSKEDR
Confirmed sites: "@S:2,@S:14"
Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVGAGGDSSKEDR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 3465: 2018.833344 from(1010.423948,2+) Elution from: 31.352 to 31.352 scan no 2830 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2018.8346
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 6.7e-005
Matched b ions: b(5)-98, b(7)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(13)-98, b(13), b(14)-98, b(16)++, b(16)-196++, b(16)-98++, b(18), b(18)-98++
Matched y ions: y(3), y(5), y(6)-98++, y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13), y(13)++, y(13)-98, y(14)-98, y(14), y(14)-98++, y(14)++, y(15), y(17)-98++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1386
NSVVSPVVGAGGDSSKEDR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVGAGGDSSKEDR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 3608: 1938.866073 from(647.295967,3+)
Elution from: 30.093 to 30.093 scan no 2654 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1938.8683

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S5: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 32 Expect: 0.0062

Matched b ions: b(3), b(5)+, b(9)-98, b(13)+, b(16)-98++, b(16)+

Matched y ions: y(4), y(6), y(11)+, y(12)+, y(14)+, y(15)+, y(15)-98++, y(16)-98++, y(16)+, y(17)+, y(17)-98++

Precursor origin neutral loss:

Peptide No.1387

NSVVSPVVAGGDSSKEDR

Confirmed sites: "@S:5,@S:14"

Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVAGGDSSKEDR

Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 2968: 2018.834187 from(673.952005,3+) Elution from: 31.272 to 31.272 scan no 2757 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2018.8346
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 5.5e-007
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5)+, b(6)-98++, b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-
98, b(11)-98, b(13)+, b(16)+, b(16)-98++, b(18)-196++
Matched y ions: y(2), y(5)+, y(5), y(6)+, y(6), y(7)+, y(8)-98++, y(9)-98++, y(9), y(9)+, y(10), y
(10)+, y(11)+, y(11)-98, y(11), y(11)-98++, y(12)-98++, y(12)-98, y(12)+, y(13)-98++, y(13)+, y
(14)+, y(14)-98++, y(15)-98++, y(15)+, y(15)-196++, y(16)-196++, y(16)+, y(16)-98++, y(17)-
98++, y(17)+, y(17)-196++, y(18)++
Precursor origin neutral loss: +

Peptide No.1388

NSVVSPVVGAGGDSKEDR
Confirmed sites: "@S:5,@S:15"
Ambiguous sites:

MS/MS Fragmentation of NSVVSPVVGAGGDSKEDR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic
acid binding / nucleotide

Match to Query 3340: 2018.832393 from(673.951407,3+)
Elution from: 32.323 to 32.323 scan no 2922 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2018.8346
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 6.8e-005
Matched b ions: b(2), b(3), b(4), b(5)++, b(5)−98, b(6)−98++, b(7), b(8)−98++, b(8), b(8)−98, b(10)−98, b(11)−98, b(14)++, b(15)−196++, b(16)++, b(16)−98++, b(16)−196++, b(17)−98++, b(18)++, b(18)−98++
Matched y ions: y(2), y(5)−98, y(6)++, y(6), y(6)−98, y(9)++, y(9)−98++, y(9)−98, y(10)++, y(11)+, y(11)−98, y(11)−98++, y(12)−98++, y(12), y(12)−98, y(12)++, y(13)−98, y(13)−98++, y(13)++, y(13)−98, y(14)−98++, y(15)−98++, y(15)−98++, y(15)++, y(16)++, y(16)−196++, y(16)−98++, y(17)−98++, y(17)+, y(17)−98++, y(17)−98, y(18)++, y(18)−98, y(18)−98++, y(18)−98, y(18)−98++, y(18)−98++
Precursor origin neutral loss: +

Peptide No.1389
NTEEDDGSGNGGGQLYVSLK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NTEEDDGSGNGGGQLYVSLK
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 4071: 2233.898944 from(1117.956748,2+)
Elution from: 41.794 to 41.794 scan no 4226 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2233.9011

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 98 Expect: 1.3e-009

Matched b ions: b(7), b(9)–98, b(9), b(13)–98, b(15), b(16)–98, b(17)–98, b(17), b(18)–98, b(18), b(20)–98

Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14)–98, y(14), y(15), y(16), y(16)–98, y(17), y(18)++, y(19)–98++, y(19)++, y(20)++, y(20)–98++

Precursor origin neutral loss: +

Peptide No.1390

NTEEGEMVNNVSPMMHSR

Confirmed sites: @S:13

Ambiguous sites:

MS/MS Fragmentation of NTEEGEMVNNVSPMMHSR

Found in AT5G45190.1, cyclin family protein

Match to Query 4406: 2254.880247 from(752.634025,3+)

Elution from: 37.237 to 37.237 scan no 3510 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2254.8806
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 8.8e-006
Matched b ions: b(5), b(6), b(12), b(14)++, b(15)++, b(17)−98++
Matched y ions: y(3), y(4), y(7)++, y(8)−98++, y(8), y(9)++, y(10)++, y(11)++, y(11)−98++, y(12)−98++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)−98++
Precursor origin neutral loss:

Peptide No.1391
NTGRVSPAVIDPPSPR
Confirmed sites: “@S:6, @S:13”
Ambiguous sites:
MS/MS Fragmentation of NTGRVSPAVIDPPSPR
Found in AT1G80180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15400.3); similar to Os06g0601100 [Oryz

Match to Query 2892: 1708.730674 from(855.372613,2+)
Elution from: 27.738 to 27.738 scan no 2232 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1708.7335
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00018
Matched b ions: b(3), b(6)-98, b(9), b(10)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(9), y(10), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1392

NTGRVSPAVDPPSPR
Confirmed sites: "@T:2,@S:13"
Ambiguous sites:

MS/MS Fragmentation of NTGRVSPAVDPPSPR
Found in AT1G80180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15400.3); similar to Os06g0601100 [Oryz
Match to Query 3081: 1708.731756 from(570.584528,3+)
Elution from: 26.271 to 26.271 scan no 2191 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1708.7335
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.011
Matched b ions: b(4), b(7), b(8)++, b(8), b(9)−98++, b(9), b(9)+, b(9)−98, b(10)+, b(10)−98++, b(11)−98++, b(13)−98++, b(14)−196++
Matched y ions: y(2), y(3), y(4)−98, y(4), y(5)+, y(5), y(5)−98, y(6), y(6)+, y(7)−98++, y(7)−98, y(7), y(7)+, y(9)−98, y(9)+, y(11)−98++, y(12)+, y(13)−98++, y(14)−98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1393

NTSQTPVEVGELVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NTSQTPVEVGELVR
Found in AT1G67580.1, protein kinase family protein

Match to Query 2197: 1508.686872 from(755.350712,2+)   
Elution from: 40.471 to 40.471 scan no 3831 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1508.6871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.003
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(9)+, b(10)-98++, b(10), b(10)-98, b(12)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(8)+, y(9), y(10), y(11)-98++, y(11), y(12)+
Precursor origin neutral loss: +

Peptide No.1394

NTSQTPVEVGELVR
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of NTSQTPVEVGELVR
Found in AT1G67580.1, protein kinase family protein

Match to Query 1988: 1508.685942 from(755.350247,2+)
Elution from: 39.442 to 39.442 scan no 3877 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1508.6871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00039
Matched b ions: b(4)-98, b(5), b(5)-98, b(7), b(8)-98, b(8)++, b(8), b(9)++, b(10)-98, b(12)
Matched y ions: y(2), y(3), y(5), y(6), y(8), y(9), y(10), y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1395

NVDSLSPENDSSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NVDSLSPENDSSR
Found in AT1G21580.1, hydroxyproline–rich glycoprotein family protein

Match to Query 1500: 1498.591152 from(750.302852,2+)
Elution from: 25.228 to 25.228 scan no 1965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1498.5937
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.014
Matched b ions: b(6)-98, b(10)
Matched y ions: y(7), y(8), y(8)-98, y(8)++, y(9)++, y(10)-98, y(10), y(11)-98, y(11), y(11)++, y(12)++
y(12)-98, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1396

NVDVGDALISQSPK
Confirmed sites: “@S:10, @S:12”
Ambiguous sites:

MS/MS Fragmentation of NVDVGDALISQSPK
Found in AT5G45190.1, cyclin family protein

Match to Query 2709: 1601.671936 from(801.843244,2+)
Elution from: 44.323 to 44.323 scan no 4566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1601.6739
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00015
Matched b ions: b(4), b(7), b(8), b(9), b(11)-98
Matched y ions: y(5), y(6)-98, y(7), y(8), y(9)--196, y(9), y(10)+, y(10)-98, y(10), y(11)-98++, y(11), y(11)-98, y(12), y(12)+, y(12)-98++, y(13)-98++, y(13)-196++, y(13)+
Precursor origin neutral loss: +

Peptide No.1397

NVDVGDALISQSPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of NVDVGDALISQSPK
Found in AT5G45190.1, cyclin family protein

Match to Query 2018: 1521.706456 from(761.860504,2+)
Elution from: 42.058 to 42.058 scan no 4223 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1521.7076
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 9.5e-009
Matched b ions: b(3), b(4), b(7), b(8), b(9), b(10), b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)
++, y(13)-98++, y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.1398

NVEPSSSPEVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NVEPSSSPEVR
Found in AT1G15940.1, similar to binding [Arabidopsis thaliana] (TAIR:AT1G80810.1); similar to Tudor [Medicago truncatula]

Match to Query 1061: 1279.543608 from(640.779080,2+)^+
Elution from: 21.179 to 21.179 scan no 1445 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1279.5445
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.039
Matched b ions: b(2), b(5)
Matched y ions: y(4), y(7), y(8), y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.1399

NVFGSSDDDEAEYVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of NVFGSSDDDEAEYVR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 3089: 1910.718896 from(956.366724,2+)
Elution from: 45.635 to 45.635 scan no 4721 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1910.7207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 1.3e-009
Matched b ions: b(9), b(10), b(10)–98, b(11)–98, b(12)–98, b(12), b(13), b(15), b(15)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)–98, y(13), y(13)–98++, y(14)–98++, y(14), y(14)++, y(15)–98, y(15)–98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1400

NVFGSSDDEDAEYVR
Confirmed sites: “@S:5,@S:6”
Ambiguous sites:

MS/MS Fragmentation of NVFGSSDDEDAEYVR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 3438: 1990.684766 from(996.349659,2+)
Elution from: 52.672 to 52.672 scan no 5566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1990.6870
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 1.4e-005
Matched b ions: b(8), b(8)-98, b(9), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(11), y(12)-98++, y(12)-196, y(13)-98, y(13)-196, y(14), y(14)-196++, y(14)+++, y(14)-98++, y(15)-98++, y(15)+, y(15)-196++
Precursor origin neutral loss: +

Peptide No.1401
NVFGSSDDDEAEEYVR
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of NVFGSSDDDEAEEYVR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)
Match to Query 2803: 1910.719568 from(956.367060,2+)
Elution from: 47.161 to 47.161 scan no 4803 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1910.7207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 2.2e–005
Matched b ions: b(10), b(12), b(15)
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(11), y(13), y(14)+, y(15)–98++, y(15)+
Precursor origin neutral loss:

Peptide No.1402

NVSLDSHDENSDQEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NVSLDSHDENSDQEK
Found in AT5G47690.1, binding

Match to Query 2217: 1795.687848 from(898.851200,2+) Elution from: 20.194 to 20.194 scan no 1320 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1795.6897
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 7.8e-007
Matched b ions: b(5), b(7), b(8), b(9), b(11)-98, b(12)-98, b(12), b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)++, y(11), y(11)-98, y(12)++, y(13)-98++, y(13)-98, y(13)++, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No. 1403

NVSLDSHDENSQEK
Confirmed sites: “@S:3, @S:11”
Ambiguous sites:

MS/MS Fragmentation of NVSLDSHDENSQEK
Found in AT5G47690.1, binding

Match to Query 3414: 1875.652960 from(938.833756,2+) Elution from: 22.855 to 22.855 scan no 1582 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1875.6561
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3  : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 Expect: 0.064
Matched b ions: b(7)-98, b(7), b(10), b(11)-98, b(12), b(13)-98, b(14)-98, b(14), b(14)-98++
Matched y ions: y(3), y(8), y(10)+, y(12)+, y(13)-98++, y(13)-196++, y(13)+++, y(14)-196++, y(14) ++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1404

NVSLDSHDENSDQEK
Confirmed sites: ”@S:3,@S:6,@S:11”
Ambiguous sites:

MS/MS Fragmentation of NVSLDSHDENSDQEK
Found in AT5G47690.1, binding

Match to Query 3637: 1955.620988 from(978.817770,2+)
Elution from: 23.871 to 23.871 scan no 1839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1955.6224
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(show in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(show in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(show in table), 97.9769
Ions Score: 24 Expect: 0.006
Matched b ions: b(7)-98, b(7), b(8)-98, b(8)-196, b(8), b(9), b(9)-196, b(13)++, b(14)++
Matched y ions: y(7), y(7)-98, y(10), y(11)-98, y(12), y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1405

NVSLDSHDENSEDQEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of NVSLDSHDENSEDQEK
Found in AT5G47690.1, binding

Match to Query 2180: 1795.688812 from(898.851682,2+)
Elution from: 20.289 to 20.289 scan no 1316 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1795.6897  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 49 Expect: 7.2e-005  
Matched b ions: b(5), b(6)–98, b(7)–98, b(7), b(8)–98, b(9)–98, b(11)–98, b(12)–98, b(12), b(13), b(13)–98, b(14)–98++, b(14)++  
Matched y ions: y(3), y(4), y(7), y(10)–98, y(10), y(11), y(11)–98, y(12), y(12)–98++, y(13)–98++, y(13)++, y(14)++, y(14)–98++  
Precursor origin neutral loss: +

Peptide No. 1406  

NVSLDSHDENSDQEK  
Confirmed sites: "@S:6,@S:11"  
Ambiguous sites:  

MS/MS Fragmentation of NVSLDSHDENSDQEK  
Found in AT5G47690.1, binding  

Match to Query 2435: 1875.654880 from(938.834716,2+)  
Elution from: 22.504 to 22.504 scan no 1540 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1875.6561
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00032
Matched b ions: b(5), b(6), b(7)–98, b(7), b(8), b(8)–98, b(9), b(10), b(12)–98, b(14)–98++, b(14)++
Matched y ions: y(3), y(4), y(5)–98, y(5), y(6)–98, y(6), y(7)–98, y(8), y(9), y(10), y(10)–98++, y(12),
y(12)–196++, y(12)–98++, y(13)–98++, y(13)–196++, y(13)++, y(14)–196++, y(14)++, y(14)–98++
Precursor origin neutral loss: +

Peptide No. 1407

NVTDSFADDNVITKGDSTVTYR
Confirmed sites: ”@T:3,@Y:21”
Ambiguous sites: @S:18 or T:19

MS/MS Fragmentation of NVTDSFADDNVITKGDSTVTYR
Found in AT2G30940.1, protein kinase family protein

Match to Query 4757: 2643.015207 from(882.012345,3+)
Elution from: 36.244 to 36.244 scan no 3488 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2643.0179
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y21 : Phospho (Y)
Ions Score: 33 Expect: 0.004
Matched b ions: b(8), b(11)++, b(12)++, b(12)−98++, b(12)−98, b(14)++, b(14), b(17)++, b(20)++
Matched y ions: y(5)++, y(5)−98, y(5), y(8), y(10)++, y(10), y(11), y(12)−98, y(12)++, y(12)−98++, y(13)++, y(13), y(14)++, y(14)−98++, y(15)−98++, y(15)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)−98++
Precursor origin neutral loss:

Peptide No.1408
NVVLDEFGSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NVVLDEFGSPK
Found in AT2G28000.1, CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded pr

Match to Query 1034: 1283.578042 from(642.796297,2+)
Elution from: 44.146 to 44.146 scan no 4371 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1283.5798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00018
Matched b ions: b(2), b(3), b(4)++, b(5), b(7), b(8)
Matched y ions: y(3)−98, y(3), y(4), y(5), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10)−98
Precursor origin neutral loss: +

Peptide No.1409

NVVTWTAMVSGYLRSK
Confirmed sites: "@T:4,@T:6,@S:10,@S:15"
Ambiguous sites:

MS/MS Fragmentation of NVVTWTAMVSGYLRSK
Found in AT2G35030.1, pentatricopeptide (PPR) repeat-containing protein

Match to Query 3802: 2130.802302 from(711.274710,3+)
Elution from: 49.157 to 49.157 scan no 5140 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2130.8052
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.038
Matched b ions: b(5)−98, b(8)++, b(9)−98++, b(9)++, b(11)++, b(13)−294++, b(14)++, b(15)++, b(15)−98++
Matched y ions: y(12)++, y(12)−294++, y(13)++, y(14)−294++, y(14)−196++, y(14)−98++, y(15)−392++, y(15)−294++, y(15)−196++
Precursor origin neutral loss:

Peptide No.1410

NYSRSPPPYR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of NYSRSPPPYR
Found in AT2G24590.1, splicing factor, putative

Match to Query 2089: 1395.536244 from(698.775398,2+)
Elution from: 23.277 to 23.277 scan no 1763 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1395.5373
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.022
Matched b ions: b(3)-98, b(3), b(4), b(5), b(5)-196, b(5)-98, b(6)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)+, y(7), y(7)-98++, y(8), y(8)-98++, y(9)-98++, y(9)
Precursor origin neutral loss: +

Peptide No.1411

NYSRSPPPYR
Confirmed sites: "@Y:2,@S:5"
Ambiguous sites:

MS/MS Fragmentation of NYSRSPPPYR
Found in AT2G24590.1, splicing factor, putative

Match to Query 2192: 1395.536248 from(698.775400,2+)
Elution from: 22.703 to 22.703 scan no 1702 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1395.5373
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0016
Matched b ions: b(4), b(5), b(5)−98, b(6), b(6)−98, b(7)−98, b(7), b(8)−98, b(9)−98, b(9), b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(7)−98++, y(8)−98++, y(9)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1412

PLSYSSPSSSEER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1966: 1504.607254 from(753.310903,2+)  
Elution from: 26.611 to 26.611 scan no 2185 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1504.6082
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 9.6e-006
Matched b ions: b(3), b(4), b(5), b(6), b(11)−98, b(12)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(10)++, y(11)−98, y(11), y(11)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1413
PLSYSSPSSSEER
Confirmed sites: @S:3
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1774: 1584.572792 from(793.293672,2+)  
Elution from: 28.649 to 28.649 scan no 2317 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 23 Expect: 0.019
Matched b ions: b(3)−98, b(3), b(4)−98, b(6)−196, b(6)−98, b(7)−196
Matched y ions: y(2), y(4), y(5)+, y(6), y(9), y(10), y(11), y(11)−98, y(12)−196++, y(12)+, y(12)−98++
Precursor origin neutral loss: +

Peptide No.1414

PLSYSSPSSSEER
Confirmed sites: "@S:3,@S:9"
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 2430: 1584.572618 from(793.293585,2+)
Elution from: 28.832 to 28.832 scan no 2262 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0047
Matched b ions: b(4)–98, b(5)
Matched y ions: y(4), y(5), y(6), y(7)–98, y(8), y(9), y(10), y(11)–98, y(11), y(11)–98++, y(11)–196++, y(12)++, y(12)–98++
Precursor origin neutral loss: +

Peptide No.1415

PLSYSSPSSSEER
Confirmed sites: "@S:3,@S:9"
Ambiguous sites: @Y:4orS:5

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1944: 1664.540266 from(833.277409,2+)
Elution from: 30.410 to 30.410 scan no 2578 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1664.5409
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  Y4 : Phospho (Y)
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.012
Matched b ions: b(5)++, b(6), b(7)−98, b(8)−98
Matched y ions: y(2), y(4), y(5), y(7), y(10), y(11)−98++, y(11)−98, y(12)++, y(12)−196++, y(12)−98++
Precursor origin neutral loss: +

Peptide No.1416

PLSYSSPSSSEER
Confirmed sites:
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 2544: 1504.607226 from(753.310889,2+)
Elution from: 25.560 to 25.560 scan no 2093 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1504.6082
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00019
Matched b ions: b(3), b(4), b(7)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(5)+, y(5), y(6), y(7), y(9), y(9)-98, y(10), y(10)+, y(11), y(11)-98, y(11)-98++, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.1417
PLSYSSPSSSEEER
Confirmed sites: @S:5
Ambiguous sites: @S:10orS:9

MS/MS Fragmentation of PLSYSSPSSSEEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)
Match to Query 2523: 1584.572964 from(793.293758,2+) Elution from: 29.487 to 29.487 scan no 2641 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.05
Matched b ions: b(6)–98, b(8)
Matched y ions: y(5), y(7), y(8), y(9), y(9)–196, y(11)–98, y(11), y(11)++, y(12)–98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1418

PLSYSSPSSSEER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1511: 1504.606908 from(753.310730,2+)
Elution from: 25.655 to 25.655 scan no 2022 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1504.6082
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.3e-007
Matched b ions: b(4), b(6)–98, b(6), b(7)–98, b(9)–98, b(12)–98++
Matched y ions: y(2), y(3), y(4), y(5)+, y(6), y(7), y(8)–98, y(8), y(9), y(9)–98, y(11)–98, y(11), y(11)–98++, y(11)+, y(12)–98, y(12)+
Precursor origin neutral loss: +

Peptide No.1419

PLSYSSPSSSEER
Confirmed sites: @S:6
Ambiguous sites: @S:10 or S:9

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1773: 1584.571852 from(793.293202,2+)
Elution from: 29.986 to 29.986 scan no 2495 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
Ions Score: 19 Expect: 0.037  
Matched b ions: b(3), b(11)−98++, b(11)−196  
Matched y ions: y(5), y(6), y(7), y(8), y(8)−196, y(9), y(11)−98, y(11), y(12)−98++, y(12)++  
Precursor origin neutral loss: +

Peptide No.1420

PLSYSSPSSSEER  
Confirmed sites: “@S:6, @S:8”  
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER  
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 2222: 1584.573350 from(793.293951,2+)  
Elution from: 28.943 to 28.943 scan no 2524 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 56 Expect: 9.2e-006  
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8)-196, b(9)-196, b(9)-98, b(9)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(12), b(12)-98  
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)-98, y(7)-98, y(7), y(8)++, y(8), y(8)-98, y(8)-98++, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(11), y(11)-98, y(11)-98++, y(11)++, y(11)-196, y(12)++, y(12)-98++  
Precursor origin neutral loss: +

Peptide No.1421

PLSYSSPSSSEER  
Confirmed sites: "@S:6,@S:9"  
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER  
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1747: 1584.573126 from(793.293839,2+)  
Elution from: 28.321 to 28.321 scan no 2391 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 1.1e-006
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(8), b(9)-98, b(9)-196, b(9)-98++, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)+, y(8), y(8)-98, y(8)-196, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(11), y(11)-98, y(11)-196++, y(11)+, y(11)-98++, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1422
PLSYSSPSSSEER
Confirmed sites: ＊@S:8,@S:10＊
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 1697: 1584.572586 from(793.293569,2+)
Elution from: 29.468 to 29.468 scan no 2533 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.5746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 8.7e-005
Matched b ions: b(4), b(8), b(9)–98++
Matched y ions: y(2), y(4), y(5), y(6), y(6)–98, y(7)–98, y(7), y(7)–196, y(8), y(9)–98, y(10), y(12)–98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1423

PLSYSSPSSSEER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of PLSYSSPSSSEER
Found in AT4G07523.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27180.1)

Match to Query 2235: 1504.606542 from(753.310547,2+)
Elution from: 27.758 to 27.758 scan no 2235 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1504.6082
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.1e-006
Matched b ions: b(3), b(5), b(6), b(7), b(9)−98, b(12), b(12)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(11)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1424

PSSFFFEDASDDELELIR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of PSSFFFEDASDDELELIR
Found in AT4G16630.1, DEAD/DEAH box helicase, putative (RH28)

Match to Query 4026: 2195.925034 from(1098.969793,2+)
Elution from: 71.899 to 71.899 scan no 7302 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2195.9299
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 3.3e-005
Matched b ions: b(7), b(8), b(11)–98, b(15), b(17)–98
Matched y ions: y(6), y(9)–98, y(10)–98, y(11)–98, y(11), y(12)–98, y(13), y(14)–98, y(15), y(17)++
Precursor origin neutral loss: +

Peptide No.1425

QANESPSSLLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QANESPSSLLK
Found in AT5G18620.1, CHR17 (CHROMATIN REMODELING FACTOR17); DNA–dependent ATPase

Match to Query 1176: 1252.569028 from(627.291790,2+)
Elution from: 34.451 to 34.451 scan no 3243 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1252.5700
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0045
Matched b ions: b(5), b(6)—98, b(7), b(9), b(10)—98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No. 1426

QANESPSSLLK
Confirmed sites: @S:5 or S:7
Ambiguous sites: @S:5 or S:7

MS/MS Fragmentation of QANESPSSLLK
Found in AT5G18620.1, CHR17 (CHROMATIN REMODELING FACTOR17); DNA-dependent ATPase

Match to Query 1115: 1252.569904 from(627.292228,2+) Elution from: 34.518 to 34.518 scan no 3251 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1252.5700
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.016
Matched b ions:
Matched y ions: y(2), y(3), y(4), y(7), y(8), y(9)−98++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1427
QDESALSPER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of QDESALSPER
Found in AT5G14720.1, protein kinase family protein

Match to Query 913: 1210.485786 from(606.250169,2+)  
Elution from: 21.279 to 21.279 scan no 1458 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1210.4867
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0017
Matched b ions: b(4)
Matched y ions: y(3), y(4), y(5), y(5)−98, y(6), y(6)−98, y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1428

QDNSRNLSQSVNGNK
Confirmed sites: "@S:4,@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of QDNSRNLSQSVNGNK
Found in AT1G48280.1, hydroxyproline-rich glycoprotein family protein

Match to Query 2475: 1899.689742 from(634.237190,3+)
Elution from: 22.772 to 22.772 scan no 1654 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1899.6914
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.056
Matched b ions: b(5), b(6), b(6)+, b(9)+, b(9)+98++, b(10)-196++, b(11)+, b(11)-294++, b(13)+, b(13)-98++, b(13)-196++, b(14)+, b(14)-98++
Matched y ions: y(2), y(8)+, y(9), y(9)-196++, y(9)+, y(9)-98++, y(10), y(10)-98++, y(10)-196++, y(10)+, y(11)-196++, y(12)+, y(12)-98++, y(13)-294++, y(13)+
Precursor origin neutral loss: +

Peptide No.1429
QDQSSPINFEMSSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QDQSSPINFEMSSR
Found in AT5G40300.1, integral membrane protein, putative

Match to Query 2884: 1704.681060 from(853.347806,2+)
Elution from: 41.424 to 41.424 scan no 4066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1704.6814
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0012
Matched b ions: b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss:

Peptide No.1430
QDTSGEFSAASPER
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of QDTSGEFSAASPER
Found in AT5G05170.1, CESA3 (CELLULASE SYNTHASE 3); cellulose synthase/ transferase, transferring glycosyl groups

Match to Query 2178: 1560.607368 from(781.310960,2+)
Elution from: 26.079 to 26.079 scan no 2111 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1560.6093
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 1.5e-006
Matched b ions: b(6), b(7), b(9), b(10), b(11)−98
Matched y ions: y(3), y(4), y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)+, y(8)−98, y(9)−98, y(10), y(11), y(11)+, y(12), y(12)+
Precursor origin neutral loss: +

Peptide No.1431
QDVESTEDSEDEDILK
Confirmed sites: @S:9
Ambiguous sites:
MS/MS Fragmentation of QDVESTEDSEDEDILK
Found in AT1G67310.1, calmodulin binding / transcription regulator

Match to Query 3280: 1930.755618 from(966.385085,2+) Elution from: 38.196 to 38.196 scan no 3745 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1930.7568
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 2.9e-006
Matched b ions: b(4), b(8), b(12), b(13)–98, b(13), b(15), b(15)–98++, b(15)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9), y(9)–98, y(10)–98, y(10), y(11), y(11)–98, y(12), y(12)–98, y(13)++, y(13), y(14)–98++, y(14)++, y(14)
Precursor origin neutral loss: +

Peptide No.1432
QESDGEEPVSLSQQPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QESDGEEPVSLSQQPK
Found in AT1G76380.1, DNA-binding bromodomain-containing protein

Match to Query 2287: 1836.774014 from(919.394283,2+)
Elution from: 30.444 to 30.444 scan no 2660 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1836.7778  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 24 Expect: 0.041  
Matched b ions: b(9)-98  
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(12)  
Precursor origin neutral loss: +

Peptide No.1433

QESTDSLAVGSPPK  
Confirmed sites: @S:11  
Ambiguous sites:

MS/MS Fragmentation of QESTDSLAVGSPPK  
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty-ac  
Match to Query 2202: 1494.659646 from(748.337099,2+))  
Elution from: 31.674 to 31.674 scan no 2763 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1494.6603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 7.4e-006
Matched b ions: b(5), b(8), b(9), b(11)–98, b(13)++
Matched y ions: y(3), y(4), y(5)–98, y(5), y(6)–98, y(6), y(7), y(7)–98, y(8), y(9), y(9)–98, y(10), y (11), y(12)
Precursor origin neutral loss: +

Peptide No.1434
QESTDSLAVGSPPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QESTDSLAVGSPPK
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty-ac

Match to Query 1486: 1494.659284 from(748.336918,2+)
Elution from: 29.530 to 29.530 scan no 2541 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1494.6603
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00066
Matched b ions: b(4)-98, b(5)-98, b(8)-98, b(9)-98, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9)++, y(10)++, y(11)
Precursor origin neutral loss: +

Peptide No.1435
QESTDSLAVGSPPK
Confirmed sites: @S:11
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of QESTDSLAVGSPPK
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1);
similar to Cytosolic fatty-ac

Match to Query 2188: 1574.625604 from(788.320078,2+)
Elution from: 34.663 to 34.663 scan no 3285 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1574.6266
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.024
Matched b ions: b(5), b(7)-98, b(8)-98, b(9)-98, b(11)-98
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.1436

QESTDSLAVGSPPKSEGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of QESTDSLAVGSPPKSEGR
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty–ac

Match to Query 3197: 1923.855822 from(642.292550,3+)  
Elution from: 26.691 to 26.691 scan no 2196 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1923.8575
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00024
Matched b ions: b(11)-98, b(15)+, b(16)-98++
Matched y ions: y(2), y(4), y(6)+, y(6), y(7)+, y(7), y(8)-98, y(8)-98++, y(8), y(9)+, y(9)-98++, y(9)-98, y(10)-98++, y(10)+, y(10)-98, y(11)+, y(11)-98++, y(12)-98++, y(13)+, y(13)-98++, y(14)+, y(15)+, y(16)+, y(16)-98++
Precursor origin neutral loss:

Peptide No. 1437
QESTDSLAVGSPPKSEGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QESTDSLAVGSPPKSEGR
Found in AT1G59710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to Cytosolic fatty-ac

Match to Query 3101: 1923.856569 from(642.292799,3+)
Elution from: 27.654 to 27.654 scan no 2293 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1923.8575
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0076
Matched b ions: b(6)-98, b(7)+, b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(17)-98++
Matched y ions: y(2), y(4), y(5), y(7)+, y(7), y(9), y(11)+, y(13)+, y(14)+, y(15)+, y(16)+
Precursor origin neutral loss:

Peptide No.1438
QFSTGSLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QFSTGSLR
Found in AT2G31800.1, ankyrin protein kinase, putative

Match to Query 527: 974.421978 from(488.218265,2+)
Elution from: 31.471 to 31.471 scan no 2621 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 974.4222
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.011
Matched b ions: b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98++
Precursor origin neutral loss: +

Peptide No.1439

QGDFPHLTSQNSWGTK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of QGDFPHLTSQNSWGTK
Found in AT5G42950.1, GYF domain-containing protein

Match to Query 3163: 1881.803010 from(628.274946,3+)
Elution from: 41.071 to 41.071 scan no 4128 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1881.8047
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0077
Matched b ions: b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)--98, y(7)--98, y(7), y(8), y(9), y(10)++, y(11)++, y(12)++, y(12)--98++, y(13)--98++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1440
QGLRNAVTEASGTGGYARASAK
Confirmed sites: ”@T:13,@Y:16”
Ambiguous sites:

MS/MS Fragmentation of QGLRNAVTEASGTGGYARASAK
Found in AT1G70520.1, protein kinase family protein

Match to Query 4528: 2324.030709 from(775.684179,3+)
Elution from: 32.246 to 32.246 scan no 2841 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2324.0310  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Y16 : Phospho (Y)  
Ions Score: 24 Expect: 0.048  
Matched b ions: b(6), b(7), b(8), b(11)+, b(12)+, b(13)+, b(13)−98++, b(15)+, b(16)+, b(18)+, b(19)−98++, b(20)+, b(20)−98++, b(21)+, b(21)−98++  
Matched y ions: y(7), y(10), y(13)+, y(14)+, y(15)−98++, y(19)+  
Precursor origin neutral loss: +

Peptide No.1441

QGSGGVWGWLAGSPQEKKDDSP  
Confirmed sites: @S:21  
Ambiguous sites:  

MS/MS Fragmentation of QGSGGVWGWLAGSPQEKKDDSP  
Found in AT3G05420.1, ACBP4 (ACYL-COA BINDING PROTEIN 4, ACYL-COA-BINDING DOMAIN 4); acyl-CoA binding

Match to Query 4306: 2351.967476 from(1176.991014,2+)  
Elution from: 62.644 to 62.644 scan no 6678 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2351.9695
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 1e-005
Matched b ions: b(12), b(13), b(21)+, b(21)−98++
Matched y ions: y(5), y(6), y(7), y(8), y(9)−98, y(9), y(11)+, y(11), y(11)−98, y(12), y(13), y(14), y(15)−98, y(15), y(16), y(16)+, y(16)−98++, y(17)−98++, y(18)+, y(19)+, y(19)−98++, y(21)−98++
Precursor origin neutral loss: +

Peptide No.1442
QGSGIIGTFGQSEELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QGSGIIGTFGQSEELR
Found in AT5G15070.1, acid phosphatase

Match to Query 2664: 1757.796586 from(879.905569,2+)
Elution from: 51.300 to 51.300 scan no 5416 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1757.7985  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 70 Expect: 8.6e-007  
Matched b ions: b(3), b(5), b(5)−98, b(6)−98, b(6), b(7)−98, b(9)−98  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(12)++, y(13)  
Precursor origin neutral loss: +  

Peptide No.1443  
QGSLTLPR  
Confirmed sites: @T:5  
Ambiguous sites:  

MS/MS Fragmentation of QGSLTLPR  
Found in AT1G45249.1, ABF2 (ABSCISIC ACID RESPONSIVE ELEMENTS–BINDING FACTOR 2)  

Match to Query 389: 950.456988 from(476.235770,2+)  
Elution from: 32.775 to 32.775 scan no 3018 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 950.4586
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.028
Matched b ions: b(3), b(4), b(6)--98
Matched y ions: y(2), y(3), y(4)--98, y(6)--98, y(7)++
Precursor origin neutral loss: +

Peptide No.1444

QGSSGIVFDDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QGSSGIVFDDR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80180.1);
similar to Os06g0601100 [Oryz]

Match to Query 1116: 1259.517760 from(630.766156,2+)
Elution from: 35.500 to 35.500 scan no 3316 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.5183
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 2.9e-005
Matched b ions: b(5), b(6)--98, b(6), b(7), b(7)--98, b(10)--98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1445

QGSSGIVFDDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of QGSSGIVFDDR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80180.1); similar to Os06g0601100 [Oryz]

Match to Query 1716: 1259.517682 from(630.766117,2+)  
Elution from: 35.596 to 35.596 scan no 3464 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1259.5183
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00016
Matched b ions: b(6)-98, b(7)-98, b(9), b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(8)+, y(9)-98, y(10)-98
Precursor origin neutral loss: +

Peptide No.1446

QGSSGIVWDDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QGSSGIVWDDR
Found in AT1G80180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15400.3);
similar to Os06g0601100 [Oryz]

Match to Query 1155: 1298.527380 from(650.270966,2+)
Elution from: 38.946 to 38.946 scan no 3652 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1298.5292
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 51 Expect: 3.8e-005
Matched b ions: b(4)-98, b(6)-98, b(7), b(7)-98, b(8), b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++
Precursor origin neutral loss: +

Peptide No.1447

QGSSGIVWDDR
Confirmed sites: @S:3orS:4
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of QGSSGIVWDDR
Found in AT1G80180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15400.3); similar to Os06g0601100 [Oryz]

Match to Query 1786: 1298.528278 from(650.271415,2+)  
Elution from: 38.581 to 38.581 scan no 3823 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1298.5292
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.016
Matched b ions:
Matched y ions: y(2), y(3), y(4), y(5)
Precursor origin neutral loss: +

Peptide No.1448
QGTASETDYVTDGGSDSDDSPKK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of QGTASETDYVTDGGSDSDDSPKK
Found in AT2G16480.1, SWIB complex BAF60b domain–containing protein / plus–3 domain–containing protein

Match to Query 3522: 2410.960956 from(804.660928,3+)
Elution from: 24.835 to 24.835 scan no 1815 polarity:+
Peptide No. 1449

QGYFSMNKINNGLRSLSSR
Confirmed sites: "@Y:3,@S:15"
Ambiguous sites: @S:17 or S:18

MS/MS Fragmentation of QGYFSMNKINNGLRSLSSR
Found in AT4G03470.1, ankyrin repeat family protein

Match to Query 4173: 2426.989128 from (607.754558, 4+)
Elution from: 21.861 to 21.861 scan no 1509 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 2426.9844
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3: Phospho (Y)
M6: Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
S15: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S18: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 22 Expect: 0.063
Matched b ions: b(4), b(6), b(6)+, b(7)+, b(7)+, b(8)+, b(9)+, b(10)+, b(16)+
Matched y ions: y(6)+98, y(9)+98++, y(9)+, y(10)+98++, y(10)+, y(12)+, y(12)+98++, y(13)+98++, y(14)+, y(16)+98+
Precursor origin neutral loss: +

Peptide No. 1450

QHSWSPDADREEAWLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QHSWSPDADREEAWLR
Found in AT4G33985.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G15590.2);
similar to Os04g0282200 [Oryz]

Match to Query 3766: 2061.868179 from(688.296669,3+)
Elution from: 41.779 to 41.779 scan no 4247 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2061.8694  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 36 Expect: 0.0024  
Matched b ions: b(3), b(6), b(9)+98++, b(9)+, b(13)+  
Matched y ions: y(4), y(6)+, y(7)+++, y(8)+, y(9)+, y(11)+++, y(12)+, y(13)+++, y(14)+++, y(14)+98++  
Precursor origin neutral loss:   

Peptide No.1451  
QIGLTSTSSPK  
Confirmed sites: @S:9  
Ambiguous sites:   

MS/MS Fragmentation of QIGLTSTSSPK  
Found in AT3G61480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28350.2); similar to unknown protein [O  

Match to Query 1210: 1197.563876 from(599.789214,2+)  
Elution from: 28.103 to 28.103 scan no 2163 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1197.5642
**Fixed modifications:** Carbamidomethyl (C)
**Variable modifications:**
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
**Ions Score:** 27  Expect: 0.012
**Matched b ions:** b(8)++, b(8), b(10)++
**Matched y ions:** y(3), y(4), y(6), y(7), y(8), y(9)
**Precursor origin neutral loss:**

**Peptide No.1452**

**QILSSTQR**
**Confirmed sites:** @S:5
**Ambiguous sites:**

**MS/MS Fragmentation of QILSSTQR**
Found in AT4G29060.1, EMB2726 (EMBRYO DEFECTIVE 2726); translation elongation factor

Match to Query 659: 1011.473154 from(338.164994,3+)  
Elution from: 15.463 to 15.463 scan no 790 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1011.4750
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.048
Matched b ions: b(1), b(4), b(5)++
Matched y ions: y(2), y(5)++, y(6)++, y(7)++
Precursor origin neutral loss:

Peptide No.1453
QLANESEEETPK
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of QLANESEEETPK
Found in AT1G80810.1, binding
Match to Query 1399: 1453.596840 from(727.805696,2+)
Elution from: 21.168 to 21.168 scan no 1430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1453.5973
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00037
Matched b ions: b(8)-98, b(9), b(11)
Matched y ions: y(2), y(3), y(5), y(7), y(8)-98, y(9), y(9)+, y(9)-98++, y(10)+, y(10), y(11)-98++
Precursor origin neutral loss: +

Peptide No. 1454

QLLEVAASKAST
Confirmed sites:
Ambiguous sites: @T:12

MS/MS Fragmentation of QLLEVAASKAST
Found in AT1G31812.1, ACBP (ACYL-COA BINDING PROTEIN); acyl-CoA binding

Match to Query 1288: 1296.630970 from(649.322761,2+)
Elution from: 34.212 to 34.212 scan no 3215 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.6326
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0061
Matched b ions: b(3), b(5), b(8), b(9), b(10)
Matched y ions: y(3), y(5), y(6)−98, y(7)++, y(7), y(7)−98, y(8)−98++, y(8), y(8)−98, y(9), y(10)−98
Precursor origin neutral loss: +

Peptide No.1455
QLNSDSYKEELTVNR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QLNSDSYKEELTVNR
Found in AT2G43130.1, ARA4 (Arabidopsis Rab GTPase homolog A5c); GTP binding

Match to Query 3448: 1874.839560 from(625.953796,3+)
Elution from: 33.526 to 33.526 scan no 3161 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1874.8411
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 32 Expect: 0.0063
Matched b ions: b(3), b(4)+, b(4), b(7)−98, b(9)−98++, b(9)+, b(10)−98++, b(11)−98++, b(11)+, b(13)++

Matched y ions: y(2), y(3), y(4), y(4)+, y(5), y(6), y(7), y(8)+, y(9)+, y(10)+, y(10)−98++, y(11)−98++, y(11)+, y(12)+, y(12)−98++, y(13)+, y(13)−98++, y(14)+

Precursor origin neutral loss: +

Peptide No.1456
QLSIDQFENEGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSIDQFENEGR
Found in AT1G08420.1, kelch repeat−containing protein / serine/threonine phosphoesterase family protein

Match to Query 2568: 1514.638876 from(758.326714,2+)
Elution from: 45.360 to 45.360 scan no 4727 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1514.6402
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 46 Expect: 0.00018
Matched b ions: b(3)–98, b(4), b(4)–98, b(5), b(6)–98, b(8)++, b(10)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)–98, y(10), y(10)++, y(10)–98++
Precursor origin neutral loss: +

Peptide No.1457
QLSIDQFENEGRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSIDQFENEGRR
Found in AT2G27210.1, kelch repeat-containing serine/threonine phosphoesterase family protein

Match to Query 2692: 1670.739975 from(557.920601,3+)
Elution from: 42.655 to 42.655 scan no 4119 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1670.7413
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1.9e-005
Matched b ions: b(2), b(3)-98, b(4), b(5)-98, b(6)-98, b(7)-98++, b(8)++
Matched y ions: y(3)+, y(4), y(5)+, y(6)+, y(7)+, y(8)+, y(9)+, y(10)+, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1458

QLSIHDNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSIHDNR
Found in AT1G10290.1, ADL6 (DYNAMIN–LIKE PROTEIN 6)

Match to Query 798: 1061.465192 from(531.739872,2+)
Elution from: 20.976 to 20.976 scan no 1397 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1061.4655
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.036
Matched b ions: b(4)
Matched y ions: y(2), y(3), y(4), y(6), y(7)++
Precursor origin neutral loss: +

Peptide No.1459

QLSLDQFQNESR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSLDQFQNESR
Found in AT4G03080.1, kelch repeat-containing serine/threonine phosphoesterase family protein

Match to Query 1595: 1543.667420 from(772.840986,2+)
Elution from: 43.326 to 43.326 scan no 4276 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1543.6668
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 4.8e-007
Matched b ions: b(4)++, b(4), b(7)−98, b(7)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10)−98, y(10), y(10)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1460
QLSMTEEEIAVDDEDSGGEGEK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of QLSMTEEEIAVDDEDSGGEGEK
Found in AT1G71080.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G38050.1); similar to hypothetical prote

Match to Query 3584: 2448.936084 from(1225.475318,2+)
Elution from: 40.415 to 40.415 scan no 3836 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2448.9363
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00016
Matched b ions: b(13), b(18)-98++, b(19)++, b(20)++
Matched y ions: y(8)-98, y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(18)
Precursor origin neutral loss: +

Peptide No.1461
QLTFSPSFSSQSR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of QLTFSPSFSSQSR
Found in AT4G31160.1, transducin family protein / WD-40 repeat family protein

Match to Query 2100: 1550.674648 from(776.344600,2+)
Elution from: 44.005 to 44.005 scan no 4513 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1550.6766
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0031
Matched b ions: b(7), b(10)
Matched y ions: y(3), y(7), y(8)+98, y(8), y(8)+, y(9)+98++, y(9)+98, y(9), y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.1462
QLTFSPSFSSQSR
Confirmed sites: @S:7
Ambiguous sites: 

MS/MS Fragmentation of QLTFSPSFSSQSR
Found in AT4G31160.1, transducin family protein / WD-40 repeat family protein

Match to Query 2152: 1550.675144 from(776.344848,2+)
Elution from: 43.991 to 43.991 scan no 4514 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1550.6766
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.011
Matched b ions:
Matched y ions: y(4), y(5), y(7), y(8)-98, y(8), y(9)+, y(9), y(9)-98, y(11), y(11)-98+
Precursor origin neutral loss: +

Peptide No.1463
QMSESSLCAEEEEDDDSK
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of QMSESSLCAEEEEDDDSK
Found in AT3G07880.1, Rho GDP–dissociation inhibitor family protein

Match to Query 3320: 2284.786380 from(1143.400466,2+)
Elution from: 29.117 to 29.117 scan no 2379 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2284.7872
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 2.7e-006
Matched b ions: b(15)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)
Precursor origin neutral loss: +

Peptide No.1464

QMSESSLCATEEEEDDSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QMSESSLCATEEEEDDSK
Found in AT3G07880.1, Rho GDP-dissociation inhibitor family protein

Match to Query 3271: 2268.790936 from(1135.402744,2+)
Elution from: 33.624 to 33.624 scan no 3081 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2268.7923
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 Expect: 7.7e-009
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98++, b(10)-98, b(11), b(15), b(16)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17)-98++, y(17)+
Precursor origin neutral loss: +

Peptide No.1465
QMSINSVPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QMSINSVPK
Found in AT1G08420.1, kelch repeat-containing protein / serine/threonine phosphoesterase family protein

Match to Query 650: 1082.481886 from(542.248219,2+)
Elution from: 32.339 to 32.339 scan no 2926 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1082.4831
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.013
Matched b ions: b(2), b(3), b(4)−98, b(5), b(7), b(8)−98
Matched y ions: y(2), y(3), y(4), y(6), y(7)−98++, y(7), y(7)−98, y(7)+++, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.1466
QNSAFENGSLPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QNSAFENGSLPR
Found in AT1G79830.1, similar to CIP1 (COP1–INTERACTIVE PROTEIN 1) [Arabidopsis thaliana]
(TAIR:AT5G41790.1); similar to

Match to Query 1883: 1398.592568 from(700.303560,2+)
Elution from: 34.264 to 34.264 scan no 3112 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1398.5929
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 3.8e-005
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)+, b(8), b(9), b(10), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10)-98, y(10)
Precursor origin neutral loss:

Peptide No.1467

QNSENVLIDMEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QNSENVLIDMEK
Found in AT5G61740.1, ATATH14 (ABC2 homolog 14); ATPase, coupled to transmembrane movement of substances

Match to Query 2017: 1498.636374 from(750.325463,2+)
Elution from: 45.620 to 45.620 scan no 4657 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1498.6374
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.4e-006
Matched b ions: b(4)-98, b(5), b(6)+, b(6)-98, b(7), b(8), b(8)-98, b(8)-98++, b(8)+, b(9), b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)+, y(8), y(9), y(10), y(10)-98, y(10)-98++, y(11)-98++
Precursor origin neutral loss:

Peptide No.1468

QNSENVLIDMEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QNSENVLIDMEK
Found in AT5G61740.1, ATATH14 (ABC2 homolog 14); ATPase, coupled to transmembrane movement of substances

Match to Query 2003: 1514.631222 from(758.322887,2+)
Elution from: 33.412 to 33.412 scan no 3070 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1514.6323
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 50 Expect: 5.9e-005
Matched b ions: b(4), b(4)-98++, b(5)+, b(5), b(6)-98++, b(6)-98, b(7)-98, b(8)-98, b(9), b(10)+, b(10)-98++, b(11)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)+
Precursor origin neutral loss: +

Peptide No. 1469
QNSETLYYADDEDGNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QNSETLYYADDEDGNR
Found in AT2G14835.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 2684: 1968.734706 from(985.374629,2+)
Elution from: 35.182 to 35.182 scan no 3170 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1968.7374
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 8.2e-007
Matched b ions: b(6)-98, b(6), b(7)-98, b(8), b(10), b(15)++
Matched y ions: y(4), y(5)+, y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15)-98++
Precursor origin neutral loss:

Peptide No.1470

QNSETLYYADDEDGNR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of QNSETLYYADDEDGNR
Found in AT2G14835.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 3323: 1968.736368 from(985.375460,2+)
Elution from: 34.318 to 34.318 scan no 3229 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1968.7374
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 4.1e-006
Matched b ions: b(6)-98, b(7), b(8), b(13), b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++, y(14)
Precursor origin neutral loss: +

Peptide No.1471

QNSETLYYADDEDGNRK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QNSETLYYADDEDGNRK
Found in AT2G14835.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 3250: 2096.830794 from(699.950874,3+)
Elution from: 29.137 to 29.137 scan no 2490 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2096.8324  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 29 Expect: 0.011  
Matched b ions: b(4)–98++, b(6)–98, b(11)–98++  
Matched y ions: y(3), y(5)++, y(6), y(7)++, y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(15)–98++, y(15)++  
Precursor origin neutral loss:  

Peptide No.1472  
QPASVPGSSSPVENVDR  
Confirmed sites: @S:10  
Ambiguous sites:  

MS/MS Fragmentation of QPASVPGSSSPVENVDR  
Found in AT3G19670.1, FF domain-containing protein / WW domain-containing protein  

Match to Query 2943: 1804.797874 from(903.406213,2+)  
Elution from: 29.801 to 29.801 scan no 2615 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.7992
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00018
Matched b ions:
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(11)+, y(11), y(12)−98++, y(12)+, y(12)−98, y(12), y(13)−98++, y(13)−98, y(14), y(14)+
Precursor origin neutral loss: +

Peptide No.1473

QPGSAFISATSE
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of QPGSAFISATSE
Found in AT1G66580.1, 60S ribosomal protein L10 (RPL10C)

Match to Query 1469: 1273.522462 from(637.768507,2+)
Elution from: 40.769 to 40.769 scan no 3979 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1273.5227
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1.4e-005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11)−98, b(11)
Matched y ions: y(2), y(2)−98, y(3), y(4), y(5), y(6)−98, y(6), y(7), y(11)++
Precursor origin neutral loss: +

Peptide No.1474

QRDEDWDSD
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of QRDEDWDSD
Found in AT3G27550.1, group II intron splicing factor CRS1-related

Match to Query 935: 1244.397444 from(623.205998,2+)
Elution from: 22.741 to 22.741 scan no 1637 polarity:+


Monoisotopic mass of neutral peptide Mr(calc): 1244.3983
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.00074
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)+, b(7), b(7)+, b(8)+, b(8)-98++
Matched y ions: y(2), y(2)-98, y(3)-98, y(3), y(4)+, y(4)-98, y(4), y(5), y(6)-98, y(7)
Precursor origin neutral loss: +

Peptide No.1475

QRSSPADFFTYLASDK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of QRSSPADFFTYLASDK
Found in AT1G05805.1, basic helix–loop–helix (bHLH) family protein

Match to Query 3233: 1911.838902 from(638.286910,3+)
Elution from: 58.326 to 58.326 scan no 6251 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1911.8404
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.012
Matched b ions: b(7)-98, b(8)++, b(8)-98++, b(9)+, b(10)-98++, b(12)++, b(13)++
Matched y ions: y(3), y(4), y(6), y(6)+, y(7), y(8)
Precursor origin neutral loss:

Peptide No.1476
QSFGSYGDESK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QSFGSYGDESK
Found in AT1G27500.1, kinesin light chain–related

Match to Query 1222: 1283.470248 from(642.742400,2+)
Elution from: 27.331 to 27.331 scan no 2248 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1283.4707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 8.5e-007
Matched b ions: b(2), b(3), b(5)–98, b(7), b(8), b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)–98, y(9)–98++, y(9)–98, y(9), y(9)++, y(10)
Precursor origin neutral loss: +

---

Peptide No.1477

QSILDSPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QSILDSPK
Found in AT2G16650.1, similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:AT4G21900.1); similar to Tetratr

Match to Query 468: 966.441572 from(484.228062,2+)
Elution from: 27.106 to 27.106 scan no 2212 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 966.4423
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 3.1e-005
Matched b ions: b(2), b(3), b(5), b(6)-98, b(7)++
Matched y ions: y(3), y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)++, y(7)
Precursor origin neutral loss:

Peptide No.1478

QSKSKLASFSSATQPCSGIPK
Confirmed sites: ”@S:11,@T:13”
Ambiguous sites:

MS/MS Fragmentation of QSKSKLASFSSATQPCSGIPK
Found in AT4G00026.1, similar to expressed protein [Oryza sativa (japonica cultivar-group)]
(GB:ABF95014.1); similar to e

Match to Query 4511: 2368.052865 from(790.358231,3+)
Elution from: 42.142 to 42.142 scan no 4249 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2368.0535
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.06
Matched b ions: b(4), b(6)++, b(9)+, b(10), b(12)++, b(13)+, b(14)++, b(14)-98++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(18)-196++, b(19)+, b(20)-98++
Matched y ions: y(11)+, y(13)-98++, y(16)-196++, y(17)-196++, y(18)-196++
Precursor origin neutral loss:

Peptide No.1479
QSLDTPSEEETSK
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of QSLDTPSEEETSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to erythrocyte membra
Match to Query 1646: 1529.612448 from(765.813500,2+)
Elution from: 23.371 to 23.371 scan no 1624 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1529.6134
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.066
Matched b ions:
Matched y ions: y(5), y(7), y(8)-98, y(8), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.1480

QSLSEGSLDK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of QSLSEGSLDK
Found in AT1G59610.1, ADL3 (ARABIDOPSIS DYNAMIN–LIKE 3)

Match to Query 782: 1142.484286 from(572.249419,2+)
Elution from: 27.181 to 27.181 scan no 2150 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1142.4856
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 3.5e-005
Matched b ions: b(4), b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1481

QSLSEGSLDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of QSLSEGSLDK
Found in AT1G10290.1, ADL6 (DYNAMIN–LIKE PROTEIN 6)

Match to Query 1271: 1142.485174 from(572.249863,2+)
Elution from: 26.250 to 26.250 scan no 2166 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1142.4856
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.013
Matched b ions: b(4), b(5), b(8), b(9)
Matched y ions: y(2), y(3), y(6), y(7), y(7)--98, y(8)--98++, y(8), y(8)--98, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.1482
QSPEIEQTDIPIK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of QSPEIEQTDIPIK
Found in AT4G31800.1, WRKY18 (WRKY DNA-binding protein 18); transcription factor

Match to Query 2091: 1576.737982 from(789.376267,2+)
Elution from: 40.516 to 40.516 scan no 4053 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1576.7385
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0062
Matched b ions: b(5)–98, b(6)–98, b(8), b(9)–98++, b(10)–98, b(10), b(11)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(10), y(11)++
Precursor origin neutral loss: +

Peptide No. 1483
QSSADDLIVNGK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of QSSADDLIVNGK
Found in AT3G12270.1, methyltransferase

Match to Query 1223: 1325.585790 from(663.800171,2+)  
Elution from: 32.649 to 32.649 scan no 2864 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1325.5864
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.021
Matched b ions: b(3), b(4), b(5), b(6), b(7)+, b(7)−98, b(9), b(9)−98, b(10), b(10)−98+
Matched y ions: y(3), y(4), y(5), y(5)+, y(6), y(7), y(8), y(9), y(11)−98+
Precursor origin neutral loss: 

Peptide No.1484

QSSADDLIVNGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QSSADDLIVNGK
Found in AT3G12270.1, methyltransferase

Match to Query 1140: 1325.585226 from(663.799889,2+)
Elution from: 31.522 to 31.522 scan no 2803 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1325.5864
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.5e-005
Matched b ions: b(4)-98, b(4), b(5), b(6)-98, b(7)++, b(8), b(9), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98++
Precursor origin neutral loss:

Peptide No.1485

QSSFDEEIEEMGR
Confirmed sites: @S:2orS:3
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of QSSFDEEIEEMGR
Found in AT3G18350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48840.1); similar to unknown protein [O

Match to Query 1885: 1635.610404 from(818.812478,2+)
Elution from: 50.658 to 50.658 scan no 4898 polarity:+

Found in AT3G18350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48840.1); similar to unknown protein [O

Match to Query 1885: 1635.610404 from(818.812478,2+)
Elution from: 50.658 to 50.658 scan no 4898 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.6123
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0024
Matched b ions:
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss:

Peptide No.1486

QSSFDEEIEEMGR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of QSSFDEEIEEMGR
Found in AT3G18350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48840.1);
similar to unknown protein [O

Match to Query 1857: 1635.610406 from(818.812479,2+)
Elution from: 49.305 to 49.305 scan no 4943 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1635.6123
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 3.6e-007
Matched b ions: b(5)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss:

Peptide No.1487

QSSLLSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QSSLLSK
Found in AT1G10290.1, ADL6 (DYNAMIN–LIKE PROTEIN 6)

Match to Query 240: 841.394196 from(421.704374,2+) Elution from: 22.801 to 22.801 scan no 1575 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 841.3946
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.011
Matched b ions:
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++
Precursor origin neutral loss:

Peptide No.1488

QSSTLVNDVR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of QSSTLVNDVR
Found in AT5G35180.1, similar to EDR2 (enhanced disease resistance 2), lipid binding
[Arabidopsis thaliana] (TAIR:AT4G190)

Match to Query 948: 1197.539188 from(599.776870,2+)
Elution from: 28.848 to 28.848 scan no 2488 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5390
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.003
Matched b ions: b(7), b(8), b(8)++, b(8)—98, b(9)—98++, b(9)—98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(9)++
Precursor origin neutral loss:

Peptide No.1489

QSSTLVNDVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QSSTLVNDVR
Found in AT5G35180.1, similar to EDR2 (enhanced disease resistance 2), lipid binding
[Arabidopsis thaliana] (TAIR:AT4G190)

Match to Query 967: 1197.538464 from(599.776508,2+)
Elution from: 28.757 to 28.757 scan no 2477 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5390
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.01
Matched b ions: b(4)-98, b(5)-98, b(7), b(7)-98, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(6)++, y(6), y(7), y(8)-98++, y(8)-98, y(9)-98++
Precursor origin neutral loss:

Peptide No.1490

QSSTLVNDVR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of QSSTLVNDVR
Found in AT5G35180.1, similar to EDR2 (enhanced disease resistance 2), lipid binding [Arabidopsis thaliana] (TAIR:AT4G190)

Match to Query 902: 1197.538482 from(599.776517,2+) Elution from: 30.012 to 30.012 scan no 2526 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5390  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 23 Expect: 0.027  
Matched b ions: b(7), b(8), b(9)−98++, b(9)−98  
Matched y ions: y(2), y(3), y(4), y(6), y(7)+, y(8), y(8)−98  
Precursor origin neutral loss:  

Peptide No.1491  

QTLMYTATWPK  
Confirmed sites: ”@T:2,@T:8”  
Ambiguous sites:  

MS/MS Fragmentation of QTLMYTATWPK  
Found in AT3G06480.1, DEAD box RNA helicase, putative  

Match to Query 1619: 1514.593425 from(505.871751,3+)  
Elution from: 17.867 to 17.867 scan no 992 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1514.5918
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.056
Matched b ions: b(6)++
Matched y ions: y(3), y(7)++, y(8)++, y(8)−98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1492
QTNVDNGGEISPTVDR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of QTNVDNGGEISPTVDR
Found in AT3G19510.1, homeobox protein (HAT 3.1)

Match to Query 2799: 1780.760128 from(891.387340,2+) Elution from: 28.073 to 28.073 scan no 2384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1780.7628
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0049
Matched b ions:
Matched y ions: y(5), y(6), y(7), y(10), y(11), y(12), y(12)--98, y(13)++
Precursor origin neutral loss: +

Peptide No.1493

QTSPKPPPSPSPLR
Confirmed sites: ”@S:3,@S:9”
Ambiguous sites:

MS/MS Fragmentation of QTSPKPPPSPSPLR
Found in AT3G46440.1, UXS5 (UDP–Xyl synthase 5); catalytic

Match to Query 2831: 1647.740916 from(550.254248,3+)
Elution from: 26.960 to 26.960 scan no 2262 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1647.7423  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 30 Expect: 0.0097  
Matched b ions: b(3), b(9)−196++, b(9)++, b(9)−98++, b(10)−98++, b(10)−196++, b(13)−196++  
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(6), y(7)−98, y(7), y(8), y(8)++, y(9), y(9)++, y(9)−98++, y(10)++, y(11)++, y(11)−98++, y(12)++, y(12)−98++  
Precursor origin neutral loss: +

Peptide No.1494

QTTAEGSANPEPDQILSPR  
Confirmed sites: @S:17  
Ambiguous sites:  

MS/MS Fragmentation of QTTAEGSANPEPDQILSPR  
Found in AT1G57990.1, ATPUP18 (Arabidopsis thaliana purine permease 18); purine transporter

Match to Query 3696: 2089.931016 from(697.650948,3+)  
Elution from: 37.607 to 37.607 scan no 3633 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2089.9317
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.017
Matched b ions: b(6), b(9), b(10)++, b(11), b(11)++, b(13)++, b(15)++, b(16)++, b(17)−98++
Matched y ions: y(3), y(5), y(8)++, y(8), y(10)++, y(11)++, y(14)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1495

QVDGDDSDGFETASER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of QVDGDDSDGFETASER
Found in AT4G30480.1, tetratricopeptide repeat (TPR)−containing protein

Match to Query 2793: 1806.657340 from(904.335946,2+)
Elution from: 29.121 to 29.121 scan no 2525 polarity:+

Found in AT4G30480.1, tetratricopeptide repeat (TPR)−containing protein

Match to Query 2793: 1806.657340 from(904.335946,2+)
Elution from: 29.121 to 29.121 scan no 2525 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1806.6581
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 9.5e-007
Matched b ions: b(3), b(7), b(9)-98, b(11)-98, b(11), b(12)+, b(12), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)-98++, y(11), y(11)-98, y(12)-98++, y(12)-98, y(13), y(13)+, y(13)-98++, y(13)-98, y(14), y(14)-98, y(14)-98++, y(14)++, y(15)-98, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1496
QVLDTKMYKQSNV
Confirmed sites: "@T:5,@S:11"
Ambiguous sites:

MS/MS Fragmentation of QVLDTKMYKQSNV
Found in AT1G61780.1, postsynaptic protein-related

Match to Query 2898: 1712.720217 from(571.914015,3+)
Elution from: 17.500 to 17.500 scan no 962 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1712.7245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.015
Matched b ions: b(5)−98, b(10)−98++, b(11)−196++
Matched y ions: y(8)++, y(10)++, y(11)++, y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1497
QVLQGPSATVNSPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of QVLQGPSATVNSPR
Found in AT3G60240.2, EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G)

Match to Query 2518: 1532.734172 from(767.374362,2+) Elution from: 29.320 to 29.320 scan no 2567 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.7348  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 76 Expect: 1.7e-007  
Matched b ions: b(3), b(5), b(7), b(9), b(12)-98  
Matched y ions: y(2), y(3), y(3)-98, y(4), y(5), y(6)-98, y(7), y(8), y(9)-98, y(9), y(9)+, y(10), y(10)-98, y(11)+, y(12), y(12)+, y(13)-98++, y(13)++  
Precursor origin neutral loss: +

Peptide No. 1498

QWEWFLEDSTNGNSDGDEDGDKKGR  
Confirmed sites:  
Ambiguous sites: @T:10 or S:9

MS/MS Fragmentation of QWEWFLEDSTNGNSDGDEDGDKKGR  
Found in AT3G13780.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02720.1); similar to SMAD/FHA [Medicago]

Match to Query 4008: 2964.183225 from(989.068351,3+)  
Elution from: 59.062 to 59.062 scan no 5685 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2964.1835
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.043
Matched b ions: b(10)−98, b(12)++, b(13)++, b(15)++, b(17)++, b(20)++, b(20)−98++
Matched y ions: y(4), y(5), y(15)++, y(17)++, y(21)++
Precursor origin neutral loss:

Peptide No.1499
QYEDVEDEEEIGSDDDLTR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of QYEDVEDEEEIGSDDDLTR
Found in AT5G14050.1, transducin family protein / WD-40 repeat family protein

Match to Query 4292: 2335.881780 from(1168.948166,2+)
Elution from: 42.195 to 42.195 scan no 4241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2335.8853
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 6.5e-006
Matched b ions: b(9), b(10), b(11), b(12), b(14)+, b(16)–98
Matched y ions: y(7)–98, y(7), y(8)–98, y(8), y(9)–98, y(9), y(10)–98, y(10), y(11)–98, y(11), y(12), y(12)–98, y(13), y(13)–98, y(14)–98++, y(14)–98, y(14), y(15)++, y(15)–98, y(16)++
Precursor origin neutral loss: +

Peptide No.1500

RAESPEAMEEDEEEIAEIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RAESPEAMEEDEEEIAEIK
Found in AT3G53230.1, cell division cycle protein 48, putative / CDC48, putative

Match to Query 3567: 2283.939438 from(1142.976995,2+)
Elution from: 44.989 to 44.989 scan no 4485 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2283.9453
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 33 Expect: 0.005
Matched b ions: b(4)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)+, b(12)-98++, b(12)+, b(13), b(14)-98++, b(14), b(15)-98++, b(15), b(15)-98, b(16)-98, b(16)-98++, b(16), b(16)+, b(17)-98++, b(17)-98, b(17)-98++, b(18)+
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15), y(16), y(16)+, y(16)-98, y(17)-98, y(17)+, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1501
RAFSEGDIQK
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of RAFSEGDIQK
Found in AT5G53420.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27900.2); similar to CCT [Medicago truncatula]
Match to Query 1316: 1229.543440 from(615.778996,2+)
Elution from: 26.346 to 26.346 scan no 2045 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1229.5441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.3e-005
Matched b ions: b(2), b(3), b(4)−98, b(5), b(5)−98, b(6), b(7)−98, b(7), b(8)−98, b(8), b(8)−98++, b(9)−98++, b(9), b(9)−98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98, y(7), y(8)++, y(8), y(8)−98, y(9), y(9)−98
Precursor origin neutral loss: +

Peptide No.1502
RASFGATIENDPCIHAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RASFGATIENDPCIHAK
Found in AT3G59770.1, SAC9 (suppressor of actin 9)

Match to Query 3647: 1965.874950 from(656.298926,3+)
Elution from: 32.418 to 32.418 scan no 3035 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1965.8768
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0053
Matched b ions: b(2), b(3)-98, b(4), b(4)-98, b(4)+, b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(7)-98++, b(7)+, b(8)-98, b(8), b(8)+, b(9), b(9)+, b(9)-98, b(9)-98++, b(11)-98, b(11), b(11)-98++, b(11)+, b(12)-98++, b(12)+, b(14)-98++, b(15)+, b(16)+, b(16)-98++
Matched y ions: y(3), y(5), y(6)+, y(6), y(7), y(7)+, y(8), y(8)+, y(9), y(9)+, y(9), y(10)+, y(10)+, y(14)+, y(15)-98++, y(15)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1503
RASFGATIENDPCIHAK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RASFGATIENDPCIHAK
Found in AT3G59770.1, SAC9 (suppressor of actin 9)

Match to Query 3603: 1965.875886 from(656.299238,3+)
Elution from: 33.510 to 33.510 scan no 3132 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1965.8768
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.0001
Matched b ions: b(2), b(7), b(7)−98++, b(7)−98, b(8), b(8)++, b(8)−98, b(9), b(9)++, b(9)−98++, b(9)−98, b(10), b(10)++, b(11)−98, b(11), b(11)−98++, b(11)++, b(12)−98++, b(12)++, b(13)++, b(13)−98++, b(14)−98++, b(15)++, b(15)−98++, b(16)++, b(16)−98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10)++, y(11)−98++, y(12)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1504
RDEETIPMSQSSPYSPK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of RDEETIPMSQSSPYSPK
Found in AT3G53520.1, UXS1 (UDP-GLUCURONIC ACID DECARBOXYLASE 1); catalytic

Match to Query 3696: 2030.864124 from(1016.439338,2+)
Elution from: 35.583 to 35.583 scan no 3176 polarity:+

200 400 600 800 1000 1200
Monoisotopic mass of neutral peptide Mr(calc): 2030.8656
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.3e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(9)+, b(10), b(12), b(14), b(15)–98
Matched y ions: y(5)–98, y(5), y(6), y(9), y(9)+, y(10), y(11)–98, y(11), y(12), y(13), y(13)–98, y (15)–98
Precursor origin neutral loss: +

Peptide No.1505
RDFNGYRSPPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of RDFNGYRSPPR
Found in AT4G28990.1, RNA–binding protein–related

Match to Query 2360: 1443.639480 from(482.220436,3+)
Elution from: 21.413 to 21.413 scan no 1503 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1443.6408
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.042
Matched b ions: b(2), b(4), b(5), b(6)++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++
Matched y ions: y(2), y(3), y(4)-98, y(7)++, y(8)-98++, y(9)-98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1506
RDSFSSKPYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RDSFSSKPYSR
Found in AT1G03350.1, BSD domain-containing protein

Match to Query 1992: 1408.612305 from(470.544711,3+)
Elution from: 20.389 to 20.389 scan no 1342 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1408.6136
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00086
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(5)–98, b(6)–98, b(6), b(7)–98, b(7), b(7)+, b(8)–98++, b(9)+, b(10)–98++, b(10)+
Matched y ions: y(1), y(2), y(3), y(4)+, y(4), y(5)+, y(5), y(6)+, y(6), y(7)+, y(8)+, y(9)+, y(9)–98++, y(10)–98++
Precursor origin neutral loss: +

Peptide No.1507
RDSVDWVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RDSVDWVK
Found in AT1G52590.1, similar to RNase H domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G24090.1); similar to

Match to Query 583: 1083.474404 from(542.744478,2+)
Elution from: 27.847 to 27.847 scan no 2315 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1083.4750
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.0005
Matched b ions: b(2), b(3), b(4)−98, b(5), b(5)−98, b(6)−98, b(6), b(7), b(7)−98
Matched y ions: y(3), y(5)
Precursor origin neutral loss: +

Peptide No. 1508

RESVGILNDDDEALFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RESVGILNDDDEALFR
Found in AT3G14120.1, similar to Nuclear pore complex, rNup107 component (sc Nup84) (ISS) [Ostreococcus tauri] (GB:CAL505

Match to Query 3271: 1927.862896 from(964.938724,2+) Elution from: 51.328 to 51.328 scan no 5441 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1927.8676
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0057
Matched b ions: b(4)–98, b(6)–98
Matched y ions: y(6), y(7), y(10), y(12), y(13), y(14)–98, y(14)
Precursor origin neutral loss: +

Peptide No.1509
RFSDVPSR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of RFSDVPSR
Found in AT3G49400.1, transducin family protein / WD-40 repeat family protein
Match to Query 718: 1042.458980 from(522.236766,2+) Elution from: 23.418 to 23.418 scan no 1656 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1042.4597
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.049
Matched b ions: b(2), b(3)−98, b(3), b(5)+, b(6)−98++, b(7)−98, b(7)
Matched y ions: y(1), y(4), y(5), y(5)+, y(6)−98, y(6), y(7)−98
Precursor origin neutral loss: +

Peptide No.1510
RFTHQVFATWYR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of RFTHQVFATWYR
Found in AT1G66750.1, AT;CDKD;2/CAK4AT/CDKD1;2/CDKD;2 (CYCLIN-DEPENDENT KINASE D1;2); kinase/ protein binding / protein s

Match to Query 2940: 1690.774701 from(564.598843,3+)
Elution from: 42.984 to 42.984 scan no 4399 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1690.7769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.024
Matched b ions: b(2), b(3), b(4)−98, b(5)++, b(5), b(5)−98++, b(6)−98++, b(6)+, b(6)−98, b(7)++, b(8)−98++, b(8)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1511
RGALLQDSEEEDG
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of RGALLQDSEEEDG
Found in AT5G64010.1, unknown protein

Match to Query 2231: 1497.598040 from(749.806296,2+)
Elution from: 30.647 to 30.647 scan no 2720 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1497.5984
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7), b(8)−98, b(9)−98, b(9), b(9)−98++, b(10), b(10)−
   98++, b(10)++, b(10)−98, b(11), b(11)−98++, b(11)+, b(11)−98, b(12)++, b(12)−98++
Matched y ions: y(3), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1512
RGGDLGSFGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of RGGDLGSFGR
Found in AT2G18040.1, PIN1AT (parvulin 1At)

Match to Query 725: 1100.475430 from(551.244991,2+)
Elution from: 26.749 to 26.749 scan no 2202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1100.4763
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0035
Matched b ions: b(4), b(5), b(7)−98, b(8)−98++, b(8)−98, b(9)−98
Matched y ions: y(3), y(6)−98, y(6), y(9)−98
Precursor origin neutral loss: +

Peptide No.1513

RGNSSNDHELGILR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RGNSSNDHELGILR
Found in AT5G47910.1, RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)

Match to Query 2691: 1646.751243 from(549.924357,3+)
Elution from: 29.847 to 29.847 scan no 2611 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1646.7525  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 38 Expect: 0.0014  
Matched b ions: b(2), b(4)−98, b(5), b(6), b(7), b(7)−98, b(8)−98++, b(9)−98++, b(9)++, b(10) ++, b(11)−98++, b(12)++, b(13)−98++  
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(10)++, y(12)−98++, y (13)++  
Precursor origin neutral loss: +  

Peptide No.1514  

RGSDDEDDDEDDIFSSK  
Confirmed sites: @S.3  
Ambiguous sites:  

MS/MS Fragmentation of RGSDDEDDDEDDIFSSK  
Found in AT5G58760.1, DDB2 (DAMAGED DNA-BINDING 2); nucleotide binding  

Match to Query 2468: 1908.688202 from(955.351377,2+)  
Elution from: 34.548 to 34.548 scan no 3202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1908.6898
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 9.1e-005
Matched b ions: b(5), b(6)–98, b(7), b(8)–98, b(10)–98, b(11)–98, b(11), b(13)
Matched y ions: y(5), y(6), y(8), y(9), y(12), y(13), y(14)–98
Precursor origin neutral loss: +

Peptide No.1515

RGSEANWALANSR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of RGSEANWALANSR
Found in AT3G15450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1);
similar to unknown [Glycine m
Match to Query 2562: 1510.667522 from(756.341037,2+)n
Elution from: 30.530 to 30.530 scan no 2753 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1510.6677
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 3.6e-007
Matched b ions: b(3)-98, b(4)-98, b(5), b(6), b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(11)-98
Precursor origin neutral loss: +

Peptide No.1516
RGSEANWSL
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of RGSEANWSL
Found in AT4G27450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15450.1); similar to unknown [Glycine m

Match to Query 674: 1098.448250 from(550.231401,2+)
Elution from: 39.875 to 39.875 scan no 3971 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1098.4495  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 30 Expect: 0.0031  
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)++, b(8), b(8)-98++  
Matched y ions: y(2), y(3), y(4), y(5)++, y(6), y(7)++  
Precursor origin neutral loss:  

Peptide No.1517  
RHSFGEEELAYLPYK  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of RHSFGEEELAYLPYK  
Found in AT3G12020.1, kinesin motor protein-related  

Match to Query 3198: 1917.862857 from(640.294895,3+)  
Elution from: 45.412 to 45.412 scan no 4667 polarity:+
**Peptide No. 1518**

**RHSGDFSDAGHFLR**

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **RHSGDFSDAGHFLR**

Found in **AT1G78020.1**, senescence-associated protein-related

Match to Query 2914: 1680.713996 from(421.185775,4+)

Elution from: 32.581 to 32.581 scan no 3006 polarity:+

---

**Monoisotopic mass of neutral peptide Mr(calc): 1917.8662**

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**

S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

**Ions Score:** 34 **Expect:** 0.0035

**Matched b ions:** b(4), b(7)++, b(8), b(8)++, b(9)++, b(10)++

**Matched y ions:** y(3), y(5), y(6), y(10)++

**Precursor origin neutral loss:** +
Monoisotopic mass of neutral peptide Mr(calc): 1680.7158
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.035
Matched b ions: b(2), b(3)-98, b(5)+, b(5), b(5)-98++, b(5)-98, b(6)+, b(6)-98++, b(7)-98++, b(8)++,
b(8)-98++, b(10)+, b(10)-98++
Matched y ions: y(2), y(3), y(4)+, y(4), y(5)+, y(5), y(6)+, y(7)+, y(8)+, y(9)+, y(11)+
Precursor origin neutral loss: +

Peptide No. 1519

RHSWSFDR

Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSWSFDR

Found in AT3G18770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49590.1);
similar to IMP dehydrogenase/

Match to Query 1332: 1169.476034 from(585.745293,2+)
Elution from: 25.543 to 25.543 scan no 2052 polarity:+
**Peptide No. 1520**

RIEVDSGDGDGER

**Confirmed sites:** @S:6

**Ambiguous sites:**

MS/MS Fragmentation of **RIEVDSGDGDGER**

Found in **AT1G80930.1**, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 2191: 1426.571486 from(714.293019,2+)

Elution from: 20.096 to 20.096 scan no 1340 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1426.5725
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 2.2e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6)—98, b(7)—98++, b(7)—98, b(8), b(9)—98, b(9), b(9)+, b(10), b(10)—98, b(11)—98
Matched y ions: y(3), y(5), y(6), y(7), y(7)—98, y(8)—98, y(9)
Precursor origin neutral loss: +

Peptide No.1521
RIEVDSDGDGERR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of RIEVDSDGDGERR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 1954: 1582.672992 from(528.564940,3+) Elution from: 18.374 to 18.374 scan no 1049 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.6736

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 39 Expect: 0.00064

Matched b ions: b(3), b(4), b(5), b(6)-98, b(7)-98, b(7)-98++, b(8)+, b(8)-98++, b(9), b(9)-98++, b(11), b(11)-98, b(12)-98++

Matched y ions: y(1), y(2)+, y(4)+, y(6)+, y(7)+, y(8)-98++, y(8)+, y(8)-98++, y(9)-98++, y(9)+, y(10)+, y(10)-98++, y(12)-98++

Precursor origin neutral loss: +

Peptide No.1522

RKADSDEEAEFDVEGR

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of RKADSDEEAEFDVEGR
Found in AT2G34357.1, binding

Match to Query 3570: 1931.789256 from(644.937028,3+)  
Elution from: 28.269 to 28.269 scan no 2467 polarity:+
Peptide No. 1523

RKETSDDEELAR

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of RKETSDDEELAR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 2396: 1527.655176 from(510.225668,3+)

Elution from: 17.964 to 17.964 scan no 1028 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1527.6566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 5.3e-006
Matched b ions: b(2), b(3), b(4)++, b(5)++, b(5)–98++, b(5)–98, b(6)–98++, b(6)–98, b(6)++, b(7)++, b(7)–98++, b(8)–98++, b(8)–98, b(9)++, b(9)–98++, b(10)++, b(11)–98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)–98, y(8)–98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1524
RKETSDDEELAR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of RKETSDDEELAR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 2238: 1527.653818 from(764.834185,2+)
Elution from: 18.156 to 18.156 scan no 976 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1527.6566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.2e-006
Matched b ions: b(2), b(4)−98, b(5)−98, b(5), b(6), b(6)−98, b(7)−98, b(7), b(9)−98, b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)−98, y(9), y(11)−98
Precursor origin neutral loss: +

Peptide No.1525
RKLEGEESEAEPEESEQK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of RKLEGEESEAEPEESEQK
Found in AT3G56860.1, UBA2A; RNA binding
Match to Query 2806: 2038.881420 from(680.634416,3+)
Elution from: 17.909 to 17.909 scan no 1020 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2038.8844
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.027
Matched b ions: b(7)++, b(7), b(10)++, b(11)−98++, b(11)++, b(12)++, b(13)−98++, b(13)++, b(14)−98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8)
Precursor origin neutral loss: +

Peptide No.1526

RKLETLDETSEGEEAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of RKLETLDETSEGEEAK
Found in AT2G19385.1, nucleic acid binding / zinc ion binding

Match to Query 3549: 1913.860320 from(638.960716,3+)
Elution from: 23.687 to 23.687 scan no 1781 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1913.8619
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00022
Matched b ions: b(3), b(4), b(5)+, b(6), b(6)+, b(7)+, b(7), b(8), b(8)+, b(9)+, b(10)+, b(10)-98+, b(12)-98+, b(12)+, b(13)+, b(13)-98+, b(14)+, b(14)-98+, b(15)-98+, b(15)+
Matched y ions: y(2), y(3), y(5), y(6), y(7)+, y(7)-98, y(7), y(8), y(8)-98, y(8)-98+, y(8)+, y(9)-98, y(9)+, y(10), y(10)-98, y(11)-98+, y(12)-98+, y(15)-98+
Precursor origin neutral loss: +

Peptide No.1527
RKPISDEVNDSDEEYK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of RKPISDEVNDSDEEYK
Found in AT3G12480.1, transcription factor, putative

Match to Query 2735: 2002.849338 from(668.623722,3+)
Elution from: 23.097 to 23.097 scan no 1697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2002.8520

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 50 Expect: 9.9e-005

Matched b ions: b(2), b(4), b(5), b(6)++, b(6), b(7)+, b(7), b(8)+, b(8), b(9)+, b(10)++, b(11)−98++, b(13)−98++, b(13)+, b(14)+, b(14)−98++, b(15)+, b(15)−98++

Matched y ions: y(2), y(4)+, y(4), y(5)+, y(6)−98, y(6), y(7)−98, y(7), y(8)−98, y(8), y(8)+, y(8)−98++, y(9), y(9)−98, y(9)+, y(9)−98++, y(10), y(10)+, y(13)+, y(14)−98++, y(14)+

Precursor origin neutral loss: +

Peptide No.1528

RKPISDEVNDSDEEYKK

Confirmed sites: @S:11

Ambiguous sites:

MS/MS Fragmentation of RKPISDEVNDSDEEYKK

Found in AT3G12480.1, transcription factor, putative

Match to Query 2998: 2130.945321 from(711.322383,3+)
Elution from: 20.491 to 20.491 scan no 1342 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2130.9470
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 4.4e-007
Matched b ions: b(2), b(6)+++, b(7), b(7)+++, b(8)+, b(9), b(9)+, b(10), b(10)+++, b(11)–98++, b(11)+, b(12)–98++, b(13)–98++, b(14)–98++, b(14)+, b(15)–98++, b(15)+, b(16)–98++, b(16)+
Matched y ions: y(3), y(4), y(5)+, y(5)+, y(6)+, y(6)+, y(7)–98++, y(7)–98, y(7)+, y(7)+, y(8)–98++, y(8)+, y(8)+, y(9)–98++, y(9)–98, y(9)+, y(9)+, y(10)–98++, y(10)–98, y(10)+, y(10)+, y(11)–98++, y(14)–98++, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.1529
RKVSNPSFIAAQSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RKVSNPSFIAAQSK
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 2734: 1611.811716 from(538.277848,3+)
Elution from: 23.714 to 23.714 scan no 1803 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1611.8133

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 35 Expect: 0.0029

Matched b ions: b(2), b(3), b(4)+, b(4)-98, b(4), b(5)-98, b(5), b(5)-98++, b(5)+, b(6)-98++, b(7)-98++, b(7)-98, b(7)+, b(8), b(8)-98++, b(8)+, b(9)-98++, b(9)+, b(10)+, b(10)-98++, b(11)-98++, b(11)+, b(12)+, b(12)-98++, b(13)+, b(13)-98++

Matched y ions: y(2), y(3), y(4), y(5), y(5)+, y(5)+, y(6), y(6)+, y(7), y(7)+, y(8), y(8)+, y(9), y(9)+, y(12)+, y(13)+, y(13)-98++

Precursor origin neutral loss: +

Peptide No.1530

RLEEEELESSDDERDK
Confirmed sites: "@S:9,@S:10"
Ambiguous sites:

MS/MS Fragmentation of RLEEEELESSDDERDK
Found in AT1G58050.1, helicase domain-containing protein

Match to Query 3009: 2137.807269 from(713.609699,3+)
Elution from: 25.753 to 25.753 scan no 1962 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2137.8089
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00018
Matched b ions: b(2), b(4), b(5), b(6), b(7)+, b(7), b(8), b(9)-98, b(10)+, b(12)-196++, b(12)-98++, b(14)-196++, b(14)+, b(15)-196++, b(15)+, b(15)-98++
Matched y ions: y(4), y(6)+, y(7)-98++, y(8)+, y(9)-196, y(10)-98++, y(10)-196++, y(11)-196++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1531
RLLPYLMQASDDGTSSSSR
Confirmed sites: "@S:17,@S:18"
Ambiguous sites:

MS/MS Fragmentation of RLLPYLMQASDDGTSSSSR
Found in AT3G23740.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14120.1); similar to Os01g0101800 [Oryz]

Match to Query 3213: 2258.925724 from(565.738707,4+)
Elution from: 21.258 to 21.258 scan no 1384 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2258.9279
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M7 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.048
Matched b ions: b(2), b(5)++, b(7)++, b(8)++, b(9)++
Matched y ions: y(3), y(6)−196, y(7)−196++, y(7)−196, y(7)−98, y(8)−196, y(9)−196++, y(10)−98++, y(11)−196++, y(12)−196++, y(12)−98++, y(14)−98++, y(14)−196++, y(15)−196++
Precursor origin neutral loss: +

Peptide No.1532

RLSFVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RLSFVR
Found in AT3G61260.1, DNA-binding family protein / remorin family protein

Match to Query 350: 856.431850 from(429.223201,2+)
Elution from: 28.169 to 28.169 scan no 2426 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 856.4320
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 43 Expect: 0.00024
Matched b ions: b(2), b(3)−98, b(4)−98, b(5), b(5)−98
Matched y ions: y(1), y(2), y(3), y(4)−98, y(4), y(5)−98, y(5)
Precursor origin neutral loss: +

Peptide No.1533

RMDDSLSPR
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of RMDDSLSPR
Found in AT2G37340.1. RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1332: 1251.434492 from(626.724522,2+) Elution from: 19.104 to 19.104 scan no 1152 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1251.4356
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.002
Matched b ions: b(3), b(4), b(5)−98, b(5), b(6)−98, b(6), b(7)−196, b(7)−98, b(7), b(7)−98++, b(8)−196
Matched y ions: y(2), y(3), y(3)−98, y(4)−98, y(4), y(5), y(5)−196, y(6)−98, y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1534

RMDDSLSPR
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of RMDDSLSPR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 913: 1235.439658 from(618.727105,2+)
Elution from: 21.944 to 21.944 scan no 1532 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1235.4407

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
- S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 45 Expect: 0.00012

Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-196, b(7)-98, b(7), b(7)-196

Matched y ions: y(1), y(2), y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-196, y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)+

Precursor origin neutral loss: +

---

**Peptide No.1535**

**RMDDSLSPR**

Confirmed sites: @S:7

Ambiguous sites:

MS/MS Fragmentation of **RMDDSLSPR**

Found in **AT2G37340.1**, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33; nucleic acid binding / nucleotide)

Match to Query 1326: 1155.472980 from(578.743766,2+)

Elution from: 20.910 to 20.910 scan no 1434 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1155.4744
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0035
Matched b ions: b(3), b(4), b(5), b(6), b(7)–98
Matched y ions: y(2), y(5), y(5)–98, y(6)
Precursor origin neutral loss: +

Peptide No.1536

RNESSCDEGDDFDAK
Confirmed sites: "@S:4,@S:5"
Ambiguous sites:

MS/MS Fragmentation of RNESSCDEGDDFDAK
Found in AT1G63250.1, DEAD box RNA helicase, putative

Match to Query 2746: 1903.593958 from(952.804255,2+)  
Elution from: 24.095 to 24.095 scan no 1813 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1903.5968
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 13 Expect: 0.051
Matched b ions: b(6)-98, b(11), b(12)+, b(13)-196, b(13)
Matched y ions: y(7), y(8), y(9), y(10), y(13)-98
Precursor origin neutral loss: +

Peptide No.1537

RNESSCDEGDDFDAK
Confirmed sites: @S:4 or S:5
Ambiguous sites: @S:4 or S:5

MS/MS Fragmentation of RNESSCDEGDDFDAK
Found in AT1G63250.1, DEAD box RNA helicase, putative

Match to Query 2976: 1823.628254 from (912.821403, 2+) Elution from: 21.536 to 21.536 scan no 1470 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1823.6305
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.02
Matched b ions: b(5)-98, b(10), b(10)-98, b(11), b(12), b(13)-98, b(13), b(14)++
Matched y ions: y(5), y(8)
Precursor origin neutral loss: +

Peptide No.1538

RNRSPSPLYR
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of RNRSPSPLYR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 2228: 1404.604902 from(469.208910,3+)
Elution from: 19.554 to 19.554 scan no 1277 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1404.6064
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0002
Matched b ions: b(3)++, b(4)++, b(4)−98++, b(4), b(4)−98, b(5)−98++, b(6)−98++, b(6)−196++, b(6)++, b(7)−196++, b(7)−98++, b(8)−196++, b(8)++, b(8)−98++, b(9)++, b(9)−196++, b(9)−98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)−98, y(5), y(6)−98, y(6), y(6)++
Precursor origin neutral loss: +

Peptide No.1539
RNSESGLELLSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RNSESGLELLSK
Found in AT3G28180.1, ATGSLCO4 (Cellulose synthase-like C4); transferase, transferring glycosyl groups

Match to Query 1668: 1411.669310 from(706.841931,2+)
Elution from: 37.049 to 37.049 scan no 3558 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6708
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 2.6e-006
Matched b ions: b(2), b(3)−98, b(4)−98, b(7), b(7)−98++, b(8)−98, b(8), b(9)−98, b(9), b(10)−98, b(10), b(10)−98++, b(11)++, b(11)−98
Matched y ions: y(2), y(3), y(4), y(8), y(9), y(10)−98
Precursor origin neutral loss: +

Peptide No.1540
RNSESGLELLSK
Confirmed sites: @S:3 or S:5
Ambiguous sites: @S:3 or S:5

MS/MS Fragmentation of RNSESGLELLSK
Found in AT3G28180.1, ATCSLC04 (Cellulose synthase-like C4); transferase, transferring glycosyl groups

Match to Query 2268: 1411.669539 from(471.563789,3+)
Elution from: 35.940 to 35.940 scan no 3487 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6708
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.048
Matched b ions: b(5), b(6), b(6)+, b(7)+, b(7)-98++, b(9)+, b(9)-98++, b(10)+, b(10)-98++, b (11)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(7)+
Precursor origin neutral loss:

Peptide No.1541

RPDSASKLPDSLEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RPDSASKLPDSLEK
Found in AT2G35920.1, helicase domain-containing protein

Match to Query 2615: 1621.770264 from(541.597364,3+)
Elution from: 28.020 to 28.020 scan no 2362 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1621.7712
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0054
Matched b ions: b(2), b(3), b(5)−98, b(5)−98++, b(7)−98++, b(7)−98, b(7), b(7)++, b(8)−98++, b(8)++, b(9)−98, b(10)−98++, b(10)++, b(11)++, b(13)−98++
Matched y ions: y(4), y(6), y(7)++, y(8)++, y(9)++, y(11)++, y(12)−98++, y(12)++, y(13)−98++)
Precursor origin neutral loss: +

Peptide No.1542
RPDTESAEHSPAQDEPHK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of RPDTESAEHSPAQDEPHK
Found in AT5G58040.1, ATFIP1[V] (ARABIDOPSIS HOMOLOG OF YEAST FIP1 [V]); RNA binding

Match to Query 3135: 2109.875564 from(528.476167,4+)
Elution from: 16.960 to 16.960 scan no 945 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2109.8753
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.032
Matched b ions: b(2), b(3), b(5), b(6)-98, b(9)-98++, b(10)+, b(10)-98++, b(11)-98++, b(12)+, b(14)+
Matched y ions: y(5)+, y(8)+, y(9)+
Precursor origin neutral loss: +

Peptide No.1543
RPSLSPPPPPYR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of RPSLSPPPPPYR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 1933: 1425.619222 from(713.816887,2+)
Elution from: 34.121 to 34.121 scan no 2979 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1425.6207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.022
Matched b ions: b(2), b(4)-98, b(5)-196, b(5)-98, b(6)-98, b(7)-98, b(7), b(7)-196, b(8)-196, b(8)-98, b(9)-196
Matched y ions: y(4), y(6), y(7), y(9)-98, y(9), y(9)-196
Precursor origin neutral loss: +

Peptide No.1544
RPSPAVRASYQR
Confirmed sites: ”@S:9,@Y:10”
Ambiguous sites:

MS/MS Fragmentation of RPSPAVRASYQR
Found in AT2G44410.1, protein binding / zinc ion binding

Match to Query 2560: 1546.683837 from(516.568555,3+) Elution from: 32.141 to 32.141 scan no 2962 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1546.6806
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y10 : Phospho (Y)
Ions Score: 26 Expect: 0.024
Matched b ions: b(2), b(3), b(5)+, b(5), b(6), b(6)+, b(7)+, b(9)−98, b(9)+, b(9)−98++, b(11)+, b(11)−98++
Matched y ions: y(1), y(3), y(5)−98, y(5)+, y(6), y(6)+, y(6)−98++, y(7)−98, y(7)−98++, y(8)−98++, y(8)−98, y(9)+, y(9)−98, y(9)−98++, y(10)−98++, y(11)+
Precursor origin neutral loss:

Peptide No.1545
RPSPDYGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RPSPDYGR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding

Match to Query 558: 1026.427680 from(514.221116,2+)
Elution from: 16.929 to 16.929 scan no 890 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1026.4284
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0019
Matched b ions: b(2), b(3)–98, b(5)–98, b(5), b(7)–98
Matched y ions: y(3), y(4)++, y(5), y(6), y(6)–98, y(7)–98
Precursor origin neutral loss: +

Peptide No.1546

RPTSSPLSAESPR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of RPTSSPLSAESPR
Found in AT1G27100.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69890.1);
similar to Cytosolic fatty-ac

Match to Query 1830: 1463.675912 from(732.845232,2+)
Elution from: 21.512 to 21.512 scan no 1497 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.6769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.005
Matched b ions: b(2), b(5), b(8), b(10), b(11)-98, b(11), b(11)+, b(12)-98++
Matched y ions: y(2), y(3), y(5), y(10)-98++, y(10), y(11), y(11)-98, y(12)-98, y(12)+
Precursor origin neutral loss: +

Peptide No.1547
RPTSSPLSAESPR
Confirmed sites: 
Ambiguous sites: @S:4 or S:5

MS/MS Fragmentation of RPTSSPLSAESPR
Found in AT1G27100.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69890.1); similar to Cytosolic fatty-ac

Match to Query 1845: 1463.675728 from(732.845140,2+)
Elution from: 22.198 to 22.198 scan no 1557 polarity:+

Peptide No.1547
Monoisotopic mass of neutral peptide Mr(calc): 1463.6769  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 20 Expect: 0.062  
Matched b ions: b(2), b(5)-98, b(6), b(7)-98, b(8)-98, b(11)-98, b(11)  
Matched y ions: y(2), y(10), y(11), y(12)++  
Precursor origin neutral loss: +  

Peptide No.1548  
RQDSFEMR  
Confirmed sites: @S:4  
Ambiguous sites:  

MS/MS Fragmentation of **RQDSFEMR**  
Found in **AT2G39480.1**, PGP6; ATPase, coupled to transmembrane movement of substances  
Match to Query 1252: 1147.447788 from(574.731170,2+)  
Elution from: 22.894 to 22.894 scan no 1691 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1147.4481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 2.8e−005
Matched b ions: b(2), b(3), b(4)−98, b(5)−98, b(6)−98, b(6), b(7)−98, b(7)
Matched y ions: y(1), y(2), y(5)−98, y(5), y(6)−98
Precursor origin neutral loss: +

Peptide No.1549
RQGSSGIVFDDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RQGSSGIVFDDR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80180.1);
similar to Os06g0601100 [Oryz]

Match to Query 2058: 1415.618996 from(708.816774,2+)
Elution from: 29.039 to 29.039 scan no 2580 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1415.6194
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 7.6e-005
Matched b ions: b(2), b(4)-98, b(5)-98, b(6)-98, b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98
Matched y ions: y(2), y(4), y(5), y(7)++, y(7), y(8), y(10)-98
Precursor origin neutral loss: +

Peptide No.1550
RQGSSGIVFDDR
Confirmed sites: ”@S:4,@S:5”
Ambiguous sites:

MS/MS Fragmentation of RQGSSGIVFDDR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80180.1); similar to Os06g0601100 [Oryz]

Match to Query 1584: 1495.584798 from(748.799675,2+)
Elution from: 34.093 to 34.093 scan no 3052 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1495.5857

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 20 Expect: 0.049
Matched b ions: b(5)-98++, b(6)-98, b(7), b(8), b(9), b(10), b(10)-99, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(11)++
Precursor origin neutral loss: +

Peptide No.1551

RQNTSEGPEFEAK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of RQNTSEGPEFEAK
Found in AT3G13235.1, ubiquitin family protein

Match to Query 2536: 1571.660926 from(786.837739,2+)
Elution from: 22.048 to 22.048 scan no 1561 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6617
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0007
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7), b(7)-98, b(9)-98, b(9), b(11)-98, b(11), b(11)-98++, b(12), b(12)-98, b(12)++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1552
RRDSEESLLLLDSR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RRDSEESLLLLDSR
Found in AT2G32040.1, integral membrane transporter family protein

Match to Query 2682: 1654.765956 from(552.595928,3+)
Elution from: 31.362 to 31.362 scan no 2897 polarity:+
**Peptide No. 1553**

**RREEQQQTDWSE**

**Confirmed sites:** @S:11

**Ambiguous sites:**

**MS/MS Fragmentation of RREEQQQTDWSE**

- Found in AT1G17930.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25010.1); similar to Os01g0738500 [Oryz]

- Match to Query 2689: 1670.665488 from(836.340020,2+)
- Elution from: 21.853 to 21.853 scan no 1354 polarity:+

**Monoisotopic mass of neutral peptide Mr(calc): 1654.7675**

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**

- S4 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score: 36 Expect: 0.0019**

**Matched b ions:** b(3)++, b(3), b(5)++, b(6)–98++, b(6)++, b(7)–98++, b(7)++, b(8), b(8)++, b(8)–98++, b(9)++, b(9)–98++, b(10)++, b(11)++, b(11)–98++

**Matched y ions:** y(2), y(3), y(4)++, y(4), y(5), y(6), y(7)

**Precursor origin neutral loss:** +
Monoisotopic mass of neutral peptide Mr(calc): 1670.6686
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.054
Matched b ions: b(2), b(8)+, b(9)+, b(10)+, b(11)−98++, b(11)++
Matched y ions:
Precursor origin neutral loss: +

Peptide No.1554
RRLAFVDNALESIFSGSSK
Confirmed sites: “@S:12,@S:15,@S:18”
Ambiguous sites:

MS/MS Fragmentation of RRLAFVDNALESIFSGSSK
Found in AT3G28040.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 4447: 2336.006295 from(779.676041,3+)
Elution from: 17.311 to 17.311 scan no 939 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2336.0003
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.057
Matched b ions: b(5), b(7), b(8), b(10)++, b(12)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)++
, b(16)-98++, b(17)-98++, b(17)++, b(17)-196++, b(18)++
Matched y ions: y(5), y(6)++, y(7)-196, y(8)-98, y(8)-196, y(8)-294, y(9)-294, y(10)++, y(12)++, y(12)-196++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++, y(14)-294++, y(15)++, y(16)-196++, y(16)-294++, y(17)-98++, y(17)++, y(17)-196++, y(18)-98++, y(18)-294++
Precursor origin neutral loss: +

Peptide No.1555

RRPSLSPPPPYR
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of RRPSLSPPPPYR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 2669: 1581.720696 from(528.247508,3+)
Elution from: 28.316 to 28.316 scan no 2430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1581.7218
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 44 Expect: 0.00035
Matched b ions: b(1), b(2), b(2)+, b(4)-98++, b(4)+, b(4)-98, b(5)-98++, b(5), b(5)-98, b(6)-196++, b(6)-98++, b(6)-98, b(6), b(6)+, b(6)-196, b(7)-196++, b(7)-98++, b(7)+, b(8)-196++, b(8)-98++, b(9)-196++, b(9)+, b(10)-98++, b(11)-98++, b(11)+, b(11)-196++
Matched y ions: y(1), y(3), y(4)+, y(4), y(5)+, y(5), y(6), y(6)+, y(7)-98, y(7), y(7)+, y(8), y(8)-98, y(8)-98++, y(8)+, y(9), y(9)-196++, y(9)+, y(9)-98++, y(10)+, y(10)-98, y(10), y(10)-98++, y(10)-196++, y(11)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.1556
RRPSLSPPPPYR
Confirmed sites: "@S:4,@Y:11"
Ambiguous sites:

MS/MS Fragmentation of RRPSLSPPPPYR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 2775: 1581.720838 from(791.867695,2+)
Elution from: 27.822 to 27.822 scan no 2405 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1581.7218
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y11 : Phospho (Y)
Ions Score: 24 Expect: 0.029
Matched b ions: b(2), b(4)−98, b(4), b(5)−98, b(5), b(6), b(6)−98, b(7)−98, b(11), b(11)−98, b(11)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(10)−98, y(11), y(11)−98++, y(11)−98
Precursor origin neutral loss: +

Peptide No.1557
RRPRLSPPPPYPYRDR
Confirmed sites: “@S:4,@S:6”
Ambiguous sites:

MS/MS Fragmentation of RRPRLSPPPPYPYRDR
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 3327: 1852.847700 from(464.219201,4+)
Elution from: 26.490 to 26.490 scan no 2182 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1852.8498
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.025
Matched b ions: b(1), b(2)+, b(2), b(4)--98++, b(5), b(5)--98++, b(6)--196++, b(6)--98++, b(6)+, b(7)--196++, b(7)--98++, b(7)+, b(8)--98++
Matched y ions: y(1), y(3), y(6), y(6)+, y(7)+, y(7)+++, y(8)+, y(8)+++, y(9)--98++, y(9)--98++, y(10)--98++, y(10)+, y(10)+++, y(11)--98++, y(11)+, y(12)--196++, y(12)--98++, y(12)+
Precursor origin neutral loss: +

Peptide No.1558
RRPSPDYGR
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of RRPSPDYGR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPlicing FACTOR 31); RNA binding

Match to Query 1177: 1182.528051 from(395.183293,3+) Elution from: 16.719 to 16.719 scan no 854 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1182.5295
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0027
Matched b ions: b(1), b(2), b(2)++, b(3)++, b(4)−98++, b(4)++, b(4)−98, b(5)−98++, b(5)++, b(6)−98++, b(7)++, b(8)−98++
Matched y ions: y(1), y(2), y(4), y(4)++, y(5), y(5)++, y(7)−98, y(8)++
Precursor origin neutral loss: +

Peptide No.1559
RRPSPDYTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RRPSPDYTR
Found in AT2G46610.1, arginine-serine-rich splicing factor, putative

Match to Query 1502: 1226.554602 from(409.858810,3+);
Elution from: 16.345 to 16.345 scan no 885 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1226.5557
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.04
Matched b ions: b(1), b(2)++, b(4)−98++, b(4)−98, b(4)++, b(5)−98++, b(6)−98++, b(6)++
Matched y ions: y(3), y(5)++, y(5)
Precursor origin neutral loss: +

Peptide No.1560

RRSEENLSVSVDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RRSEENLSVSVDK
Found in AT1G24706.1, similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:AT1G20920.1); similar to F5

Match to Query 2543: 1783.808646 from(595.610158,3+)  
Elution from: 25.317 to 25.317 scan no 1978 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1783.8101

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

**Ions Score:** 45  **Expect:** 0.00024

**Matched b ions:** b(3)-98++, b(3)+, b(3)-98, b(4)-98++, b(4)-98, b(4), b(5)+, b(5)-98++, b(5), b(6)+, b(6), b(6)-98++, b(7)+, b(7), b(7)-98++, b(8)+, b(8)-98++, b(9)-98++, b(9)+, b(10)+, b(10)-98++, b(11)-98++, b(11)+, b(12)-98++, b(12)+, b(13)+, b(13)-98++, b(14)+, b(14)-98++

**Matched y ions:** y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)+, y(13)-98++, y(13)+

**Precursor origin neutral loss:** +

---

**Peptide No.1561**

**RRSPDYGYAR**

**Confirmed sites:** @S:3

**Ambiguous sites:**

**MS/MS Fragmentation of RRSPDYGYAR**

**Found in AT1G23860.1, SRZ-21**

**Match to Query 1793:** 1319.576457 from (440.866095, 3+)

**Elution from:** 17.982 to 17.982 scan no 1082 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1319.5771
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00013
Matched b ions: b(1), b(2)++, b(3)++, b(3)-98++, b(3), b(3)-98, b(4)-98++, b(4)-98, b(4)++, b(5)++, b(5)-98++, b(6)++, b(6)-98++, b(7)-98++, b(7)++, b(9)++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(9)++
Precursor origin neutral loss: +

Peptide No.1562
RRSPEYDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RRSPEYDR
Found in AT2G46610.1, arginine-serine-rich splicing factor, putative

Match to Query 1322: 1157.495634 from(386.839154,3+)
Elution from: 14.169 to 14.169 scan no 684 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1157.4978
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0073
Matched b ions: b(1), b(2)+, b(3)+, b(3)−98++, b(4)−98++, b(5)+, b(6)+, b(7)+
Matched y ions: y(1), y(3), y(3)+, y(5)+, y(5), y(6)−98++, y(7)−98++, y(7)+
Precursor origin neutral loss: +

Peptide No.1563

RRSPLPLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RRSPLPLR
Found in AT1G16610.1, SR45 (arginine/serine-rich 45); RNA binding

Match to Query 928: 1073.584575 from(358.868801,3+)
Elution from: 19.162 to 19.162 scan no 1189 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1073.5859
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.016
Matched b ions: b(1), b(2)+, b(2), b(3)+, b(3), b(3)−98++, b(3)−98, b(4)−98++, b(4)−98, b(4)+, b(5), b(5)+, b(5)−98++, b(6)−98++, b(6)+, b(7)+, b(7)−98++
Matched y ions: y(1), y(3), y(4), y(5), y(5)+, y(6)+, y(6)−98++, y(7)+
Precursor origin neutral loss: +

Peptide No.1564
RRSPSPLYR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:
MS/MS Fragmentation of RRSPSPLYR
Found in AT2G29210.1, splicing factor PWI domain-containing protein

Match to Query 1132: 1290.562287 from(431.194705,3+)
Elution from: 20.153 to 20.153 scan no 1253 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1290.5635

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**

- **S3**: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- **S5**: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 35  **Expect:** 0.0026

**Matched b ions:** b(1), b(2)++, b(2), b(3)++, b(3)–98++, b(3)–98, b(3), b(4)–98++, b(5)–98++, b(5)–196, b(5)–98, b(5)–196++, b(5)++, b(6)–196++, b(6)–196, b(6)–98++, b(7)++, b(7)–196++, b(8)++, b(8)–98++

**Matched y ions:** y(1), y(2), y(3)++, y(3), y(4), y(4)++, y(5), y(5)++, y(6)–98, y(6), y(6)++, y(6)–98++, y(7)–196++, y(8)–98++, y(8)++

**Precursor origin neutral loss:** +

---

**Peptide No.1565**

**RRSPSPLYR**

**Confirmed sites:** “@S:3,@Y:8”

Ambiguous sites:

**MS/MS Fragmentation of RRSPSPLYR**

Found in **AT2G29210.1**, splicing factor PWI domain–containing protein

**Match to Query 1456: 1290.563157 from (431.194995, 3+)**

**Elution from:** 20.030 to 20.030 scan no 1273 polarity: +
Peptide No. 1566

RRSPSPYR

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of RRSPSPYR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 1040: 1097.511546 from(366.844458,3+)
Elution from: 14.583 to 14.583 scan no 725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1097.5131
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.042
Matched b ions: b(1), b(2)+, b(2), b(3)+, b(3), b(3)-98++, b(3)-98, b(4)-98++, b(4)-98, b(5)+, b(5)-98++, b(5)-98++, b(6)-98++, b(7)+
Matched y ions: y(1), y(3), y(3)+, y(4), y(5), y(5)+
Precursor origin neutral loss: +

Peptide No.1567
RRSVSPSPVR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of RRSVSPSPVR
Found in AT1G70620.1, cyclin-related

Match to Query 1130: 1299.583236 from(434.201688,3+)
Elution from: 17.181 to 17.181 scan no 952 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1299.5849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.038
Matched b ions: b(3)++, b(4)−98++, b(5)−98++, b(5)−196++, b(6)−196++, b(7)−98++, b(8)−196++
Matched y ions: y(4), y(5), y(8)−196++
Precursor origin neutral loss: +

Peptide No.1568
RRSVTPPR
Confirmed sites: “@S:3,@T:5”
Ambiguous sites:

MS/MS Fragmentation of RRSVTTPPR
Found in AT1G23860.1, SRZ−21

Match to Query 971: 1127.498919 from(376.840249,3+)
Elution from: 16.812 to 16.812 scan no 892 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1127.5002
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0093
Matched b ions: b(3)++, b(3)−98++, b(4)−98++, b(4)++, b(5)−196++, b(5)−98++, b(6)−196++
Matched y ions: y(3), y(4)−98, y(5), y(6)−98++
Precursor origin neutral loss: +

Peptide No.1569
RSADPAAVSSVDDQFALSSSE
Confirmed sites: “@S:9,@S:10”
Ambiguous sites: @S:18orS:19orS:20

MS/MS Fragmentation of RSADPAAVSSVDDQFALSSSE
Found in AT1G71770.1, PAB5 (POLY(A)−BINDING PROTEIN); RNA binding

Match to Query 3887: 2377.878336 from(793.633388,3+)
Elution from: 49.755 to 49.755 scan no 5173 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2377.8753
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 24 Expect: 0.026
Matched b ions: b(12)++, b(13)++, b(14)−98++, b(15)−196++
Matched y ions: y(10)−98++, y(13)−294++, y(15)−294++, y(15)++, y(16)−196++, y(17)−294++, y(20)−294++

Precursor origin neutral loss:

Peptide No.1570

RSASWPQL
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSASWPQL
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 859: 1023.453394 from(512.733973,2+)
Elution from: 42.940 to 42.940 scan no 4417 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1023.4539
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0014
Matched b ions: b(2)-98, b(3)+, b(4)+, b(4)-98, b(4), b(5)-98, b(5), b(5)+, b(6)-98, b(6), b(6)-98++, b(6)+, b(7)-98, b(7), b(7)-98++, b(7)+
Matched y ions: y(2), y(3), y(4), y(5)+, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1571
RSASWPQL
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RSASWPQL
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 663: 1023.453490 from(512.734021,2+)
Elution from: 45.725 to 45.725 scan no 4510 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1023.4539
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00013
Matched b ions: b(2), b(3), b(4)+, b(4)-98, b(4), b(5)-98, b(5), b(5)+, b(6)-98, b(6), b(6)+, b(6)-98++, b(7)-98, b(7), b(7)-98++, b(7)+
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6)+, y(6)-98++
Precursor origin neutral loss: +

Peptide No.1572
RSDKASASK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of RSDKASASK
Found in AT5G39860.1, PRE1 (PACLOBUTRAZOL RESISTANCE1); DNA binding / transcription factor

Match to Query 716: 1028.465860 from(515.240206,2+)
Elution from: 27.560 to 27.560 scan no 2339 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1028.4651
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.044
Matched b ions: b(2), b(3), b(4)++, b(6)++, b(7)++, b(8)−98
Matched y ions: y(4), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1573
RSFCIPNITETPKSSR
Confirmed sites: "@S:2,@S:14,@S:15"
Ambiguous sites:

MS/MS Fragmentation of RSFCIPNITETPKSSR
Found in AT2G40640.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05230.1); similar to hypothetical prote

Match to Query 3038: 2131.850304 from(711.624044,3+)  
Elution from: 43.720 to 43.720 scan no 4332 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2131.8564
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.032
Matched b ions: b(4)-98, b(5)++, b(5)-98, b(6)-98++, b(6)-98, b(7)-98, b(8)-98++, b(11)++, b(12)-98++, b(13)-98++, b(15)-294++
Matched y ions: y(4)++, y(5)-98++, y(8)++, y(10)++, y(11)-98++, y(12)-196++, y(13)+, y(14)-98++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.1574

RSLSPRSPALQK
Confirmed sites: "@S:2,@S:4,@S:7"
Ambiguous sites:

MS/MS Fragmentation of RSLSPRSPALQK
Found in AT5G64200.1, ATSC35 (""Arabidopsis thaliana arginine-serine-rich splicing factor 35, 35 kDa protein""); RNA bindin

Match to Query 2178: 1578.670110 from(790.342331,2+) Elution from: 23.532 to 23.532 scan no 1768 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1578.6721
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.03
Matched b ions: b(2), b(3)-98, b(4)-98, b(5), b(5)-196, b(6), b(6)-98, b(7)-196, b(7)-98, b(9), b(10)-294++, b(10), b(10)++, b(11)-196++, b(11)-98++, b(11)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10)-98, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1575
RSLSPVYR
Confirmed sites: “@S:2,@S:4”
Ambiguous sites:

MS/MS Fragmentation of RSLSPVYR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding

Match to Query 927: 1136.477402 from(569.245977,2+)
Elution from: 27.552 to 27.552 scan no 2279 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1136.4780
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 30 Expect: 0.0063
Matched b ions: b(2), b(3)-98, b(4)-196, b(4)-98, b(5)-98, b(5), b(6)-196, b(6)-98, b(6), b(7), b(7)-98
Matched y ions: y(1), y(2), y(4), y(5)-98, y(5), y(6), y(6)+, y(6)-98
Precursor origin neutral loss: +

Peptide No.1576
RSLSRSPIQLSR
Confirmed sites: “@S:2,@S:4,@S:6”
Ambiguous sites:

MS/MS Fragmentation of RSLSRSPIQLSR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 2389: 1638.703410 from(820.358981,2+)
Elution from: 32.369 to 32.369 scan no 2930 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 1638.7045
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.011
Matched b ions: b(2), b(3)−98, b(4)−98, b(5), b(5)−98, b(6)−196, b(6)−98, b(8), b(8)−98, b(9)−98, b(9), b(10), b(11)−196, b(11)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)−98, y(8), y(9), y(9)−98, y(9)−196++, y(10), y(10)−98, y(11)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1577

RSPDYQDYQDVITGSR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSPDYQDYQDVITGSR
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to unnamed protein pr

Match to Query 3442: 1978.839316 from(990.426934,2+)
Elution from: 42.260 to 42.260 scan no 4285 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1978.8422
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.7e-006
Matched b ions: b(4), b(5), b(6), b(7), b(7)-98, b(8), b(10)-98, b(10), b(11)-98, b(12), b(13)
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(14)
Precursor origin neutral loss: +

Peptide No.1578
RSPEGNTNSEIEGSLLCK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSPEGNTNSEIEGSLLCK
Found in AT2G04235.1, similar to hypothetical protein [Trifolium pratense] (GB:BAE71230.1)

Match to Query 3529: 2069.906412 from(690.976080,3+)
Elution from: 36.999 to 36.999 scan no 3585 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2069.9088  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
**Ions Score:** 50 Expect: 0.00012  
**Matched b ions:** b(4), b(6), b(8), b(8)−98++, b(9)+, b(10)+, b(11)+, b(13)−98++, b(14)−98++, b(14)+, b(15)+, b(16)+, b(17)+, b(17)−98++  
**Matched y ions:** y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)+, y(11)+, y(15)+, y(16)+  
**Precursor origin neutral loss:**

---

**Peptide No. 1579**

RSPEGNTNSEIEGSLLCK  
**Confirmed sites:** @T:7  
**Ambiguous sites:**

MS/MS Fragmentation of RSPEGNTNSEIEGSLLCK  
**Found in** AT2G04235.1, similar to hypothetical protein [Trifolium pratense] (GB:BAE71230.1)

Match to Query 3646: 2069.906094 from(690.975974,3+)  
**Elution from:** 37.729 to 37.729 scan no 3649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2069.9088  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 31 Expect: 0.01  
Matched b ions: b(5), b(6), b(8)–98++, b(8), b(9)–98, b(10)++, b(10), b(10)–98++, b(11)–98++, b(11) ++, b(13)–98++, b(14)++, b(15)–98++, b(16)++, b(16)–98++, b(17)++  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(10)++, y(11)++  
Precursor origin neutral loss:  

Peptide No.1580

RSPSSQDSLPGIALYR  
Confirmed sites: @S:2  
Ambiguous sites: @S:4 or S:5  

MS/MS Fragmentation of RSPSSQDSLPGIALYR  
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/  

Match to Query 3205: 1905.836470 from(953.925511,2+)  
Elution from: 51.042 to 51.042 scan no 5361 polarity:+  

---
Monoisotopic mass of neutral peptide Mr(calc): 1905.8387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.024
Matched b ions: b(2), b(7)−98, b(7), b(9), b(9)−98, b(12), b(12)−98, b(13), b(15)
Matched y ions: y(4), y(7), y(8), y(9), y(11), y(14)−98, y(14)
Precursor origin neutral loss: +

Peptide No.1581
RSPTYEAYPR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSPTYEAYPR
Found in AT4G36980.1, similar to peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thaliana]

Match to Query 1789: 1318.570124 from(660.292338,2+) Elution from: 22.951 to 22.951 scan no 1750 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1318.5707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0014
Matched b ions: b(2), b(2)-98, b(6), b(6)-98, b(7), b(8), b(8)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9)++
Precursor origin neutral loss: +

Peptide No.1582

RSPTYEAYPR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of RSPTYEAYPR
Found in AT4G36980.1, similar to peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thalian]

Match to Query 1671: 1318.568986 from(660.291769,2+)
Elution from: 24.176 to 24.176 scan no 1847 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1318.5707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 27 Expect: 0.013
Matched b ions: b(2), b(6), b(6)-98, b(7), b(8), b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(9)
Precursor origin neutral loss: +

Peptide No.1583
RSPYANGV
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSPYANGV
Found in AT1G23860.1, SRZ-21

Match to Query 457: 942.395230 from(472.204891,2+)
Elution from: 20.862 to 20.862 scan no 1443 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 942.3960
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00037
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(7)++
Matched y ions: y(2), y(3), y(4)
Precursor origin neutral loss: +

Peptide No.1584
RSPYANGV
Confirmed sites:
Ambiguous sites: @S:2orY:4

MS/MS Fragmentation of RSPYANGV
Found in AT1G23860.1, SRZ-21

Match to Query 565: 942.395128 from(472.204840,2+)
Elution from: 20.588 to 20.588 scan no 1415 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 942.3960
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Y4 : Phospho (Y)
Ions Score: 36 Expect: 0.00086
Matched b ions: b(4), b(5), b(6), b(7)
Matched y ions: y(2), y(3)
Precursor origin neutral loss: +

Peptide No.1585

RSRSPPR
Confirmed sites: "@S:2,@S:4"
Ambiguous sites:

MS/MS Fragmentation of RSRSPPR
Found in AT5G64200.1. ATSC35 (""Arabidopsis thaliana arginine-serine-rich splicing factor 35, 35 kDa protein""); RNA bindin

Match to Query 504: 1014.415602 from(339.145810,3+)
Elution from: 12.422 to 12.422 scan no 623 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1014.4161
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.036
Matched b ions: b(2)−98++, b(2), b(3)−98++, b(3)++, b(4)+, b(4)−98++, b(5)−98++, b(5)−196++, b(6)−196++
Matched y ions: y(2), y(4)−98, y(4)++
Precursor origin neutral loss: +

Peptide No.1586

RSSLRENIAEDDTNR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of RSSLRENIAEDDTNR
Found in AT3G19370.1, similar to transport protein-related [Arabidopsis thaliana] (TAIR:AT2G23360.1); similar to Prefoldi

Match to Query 2374: 1854.821211 from(619.281013,3+)  
Elution from: 23.437 to 23.437 scan no 1661 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1854.8221
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.05
Matched b ions: b(3)−98, b(7)−98++, b(7)++, b(8)−98++, b(8)++, b(9)−98++, b(9)++, b(10)−98++, b(12)−98++, b(13)++
Matched y ions: y(3), y(4), y(6), y(7), y(12)++
Precursor origin neutral loss: +

Peptide No.1587
RSPIKPIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RSSPIKPIR
Found in AT2G03150.1, EMB1579 (EMBRYO DEFECTIVE 1579); binding

Match to Query 1182: 1132.610307 from(378.544045,3+) Elution from: 17.669 to 17.669 scan no 1013 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1132.6118
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.018
Matched b ions: b(2), b(3)−98, b(3), b(4)−98, b(5)−98, b(5)
Matched y ions: y(1), y(3)++, y(3), y(4), y(4)++, y(5)++, y(6)++, y(7)++, y(7)−98++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1588
RSSSMEKIMR
Confirmed sites: 
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of RSSSMEKIMR
Found in AT1G45207.2, remorin family protein

Match to Query 1892: 1319.574952 from(660.794752,2+) 
Elution from: 18.406 to 18.406 scan no 1101 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1319.5727
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 Expect: 0.028
Matched b ions: b(3)-98, b(4), b(5), b(9)-98++, b(9)++
Matched y ions: y(5), y(6), y(7), y(9)-98++, y(9)-98, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1589

RSTFGSNTYTRQPSK
Confirmed sites:
Ambiguous sites: @T:3

MS/MS Fragmentation of RSTFGSNTYTRQPSK
Found in AT3G22910.1, calcium-transporting ATPase, plasma membrane-type, putative / Ca (2+)-ATPase, putative (ACA13)

Match to Query 3306: 1808.818896 from(603.946908,3+)
Elution from: 23.283 to 23.283 scan no 1781 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1808.8206
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.054
Matched b ions: b(4), b(5)−98, b(6)++, b(6), b(7), b(7)++, b(8)++, b(9)++, b(9), b(9)−98++, b(14)−98++
Matched y ions: y(6)++, y(6), y(8)++, y(9)++, y(9), y(13)++
Precursor origin neutral loss: +

Peptide No.1590

RSYSPGYEGAAAAAPDR
Confirmed sites: @S:2
Ambiguous sites: @Y:3orS:4

MS/MS Fragmentation of RSYSPGYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3173: 1897.738452 from(949.876502,2+)
Elution from: 30.384 to 30.384 scan no 2661 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.7396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y3 : Phospho (Y)
Ions Score: 89 Expect: 6.9e-009
Matched b ions: b(4)--98, b(6)--98, b(7), b(7)--98, b(8)--98, b(8), b(10)--98, b(10), b(11)--98++, b(11), b (12), b(13)--98, b(13), b(14), b(14)--98, b(16), b(16)--98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(15)
Precursor origin neutral loss: +

Peptide No.1591

RSYSPGYEGAAAAAPDR
Confirmed sites: "@S:2,@Y:7"
Ambiguous sites:

MS/MS Fragmentation of RSYSPGYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3170: 1897.738336 from(949.876444,2+)
Elution from: 29.623 to 29.623 scan no 2607 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.7396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 89 Expect: 7.8e-009
Matched b ions: b(3)–98, b(5), b(7), b(7)–98, b(8)–98, b(8), b(9)–98, b(10)–98, b(10), b(11), b(11)–98, b(12), b(12)–98, b(13), b(13)–98, b(14), b(14)–98, b(15)–98, b(16), b(16)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(12), y(14), y(15)
Precursor origin neutral loss: +

Peptide No. 1592

RSYSPGYEAAAAAPDR
Confirmed sites: ”@S:4,@Y:7”
Ambiguous sites:

MS/MS Fragmentation of RSYSPGYEAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3167: 1897.738686 from(633.586838,3+)
Elution from: 29.640 to 29.640 scan no 2662 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.7396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 61 Expect: 5.2e-006
Matched b ions: b(4), b(5), b(7), b(7)-98++, b(8)-98++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11)++, y(12), y(12)++, y(13)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1593

RSYPYEGAAAAAPDR
Confirmed sites:
Ambiguous sites: ”@S:2orY:3orS:4, @S:2orY:3orS:4”

MS/MS Fragmentation of RSYPYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30; RNA binding

Match to Query 3128: 1897.738101 from(633.586643,3+)
Elution from: 29.624 to 29.624 scan no 2595 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.7396
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00013
Matched b ions: b(4)-98, b(5)+, b(6)-98, b(7), b(7)-98++, b(8), b(8)+, b(8)-98++, b(9)-98++, b(9)+, b(10)-98++, b(10)+, b(11)-98++, b(11)+, b(12)+, b(12)-98++, b(13)-98++, b(13)+, b(14)-98++, b(14)+, b(15)-98++, b(15)+, b(16)-98++, b(16)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)+, y(12)+, y(13)+
Precursor origin neutral loss: +

Peptide No.1594
RSYSPGYEGAAAAAPDR
Confirmed sites: @Y:7
Ambiguous sites: @S:2orY:3orS:4

MS/MS Fragmentation of RSYSPGYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3506: 1897.737666 from(633.586498,3+)
Elution from: 30.547 to 30.547 scan no 2716 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.7396

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
Y7 : Phospho (Y)

Ions Score: 41 Expect: 0.00049
Matched b ions: b(4), b(5), b(7), b(8), b(8)+, b(9)+, b(10)+, b(11)+, b(12)+, b(13)+, b(14)+, b(15)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)+, y(10), y(11)+, y(12)+, y(13)+
Precursor origin neutral loss: +

Peptide No.1595

RSYSPGYEGAAAAAPDRDR
Confirmed sites: @S:2
Ambiguous sites: @Y:3 or S:4

MS/MS Fragmentation of RSYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 4170: 2168.865756 from(723.962528,3+)
Elution from: 28.563 to 28.563 scan no 2344 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2168.8677
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Y3: Phospho (Y)
Ions Score: 37 Expect: 0.0017
Matched b ions: b(2), b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(10)-98++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(16)-98, b(17)-98++, b(18)-98++, b(18)++
Matched y ions: y(3)++, y(5), y(6)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1596
RSYSPGYEGAAAAAPDRDR
Confirmed sites: "@S:2,@Y:7"
Ambiguous sites:
MS/MS Fragmentation of RSYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding
Match to Query 4169: 2168.865388 from(1085.439970,2+)
Elution from: 28.570 to 28.570 scan no 2345 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2168.8677
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Y7 : Phospho (Y)
Ions Score: 29 Expect: 0.011
Matched b ions: b(3)−98, b(4)−98, b(7), b(8), b(8)−98, b(10), b(13), b(14), b(15)−98, b(16)−98, b(16), b(17)−98, b(18)−98, b(18), b(18)−98++, b(18)++
Matched y ions: y(3), y(10), y(11), y(12), y(14), y(16), y(17), y(18)−98, y(18)−98++
Precursor origin neutral loss: +

Peptide No.1597
RSYSPGYEGAAAAAPDRDR
Confirmed sites: @S:4
Ambiguous sites: @S:2orY:3

MS/MS Fragmentation of RSYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3936: 2168.863836 from(543.223235,4+)
Elution from: 28.071 to 28.071 scan no 2413 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2168.8677
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 3.3e-005
Matched b ions: b(3), b(4)+, b(4)+98, b(5)+98+, b(6)+98, b(6)+, b(6)+98++, b(7)+98, b(7)+, b(7)+98++, b(8)+98++, b(9)+98++, b(10)+98++, b(11)+98++
Matched y ions: y(1)+, y(3)+, y(6)+, y(7)+, y(8)+, y(9)+, y(10)+, y(11)+, y(12)+, y(13)+, y(14)+, y(15)+
Precursor origin neutral loss: +

Peptide No.1598
RTDESEAMSEDVNK
Confirmed sites: @S:5
Ambiguous sites:
MS/MS Fragmentation of RTDESEAMSEDVNK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1);
similar to nuclear matrix con

Match to Query 2749: 1689.651940 from(845.833246,2+)
Elution from: 21.790 to 21.790 scan no 1346 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1689.6553
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.4e-005
Matched b ions: b(3), b(6)–98, b(6), b(7)–98, b(9)–98, b(10)–98, b(11)–98, b(11), b(12)–98, b(12), b(13), b(13)–98
Matched y ions: y(3), y(10)–98, y(11)–98, y(13)–98++
Precursor origin neutral loss: +

Peptide No.1599
RTDESEAMSEDVNK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of RTDESEAMSEDVNK
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68790.1); similar to nuclear matrix con

Match to Query 1930: 1689.654006 from(845.834279,2+)
Elution from: 20.688 to 20.688 scan no 1368 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1689.6553
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 2.5e-009
Matched b ions: b(3), b(4), b(5), b(6), b(6)+, b(7), b(8), b(9)-98, b(10)-98, b(11), b(11)+, b(12)-98, b(12), b(12)+, b(13)-98, b(13), b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(8)-98, y(8), y(9)-98++, y(9)-98, y(11)-98, y(12), y(13)-98++
Precursor origin neutral loss: +

Peptide No.1600

RTSFGYDQEAR
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of RTSFGYDQEAR
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 1647: 1408.577002 from(705.295777,2+)
Elution from: 25.238 to 25.238 scan no 1965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1408.5772
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0022
Matched b ions: b(3)−98, b(4)−98, b(6), b(7)−98, b(7), b(8), b(9)−98, b(9), b(10)+
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(10)−98
Precursor origin neutral loss: +

Peptide No.1601
RTSSAPF
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RTSSAPF
Found in AT3G56850.1, AREB3 (ABA–RESPONSIVE ELEMENT BINDING PROTEIN 3); DNA binding / transcription factor/ transcription

Match to Query 240: 844.346446 from(423.180499,2+)
Elution from: 25.300 to 25.300 scan no 1902 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 844.3480
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.059
Matched b ions: b(3), b(4)−98, b(5)−98, b(5), b(5)++, b(6), b(6)++, b(6)−98++
Matched y ions: y(2), y(3), y(6)++
Precursor origin neutral loss: +

Peptide No.1602

RTSSTKISTSSSESNK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of RTSSTKISTSSSESNK
Found in AT1G65920.1, regulator of chromosome condensation (RCC1) family protein / zinc finger protein−related

Match to Query 2950: 1691.777766 from(564.933198,3+)
Elution from: 42.973 to 42.973 scan no 4402 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1691.7727
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.048
Matched b ions: b(8)-98
Matched y ions: y(4), y(6)++, y(7)++, y(8)-98++, y(10)-98++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1603
RTVLDER
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of RTVLDER
Found in AT1G08840.1, EMB2411 (EMBRYO DEFECTIVE 2411); ATP–dependent DNA helicase

Match to Query 599: 967.448436 from(484.731494,2+)
Elution from: 19.091 to 19.091 scan no 1230 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.4488
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0068
Matched b ions: b(1), b(3), b(3)−98, b(4)−98, b(4), b(4)−98++, b(5)−98, b(5), b(6), b(6)−98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)−98
Precursor origin neutral loss: +

Peptide No.1604

RVRVETLCLTK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of RVRVETLCLTK
Found in AT2G44930.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G28580.1); similar to Plant protein of u

Match to Query 1866: 1453.747848 from(485.589892,3+)
Elution from: 35.065 to 35.065 scan no 3286 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1453.7476  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 26 Expect: 0.015  
Matched b ions: b(7)++, b(8)++, b(9)++, b(10)++, b(10)-98++  
Matched y ions:  
Precursor origin neutral loss:  

Peptide No.1605  
RVSDTSELSDGEVK  
Confirmed sites: @S:6  
Ambiguous sites:  

MS/MS Fragmentation of RVSDTSELSDGEVK  
Found in AT4G02860.1, catalytic  

Match to Query 2560: 1600.696870 from(801.355711,2+)  
Elution from: 23.611 to 23.611 scan no 1839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1600.6981
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.019
Matched b ions: b(4), b(5), b(6), b(7)-98, b(10)-98, b(12), b(12)-98, b(13)
Matched y ions:
Precursor origin neutral loss: +

Peptide No.1606

RVSDTSELSDGEVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of RVSDTSELSDGEVK
Found in AT4G02860.1, catalytic

Match to Query 1808: 1600.696800 from(801.355676,2+) Elution from: 24.673 to 24.673 scan no 1821 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1600.6981
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.5e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(11)-98++, b(12)-98++, b(12)-98, b(13)-98, b(13)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7)-98, y(10)-98, y(10), y(11)++, y(11)
Precursor origin neutral loss: +

Peptide No.1607
RVSSFEALQPATR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RVSSFEALQPATR
Found in AT1G74910.1, ADP-glucose pyrophosphorylase family protein

Match to Query 2066: 1540.737664 from(771.376108,2+)
Elution from: 34.594 to 34.594 scan no 3224 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.7399
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 31 Expect: 0.0067  
Matched b ions: b(4)−98, b(5)−98, b(6)−98, b(7), b(7)−98, b(8)−98, b(8), b(9), b(9)−98  
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(11)−98  
Precursor origin neutral loss: +

Peptide No.1608

RVSSFEALQPATR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RVSSFEALQPATR
Found in AT1G74910.1, ADP-glucose pyrophosphorylase family protein

Match to Query 2640: 1540.737876 from(771.376214,2+)  
Elution from: 33.488 to 33.488 scan no 3181 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.7399
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 60 Expect: 1e-005
Matched b ions: b(2), b(4)+, b(4)−98, b(5)−98, b(6), b(6)−98, b(7)−98, b(7), b(8), b(8)−98, b(9), b(9)−98, b(10)−98, b(11)−98++, b(12)−98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)−98, y(11)−98, y(11), y(12)−98, y(12)++
Precursor origin neutral loss: +

Peptide No.1609
RVSTGSASSLLGTTTR
Confirmed sites: @S:6
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of RVSTGSASSLLGTTTR
Found in AT5G06560.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11850.2); similar to expressed protein

Match to Query 2935: 1651.732326 from(826.873439,2+)
Elution from: 36.487 to 36.487 scan no 3586 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1651.7331
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0075
Matched b ions: b(2), b(5), b(6)−98, b(7)−98, b(8), b(8)−98, b(8)−196
Matched y ions: y(3), y(4), y(5), y(9), y(10), y(13), y(13)−98++, y(14)−196++
Precursor origin neutral loss: +

Peptide No.1610

RVSVVDSMLLEDLSKR
Confirmed sites: "@S:8,@S:14"
Ambiguous sites:

MS/MS Fragmentation of RVSVVDSMLLEDLSKR
Found in AT2G32050.1, cell cycle control protein-related

Match to Query 3266: 1979.875452 from(495.976139,4+) Elution from: 35.165 to 35.165 scan no 3297 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1979.8788
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0017
Matched b ions: b(4), b(5), b(6)++, b(7)++, b(7), b(8)++, b(9)−98++, b(9)++, b(11)−98++, b(12)−98++, b(13)−98++, b(14)−196++
Matched y ions: y(3)−98, y(3), y(8)−98++, y(9)−98++, y(10)−196++, y(11)−196++
Precursor origin neutral loss: +

Peptide No.1611
RVYSEIR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RVYSEIR
Found in AT4G30010.1, similar to fiber protein Fb15 [Gossypium barbadense] (GB:AAP34362.1)

Match to Query 635: 1001.468608 from(501.741580,2+)
Elution from: 23.162 to 23.162 scan no 1688 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1001.4695
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00016
Matched b ions: b(1), b(2), b(3), b(4)–98, b(5)–98, b(5), b(6), b(6)–98
Matched y ions: y(1), y(2), y(3), y(4), y(4)–98, y(5)
Precursor origin neutral loss: +

Peptide No.1612

RYSPPYYSPPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RYSPPYYSPPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2311: 1461.642662 from(731.828607,2+) Elution from: 32.948 to 32.948 scan no 3056 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1461.6442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0013
Matched b ions: b(2), b(3)--98, b(3), b(4)--98, b(4)+, b(5)--98++, b(6), b(6)--98, b(7), b(7)--98, b(8), b(8)--98, b(9), b(10)--98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)--98, y(10)++
Precursor origin neutral loss: +

Peptide No.1613

RYSPPYYSPPR
Confirmed sites: “@S:3,@S:8”
Ambiguous sites:

MS/MS Fragmentation of RYSPPYYSPPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2129: 1541.609733 from(514.877187,3+)
Elution from: 37.644 to 37.644 scan no 3679 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0017
Matched b ions: b(2), b(3)++, b(3), b(4)−98++, b(4)++, b(4)−98, b(5), b(5)−98++, b(5)++, b(6), b(7), b(7)−98++, b(8)−196++, b(8)−98++, b(9)−196++
Matched y ions: y(3)++, y(3), y(4)++, y(4), y(4)−98++, y(4)−98, y(5)++, y(5), y(5)−98++, y(6), y(7), y(7)++, y(8)++, y(8)−98++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.1614

RYSPPYYSPPR
Confirmed sites: ”@S:3,@Y:6”
Ambiguous sites:

MS/MS Fragmentation of RYSPPYYSPPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2546: 1541.609182 from(771.811867,2+)
Elution from: 36.099 to 36.099 scan no 3480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 43 Expect: 0.00035
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(8)-98, b(8), b(9)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98
Precursor origin neutral loss: +

Peptide No.1615

RYSPPYYSSPR
Confirmed sites: @S:3
Ambiguous sites: @Y:7orS:8

MS/MS Fragmentation of RYSPPYYSSPR
Found in AT3G55460.1, SCL30 (SC35–like splicing factor 30); RNA binding

Match to Query 1836: 1541.609744 from(771.812148,2+) Elution from: 35.928 to 35.928 scan no 3373 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 33 Expect: 0.004
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(6), b(8)-98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9)-98
Precursor origin neutral loss: +

Peptide No. 1616

RYSPPYYSPPR
Confirmed sites: “@Y:2,@S:8”
Ambiguous sites:

MS/MS Fragmentation of RYSPPYYSPPR
Found in AT3G55460.1, SCL30 (SC35–like splicing factor 30); RNA binding

Match to Query 2536: 1541.609361 from(514.877063,3+)  
Elution from: 36.579 to 36.579 scan no 3556 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.014
Matched b ions: b(1), b(2), b(3)++, b(3), b(4), b(4)++, b(5), b(5)++, b(6), b(6)++, b(7), b(7)++, b(8)-98, b(8)-98++, b(10)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4)-98++, y(4), y(4)++, y(4)-98, y(5)++, y(5), y(5)-98++, y(5)-98, y(6), y(7)++, y(8)-98++, y(8)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1617

RYSPPYYSSPR
Confirmed sites: "@Y:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of RYSPPYYSSPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2647: 1541.609502 from(771.812027,2+)
Elution from: 36.928 to 36.928 scan no 3645 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1541.6105
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y6 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0032
Matched b ions: b(2), b(3), b(5), b(6), b(7), b(8)−98, b(8), b(9), b(9)−98, b(10)++
Matched y ions: y(2), y(3), y(4), y(4)−98, y(5)−98, y(5), y(6)−98, y(7)−98, y(7), y(8)−98, y(8)−98++, y(8), y(9), y(9)−98
Precursor origin neutral loss: +

Peptide No.1618

RYSPYYSSPWR
Confirmed sites: @S:3
Ambiguous sites: @Y:7orS:8

MS/MS Fragmentation of RYSPYYSSPWR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2963: 1697.710188 from(566.910672,3+)
Elution from: 32.287 to 32.287 scan no 2982 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1697.7116
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 39 Expect: 0.00091
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(6), b(6)-98, b(8)-98, b(8)-98++, b(11)+
Matched y ions: y(1), y(3)+, y(3), y(4)+, y(4), y(6)+, y(7)+, y(8)+, y(9)+, y(10)-98++, y(10)+, y(11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.1619
RYSSFQAAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RYSSFQAAK
Found in AT2G04560.1, glycotransferase family protein 19

Match to Query 943: 1136.504241 from(379.842023,3+)
Elution from: 32.495 to 32.495 scan no 2940 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1136.5015
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.065
Matched b ions: b(2), b(3)++, b(4)++, b(5)++, b(6)++, b(7)++, b(7)−98++, b(8)−98++, b(8)++
Matched y ions: y(6)++, y(7)−98++
Precursor origin neutral loss: +

Peptide No.1620
SAADLTTVLER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SAADLTTVLER
Found in AT1G14650.1, SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein

Match to Query 1410: 1254.585206 from(628.299879,2+)  
Elution from: 48.550 to 48.550 scan no 4873 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1254.5857
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00012
Matched b ions: b(5)-98, b(5), b(9)-98, b(9)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1621

SAANDSDHSDLEASVVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SAANDSDHSDLEASVVK
Found in AT5G46760.1, basic helix–loop–helix (bHLH) family protein

Match to Query 2300: 1823.756584 from(912.885568,2+)
Elution from: 29.117 to 29.117 scan no 2497 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1823.7574
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0005
Matched b ions: b(7), b(8)--98, b(8), b(9)--98, b(10), b(11), b(12), b(12)--98, b(13)--98, b(13), b(14)--98++, b(14)++, b(15)--98, b(15)++, b(15)--98++, b(16)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(13)--98++, y(13), y(13)--98, y(13)++, y(14)--98++, y(14)++, y(15)++, y(15)--98++
Precursor origin neutral loss: +

Peptide No.1622
SAANDSDHSDLEASVVK
Confirmed sites: "@S:6,@S:14"
Ambiguous sites:

MS/MS Fragmentation of SAANDSDHSDLEASVVK
Found in AT5G46760.1, basic helix–loop–helix (bHLH) family protein

Match to Query 2813: 1903.722768 from(635.581532,3+)
Elution from: 31.835 to 31.835 scan no 2833 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1903.7237
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0043
Matched b ions: b(7)−98, b(11)++, b(12)++, b(14)−98++, b(15)−196++, b(15)−98++, b(15)++, b(16)++,
b(16)−196++, b(16)−98++
Matched y ions: y(3), y(5), y(6)−98, y(7), y(9), y(10)++, y(11)−98++, y(12)++, y(13)−98++, y(13)++, y
(14)++, y(14)−98++, y(15)−98++, y(15)++, y(15)−196++, y(16)++
Precursor origin neutral loss: +

Peptide No.1623

SAANDSDHSDLEASVVK
Confirmed sites: “@S:6,@S:9”
Ambiguous sites:

MS/MS Fragmentation of SAANDSDHSDLEASVVK
Found in **AT5G46760.1**, basic helix-loop-helix (bHLH) family protein

Match to Query 2505: 1903.722614 from(952.868583,2+)
Elution from: 32.913 to 32.913 scan no 2899 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1903.7237
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00016
Matched b ions: b(7)-98, b(7), b(8)-98, b(10)-98, b(10), b(10)-196, b(11), b(12), b(12)-196++, b(12)-98, b(13), b(13)-98++, b(14)-196++, b(14)+, b(14)-98++, b(15), b(15)-98, b(15)+, b(15)-196, b(15)-196++, b(16), b(16)-98+-
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)+, y(10), y(12), y(12)+, y(12)-98, y(13), y(13)-98++, y(13)-98, y(13)-98++, y(14)-98++, y(15)-98++, y(15)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1624

SAANDSDHSDLEASVVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SAANDSDHSDLEASVVK
Found in AT5G46760.1, basic helix-loop-helix (bHLH) family protein

Match to Query 2304: 1823.756214 from(608.926014,3+)
Elution from: 30.518 to 30.518 scan no 2592 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1823.7574  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 24 Expect: 0.035  
Matched b ions: b(8), b(11)++, b(14)++, b(15)−98++, b(15)++  
Matched y ions: y(4), y(6), y(8)++, y(10)−98++, y(11)−98++, y(12)++, y(13)−98++, y(13)++, y(14)++,  
y(14)−98++, y(15)++  
Precursor origin neutral loss:  
Peptide No.1625

SAANDSDHSDLEASVVK  
Confirmed sites: “@S:9,@S:14”  
Ambiguous sites:  

MS/MS Fragmentation of SAANDSDHSDLEASVVK  
Found in AT5G46760.1, basic helix-loop-helix (bHLH) family protein  

Match to Query 2747: 1903.722504 from(635.581444,3+)  
Elution from: 32.760 to 32.760 scan no 2982 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1903.7237
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0091
Matched b ions: b(8)+, b(11)+, b(12)+98+, b(14)+, b(15)+98+, b(15)+196+, b(15)+, b(16)+
Matched y ions: y(5), y(6)+98, y(7), y(8)+98+, y(9)+, y(10)+98+, y(11)+196+, y(11)+, y(12)+, y(13)+,
y(13)+98+, y(14)+98+, y(14)+, y(15)+, y(15)+98+, y(15)+196+
Precursor origin neutral loss: +

Peptide No.1626

SAANDTEMDDDSGNEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of SAANDTEMDDDSGNEK
Found in AT5G09390.1, CD2-binding protein-related

Match to Query 2181: 1777.597674 from(889.806113,2+)
Elution from: 18.660 to 18.660 scan no 1123 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1777.5985
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 2.3e-007
Matched b ions: b(5), b(7), b(15)++
Matched y ions: y(5), y(6), y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(11), y(11)−98, y(12), y(12)−98,
y(13)++, y(14), y(14)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1627

SAASFTELDR
Confirmed sites: @S:1orS:4
Ambiguous sites: @S:1orS:4

MS/MS Fragmentation of SAASFTELDR
Found in AT1G79610.1, sodium proton exchanger, putative (NHX6)

Match to Query 935: 1175.484718 from(588.749635,2+)
Elution from: 36.718 to 36.718 scan no 3480 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1175.4859
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.013
Matched b ions: b(5)-98
Matched y ions: y(2), y(3), y(4), y(5)
Precursor origin neutral loss: +

Peptide No.1628
SAASFTELDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SAASFTELDR
Found in AT1G79610.1, sodium proton exchanger, putative (NHX6)

Match to Query 863: 1175.484430 from(588.749491,2+)  
Elution from: 37.929 to 37.929 scan no 3546 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1175.4859
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00013
Matched b ions: b(5)-98, b(9)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.1629

SADEQIPSSTSFVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SADEQIPSSTSFVK
Found in AT1G26270.1, phosphatidylinositol 3- and 4-kinase family protein

Match to Query 2380: 1574.685508 from(788.350030,2+)
Elution from: 41.264 to 41.264 scan no 3935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1574.6865
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.00011
Matched b ions: b(3), b(4)−98, b(5)−98, b(5), b(6)−98, b(6), b(12), b(13)−98, b(13)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1630

SADNISSFTSTDDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SADNISSFTSTDDK
Found in AT5G53620.1, similar to intracellular protein transport protein USO1–related [Arabidopsis thaliana] (TAIR:AT2G46)

Match to Query 1644: 1566.606230 from(784.310391,2+) 
Elution from: 35.785 to 35.785 scan no 3362 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1566.6087
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.021
Matched b ions: b(5), b(5)-98, b(6), b(7)
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++
Precursor origin neutral loss: +

Peptide No.1631

SADTLIDNDTHLIK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SADTLIDNDTHLIK
Found in AT5G42950.1, GYF domain-containing protein

Match to Query 2641: 1634.754020 from(818.384286,2+)
Elution from: 44.493 to 44.493 scan no 4466 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1634.7553
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0012
Matched b ions: b(5)-98, b(5), b(6)-98, b(7), b(11)-98++, b(12)-98, b(13)-98, b(13), b(13)-98++
Matched y ions: y(5), y(7), y(8), y(9), y(10)+, y(11)+, y(12)+, y(13)+
Precursor origin neutral loss: +

Peptide No.1632
SAENIDLEFQESR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SAENIDLEFQESR
Found in AT1G67900.1, phototropic-responsive NPH3 family protein

Match to Query 1811: 1616.669730 from(809.342141,2+)
Elution from: 43.682 to 43.682 scan no 4329 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1616.6719
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 6e-008
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++
Precursor origin neutral loss: +

Peptide No.1633
SAGDTLEYNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SAGDTLEYNR
Found in AT5G25110.1, CIPK25 (CBL–INTERACTING PROTEIN KINASE 25); kinase

Match to Query 1238: 1204.475864 from(603.245208,2+)
Elution from: 27.472 to 27.472 scan no 2078 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1204.4761
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.024
Matched b ions: b(4), b(6)–98, b(7)–98, b(8)
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.1634
SANEQLPVSASFVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SANEQLPVSASFVK
Found in AT2G03890.1, phosphatidylinositol 3- and 4-kinase family protein

Match to Query 2037: 1555.726558 from(778.870555,2+)
Elution from: 45.412 to 45.412 scan no 4692 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1555.7283
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 2.8e-006
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(12)-98++, b(13)-98, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1635
SAPTTPINQNAAAFAAVSEEER
Confirmed sites:
Ambiguous sites: @S:1orT:4orT:5

MS/MS Fragmentation of SAPTTPINQNAAAFAAVSEEER
Found in AT4G37870.1, phosphoenolpyruvate carboxykinase (ATP), putative / PEP carboxykinase, putative / PEPCK, putative

Match to Query 4361: 2424.093384 from(809.038404,3+)
Elution from: 56.566 to 56.566 scan no 6018 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2424.0958
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 5.9e-005
Matched b ions: b(7)-98, b(7), b(8)-98, b(11), b(12), b(14), b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(21)++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(15)++, y(16)++, y(18)++
Precursor origin neutral loss: +

Peptide No.1636

SASDEEEDGTVQR
Confirmed sites: @S:1orS:3
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SASDEEEDGTVQR
Found in AT5G04420.1, kelch repeat-containing protein

Match to Query 1509: 1501.555236 from(751.784894,2+) Elution from: 18.912 to 18.912 scan no 1139 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1501.5569
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 38 Expect: 0.00042
Matched b ions: b(8), b(8)−98, b(9)−98
Matched y ions: y(2), y(3), y(5), y(6), y(7)++, y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1637
SASFHTLDELEVR
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SASFHTLDELEVR
Found in AT1G64500.1, glutaredoxin family protein

Match to Query 2781: 1582.700464 from(792.357508,2+)
Elution from: 45.294 to 45.294 scan no 4746 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.7028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00044
Matched b ions: b(7)-98, b(10)-98, b(11)++, b(12)-98, b(12)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1638

SASFHTLDELEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASFHTLDELEVR
Found in AT1G64500.1, glutaredoxin family protein

Match to Query 2674: 1582.701586 from(792.358069,2+)
Elution from: 46.591 to 46.591 scan no 4852 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1582.7028
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00038
Matched b ions: b(6)-98, b(7)-98, b(8)-98, b(11)-98, b(11)+, b(12)-98, b(12), b(12)-98++
Matched y ions: y(5), y(6), y(8), y(9), y(10)+, y(11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.1639
SASFKEESDFFADLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASFKEESDFFADLK
Found in AT1G30690.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 3053: 1799.764398 from(900.889475,2+)
Elution from: 56.801 to 56.801 scan no 5865 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1799.7654
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 2.9e-006
Matched b ions: b(4)–98, b(7)–98, b(9), b(10), b(12)–98, b(12)++, b(12), b(12)–98++, b(13)–98, b(13), b(14)–98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)++, y(12)++, y(12), y(13)–98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1640
SASFLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASFLR
Found in AT5G37810.1, NIP4;1/NLM4 (NOD26–LIKE INTRINSIC PROTEIN 4;1); water channel

Match to Query 133: 759.329604 from(380.672078,2+)
Elution from: 24.911 to 24.911 scan no 1851 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 759.3316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.047
Matched b ions: b(2)
Matched y ions: y(1), y(2), y(3), y(4)-98++, y(4)-98, y(4), y(5)-98++
Precursor origin neutral loss:

Peptide No.1641

SASPPAAPADSSAPPHPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASPPAAPADSSAPPHPK
Found in AT5G62810.1, PEX14 (PEROXISOME DEFECTIVE 2)

Match to Query 2759: 1763.787528 from(588.936452,3+)
Elution from: 21.794 to 21.794 scan no 1535 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1763.7879
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0015
Matched b ions: b(6)-98, b(7)-98
Matched y ions: y(2), y(5)+, y(5), y(6), y(10)+, y(11)+, y(13)+, y(14)+, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.1642

SASVLESPDIENGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SASVLESPDIENGK
Found in AT3G54030.1, protein kinase family protein

Match to Query 2116: 1581.690782 from(791.852667,2+)
Elution from: 34.820 to 34.820 scan no 3292 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1581.6923  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 60 Expect: 9.3e-006  
Matched b ions: b(4), b(5), b(6), b(7)–98, b(7), b(8)–98, b(9), b(10)–98, b(10), b(11), b(11)–98, b(12), b(13), b(14), b(14)–98++  
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)–98, y(10), y(10)–98, y(11)+, y(11), y(11)–98, y(11)–98++, y(12)–98++, y(12), y(12)–98, y(12)++, y(13)+, y(13)–98++  
Precursor origin neutral loss: +  

Peptide No. 1643  
SASWPQL  
Confirmed sites:  
Ambiguous sites: @S:1orS:3  

MS/MS Fragmentation of SASWPQL  
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase  
Match to Query 355: 867.352162 from(434.683357,2+)  
Elution from: 53.426 to 53.426 scan no 5566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 867.3528
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.013
Matched b ions: b(4), b(4)–98, b(5)–98, b(6)–98, b(6), b(6)++
Matched y ions: y(1), y(3)
Precursor origin neutral loss: +

Peptide No.1644
SASYGALSDHQFSRPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASYGALSDHQFSRPR
Found in AT2G44160.1, MTHFR2 (METHYLENETETRAHYDROFOLATE REDUCTASE 2); methylenetetrahydrofolate reductase (NADPH)

Match to Query 3093: 1857.813399 from(620.278409,3+)
Elution from: 31.198 to 31.198 scan no 2823 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1857.8159
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00029
Matched b ions: b(3)–98, b(5)–98, b(10)–98, b(10)++, b(14)++
Matched y ions: y(7)++, y(8)++, y(9)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)–98++, y(15)–98++
Precursor origin neutral loss: +

Peptide No.1645

SAVDETDSGAFQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SAVDETDSGAFQR
Found in AT4G19880.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45020.1); similar to Glutathione S–tran

Match to Query 1693: 1548.609804 from(775.312178,2+)
Elution from: 28.603 to 28.603 scan no 2311 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1548.6093
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00014
Matched b ions: b(3), b(5)–98, b(6), b(9)–98, b(13)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(9)++, y(11)
Precursor origin neutral loss: +

Peptide No.1646

SCGMSISPSVYR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SCGMSISPSVYR
Found in AT4G08310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G44780.2); similar to hypothetical prote

Match to Query 1698: 1422.565088 from(712.289820,2+)
Elution from: 39.143 to 39.143 scan no 3874 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1422.5672
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00013
Matched b ions: b(4), b(6), b(10)-98
Matched y ions: y(2), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(10), y(10)-98, y(11)++
Precursor origin neutral loss: +

Peptide No.1647

SCSDTVNASYQEVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SCSDTVNASYQEVK
Found in AT1G54480.1, similar to WDL1 (WVD2−LIKE 1) [Arabidopsis thaliana]
(TAIR:AT3G04630.3); similar to Targeting prote

Match to Query 2487: 1666.653692 from(834.334122,2+)
Elution from: 29.605 to 29.605 scan no 2556 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1666.6545
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 70 Expect: 6e-007

Matched b ions: b(4)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(11)-98, b(12)-98, b(12)++, b(13)-98, b(13), b(13)-98++

Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++

Precursor origin neutral loss: +

Peptide No. 1648

SCSDTVNASYQEVK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SCSDTVNASYQEVK
Found in AT1G54460.1, similar to WDL1 (WVD2-LIKE 1) [Arabidopsis thaliana] (TAIR:AT3G04630.3); similar to Targeting prote

Match to Query 2529: 1666.653700 from(834.334126,2+) Elution from: 29.114 to 29.114 scan no 2522 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1666.6545
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 7e-005
Matched b ions: b(4), b(6)−98, b(8)−98, b(8), b(9)−98, b(12), b(12)++, b(13)−98, b(13), b(13)−98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1649
SDDDERGEEYLFK
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SDDDERGEEYLFK
Found in AT2G43130.1, ARA4 (Arabidopsis Rab GTPase homolog A5c); GTP binding

Match to Query 2002: 1681.648848 from(841.831700,2+)
Elution from: 40.977 to 40.977 scan no 3901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1681.6508
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0019
Matched b ions: b(6)-98, b(8), b(9), b(10)-98, b(11)-98, b(12)-98++
Matched y ions: y(9)+, y(10)+, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.1650

SDEENETVNSPTIWR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SDEENETVNSPTIWR
Found in AT5G04020.1, calmodulin-binding protein-related (PICBP)

Match to Query 3049: 1855.760158 from(928.887355,2+)
Elution from: 41.146 to 41.146 scan no 4103 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1855.7625
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.042
Matched b ions: b(9)++, b(13), b(13)–98, b(14)–98
Matched y ions: y(2), y(5), y(6), y(7)–98, y(7), y(8), y(8)–98, y(9)
Precursor origin neutral loss: +

Peptide No.1651
SDEKEEILSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SDEKEEILSPR
Found in AT2G34310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29530.1); similar to expressed protein,

Match to Query 1685: 1381.611622 from(691.813087,2+)
Elution from: 26.935 to 26.935 scan no 2189 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1381.6126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.011
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98
Matched y ions: y(2), y(3)-98, y(3), y(4)-98, y(6), y(7)-98, y(7), y(8)-98++, y(8)+, y(9)-98++, y(9) ++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1652
SDETSDEDELTSFGSMPVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDETSDEDELTSFGSMPVK
Found in AT2G39810.1, HOS1 (High expression of osmotically responsive genes 1)

Match to Query 4235: 2267.868332 from(1134.941442,2+)
Elution from: 54.023 to 54.023 scan no 5542 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2267.8664
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 1.7e-005
Matched b ions: b(6), b(8), b(9–98), b(9), b(10), b(11), b(11–98), b(12), b(12–98), b(15), b(17), b (18–98)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(17)++
Precursor origin neutral loss: +

Peptide No.1653
SDETSDEDELTSGSMPVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SDETSDEDELTSGSMPVK
Found in AT2G39810.1, HOS1 (High expression of osmotically responsive genes 1)

Match to Query 3269: 2267.864252 from(1134.939402,2+)  
Elution from: 52.619 to 52.619 scan no 5278 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2267.8664
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 7.5e-007
Matched b ions: b(9), b(10), b(11), b(14), b(14)−98, b(17), b(18)−98, b(19)++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(16), y(17)−98++
Precursor origin neutral loss: +

Peptide No.1654
SDEVIEVLSASPSK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 1980: 1539.706222 from(770.860387,2+)
Elution from: 46.086 to 46.086 scan no 4780 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1539.7069
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 5.7e-009
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9), b(10), b(11)–98, b(11), b(12)–98, b(12)++, b(13)–98, b(13)
Matched y ions: y(3), y(4), y(4)–98, y(5), y(5)–98, y(6)–98, y(6), y(7)–98, y(8), y(9), y(10), y(10)–98++, y(10)–98, y(11)–98, y(11)
Precursor origin neutral loss: +

Peptide No. 1655

SDEVIEVLSASPSK
Confirmed sites:
Ambiguous sites: "@S:11orS:13orS:9, @S:11orS:13orS:9"

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2599: 1619.672254 from(810.843403,2+)  
Elution from: 47.143 to 47.143 scan no 4916 polarity:+

Peptide No. 1655

SDEVIEVLSASPSK
Confirmed sites:
Ambiguous sites: "@S:11orS:13orS:9, @S:11orS:13orS:9"

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2599: 1619.672254 from(810.843403,2+)  
Elution from: 47.143 to 47.143 scan no 4916 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1619.6732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0018
Matched b ions: b(5), b(7), b(8)
Matched y ions: y(6)−98, y(6), y(7), y(7)−98, y(8), y(9), y(9)−98, y(10)
Precursor origin neutral loss: +

Peptide No.1656
SDEVIEVLSASPSK
Confirmed sites: 
Ambiguous sites: @S:11 or S:13

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2390: 1539.705342 from(770.859947,2+)
Elution from: 46.111 to 46.111 scan no 4798 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1539.7069
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 7.4e-005
Matched b ions: b(5), b(8), b(9)
Matched y ions: y(4), y(5), y(6), y(6)−98, y(7)−98, y(8), y(9), y(10), y(11)−98, y(11)
Precursor origin neutral loss: +

Peptide No.1657
SDEVIEVLSASPSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2062: 1539.706332 from(770.860442,2+) Elution from: 47.211 to 47.211 scan no 4741 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1539.7069
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1.5e-005
Matched b ions: b(4), b(6), b(8), b(9)–98, b(10)–98, b(11), b(11)–98, b(12)–98
Matched y ions: y(3), y(6)–98, y(6), y(7)–98, y(8), y(9), y(10), y(11), y(11)–98, y(13)++
Precursor origin neutral loss: +

Peptide No.1658
SDEVIEVLSASPSK
Confirmed sites: ”@S:9,@S:11”
Ambiguous sites:

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2857: 1619.670596 from(810.842574,2+)
Elution from: 47.175 to 47.175 scan no 4957 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1619.6732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0072
Matched b ions: b(3), b(7), b(8), b(9)+98, b(10)+98, b(11), b(11)+98, b(12)+196
Matched y ions: y(4), y(6), y(7), y(7)+98, y(8)+98, y(10)+196++, y(10)+98, y(10), y(11)+98
Precursor origin neutral loss: +

Peptide No.1659
SDEVIEVLSASPSK
Confirmed sites: @S:9
Ambiguous sites: @S:11orS:13

MS/MS Fragmentation of SDEVIEVLSASPSK
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra

Match to Query 2232: 1619.671308 from(810.842930,2+)
Elution from: 48.241 to 48.241 scan no 4835 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1619.6732
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 9e−005
Matched b ions: b(6), b(7), b(8)
Matched y ions: y(4), y(6)−98, y(6), y(7), y(8), y(8)−98, y(8)−196, y(9), y(9)−98, y(10)−196++, y(10)
Precursor origin neutral loss: +

Peptide No.1660
SDFSPESGIADYSASPDAK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of SDFSPESGIADYSASPDAK
Found in AT3G16310.1, mitotic phosphoprotein N' end (MPPN) family protein

Match to Query 3429: 2022.807356 from(1012.410954,2+)
Elution from: 42.766 to 42.766 scan no 4347 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2022.8095
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 Expect: 8.3e-008
Matched b ions: b(6), b(9), b(10), b(11), b(12), b(14), b(15)−98, b(17)−98, b(17)
Matched y ions: y(4), y(5), y(6)−98, y(6), y(7)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y(10), y(11), y(12)−98, y(12), y(13), y(13)−98, y(14)++, y(15)++, y(15), y(15)−98, y(15)−98++, y(16)−98++, y(16)++, y(17)++, y(17)−98++, y(18)−98++
Precursor origin neutral loss: +

Peptide No. 1661
SDIQSPNFQEQAEFR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SDIQSPNFQEQAEFR
Found in AT1G08680.1, ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAINING PROTEIN ZIGA4); DNA binding

Match to Query 3108: 1874.781268 from(938.397910,2+)
Elution from: 44.085 to 44.085 scan no 4489 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1874.7836
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 8.2e-007
Matched b ions: b(5)—98, b(7), b(7)—98, b(8), b(8)—98, b(9)—98, b(9), b(10)—98, b(10), b(13), b(14), b(14)—98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)—98, y(11), y(11)—98++, y(12)++, y(12)—98++, y(13)++, y(13)—98++
Precursor origin neutral loss: +

Peptide No. 1662
SDLQTPLVRPK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDLQTPLVRPK
Found in AT3G19820.1, DWF1 (DIMINUTO 1); catalytic

Match to Query 1938: 1332.679210 from(667.346881,2+)
Elution from: 31.010 to 31.010 scan no 2794 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1332.6802
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0011
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1663
SDNLCLYVQSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of SDNLCLYVQSR
Found in AT2G40120.1, protein kinase family protein

Match to Query 2007: 1433.600356 from(717.807454,2+)
Elution from: 38.794 to 38.794 scan no 3717 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1433.6010
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 72 Expect: 4.7e-007
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(8), b(9), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++
Precursor origin neutral loss:

Peptide No.1664

SDPFSEGNEQVMAFPGAR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SDPFSEGNEQVMAFPGAR
Found in AT1G17210.1, zinc ion binding

Match to Query 3516: 2017.820138 from(1009.917345,2+)
Elution from: 55.766 to 55.766 scan no 5935 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2017.8240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0014
Matched b ions: b(7)++, b(11)–98, b(12)–98, b(13)–98, b(13), b(14)–98, b(14), b(15)–98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12), y(15)++, y(16)–98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1665
SDPTLSEPCSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SDPTLSEPCSPK
Found in AT3G52710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G36220.1); similar to Os11g0153300 [Oryz]

Match to Query 1725: 1396.557396 from(699.285974,2+) Elution from: 26.659 to 26.659 scan no 2158 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1396.5582
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.03
Matched b ions: b(5), b(6), b(7)
Matched y ions: y(5), y(6), y(7), y(8), y(9)+, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1666

SDPVVSFR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SDPVVSFR
Found in AT1G56070.1, LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/translation

Match to Query 453: 985.426254 from(493.720403,2+)
Elution from: 36.389 to 36.389 scan no 3350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 985.4270
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0058
Matched b ions:
Matched y ions: y(2), y(3)−98, y(4), y(5)++, y(6)++, y(6), y(6)−98++, y(7)++
Precursor origin neutral loss: +

Peptide No.1667
SDQEEDDLEDGFSELEGSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDQEEDDLEDGFSELEGSK
Found in AT1G80270.1, DNA−binding protein, putative

Match to Query 3202: 2207.823738 from(1104.919145,2+);
Elution from: 59.255 to 59.255 scan no 5702 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2207.8267
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 112 Expect: 3.9e-011
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(9)+, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(15)-98++, b(16), b(16)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)+, y(14), y(15), y(16), y(17)++
Precursor origin neutral loss: +

Peptide No.1668

SDQEDDDLEDGFSELEGSK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SDQEDDDLEDGFSELEGSK
Found in AT1G80270.1, DNA-binding protein, putative

Match to Query 4102: 2207.823540 from(1104.919046,2+)
Elution from: 53.850 to 53.850 scan no 5749 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2207.8267
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 9.2e-007
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(12), b(14)−98, b(15)−98, b(15), b(16), b(16)−98
Matched y ions: y(5), y(6), y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(10), y(10)−98, y(11), y(11)−98, y(12), y(13)−98++, y(13), y(14), y(15), y(17)−98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1669
SDSESITAPK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDSESITAPK
Found in AT3G51160.1, MUR1 (MURUS 1)

Match to Query 725: 1113.458714 from(557.736633,2+)
Elution from: 22.701 to 22.701 scan no 1624 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1113.4591
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00064
Matched b ions: b(4)−98, b(4), b(5)−98++, b(7)++, b(8)−98, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8)++, y(8)
Precursor origin neutral loss: +

Peptide No.1670

SDSESITAPK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SDSESITAPK
Found in AT3G51160.1, MUR1 (MURUS 1)

Match to Query 720: 1113.459002 from(557.736777,2+)
Elution from: 22.136 to 22.136 scan no 1581 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1113.4591
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.025
Matched b ions: b(3), b(4), b(5)–98++, b(5), b(7), b(8)++, b(8)–98, b(8), b(9)–98++
Matched y ions: y(2), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1671

SDSGINGVDFTEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDSGINGVDFTEK
Found in AT5G40390.1, SIP1 (SEED IMBIBITION 1–LIKE); galactinol–sucrose galactosyltransferase/ hydrolase, hydrolyzing O–g

Match to Query 1868: 1447.586074 from(724.800313,2+)
Elution from: 39.572 to 39.572 scan no 3894 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1447.5868
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 4.3e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98++, b(9), b(9)-98, b(10), b(12)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1672
SDSGINGVDFTEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSGINGVDFTEK
Found in AT5G40390.1, SIP1 (SEED IMBIBITION 1-LIKE); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-g

Match to Query 1702: 1447.585676 from(724.800114,2+)
Elution from: 38.623 to 38.623 scan no 3802 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1447.5868
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 2.1e-007
Matched b ions: b(3)–98, b(3), b(4)–98, b(5)–98, b(5), b(6)–98, b(6)++, b(6), b(7)–98, b(8), b(8)–98, b(9)–98++, b(9), b(9)–98, b(10)–98, b(12)–98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)–98++, y(11)–98
Precursor origin neutral loss: +

Peptide No.1673
SDSNGNVEPVASER
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of SDSNGNVEPVASER
Found in AT4G24100.1, protein kinase family protein

Match to Query 1673: 1539.619722 from(770.817137,2+)  
Elution from: 23.051 to 23.051 scan no 1611 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1539.6202
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 8.1e-005
Matched b ions: b(7)-98, b(7), b(8), b(8)-98, b(11)-98, b(13)++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(8)++, y(9), y(12)-98++
Precursor origin neutral loss: +

Peptide No.1674

SDSPGKDEPGYNK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SDSPGKDEPGYNK
Found in AT2G04410.1, similar to NOI [Arabidopsis thaliana] (TAIR:AT5G55850.1); similar to nitrate-induced NOI protein [Z

Match to Query 1502: 1472.581536 from(737.298044,2+)
Elution from: 17.810 to 17.810 scan no 1023 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1472.5820
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00018
Matched b ions: b(4), b(6)--98, b(7), b(7)--98, b(8), b(8)--98, b(10), b(11), b(12)--98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.1675

SDSPGKDEPGYNK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSPGKDEPGYNK
Found in AT2G04410.1, similar to NOI [Arabidopsis thaliana] (TAIR:AT5G55850.1); similar to nitrate-induced NOI protein [Z

Match to Query 1945: 1472.581186 from(737.297869,2+)  
Elution from: 18.070 to 18.070 scan no 1021 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1472.5820
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
 S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00014
Matched b ions: b(6)-98, b(8)
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(10)++, y(10), y(11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.1676

SDSPVSAVSEPQLPEQK
Confirmed sites: ”@S:1, @S:3”
Ambiguous sites:

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1);
similar to Os06g0206100 [Oryz

Match to Query 3629: 1956.810174 from(979.412363,2+)
Elution from: 41.483 to 41.483 scan no 4255 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1956.8118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 35 Expect: 0.0025
Matched b ions: b(7)-98, b(7), b(8)-98, b(8)-196, b(8), b(9)-98, b(9)-196, b(9)-98, b(10)-98, b(10)-196, b(10)-98, b(10), b(10)-196, b(10)-98, b(10), b(10)-196, b(11)-196, b(11)-98, b(11), b(11)-196, b(11)-98, b(13)-98, b(13), b(13)-196, b(14)-98
Matched y ions: y(4), y(5), y(7), y(9), y(10), y(11), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1677
SDSPVSAVSEPQLPEQK
Confirmed sites: "@S:6,@S:9"
Ambiguous sites: @S:1 or @S:3

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 2822: 2036.774840 from(1019.394696,2+)
Elution from: 43.706 to 43.706 scan no 4192 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2036.7782
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0036
Matched b ions: b(5), b(6)-98, b(7)-98, b(8)-98, b(10)-98, b(10)-196, b(10), b(11)-294++, b(11)-196, b(11)-294, b(11)-98, b(12)-196++, b(12)-98, b(13)-196, b(13)-98, b(13), b(14)-294, b(14)-196, b(14)-98, b(15)-98, b(16)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(12), y(13)++, y(14)-98++, y(14)-196, y(14)++
Precursor origin neutral loss: +

Peptide No.1678

SDSPVSAVSEPQLPEQK
Confirmed sites: @S:9
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 3217: 1956.810340 from(979.412446,2+)
Elution from: 39.891 to 39.891 scan no 3970 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1956.8118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00021
Matched b ions: b(5), b(7)-98, b(8)-98, b(9)-196, b(9), b(10)-98, b(10), b(11)-98, b(11), b(13)-98, b(13), b(13)-196, b(14)-98, b(14)-98
Matched y ions: y(4), y(5), y(7), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1679

SDSPVSAVSEPQLPEQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 3002: 1876.843396 from(939.428974,2+)
Elution from: 38.494 to 38.494 scan no 3785 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1876.8455
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.7e-007
Matched b ions: b(5), b(5)-98, b(7)-98, b(8), b(9)-98++, b(9), b(9)-98, b(10), b(12), b(13)-98, b(13), b(14)-98, b(15), b(16)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(14)+, y(14), y(15)+, y(15)-98++
Precursor origin neutral loss:

Peptide No.1680

SDSPVSAVSEPQLPEQK
Confirmed sites: “@S:3,@S:6”
Ambiguous sites:

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1);
similar to Os06g0206100 [Oryz]

Match to Query 3203: 1956.810092 from(979.412322,2+)
Elution from: 42.483 to 42.483 scan no 4241 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1956.8118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00074
Matched b ions: b(3), b(5), b(7)-98, b(7), b(8)-98, b(8)-196, b(8), b(9)-196, b(9)-98, b(10)-98, b(10), b(10)-196, b(11)-196, b(12)-98, b(12)-98, b(13)-98, b(13), b(14)-196, b(14)-98, b(14)+, b(16)
Matched y ions: y(4), y(5), y(7), y(9), y(10), y(11), y(12)-98, y(12), y(13)+, y(14)-98++, y(14)+, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1681

SDSPVSAVSEPQLPEQK
Confirmed sites: "@S:3,@S:6,@S:9"
Ambiguous sites:

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 3738: 2036.775352 from(1019.394952,2+)
Elution from: 44.345 to 44.345 scan no 4578 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2036.7782
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0025
Matched b ions: b(5), b(6)-98, b(7)-196, b(7)-98, b(8)-196, b(8), b(9)-98, b(10)-196++, b(10)-98, b(10)-196, b(10), b(10)-294, b(11)-294++, b(11)-196, b(11)-98, b(11), b(12)-294, b(12)-196++, b(12)-98, b(12), b(13)-196, b(13)-98, b(13), b(14)-294, b(14)-196, b(14)-98, b(15), b(16)-98, b(16)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(12), y(12)-98, y(12), y(13)-98++, y(13)-98++, y(14)-196, y(14)-196++, y(14)-196++, y(14)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1682
SDSPVSAVSEPQLPEQK
Confirmed sites: ”@S:3,@S:9”
Ambiguous sites:

MS/MS Fragmentation of SDSPVSAVSEPQLPEQK
Found in AT3G13990.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07660.1); similar to Os06g0206100 [Oryz]

Match to Query 2893: 1956.810092 from(979.412322,2+)
Elution from: 41.027 to 41.027 scan no 4100 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1956.8118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 48 Expect: 0.00013
Matched b ions: b(5), b(6), b(7)-98, b(7), b(8)-98, b(9)-196, b(10)-98, b(10), b(10)-196, b(11)-196, b(12)-98, b(13)-98, b(13), b(13)-196, b(14)-196, b(16)-98
Matched y ions: y(4), y(5), y(7), y(9)-98, y(9), y(10), y(10)-98, y(11)++, y(11), y(11)-98, y(12), y(12)-98, y(13)+, y(13)-98, y(14)+++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1683
SDSQSELSSGNSDALAEQR
Confirmed sites:
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SDSQSELSSGNSDALAEQR
Found in AT1G01960.1, EDA10 (embryo sac development arrest 10); guanyl-nucleotide exchange factor

Match to Query 3663: 2172.912972 from(1087.463762,2+)
Elution from: 39.901 to 39.901 scan no 3984 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2172.9172
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 6.5e-009
Matched b ions: b(6)-98, b(7)-98, b(7), b(8)-98, b(11), b(13), b(13)-98, b(14), b(15)-98, b(15), b(15)-98, b(16), b(17), b(17)-98, b(18)-98, b(18), b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(15), y(16)
Precursor origin neutral loss: +

Peptide No.1684
SDSQSELSSGNSDALAIEQR
Confirmed sites: @S:1orS:3orS:5
Ambiguous sites: 
MS/MS Fragmentation of SDSQSELSSGNSDALAIEQR
Found in AT1G01960.1, EDA10 (embryo sac development arrest 10); guanyl-nucleotide exchange factor
Match to Query 4040: 2172.918022 from(1087.466287,2+)
Elution from: 39.885 to 39.885 scan no 4041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2172.9172
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 1.3e-007
Matched b ions: b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(10), b(11), b(14)-98, b(15)-98, b(15), b(16), b(17)-98, b(17), b(18)-98, b(19)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(15)
Precursor origin neutral loss: +

Peptide No.1685
SDSQVFLFLNSK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SDSQVFLFLNSK
Found in AT2G36620.1, RPL24A (RIBOSOMAL PROTEIN L24); structural constituent of ribosome

Match to Query 1829: 1463.668298 from(732.841425,2+) 
Elution from: 59.348 to 59.348 scan no 6360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.6697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 9e-005
Matched b ions: b(3)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1686
SDSQVFLFLNSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSQVFLFLNSK
Found in AT2G36620.1, RPL24A (RIBOSOMAL PROTEIN L24); structural constituent of ribosome

Match to Query 2105: 1463.669434 from(732.841993,2+)
Elution from: 61.550 to 61.550 scan no 6509 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.6697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 3.6e-005
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1687

SDSVELDDDLSPPR
Confirmed sites: "@S:1,@S:11"
Ambiguous sites:

MS/MS Fragmentation of SDSVELDDDLSPPR
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);
Match to Query 2787: 1703.631596 from(852.823074,2+)
Elution from: 46.067 to 46.067 scan no 4749 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1703.6328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 9.2e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(9), b(10)-98++, b(10)-98, b(11)-98, b(11)-196, b(12)-98, b(12)-196
Matched y ions: y(3), y(4), y(4)-98, y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)++
Precursor origin neutral loss: +

Peptide No.1688

SDSVELDDLSPPR
Confirmed sites: @S:11
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SDSVELDDLSPPR
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 2459: 1703.629656 from(852.822104,2+) 
Elution from: 46.724 to 46.724 scan no 4755 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1703.6328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 7.9e-006
Matched b ions: b(3), b(4)−98, b(5), b(6)−98, b(7), b(10)−98++, b(10)−98, b(10), b(11), b(11)−98, b(11)−196, b(12)−98, b(12)−196, b(13)−196
Matched y ions: y(3), y(4), y(4)−98, y(5), y(5)−98, y(6), y(7), y(8), y(9), y(10), y(11), y(11)−98
Precursor origin neutral loss: +

Peptide No.1689

SDVVSENSTIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SDVVSENSTIR
Found in AT5G43310.1, COP1-interacting protein-related

Match to Query 1040: 1285.556130 from(643.785341,2+)
Elution from: 27.267 to 27.267 scan no 2238 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1285.5551
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00094
Matched b ions: b(3), b(4), b(6)−98, b(8)−98++
Matched y ions: y(3), y(5), y(6), y(7)−98, y(7), y(8), y(8)−98, y(8)++, y(9)−98++, y(9)−98, y(10)++
Precursor origin neutral loss: +

Peptide No.1690
SEEEAVVGEQSDAK
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of SEEEAVVGEQSDAK
Found in AT5G62000.1, ARF2 (AUXIN RESPONSE FACTOR 2); transcription factor

Match to Query 1750: 1485.586380 from(743.800466,2+)
Elution from: 22.966 to 22.966 scan no 1662 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1485.5871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.01
Matched b ions: b(6), b(9), b(10), b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)-98++, y(10)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1691
SEHADSDSDTFYIPSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SEHADSDSDTFYIPSK
Found in AT5G57110.1, ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calcium-transporting ATPase/ calmodulin binding

Match to Query 3078: 1877.734779 from(626.918869,3+)
Elution from: 36.392 to 36.392 scan no 3508 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1877.7356  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S1 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
**Ions Score:** 50 **Expect:** 6e-005  
**Matched b ions:** b(2), b(3)+, b(4), b(6)–98, b(6)+, b(6), b(7), b(7)–98++, b(7)+, b(7)–98, b(8), b(8)+, b(8)–98++, b(8)–98, b(9), b(9)–98++, b(9)+, b(10), b(10)+, b(10)–98++, b(11)–98++, b(11), b(11)+, b(12), b(12)–98++, b(12)+, b(13)+, b(13)–98++, b(14)–98++, b(14)+, b(15)–98++, b(15)+  
**Matched y ions:** y(2), y(3), y(4), y(5), y(5)+, y(6)+, y(6), y(7)+, y(7), y(8), y(8)+, y(13)+, y(15)+  
**Precursor origin neutral loss:**

Peptide No. 1692  
SEHADSDSTFYIPSK  
**Confirmed sites:** @S:6  
**Ambiguous sites:**

**MS/MS Fragmentation of SEHADSDSTFYIPSK**  
Found in AT5G57110.1, ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calcium transporting ATPase/ calmodulin binding  

Match to Query 2753: 1877.733680 from(939.874116,2+)  
Elution from: 36.356 to 36.356 scan no 3433 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1877.7356
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.3e-006
Matched b ions: b(3), b(4), b(5), b(6)+, b(6)-98, b(7), b(7)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98++, b(12), b(12)-98, b(13)-98, b(13), b(14)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1693
SEHADSDSDTFYIPS
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SEHADSDSDTFYIPS
Found in AT5G57110.1, ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calcium-transporting ATPase/ calmodulin binding

Match to Query 3276: 1877.735331 from(626.919053,3+);
Elution from: 38.460 to 38.460 scan no 3562 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1877.7356
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 8.2e-005
Matched b ions: b(5), b(6)++, b(7)++, b(7), b(8), b(8)−98++, b(8)++, b(8)−98, b(9), b(9)−98++, b(9)++, b(10), b(10)++, b(10)−98++, b(11)−98++, b(11), b(11)++, b(12)−98++, b(12)++, b(13)++, b(13)−98++, b(14)++, b(14)−98++, b(15)++
Matched y ions: y(2), y(3), y(4)++, y(4)−98++, y(5), y(5)++, y(6)++, y(6), y(7), y(7)++, y(8), y(9)++, y(9)−98++, y(10)−98++, y(14)−98++
Precursor origin neutral loss:

Peptide No.1694

SEINDEASGEEELLEK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SEINDEASGEEELLEK
Found in AT3G51880.1, HMGB1 (HIGH MOBILITY GROUP B 1); transcription factor

Match to Query 3815: 2114.839466 from(1058.427009,2+)
Elution from: 41.984 to 41.984 scan no 4249 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2114.8416
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
    S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 5e-009
Matched b ions: b(5), b(6), b(7), b(8), b(9)+, b(9), b(10), b(10)−98, b(12)−98, b(12), b(13)−98, b(13), b(14)−98, b(14), b(15)−98, b(15), b(16)−98, b(16), b(17)−98, b(17), b(17)+, b(17)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)−98, y(10), y(10)−98, y(11)−98, y(11), y(12), y(12)−98, y(13)−98, y(13), y(14)−98, y(14), y(15)−98++, y(15)−98, y(15)+, y(16)−98++, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.1695

SELESTDDGPEEVVEIPK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of SELESTDDGPEEVVEIPK
Found in AT1G20970.1, adhesin−related

Match to Query 2865: 2051.882892 from(1026.948722,2+)
Elution from: 49.396 to 49.396 scan no 4773 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2051.8823

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- T6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 26 **Expect:** 0.028

**Matched b ions:** b(8), b(16)–98, b(16), b(17)–98

**Matched y ions:** y(7), y(10), y(11), y(12), y(13)–98, y(15)–98++

**Precursor origin neutral loss:** +

---

**Peptide No.1696**

**SEMSQSQNSPIDTGR**

**Confirmed sites:** @S:9

**Ambiguous sites:**

**MS/MS Fragmentation of SEMSQSQNSPIDTGR**

**Found in** AT5G01400.1, ESP4 (ENHANCED SILENCING PHENOTYPE 4); binding

Match to Query 2695: 1731.676272 from(866.845412,2+)

Elution from: 19.866 to 19.866 scan no 1251 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1731.6771
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0022
Matched b ions: b(6)++, b(8), b(9)−98, b(11), b(11)−98, b(12), b(12)++
Matched y ions: y(3), y(4), y(6), y(7)−98, y(7), y(8), y(10)−98, y(10), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No. 1697
SEMSQSQNPSPTGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SEMSQSQNPSPTGR
Found in AT5G01400.1, ESP4 (ENHANCED SILENCING PHENOTYPE 4); binding

Match to Query 2650: 1715.681320 from(858.847936,2+)
Elution from: 23.802 to 23.802 scan no 1771 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.6822
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.6e-005
Matched b ions: b(3), b(5), b(6)-98, b(7)++, b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)++, b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(8)++, y(10), y(10)-98, y(11)-98, y(11)++, y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++, y(13)-98, y(14)++
Precursor origin neutral loss: +

Peptide No. 1698
SEMSQSQNSPIDTGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SEMSQSQNSPIDTGR
Found in AT5G01400.1, ESP4 (ENHANCED SILENCING PHENOTYPE 4); binding

Match to Query 2061: 1715.681216 from(858.847884,2+)
Elution from: 23.902 to 23.902 scan no 1722 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.6822
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.4e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9–98), b(9), b(10–98), b(11), b(11–98), b(12), b(12–98), b(13), b(13–98), b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7–98), y(8–98), y(8), y(10), y(10–98++), y(10–98), y(11)++, y(12)++, y(12)–98++, y(13)–98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1699
SEMSQSQNSPIDTGR
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of SEMSQSQNSPIDTGR
Found in AT5G01400.1, ESP4 (ENHANCED SILENCING PHENOTYPE 4); binding

Match to Query 2040: 1715.679105 from(572.900311,3+)
Elution from: 23.059 to 23.059 scan no 1692 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1715.6822
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0066
Matched b ions: b(5)
Matched y ions: y(3), y(4), y(5), y(7)++, y(8)++, y(9)++, y(10)−98++, y(10)++, y(11)++, y(11)−98++, y(12)++, y(13)++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.1700
SEPDSDSDSDGPQYEYFTGGEK
Confirmed sites: 
Ambiguous sites: @S:5orS:7

MS/MS Fragmentation of SEPDSDSDSDGPQYEYFTGGEK
Found in AT4G22150.1, PUX3 (LANT UBX DOMAIN−CONTAINING PROTEIN 3)
Match to Query 3371: 2325.845118 from(1163.929835,2+)
Elution from: 41.989 to 41.989 scan no 4142 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2325.8434
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.01
Matched b ions: b(10), b(10)-98, b(14), b(16)-98, b(20)++
Matched y ions: y(7), y(11), y(14), y(17)-98++, y(18)-98++, y(18)+++, y(19)+++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.1701

SERDSPDTSLR
Confirmed sites: @S:1orS:5
Ambiguous sites: @S:1orS:5

MS/MS Fragmentation of SERDSPDTSLR
Found in AT3G45830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G02290.1); similar to unknow protein [Or

Match to Query 1383: 1341.555182 from(671.784867,2+)
Elution from: 19.028 to 19.028 scan no 1142 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1341.5562
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 18 Expect: 0.068
Matched b ions: b(5)−98, b(5), b(6)−98, b(7), b(7)−98
Matched y ions: y(4), y(6)
Precursor origin neutral loss: +

Peptide No.1702

SESDLAAAIEELDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SEDSLAAAIEELDK
Found in AT1G80950.1, phospholipid/glycerol acyltransferase family protein

Match to Query 2430: 1569.682422 from(785.848487,2+)
Elution from: 64.465 to 64.465 scan no 6783 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.6811
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.7e-005
Matched b ions: b(5)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.1703

SESLGHRSDVSSPEAK
Confirmed sites: ”@S:3,@S:8,@S:11”
Ambiguous sites:

MS/MS Fragmentation of SESLGHRSDVSSPEAK
Found in AT3G48530.1, CBS domain-containing protein

Match to Query 3510: 1924.700196 from(642.574008,3+)
Elution from: 22.023 to 22.023 scan no 1574 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1924.7006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 36 Expect: 0.0015
Matched b ions: b(4)-98, b(6)-98, b(8)--, b(8)--98++, b(9)-98++, b(9)--, b(10)-196++, b(10)--98++, b(10)--, b(11)-196++, b(12)-98++, b(12)-98++, b(12)-98++, b(14)-98++, b(14)-98++, b(14)-98++, b(14)-98++
Matched y ions: y(2), y(4), y(6), y(6)-98, y(7)--, y(7), y(10)-++, y(12)-98++, y(12)-98++, y(12)-98++, y(12)-98++, y(13)-98++, y(14)-98++, y(15)-294++
Precursor origin neutral loss: +

Peptide No.1704
SESLGHRSDVSSPEAK
Confirmed sites: "@S:3,@S:8,@S:12"
Ambiguous sites:

MS/MS Fragmentation of SESLGHRSDVSSPEAK
Found in AT3G48530.1, CBS domain-containing protein

Match to Query 3555: 1924.699047 from (642.573625,3+)
Elution from: 21.602 to 21.602 scan no 1552 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1924.7006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.022
Matched b ions: b(3)-98, b(6)-98, b(7)-98, b(9)+++, b(9)-98++, b(10)-98++, b(10)-196++
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(10)+++, y(12)+++, y(12)-196++, y(12)-98++, y(13)+++, y(14)+++, y(14)-98++, y(14)-196++, y(15)-294++
Precursor origin neutral loss: +

Peptide No.1705

SETDFMTEYVVTR
Confirmed sites: @Y:9
Ambiguous sites:

MS/MS Fragmentation of SETDFMTEYVVTR
Found in AT1G01560.1, ATMPK11 (Arabidopsis thaliana MAP kinase 11); MAP kinase/ kinase

Match to Query 2454: 1656.671534 from(829.343043,2+)
Elution from: 48.354 to 48.354 scan no 5040 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1656.6742
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y9 : Phospho (Y)
Ions Score: 69 Expect: 9.6e-007
Matched b ions: b(5), b(6), b(7), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1706
SETHDEVFETSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SETHDEVFETSPK
Found in AT1G18190.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19950.1); similar to Os04g0652500 [Oryz]

Match to Query 2593: 1584.632210 from(793.323381,2+)
Elution from: 27.115 to 27.115 scan no 2246 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1584.6345
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0023
Matched b ions: b(5), b(6), b(9), b(11)−98, b(11)−98++
Matched y ions: y(2), y(3), y(4), y(4)−98, y(6)−98, y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)+, y(11)−98++
Precursor origin neutral loss: +

Peptide No.1707

SEVLSEQARSE
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SEVLSEQARSE
Found in AT3G59430.1, unknown protein

Match to Query 1169: 1313.549204 from(657.781878,2+)
Elution from: 22.710 to 22.710 scan no 1646 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1313.5500
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00017
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8), b(9), b(9)+++, b(10)--98++
Matched y ions: y(2), y(2)--98, y(3)--98, y(4), y(7)--98, y(7), y(8), y(9)--98, y(9)--98++, y(9)+++, y(10)++
Precursor origin neutral loss: +

Peptide No.1708

SEYGSTLDDDQR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SEYGSTLDDDQR
Found in AT1G66680.1, AR401

Match to Query 1522: 1464.539342 from(733.276947,2+)
Elution from: 28.574 to 28.574 scan no 2307 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1464.5406
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 8.6e-007
Matched b ions: b(2), b(3), b(4), b(5)+, b(5)−98, b(6)−98, b(7)−98, b(8)−98++, b(8), b(8)−98, b(9), b(9)−98, b(10), b(10)−98, b(10)−98++, b(11), b(11)−98, b(11)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), (7), y(8)−98, y(8), y(8)−98++, y(9)−98, y(9), y(10)−98++, y(10), y(10)−98, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.1709
SFADILQEGLER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFADILQEGLER
Found in AT3G10360.1, APUM4 (ARABIDOPSIS PUMILIO 4); RNA binding

Match to Query 2152: 1456.659174 from(729.336863,2+)
Elution from: 62.722 to 62.722 scan no 6748 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1456.6599
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 4.7e-007
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.1710

SFDDSPPAAAELR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFDDSPPAAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22960.1); similar to hypothetical prote

Match to Query 1727: 1454.604856 from(728.309704,2+)
Elution from: 40.119 to 40.119 scan no 4001 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 72 Expect: 4.4e-007
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(7), b(8), b(9), b(10)-98, b(11)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No. 1711

SFDDSPAAALR
Confirmed sites: "@S:1,@S:5"
Ambiguous sites:

MS/MS Fragmentation of SFDDSPAAALR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22960.1); similar to hypothetical prote

Match to Query 2052: 1534.572614 from(768.293583,2+) Elution from: 45.948 to 45.948 scan no 4606 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1534.5742
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.015
Matched b ions: b(5)-98, b(6)-196, b(6)-98, b(7)-196, b(8)+, b(9)-98, b(10)-98, b(10)-196, b(11)-98, b(11)
Matched y ions: y(3), y(4), y(8), y(9), y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.1712

SFDDSPAAELR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SFDDSPAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22960.1); similar to hypothetical prote

Match to Query 2071: 1454.608240 from(728.311396,2+)
Elution from: 41.279 to 41.279 scan no 4047 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.018
Matched b ions: b(5), b(8)−98, b(9)−98, b(12)++
Matched y ions: y(3), y(4), y(5), y(8), y(9)−98++, y(9)−98, y(10), y(11)−98++
Precursor origin neutral loss: +

Peptide No.1713
SFDDSPPAAELRR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFDDSPPAAELRR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22960.1); similar to hypothetical prote

Match to Query 2200: 1610.706534 from(806.360543,2+)  
Elution from: 35.549 to 35.549 scan no 3390 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1610.7090
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0057
Matched b ions: b(5)-98, b(6), b(7)-98, b(12)-98++, b(12)++
Matched y ions: y(6), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++
Precursor origin neutral loss: +

**Peptide No.1714**

SFDELLELSHHGNNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SFDELLELSHHGNNR**
Found in **AT1G60440.1**, ATCOAA/ATPANK1 (PANTOTHENATE KINASE 1); pantothenate kinase

Match to Query 2908: 1846.797324 from(616.606384,3+)
Elution from: 45.419 to 45.419 scan no 4693 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1846.7999
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.6e-005
Matched b ions: b(2), b(3)–98, b(4)–98, b(4), b(5)–98, b(6)–98, b(11)–98++
Matched y ions: y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1715
SFDELLELSQK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFDELLELSQK
Found in AT4G32180.1, ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase

Match to Query 1858: 1387.625654 from(694.820103,2+)
Elution from: 59.647 to 59.647 scan no 6309 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1387.6272
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 6.5e-007
Matched b ions: b(3), b(3)–98, b(4), b(5)–98, b(5), b(6), b(7)–98, b(7), b(8)–98, b(8), b(9), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1716

SFDFDQNER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFDFDQNER
Found in AT1G65710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G37010.1); similar to OSIGBa0115K01–H031

Match to Query 978: 1236.443762 from(619.229157,2+)  
Elution from: 37.850 to 37.850 scan no 3536 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1236.4448
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 Expect: 0.055
Matched b ions: b(3)
Matched y ions: y(4), y(5), y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.1717

SFETIPESR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFETIPESR
Found in AT3G14205.1, phosphoinositide phosphatase family protein

Match to Query 807: 1144.480168 from(573.247360,2+)
Elution from: 34.651 to 34.651 scan no 3100 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1144.4801
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.054
Matched b ions: b(4), b(5), b(5)-98, b(6)-98
Matched y ions: y(4), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1718

SFGDVNEIGAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFGDVNEIGAR
Found in AT4G32285.1, epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related

Match to Query 1087: 1243.523112 from(622.768832,2+)
Elution from: 38.028 to 38.028 scan no 3723 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1243.5234
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 3.4e-009
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.1719

SFGEFDLDGLLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFGEFDLDGLLK
Found in AT3G02880.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 1690: 1419.629742 from(710.822147,2+)
Elution from: 70.310 to 70.310 scan no 7370 polarity:+
Peptide No. 1720

SFGNLGEIGSVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFGNLGEIGSVK
Found in AT5G24890.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G31510.1); similar to putative KID-conta

Match to Query 1523: 1286.589960 from(644.302256,2+)
Elution from: 49.532 to 49.532 scan no 4995 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1286.5907
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 78 Expect: 1.2e-007
Matched b ions: b(3)–98, b(4)–98, b(4), b(5)–98, b(5), b(6)–98, b(7)–98, b(8)–98, b(9)–98, b(10), b(11)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No. 1721

SFGSNADLSPPPGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SFGSNADLSPPPGR
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 1579: 1383.581252 from(692.797902,2+) Elution from: 34.521 to 34.521 scan no 3256 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1383.5820

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 53 Expect: 2.9e-005
Matched b ions: b(6), b(7), b(8), b(9)--98, b(9), b(10)--98, b(10)--++, b(11)--98++
Matched y ions: y(3), y(4), y(5)--98, y(6)--98, y(6), y(7), y(7)--98, y(8), y(8)--98, y(9), y(9)--, y(9), y(9)--, y(10), y(10), y(10), y(11), y(11)++

Precursor origin neutral loss: +

Peptide No.1722

SFLGSHIVEDGSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFLGSHIVEDGSK
Found in AT2G47800.1, ATMNP4 (Arabidopsis thaliana multidrug resistance-associated protein 4)

Match to Query 1799: 1454.643080 from(728.328816,2+)
Elution from: 39.658 to 39.658 scan no 3942 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.6e-006
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6)-98, b(7), b(8)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.1723
SFLGSHIVEDGSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SFLGSHIVEDGSK
Found in AT2G47800.1, ATMRP4 (Arabidopsis thaliana multidrug resistance-associated protein 4)

Match to Query 2289: 1454.643644 from(728.329098,2+)
Elution from: 40.516 to 40.516 scan no 4073 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.6442
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0098
Matched b ions: b(6), b(6)-98, b(8), b(9), b(10), b(10)-98, b(11)-98++, b(11)++
Matched y ions: y(4), y(5), y(6), y(8), y(9)-98++, y(10)-98++, y(10)-98, y(10), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1724
SFQDLQEMR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFQDLQEMR
Found in AT1G79940.1, heat shock protein binding / unfolded protein binding

Match to Query 1322: 1232.489278 from(617.251915,2+)
Elution from: 40.830 to 40.830 scan no 3987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1232.4897
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 1.2e-005
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(4), b(5), b(5)–98, b(6), b(6)–98, b(7)–98, b(7), b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.1725

SFSAEGLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSAEGLK
Found in AT2G25620.1, protein phosphatase 2C, putative / PP2C, putative

Match to Query 386: 917.388496 from(459.701524,2+)
Elution from: 33.155 to 33.155 scan no 2849 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 917.3895
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 6.6e-005
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(5), b(5)–98, b(7), b(7)–98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)–98, y(6), y(6)–98++, y(7), y(7)–98, y(7)++, y(7)–98++
Precursor origin neutral loss: +

Peptide No.1726

SFSDAVSSSSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFSDAVSSSSR
Found in AT3G04630.1, WDL1 (WVD2–LIKE 1)

Match to Query 981: 1208.470548 from(605.242550,2+)
Elution from: 26.270 to 26.270 scan no 2139 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1208.4710
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 67 Expect: 6.6e-007
Matched b ions: b(2), b(4)–98, b(5)–98, b(5), b(6), b(6)–98, b(7), b(8)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No. 1727

SFSDAVSSSSR
Confirmed sites:
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SFSDAVSSSSR
Found in AT3G04630.1, WDL1 (WVD2-LIKE 1)

Match to Query 1425: 1208.469744 from(605.242148, 2+)
Elution from: 26.357 to 26.357 scan no 2162 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 1208.4710
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00053
Matched b ions: b(5)--98, b(5), b(6), b(6)--98
Matched y ions: y(2), y(4), y(5)+++, y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1728

SFSGDADLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSGDADLR
Found in AT4G342401, ALDH3I1 (Aldehyde dehydrogenase 3I1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase

Match to Query 605: 1046.407484 from(524.211018,2+) Elution from: 32.226 to 32.226 scan no 2786 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1046.4070
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1e-005
Matched b ions: b(2), b(3)−98, b(5)++, b(5)−98, b(5), b(7), b(7)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98++, y(7), y(7)−98, y(8)−98++
Precursor origin neutral loss: +

Peptide No. 1729

SFSGGECADWSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSGGECADWSK
Found in AT4G38900.1, bZIP protein

Match to Query 2061: 1409.495360 from(705.754956,2+)
Elution from: 35.178 to 35.178 scan no 3361 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1409.4959
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 Expect: 3.3e-008
Matched b ions: b(2), b(3)–98, b(3), b(5)–98, b(5), b(6)–98, b(6), b(8)–98, b(9), b(9)–98, b(10)–98++, b(10)–98, b(10), b(10)++, b(11)–98
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)++, y(8), y(9), y(10)–98++, y(10), y(10)–98, y(10)++
Precursor origin neutral loss: +

Peptide No.1730
SFSHELGPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSHELGPR
Found in AT1G45160.1, kinase

Match to Query 1061: 1108.468894 from(555.241723,2+) Elution from: 28.614 to 28.614 scan no 2487 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1108.4702
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 7.8e-005
Matched b ions: b(4)-98, b(5)
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)-98++, y(7)-98, y(7)++, y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1731

SFSHELNSK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SFSHELNSK
Found in AT3G17850.1, protein kinase, putative

Match to Query 1162: 1127.463532 from(564.739042,2+) Elution from: 24.050 to 24.050 scan no 1848 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1127.4648
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 19 Expect: 0.051
Matched b ions: b(3)-98, b(4)+, b(4), b(5)-98, b(6)-98, b(6), b(7)-98++, b(7), b(7)+, b(7)-98, b(8)-98, b(8)+
Matched y ions: y(3), y(4), y(5), y(6), y(6)+
Precursor origin neutral loss: +

Peptide No.1732

SFSSGSVPFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSSGSVPPER
Found in AT1G53240.1, malate dehydrogenase (NAD), mitochondrial

Match to Query 985: 1131.458632 from(566.736592,2+)
Elution from: 28.251 to 28.251 scan no 2183 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1131.4597
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 2.7e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6)++, b(6), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)-98, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(9)++
Precursor origin neutral loss: +

Peptide No.1733

SFSSGSVPER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SFSSGSVPER
Found in AT1G53240.1, malate dehydrogenase (NAD), mitochondrial

Match to Query 744: 1131.459362 from(566.736957,2+)
Elution from: 26.590 to 26.590 scan no 2160 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1131.4597
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0014
Matched b ions: b(2), b(4)–98, b(5)–98, b(5), b(6)+++, b(6), b(6)–98, b(7)–98, b(7)–98++, b(7), b(8)–98, b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7)–98, y(8)–98++, y(8), y(8)–98, y(8)+++, y(9)++
Precursor origin neutral loss: +

Peptide No.1734
SFSVDSDFDSDLGVTEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSVDSDFDSDLGVTEEK
Found in AT1G43700.1, VIP1 (VIRE2–INTERACTING PROTEIN 1); transcription factor

Match to Query 3973: 2115.852526 from(1058.933539,2+)  
Elution from: 70.983 to 70.983 scan no 7473 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2115.8561
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 6.8e-009
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(8), b(9)-98, b(10), b(11), b(12)-98, b(12), b(13)-98, b(14)-98, b(16)-98, b(17)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1735
SFSYPNTFAFK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SFSYPNTFAFK
Found in AT5G50530.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 1590: 1387.584598 from(694.799575,2+)
Elution from: 53.779 to 53.779 scan no 5741 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1387.5849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 21  Expect: 0.051
Matched b ions: b(2), b(3), b(4), b(5)-98, b(7)++
Matched y ions: y(3), y(7), y(8), y(8)++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1736
SFVVEESDDDMDETEEVKPK
Confirmed sites: @S:7
Ambiguous sites:
MS/MS Fragmentation of SFVVEESDDDMDETEEVKPK
Found in AT4G22670.1, tetratricopeptide repeat (TPR)–containing protein
Match to Query 4687: 2406.965242 from(1204.489897,2+)
Elution from: 40.638 to 40.638 scan no 4064 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2406.9661
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 124 Expect: 3.4e-012
Matched b ions: b(6), b(8)−98, b(8), b(9)++, b(9)−98, b(9), b(10)−98, b(11)−98, b(11), b(12)−98, b(12), b(13)−98, b(14)−98, b(14), b(15), b(16), b(16)−98, b(17)−98, b(18)−98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)−98, y(15)−98, y(15)−98++, y(16)−98, y(16)−98++, y(17)−98, y(17)−98++, y(18)−98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1737
SFVVEESDDDMDETEEVKPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SFVVEESDDDMDETEEVKPK
Found in AT4G22670.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 4157: 2422.959944 from(1212.487248,2+)
Elution from: 36.190 to 36.190 scan no 3441 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2422.9610
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 88 Expect: 1.5e-008
Matched b ions: b(5), b(6), b(8)–98, b(8), b(9)++, b(9), b(9)–98, b(10)–98, b(11), b(11)–98, b(12)–98, b(12), b(13)–98, b(14)–98, b(15)–98, b(15), b(16)–98, b(16), b(16)++, b(17)–98, b(17)–98++, b(18)++,
b(19)–98++
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(11), y(12), y(13), y(14)–98, y(14)–98++, y
(14)++, y(15)–98++, y(15)–98, y(15), y(16)++, y(16)–98, y(16)–98++, y(17)–98++, y(17)++, y(17)–98, y(18)–98++
Precursor origin neutral loss: +

Peptide No.1738
SGDESIETAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGDESIETAR
Found in AT4G24680.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to expressed protein

Match to Query 1040: 1143.442210 from(572.728381,2+) Elution from: 21.659 to 21.659 scan no 1339 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1143.4445
Fixed modifications: Carbamidomethyl (C)
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.011
Matched b ions: b(4), b(5)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1739

SGDSGGGENLMDSDK
Confirmed sites: @S:1
Ambiguous sites: 

MS/MS Fragmentation of SGDSGGGENLMDSDK
Found in AT1G11360.1, universal stress protein (USP) family protein

Match to Query 2127: 1490.522696 from(746.268624,2+)
Elution from: 28.294 to 28.294 scan no 2189 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1490.5232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 1.2e-007
Matched b ions: b(4), b(5)–98, b(6)–98, b(7)–98, b(7), b(8), b(8)–98, b(9)–98, b(9), b(10)–98, b(10), b(10)–98++, b(11), b(11)–98, b(11)++, b(13)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.1740
SGDSGGGENLMDSDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGDSGGGENLMDSDK
Found in AT1G11360.1, universal stress protein (USP) family protein

Match to Query 1816: 1506.516770 from(754.265661,2+)
Elution from: 18.833 to 18.833 scan no 1116 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1506.5181
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 66 Expect: 8.7e-007
Matched b ions: b(7)-98, b(7), b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.1741

SGDSGGENLMDSDK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SGDSGGENLMDSDK
Found in AT1G11360.1, universal stress protein (USP) family protein

Match to Query 1984: 1490.522414 from(746.268483,2+)
Elution from: 27.875 to 27.875 scan no 2323 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1490.5232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:

S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 87 Expect: 6.3e-009
Matched b ions: b(3), b(4)−98, b(4), b(5)−98, b(6)−98, b(7)−98, b(7), b(8), b(8)−98, b(9)−98, b(9), b (10)−98, b(10)−98++, b(10), b(11), b(11)++, b(11)−98, b(12)−98, b(13), b(13)−98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)−98, y(11)−98++, y(11) ++, y(12)−98++, y(12)++, y(13)++

Precursor origin neutral loss: +

Peptide No. 1742
SGDSGGENLMDSDK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SGDSGGENLMDSDK
Found in AT1G11360.1, universal stress protein (USP) family protein

Match to Query 1750: 1506.517162 from(754.265857,2+)
Elution from: 18.935 to 18.935 scan no 1121 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1506.5181
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 Expect: 3.2e−006
Matched b ions: b(4)−98, b(6)−98, b(7)−98, b(7), b(9), b(10)−98, b(10), b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11)−98++, y(12)−98++, y(13)−98++
Precursor origin neutral loss: +

Peptide No.1743
SGEACNISGNISGQDDNK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of SGEACNISGNISGQDDNK
Found in AT1G72090.1, radical SAM domain-containing protein / TRAM domain-containing protein
Match to Query 3260: 1944.749546 from(973.382049,2+)
Elution from: 25.229 to 25.229 scan no 1998 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1944.7520
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 5.3e-005
Matched b ions: b(7), b(10), b(12)−98, b(13)−98, b(14)−98, b(16)−98, b(16), b(16)++, b(17)
Matched y ions: y(4), y(6), y(7), y(7)−98, y(8)−98, y(8), y(10)−98, y(10), y(11), y(11)−98, y(12)−98, y(13), y(14)++, y(15)−98++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1744
SGEMTDSSLLSISPPSAR
Confirmed sites: @S:13
Ambiguous sites:
MS/MS Fragmentation of SGEMTDSSLLSISPPSAR
Found in AT3G23920.1, BMY7/TR-BAMY (beta-amylase 7); beta-amylase

Match to Query 3098: 1913.842618 from(957.928585,2+) Elution from: 50.377 to 50.377 scan no 5301 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1913.8441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 6.5e-005
Matched b ions: b(9), b(12), b(13)++, b(14)-98++
Matched y ions: y(5), y(6), y(6)-98, y(7), y(8), y(9), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.1745

SGESDSDAEDLEHADK
Confirmed sites:
Ambiguous sites: @S:1orS:4orS:6

MS/MS Fragmentation of SGESDSDAEDLEHADK
Found in AT5G15070.1, acid phosphatase

Match to Query 2783: 1783.639044 from(892.826798,2+)
Elution from: 25.847 to 25.847 scan no 2042 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1783.6421
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.035
Matched b ions: b(9)-98, b(10)-98, b(13)++, b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(15)++
Matched y ions: y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1746

SGESDSDAEDLEHADK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SGESDSDAEDLEHADK
Found in AT5G15070.1, acid phosphatase

Match to Query 2720: 1783.637448 from(892.826000,2+)
Elution from: 24.935 to 24.935 scan no 1961 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1783.6421
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.016
Matched b ions: b(8), b(14), b(14)++, b(14)−98++
Matched y ions: y(5), y(6), y(7), y(9), y(11), y(12)++, y(13)++, y(13)−98++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1747

SGESVDDESENYLSDLGK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SGESVDDESENYLSDLGK
Found in AT1G42550.1, PMI1 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 3737: 2022.791846 from(1012.403199,2+)
Elution from: 50.442 to 50.442 scan no 5308 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2022.7942
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 1.5e-009
Matched b ions: b(5)–98, b(6)–98, b(6), b(7)–98, b(7), b(8)–98, b(9)–98, b(9), b(10), b(11)–98++, b(11)–98, b(11), b(12)–98, b(12), b(13)–98, b(13), b(15), b(15)++, b(16)–98, b(16), b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(13), y(14), y(15)++, y(15), y(16)–98++
Precursor origin neutral loss: +

Peptide No. 1748
SGGEGECYMCGDVGHFAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGGEGECYMCGDVGHFAR
Found in AT2G17870.1, cold–shock DNA–binding family protein

Match to Query 3639: 2067.724376 from(1034.869464,2+)
Elution from: 39.913 to 39.913 scan no 3939 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2067.7274
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 3.7e-009
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(11), b(12)-98, b(13)-98, b(15)-98, b(15), b(16), b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.1749
SGGGGAYPSSSTFDRY
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGGGGAYPSSSTFDRY
Found in AT5G04280.1, glycine-rich RNA-binding protein

Match to Query 2590: 1687.651380 from(844.832966,2+)
Elution from: 39.432 to 39.432 scan no 3909 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6515
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 7e-008
Matched b ions: b(4), b(5)–98, b(6)–98, b(7)–98, b(7), b(8)–98, b(13)–98, b(14), b(15)++, b(15)–98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1750
SGGSPNRAELR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SGGSPNRAELR
Found in AT1G03350.1, BSD domain-containing protein

Match to Query 1255: 1222.543377 from(408.521735,3+)
Elution from: 17.750 to 17.750 scan no 984 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1222.5455
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0012
Matched b ions: b(2), b(4)−98, b(5)−98, b(6)−98, b(7)++, b(9)−98++
Matched y ions: y(2)++, y(2), y(4), y(6)++, y(7)++, y(8)++, y(9)−98++, y(9)++, y(10)++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.1751

SGLFMSGPIER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SGLFMSGPIER
Found in AT2G35350.1, PLL1 (POLTERGEIST LIKE 1); protein phosphatase type 2C

Match to Query 1186: 1272.555614 from(637.285083,2+)  
Elution from: 49.746 to 49.746 scan no 5224 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1272.5573
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.023
Matched b ions: b(9)–98
Matched y ions: y(5), y(6), y(7), y(7)–98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.1752

SGLRISDPSK
Confirmed sites: “@S:1,@S:6,@S:9”
Ambiguous sites:

MS/MS Fragmentation of SGLRISDPSK
Found in AT1G14460.1, DNA polymerase–related

Match to Query 1868: 1298.474307 from(433.832045,3+)
Elution from: 22.077 to 22.077 scan no 1617 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1298.4710
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.048
Matched b ions: b(4)-98, b(5)++, b(5)-98++, b(6)-196, b(6)-196++, b(6)++, b(7)-196, b(7)-98++, b(8)-196++, b(8)++
Matched y ions: y(4), y(5), y(5)-196, y(7)-196++
Precursor origin neutral loss: +

Peptide No.1753
SGLTEVGVSGLAQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGLTEVGVSGLAQR
Found in AT3G28450.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 2264: 1452.695370 from(727.354961,2+)
Elution from: 43.596 to 43.596 scan no 4482 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1452.6973
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 2.4e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(8), b(10)-98, b(11)-98
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1754
SGPELEESGTR
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SGPELEESGTR
Found in AT2G35490.1, plastid-lipid associated protein PAP, putative

Match to Query 1353: 1240.496536 from(621.255544,2+)
Elution from: 24.115 to 24.115 scan no 1748 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1240.4972
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.047
Matched b ions: b(5)-98
Matched y ions: y(3), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1755

SGRTSEPNSEDEAAGVGK
Confirmed sites: @S:9
Ambiguous sites: @S:1orT:4orS:5

MS/MS Fragmentation of SGRTSEPNSEDEAAGVGK
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 3267: 1949.737498 from(975.876025,2+)
Elution from: 19.768 to 19.768 scan no 1321 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1949.7404
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.015
Matched b ions: b(6)–98, b(6), b(7), b(8), b(8)–98, b(10)–98, b(10), b(11), b(11)–98, b(12)–196, b(13)–98, b(13), b(13)–98++, b(14)–196++, b(14)–98, b(14), b(14)++, b(15)–98++, b(16)–98, b(16), b(16)–196++, b(16)–98++, b(17)–98++
Matched y ions: y(4), y(5), y(7), y(8), y(10)–98, y(12)–98, y(12)
Precursor origin neutral loss: +

Peptide No.1756
SGRTSEPNSDEAAGVGK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SGRTSEPNSDEAAGVGK
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 2375: 1869.771501 from(624.264443,3+)
Elution from: 19.509 to 19.509 scan no 1215 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1869.7741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.01
Matched b ions: b(6), b(6)-98, b(7)+, b(8)+, b(8)-98+, b(8)-98++, b(9)-98++, b(9)-98+++, b(10)+, b(10)-98++, b(10)+, b(10)-98++, b(13)+, b(14)-98++, b(15)+, b(15)-98++, b(16)+, b(16)-98++
Matched y ions: y(4), y(7), y(8), y(9), y(12)+, y(14)+, y(15)+
Precursor origin neutral loss:

Peptide No. 1757

SGRTSEPNSEDEAAGVGK
Confirmed sites: “@S:5,@S:9”
Ambiguous sites:

MS/MS Fragmentation of SGRTSEPNSEDEAAGVGK
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 3266: 1949.738676 from(650.920168,3+)
Elution from: 19.979 to 19.979 scan no 1298 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1949.7404
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00017
Matched b ions: b(3), b(4), b(5)-98, b(6)-98++, b(6)-98, b(6), b(8), b(8)-98++, b(9)-196, b(10)++, b(10)-98++, b(10)-196++, b(11)-98++, b(12)-98++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)-196++, b(16)-98++, b(16)++, b(17)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)-98++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)++
Precursor origin neutral loss: +

Peptide No.1758
SGRTSEPNSEDEAAGVGK
Confirmed sites: @T:4
Ambiguous sites: @T:4

MS/MS Fragmentation of SGRTSEPNSEDEAAGVGK
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 2452: 1869.773118 from(624.264982,3+)
Elution from: 20.107 to 20.107 scan no 1211 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1869.7741
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0063
Matched b ions: b(4)-98, b(4), b(6), b(6)-98, b(8), b(10)++, b(11)-98++, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(8), y(10), y(10)++, y(12)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1759

SGSFESGSLR
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SSGFESGSLR
Found in AT5G55900.1, sucrase-related
Match to Query 1069: 1105.443152 from(553.728852,2+) Elution from: 27.789 to 27.789 scan no 2359 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1105.4441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.013
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(6)-98, b(8)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1760
SGSFESGSLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSFESGSLR
Found in AT5G55900.1, sucrase-related

Match to Query 745: 1105.443216 from(553.728884,2+)
Elution from: 27.549 to 27.549 scan no 2311 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1105.4441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00099
Matched b ions: b(4), b(5)–98, b(7)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)–98++, y(8)–98
Precursor origin neutral loss: +

Peptide No.1761

SGSFGSGLVNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSFGSGLVNR
Found in AT4G22740.1, glycine-rich protein

Match to Query 863: 1159.501348 from(580.757950,2+)
Elution from: 35.217 to 35.217 scan no 3350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1159.5022
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.2e-006
Matched b ions: b(3)–98, b(4), b(4)–98, b(5)–98, b(6)–98, b(7)–98, b(8)–98, b(9)–98, b(9)–98++, b (10)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)–98++, y(9)–98, y(9)++, y(10)–98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1762
SGSGTSLNGDLPQSVSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGSGLNLGDPQSVSR
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 3002: 1740.766778 from(871.390665,2+)
Elution from: 37.500 to 37.500 scan no 3545 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0011
Matched b ions: b(5), b(7)-98, b(8)-98, b(8), b(9), b(10), b(10)-98, b(11)-98, b(11), b(12)-98, b(13), b(15)-98, b(15), b(15)+, b(16)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(16)++
Precursor origin neutral loss: +

**Peptide No.1763**

SGSGTSLNGDLPSVSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SGSGTSLNGDLPSVSR**
Found in **AT5G47480.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2720: 1740.766926 from(871.390739,2+)  
Elution from: 36.961 to 36.961 scan no 3546 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 39 Expect: 0.001
Matched b ions: b(5)-98, b(5), b(7)-98, b(7), b(8)-98, b(8), b(9)-98++, b(9), b(10), b(10)-98, b(11)-98, b(11), b(13), b(13)-98, b(15)-98, b(15), b(16)++
Matched y ions: y(2), y(4), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(13), y(13)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1764
SGSGTSLNGDLPQSVSR
Confirmed sites: 
Ambiguous sites: "@S:1orS:3, @T:5orS:6"

MS/MS Fragmentation of SGSGTSLNGDLPQSVSR
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 3034: 1820.732040 from(911.373296,2+)
Elution from: 40.254 to 40.254 scan no 4028 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1820.7342
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.011
Matched b ions: b(9)-98, b(10), b(10)-196, b(16)
Matched y ions: y(4), y(6), y(7), y(9), y(10), y(11), y(14)++
Precursor origin neutral loss: +

**Peptide No.1765**

SGSGTSLNGDLPQSVSR
Confirmed sites:
Ambiguous sites: @S:3orT:5orS:6

MS/MS Fragmentation of SGSGLNSDLPQSVSR
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2874: 1740.767840 from(871.391196,2+)
Elution from: 36.098 to 36.098 scan no 3485 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0086
Matched b ions: b(11)–98
Matched y ions: y(3), y(6), y(7), y(9), y(10), y(11), y(15)–98++
Precursor origin neutral loss: +

Peptide No.1766

SGSGTSLNGDLPQSVSR
Confirmed sites:
Ambiguous sites: @S:3 or T:5

MS/MS Fragmentation of SGSGTSLNGDLPQSVSR

Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 3077: 1740.766244 from(871.390398,2+)
Elution from: 37.267 to 37.267 scan no 3625 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00019
Matched b ions: b(5), b(7)--98, b(7), b(8)--98, b(8), b(9)--98, b(10), b(10)--98, b(11)--98, b(11), b(13), b(13)--98, b(15), b(15)--98, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(15)++
Precursor origin neutral loss: +

Peptide No.1767

SGSGTSLNGDLPQSVSR

Confirmed sites: 
Ambiguous sites: "@S:1orS:3orT:5orS:6, @S:1orS:3orT:5orS:6"

MS/MS Fragmentation of SGSGTSLNGDLPQSVSR
Found in AT5G47480.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47490.1); similar to hypothetical prote

Match to Query 2930: 1820.731714 from(911.373133,2+)
Elution from: 40.082 to 40.082 scan no 3999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1820.7342
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T5: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  S6: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 30 Expect: 0.0069
Matched b ions: b(8), b(10), b(10)−196, b(10)−98, b(11), b(11)−98, b(12)−98, b(12)−196
Matched y ions: y(4), y(6), y(7), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1768

SGSNNGVDTNLDAEDR
Confirmed sites:
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SGSNNGVDTNLDAEDR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2752: 1742.672414 from(872.343483,2+) 
Elution from: 28.264 to 28.264 scan no 2407 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1742.6744
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 Expect: 1.4e-009
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10)-98++, b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(14)-98++, b(15)-98, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(13)
Precursor origin neutral loss: +

Peptide No.1769

SGSNNGVDTNLDAEDR
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of SGSNNGVDTNLDAEDR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose–phosphate synthase

Match to Query 3009: 1742.674576 from(872.344564,2+)
Elution from: 29.079 to 29.079 scan no 2413 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1742.6744
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 1.4e-009
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(11)-98, b(12), b(12)-98, b(13)-98, b(14)-98, b(14)-98++, b(15), b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1770
SGSPPEEHASINPAER
Confirmed sites: 
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SGSPEEHASINPAER
Found in AT4G11740.1, SAY1

Match to Query 2453: 1788.729480 from(895.372016,2+)
Elution from: 23.209 to 23.209 scan no 1684 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1788.7315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.9e-006
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(15)-98, b(15)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1771

SGSPEEEHASINPAER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSPEEEHASINPAER
Found in AT4G11740.1, SAY1

Match to Query 3272: 1788.729966 from(895.372259,2+)
Elution from: 23.480 to 23.480 scan no 1785 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1788.7315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 1.1e-006
Matched b ions: b(6)-98, b(8), b(8)-98, b(9), b(9)-98, b(11)-98, b(11), b(12), b(12)-98, b(14), b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)+, y(11), y(12), y(13)+, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1772
SGSPDPLLASLSINDHL
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of SGSPDPLLASLSINDHL
Found in AT2G23350.1, PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor

Match to Query 2944: 1804.821940 from(903.418246,2+)
Elution from: 65.682 to 65.682 scan no 6987 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.8244
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0011
Matched b ions: b(8), b(9)
Matched y ions: y(4), y(6)–98, y(7)–98, y(8), y(8)–98, y(9), y(9)–98, y(10), y(10)–98, y(11), y (13)++, y(14)++, y(14)–98++, y(16)–98++
Precursor origin neutral loss: +

Peptide No. 1773

SGSPSDLASLSINDHL
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSPSDLASLSINDHL
Found in AT2G23350.1, PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor

Match to Query 3077: 1804.821598 from(903.418075,2+) Elution from: 70.323 to 70.323 scan no 7228 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.8244
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 7.3e-006
Matched b ions: b(6), b(8)-98, b(9), b(9)-98, b(10)++, b(11)-98, b(12), b(15)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(13)++, y(14), y(14)++, y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1774

SGSPDLLASLSINDHL
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SGSPDLLASLSINDHL
Found in AT2G23350.1, PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor

Match to Query 3159: 1804.821732 from(903.418142,2+) Elution from: 69.659 to 69.659 scan no 7360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1804.8244
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00021
Matched b ions: b(6)−98, b(7)−98, b(8)−98, b(9)−98, b(10)++, b(12), b(15)−98++
Matched y ions: y(4), y(6), y(9), y(10), y(11), y(13)−98, y(13)++, y(14)−98++, y(15)−98++, y(15)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.1775
SGSRPQLDLSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGSRPQLDLSK
Found in AT4G32180.1, ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase

Match to Query 1456: 1266.595740 from(634.305146,2+)
Elution from: 28.082 to 28.082 scan no 2160 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1266.5969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.032
Matched b ions: b(4), b(4)++, b(4)−98, b(5)−98++, b(5), b(6)++, b(6)−98, b(7)−98++, b(7)−98, b(7), b(8)−98, b(8), b(9)−98++, b(9), b(9)−98, b(10)−98, b(10), b(10)−98++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1776
SGSRPQLDLSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSRPQLDLSK
Found in AT4G32180.1, ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase

Match to Query 1655: 1266.595116 from(423.205648,3+)
Elution from: 26.639 to 26.639 scan no 2218 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1266.5969
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 49 Expect: 9.6e-005
Matched b ions: b(2), b(4)+, b(4)−98++, b(4), b(4)−98, b(5)−98++, b(6), b(6)−98++, b(6)−98, b(6)++, b(7)−98++, b(7)++, b(8), b(8)−98++, b(8)++, b(9)−98, b(9)−98++, b(9)++, b(10)−98++, b(10)−98, b(10)++, b(10)−98++, b(10)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)+, y(6), y(7)+, y(8)+, y(9)−98++, y(9)+, y(10)−98++, y(10)+
Precursor origin neutral loss: +

Peptide No.1777
SGVMVSSVDELIDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SGVMVSSVDELIDK
Found in AT5G43430.1, ETFBETA; electron carrier

Match to Query 2700: 1557.697914 from(779.856233,2+)
Elution from: 55.100 to 55.100 scan no 5897 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1557.6997  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 55 Expect: 3e-005  
Matched b ions: b(3), b(4), b(5)–98, b(5), b(12)–98, b(12)  
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++  
Precursor origin neutral loss: +  

**Peptide No.1778**  
SGVQSPPDLLNL  
Confirmed sites: @S:5  
Ambiguous sites:  

MS/MS Fragmentation of SGVQSPPDLLNL  
Found in AT5G65700.1, BAM1 (big apical meristem 1); ATP binding / kinase/ protein serine/threonine kinase  

Match to Query 1626: 1318.616044 from(660.315298,2+)  
Elution from: 67.359 to 67.359 scan no 6947 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1318.6170
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0013
Matched b ions: b(4), b(5)−98, b(6)−98, b(9)−98, b(9)+, b(9), b(10)+, b(10), b(10)−98, b(11)+, b(11), b(11)−98++
Matched y ions: y(2), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1779

SGYVPTLPDSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SGYVPTLPDSPK
Found in AT2G03150.1, EMB1579 (EMBRYO DEFECTIVE 1579); binding

Match to Query 2012: 1339.604870 from(670.809711,2+)
Elution from: 40.611 to 40.611 scan no 4138 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1339.6061
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00032
Matched b ions: b(3), b(4), b(7), b(8)++, b(10)
Matched y ions: y(4)++, y(5), y(5)−98++, y(6)−98, y(6), y(8), y(8)++, y(9)++, y(9), y(9)−98++, y(9)−98, y(10)++
Precursor origin neutral loss:

Peptide No.1780

SIAAAHTKTTR
Confirmed sites: "@S:1,@T:7"
Ambiguous sites:

MS/MS Fragmentation of SIAAAHTKTTR
Found in AT2G07728.1, unknown protein

Match to Query 1613: 1315.569855 from(439.530561,3+)
Elution from: 21.167 to 21.167 scan no 1483 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1315.5686
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.053
Matched b ions: b(5)-98, b(6)++, b(7)++, b(8)++, b(8)-98++, b(9)++, b(9)-98++
Matched y ions: y(9)++
Precursor origin neutral loss: +

Peptide No.1781
SIAADSWSIK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SIAADSWSIK
Found in AT1G66680.1, AR401

Match to Query 880: 1156.516212 from(579.265382,2+) Elution from: 41.468 to 41.468 scan no 4181 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1156.5165
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00039
Matched b ions: b(2), b(3), b(4), b(5), b(7)–98, b(7), b(8)–98, b(9)–98++, b(9)
Matched y ions: y(3), y(5), y(6), y(6)–98, y(7), y(8)++, y(8), y(8)–98
Precursor origin neutral loss: +

Peptide No.1782

SIAADSWSIK
Confirmed sites: "@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of SIAADSWSIK
Found in AT1G66680.1, AR401

Match to Query 996: 1236.481714 from(619.248133,2+) Elution from: 47.231 to 47.231 scan no 4552 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1236.4828
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.002
Matched b ions: b(2), b(3), b(7)–98, b(8)–98, b(9)–196, b(9)–98
Matched y ions: y(3), y(5), y(5)–98, y(6), y(7), y(7)–98, y(8), y(8)–98++, y(8)+++, y(8)–98, y(8)–196
Precursor origin neutral loss: +

Peptide No.1783
SIAADSWSIK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SIAADSWSIK
Found in AT1G66680.1, AR401

Match to Query 843: 1156.515118 from(579.264835,2+)
Elution from: 41.423 to 41.423 scan no 4173 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1156.5165
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00036
Matched b ions: b(2), b(3), b(4)
Matched y ions: y(3), y(4), y(4)−98, y(5), y(6)−98, y(6), y(7), y(7)−98, y(8)++, y(8)−98, y(8), y(8)−98++
Precursor origin neutral loss: +

Peptide No.1784

SIDPYKDYIHVRAR
Confirmed sites: “@Y:5,@Y:8”
Ambiguous sites:

MS/MS Fragmentation of SIDPYKDYIHVRAR
Found in AT3G07340.1, basic helix–loop–helix (bHLH) family protein

Match to Query 3183: 1891.838580 from(631.620136,3+)
Elution from: 38.430 to 38.430 scan no 3776 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1891.8383
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
Y8 : Phospho (Y)
Ions Score: 27 Expect: 0.023
Matched b ions: b(5), b(11)++
Matched y ions: y(3)++, y(7)++, y(9)++, y(11)++, y(12)++, y(13)++
Precursor origin neutral loss:

Peptide No.1785
SIEVEETGHR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SIEVEETGHR
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to unnamed protein pr

Match to Query 1055: 1235.517726 from(618.766139,2+)
Elution from: 20.946 to 20.946 scan no 1383 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1235.5183
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 3e-006
Matched b ions: b(3)-98, b(5)-98, b(8)-98, b(9)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)+, y(8), y(9)+
Precursor origin neutral loss: +

Peptide No.1786

SIEYEDDDMAVDDQDIQK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SIEYEDDDMAVDDQDIQK
Found in AT5G21160.1, La domain-containing protein / proline-rich family protein

Match to Query 4329: 2207.840480 from(1104.927516,2+)
Elution from: 43.685 to 43.685 scan no 4452 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2207.8453
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 Expect: 6.7e-008
Matched b ions: b(5), b(7), b(8), b(9)−98, b(10)−98, b(10), b(11)−98, b(13), b(15), b(16), b(17)++, b(17)−98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(13), y(14), y(15), y(15)++
Precursor origin neutral loss: +

**Peptide No.1787**

SIGELSQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SIGELSQR
Found in AT4G01290.1, similar to unknown [Oryza sativa] (GB:AAF00138.1); similar to Os06g0105900 [Oryza sativa (japonica

Match to Query 439: 968.431264 from(485.222908,2+) Elution from: 28.056 to 28.056 scan no 2237 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 968.4328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0068
Matched b ions: b(2), b(3)−98, b(4), b(4)−98, b(5), b(6)−98
Matched y ions: y(2), y(3), y(4), y(6)
Precursor origin neutral loss: +

Peptide No.1788
SIGFNPTSPTR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SIGFNPTSPTR
Found in AT1G65320.1, CBS domain−containing protein

Match to Query 1617: 1255.558696 from(628.786624,2+) Elution from: 36.718 to 36.718 scan no 3575 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1255.5598
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.015
Matched b ions: b(5), b(6), b(7)++, b(8), b(9)--98
Matched y ions: y(3), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1789

SIPGAPPVTPAGSFGR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SIPGAPPVTPAGSFGR
Found in AT2G47970.1, NPL4 family protein

Match to Query 2525: 1589.757382 from(795.885967,2+)
Elution from: 43.998 to 43.998 scan no 4496 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1589.7602
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00072
Matched b ions: b(5)
Matched y ions: y(6)++, y(6), y(7)−98, y(8), y(9), y(9)−98, y(10)++, y(10)−98, y(10), y(11)−98++, y(11)++, y(11)−98, y(11), y(13)++, y(14)++, y(14), y(14)−98++
Precursor origin neutral loss: +

Peptide No.1790
SIPSIVELDSLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SIPSIVELDSLK
Found in AT3G03250.1, UGP (UDP−glucose pyrophosphorylase); UTP:glucose−1−phosphate uridylyltransferase

Match to Query 1564: 1379.694078 from(690.854315,2+)
Elution from: 59.408 to 59.408 scan no 6336 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1379.6949
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00027
Matched b ions: b(2), b(3)-98, b(6)-98, b(6), b(8)-98, b(9)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10)++, y(10)
Precursor origin neutral loss: +

Peptide No.1791
SIQELDLSDCER
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of SIQELDLSDCER
Found in AT5G15020.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G01320.1); similar to paired amphipathic

Match to Query 2295: 1543.621630 from(772.818091,2+) Elution from: 42.391 to 42.391 scan no 4084 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1543.6225
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.2e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)−98, b(10)−98, b(11)−98, b(11), b(11)++
Matched y ions: y(3), y(4), y(5)−98, y(6), y(6)−98, y(7)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y(10)−98++, y(10)++, y(10)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.1792
SISELTLDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISELTLDK
Found in AT5G52882.1, ATP binding / nucleoside-triphosphatase / nucleotide binding
Match to Query 657: 1084.503586 from(543.259069,2+)
Elution from: 42.873 to 42.873 scan no 4330 polarity:+

---

Monoisotopic mass of neutral peptide Mr(calc): 1543.6225
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.2e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)−98, b(10)−98, b(11)−98, b(11), b(11)++
Matched y ions: y(3), y(4), y(5)−98, y(6), y(6)−98, y(7)−98, y(7), y(8), y(8)−98, y(9), y(9)−98, y(10)−98++, y(10)++, y(10)−98, y(11)++
Precursor origin neutral loss: +

Peptide No.1792
SISELTLDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISELTLDK
Found in AT5G52882.1, ATP binding / nucleoside-triphosphatase / nucleotide binding
Match to Query 657: 1084.503586 from(543.259069,2+)
Elution from: 42.873 to 42.873 scan no 4330 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1084.5053
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0054
Matched b ions: b(2), b(4)-98, b(5), b(8)++
Matched y ions: y(2), y(3), y(4), y(6), y(7)-98, y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.1793
SISFHLGNK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISFHLGNK
Found in AT5G56760.1, AtSerat1;1 (SERINE ACETYLTRANSFERASE 52); serine O-acetyltransferase

Match to Query 969: 1081.495226 from(541.754889,2+)
Elution from: 38.155 to 38.155 scan no 3766 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1081.4957
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0011
Matched b ions: b(2), b(3)--98, b(5)--98, b(8)--98
Matched y ions: y(3), y(4), y(5)--, y(5), y(6), y(7)--98++, y(7), y(7)--98, y(7)++
Precursor origin neutral loss: +

Peptide No.1794

SISFNPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISFNPR
Found in AT3G12100.1, cation efflux family protein / metal tolerance protein, putative

Match to Query 272: 899.389374 from(450.701963,2+)
Elution from: 33.010 to 33.010 scan no 3016 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 899.3902
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.038
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(5)-98++, y(6)++
Precursor origin neutral loss: +

Peptide No.1795

SISGEDTSDWSNLVK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SISGEDTSDWSNLVK
Found in AT2G21230.1, bZIP family transcription factor

Match to Query 2841: 1716.721738 from(859.368145,2+)
Elution from: 52.595 to 52.595 scan no 5363 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1716.7243
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.0002
Matched b ions: b(6), b(7)–98, b(8), b(9)–98, b(10)–98, b(13)–98, b(14)–98, b (14)
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(12)
Precursor origin neutral loss: +

Peptide No.1796

SISGEDTSDWSNLVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISGEDTSDWSNLVK
Found in AT2G21230.1, bZIP family transcription factor

Match to Query 2683: 1716.723456 from(859.369004,2+)
Elution from: 50.819 to 50.819 scan no 5377 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1716.7243  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 64 Expect: 3.5e-006  
Matched b ions: b(5)-98, b(6), b(6)-98, b(7)-98, b(8)-98, b(9), b(11)-98, b(14)-98  
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13)++, y(13), y(13)-98++  
Precursor origin neutral loss: +

**Peptide No.1797**

SISIESPR  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of SISIESPR
Found in AT3G62700.1, ATMRTP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)

Match to Query 381: 967.436924 from(484.725738,2+)
Elution from: 28.782 to 28.782 scan no 2479 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.4375
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00041
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(5)−98, b(5), b(6), b(7)−98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)−98, y(6), y(6)++, y(6)−98++
Precursor origin neutral loss: +

Peptide No.1798

SISIESPR
Confirmed sites: "@S:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of SISIESPR
Found in AT3G62700.1, ATMRP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)

Match to Query 572: 1047.402088 from(524.708320,2+)
Elution from: 29.192 to 29.192 scan no 2507 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1047.4039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 26 Expect: 0.0083
Matched b ions: b(2), b(4)-98, b(5), b(6)-196, b(6)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(4)-98, y(5), y(6)-98, y(6), y(6)-98++, y(7)-196++
Precursor origin neutral loss: +

Peptide No.1799

SISIESPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SISIESPR
Found in AT3G62700.1, ATMRP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)

Match to Query 415: 967.436866 from(484.725709,2+)
Elution from: 26.964 to 26.964 scan no 2189 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 967.4375
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.025
Matched b ions: b(2), b(4)++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6)
Precursor origin neutral loss: +

Peptide No.1800

SISIESPRQPK
Confirmed sites: ”@S:3,@S:6”
Ambiguous sites:

MS/MS Fragmentation of SISIESPRQPK
Found in AT3G62700.1, ATMRP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)

Match to Query 1893: 1400.610910 from(701.312731,2+)
Elution from: 28.224 to 28.224 scan no 2298 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1400.6102
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.059
Matched b ions: b(3)-98, b(5)-98, b(6)-98, b(7)-196, b(8), b(9)
Matched y ions: y(2), y(3), y(6), y(7), y(8), y(8)++, y(9)-196++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1801

SISITPEIGDDIVR
Confirmed sites: @S:1 or S:3
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SISITPEIGDDIVR
Found in AT3G58640.1, protein kinase family protein

Match to Query 2155: 1593.764716 from(797.889634,2+)
Elution from: 53.146 to 53.146 scan no 5632 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1593.7651
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.019
Matched b ions: b(3)-98, b(4)-98, b(5), b(5)-98, b(6)-98, b(8)-98
Matched y ions: y(6), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.1802

SISPLPLSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SISPLPLSK
Found in AT5G43310.1, COP1-interacting protein–related

Match to Query 495: 1020.525346 from(511.269949,2+) 
Elution from: 37.911 to 37.911 scan no 3707 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1020.5256  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 26 Expect: 0.022  
Matched b ions: b(2), b(3), b(3)-98, b(5)-98, b(5)  
Matched y ions: y(4), y(5), y(6), y(7)-98++, y(7), y(7)-98, y(7)++, y(8)++  
Precursor origin neutral loss: +

Peptide No.1803  
SISSAQYFGDQNK  
Confirmed sites: @S:1  
Ambiguous sites: 

MS/MS Fragmentation of SISSAQYFGDQNK  
Found in AT4G17890.1, UBP20 (UBIQUITIN–SPECIFIC PROTEASE 20); DNA binding  
Match to Query 1941: 1523.626902 from(762.820727,2+)  
Elution from: 35.774 to 35.774 scan no 3420 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1523.6293
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 62 Expect: 5.6e-006
Matched b ions: b(2), b(3), b(3)-98, b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(4), y(5)++, y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No. 1804
SISSPTVVEVDLGDR
Confirmed sites:
Ambiguous sites: @S:1 or S:3 or S:4

MS/MS Fragmentation of SISSPTVVEVDLGDR
Found in AT5G66120.2, 3-dehydroquinate synthase, putative

Match to Query 2400: 1652.762762 from (827.388657, 2+).
Elution from: 47.769 to 47.769 scan no 4999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1652.7658
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.033
Matched b ions: b(7)-98, b(10), b(10)-98, b(11), b(12)+, b(14), b(14)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)
Precursor origin neutral loss:

Peptide No.1805

SISSPTVVEVDLGDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SISSPTVVEVDLGDR
Found in AT5G66120.2, 3-dehydroquinate synthase, putative

Match to Query 2337: 1652.763872 from(827.389212,2+)  
Elution from: 47.844 to 47.844 scan no 4999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1652.7658
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00021
Matched b ions: b(7), b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12)−98++, y(13)−98++, y(13), y(13)+, y(14)−98++
Precursor origin neutral loss:

Peptide No.1806
SITSGDNFGNPSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SITSGDNFGNPSK
Found in AT5G21160.1, La domain-containing protein / proline-rich family protein

Match to Query 1865: 1402.575602 from(702.295077,2+)
Elution from: 31.137 to 31.137 scan no 2575 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1402.5765
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 2.8e-005
Matched b ions: b(3), b(5)–98, b(6)–98, b(7)–98, b(8)–98, b(8)++, b(9), b(10), b(10)–98, b(12)
Matched y ions: y(3), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11)++, y(11)
Precursor origin neutral loss: +

Peptide No.1807

SITSGDNFGNPSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SITSGDNFGNPSK
Found in AT5G21160.1, La domain-containing protein / proline–rich family protein

Match to Query 1864: 1402.575340 from(702.294946,2+)
Elution from: 32.832 to 32.832 scan no 2805 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1402.5765
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1.1e-005
Matched b ions: b(3), b(4)++, b(6), b(7), b(8), b(9), b(10), b(11)−98++, b(11)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)−98++, y(10), y(11)++, y(11), y(11)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1808

SKDTEAAVDAEDESAAEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of SKDTEAAVDAEDESAAEK
Found in AT3G57150.1, NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)

Match to Query 2623: 1944.781584 from(973.398068,2+)
Elution from: 22.377 to 22.377 scan no 1494 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1944.7837
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 5.7e-009
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(11), b(12)++, b(12), b(13), b(15), b(16)–98, b(16), b(17)–98, b(17)++
Matched y ions: y(5)–98, y(6)–98, y(7)–98, y(7), y(8)–98, y(8), y(9), y(10)–98, y(10), y(11)–98, y(11), y(12), y(12)–98, y(13), y(13)–98, y(15), y(16), y(16)–98
Precursor origin neutral loss: +

Peptide No. 1809
SKPIEEEETGSGSQSGGESPEAK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of SKPIEEEETGSGSQSGGESPEAK
Found in AT1G43690.1, ubiquitin interaction motif-containing protein

Match to Query 3919: 2398.999104 from(800.673644,3+)
Elution from: 19.841 to 19.841 scan no 1280 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2399.0012
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00078
Matched b ions: b(8), b(9), b(10), b(11), b(12), b(13)++, b(14)++, b(15)++, b(18)++, b(19)–98++, b(21)–98++, b(21)++, b(22)++
Matched y ions: y(4), y(5), y(7)–98, y(8), y(8)–98, y(9), y(11)++, y(15)++, y(17)++, y(21)–98++, y(21)++
Precursor origin neutral loss: +

Peptide No.1810
SKSEVDEAVSEEAAEDDD
Confirmed sites: @S:10
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SKSEVDEAVSEEAAEDDD
Found in AT2G17560.1, HMGB4 (HIGH MOBILITY GROUP B 4); transcription factor

Match to Query 3018: 2141.706662 from(1071.860607,2+)
Elution from: 33.578 to 33.578 scan no 3075 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2141.7086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 5.7e-005
Matched b ions: b(5), b(5)−98, b(7)−98, b(8), b(8)−98, b(9)−98, b(9)+, b(9), b(11)−98, b(11)−196, b(12), b(13)−98, b(14), b(15), b(15)−98, b(15)−98++, b(15)+, b(16)−98++, b(16)++, b(16)−196++, b(17)−98++, b(17)+, b(17)−196++
Matched y ions: y(5), y(6), y(9), y(10)−98, y(10), y(11), y(12), y(13), y(13)−98, y(14)−98, y(15)−98++
Precursor origin neutral loss: +

Peptide No.1811
SKSEVDEAVSEEEAEDDD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SKSEVDEAVSEEEAEDDD
Found in AT2G17560.1, HMGB4 (HIGH MOBILITY GROUP B 4); transcription factor

Match to Query 3831: 2061.739960 from(1031.877256,2+)
Elution from: 34.688 to 34.688 scan no 3266 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2061.7423
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 2.2e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(14)-98++, b(14)-98, b(14)+, b(15), b(15)+, b(15)-98, b(15)-98++, b(16)+, b(16)-98++, b(16)-98++, b(17)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)+, y(10)-98, y(10), y(10)-98++, y(11)-98, y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(15), y(16)+
Precursor origin neutral loss: +

Peptide No.1812
SKSEVDEAVSEEEAEDDD
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SKSEVDEAVSEEEAEDDD
Found in AT2G17560.1, HMGB4 (HIGH MOBILITY GROUP B 4); transcription factor

Match to Query 3512: 2061.739534 from(1031.877043,2+)
Elution from: 33.331 to 33.331 scan no 3092 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2061.7423
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 5e–008
Matched b ions: b(4)–98, b(5)–98, b(5), b(6), b(7), b(7)–98, b(8)–98, b(8)–98++, b(8), b(9)+, b(9)–
98, b(10), b(10)–98, b(11), b(11)–98, b(12), b(12)–98, b(13), b(14), b(14)–98++, b(14)+, b(15), b
(15)–98, b(15)–98++, b(15)++, b(16)++, b(17)++, b(17)–98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)+, y(13), y(14), y(16)
Precursor origin neutral loss: +

Peptide No.1813
SKSEVDEAVSEEEAEDDD
Confirmed sites: @S:10
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SKSEVDEAVSEEEAEDDD
Found in AT2G17560.1, HMGB4 (HIGH MOBILITY GROUP B 4); transcription factor

Match to Query 3020: 2141.706198 from(1071.860375,2+)
Elution from: 34.508 to 34.508 scan no 3106 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2141.7086
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 25 Expect: 0.009
Matched b ions: b(5)-98, b(6), b(7), b(7)-98, b(8), b(9)+, b(9)-98, b(9), b(12)+, b(12)-98, b(13), b(14)-98, b(16)+, b(17)-98++, b(17)+
Matched y ions: y(9), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.1814

SKSLDEDYDMK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SKSLDEDYDMK
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 2241: 1409.540598 from(705.777575,2+)
Elution from: 25.489 to 25.489 scan no 2083 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1409.5421
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 1.4e-005
Matched b ions: b(5)–98, b(5), b(6), b(6)–98, b(7), b(7)–98, b(8)–98, b(9), b(9)–98, b(10)
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1815

SKSLDEDYDMK
Confirmed sites: "@S:1,@S:3"
Ambiguous sites:

MS/MS Fragmentation of SKSLDEDYDMK
Found in AT3G23900.1, RNA recognition motif (RRM)–containing protein

Match to Query 2479: 1489.508198 from(745.761375,2+) Elution from: 29.800 to 29.800 scan no 2677 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1489.5085
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00011
Matched b ions: b(4)-196, b(4)-98, b(5)-98, b(5), b(6)-196, b(6)-98, b(7)-98, b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98
Precursor origin neutral loss: +

Peptide No.1816

SKSLDEDYDMK
Confirmed sites: ”@S:1,@S:3”
Ambiguous sites:

MS/MS Fragmentation of SKSLDEDYDMK
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 1607: 1505.502636 from(753.758594,2+)
Elution from: 24.126 to 24.126 scan no 1751 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1505.5034
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 Expect: 0.0013
Matched b ions: b(7), b(9)-196, b(9)-196++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1817

SKSLDEDYDMK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SKSLDEDYDMK
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 1653: 1409.541608 from(705.778080,2+)
Elution from: 26.219 to 26.219 scan no 2097 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1409.5421
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 6.7e-007
Matched b ions: b(3)-98, b(5), b(7)-98, b(7), b(9)-98, b(9), b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9)
Precursor origin neutral loss: +

Peptide No.1818
SKSSEDIYSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SKSSEDIYSR
Found in AT2G37550.1, ASP1 (PDE1 SUPPRESSOR 1); DNA binding

Match to Query 1091: 1250.516816 from(626.265684,2+)
Elution from: 19.185 to 19.185 scan no 1153 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1250.5180
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 8e-005
Matched b ions: b(2)-98, b(3)-98, b(5), b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1819
SKSSEDIYSR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SKSSEDIYSR
Found in AT2G37550.1, ASP1 (PDE1 SUPPRESSOR 1); DNA binding
Match to Query 1266: 1250.517358 from(626.265955,2+) Elution from: 19.804 to 19.804 scan no 1246 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1250.5180
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00025
Matched b ions: b(2), b(3)-98, b(5), b(6), b(6)-98, b(7), b(8), b(8)-98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1820

SKSSEDIYTR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SKSSEDIYTR
Found in AT3G53710.1, AGD6; DNA binding

Match to Query 1596: 1264.532462 from(633.273507,2+ )
Elution from: 19.544 to 19.544 scan no 1240 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1264.5336
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00015
Matched b ions: b(3)-98, b(5), b(6), b(6)-98, b(7), b(8)-98, b(9)
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9)++
Precursor origin neutral loss: +

Peptide No.1821

SKSSEDIYTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SKSSEDIYTR
Found in AT3G53710.1, AGD6; DNA binding

Match to Query 1023: 1264.532610 from(633.273581,2+) Elution from: 19.690 to 19.690 scan no 1255 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1264.5336
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 2.9e-005
Matched b ions: b(2), b(3)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7), y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.1822

SKSVTDEDELK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SKSVTDEDELK
Found in AT4G33985.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G15590.2); similar to Os04g0282200 [Oryz

Match to Query 2437: 1571.695826 from(786.855189,2+) Elution from: 34.637 to 34.637 scan no 3162 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6967
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 64 Expect: 3.1e-006
Matched b ions: b(3)-98, b(5)-98, b(6)-98, b(6)+, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(4)+, y(5), y(6), y(7), y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.1823
SKSVTDEDLEELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SKSVTDEDLEELK
Found in AT4G33985.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G15590.2);
similar to Os04g0282200 [Oryz]

Match to Query 2625: 1571.695500 from(786.855026,2+)
Elution from: 33.905 to 33.905 scan no 3185 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6967
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 3.8e-005
Matched b ions: b(3)–98, b(6)–98, b(6), b(7)–98, b(8), b(11), b(11)–98, b(12), b(12)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)–98, y(11), y(12)–98++
Precursor origin neutral loss: +

Peptide No.1824
SKSVTDEDLEELK
Confirmed sites:
Ambiguous sites: @S:3orT:5

MS/MS Fragmentation of SKSVTDEDLEELK
Found in AT4G33985.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G15590.2); similar to Os04g0282200 [Oryz]
Match to Query 2438: 1571.696040 from(524.905956,3+)
Elution from: 34.652 to 34.652 scan no 3164 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6967
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0017
Matched b ions: b(2), b(5), b(5)+, b(6)+, b(6), b(7)+98+, b(7)+98, b(7)+, b(8)+, b(8), b(8)+98+, b(9)+98+, b(11)+98+, b(11)+
Matched y ions: y(2), y(4)+, y(5), y(5)+, y(6), y(7), y(8)
Precursor origin neutral loss:

Peptide No.1825

SKTMSPLSSKSMLPPPPR
Confirmed sites: "@T:3,@S:5,@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of SKTMSPLSSKSMLPPPPR
Found in AT3G29390.1, RIK (RS2–INTERACTING KH PROTEIN)

Match to Query 3325: 2275.877466 from(759.633098,3+)
Elution from: 22.810 to 22.810 scan no 1703 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2275.8825
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M12 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 21 Expect: 0.055
Matched b ions: b(3)-98, b(4)-98, b(4)++, b(5)-98++, b(5)-196++, b(6)-196++, b(6)-98, b(7)-196++, b(7)++, b(7)-196, b(9)++, b(9)-392, b(9)-98++, b(10)-392, b(10)++, b(11)-196++, b(11)++, b(11)-98++, b(13)-392++, b(13)-294++, b(14)-392++, b(17)-294++
Matched y ions: y(5)++, y(11)-98++, y(11)++, y(12)-196++, y(12)++, y(12)-98++, y(13)-98, y(13)-98++, y(13)-196++, y(14)++, y(15)-98++, y(15)-196++, y(16)-294++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1826

SKTPELSPPVTPLVATPVNK
Confirmed sites: @S:7
Ambiguous sites: @S:1orT:3

MS/MS Fragmentation of SKTPELSPPVTPLVATPVNK
Found in AT2G27090.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G39790.1); similar to Protein of unknown

Match to Query 4070: 2234.099088 from(745.706972,3+) Elution from: 49.216 to 49.216 scan no 5167 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 2234.1000

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- **T3:** Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
- **S7:** Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 41  **Expect:** 0.00085

**Matched b ions:** b(6)-98, b(7)-196, b(10)+, b(11)-98++, b(11)-98, b(12)-196++, b(12)-196, b(12)+, b(13)-98++, b(14)-196++, b(15)+, b(16)-98++, b(16)+, b(17)+, b(17)-196++, b(17)-98++, b(18)-98++, b(18)-196+

**Matched y ions:** y(6), y(7), y(8), y(9)+, y(9), y(10), y(10)+, y(13)+, y(14)-98++, y(15)-98++, y(17)+, y(18)-196+

**Precursor origin neutral loss:**

---

**Peptide No.1827**

**SLADTLSR**

**Confirmed sites:** @S:7

**Ambiguous sites:**

**MS/MS Fragmentation of SLADTLSR**

Found in **AT2G22010.1**, zinc finger (C3HC4-type RING finger) family protein

**Match to Query 366:** 941.423380 from(471.718966,2+)

**Elution from:** 25.768 to 25.768 scan no 2069 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 941.4219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.027
Matched b ions: b(3), b(6), b(7), b(7)-98++
Matched y ions: y(1), y(2)++, y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(7)++
Precursor origin neutral loss:

Peptide No.1828
SLADTLSR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of SLADTLSR
Found in AT2G22010.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 341: 941.423988 from(471.719270,2+)(471.719270,2+)
Elution from: 26.195 to 26.195 scan no 2094 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 941.4219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.036
Matched b ions: b(5)−98++, b(5), b(6), b(6)++
Matched y ions: y(1), y(3), y(4)+, y(4), y(5), y(6)+, y(7)+
Precursor origin neutral loss:

Peptide No.1829

SLAPDSPEVGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SLAPDSPEVGR
Found in AT3G48190.1, ATM (ATAXIA–TELANJICTASIA MUTATED)

Match to Query 858: 1206.527000 from(604.270776,2+)
Elution from: 27.579 to 27.579 scan no 2279 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1206.5281
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 2.5e-005
Matched b ions: b(2), b(3), b(6)−98, b(9)−98, b(10)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(8)−98++, y(8)−98, y(9)++, y(9), y(9)−98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1830
SLDEDYDMK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLDEDYDMK
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 991: 1194.414286 from(598.214419,2+)
Elution from: 32.146 to 32.146 scan no 2933 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1194.4152  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 58 Expect: 4.1e-006  
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(7)-98, b(7), b(8), b(8)-98, b(8)++  
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7)  
Precursor origin neutral loss: +  

Peptide No.1831  
SLDEDYDMK  
Confirmed sites: @S:1  
Ambiguous sites:  
MS/MS Fragmentation of SLDEDYDMK  
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein  
Match to Query 988: 1210.409470 from(606.212011,2+)  
Elution from: 24.813 to 24.813 scan no 1899 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1210.4101
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 52 Expect: 1.5e-005
Matched b ions: b(2), b(3)−98, b(4)−98, b(4), b(5), b(5)−98, b(6)−98, b(7)−98, b(8)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(7)+
Precursor origin neutral loss: +

Peptide No.1832
SLDNDESSRPDWSNR
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SLDNDESSRPDWSNR
Found in AT1G29220.1, transcriptional regulator family protein

Match to Query 3081: 1856.730840 from(929.372696,2+) 
Elution from: 29.236 to 29.236 scan no 2607 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1856.7326
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00081
Matched b ions: b(9), b(11)-98, b(11)
Matched y ions: y(4), y(6), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1833

SLDSHIEDQFASGR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLDHIEDQFASGR
Found in AT5G20290.1, 40S ribosomal protein S8 (RPS8A)

Match to Query 2814: 1640.681974 from(821.348263,2+)
Elution from: 40.947 to 40.947 scan no 4130 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1640.6831
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.011
Matched b ions: b(5)-98, b(7)-98, b(8), b(8)-98
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1834
SLEANQVQQQQGAAASVSC
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of SLEANQVQQQQGAAASVSC
Found in AT1G15340.1, MBD10 (methyl-CpG-binding domain 10); DNA binding

Match to Query 3877: 2054.871144 from(1028.442848,2+)
Elution from: 31.646 to 31.646 scan no 2759 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2054.8728
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 8.5e-007
Matched b ions: b(8), b(9), b(10), b(11), b(14), b(15), b(16), b(17)
Matched y ions: y(2), y(4), y(6), y(9), y(11), y(12), y(14), y(15)
Precursor origin neutral loss: +

Peptide No. 1835
SLEEMSGENEDNENSNNDSR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of SLEEMSGENEDNENSNNDSR
Found in AT2G38940.1, ATPT2 (PHOSPHATE TRANSPORTER 2); carbohydrate transporter/phosphate transporter/sugar porter

Match to Query 4394: 2348.831634 from(1175.423093,2+)
Elution from: 28.096 to 28.096 scan no 2162 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2348.8335
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 Expect: 9.1e-008
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(10), b(11), b(12), b(13), b(14), b(15)-98, b(16)-98, b(18)-98
Matched y ions: y(6)-98, y(6), y(7)-98, y(7), y(8)-98++, y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(14)-98++, y(14), y(14)-98, y(15), y(15)-98, y(16)+, y(16)-98, y(16), y(16)-98++, y(17)+, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1836

SLEFPEPTSFR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLEFPEPTSFR
Found in AT4G08500.1, MEKK1 (MYTOGEN ACTIVATED PROTEIN KINASE KINASE); kinase

Match to Query 1630: 1388.600586 from(695.307569,2+)
Elution from: 53.000 to 53.000 scan no 5644 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1388.6013
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0012
Matched b ions: b(2), b(3)−98, b(3), b(4), b(4)−98, b(6), b(7)−98, b(8), b(8)++, b(9)
Matched y ions: y(5), y(7), y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.1837
SLEHSDGPSILDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLEHSDGPSILDK
Found in AT4G01290.1, similar to unknown [Oryza sativa] (GB:AAF00138.1); similar to Os06g0105900 [Oryza sativa (japonica

Match to Query 2233: 1476.648388 from(739.331470,2+)
Elution from: 32.463 to 32.463 scan no 3045 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1476.6497
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 6.1e-005
Matched b ions: b(3)−98, b(4)−98, b(5)−98, b(5), b(6)++, b(10)−98, b(10), b(12)
Matched y ions: y(2), y(3), y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1838

SLEIEPK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLEIEPK
Found in AT2G16940.1, RNA recognition motif (RRM)−containing protein

Match to Query 397: 894.409698 from(448.212125,2+)  
Elution from: 29.863 to 29.863 scan no 2640 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 894.4099
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 5e-005
Matched b ions: b(2)–98, b(2), b(3)–98, b(3), b(4), b(4)–98, b(5), b(5)–98, b(6)–98
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6)
Precursor origin neutral loss: +

Peptide No.1839
SLEPLEAEQAVSEK
Confirmed sites: @S:1
Ambiguous sites: 

MS/MS Fragmentation of SLEPLEAEQAVSEK
Found in AT2G27285.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27280.1); similar to PREDICTED: similar

Match to Query 2295: 1608.726320 from(805.370436,2+) Elution from: 43.986 to 43.986 scan no 4476 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1608.7283
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 81 Expect: 7.2e-008
Matched b ions: b(2), b(3), b(3)-98, b(5)-98, b(6)-98, b(6), b(7)++, b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(12), y(12)++, y(13)++

Precursor origin neutral loss: +

Peptide No.1840

SLEWTNSSLSEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SLEWTNSSLSEK
Found in ATCG01130.1, Identical to Putative membrane protein ycf1 (ycf1-B) [Arabidopsis Thaliana] (GB:P56785); similar to

Match to Query 1749: 1459.622008 from(730.818280,2+)
Elution from: 41.409 to 41.409 scan no 4171 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1459.6232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 43 Expect: 0.00026
Matched b ions: b(3), b(4), b(5), b(9)-98, b(9), b(11), b(11)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(8)++, y(9)+++, y(9), y(9)-
98++, y(9)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.1841
SLEWTNSSLSEK
Confirmed sites:
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of SLEWTNSSLSEK
Found in ATCG01130.1, Identical to Putative membrane protein ycf1 (ycf1-B) [Arabidopsis Thaliana] (GB:P56785); similar to

Match to Query 1858: 1459.622476 from(730.818514,2+) Elution from: 41.447 to 41.447 scan no 4178 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1459.6232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0015
Matched b ions: b(3), b(4), b(4)++, b(5), b(9)−98, b(9), b(11)++
Matched y ions: y(3), y(4), y(7), y(7)−98, y(8), y(8)++, y(8)−98, y(9)−98, y(9), y(9)++, y(10)++, y(10), y(10)−98++
Precursor origin neutral loss: +

Peptide No. 1842

SLEWTNSSLEK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of SLEWTNSSLEK
Found in ATCG01130.1, Identical to Putative membrane protein ycf1 (ycf1-B) [Arabidopsis Thaliana] (GB:P56785); similar to

Match to Query 1825: 1459.622506 from(730.818529,2+) Elution from: 42.248 to 42.248 scan no 4248 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1459.6232
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0027
Matched b ions: b(3), b(4), b(5)–98, b(6)–98, b(9)–98, b(9), b(10)++, b(11), b(11)++
Matched y ions: y(3), y(4), y(7), y(8), y(8)–98, y(8)++, y(9), y(9)–98, y(9)++, y(10)++, y(10), y(10)–98++
Precursor origin neutral loss: +

Peptide No.1843
SLFSDVQGK
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SLFSDVQGK
Found in AT2G45200.1, GOS12 (GOLGI SNARE 12); SNARE binding
Match to Query 619: 1059.463448 from(530.739000,2+)
Elution from: 40.689 to 40.689 scan no 4042 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1059.4637
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00023
Matched b ions: b(3)-98, b(3), b(4), b(6)-98, b(6), b(7)-98, b(7)++, b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7)
Precursor origin neutral loss: +

Peptide No.1844

SLGSFRSAANV
Confirmed sites: “@S:4,@S:7”
Ambiguous sites:

MS/MS Fragmentation of SLGSFRSAANV
Found in AT2G37170.1, PIP2B (plasma membrane intrinsic protein 2;2); water channel

Match to Query 1447: 1267.498610 from(634.756581,2+) Elution from: 45.180 to 45.180 scan no 4653 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1267.4999
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0038
Matched b ions: b(5)–98, b(5)+, b(6), b(7)–98, b(7)–98, b(8)–98, b(8), b(8)–196, b(9)–98, b(9)–98++, b(9)–98++, b(9)–196++, b(10)–196++, b(10)++, b(10)–98++
Matched y ions: y(2), y(3), y(5), y(6), y(6)–98, y(7), y(8), y(9)–98++, y(9)–98, y(9), y(9)–196, y(9)+, y(9)+, y(9)+++, y(10)–196++, y(10)++
Precursor origin neutral loss: +

Peptide No.1845

SLHSIDEEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SLHSIDEEEK
Found in AT1G55535.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13420.1); similar to hypothetical prote

Match to Query 790: 1136.474070 from(569.244311,2+)
Elution from: 20.985 to 20.985 scan no 1397 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1136.4751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 2.6e-005
Matched b ions: b(4)-98, b(5)-98, b(6), b(6)-98, b(7), b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98++, y(7)++, y(7)-98
Precursor origin neutral loss: +

Peptide No.1846
SLLNESPSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SLLNESPSR
Found in AT1G19485.1, AT hook motif-containing protein

Match to Query 797: 1081.479266 from(541.746909,2+) Elution from: 30.002 to 30.002 scan no 2633 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1081.4805
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.038
Matched b ions: b(2), b(5)
Matched y ions: y(3), y(4), y(5), y(5)−98, y(6), y(6)−98, y(7)++, y(7)
Precursor origin neutral loss: +

Peptide No.1847
SLNLAAESSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLNLAAESSR
Found in AT3G60380.1, similar to hydroxyproline–rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT4G16790.1)
Match to Query 1127: 1126.501082 from(564.257817,2+) Elution from: 31.993 to 31.993 scan no 2942 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1126.5019
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1e-005
Matched b ions: b(3), b(4), b(5), b(5)–98, b(6), b(6)–98, b(7)–98, b(7), b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++
Precursor origin neutral loss: +

Peptide No.1848
SLNRSPPSYGSHP
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SLNRSPPSYGSHP
Found in AT3G13224.2, RNA recognition motif (RRM)–containing protein

Match to Query 2069: 1633.734258 from(545.585362,3+)
Elution from: 20.440 to 20.440 scan no 1317 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1633.7362
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0073
Matched b ions: b(5), b(6)−98, b(6)++, b(7)−98++, b(8)−98++, b(10)−98++, b(12)++, b(13)−98++, b(13)++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7)++, y(8)++, y(9)++, y(10)−98++, y(12)−98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1849
SLPAEQLAGPSEPAK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLPAEQLAGPSEPAK
Found in AT4G32350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79910.1); similar to hypothetical prote

Match to Query 2159: 1573.738394 from(787.876473,2+)
Elution from: 36.125 to 36.125 scan no 3472 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1573.7388
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 Expect: 2.7e-008
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9)-98++, b(10)+, b (10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(14)-98, b(14)
Matched y ions: y(3), y(4), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.1850

SLPAISGSEDQSSPQK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SLPAISGSEDQSSPQK
Found in AT1G10520.1, DNA polymerase lambda (POLL)

Match to Query 2897: 1709.752072 from(855.883312,2+) Elution from: 32.141 to 32.141 scan no 2827 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1709.7509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 Expect: 2.8e-008
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(10), b(11), b(12), b(13)−98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(14)++, y(14), y(14)−98++
Precursor origin neutral loss:

Peptide No.1851

SLQSSLIAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SLQSSLIAK
Found in AT1G50360.1, VIIIA (Myosin-like protein VIIA); motor

Match to Query 911: 1112.547542 from(557.281047,2+)
Elution from: 37.163 to 37.163 scan no 3500 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1112.5478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.003
Matched b ions: b(4), b(5)−98, b(6)−98, b(8), b(8)++, b(8)−98++, b(8)−98, b(9)−98
Matched y ions: y(2), y(4), y(5), y(6)−98, y(7)−98, y(7), y(8)++, y(8), y(8)−98, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1852
SLQSSLIAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SLQSSLIAK
Found in AT1G50360.1, VIIIA (Myosin−like protein VIIA); motor

Match to Query 759: 1112.546792 from(557.280672,2+)
Elution from: 35.524 to 35.524 scan no 3388 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1112.5478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00041
Matched b ions: b(2), b(3), b(6), b(8), b(8)+, b(8)–98, b(8)–98++, b(9)–98
Matched y ions: y(2), y(4), y(4)–98++, y(4)–98, y(5), y(5)–98, y(6), y(7), y(7)–98, y(8)+, y(8)–98++, y(8), y(9)+
Precursor origin neutral loss: +

Peptide No.1853

SLRKSEDHVENNLSAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SLRKSEDHVENNLSAK
Found in AT2G35050.1, protein kinase family protein

Match to Query 3474: 1905.892932 from(477.480509,4+) 
Elution from: 19.574 to 19.574 scan no 1253 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1905.8945
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.023
Matched b ions: b(4)++, b(4), b(5)−98++, b(7)++, b(8)++, b(8)−98++, b(9)−98++, b(9)++, b(10)−98++, b(10)++, b(11)−98++, b(11)++, b(12)++, b(12)−98++
Matched y ions: y(1), y(3), y(4), y(6), y(8)++, y(9)++, y(10)++, y(11)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1854

SLSASGSFR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SLSASGSFR
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 551: 990.416288 from(496.215420,2+)
Elution from: 27.050 to 27.050 scan no 2229 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 990.4171
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00062
Matched b ions: b(2), b(3), b(4), b(5)—98++, b(5)—98, b(6)—98, b(7), b(7)—98, b(8)—98
Matched y ions: y(1), y(2), y(5), y(5)—98, y(6), y(6)—98, y(7), y(7)—98, y(7)++
Precursor origin neutral loss: +

Peptide No.1855

SLSASGSFR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SLSASGSFR
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 490: 990.416666 from(496.215609,2+) Elution from: 26.154 to 26.154 scan no 2121 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 990.4171
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00029
Matched b ions: b(2), b(3), b(4), b(5), b(7)−98, b(8)−98, b(8)++
Matched y ions: y(1), y(2), y(3)−98, y(4), y(4)−98, y(5), y(5)−98, y(6), y(6)−98, y(7), y(7)−98, y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No. 1856
SLSASGSFRNDSTPK
Confirmed sites:
Ambiguous sites: @S:5 or S:7

MS/MS Fragmentation of SLSASGSFRNDSTPK
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 2403: 1632.713214 from(817.363883,2+)
Elution from: 25.029 to 25.029 scan no 1970 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1632.7144
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0019
Matched b ions: b(4), b(7)–98, b(8)–98, b(8)–98++, b(11)–98, b(11), b(12), b(13)–98
Matched y ions: y(2), y(4), y(6), y(8), y(11)++, y(12), y(13)++, y(13)–98++
Precursor origin neutral loss: +

Peptide No.1857

SLSASSFLIDTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSASSFLIDTK
Found in AT1G07110.1, F2KP (FRUCTOSE–2,6–BISPHOSPHATASE); fructose–2,6–bisphosphate 2–phosphatase

Match to Query 1469: 1347.630852 from(674.822702,2+)
Elution from: 53.574 to 53.574 scan no 5680 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1347.6323 
Fixed modifications: Carbamidomethyl (C) 
Variable modifications: 
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 
Ions Score: 78 Expect: 8.3e-008 
Matched b ions: b(3)-98, b(4)-98, b(5), b(5)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98 
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(10)-98, y(10)+, y (11)++ 
Precursor origin neutral loss: + 

Peptide No.1858 
SLSDHIQK 
Confirmed sites: @S:1 
Ambiguous sites: 

MS/MS Fragmentation of SLSDHIQK 
Found in AT5G40450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to erythrocyte membra 

Match to Query 484: 1006.447926 from(504.231239,2+) 
Elution from: 20.138 to 20.138 scan no 1312 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1006.4485
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.00092
Matched b ions: b(2)-98, b(3)−98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(6)++, b(7)-98, b(7)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No.1859

SLSEDLSSGDL SK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSEDLSSGDL SK
Found in AT1G28530.1, similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD07831.1)

Match to Query 2018: 1416.601786 from(709.308169,2+)
Elution from: 42.567 to 42.567 scan no 4305 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1416.6021
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 4.2e-008
Matched b ions: b(3), b(4)–98, b(5)–98, b(5), b(6)–98, b(7), b(7)–98, b(8), b(8)++, b(8)–98, b(9)–98, b(9), b(10)–98, b(11)++, b(11)–98, b(11), b(12), b(12)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(10)++, y(11)–98, y(11), y(11)–98++, y(11)++
Precursor origin neutral loss: +

Peptide No. 1860
SLSEISEVDAVR
Confirmed sites: @S:6
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SLSEISEVDAVR
Found in AT1G56230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22660.2); similar to Os01g0347100 [Oryza]

Match to Query 2111: 1463.593394 from(732.803973,2+) Elution from: 50.258 to 50.258 scan no 5284 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.5946
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.02
Matched b ions: b(4), b(5)−98, b(5), b(7), b(8)−98, b(9), b(9)−98++, b(10)−98, b(11)−98, b(11)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1861

SLSEISEVDAVR
Confirmed sites: “@S:3,@S:6”
Ambiguous sites:

MS/MS Fragmentation of SLSEISEVDAVR
Found in AT1G56230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22660.2);
similar to Os01g0347100 [Oryz

Match to Query 1510: 1463.592494 from(732.803523,2+)
Elution from: 50.376 to 50.376 scan no 4887 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.5946
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00055
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-196, b(7), b(8)-98, b(8), b(9)-98++, b(10)-98, b(11)-98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6)+, y(6), y(7), y(7)-98, y(8)-98, y(8), y(10)-98++, y(10)-196++, y(10), y(10)-98
Precursor origin neutral loss: +

Peptide No.1862
SLSESEDEEEGR
Confirmed sites: ”@S:3,@S:5”
Ambiguous sites:

MS/MS Fragmentation of SLSESEDEEEGR
Found in AT2G28910.1, CXIP4 (CAX INTERACTING PROTEIN 4); nucleic acid binding / zinc ion binding

Match to Query 1638: 1525.485076 from(763.749814,2+) Elution from: 22.498 to 22.498 scan no 1510 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1525.4858
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.0096
Matched b ions: b(5)−98, b(8)−98
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(10)−196++, y(10)−98, y(10), y(10)−98++
Precursor origin neutral loss: +

Peptide No. 1863

SLSFSGHSFQGR
Confirmed sites: “@S:1,@S:8”
Ambiguous sites:

MS/MS Fragmentation of SLSFSGHSFQGR
Found in AT5G50530.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 2332: 1468.552390 from(735.283471,2+)
Elution from: 40.267 to 40.267 scan no 4040 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1468.5537

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

Ions Score: 30 Expect: 0.0042
Matched b ions: b(3)−98, b(4)−98, b(5)−98, b(6), b(7), b(7)−98, b(8)−98, b(9)−98++, b(9)−98, b(10), b(10)−98, b(10)++, b(11)−98, b(11)−98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(7), y(7)−98++, y(7)−98, y(7)++, y(8), y(8)−98, y(9)−98++, y(9), y(9)++, y(9)−98, y(10)−98, y(11)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No. 1864

SLSFGHQSFQGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSFGHQSFQGR
Found in AT5G50530.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 2097: 1388.585660 from (695.300106,2+)
Elution from: 37.630 to 37.630 scan no 3686 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1388.5874

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 40 Expect: 0.00068

Matched b ions: b(3)–98, b(4)–98, b(5)–98, b(5), b(7), b(10)–98, b(11), b(11)++

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10)–98++, y(10)++, y(11)–98++

Precursor origin neutral loss: +

Peptide No. 1865

SLSGEGGSGTGSLR

Confirmed sites: @S:8

Ambiguous sites:

MS/MS Fragmentation of SLSGEGGSGTGSLR

Found in AT5G03280.1, EIN2 (ETHYLENE INSENSITIVE 2); transporter

Match to Query 1441: 1430.602084 from(716.308318,2+)

Elution from: 24.897 to 24.897 scan no 1849 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1430.6038
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(5), b(8)--98, b(12)--98
Matched y ions: y(2), y(5), y(6), y(7), y(9), y(10), y(11)--98, y(12)--98++, y(12), y(13)++, y(13)--98++
Precursor origin neutral loss: +

Peptide No.1866

SLSGISLNEPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSGISLNEPK
Found in AT4G11270.1, transducin family protein / WD-40 repeat family protein

Match to Query 1065: 1223.579490 from(612.797021,2+)
Elution from: 39.926 to 39.926 scan no 3975 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1223.5798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.0001
Matched b ions: b(2), b(3)–98, b(4)–98, b(5)–98, b(5)++, b(6), b(6)–98, b(7)–98, b(7)++, b(8), b(8)–98, b(9)–98, b(9), b(9)++, b(10)–98, b(10)–98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(4)+, y(5), y(5)+, y(6), y(7), y(8), y(9)–98, y(9), y(9)–98++, y(9)++, y(10)–98, y(10)–98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1867

SLSIAPTGR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLSIAPTGR
Found in AT1G15440.1, transducin family protein / WD-40 repeat family protein

Match to Query 434: 980.470536 from(491.242544,2+)
Elution from: 31.856 to 31.856 scan no 2861 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 980.4692

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 25 Expect: 0.024
Matched b ions: b(3), b(5), b(5)-98
Matched y ions: y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No. 1868

SLSIPITK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSIPITK
Found in AT4G39390.1, transporter-related

Match to Query 319: 937.487120 from(469.750836,2+) Elution from: 39.369 to 39.369 scan no 3901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 937.4885
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.022
Matched b ions: b(2), b(4)−98
Matched y ions: y(4), y(5), y(6)++, y(6)−98, y(6)
Precursor origin neutral loss: +

Peptide No.1869
SLSIPPVGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSIPPVGK
Found in AT3G45090.1, 2-phosphoglycerate kinase–related

Match to Query 536: 976.500360 from(489.257456,2+)
Elution from: 39.678 to 39.678 scan no 3725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 976.4994
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0045
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(7)-98
Matched y ions: y(4)++, y(4), y(5), y(6), y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.1870

SLSLNFDSEDYEPER
Confirmed sites:
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SLSLNFDSEDYEPER
Found in AT2G31270.1, ATCDT1A/CDT1/CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein

Match to Query 2748: 1750.704836 from(876.359694,2+)
Elution from: 52.708 to 52.708 scan no 5571 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1750.7087
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0011
Matched b ions: b(5), b(6)−98, b(7)−98, b(7), b(9)−98, b(9)
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(10)
Precursor origin neutral loss: +

Peptide No.1871

SLSLNFDSEPDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSLNFDSEPDER
Found in AT2G31270.1, ATCDT1A/CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin−dependent protein kinase/ protein

Match to Query 2995: 1750.705018 from(876.359785,2+)
Elution from: 53.003 to 53.003 scan no 5633 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1750.7087
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 57 Expect: 1.1e-005
Matched b ions: b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++
Precursor origin neutral loss: +

Peptide No.1872

SLSLQER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSLQER
Found in AT1G53350.1, disease resistance protein (CC-NBS-LRR class), putative

Match to Query 297: 911.410246 from(456.712399,2+)  
Elution from: 26.278 to 26.278 scan no 2105 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 911.4113
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0021
Matched b ions: b(2), b(3), b(4)−98, b(5)+, b(5)−98, b(5), b(6)−98
Matched y ions: y(1), y(2), y(3), y(4), y(5)−98++, y(5)−98, y(5), y(5)+, y(6)+
Precursor origin neutral loss: +

Peptide No.1873

SLSPETLALMCDER
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SLSPETLALMCDER
Found in AT2G20110.1, tesmin/TSO1–like CXC domain–containing protein

Match to Query 2494: 1700.714346 from(851.364449,2+)
Elution from: 51.117 to 51.117 scan no 5395 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1700.7150
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00019
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(9), b(12)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.1874

SLSPETLALMCDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSPETLALMCDER
Found in AT2G20110.1, tesmin/TSO1-like CXC domain-containing protein

Match to Query 2598: 1700.714322 from(851.364437,2+)
Elution from: 52.172 to 52.172 scan no 5505 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1700.7150
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.2e-005
Matched b ions: b(7)-98, b(8)-98, b(9), b(10)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1875

SLSKPFPDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSKPFPDR
Found in AT2G43680.1, IQD14; calmodulin binding

Match to Query 753: 1125.520666 from(563.767609,2+)
Elution from: 27.537 to 27.537 scan no 2310 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1125.5219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 31 Expect: 0.0062
Matched b ions: b(2), b(3)−98, b(3), b(4), b(5), b(5)−98, b(6)−98, b(6)−98++, b(8)−98, b(8), b(8)++
Matched y ions: y(1), y(4), y(5), y(6), y(6)++, y(7)−98++, y(7)++, y(7)−98, y(7), y(8)−98++
Precursor origin neutral loss: +

Peptide No. 1876
SLSPVYR
Confirmed sites: "@S:1,@S:3"
Ambiguous sites:
MS/MS Fragmentation of SLSPVYR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding
Match to Query 518: 980.376164 from(491.195358,2+)
Elution from: 34.382 to 34.382 scan no 3225 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 980.3769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.018
Matched b ions: b(2)-98, b(2), b(3)-98, b(3), b(3)-98++, b(4)-196++, b(4), b(5), b(5)-196, b(5)-98, b(5)++, b(6), b(6)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(5)-98++, y(5)-98
Precursor origin neutral loss: +

Peptide No. 1877

SLSRSPIQLSR
Confirmed sites: ”@S:1,@S:3,@S:5”
Ambiguous sites:

MS/MS Fragmentation of SLSRSPIQLSR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1888: 1482.603088 from(742.308820,2+)
Elution from: 37.812 to 37.812 scan no 3697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1482.6034

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 24 Expect: 0.022

Matched b ions: b(4), b(4)-98, b(5)-98, b(5)-196, b(7), b(7)-98, b(8), b(8)-98, b(8)-98++, b(9), b(9)-98, b(10)

Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(10)-196++, y(10)++

Precursor origin neutral loss: +

Peptide No.1878

SLSRPIQLSR

Confirmed sites: "@S:1,@S:5"

Ambiguous sites:

MS/MS Fragmentation of SLSRPIQLSR

Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1902: 1402.636230 from(702.325391,2+)
Elution from: 35.509 to 35.509 scan no 3279 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1402.6371
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 22 Expect: 0.048
Matched b ions: b(4)++, b(4), b(5)−196, b(5)−98, b(7)−98, b(7), b(8), b(8)−98, b(9), b(9)−98, b(10), b(10)−196
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)++, y(8), y(8)−98++, y(9)++, y(9)−98++, y(10)++, y(10)−98++
Precursor origin neutral loss: +

Peptide No.1879

SLSSLQVLQETK
Confirmed sites:
Ambiguous sites: @S:1 or S:3 or S:4

MS/MS Fragmentation of SLSSLQVLQETK
Found in AT3G13360.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56210.1); similar to hypothetical prote

Match to Query 1605: 1411.696264 from(706.855408,2+)
Elution from: 48.040 to 48.040 scan no 5022 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1411.6959
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.03
Matched b ions: b(6), b(7)+, b(7)−98, b(8), b(8)−98
Matched y ions: y(2), y(4), y(5), y(7)
Precursor origin neutral loss: +

Peptide No.1880
SLSWSVSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSWSVSR
Found in AT1G74450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18740.1);
similar to Protein of unknown

Match to Query 726: 1000.437908 from(501.226230,2+)
Elution from: 39.078 to 39.078 scan no 3890 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1000.4379
Fixed modifications: Carbamidomethyl (C)
Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00073
Matched b ions: b(2), b(4)–98, b(5)–98, b(6)–98, b(7)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6)–98++, y(6)–98, y(6), y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No. 1881

SLTDDELDELK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SLTDDELDELK
Found in AT3G50350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G33985.1);
similar to Os04g0282200 [Oryz]

Match to Query 1493: 1356.568874 from(679.291713,2+)  
Elution from: 44.417 to 44.417 scan no 4532 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1356.5697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 1.7e-006
Matched b ions: b(2), b(3), b(3)–98, b(4)–98, b(5)–98, b(5), b(7)–98, b(8)–98, b(8), b(9)–98, b(9), b(10), b(10)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1882

SLTELTGSPQLR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SLTELTGSPQLR
Found in AT4G34860.1, beta–fructofuranosidase, putative / invertase, putative / saccharase, putative / beta–fructosidase,

Match to Query 1569: 1380.663690 from(691.339121,2+)
Elution from: 41.907 to 41.907 scan no 4203 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1380.6650
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 5.5e-005
Matched b ions: b(3), b(4), b(5), b(6), b(8)−98, b(8), b(9)−98, b(10)−98++, b(11), b(11)−98
Matched y ions: y(2), y(3), y(4), y(5)−98, y(5), y(6), y(6)−98, y(7), y(7)−98, y(8), y(8)−98, y(9), y(9)−98, y(9)++, y(10)++, y(10), y(10)−98++, y(11)++
Precursor origin neutral loss: +

Peptide No. 1883

SMAQYPEAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMAQYPEAR
Found in AT5G64220.1, calmodulin-binding protein

Match to Query 768: 1131.441672 from(566.728112,2+) Elution from: 24.728 to 24.728 scan no 1933 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1131.4420
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 3.9e-005
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6), b(8)-98
Matched y ions: y(1), y(2), y(4), y(5), y(6), y(6)++, y(7)
Precursor origin neutral loss: +

Peptide No.1884

SMAQYPEAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMAQYPEAR
Found in AT5G64220.1, calmodulin-binding protein

Match to Query 780: 1147.436688 from(574.725620,2+) Elution from: 20.188 to 20.188 scan no 1319 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1147.4369
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 51 Expect: 3.5e-005
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1885

SMDFETVDQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMDFETVDQR
Found in AT1G27750.1, nucleotide binding

Match to Query 1173: 1306.487708 from(654.251130,2+)  
Elution from: 39.559 to 39.559 scan no 3727 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1306.4901
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.011
Matched b ions: b(3)−98, b(4), b(5)−98, b(8)++
Matched y ions: y(2), y(3), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1886

SMESNVANGNTTIDIHHPCR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMESNVANGNTTIDIHHPCR
Found in AT4G24520.1, ATR1 (ARABIDOPSIS CYTOCHROME REDUCTASE)

Match to Query 3797: 2331.968655 from(778.330161,3+)
Elution from: 31.519 to 31.519 scan no 2918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2331.9725  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 28 Expect: 0.017  
Matched b ions: b(2), b(3)-98, b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(15)-98++, b(17)++, b(17)-98++  
Matched y ions: y(3), y(6), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++  
Precursor origin neutral loss: +

Peptide No.1887

SMFSGFTETPKSPK  
Confirmed sites: @S:12  
Ambiguous sites:

MS/MS Fragmentation of SMFSGFTETPKSPK  
Found in AT5G64680.1, similar to Os01g0259900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042641.1); similar to hy  
Match to Query 2757: 1622.702162 from(812.358357,2+)  
Elution from: 41.090 to 41.090 scan no 4156 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1622.7051
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00068
Matched b ions: b(6), b(9), b(11), b(12)–98
Matched y ions: y(2), y(3)–98, y(4), y(5)–98, y(5), y(6)–98, y(6), y(7)–98, y(8)–98, y(8), y(9), y(10), y(10)–98++, y(10)–98, y(10)++, y(11)++, y(11), y(12)++, y(12)–98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1888
SMGTSYTEEELNR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SMGTSYTEEELNR
Found in AT1G73630.1, calcium–binding protein, putative

Match to Query 1793: 1595.615948 from(798.815250,2+)
Elution from: 37.791 to 37.791 scan no 3506 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1595.6174
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.06
Matched b ions: b(6), b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9)-98, y(10), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1889
SMIPQNLGSFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 1375: 1316.584448 from(659.299500,2+)
Elution from: 41.702 to 41.702 scan no 4176 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1316.5835
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.054
Matched b ions:
Matched y ions: y(7), y(8)-98, y(8), y(9)
Precursor origin neutral loss: +

Peptide No. 1890

SMIPQNLGSFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 1346: 1300.587948 from(651.301250,2+) Elution from: 48.227 to 48.227 scan no 5060 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1300.5886
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0046
Matched b ions: b(2), b(3), b(5)
Matched y ions: y(4), y(6), y(7), y(7)+, y(8)+, y(8)−98, y(8), y(8)−98++, y(9)+, y(9), y(9)−98++
Precursor origin neutral loss: +

Peptide No.1891
SMIPQNLGSFKEESSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFKEESSK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 3000: 1876.824988 from(939.419770,2+)
Elution from: 36.024 to 36.024 scan no 3454 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1876.8277
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 2.4e-005
Matched b ions: b(7), b(8), b(9)--98, b(10)--98, b(13)--98, b(14)--98++, b(14)++, b(15)--98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)--98, y(9), y(11), y(11)--98, y(12)++, y(12), y(12)--98, y(13)--98++, y(13)++, y(13)--98, y(13), y(14)--98++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1892
SMIPQNLGSFKEESSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFKEESSK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 2676: 1860.829652 from(931.422102,2+)
Elution from: 43.143 to 43.143 scan no 4286 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1860.8328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.036
Matched b ions: b(10), b(14)-98++, b(14)-98
Matched y ions: y(9)-98, y(9), y(11)-98, y(12)+, y(13)-98++, y(13)+, y(13), y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.1893

SMIPQNLGSFKEESSK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFKEESSK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 2960: 1860.830598 from(621.284142,3+)
Elution from: 43.212 to 43.212 scan no 4350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1860.8328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0041
Matched b ions: b(2), b(3), b(11)++, b(14)++
Matched y ions: y(8)++, y(9)++, y(10)++, y(11)++, y(11)−98++, y(12)++, y(13)++, y(13)−98++, y(14)++,
y(14)−98++
Precursor origin neutral loss:

Peptide No.1894

SMIPQNLGSFKEESSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SMIPQNLGSFKEESSK
Found in AT1G72160.1, SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein

Match to Query 3236: 1860.831196 from(931.422874,2+)
Elution from: 44.605 to 44.605 scan no 4367 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1860.8328
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 2.3e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9)--98, b(10)--98, b(11), b(12), b(12)--98, b(13), b(13)--98, b(13)--98++, b(14)--98++, b(14)--98, b(15)--98, b(15)--98++  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)--98, y(9), y(10), y(10)--98, y(11)--98, y(11), y(11)++, y(12)++, y(12), y(13)--98++, y(13)++, y(13)--98, y(13), y(14)--98++, y(14)++, y(15)++  
Precursor origin neutral loss: +

Peptide No.1895
SMSDSNLNNVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SMSDSNLNNVR
Found in AT5G56850.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22795.1); similar to Os05g0232200 [Oryz]

Match to Query 1771: 1315.522100 from(658.768326,2+)  
Elution from: 26.894 to 26.894 scan no 2287 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1315.5227
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0002
Matched b ions: b(4), b(7)-98, b(7), b(8), b(10)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9)-98, y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.1896

SMSELSTGYSR
Confirmed sites: "@S:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1350: 1392.467390 from(697.240971,2+)
Elution from: 28.210 to 28.210 scan no 2258 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1392.4669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.001
Matched b ions: b(2), b(4)–98, b(5)–98, b(5), b(7)–98, b(9)–98, b(9), b(10)–98
Matched y ions: y(2), y(4), y(5), y(6), y(6)–98, y(7), y(7)–98, y(9)–196++, y(9)–98, y(9)–196, y(10)++
Precursor origin neutral loss: +

Peptide No.1897

SMSELSTGYSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1265: 1312.500572 from(657.257562,2+)
Elution from: 24.684 to 24.684 scan no 1882 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1312.5006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 9.8e-006
Matched b ions: b(2), b(4), b(5), b(6)−98, b(7)−98, b(8)−98, b(9)−98, b(10)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)−98, y(9)−98, y(9), y(10)−98++
Precursor origin neutral loss: +

Peptide No.1898
SMSELSTGYSR
Confirmed sites: 
Ambiguous sites: @S:6orT:7

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1335: 1312.500290 from(657.257421,2+) 
Elution from: 24.917 to 24.917 scan no 1956 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1312.5006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
  T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 1.8e-005
Matched b ions: b(2), b(4), b(5), b(7)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(10)-98++
Precursor origin neutral loss: +

Peptide No.1899
SMSELSTGYSR
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase
Match to Query 1767: 1296.505208 from(649.259880,2+)
Elution from: 33.280 to 33.280 scan no 3115 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.5057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 7.3e-007
Matched b ions: b(2), b(2)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(8)-98, b(9), b(9)-98, b(10), b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No. 1900

SMSELSTGYSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1362: 1312.499308 from(657.256930,2+) 
Elution from: 26.167 to 26.167 scan no 2090 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1312.5006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 Expect: 1.9e-006
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(8)-98, b(9)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)+, y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1901
SMSELSTGYSR
Confirmed sites: @S:1
Ambiguous sites: @S:6orT:7

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1594: 1392.466162 from(697.240357,2+)
Elution from: 28.876 to 28.876 scan no 2457 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1392.4669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
M2 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 35 Expect: 0.00065
Matched b ions: b(2), b(4), b(5)–98, b(5), b(9)–98
Matched y ions: y(2), y(3), y(4), y(6), y(6)–98, y(7)–98, y(7), y(8)–98, y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1902
SMSELSTGYSR
Confirmed sites: ”@S:1,@S:3”
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1950: 1376.473138 from(689.243845,2+)
Elution from: 37.809 to 37.809 scan no 3755 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 16 Expect: 0.055
Matched b ions: b(4)-98, b(5), b(5)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)
Precursor origin neutral loss: +

Peptide No.1903

SMSELSTGYSR
Confirmed sites: “@S:1,@S:6”
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1763: 1376.471314 from(689.242933,2+) Elution from: 35.597 to 35.597 scan no 3409 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00017
Matched b ions: b(2), b(2)-98, b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-196, b(6)-98, b(7)-98, b(7)-98++, b(7)+, b(7)-196, b(7), b(8)-98, b(8)-196, b(8)+, b(9)-98, b(9), b(9)-196, b(9)-196++, b(10)-98
Matched y ions: y(2), y(3), y(4), y(4)+, y(5), y(6)-98, y(6), y(7)-98, y(7)+, y(8)+, y(8), y(8)-98, y(8)-98++, y(9), y(9)-98, y(9)+, y(9)-98++, y(10)-98++
Precursor origin neutral loss: +

---

Peptide No.1904

SMSELSTGYSR
Confirmed sites: @S:1
Ambiguous sites: @T:7 or Y:9

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1592: 1376.472130 from(689.243341,2+)
Elution from: 34.820 to 34.820 scan no 3293 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
  Y9 : Phospho (Y)
Ions Score: 22 Expect: 0.014
Matched b ions: b(2), b(4)--98, b(4), b(5)--98, b(5), b(6)++, b(9)--98
Matched y ions: y(2), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1905
SMSELSTGYSR
Confirmed sites: “@S:1,@T:7”
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1826: 1376.471244 from(689.242898,2+)
Elution from: 35.309 to 35.309 scan no 3252 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00013
Matched b ions: b(2), b(2)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(9), b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(6)-98, y(7), y(7)-98, y(7)++, y(8), y(8)-98, y(8)++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.1906

SMSELSTGYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1252: 1296.505226 from(649.259889,2+)
Elution from: 34.458 to 34.458 scan no 3243 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.5057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 2.5e-005
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(8)-98++, b(9), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1907

SMSELSTGYSR
Confirmed sites: "@S:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1949: 1376.471720 from(689.243136,2+) Elution from: 36.138 to 36.138 scan no 3537 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720

Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 36 Expect: 0.00044
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5), b(5)-98, b(6)-196, b(7)-98, b(7)-196, b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(7)+, y(8), y(8)-98, y(9)-196++, y(9)-98, y(9), y(9)-98++, y(9)-196, y(9)+++, y(10)-98++, y(10)-196++, y(10)+

Precursor origin neutral loss: +

Peptide No.1908
SMSELSTGYSR
Confirmed sites: @S:3
Ambiguous sites: @S:6orT:7orY:9

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1327: 1376.471286 from(689.242919,2+)
Elution from: 36.786 to 36.786 scan no 3401 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y9 : Phospho (Y)
Ions Score: 27 Expect: 0.0029
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(9)-98, b(9)
Matched y ions: y(2), y(6), y(7), y(7)+, y(9)-98, y(9), y(9)-98++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1909

SMSELSTGYSR
Confirmed sites: "@S:3,@T:7"
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 2063: 1376.472578 from(689.243565,2+)
Elution from: 36.797 to 36.797 scan no 3574 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.4720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.011
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(7)-98, b(8)-98, b(9)-98, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)+, y(7), y(7)-98, y(7)-98++, y(9)-98++, y(9), y(9)-196++, y(9)-98, y(9)+, y(10)-98++, y(10)-196++, y(10)+
Precursor origin neutral loss: +

Peptide No.1910

SMSELSTGYSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1066: 1296.504716 from(649.259634,2+)
Elution from: 30.678 to 30.678 scan no 2691 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.5057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 4.9e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6)−98, b(7)−98, b(8)−98, b(9)−98, b(10)−98, b(10)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)−98, y(7), y(7)−98, y(7)++, y(8)−98, y(9)−98++, y(9), y(9)−98, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1911
SMSELSTGYSR
Confirmed sites: @T:7
Ambiguous sites:
MS/MS Fragmentation of SMSELSTGYSR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase
Match to Query 1145: 1296.506588 from(649.260570,2+)
Elution from: 31.806 to 31.806 scan no 2730 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.5057
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 1.1e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)--98, b(8)--98, b(9)--98, b(10)--98
Matched y ions: y(2), y(3), y(4), y(5)--98, y(6), y(7), y(7)--98, y(8)--98++, y(9)--98, y(9), y(9)--98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1912
SMTGEIQAPSSPR
Confirmed sites: @S:12
Ambiguous sites:
MS/MS Fragmentation of SMTGEIQAPSSPR
Found in AT1G30450.1, CCC1; cation:chloride symporter

Match to Query 2153: 1567.669054 from(784.841803,2+)
Elution from: 29.385 to 29.385 scan no 2526 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1567.6701
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 5e−005
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)+, b(11), b(12)−98, b(12)+, b(13)−98+
Matched y ions: y(2), y(3), y(4), y(5), y(5)−98, y(6), y(6)−98, y(7)−98, y(8), y(8)−98, y(10)+, y(11), y(11)+, y(12), y(12)+, y(13)+
Precursor origin neutral loss:

Peptide No.1913
SMVQYPEAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMVQYPEAR
Found in AT2G22300.1, ethylene-responsive calmodulin−binding protein, putative (SR1)

Match to Query 858: 1159.472292 from(580.743422,2+)
Elution from: 29.769 to 29.769 scan no 2612 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1159.4733
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 3.6e-005
Matched b ions: b(2), b(2)–98, b(3)–98, b(3), b(4)–98, b(4), b(5), b(5)–98, b(6)–98, b(7), b(7)–98, b(8), b(8)–98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No.1914

SMVQYPEAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SMVQYPEAR
Found in AT2G22300.1, ethylene-responsive calmodulin-binding protein, putative (SR1)

Match to Query 945: 1175.468302 from(588.741427,2+) Elution from: 23.834 to 23.834 scan no 1808 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1175.4682
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 Expect: 0.00045
Matched b ions: b(3)–98, b(3), b(4)–98, b(4), b(5), b(5)–98
Matched y ions: y(2), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1915

SNATTLPVTQSPR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SNATTLPVTQSPR
Found in AT3G17420.1, GPK1 (Glyoxysomal protein kinase 1); kinase

Match to Query 1715: 1450.680114 from(726.347333,2+)
Elution from: 28.465 to 28.465 scan no 2436 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1450.6817
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 5.3e-006
Matched b ions: b(5), b(6), b(10), b(11), b(12)-98
Matched y ions: y(2), y(3), y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98++, y(9), y(9)-98, y(10)
Precursor origin neutral loss:

Peptide No.1916

SNDLSPPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SNDLSPPR
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 393: 964.401020 from(483.207786,2+)
Elution from: 24.331 to 24.331 scan no 1842 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 964.4015
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.00065
Matched b ions: b(4), b(5)–98
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.1917
SNEAVLMGIGK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNEAVLMGIGK
Found in AT5G35620.1, LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES); RNA binding / translation initiation factor

Match to Query 1209: 1197.546032 from(599.780292,2+) Elution from: 44.686 to 44.686 scan no 4378 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1197.5464
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.4e-005
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(7)-98, b(8)-98, b(9)-98, b(9)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1918
SNEAVLMGIGK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNEAVLMGIGK
Found in AT5G35620.1, LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES); RNA binding / translation initiation factor

Match to Query 1283: 1213.539864 from(607.777208,2+)  
Elution from: 37.221 to 37.221 scan no 3396 polarity:+

Peptide No.1918
SNEAVLMGIGK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNEAVLMGIGK
Found in AT5G35620.1, LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES); RNA binding / translation initiation factor

Match to Query 1283: 1213.539864 from(607.777208,2+)  
Elution from: 37.221 to 37.221 scan no 3396 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1213.5413
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 Expect: 0.0045
Matched b ions: b(3), b(4)–98, b(5)–98, b(5), b(6)–98, b(7), b(9)–98, b(9), b(9)++
Matched y ions: y(2), y(4), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1919

SNERSPSPGSPAPLR
Confirmed sites: “@S:5,@S:7,@S:10”
Ambiguous sites:

MS/MS Fragmentation of SNERSPSPGSPAPLR
Found in AT5G64200.1, ATSC35 (“Arabidopsis thaliana arginine/serine-rich splicing factor 35, 35 kDa protein”); RNA bindin

Match to Query 2167: 1790.676684 from(896.345718,2+)
Elution from: 25.596 to 25.596 scan no 2014 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1790.6790
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.028
Matched b ions: b(5), b(5)−98, b(6)−98, b(7)−98, b(8)−196, b(10)−196, b(10)−98, b(12)−98, b(12), b(13)−196+
Matched y ions: y(3), y(5), y(6), y(7), y(8)−98, y(8), y(10), y(12)++
Precursor origin neutral loss: +

Peptide No.1920

SNERSPSPGSPAPLRK
Confirmed sites: “@S:1,@S:7,@S:10”
Ambiguous sites:

MS/MS Fragmentation of SNERSPSPGSPAPLRK
Found in AT5G64200.1, ATSC35 ("Arabidopsis thaliana arginine/serine-rich splicing factor 35, 35 kDa protein"); RNA bindin

Match to Query 2765: 1918.772196 from(640.598008,3+)
Elution from: 22.443 to 22.443 scan no 1591 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1918.7740
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0034
Matched b ions: b(4), b(5), b(5)-98, b(7)-98, b(7), b(8)-98, b(9)++, b(10)-98, b(10)-196++, b(10)-98++, b(11)-294++, b(11)-196++, b(12)-98++, b(12)-294++, b(13)-196++, b(15)++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)-98++, y(11)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.1921

SNERSPSPGSPAPLRK
Confirmed sites: "@S:5,@S:7,@S:10"
Ambiguous sites:

MS/MS Fragmentation of SNERSPSPGSPAPLRK
Found in AT5G64200.1, ATSC35 ("Arabidopsis thaliana arginine-serine-rich splicing factor 35, 35 kDa protein"); RNA bindin

Match to Query 3488: 1918.772931 from(640.598253,3+)
Elution from: 22.089 to 22.089 scan no 1603 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1918.7740
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.034
Matched b ions: b(4), b(5), b(5)-98, b(6)+, b(7)-98, b(7)-196, b(9)-98++, b(9)+, b(10)-196, b(10)-98, b(10)-196++, b(10)-98++, b(11)-294++, b(11)+, b(11)-196++, b(12)-98++, b(12)-294++, b(12)-196++, b(13)-196++, b(13)-294++, b(15)-98++, b(15)+
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(7)-98++, y(8)+, y(9)-98++, y(10)+, y(10)-196++, y(10)-98++, y(11)-98++, y(11)-196++, y(12)-98++, y(12)-294++, y(13)+, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1922
SNGISDAASEQISDR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SNGISDAASEQISDR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1869: 1628.667680 from(815.341116,2+)
Elution from: 30.355 to 30.355 scan no 2571 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1628.6679
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.019
Matched b ions: b(8)++, b(8), b(9), b(12)
Matched y ions: y(3)-98, y(4)-98, y(5), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(11)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.1923

SNGSEPESPVSPLLTSDPK
Confirmed sites: "@S:8,@S:11"
Ambiguous sites:

MS/MS Fragmentation of SNGSEPESPVSPLLTSDPK
Found in AT3G55320.1, PGP20 (P–GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances

Match to Query 3161: 2099.868692 from(1050.941622,2+)
Elution from: 42.638 to 42.638 scan no 4198 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2099.8701
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.045
Matched b ions: b(7), b(11)-98, b(17), b(17)-98, b(18)-98
Matched y ions: y(5), y(8), y(9), y(12)++, y(12), y(13)++, y(14)++, y(14), y(14)-98++, y(14)-98
Precursor origin neutral loss: +

Peptide No.1924

SNPFYSEAYTTNGSGTGFK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of SNPFYSEAYTTNGSGTGFK
Found in AT5G19450.1, CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); calcium- and calmodulin-dependent protein kinase/kin

Match to Query 3780: 2106.854628 from(1054.434590,2+) Elution from: 46.170 to 46.170 scan no 4798 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2106.8571
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 1.2e-005
Matched b ions: b(5), b(6), b(7), b(8), b(10), b(11), b(12), b(14)-98, b(17)-98++, b(18)-98, b(18)-98++
Matched y ions: y(5), y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15)-98, y(15), y(16)++, y(17)-98++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.1925

SNPFYSEAYTTNGSGTGFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SNPFYSEAYTTNGSGTGFK**
Found in **AT5G19450.1**, CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); calcium- and calmodulin-dependent protein kinase/kin

Match to Query 3733: 2106.853092 from(1054.433822,2+)
Elution from: 47.217 to 47.217 scan no 4894 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2106.8571
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 4.3e-005
Matched b ions: b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(16), b(16)+, b(17)-98++, b(18)
Matched y ions: y(5), y(14), y(14)-98, y(14)+, y(15)-98, y(15), y(16)+, y(17)-98++, y(17)+
Precursor origin neutral loss: +

Peptide No.1926

SNPFYSEAYTTNGSGTGFK
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of SNPFYSEAYTTNGSGTGFK
Found in AT5G19450.1, CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); calcium- and calmodulin-dependent protein kinase/kin

Match to Query 3856: 2106.854226 from(1054.434389,2+)
Elution from: 47.349 to 47.349 scan no 4946 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2106.8571
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.027
Matched b ions: b(4), b(5), b(7), b(8), b(11)-98, b(12)-98, b(14)-98, b(15)++, b(16)-98++, b(16)++, b(18)
Matched y ions: y(9), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(14), y(14)++, y(15)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.1927
SNPFYSEAYTTNGSGTGFK
Confirmed sites:
Ambiguous sites: @S:14orT:16

MS/MS Fragmentation of SNPFYSEAYTTNGSGTGFK
Found in AT5G19450.1, CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); calcium- and calmodulin-dependent protein kinase/ kin

Match to Query 3260: 2106.853028 from(1054.433790,2+)
Elution from: 46.189 to 46.189 scan no 4649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2106.8571
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 9.8e-005
Matched b ions: b(5), b(6), b(8), b(9)
Matched y ions: y(6), y(8)−98, y(8), y(9)−98, y(10)−98, y(11), y(11)−98, y(12)−98, y(12), y(13),
y(14)−98, y(14), y(15), y(16)++, y(17)++, y(17)−98++, y(18)−98++
Precursor origin neutral loss: +

Peptide No.1928

SNQVEEKSEGEGEDVEPEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNQVEEKSEGEGEDVEPEK
Found in AT5G20360.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-contain

Match to Query 4279: 2197.888296 from(733.636708,3+)
Elution from: 22.073 to 22.073 scan no 1479 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2197.8899  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 36 Expect: 0.0023  
Matched b ions: b(10)++, b(11)+, b(11)--98++, b(12)++, b(12)--98++, b(13)--98++, b(14)+, b(15)--98++, b(16)--98++, b(16)+, b(17)--98++  
Matched y ions: y(3), y(4), y(6), y(7), y(8)++, y(8), y(9), y(13)+, y(15)++  
Precursor origin neutral loss: +  

Peptide No. 1929  
SNQVEEKSEGEGEDVEPEKK  
Confirmed sites: @S:8  
Ambiguous sites:  

MS/MS Fragmentation of SNQVEEKSEGEGEDVEPEKK  
Found in AT5G20360.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-contain  

Match to Query 4538: 2325.982536 from(776.334788,3+)  
Elution from: 19.796 to 19.796 scan no 1195 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2325.9848
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0063
Matched b ions: b(7), b(12)−98++, b(14)++, b(14)−98++, b(15)−98++, b(16)−98++, b(18)++
Matched y ions: y(4), y(6), y(7), y(9)++, y(11)++, y(12)++, y(13)−98++, y(16)++, y(16)−98++, y(17)−98++
Precursor origin neutral loss: +

Peptide No.1930

SNRYSDEDEEEEEEVAGGR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SNRYSDEDEEEEEEVAGGR
Found in AT5G61150.1, VIP4 (VERNALIZATION INDEPENDENCE 4)

Match to Query 3395: 2149.805336 from(1075.909944,2+) Elution from: 27.926 to 27.926 scan no 2328 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2149.8072

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 95 Expect: 1.5e-009

Matched b ions: b(3), b(4), b(5)−98, b(5), b(6)−98, b(6), b(7)−98, b(7), b(8)−98, b(8), b(9)++, b(9), b(10)−98, b(10), b(11), b(11)+, b(11)−98, b(12), b(12)−98, b(13), b(13)+, b(13)−98, b(14)−98, b(14), b(14)−98++, b(15), b(15)+, b(16)−98, b(16)+, b(17), b(17)+

Matched y ions: y(4), y(5), y(6), y(7)+, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)−98, y(15)−98, y(16)−98++, y(16)+

Precursor origin neutral loss: +

Peptide No.1931

SNSAGVHFSAPLGGVYSK

Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNSAGVHFSAPLGGVYSK

Found in AT2G35350.1, PLL1 (POLTERGEIST LIKE 1); protein phosphatase type 2C

Match to Query 3409: 1856.845372 from(929.429962,2+)

Elution from: 43.145 to 43.145 scan no 4474 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1856.8457
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.028
Matched b ions: b(7), b(8), b(12), b(14)−98++
Matched y ions: y(8), y(10), y(11), y(12)++, y(13), y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.1932
SNSAGVHFSAPLGGVYSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SNSAGVHFSAPLGGVYSK
Found in AT2G35350.1, PLL1 (POLTERGEIST LIKE 1); protein phosphatase type 2C

Match to Query 3408: 1856.842620 from(619.954816,3+)
Elution from: 43.153 to 43.153 scan no 4475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1856.8457
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.028
Matched b ions: b(8)−98++, b(9)−98++, b(10)
Matched y ions: y(6), y(7), y(8)++, y(8), y(9)++, y(10), y(14)++, y(15)++, y(16)−98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1933

SNSLSFLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SNSLSFLGK
Found in AT5G22030.1, ubiquitin–specific protease 8, putative (UBP8)

Match to Query 828: 1031.468378 from(516.741465,2+)
Elution from: 43.545 to 43.545 scan no 4475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1031.4688
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.7e-005
Matched b ions: b(2), b(3)++, b(3)−98, b(4)−98, b(5)−98, b(5), b(6)−98, b(7)−98, b(7)−98++, b(8)−98,
b(8)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98++, y(7), y(7)−98, y(7)++, y(8)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1934
SNSSNLDEVMPR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SNSSNLDEVMPR
Found in AT1G27500.1, kinesin light chain-related

Match to Query 2112: 1540.657376 from(771.335964,2+)
Elution from: 45.497 to 45.497 scan no 4710 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1540.6592  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
**Ions Score:** 75  
**Expect:** 2.6e-007  
**Matched b ions:** b(6)–98, b(6), b(8)–98, b(9), b(9)–98, b(10)–98, b(10), b(11)–98, b(11), b(12)–98  
**Matched y ions:** y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)+, y(11)  
**Precursor origin neutral loss:** +  

---

**Peptide No.1935**  

SNSSNLDLEVRMP  

**Confirmed sites:** @S:3  

**Ambiguous sites:**  

**MS/MS Fragmentation of SNSSNLDLEVRMP**  

Found in **AT1G27500.1**, kinesin light chain–related  

Match to Query 2640: 1540.658504 from(771.336528,2+)  

Elution from: 45.451 to 45.451 scan no 4739 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.6592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 67 Expect: 1.7e-006
Matched b ions: b(6)-98, b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(12)++
Precursor origin neutral loss: +

Peptide No.1936

SNSSNLDELLEVR
Confirmed sites: @S:4
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SNSSNLDELLEVR
Found in AT1G27500.1, kinesin light chain-related

Match to Query 2860: 1620.624760 from(811.319656,2+) Elution from: 50.958 to 50.958 scan no 5446 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1620.6255
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00018
Matched b ions: b(6)-98, b(6), b(8)-98, b(8), b(11), b(11)-196, b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10)-98, y(10)
Precursor origin neutral loss: +

Peptide No.1937
SNSSNLDELVEPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SNSSNLDELVEPR
Found in AT1G27500.1, kinesin light chain–related

Match to Query 2348: 1540.656830 from(771.335691,2+) Elution from: 47.206 to 47.206 scan no 4820 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1540.6592
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 7.5e-007
Matched b ions: b(6)–98, b(6), b(7)–98, b(8)–98, b(9)–98, b(10)–98, b(10), b(11)–98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)–98
Precursor origin neutral loss: +

Peptide No.1938

SNSSNLDEVMR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SNSSNLDEVMR
Found in AT1G27500.1, kinesin light chain–related

Match to Query 2039: 1556.654932 from(779.334742,2+)
Elution from: 37.539 to 37.539 scan no 3657 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1556.6541
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 Expect: 0.0012
Matched b ions: b(6)-98, b(8), b(9), b(9)-98, b(10)-98, b(11)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)-98++
Precursor origin neutral loss: +

Peptide No.1939

SPADGEGDSDEANEYYTGGQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SPADGEGDSDEANEYYTGGQK
Found in AT4G15410.1, ATB' GAMMA (Arabidopsis thaliana serine/threonine protein phosphatase 2A 55 kDa regulatory subunit

Match to Query 3429: 2355.862245 from(786.294691,3+)
Elution from: 30.499 to 30.499 scan no 2562 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2355.8652
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 71 Expect: 4.8e-007
Matched b ions: b(4), b(6), b(7), b(9), b(9)++, b(10)++, b(12)-98++, b(12)++, b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(13)-98++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(20)++, b(21)++
Matched y ions: y(4), y(5), y(6), y(6), y(6), y(7), y(7)++, y(8), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)-98++, y(16)++, y(18)-98++

Precursor origin neutral loss: +
Peptide No.1940
SPDGEKSDEAMEYTTGGK
Found in AT4G15410.1, ATB GAMMA (Arabidopsis thaliana serine/threonine protein phosphatase 2A 55 kDa regulatory subunit)
Confirmed sites: @S:8

Match to Query 4601: 2355.863500 from(1178.939026,2+,2+)
Elution from: 30.725 to 30.725 scan no 2635 polarity:+

Mass Score: 71 Expect: 4.8e-007
Matched b ions: b(4), b(6), b(7), b(9), b(9)++, b(10)++, b(12)-98++, b(12)++, b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(13)-98++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(20)++, b(21)++
Matched y ions: y(4), y(5), y(6), y(6), y(6), y(7), y(7)++, y(8), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)-98++, y(16)++, y(18)-98++

Precursor origin neutral loss: +
Monoisotopic mass of neutral peptide Mr(calc): 2355.8652
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 2.1e-009
Matched b ions: b(9)-98, b(11)-98, b(12)-98, b(15)-98, b(17)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15)-98, y(15), y(18)-98++, y(18)+, y(19)-98++
Precursor origin neutral loss: +

Peptide No.1941

SPADGEGSDSDEANEYYTGGQK
Confirmed sites: “@S:8,@S:10”
Ambiguous sites:

MS/MS Fragmentation of SPADGEGSDSDEANEYYTGGQK
Found in AT4G15410.1, ATB’ GAMMA (Arabidopsis thaliana serine/threonine protein phosphatase 2A 55 kDa regulatory subunit

Match to Query 4496: 2435.829050 from(1218.921801,2+)
Elution from: 33.183 to 33.183 scan no 3039 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2435.8315
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 7.5e-005
Matched b ions: b(9), b(11), b(12)+, b(12)−196, b(14)−98, b(15), b(16)−196, b(17)−196, b(17)−98, b(18)−98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(14), y(16)−98, y(16), y(18)−98, y(18)−98+, y(19)−98++, y(20)−98++, y(21)−196++
Precursor origin neutral loss: +

Peptide No.1942

SPARPEILNDWR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPARPEILNDWR
Found in AT4G13350.1, human Rev interacting–like protein–related / hRIP protein–related

Match to Query 2506: 1532.712108 from(511.911312,3+)
Elution from: 44.428 to 44.428 scan no 4589 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.7137
Fixed modifications: Carbamidomethyl (C)
Variable modifications: S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00065
Matched b ions: b(3)-98, b(4), b(5)++, b(6)-98, b(7), b(7)-98++, b(7)-98++, b(8)-98++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)+++, b(11)-98++
Matched y ions: y(2), y(3)++, y(3), y(4), y(4)++, y(5)++, y(5), y(7)++, y(8), y(8)++, y(9)++, y(9)++, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.1943

SPASLPDATPFTDGGGGGGGDTGR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPASLPDATPFTDGGGGGGGDTGR
Found in AT2G38280.1, FAC1 (EMBRYONIC FACTOR1); AMP deaminase

Match to Query 4085: 2225.920634 from(1113.967593,2+)
Elution from: 45.659 to 45.659 scan no 4692 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2225.9225
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 8.9e-006
Matched b ions: b(4), b(8)–98, b(9)–98, b(9), b(10)–98, b(11)–98, b(13), b(17)++, b(21)++
Matched y ions: y(7), y(10), y(11), y(12), y(13), y(15), y(16), y(17), y(19)++, y(19), y(20), y(20)++, y (21)+, y(22)++
Precursor origin neutral loss: +

Peptide No.1944

SPASPGPLSD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SPASPGPLSD
Found in AT5G16590.1, leucine–rich repeat transmembrane protein kinase, putative

Match to Query 529: 1006.400106 from(504.207329,2+) Elution from: 28.412 to 28.412 scan no 2285 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1006.4008
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0012
Matched b ions: b(3), b(4), b(5), b(8), b(9), b(9)–98
Matched y ions: y(2), y(2)–98, y(4)++, y(5), y(5)–98, y(6)–98, y(6), y(7), y(9)++
Precursor origin neutral loss: +

Peptide No.1945

SPASSADGDVYIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SPASSADGDVYIR
Found in AT3G23150.1, ETR2 (ETHYLENE RESPONSE 2); receptor

Match to Query 1963: 1416.590428 from(709.302490,2+)
Elution from: 33.038 to 33.038 scan no 3041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1416.5922
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 6.3e-007
Matched b ions: b(3), b(5)+, b(5), b(6)-98, b(6), b(7), b(9)+, b(9), b(10)-98++, b(10)-98, b(10), b(11)-98++, b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98++, y(9)-98, y(10), y(10)-98, y(11)++, y(11)-98++, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No. 1946
SPDPLEEQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPDPLEEQR
Found in AT1G67580.1, protein kinase family protein

Match to Query 819: 1149.469272 from (575.741912, 2+)
Elution from: 26.432 to 26.432 scan no 2023 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1149.4703
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 4.9e-005
Matched b ions: b(2), b(3)-98, b(3), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No.1947

SPDYGYAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPDGYAR
Found in AT1G23860.1, SRZ-21

Match to Query 532: 1007.374328 from(504.694440,2+) Elution from: 24.390 to 24.390 scan no 1757 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1007.3749
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 8.7e-005
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5)++, b(6)-98, b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.1948

SPDYQDYQDVITGSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPDYQDYQDVITGSR
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1);
similar to unnamed protein pr

Match to Query 3309: 1822.739402 from(912.376977,2+)
Elution from: 48.165 to 48.165 scan no 5043 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1822.7411
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.8e-007
Matched b ions: b(3)-98, b(4), b(5)-98, b(8), b(10)-98, b(10), b(11)-98++, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.1949
SPEAPLVVATPLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPEAPLVVATPLK
Found in AT3G19240.1, similar to dem protein-related / defective embryo and meristems protein-related [Arabidopsis thalia]

Match to Query 1625: 1400.730058 from(701.372305,2+) Elution from: 46.384 to 46.384 scan no 4820 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1400.7316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
- S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 31 Expect: 0.0073
Matched b ions: b(3)−98, b(3), b(4)−98, b(4), b(6), b(7), b(7)−98, b(8)−98, b(9)−98, b(10)−98, b(12)−98, b(12)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.1950

SPESVSAVSVVSNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPESVSAVSVVSNR
Found in AT2G34680.1, AIR9 (Auxin–Induced in Root cultures 9); protein binding

Match to Query 1945: 1496.685430 from(749.349991,2+)
Elution from: 36.223 to 36.223 scan no 3447 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1496.6871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.3e-007
Matched b ions: b(3)-98, b(3), b(4), b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(9)+, b(9), b(10)-98, b(10), b(10)-98++, b(11)+, b(11)-98, b(11), b(13)+, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.1951
SPEVSNQIR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPEVSNQIR
Found in AT5G59560.1, SRR1 (SENSITIVITY TO RED LIGHT REDUCED 1)

Match to Query 901: 1108.494406 from(555.254479,2+)
Elution from: 28.302 to 28.302 scan no 2409 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1108.4914
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.031
Matched b ions: b(3)−98, b(4)−98, b(7)−98
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(8)++
Precursor origin neutral loss: +

Peptide No.1952

SPGFETGSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPGFETGSR
Found in AT4G13350.1, human Rev interacting−like protein−related / hRIP protein−related

Match to Query 548: 1016.395776 from(509.205164,2+)
Elution from: 22.345 to 22.345 scan no 1490 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1016.3964
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00015
Matched b ions: b(3)-98, b(4), b(5)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7)
Precursor origin neutral loss: +

Peptide No.1953

SPGSSDVVVQNESLLSGR
Confirmed sites:
Ambiguous sites: @S:1orS:4orS:5

MS/MS Fragmentation of SPGSSDVVVQNESLLSGR
Found in AT4G15020.1, similar to DNA binding / protein dimerization [Arabidopsis thaliana] (TAIR:AT3G22220.2); similar to

Match to Query 3088: 1909.878018 from(955.946285,2+)
Elution from: 45.326 to 45.326 scan no 4681 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1909.8782
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0021
Matched b ions: b(10)-98
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.1954

SPITPSGYNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPITPSGYNR
Found in AT3G43590.1, zinc knuckle (CCHC-type) family protein

Match to Query 885: 1170.506050 from(586.260301,2+)
Elution from: 24.613 to 24.613 scan no 1918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1170.5070
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00064
Matched b ions: b(3)-98, b(3), b(4), b(4)-98, b(5)-98, b(5)++, b(7)-98, b(7)++, b(7)-98, b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)++, y(8)
Precursor origin neutral loss: +

Peptide No.1955

SPKEDCLEVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPKEDCLEVK
Found in AT3G58110.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42370.1);
similar to Os06g0538200 [Oryz

Match to Query 1237: 1283.546268 from(642.780410,2+)
Elution from: 22.210 to 22.210 scan no 1591 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1283.5468
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00088
Matched b ions: b(3)–98, b(4)–98, b(5)–98, b(8), b(8)–98, b(8)–98++, b(9), b(9)–98
Matched y ions: y(2), y(6), y(7), y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.1956

SPKEDCLEVKEEDVGAADSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPKEDCLEVKEEDVGAADSR
Found in AT3G58110.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42370.1); similar to Os06g0538200 [Oryz

Match to Query 3398: 2312.981559 from(772.001129,3+)
Elution from: 29.525 to 29.525 scan no 2550 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2312.9831

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 59 Expect: 1.4e-005

Matched b ions: b(3)−98, b(4)++, b(5)−98, b(5), b(6)−98, b(7), b(8)−98, b(8)++, b(9), b(9)−98, b(9)−98++, b(9), b(10)−98++, b(10)++, b(11)−98++, b(11)+, b(12)−98++, b(13)+, b(13)++, b(14)−98++, b(14)++, b(15)−98++, b(15)++, b(16)−98++, b(16)+, b(17)−98++, b(17)+, b(17)−98++, b(18)−98++, b(18)+, b(19)−98++

Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)+, y(12), y(12)+, y(14)+, y(15)+, y(16)+, y(17)+, y(18)+, y(19)+

Precursor origin neutral loss: +

Peptide No.1957

SPLGLTGGER

Confirmed sites: @S:1

Ambiguous sites:

MS/MS Fragmentation of SPLGLTGGER

Found in AT5G63490.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 791: 1065.484314 from(533.749433,2+)

Elution from: 32.648 to 32.648 scan no 2780 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1065.4855  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 20 Expect: 0.055  
Matched b ions: b(3), b(3)–98, b(5)–98, b(6)–98  
Matched y ions: y(4), y(5), y(6), y(7), y(9)++  
Precursor origin neutral loss: +  

Peptide No.1958  
SPLPLR  
Confirmed sites: @S:1  
Ambiguous sites:  
MS/MS Fragmentation of SPLPLR  
Found in AT1G16610.1, SR45 (arginine/serine-rich 45); RNA binding  
Match to Query 150: 761.382880 from(381.698716,2+)  
Elution from: 28.651 to 28.651 scan no 2484 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 761.3837
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.0059
Matched b ions: b(3)-98
Matched y ions: y(1), y(2), y(3), y(4)
Precursor origin neutral loss: +

Peptide No.1959

SPPALVYDFSQSDLDEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPALVYDFSQSDLDEK
Found in AT1G62020.1, coatamer protein complex, subunit alpha, putative

Match to Query 3134: 1787.799120 from(894.906836,2+)
Elution from: 63.269 to 63.269 scan no 6667 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1787.8018
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.057
Matched b ions: b(6)−98, b(9)−98, b(12)−98, b(14)++
Matched y ions: y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.1960

SPPVPSLFGK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPVPSLFGK
Found in AT3G45190.1, SIT4 phosphatase−associated family protein

Match to Query 749: 1107.535538 from(554.775045,2+)
Elution from: 47.112 to 47.112 scan no 4916 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1107.5365
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 24 Expect: 0.027
Matched b ions: b(2), b(3)–98, b(4)–98, b(4), b(8)–98, b(9)–98++, b(9)–98
Matched y ions: y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.1961
SPPVVVSDVSEDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPVVVSDVSEDK
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17410.1); similar to hypothetical prote

Match to Query 2024: 1436.642514 from(719.328533,2+) Elution from: 35.294 to 35.294 scan no 3348 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1436.6436
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.7e-006
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(8)-98, b(8), b(9)-98, b(9), b(11), b(12), b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1962
SPPYEDGYDR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPYEDGYDR
Found in AT4G13350.1, human Rev interacting–like protein–related / hRIP protein–related

Match to Query 1195: 1277.459468 from(639.737010,2+)
Elution from: 27.167 to 27.167 scan no 2261 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1277.4601
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00041
Matched b ions: b(3)—98, b(5)—98, b(9)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.1963

SPPYEDGYDRR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPYEDGYDRR
Found in AT4G13350.1, human Rev interacting–like protein–related / hRIP protein–related

Match to Query 2006: 1433.559776 from(717.787164,2+)
Elution from: 25.394 to 25.394 scan no 1918 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1433.5612
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0024
Matched b ions: b(5)–98, b(6)–98, b(9)–98
Matched y ions: y(2), y(5), y(8)++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1964
SPRSRGNMGPKPTPLK
Confirmed sites: @T:13
Ambiguous sites: @S:1orS:4

MS/MS Fragmentation of SPRSRGNMGPKPTPLK
Found in AT1G21320.1, VQ motif-containing protein

Match to Query 3061: 1897.864944 from(475.473512,4+)
Elution from: 13.049 to 13.049 scan no 658 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1897.8634
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M8 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.033
Matched b ions: b(5)−98++, b(5)−98, b(6)−98, b(7)−98, b(7)−98++, b(8)−98++
Matched y ions: y(3), y(4)++, y(4)−98, y(4), y(5)−98++, y(5)−98, y(8)++
Precursor origin neutral loss: +

Peptide No.1965

SPSATSTVSNEEFPR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPSATSTVSNEEFPR
Found in AT2G23140.1, armadillo/beta-catenin repeat family protein / U-box domain-containing protein

Match to Query 2548: 1687.706796 from(844.860674,2+)
Elution from: 35.141 to 35.141 scan no 3302 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.7090
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 3.5e-005
Matched b ions: b(8)−98, b(9)−98, b(13)−98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++
Precursor origin neutral loss: +

Peptide No.1966

SPSATSTVSNEEFPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SPSATSTVSNEEFPR
Found in AT2G23140.1, armadillo/beta-catenin repeat family protein / U-box domain-containing protein

Match to Query 2914: 1687.708106 from(844.861329,2+) Elution from: 34.106 to 34.106 scan no 3196 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.7090
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00015
Matched b ions: b(3), b(12)–98, b(13)–98, b(13)
Matched y ions: y(2), y(3), y(4), y(7), y(7)–98, y(8)–98, y(10)–98, y(10), y(12)–98, y(12), y(13)+, y
(14)–98++
Precursor origin neutral loss: +

Peptide No.1967

SPSATSTVSNEEFPR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of SPSATSTVSNEEFPR
Found in AT2G23140.1, armadillo/beta-catenin repeat family protein / U-box domain-containing protein

Match to Query 2454: 1687.707678 from(844.861115,2+)
Elution from: 34.479 to 34.479 scan no 3246 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.7090
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0044
Matched b ions: b(3), b(8), b(9)-98, b(13)-98, b(13), b(14)++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(12)-98, y(12), y(13)-98++
Precursor origin neutral loss: +

Peptide No.1968

SPSFILDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSFILDER
Found in AT1G72340.1, eukaryotic translation initiation factor 2B family protein / eIF-2B family protein

Match to Query 823: 1142.498154 from(572.256353,2+)
Elution from: 44.781 to 44.781 scan no 4580 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1142.5009
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.1e-005
Matched b ions: b(5)−98, b(6), b(7)−98, b(7), b(7)−98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)−98++, y(7), y(7)−98, y(8)−98, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1969

SPSLNALR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SPSLNALR
Found in AT4G20780.1, calcium-binding protein, putative

Match to Query 335: 936.442490 from(469.228521,2+)
Elution from: 32.487 to 32.487 scan no 2946 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 936.4430
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0077
Matched b ions: b(2), b(3)-98, b(4)-98
Matched y ions: y(1), y(3), y(6)-98++, y(6)-98, y(6), y(6)++, y(7)++, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1970

SPSSDLLSILQGVTDR
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SPSSDLLSILQGVTDR
Found in AT5G42950.1, GYF domain-containing protein

Match to Query 3160: 1766.841080 from(884.427816.2+)
Elution from: 77.602 to 77.602 scan no 8016 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1766.8451
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 5.3e-005
Matched b ions: b(7)++, b(10)++, b(10)—98
Matched y ions: y(3), y(5), y(7), y(8), y(9), y(10), y(11), y(13)
Precursor origin neutral loss: +

Peptide No.1971

SPSSDLLSILQGVTDR
Confirmed sites: @S:1 or S:3 or S:4
Ambiguous sites: @S:1 or S:3 or S:4

MS/MS Fragmentation of SPSSDLLSILQGVTDR
Found in AT5G42950.1, GYF domain-containing protein

Match to Query 2829: 1766.843296 from(884.428924,2+)
Elution from: 75.762 to 75.762 scan no 7859 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1766.8451
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.001
Matched b ions: b(6), b(7)++, b(7), b(10)++, b(10)--98, b(11), b(13)–98
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.1972

SPSSHPYLSVSVTDPVK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of SPSSHPYLSVSVTDPVK
Found in AT5G06140.1, phox (PX) domain-containing protein

Match to Query 3406: 1878.873453 from(627.298427,3+)
Elution from: 42.644 to 42.644 scan no 4355 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1878.8764
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0054
Matched b ions: b(8), b(8)-98++, b(9)+, b(10)-98, b(10)-98++, b(10)+, b(11)+, b(11)-98++, b(12)-98++, b(12)+, b(13)-98++, b(13)+, b(14)+, b(15)-98++, b(16)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(11)+, y(15)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1973

SPSSLPPSLSLQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSSLPPSLSLQR
Found in AT3G58600.1, similar to ATNAP4 (ARABIDOPSIS THALIANA NON–INTRINSIC ABC PROTEIN 4) [Arabidopsis thaliana] (TAIR:A)

Match to Query 2264: 1447.705100 from(724.859826,2+)
Elution from: 42.946 to 42.946 scan no 4394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1447.7072
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.029
Matched b ions: b(5), b(5)-98, b(6), b(6)-98, b(7)-98
Matched y ions: y(4)++, y(8)++, y(8), y(9), y(10), y(11)-98++
Precursor origin neutral loss: +

Peptide No.1974

SPSSLSSDYIK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPSSLSSDYIK
Found in AT5G07120.1, phox (PX) domain-containing protein

Match to Query 1428: 1262.542168 from(632.278360,2+)  
Elution from: 36.614 to 36.614 scan no 3426 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1262.5431
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0026
Matched b ions: b(2), b(3)-98, b(5)-98, b(5), b(8)-98, b(9)-98++, b(10)-98
Matched y ions: y(3), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.1975

SPSSLSSDYIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSSLSSDYIK
Found in AT5G07120.1, phox (PX) domain-containing protein

Match to Query 1740: 1262.543366 from(632.278959,2+)
Elution from: 35.913 to 35.913 scan no 3483 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1262.5431
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 7.8e-006
Matched b ions: b(4)-98, b(10)-98, b(10)
Matched y ions: y(3), y(4)+, y(4), y(6), y(7), y(8), y(9)-98++, y(9)-98, y(9), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.1976

SPSSQDSLPGIALYR
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SPSSQDSLPGIALYR
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/

Match to Query 2544: 1669.768960 from(835.891756,2+)  
Elution from: 51.116 to 51.116 scan no 5415 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.7712
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 4.6e-005
Matched b ions: b(5), b(6)++, b(6), b(7)-98, b(7), b(8)-98, b(11)-98, b(11), b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.1977

SPSSQDSLPGIALYR
Confirmed sites: ”@S:1,@S:3”
Ambiguous sites:

MS/MS Fragmentation of SPSSQDSLPGIALYR
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1);
similar to IMP dehydrogenase/

Match to Query 3026: 1749.736366 from(875.875459,2+)
Elution from: 59.781 to 59.781 scan no 6324 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1749.7375
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0032
Matched b ions: b(5)-196, b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(8)-196, b(9)-98, b(12)-196, b(14)++
Matched y ions: y(2), y(3), y(4), y(7), y(8)++, y(8), y(9), y(10), y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1978
SPSSQDSLPGIALYR
Confirmed sites: @S:1
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of SPSSQDSLPGIALYR
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/

Match to Query 2746: 1749.734508 from(875.874530,2+) 
Elution from: 59.543 to 59.543 scan no 6351 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1749.7375  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 43 Expect: 0.00038  
Matched b ions: b(5)−196, b(6)−98, b(8), b(8)−98, b(8)−196, b(9)−98, b(11)−98, b(12)−196, b(14)++  
Matched y ions: y(3), y(4), y(7), y(8)++, y(8), y(9), y(10), y(13)++  
Precursor origin neutral loss: +

Peptide No.1979

SPSSQDSLPGIALYR  
Confirmed sites: @S:3  
Ambiguous sites:

MS/MS Fragmentation of SPSSQDSLPGIALYR  
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/  

Match to Query 2399: 1669.770288 from(835.892420,2+)  
Elution from: 51.254 to 51.254 scan no 5410 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.7712
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 6.2e-006
Matched b ions: b(6)--98, b(6), b(7), b(8), b(8)--98, b(9)--98, b(9), b(11)--98, b(11), b(14)++
Matched y ions: y(2), y(3), y(4), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)--98++, y (13)+, y(14)++
Precursor origin neutral loss: +

Peptide No.1980
SPSSQDSLPGIALYR
Confirmed sites:
Ambiguous sites: "@S:1orS:3orS:4, @S:1orS:3orS:4"

MS/MS Fragmentation of SPSSQDSLPGIALYR
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/
Match to Query 2637: 1749.734938 from(875.874745,2+)
Elution from: 58.673 to 58.673 scan no 6251 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1749.7375
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.041
Matched b ions: b(5)-196, b(6), b(8), b(8)-98, b(8)-196, b(11)-98, b(14)++
Matched y ions: y(3), y(4), y(7), y(8), y(8)++, y(9)
Precursor origin neutral loss: +

Peptide No.1981

SPSSQDSLPGIALYR
Confirmed sites: @S:3orS:4
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of SPSSQDSLPGIALYR
Found in AT3G49590.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G18770.1); similar to IMP dehydrogenase/

Match to Query 2471: 1669.772900 from(835.893726,2+)
Elution from: 51.118 to 51.118 scan no 5416 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1669.7712
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.036
Matched b ions: b(6), b(7), b(8)-98, b(8), b(11), b(14)+
Matched y ions: y(2), y(3), y(4), y(7), y(8)+, y(8), y(9), y(10), y(11), y(13)-98++
Precursor origin neutral loss: +

Peptide No.1982

SPSSSLDDVEAK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPSSSLDDVEAK
Found in AT4G33400.1, dem protein-related / defective embryo and meristems protein-related

Match to Query 1645: 1313.537344 from(657.775948,2+)
Elution from: 29.252 to 29.252 scan no 2539 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1313.5388
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 3.3e-007
Matched b ions: b(2), b(3)–98, b(4), b(5), b(6), b(6)–98, b(7)–98++, b(7), b(8)–98, b(8), b(9)–98, b(10)–98, b(10), b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.1983
SPSSSLDDVEAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSSSLDDVEAK
Found in AT4G33400.1, dem protein–related / defective embryo and meristems protein–related

Match to Query 1531: 1313.537032 from(657.775792,2+)
Elution from: 29.000 to 29.000 scan no 2477 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1313.5388
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 5.8e-006
Matched b ions: b(4), b(6), b(8), b(9)-98, b(10)-98, b(11), b(11)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)-98
Precursor origin neutral loss: +

Peptide No.1984

SPSSSSSDYIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSSSSSDYIK
Found in AT5G58440.1, phox (PX) domain-containing protein

Match to Query 1102: 1236.490308 from(619.252430,2+)  
Elution from: 24.434 to 24.434 scan no 1856 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1236.4911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 7.6e-005
Matched b ions: b(2), b(3)–98, b(4)–98, b(5), b(7)–98, b(8), b(8)–98, b(9)–98, b(9)+, b(10)–98
Matched y ions: y(3), y(4), y(6), y(7), y(7)+, y(8), y(9)–98, y(9), y(9)–98++, y(10)+, y(10)–98++
Precursor origin neutral loss: +

Peptide No. 1985

SPSSSSSDYIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SPSSSSSDYIK
Found in AT5G58440.1, phox (PX) domain-containing protein

Match to Query 1357: 1236.490142 from(619.252347,2+)
Elution from: 25.360 to 25.360 scan no 1798 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1236.4911
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00052
Matched b ions: b(3), b(5), b(7)–98, b(9)–98, b(9)++, b(10)
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)–98, y(9)–98, y(9), y(9)–98++, y(10)++, y(10)–98++
Precursor origin neutral loss: +

Peptide No.1986

SPSVAPSDAGDEHFR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPSVAPSDAGDEHFR
Found in AT4G17410.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47430.1); similar to hypothetical prote

Match to Query 2426: 1650.665042 from(826.339797,2+) 
Elution from: 28.214 to 28.214 scan no 2367 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1650.6675  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 36  Expect: 0.0014  
Matched b ions: b(3)--98, b(5)--98, b(9)--98, b(11), b(13)--98  
Matched y ions: y(3), y(4), y(5), y(10), y(10)++, y(11), y(11)++, y(13)++, y(14)++  
Precursor origin neutral loss: +

Peptide No.1987  
SPTGEVIFGGETMR  
Confirmed sites:  
Ambiguous sites: @S:1 or T:3

MS/MS Fragmentation of SPTGEVIFGGETMR  
Found in ATCG00280.1, chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains

Match to Query 2342: 1559.667296 from (780.840924, 2+)  
Elution from: 47.919 to 47.919 scan no 4792 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1559.6690
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 7.8e-006
Matched b ions: b(5), b(5)−98, b(6)−98, b(6), b(7)−98, b(7), b(8)−98++, b(8)−98, b(8)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.1988

SPTGEVIFGGETMR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of SPTGEVIFGGETMR
Found in ATCG00280.1, chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains

Match to Query 2046: 1559.668824 from(780.841688,2+)
Elution from: 46.017 to 46.017 scan no 4771 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1559.6690  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T3: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 50 Expect: 8.9e-005  
Matched b ions: b(5), b(6)−98, b(6), b(7), b(7)−98, b(8)−98++, b(8), b(8)−98, b(9)−98  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12)−98++  
Precursor origin neutral loss: +  

Peptide No. 1989  
SPTGEVIFGGETMR  
Confirmed sites: @T:3  
Ambiguous sites:  

MS/MS Fragmentation of SPTGEVIFGGETMR  
Found in ATCG00280.1, chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains  

Match to Query 2182: 1575.662798 from(788.838675,2+)  
Elution from: 41.070 to 41.070 scan no 4093 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1575.6640
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  T3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  M13 : Oxidation (M), with neutral losses 0.0000 (shown in table), 63.9983
Ions Score: 52 Expect: 5e-005
Matched b ions: b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(10), b(10)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12)-98++
Precursor origin neutral loss: +

Peptide No.1990

SPTSPQLR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SPTSPQLR
Found in AT3G55600.1, similar to cation exchanger, putative (CAX10) [Arabidopsis thaliana]
(TAIR:AT1G54110.1); similar to

Match to Query 374: 964.437862 from(483.226207,2+)
Elution from: 20.787 to 20.787 scan no 1410 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 964.4379
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0043
Matched b ions: b(4)-98
Matched y ions: y(1), y(3), y(4), y(5)-98, y(5), y(6)-98++, y(6), y(6)+, y(7)+, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1991

SPTVVTVPSSPR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SPTVVTVPSSPR
Found in AT1G11360.1, universal stress protein (USP) family protein

Match to Query 2225: 1433.691624 from(717.853088,2+)
Elution from: 28.906 to 28.906 scan no 2511 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1433.6915
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69  Expect: 8.7e-007
Matched b ions: b(4), b(5), b(6), b(7), b(8)
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(6)-98, y(6), y(7), y(8), y(9), y(9)-98, y(9)+, y(10), y(10)-98, y(10)-98+
Precursor origin neutral loss: +

Peptide No.1992

SPTYEAYPR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPTYEAYPR
Found in AT4G36980.1, similar to peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thalian]

Match to Query 833: 1162.469322 from(582.241937,2+)
Elution from: 28.677 to 28.677 scan no 2349 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1162.4696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00049
Matched b ions: b(6)-98, b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7)
Precursor origin neutral loss: +

Peptide No.1993

SPTYSPPF
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPTYSPPF
Found in AT3G23900.1, RNA recognition motif (RRM)–containing protein

Match to Query 778: 1130.479646 from(566.247099,2+)  
Elution from: 37.109 to 37.109 scan no 3566 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1130.4798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0015
Matched b ions: b(2), b(2)−98, b(3), b(4)++, b(5)−98, b(5)
Matched y ions: y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.1994

SPTYSPPFR
Confirmed sites: ”@S:1,@S:5”
Ambiguous sites:

MS/MS Fragmentation of SPTYSPPFR
Found in AT3G23900.2, nucleic acid binding

Match to Query 1277: 1210.444492 from(606.229522,2+)
Elution from: 42.692 to 42.692 scan no 4124 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1210.4461
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.065
Matched b ions: b(3), b(4), b(5)−196, b(6)−196
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8)−98++
Precursor origin neutral loss: +

Peptide No.1995

SPTYSPPFR
Confirmed sites: “@S:1,@S:5”
Ambiguous sites: @T:3orY:4

MS/MS Fragmentation of SPTYSPPFR
Found in AT3G23900.1, RNA recognition motif (RRM)-containing protein

Match to Query 1692: 1290.410792 from(646.212672,2+)
Elution from: 48.273 to 48.273 scan no 5003 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1290.4124
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y4 : Phospho (Y)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 15 Expect: 0.056
Matched b ions: b(4)−98, b(5)−98, b(6)−196
Matched y ions: y(3), y(4), y(5), y(7)−98
Precursor origin neutral loss: +

Peptide No.1996

SPTYSPPFR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of SPTYSPPFR
Found in AT3G23900.1, RNA recognition motif (RRM)−containing protein

Match to Query 1174: 1130.477866 from(566.246209,2+)
Elution from: 37.096 to 37.096 scan no 3614 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1130.4798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.0002
Matched b ions: b(3)–98, b(3), b(4)++, b(5)–98, b(5), b(6)–98, b(8)–98
Matched y ions: y(3), y(4), y(5), y(6), y(7)–98, y(7)–98++
Precursor origin neutral loss: +

Peptide No.1997
SPVDDYEPNRTSPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SPVDDYEPNRTSPR
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 3005: 1826.746664 from(914.380608,2+)
Elution from: 24.812 to 24.812 scan no 1941 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1826.7472
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00053
Matched b ions: b(5), b(6), b(11), b(11)++, b(12), b(13)−98, b(13), b(14)−98
Matched y ions: y(2), y(3), y(4)−98, y(6)++, y(6), y(7)−98++, y(7)−98, y(8), y(9)−98, y(9), y(9)++, y(10), y(10)++, y(11)++, y(11)−98++, y(11), y(12), y(12)−98++, y(12)++, y(13)−98++, y(13)++, y(14)−98++
Precursor origin neutral loss: +

Peptide No.1998

SPVFGLSPTR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPVFGLSPTR
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RNA binding

Match to Query 1215: 1139.536836 from(570.775694,2+)
Elution from: 42.162 to 42.162 scan no 4291 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1139.5376
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.022
Matched b ions: b(3)-98, b(3), b(4), b(4)-98, b(5)-98, b(6)-98, b(9)-98
Matched y ions: y(3), y(4), y(6), y(7), y(9)++
Precursor origin neutral loss: +

Peptide No.1999

SPVFGLSPTR
Confirmed sites: "@S:1,@S:7"
Ambiguous sites:

MS/MS Fragmentation of SPVFGLSPTR
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2–LIKE PROTEIN 5); RNA binding

Match to Query 1554: 1219.503082 from(610.758817,2+)
Elution from: 46.033 to 46.033 scan no 4840 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1219.5039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.018
Matched b ions: b(2), b(3)−98, b(3), b(4)−98, b(4), b(4)−98++, b(5)++, b(5)−98, b(6)−98, b(6), b(7)−98, b(8)−196
Matched y ions: y(3), y(4)−98++, y(4), y(5), y(5)−98, y(6)++, y(6), y(7), y(7)−98, y(7)++, y(8)++, y(8)−98, y(8)−98++, y(9)−98++, y(9)++
Precursor origin neutral loss: +

Peptide No.2000

SPVFGLSPTTR
Confirmed sites: "@S:1,@T:9"
Ambiguous sites:

MS/MS Fragmentation of SPVFGLSPTTR
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RNA binding

Match to Query 1279: 1219.502850 from(610.758701,2+)
Elution from: 46.933 to 46.933 scan no 4785 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1219.5039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.017
Matched b ions: b(2), b(3), b(3)−98, b(4)−98, b(4), b(4)−98++, b(5)++, b(5)−98, b(5), b(6), b(6)−98, b(6)++
Matched y ions: y(2), y(3)−98, y(4)−98++, y(4), y(5), y(5)++, y(6), y(7), y(7)−98, y(7)++, y(8), y(8)++, y(8)−98, y(8)−98++, y(9)−98++
Precursor origin neutral loss: +

Peptide No.2001

SPVFLSPTDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SPVFLSPTDR
Found in AT1G29400.1, AML5 (ARABIDOPSIS MEI2–LIKE PROTEIN 5); RNA binding

Match to Query 804: 1139.536918 from(570.775735,2+)
Elution from: 41.823 to 41.823 scan no 4230 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1139.5376
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.018
Matched b ions: b(3), b(4)++, b(4)
Matched y ions: y(3), y(4), y(4)−98, y(5), y(5)−98, y(6), y(7)++, y(7)−98, y(7), y(8)−98++, y(8)−98
Precursor origin neutral loss: +

Peptide No.2002

SPVLDEEGSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SPVLDEEGSPK
Found in AT2G37340.1, RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33); nucleic acid binding / nucleotide

Match to Query 1003: 1222.511316 from(612.262934,2+)
Elution from: 23.681 to 23.681 scan no 1747 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1222.5118

**Fixed modifications:** Carbamidomethyl (C)

**Variable modifications:**
- S9 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000

**Ions Score:** 45  **Expect:** 0.00014

**Matched b ions:** b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8), b(9)-98, b(9)+, b(10)-98++

**Matched y ions:** y(2), y(3), y(4)-98, y(4)-98++, y(5), y(5)-98, y(5)-98++, y(6)+, y(6), y(7)-98, y(7), y(8), y(8)+, y(8)-98, y(9), y(9)-98, y(9)-98++, y(9)+, y(10)-98++, y(10)+

**Precursor origin neutral loss:** +

---

**Peptide No.2003**

**SQDFDSEYSR**

**Confirmed sites:** @S:1

**Ambiguous sites:**

**MS/MS Fragmentation of SQDFDSEYSR**

Found in **AT5G08660.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G34320.1); similar to Trp repressor/repl

Match to Query 1828: 1312.460152 from(657.237352,2+)  
Elution from: 28.670 to 28.670 scan no 2495 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1312.4609
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 1.6e-005
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6), y(7), y(8), y(8)+, y(9)+
Precursor origin neutral loss: +

Peptide No.2004

SQDVENENQDESLGR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of SQDVENENQDESLGR
Found in AT2G23520.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66950.1); similar to unknown protein [A

Match to Query 2880: 1798.699366 from(900.356959,2+)
Elution from: 23.681 to 23.681 scan no 1755 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1798.7006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.037
Matched b ions: b(4), b(5), b(10), b(13)−98++, b(13)−98
Matched y ions: y(6), y(7), y(8), y(9)−98, y(10)−98, y(10), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.2005

SQGMYTMEQLMR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQGMYTMEQLMR
Found in AT5G67200.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 2580: 1553.604878 from(777.809715,2+)
Elution from: 53.522 to 53.522 scan no 5661 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1553.6077
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0011
Matched b ions: b(3), b(6), b(8)-98, b(10)-98, b(11)-98, b(11)
Matched y ions: y(6), y(7), y(8), y(10)
Precursor origin neutral loss: +

Peptide No.2006

SQGSEVLLEETIK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQGSEVLLEETIK
Found in AT2G38580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65010.1); similar to PREDICTED: similar

Match to Query 2204: 1511.710572 from(756.862562,2+)  
Elution from: 49.707 to 49.707 scan no 5017 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1511.7120
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 6.1e-007
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(11)-98, b(12)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.2007

SQGSEVLLEETIK
Confirmed sites: "@S:1,@S:4"
Ambiguous sites:

MS/MS Fragmentation of SQGSEVLLEETIK
Found in AT2G38580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65010.1);
similar to PREDICTED: similar

Match to Query 2544: 1591.676896 from(796.845724,2+)
Elution from: 53.346 to 53.346 scan no 5558 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1591.6783
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 27 Expect: 0.019
Matched b ions: b(5)–98, b(5), b(6), b(6)–98, b(6)–196, b(7)–196, b(7)–98, b(8)–98, b(9)–98, b(9)–196, b(9)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(11)++
Precursor origin neutral loss: +

Peptide No.2008

SQGSEVLLEETIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SQGSEVLLEETIK
Found in AT2G38580.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65010.1); similar to PREDICTED: similar

Match to Query 2262: 1511.709888 from(756.862220,2+) Elution from: 49.446 to 49.446 scan no 5107 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1511.7120
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 37 Expect: 0.0017
Matched b ions: b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(12)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.2009

SQLLGKLKGFLGMAEANK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQLLGKLKGFLGMAEANK
Found in AT1G71430.1, similar to Os01g0617800 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001043585.1)

Match to Query 3644: 2083.085259 from(695.369029,3+)
Elution from: 43.682 to 43.682 scan no 4471 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2083.0900
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.054
Matched b ions: b(5)++, b(5), b(7), b(10), b(10)++, b(12)++, b(13)−98++, b(14)++, b(15)++, b(16)++, b(18)++
Matched y ions: y(5), y(8), y(9)++, y(9), y(11)++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss:

Peptide No.2010
SQLSFTNHDSLAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SQLSFTNHDSLAR
Found in AT1G05805.1, basic helix-loop-helix (bHLH) family protein

Match to Query 2581: 1554.680768 from(778.347660,2+)
Elution from: 35.616 to 35.616 scan no 3428 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1554.6828
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00017
Matched b ions: b(7)-98, b(9)-98, b(9), b(10)+, b(12)+
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10)-98, y(11)-98++, y(11)-98
Precursor origin neutral loss: +

Peptide No.2011
SQNGFTSSPADDVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SQNGFTSSPADDVK
Found in AT4G22140.1, DNA binding

Match to Query 1650: 1531.617038 from(766.815795,2+) Elution from: 29.808 to 29.808 scan no 2471 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1531.6191
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 Expect: 4.1e-008
Matched b ions: b(5), b(6), b(7)+, b(8)−98, b(11), b(12)+, b(12), b(13)−98++, b(13), b(13)−98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)−98, y(8), y(9), y(9)+, y(10), y(11), y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.2012

SQSFENEDPAFWK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SQSFENEDPAFWK
Found in AT3G44050.1, kinesin motor protein–related

Match to Query 2929: 1810.721924 from(906.368238,2+)
Elution from: 58.847 to 58.847 scan no 6278 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1810.7239
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 1.2e-006
Matched b ions: b(6)-98, b(8), b(8)-98, b(9), b(9)-98, b(12)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2013

SQSPPVELFNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SQSPPVELFNR
Found in AT2G37840.1, protein kinase family protein

Match to Query 1431: 1352.611550 from(677.313051,2+) Elution from: 43.639 to 43.639 scan no 4462 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1352.6125
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 6.1e-005
Matched b ions: b(9)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8)++, y(8), y(9)-98++, y(9)-98, y(9)
Precursor origin neutral loss: +

Peptide No.2014
SRGPVIEEIDSDDEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SRGPVIEEIDSDDEK
Found in AT4G22740.1, glycine-rich protein

Match to Query 2127: 1767.754299 from(590.258709,3+)
Elution from: 31.771 to 31.771 scan no 2836 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1767.7563
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 3.7e-005
Matched b ions: b(5), b(6), b(7), b(8), b(8)++, b(9)++, b(10)++, b(12)--98++, b(12)-98++, b(13)++, b(14)++, b(14)--98++
Matched y ions: y(4), y(6), y(6)--98, y(7), y(7)++, y(7)--98, y(7)--98++, y(8)++, y(8), y(9)++, y(10)++, y(11)--98++, y(13)++
Precursor origin neutral loss: +

Peptide No. 2015

SRLSSAAAKPSVTA
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SRLSSAAAKPSVTA
Found in AT4G31700.1, RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome

Match to Query 2289: 1424.701210 from (713.357881, 2+)
Elution from: 23.620 to 23.620 scan no 1827 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1424.7024
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00063
Matched b ions: b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(8)+, b(9), b(9)-98, b(11)+, b(11)-98++, b(12)-98++, b(12)+, b(13)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.2016
SRPAVSYSSRLSPER
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of SRPAVSYSSRLSPER
Found in AT2G44710.1, RNA recognition motif (RRM)-containing protein

Match to Query 2780: 1770.840366 from(591.287398,3+)
Elution from: 24.294 to 24.294 scan no 1872 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1770.8414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.057
Matched b ions: b(10)+, b(11)+, b(12)-98++, b(14)-98++, b(14)+
Matched y ions: y(3)+, y(4)-98, y(9)-98++, y(10)-98++, y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2017

SRRNDECGSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SRRNDECGSK
Found in AT1G51538.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18510.1);
similar to unknown protein [A

Match to Query 1087: 1287.503994 from(644.759273,2+)
Elution from: 21.075 to 21.075 scan no 1431 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1287.5027
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.031
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(9)
Matched y ions: y(4), y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.2018
SRSDLGSDLGYGK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SRSDLGSDLGYGK
Found in AT1G20110.1, zinc finger (FYVE type) family protein

Match to Query 2065: 1376.596000 from(689.305276,2+)
Elution from: 30.515 to 30.515 scan no 2727 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1376.5973
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.5e-007
Matched b ions: b(2), b(3)–98, b(3), b(4)–98, b(4), b(5)–98, b(5), b(7), b(8)–98, b(8), b(9)–98, b(9), b(10)–98, b(10), b(11), b(11)–98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(10)–98, y(11)–98++
Precursor origin neutral loss: +

Peptide No.2019
SRSFGDVNEIGAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SRSFGDVNEIGAR
Found in AT4G32285.1, epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related

Match to Query 2255: 1486.656927 from(496.559585,3+) Elution from: 31.571 to 31.571 scan no 2925 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.6565
Fixed modifications: Carbamidomethyl (C)
 Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0029
Matched b ions: b(3), b(4)++, b(6), b(6)++, b(7), b(7)–98++, b(7)++, b(8)++, b(8)–98++, b(9)++, b(9)–98++, b(10)++, b(10)–98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(12)++
Precursor origin neutral loss:

Peptide No.2020
SRSFGDVNEIGAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSFGDVNEIGAR
Found in AT4G32285.1, epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related

Match to Query 2161: 1486.654752 from(744.334652,2+)
Elution from: 33.163 to 33.163 scan no 2964 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.6565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.2e-005
Matched b ions: b(3)–98, b(3), b(4)–98, b(6)–98, b(6), b(7), b(7)–98, b(8)–98, b(8), b(9)–98, b(9), b(10), b(10)–98, b(11), b(12)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11)–98
Precursor origin neutral loss: +

Peptide No.2021
SRSFLGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSFLGR
Found in AT4G33650.1, ADL2 (ARABIDOPSIS DYNAMIN-LIKE 2); GTP binding / GTPase

Match to Query 436: 901.416368 from(451.715460,2+)
Elution from: 22.828 to 22.828 scan no 1703 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 901.4171
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0071
Matched b ions: b(2), b(3), b(5), b(5)−98, b(6), b(6)−98, b(6)++
Matched y ions: y(1), y(2), y(3), y(4)
Precursor origin neutral loss: +

Peptide No.2022

SRSGPLNER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSGPLNER
Found in AT2G42670.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58670.2); similar to OSJNBb0040D15.1 [O

Match to Query 859: 1094.485768 from(548.250160,2+)
Elution from: 18.053 to 18.053 scan no 1018 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1094.4869
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 42 Expect: 0.00032
Matched b ions: b(2), b(3)–98, b(4)–98, b(7), b(8)–98, b(8), b(8)++
Matched y ions: y(2), y(3), y(4), y(6), y(7)–98
Precursor origin neutral loss: +

Peptide No.2023

SRSGSEEEHASINPAER
Confirmed sites: @S:1
Ambiguous sites: @S:3 or S:5

MS/MS Fragmentation of SRSGSEEEHASINPAER
Found in AT4G11740.1, SAY1

Match to Query 3901: 2111.828196 from (1056.921374, 2+)
Elution from: 22.960 to 22.960 scan no 1714 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2111.8310
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0084
Matched b ions: b(5)−98, b(5)−196, b(5), b(7), b(8), b(9), b(11)−98, b(11), b(14)−98, b(14), b(17)−98, b(17)−98++, b(17), b(17)−196++, b(17)++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(13), y(17)++
Precursor origin neutral loss: +

Peptide No. 2024

SRGSPEEEHASINPAER
Confirmed sites: @S.3
Ambiguous sites:

MS/MS Fragmentation of SRGSPEEEHASINPAER
Found in AT4G11740.1, SAY1

Match to Query 3613: 2031.862899 from(678.294909,3+)
Elution from: 21.003 to 21.003 scan no 1430 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2031.8647
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 40 Expect: 0.00078
Matched b ions: b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(14)++, b(14)-98++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(13)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.2025
SRSGSPEEEHASINPAER
Confirmed sites: “@S:3,@S:5”
Ambiguous sites:

MS/MS Fragmentation of SRSGSPEEEHASINPAER
Found in AT4G11740.1, SAY1

Match to Query 3531: 2111.829438 from(1056.921995,2+)
Elution from: 22.943 to 22.943 scan no 1749 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2111.8310
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00021
Matched b ions: b(5)–98, b(5), b(5)–196, b(8)–196, b(8)–98, b(8), b(9), b(9)–98, b(11)–98, b(11), b(13)–98, b(14), b(17), b(17)–98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(15), y(16)–98, y(16)
Precursor origin neutral loss: +

Peptide No.2026

SRSLPAEQLAGPSEPAK
Confirmed sites: 
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SRSLPAEQLAGPSEPAK
Found in AT4G32350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79910.1); similar to hypothetical prote

Match to Query 3235: 1816.871784 from(606.631204,3+) 
Elution from: 32.691 to 32.691 scan no 2901 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1816.8720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.02
Matched b ions: b(4)-98, b(5)-98, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(10), b(11)-98++, b(11)++, b(12)-98++, b(13)++, b(14)++
Matched y ions: y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss:

Peptide No.2027
SRSLPAEQLAGPSEPAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSLPAEQLAGPSEPAK
Found in AT4G32350.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79910.1);
similar to hypothetical prote

Match to Query 3327: 1816.870964 from(909.442758,2+)
Elution from: 31.042 to 31.042 scan no 2847 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1816.8720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 6e-006
Matched b ions: b(4)−98, b(7), b(8)−98++, b(8), b(8)−98, b(9), b(10), b(10)−98, b(11), b(11)−98, b(13)−98, b(14)
Matched y ions: y(3), y(6)++, y(6), y(7), y(8), y(9), y(10), y(13), y(14), y(15)−98
Precursor origin neutral loss: +

Peptide No.2028
SRSLPRPVSPSR
Confirmed sites: “@S:1,@S:3,@S:11”
Ambiguous sites:

MS/MS Fragmentation of SRSLPRPVSPSR
Found in AT4G35785.1, transformer serine/arginine-rich ribonucleoprotein, putative

Match to Query 2751: 1577.650714 from(789.832633,2+)
Elution from: 26.098 to 26.098 scan no 2167 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1577.6517
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.038
Matched b ions: b(2), b(4)–98, b(4)–196, b(5), b(6), b(6)++, b(6)–98, b(7)–98++, b(8)–196, b(8), b(8)–98, b(8)–196++, b(9), b(9)–98, b(10), b(10)–196, b(11)–98
Matched y ions: y(4), y(4)–98, y(6), y(6)–98, y(7), y(8), y(9), y(11)++, y(11)–98++
Precursor origin neutral loss: +

Peptide No.2029

SRSLPRPVSPSR
Confirmed sites: “@S:1,@S:3,@S:9”
Ambiguous sites:

MS/MS Fragmentation of SRSLPRPVSPSR
Found in AT4G35785.1, transformer serine/arginine-rich ribonucleoprotein, putative

Match to Query 2749: 1577.650898 from(789.832725,2+)
Elution from: 26.236 to 26.236 scan no 2164 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1577.6517
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.028
Matched b ions: b(2), b(3)-98, b(3)-196, b(4)-196, b(4)-98, b(5), b(6), b(6)-196, b(6)-98, b(8)-196, b(8), b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(8), y(8)-98, y(9), y(10), y(10)-98, y(11)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2030
SRSQEWSAEK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SRSQEWSAEK
Found in AT1G64650.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27720.1);
similar to unknown protein [A

Match to Query 1521: 1286.528056 from(644.271304,2+)  
Elution from: 20.549 to 20.549 scan no 1216 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1286.5292
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.00039
Matched b ions: b(2), b(3), b(5), b(5)−98, b(6), b(8)−98, b(9), b(9)−98, b(9), b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(8)−98
Precursor origin neutral loss: +

Peptide No.2031

SRSRSVEDSADIK
Confirmed sites: “@S:1,@S:3,@S:5”
Ambiguous sites:

MS/MS Fragmentation of SRSRSVEDSADIK
Found in AT3G23900.1, RNA recognition motif (RRM)−containing protein

Match to Query 1928: 1688.619800 from(845.317176,2+)
Elution from: 22.079 to 22.079 scan no 1550 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1688.6209
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S3: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S5: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 24 Expect: 0.011
Matched b ions: b(2), b(4)++, b(4)-98, b(5)-294++, b(5)-98, b(6)-196, b(7)-98, b(8)-98, b(8), b(10)-98, b(11)-98, b(11), b(11)-98++, b(12)++, b(12)-196++, b(12)-98++
Matched y ions: y(2), y(5), y(6), y(6)++, y(9), y(10), y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No. 2032
SRSVEALSGCLK
Confirmed sites: @S:3
Ambiguous sites: 

MS/MS Fragmentation of SRSVEALSGCLK
Found in AT3G52990.1, pyruvate kinase, putative

Match to Query 1970: 1385.636830 from (693.825691, 2+)
Elution from: 30.451 to 30.451 scan no 2773 polarity: +
Monoisotopic mass of neutral peptide Mr(calc): 1385.6374
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00021
Matched b ions: b(2), b(4)--98, b(5), b(7)++, b(7), b(7)--98, b(10)++, b(10), b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)--98, y(10)
Precursor origin neutral loss: +

Peptide No.2033

SRSVSPGLCYR
Confirmed sites: @S:5
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SRSVSPGLCYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin–type family protein

Match to Query 2129: 1440.560206 from(721.287379,2+)
Elution from: 28.605 to 28.605 scan no 2520 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1440.5622
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
  S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 24 Expect: 0.017
Matched b ions: b(4)-98, b(5)-196, b(5)+, b(5)-98, b(5), b(6)-98++, b(8)
Matched y ions: y(2), y(3), y(6), y(7), y(7)-98, y(8)-98
Precursor origin neutral loss: +

Peptide No.2034
SRSVSPGLCYR
Confirmed sites: @S:5
Ambiguous sites: @S:1 or S:3

MS/MS Fragmentation of SRSVSPGLCYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 2332: 1440.561524 from(721.288038,2+)
Elution from: 28.640 to 28.640 scan no 2518 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1440.5622
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 20 Expect: 0.048
Matched b ions: b(3), b(3)−98, b(4)−98, b(5)−196, b(5)−98, b(8)
Matched y ions: y(3), y(6), y(7), y(7)−98, y(8)−98, y(10)−196++
Precursor origin neutral loss: +

Peptide No.2035

SRYLEVMNTKSDK
Confirmed sites: @S:1 or Y:3
Ambiguous sites: @S:1 or Y:3

MS/MS Fragmentation of SRYLEVMNTKSDK
Found in AT2G34920.1, EDA18 (embryo sac development arrest 18); protein binding / zinc ion binding

Match to Query 2412: 1649.749212 from (550.923680, 3+) Elution from: 18.344 to 18.344 scan no 1058 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1649.7484
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.042
Matched b ions: b(4)--98, b(6)--98, b(7)--98, b(7)--98++, b(8)+, b(9)--98++, b(10)--98++, b(12)--98++
Matched y ions:
Precursor origin neutral loss:

Peptide No.2036
SRYSPSLSPYDK
Confirmed sites: "@S:6,@S:8"
Ambiguous sites: @S:1orY:3orS:4

MS/MS Fragmentation of SRYSPSLSPYDK
Found in AT1G07350.1, transformer serine/arginine-rich ribonucleoprotein, putative

Match to Query 1891: 1638.574682 from(820.294617,2+)
Elution from: 37.560 to 37.560 scan no 3499 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1638.5769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.0084
Matched b ions: b(4), b(7)++, b(7)--98, b(8)--98, b(8)--196, b(9)--196, b(10)--196++, b(10)++, b(11)--196, b(11)
Matched y ions: y(4), y(5)--98, y(5), y(6), y(7), y(8)--98, y(8)
Precursor origin neutral loss: +

Peptide No. 2037

SRYSPSLSPYDK
Confirmed sites: @S:6
Ambiguous sites: "@Y:3orS:4, @Y:10orS:8"

MS/MS Fragmentation of SRYSPSLSPYDK
Found in AT1G07350.1, transformer serine/arginine-rich ribonucleoprotein, putative

Match to Query 2803: 1638.576240 from(820.295396,2+)
Elution from: 37.717 to 37.717 scan no 3698 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1638.5769
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y10 : Phospho (Y)
Ions Score: 21 Expect: 0.02
Matched b ions: b(5), b(6)−98, b(7)++, b(7), b(7)−98, b(10)++, b(11)−98, b(11)
Matched y ions: y(5), y(6), y(7), y(8)−98, y(8), y(10)−98, y(10)
Precursor origin neutral loss: +

Peptide No.2038
SSCNSGSEEENADVHR
Confirmed sites: @S:5
Ambiguous sites:
MS/MS Fragmentation of SSCNSGSEEENADVHR
Found in AT4G01000.1, ubiquitin family protein
Match to Query 3271: 1987.699584 from(663.573804,3+) Elution from: 22.399 to 22.399 scan no 1587 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1987.7037
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.049
Matched b ions: b(11)++, b(12)++, b(16)++
Matched y ions: y(3), y(7)++, y(9)++, y(12)++, y(13)++, y(13)−98++, y(14)++, y(14)−98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2039
SSDAEEVSDTEDEWLK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SSDAEEVSDTEDEWLK
Found in AT5G52960.1, similar to hypothetical protein asr2994 [Nostoc sp. PCC 7120] (GB:NP_487034.1); similar to Os05g0566

Match to Query 3108: 1918.734672 from(960.374612,2+) Elution from: 48.595 to 48.595 scan no 5081 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1918.7357
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 7.2e-008
Matched b ions: b(5), b(6), b(7), b(8)-98, b(9)-98, b(9), b(12)-98, b(12)+, b(13), b(13)-98, b (14)-98, b(14), b(15)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)+, y(9)-98, y(9), y(10), y(10)-98, y(11)-98, y (12)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2040
SSDGFLYCEGTK
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSDGFLYCEGTK
Found in AT3G14390.1, diaminopimelate decarboxylase, putative / DAP carboxylase, putative

Match to Query 1466: 1442.541550 from(722.278051,2+)
Elution from: 40.078 to 40.078 scan no 3813 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1442.5425
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.015
Matched b ions: b(5)–98, b(5), b(6)–98, b(7)–98
Matched y ions: y(5), y(6), y(7), y(9)
Precursor origin neutral loss: +

Peptide No.2041
SSDLAEGDEDLIAGIR
Confirmed sites:
Ambiguous sites: @S:1 or S:2

MS/MS Fragmentation of SSDLAEGDEDLIAGIR
Found in AT3G49800.1, BSD domain-containing protein

Match to Query 2997: 1739.760932 from(870.887742,2+)
Elution from: 55.148 to 55.148 scan no 5802 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1739.7614
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00095
Matched b ions: b(3), b(5)−98, b(6)−98, b(7++)−98, b(9)−98, b(10)−98, b(11)−98, b(12)−98++, b(12)−98, b(12), b(13)−98, b(13), b(15)−98
Matched y ions: y(4), y(5), y(8), y(9), y(10), y(10)++, y(11), y(12), y(13)
Precursor origin neutral loss: +

Peptide No.2042
SSDSLSGTNEILLNINSETPMK
Confirmed sites:
Ambiguous sites: ”@S:1orS:2orS:4, @S:1orS:2orS:4”

MS/MS Fragmentation of SSDSLSGTNEILLNINSETPMK
Found in AT3G19770.1, vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein

Match to Query 4404: 2395.979004 from(1198.996778,2+)
Elution from: 58.695 to 58.695 scan no 6296 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2395.9855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S2 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 39 Expect: 0.0013
Matched b ions: b(12)-98, b(12), b(12)-196, b(14), b(17)-98, b(17)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(14), y(15), y(16)
Precursor origin neutral loss: +

Peptide No.2043
SSDSLSGTNELLNINSETPMK
Confirmed sites: 
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSDSLSGTNELLNINSETPMK
Found in AT3G19770.1, vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein

Match to Query 3975: 2316.017102 from(1159.015827,2+) 
Elution from: 54.918 to 54.918 scan no 5742 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2316.0192
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 2.8e-005
Matched b ions: b(11)-98, b(12)-98, b(14), b(14)-98, b(15), b(17), b(18), b(18)++, b(19)-98, b(19)-98++, b(19)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(15), y(16), y(18)++
Precursor origin neutral loss: +

Peptide No.2044
SSDSLSGTNELLNINSETPMK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SSDSLSGTNELLNINSETPMK
Found in AT3G19770.1, vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein

Match to Query 4186: 2316.015228 from(1159.014890,2+)
Elution from: 53.536 to 53.536 scan no 5737 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2316.0192
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00058
Matched b ions: b(9), b(10)–98, b(11)–98, b(12)–98, b(12), b(13)++, b(14)–98, b(14), b(15), b(17), b (18), b(19)–98
Matched y ions: y(3), y(4), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(16), y(17)++, y(18)–98++
Precursor origin neutral loss: +

Peptide No.2045
SSDSLSGNELLNINSETPMK
Confirmed sites:
Ambiguous sites: @S:1orS:2orS:4

MS/MS Fragmentation of SSDLSGTLNELLNINSETPMK
Found in AT3G19770.1, vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein

Match to Query 4266: 2332.010944 from(1167.012748,2+)
Elution from: 49.191 to 49.191 scan no 5170 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2332.0141
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 61 Expect: 1e-005
Matched b ions: b(12)-98, b(13), b(14), b(18), b(19)-98
Matched y ions: y(3), y(7), y(8), y(9), y(11), y(13), y(15), y(16), y(17)+, y(17)
Precursor origin neutral loss: +

Peptide No.2046
SSDTDSSSPVDLLSR
Confirmed sites:
Ambiguous sites: "@S:1orS:2orT:4orS:6, @S:7orS:8"

MS/MS Fragmentation of SSDTDSSSPVDLLSR
Found in AT5G13240.1, similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE92223.1); contains domain FA

Match to Query 3338: 1837.735832 from(919.875192,2+)
Elution from: 61.341 to 61.341 scan no 6609 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1837.7384
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 24 Expect: 0.019
Matched b ions: b(11), b(12)–98
Matched y ions: y(4), y(5), y(6), y(10)–98, y(12)–196
Precursor origin neutral loss: +

Peptide No. 2047

SSDTDSSSPVDLLSR
Confirmed sites:
Ambiguous sites: @S:7

MS/MS Fragmentation of SSDTDSSSPVDLLSR
Found in AT5G13240.1, similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE92223.1); contains domain FA

Match to Query 2736: 1757.767122 from (879.890837, 2+) Elution from: 52.930 to 52.930 scan no 5634 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1757.7720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0017
Matched b ions: b(6), b(8), b(10), b(11), b(12), b(13), b(14)
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(11)
Precursor origin neutral loss:

Peptide No.2048

SSDTSSTSPVDLLLSR
Confirmed sites: @S:8
Ambiguous sites: 

MS/MS Fragmentation of SSDTSSSPVDLLLSR
Found in AT5G13240.1, similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE92223.1); contains domain FA

Match to Query 2798: 1757.767068 from(879.890810,2+)
Elution from: 52.906 to 52.906 scan no 5632 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1757.7720
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 Expect: 5.7e-008
Matched b ions: b(5), b(8)-98++, b(9), b(11), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9)-98, y(9), y(10), y(11), y(12)
Precursor origin neutral loss:

Peptide No.2049
SSDVEMVDAEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSDVEMVDAEK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1519: 1288.488238 from(645.251395,2+)
Elution from: 27.999 to 27.999 scan no 2359 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1288.4894
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 5.8e-006
Matched b ions: b(3)–98, b(3), b(4)–98, b(4), b(5)–98, b(5), b(7), b(8), b(8)–98, b(10)–98, b(10)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.2050
SSDVEMVDAEK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSDVEMVDAEK
Found in AT1G48920.1, nucleolin, putative

Match to Query 1293: 1288.487690 from(645.251121,2+)
Elution from: 27.128 to 27.128 scan no 2254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1288.4894
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 1.8e-005
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(7)-98, b(8)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(10)-98++
Precursor origin neutral loss: +

Peptide No.2051
SSDVEMVDAEKSSAK
Confirmed sites: @S:12orS:13
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of SSDVEMVDAEKSSAK
Found in AT1G48920.1, nucleolin, putative

Match to Query 2207: 1661.684986 from(831.849769,2+)
Elution from: 23.341 to 23.341 scan no 1712 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.035
Matched b ions: b(6), b(7), b(8), b(10), b(11)
Matched y ions: y(6), y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(10)-98
Precursor origin neutral loss: +

Peptide No.2052

SSESDLLAFAEK
Confirmed sites: @S:1orS:2
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSESDLLAFAEK
Found in AT3G28180.1, ATCSLC04 (Cellulose synthase-like C4); transferase, transferring glycosyl groups

Match to Query 1552: 1375.589728 from(688.802140,2+) Elution from: 52.575 to 52.575 scan no 5591 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1375.5908  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 62 Expect: 4.7e-006  
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(7), b(7)-98++, b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(11), b(11)-98, b(11)-98++  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)  
Precursor origin neutral loss: +  

Peptide No.2053  
SSESDDLFAEK  
Confirmed sites: @S:4  
Ambiguous sites:  
MS/MS Fragmentation of SSESDDLFAEK  
Found in AT3G28180.1, ATCSLC04 (Cellulose synthase-like C4); transferase, transferring glycosyl groups  
Match to Query 1966: 1375.589580 from(688.802066,2+)  
Elution from: 52.483 to 52.483 scan no 5472 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1375.5908
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0016
Matched b ions: b(5), b(6)−98, b(7)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.2054

SSESDDLSSITEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SSESDDLSSITEK**
Found in AT4G31590.1, ATCSLC05 (Cellulose synthase-like C5); transferase, transferring glycosyl groups

Match to Query 1626: 1387.611702 from(694.813127,2+)
Elution from: 45.727 to 45.727 scan no 4740 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1387.6119  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 26 Expect: 0.015  
Matched b ions: b(5)  
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(10)—98++  
Precursor origin neutral loss: +  

Peptide No.2055  
SSFASDEFSEDEKFPESK  
Confirmed sites: @S:9  
ambiguous sites:  
MS/MS Fragmentation of SSFASDEFSEDEKFPESK  
Found in AT1G55040.1, zinc finger (Ran-binding) family protein  
Match to Query 3068: 2144.842527 from(715.954785,3+)  
Elution from: 41.816 to 41.816 scan no 4135 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2144.8463
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.042
Matched b ions: b(3), b(12)−98++, b(16)−98++
Matched y ions: y(5)++, y(9)++, y(11)−98++, y(13)−98++, y(14)++, y(14)−98++, y(15)++, y(16)++, y(16)−98++
Precursor origin neutral loss: +

Peptide No.2056

SSFDSDDDEYRGSSSSASR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SSFDSDDDEYRGSSSSASR
Found in AT1G55040.1, zinc finger (Ran-binding) family protein

Match to Query 3001: 2133.774712 from(1067.894632,2+)
Elution from: 25.123 to 25.123 scan no 1951 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2133.7760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 9.5e-006
Matched b ions: b(6), b(7)−98, b(9)−98, b(14)−98++, b(15)++, b(16)++, b(18)−98++
Matched y ions: y(8), y(10)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(15)−98++, y(16)−98++, y(16)++, y(17)++, y(17)−98++
Precursor origin neutral loss: +

Peptide No.2057
SSFGSSGSGYGGSGSGAGSGNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSFGSSGSGYGGSGSGAGSGNR
Found in AT2G37220.1, 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative

Match to Query 2647: 1985.745370 from(993.879961,2+)
Elution from: 23.666 to 23.666 scan no 1759 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.7499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 66 Expect: 1.6e-006
Matched b ions:
Matched y ions: y(5), y(6), y(7), y(10), y(12), y(15), y(16), y(20), y(20)++, y(21)++, y(22)++
Precursor origin neutral loss: +

Peptide No.2058

SSFGSSGSGYGGGGGSGAGSGNR
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSFGSSGSGYGGGGGSGAGSGNR
Found in AT2G37220.1, 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative

Match to Query 3622: 1985.746858 from(993.880705,2+) Elution from: 24.553 to 24.553 scan no 1889 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.7499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 3.8e-009
Matched b ions: b(7)+, b(10)-98, b(11)-98, b(15)+, b(16)-98, b(18)-98++, b(21)+, b(22)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(15), y(16), y(17), y(18), y(18)+, y(19), y(19)+, y(20)+, y(21)+
Precursor origin neutral loss: +

Peptide No.2059

SSFGSSGSGYGGGGGSGAGSGNR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SSFGSSGSGYGGGGGSGAGSGNR
Found in AT2G37220.1, 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative

Match to Query 3681: 1985.747990 from(993.881271,2+)
Elution from: 23.490 to 23.490 scan no 1809 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.7499

Fixed modifications: Carbamidomethyl (C)

Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 73 Expect: 3.7e-007
Matched b ions: b(14)-98
Matched y ions: y(4), y(5), y(7), y(9), y(10), y(11), y(12), y(14), y(15), y(16), y(17), y(18), y(19)++

Precursor origin neutral loss: +

---

**Peptide No.2060**

SSFGSSGSGYGGGGGSGAGSGNR

Confirmed sites:
Ambiguous sites: @S:1orS:2orS:5orS:6

MS/MS Fragmentation of SSFGSSGSGYGGGGGSGAGSGNR

Found in AT2G37220.1, 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative

Match to Query 3377: 1985.748774 from(662.923534,3+) 
Elution from: 23.642 to 23.642 scan no 1783 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1985.7499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.051
Matched b ions: b(6)-98, b(7)++, b(8), b(13)-98++, b(14)++, b(15)++, b(18)++, b(19)++, b(20)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(13)++, y(15)++, y(16)++
Precursor origin neutral loss:

Peptide No.2061

SSFVSYP PPPGSISP DQR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SSFVSYP PPPGSISP DQR
Found in AT1G79090.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22270.1);
similar to Os02g0517300 [Oryz

Match to Query 3209: 1899.836294 from(950.925423,2+) 
Elution from: 42.145 to 42.145 scan no 4270 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1899.8404
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.046
Matched b ions: b(6), b(12)
Matched y ions: y(5), y(6), y(10), y(11)+, y(11)−98, y(11), y(12), y(13)+, y(14)−98++
Precursor origin neutral loss: +

Peptide No.2062

SSGEISPEREPLIK
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSGEISPEREPLIK
Found in AT5G17010.1, sugar transporter family protein

Match to Query 1849: 1620.774446 from(811.394499,2+)
Elution from: 33.683 to 33.683 scan no 3000 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1620.7760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00056
Matched b ions: b(4)-98, b(6)-98, b(9)-98, b(10)-98, b(10), b(12)-98, b(13)-98, b(13), b(13)-98++
Matched y ions: y(4), y(5), y(6), y(8)
Precursor origin neutral loss: +

Peptide No.2063
SSGEISPEREPLIK
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of SSGEISPEREPLIK
Found in AT5G17010.1, sugar transporter family protein

Match to Query 2229: 1620.774530 from(811.394541,2+) Elution from: 32.415 to 32.415 scan no 2968 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1620.7760  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 37 Expect: 0.002  
Matched b ions: b(6)-98, b(6), b(7), b(9)-98, b(9), b(10)-98, b(10), b(12)-98, b(12)-98++, b(12), b(13)-98, b(13), b(13)-98++, b(13)++  
Matched y ions: y(4), y(5), y(6), y(8), y(8)++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++  
Precursor origin neutral loss: +

Peptide No.2064  
SSGGLSDDEINR  
Confirmed sites: @S:6  
Ambiguous sites: 

MS/MS Fragmentation of SSGGLSDDEINR  
Found in AT4G37910.1, MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding  
Match to Query 1198: 1328.523872 from(665.269212,2+)  
Elution from: 26.642 to 26.642 scan no 2167 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1328.5245
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.3e-007
Matched b ions: b(4), b(5), b(6)—98, b(7)—98, b(8)—98, b(9)—98, b(10)—98, b(10), b(10)++, b(11)—98++, b(11)—98, b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)—98, y(7), y(8)—98, y(8), y(8)++, y(9), y(9)—98, y(9)—98++, y(10)—98++, y(10)—98, y(10), y(10)++, y(11)—98++, y(11)++
Precursor origin neutral loss: +

Peptide No.2065
SSGTASSSSSICQR
Confirmed sites:
Ambiguous sites: @S:6

MS/MS Fragmentation of SSGTASSSSSICQR
Found in AT4G35210.1, carrier

Match to Query 1645: 1406.552612 from(704.283582,2+)
Elution from: 33.225 to 33.225 scan no 3082 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1406.5497  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 25 Expect: 0.014  
Matched b ions: b(6)-98, b(6), b(7)-98, b(8)+, b(8)-98, b(9)-98, b(10)+, b(10), b(10)-98, b(11)-98  
Matched y ions: y(5), y(9)+  
Precursor origin neutral loss: +  

Peptide No.2066  
SSHVESEEESESELK  
Confirmed sites: @S:10  
Ambiguous sites:  

MS/MS Fragmentation of SSHVESEEESESELK  
Found in AT3G01160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to conserved hypothet  

Match to Query 2152: 1784.697190 from(893.355871,2+)  
Elution from: 20.884 to 20.884 scan no 1393 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1784.6989
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 6.6e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9), b(10)-98, b(11)-98, b(11), b(13), b(13)-98, b(13)+, b(14), b(14)-98++, b(14)++
Matched y ions: y(4), y(5), y(6)-98, y(6), y(7)-98, y(8)-98, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(12)+, y(13)-98++, y(13)+++, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2067
SSHVESEEESESELK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SSHVESEEESESELK
Found in AT3G01160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to conserved hypothet

Match to Query 2445: 1784.697462 from(893.356007,2+)
Elution from: 20.739 to 20.739 scan no 1356 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1784.6989
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0012
Matched b ions: b(4), b(5), b(7), b(7)-98, b(8)-98, b(13), b(13)-98, b(14)-98, b(14)-98++
Matched y ions: y(7)+, y(9)+, y(10)-98, y(10), y(11)-98, y(12), y(12)-98, y(12)+, y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.2068

SSHVESEEESESELK
Confirmed sites: "@S:6,@S:10"
Ambiguous sites:

MS/MS Fragmentation of SSHVESEEESESELK
Found in AT3G01160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to conserved hypothet

Match to Query 2409: 1864.664104 from(933.339328,2+)
Elution from: 25.536 to 25.536 scan no 1933 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1864.6652
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 2.6e-006
Matched b ions: b(3), b(4), b(5), b(6)–98, b(7)–98, b(7), b(8), b(8)–98, b(9), b(9)–98, b(10)–98, b(10), b(11)–98, b(11), b(12), b(13), b(13)++, b(13)–98, b(13)–98++, b(14)–98, b(14), b(14)–196++
Matched y ions: y(4), y(5), y(6)–98, y(6), y(7)–98, y(7), y(10)–98, y(10), y(11), y(12), y(12)–98, y(13)–98++, y(13)–196++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.2069

SSHVESEESESELK
Confirmed sites: @S:6
Ambiguous sites: @S:10orS:12

MS/MS Fragmentation of SSHVESEESESELK
Found in AT3G01160.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to conserved hypothet

Match to Query 3251: 1864.663274 from(933.338913,2+)
Elution from: 26.026 to 26.026 scan no 1888 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1864.6652
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S12: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 43 Expect: 0.00018
Matched b ions: b(4), b(5), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(12)+, b(12), b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(6), y(7), y(10)-98, y(10)-196, y(10), y(12), y(13)-196++, y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.2070

SSISLSGER
Confirmed sites:
Ambiguous sites: @S:1 or S:2

MS/MS Fragmentation of SSISLSGER
Found in AT5G50530.1, CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein

Match to Query 506: 1014.437454 from(508.226003,2+)
Elution from: 26.071 to 26.071 scan no 2112 polarity:+
**Monoisotopic mass of neutral peptide Mr(calc):** 1014.4383  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:**  
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
**Ions Score:** 48  
**Expect:** 6e-005  
**Matched b ions:** b(3)−98, b(3), b(4), b(5), b(5)−98, b(6), b(6)−98, b(7)−98, b(8), b(8)−98++, b(8)++  
**Matched y ions:** y(1), y(3), y(4), y(5), y(6), y(7)  
**Precursor origin neutral loss:** +

---

### Peptide No.2071

**SSISLSGER**  
**Confirmed sites:** @S:4  
**Ambiguous sites:**

**MS/MS Fragmentation of SSISLSGER**  
Found in **AT5G50530.1**, CBS domain−containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain−containing protein

Match to Query 603: 1014.437122 from(508.225837,2+)  
Elution from: 26.898 to 26.898 scan no 2184 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1014.4383
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00021
Matched b ions: b(4), b(5)−98, b(5), b(6)−98, b(8), b(8)+, b(8)−98, b(8)−98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)−98, y(6)−98++, y(7), y(7)+, y(7)−98, y(7)−98++
Precursor origin neutral loss: +

Peptide No.2072

SSKPNPFDSDDESDNK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SSKPNPFDSDDESDNK
Found in AT5G61210.1, SNAP33 (synaptosomal-associated protein 33); t-SNARE

Match to Query 2714: 1860.702206 from(931.358379,2+)
Elution from: 23.145 to 23.145 scan no 1686 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1860.7051
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 1.9e-005
Matched b ions: b(8), b(10), b(11), b(12), b(13), b(14), b(14)-98, b(14)++
Matched y ions: y(4), y(5), y(6), y(8), y(8)-98, y(10), y(11)-98, y(11), y(12)++, y(12), y(13)-98++, y(13), y(13)-98, y(14)-98++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2073

SSLPEVEASPPAGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SSLPEVEASPPAGK
Found in AT4G15930.1, dynein light chain, putative

Match to Query 1450: 1447.659202 from(724.836877,2+) Elution from: 33.286 to 33.286 scan no 3045 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1447.6595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 1.2e-005
Matched b ions: b(5), b(6), b(9)-98, b(12)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(10)+, y(11)+, y(11), y(11)-98++, y(12)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2074

SSNAISASPPLTER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SSNAISASPPLTER
Found in AT3G27390.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40640.1); similar to Steroid nuclear re

Match to Query 1977: 1508.686222 from(755.350387,2+) Elution from: 32.592 to 32.592 scan no 2997 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1508.6872
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.022
Matched b ions: b(4), b(7), b(10), b(12)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(13)++
Precursor origin neutral loss: +

Peptide No.2075
SSNFDSSPPR
Confirmed sites: @S:6orS:7
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of SSNFDSSPPR
Found in AT1G31870.1, similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G29210.1);

Match to Query 918: 1172.449434 from(587.231993,2+) Elution from: 23.434 to 23.434 scan no 1722 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1172.4499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0032
Matched b ions: b(4), b(5), b(9), b(9)++
Matched y ions: y(3), y(5), y(6)++, y(6), y(7), y(7)–98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.2076

SSNMVEESDAEAENEEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SSNMVEESDAEAENEEK
Found in AT4G24230.1, ACBP3 (ACYL-COA-BINDING DOMAIN 3); acyl-CoA binding

Match to Query 2662: 1976.713454 from(989.364003,2+)  
Elution from: 25.409 to 25.409 scan no 2003 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1976.7193
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00047
Matched b ions: b(5), b(6), b(8), b(10)–98, b(11)–98, b(12), b(13)–98, b(13)
Matched y ions: y(4), y(5), y(6), y(7), y(10), y(11), y(12)–98, y(12), y(13)–98
Precursor origin neutral loss: +

Peptide No.2077

SSPADFFTYLASDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSPADFFTYLASDK
Found in AT1G05805.1, basic helix–loop–helix (bHLH) family protein

Match to Query 2317: 1627.678646 from(814.846599,2+)
Elution from: 67.211 to 67.211 scan no 7119 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1627.6807
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0037
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(10)-98, b(11), b(12)
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.2078
SSPADFFTYLASDK
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPADFFTYLASDK
Found in AT1G05805.1, basic helix–loop–helix (bHLH) family protein

Match to Query 2719: 1627.677942 from(814.846247,2+)
Elution from: 69.076 to 69.076 scan no 7340 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1627.6807
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 Expect: 1.7e-008
Matched b ions: b(4)-98, b(6)-98, b(7)-98, b(8)-98, b(10)-98, b(11)-98
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12)++
Precursor origin neutral loss: +

Peptide No.2079

SSPAPPESSVAPVSSGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSPAPPESSVAPVSSGR
Found in AT4G17410.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47430.1); similar to hypothetical prote

Match to Query 2529: 1690.754262 from(846.384407,2+)
Elution from: 27.715 to 27.715 scan no 2335 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1690.7563
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0017
Matched b ions: b(4), b(4)−98, b(7)−98++, b(10)−98, b(11), b(12)−98, b(13)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(12), y(13)++, y(13), y(14)++, y(15)++, y(16)−98++, y
(16)++
Precursor origin neutral loss: +

Peptide No.2080
SSPENGQVESPGQIMEVEAGR
Confirmed sites: @S:10
Ambiguous sites: @S:1or S:2

MS/MS Fragmentation of SSPENGQVESPGQIMEVEAGR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine-serine-rich splicing factor 41); RNA binding

Match to Query 3364: 2359.935536 from(1180.975044,2+)
Elution from: 51.197 to 51.197 scan no 4958 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2359.9392
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.7e-005
Matched b ions: b(5)-98, b(6), b(7)-98, b(9), b(10)-98, b(12)-98, b(13)-98, b(14), b(15), b(16), b(17), b(17)-98, b(19)+++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(12)-98, y(12), y(13)-98, y(14)+++, y(14), y(14)-98, y(16), y(17)-98++, y(17)+++, y(18)+++, y(19)-98++, y(19)+
Precursor origin neutral loss: +

Peptide No.2081

SSPENGQVESPGQIMEVEAGR
Confirmed sites: @S:10
Ambiguous sites: @S:1 or S:2

MS/MS Fragmentation of SSPENGQVESPGQIMEVEAGR
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 4266: 2375.930998 from(1188.972775,2+)
Elution from: 40.161 to 40.161 scan no 4078 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2375.9341
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 Expect: 0.03
Matched b ions: b(10)-98, b(11)-196, b(12)++, b(12)-98, b(13), b(13)-98, b(15)-196, b(16)-98, b(18)-196++, b(20)-98++
Matched y ions: y(4), y(7), y(8), y(12), y(13)-98, y(13), y(14)-98, y(14), y(16), y(16)-98, y(16)++, y(17)++, y(17)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.2082
SSPGGRSPGFETGSR
Confirmed sites: "@S:1,@S:7"
Ambiguous sites:

MS/MS Fragmentation of SSPGGRSPGFETGSR
Found in AT4G13350.1, human Rev interacting-like protein-related / hRIP protein-related

Match to Query 2407: 1637.622858 from(546.881562,3+)
Elution from: 23.018 to 23.018 scan no 1664 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1637.6236
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S1 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
  S7 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 27 Expect: 0.01
Matched b ions: b(4)-98, b(5)+, b(5), b(6)-98++, b(6)+, b(7)-98++, b(8)-196++, b(10)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(6), y(8)+, y(8), y(9)+, y(10)-98++, y(11)++, y(12)+, y(13)+, y(13)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No. 2083
SSPGGRSPGFETGSR
Confirmed sites: @S:7
Ambiguous sites: @S:1 or S:2

MS/MS Fragmentation of SSPGGRSPGFETGSR
Found in AT4G13350.1, human Rev interacting–like protein–related / hRIP protein–related

Match to Query 2901: 1637.622466 from(819.818509,2+)
Elution from: 22.179 to 22.179 scan no 1607 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1637.6236
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00011
Matched b ions: b(7)-98, b(9), b(9)-196, b(10), b(11), b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2084

SSPGGRSPGFETGSR
Confirmed sites: @S:7
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPGGRSPGFETGSR
Found in AT4G13350.1, human Rev interacting-like protein-related / hRIP protein-related

Match to Query 2902: 1637.622848 from(819.818700,2+);
Elution from: 22.136 to 22.136 scan no 1625 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1637.6236
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 24 Expect: 0.02
Matched b ions: b(6)−98, b(6), b(7)−196, b(7)−98, b(9)−98, b(10)−98, b(11), b(14)−98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(12)+, y(13)+, y(13)−98++
Precursor origin neutral loss: +

Peptide No. 2085

SSPIHAMQCR
Confirmed sites:
Ambiguous sites: @S:1 or S:2

MS/MS Fragmentation of SSPIHAMQCR
Found in AT5G14620.1, DRM2 (DOMAINS REARRANGED METHYLTRANSFERASE 2)

Match to Query 1677: 1265.503992 from(633.759272,2+)
Elution from: 22.546 to 22.546 scan no 1644 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1265.5046
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.0086
Matched b ions: b(5), b(6)-98, b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++
Precursor origin neutral loss: +

Peptide No.2086

SSPLGSSDNLAK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein

Match to Query 1142: 1254.549260 from(628.281906,2+) Elution from: 26.772 to 26.772 scan no 2207 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1254.5493
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.014
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)++, b(8)++, b(11)
Matched y ions: y(2), y(4), y(6), y(7)++, y(7), y(8), y(10)++, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.2087

SSPLGSSDNLAK
Confirmed sites: @S:6
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein

Match to Query 1153: 1334.515382 from(668.264967,2+) Elution from: 30.836 to 30.836 scan no 2712 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1334.5156
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.016
Matched b ions: b(4)-98, b(4), b(6)-196, b(8)++, b(8), b(11)-98
Matched y ions: y(4), y(6), y(7), y(8)-98, y(8), y(9)++, y(9), y(10)-98++, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.2088
SSPLGSSDNLAK
Confirmed sites: @S:7
Ambiguous sites: @S:1orS:2
MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein
Match to Query 1378: 1334.514338 from(668.264445,2+) Elution from: 30.928 to 30.928 scan no 2769 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1334.5156
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.024
Matched b ions: b(4)-98, b(5)-98, b(5), b(8)++, b(9)++, b(11)-98
Matched y ions: y(2), y(4), y(6)-98++, y(7)++, y(8), y(8)-98, y(9), y(9)++, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.2089
SSPLGSSDNLAK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein

Match to Query 1018: 1254.548826 from(628.281689,2+)
Elution from: 27.909 to 27.909 scan no 2246 polarity:+
Peptide No. 2090

SSPLGSSDNLAK

Confirmed sites: "@S:2,@S:6"

Ambiguous sites:

MS/MS Fragmentation of SSPLGSSDNLAK

Found in AT1G80530.1, nodulin family protein

Match to Query 1592: 1334.514692 from (668.264622, 2+)

Elution from: 31.688 to 31.688 scan no 2840 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1334.5156
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.024
Matched b ions: b(2), b(4)−98, b(4), b(5)−98, b(6)−196, b(7)−98++, b(8)−98, b(8), b(8)++, b(10)−98, b(10), b(11), b(11)−98
Matched y ions: y(2), y(4), y(6), y(7), y(8)−98, y(8), y(9)++, y(9), y(10)−98++, y(10), y(10)++, y(10)−98, y(11)−196, y(11)−98++
Precursor origin neutral loss: +

Peptide No.2091
SSPLGSSDNLAK
Confirmed sites: @S:7
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein

Match to Query 1211: 1334.514192 from(668.264372,2+)
Elution from: 30.770 to 30.770 scan no 2713 polarity:+
Peptide No.2092

**SSPLGSSDNLAK**

**Confirmed sites:** @S:6

**Ambiguous sites:**

**MS/MS Fragmentation of SSPLGSSDNLAK**

Found in **AT1G80530.1**, nodulin family protein

Match to Query 1004: 1254.548640 from (628.281596, 2+)

Elution from: 29.912 to 29.912 scan no 2599 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1254.5493
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.6e-006
Matched b ions: b(4), b(5), b(6)−98, b(8)−98++, b(9)−98, b(10)−98, b(10), b(11), b(11)−98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)−98, y(8), y(9)++, y(9), y(10)−98++, y(10)++, y(10), y(10)−98
Precursor origin neutral loss: +

Peptide No.2093
SSPLGSSDNLAK
Confirmed sites:
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of SSPLGSSDNLAK
Found in AT1G80530.1, nodulin family protein

Match to Query 1035: 1254.548270 from(628.281411,2+) Elution from: 31.343 to 31.343 scan no 2668 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1254.5493
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 9.1e-005
Matched b ions: b(4), b(9)-98, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7)-98, y(7), y(8)-98, y(8), y(9)+++, y(9), y(10)-98++, y(10)+++, y(10)-98, y(10), y(11)+
Precursor origin neutral loss: +

Peptide No.2094
SSPLSLGNSSEEDK
Confirmed sites: 
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPLSLGNSSEEDK
Found in AT5G53830.1, VQ motif-containing protein

Match to Query 1794: 1528.627070 from(765.320811,2+)
Elution from: 30.493 to 30.493 scan no 2652 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1528.6294
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00096
Matched b ions: b(4), b(8)++, b(8)-98, b(12), b(13)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(12)
Precursor origin neutral loss: +

Peptide No.2095
SSPNESVSSATWFSGR
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSPNESVSSATWFSGR
Found in AT1G68720.1, cytidine/deoxycytidylate deaminase family protein

Match to Query 2939: 1777.729606 from(889.872079,2+)
Elution from: 46.104 to 46.104 scan no 4754 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1777.7308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 2.8e-006
Matched b ions: b(4), b(8)-98, b(12), b(13), b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14)+
Precursor origin neutral loss: +

Peptide No.2096

SSPSLLLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSPSLLLR
Found in AT5G20280.1, ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glyc

Match to Query 429: 951.478374 from(476.746463,2+)
Elution from: 39.373 to 39.373 scan no 3900 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 951.4790
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0067
Matched b ions: b(2), b(2)-98, b(6)-98, b(7)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)+, y(6), y(7)-98++
Precursor origin neutral loss: +

Peptide No.2097
SSDSGLTELSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSDSGLTELSK
Found in AT3G07330.1, ATCSLC06 (Cellulose synthase-like C6); transferase, transferring glycosyl groups

Match to Query 1742: 1289.538096 from(645.776324,2+)
Elution from: 31.422 to 31.422 scan no 2870 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1289.5388
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 2.4e-007
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6), b(7), b(7)-98, b(8)-98++, b(8)+, b(8), b(9), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(10)-98, y(10)+, y(11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.2098

SSSFLQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSFLQR
Found in AT5G11060.1, KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4); transcription factor

Match to Query 357: 903.383702 from(452.699127,2+)
Elution from: 28.315 to 28.315 scan no 2192 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 903.3851
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 5.2e-005
Matched b ions: b(2), b(4)-98, b(6)-98++, b(6)-98, b(6)
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98++, y(5)-98, y(5), y(6)-98, y(6)++
Precursor origin neutral loss: +

Peptide No.2099

SSSGVSAPLIPK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of SSSGVSAPLIPK
Found in AT5G20650.1, COPT5 (copper transporter 5); copper ion transporter

Match to Query 1283: 1221.600304 from(611.807428,2+)
Elution from: 39.244 to 39.244 scan no 3777 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1221.6006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 3.9e-006
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(5)+, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(9), b(9)-98++, b(10), b(10)-98, b(10)+, b(10)-98++, b(11)-98, b(11)-98++, b(11)+
Matched y ions: y(2), y(3), y(4), y(5), y(5)+, y(6), y(7), y(8), y(9), y(9)+, y(11)-98++, y(11)+
Precursor origin neutral loss:

Peptide No.2100

SSSGVSAPLIPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSGVSAPlPK
Found in AT5G20650.1, COPT5 (copper transporter 5); copper ion transporter

Match to Query 1044: 1221.599642 from(611.807097,2+)
Elution from: 38.237 to 38.237 scan no 3716 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1221.6006
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 4.2e-007
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(5)+, b(6)-98++, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(10)-98++, b(10)+, b(11)-98, b(11)-98++, b(11)+
Matched y ions: y(2), y(3), y(4), y(5), y(5)+, y(6), y(7), y(8), y(9), y(9)+, y(10)-98++, y(10), y(10)-98, y(10)+, y(11)+
Precursor origin neutral loss:

Peptide No.2101

SSSIGNSDADIYAENDSGR
Confirmed sites: @S:1orS:2

MS/MS Fragmentation of SSSIEGNSDADIYAENDSGR
Found in AT2G16920.1, UBC23 (ubiquitin-conjugating enzyme 22); ubiquitin-protein ligase

Match to Query 3120: 2165.836200 from(1083.925376,2+)
Elution from: 33.461 to 33.461 scan no 3068 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2100/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 2165.8386  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 97 Expect: 1.3e-09  
Matched b ions: b(6), b(7), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(15)-98, b(16), b(17), b(19)-98++, b(19)+  
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(15)+, y(16), y(17)+, y(18)+  
Precursor origin neutral loss: +  

Peptide No.2102  
SSNLIPVSR  
Confirmed sites:  
Ambiguous sites: @S:1orS:2orS:3  

MS/MS Fragmentation of SSSNLIPVSR  
Found in AT5G18500.1, protein kinase family protein  
Match to Query 811: 1138.536812 from(570.275682,2+)  
Elution from: 35.313 to 35.313 scan no 3325 polarity:+  

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2101/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 1138.5383
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.039
Matched b ions: b(5)-98, b(6), b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(4)
Precursor origin neutral loss: +

Peptide No.2103

SSSPGLAAAAAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSPGLAAAAAR
Found in AT2G14835.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 834: 1137.516708 from(569.765630,2+)
Elution from: 24.628 to 24.628 scan no 1916 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2102/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 1137.5179
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00025
Matched b ions: b(5), b(6)-98, b(8)-98, b(8), b(9)-98, b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)+, y(10)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.2104

SSPGYVGSYSVNK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of SSSPGYVGSYSVNK
Found in AT3G07810.1, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative

Match to Query 2065: 1510.633070 from(756.323811,2+)
Elution from: 31.727 to 31.727 scan no 2836 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1510.6340
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0037
Matched b ions: b(3), b(6)-98, b(6), b(7)-98, b(8)-98, b(11), b(11)-98++, b(12), b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(8), y(9), y(9)++, y(11), y(11)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.2105
SSSPGYVGSYSVNK
Confirmed sites: @Y:6
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSSPGYVGSYSVNK
Found in AT3G07810.1, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative

Match to Query 2692: 1590.598172 from(796.306362,2+)
Elution from: 36.062 to 36.062 scan no 3475 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1590.6004
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 27 Expect: 0.0098
Matched b ions: b(6)-98, b(6), b(7)-98, b(10)-98, b(12)-98, b(13)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(12)++
Precursor origin neutral loss: +

Peptide No.2106
SSSPGYVGYSVNNK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSPGYVGYSVNNK
Found in AT3G07810.1, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative

Match to Query 2450: 1510.632162 from(756.323357,2+)
Elution from: 31.472 to 31.472 scan no 2877 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea1ist.htm (2105/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 1510.6340  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 50 Expect: 6.7e-005  
Matched b ions: b(3), b(3)-98, b(6)-98, b(6), b(7)++, b(7)-98, b(8), b(8)-98, b(10)-98, b(11), b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-98++, b(13)-98, b(13)  
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(8), y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)-98++, y(12)++, y(13)++  
Precursor origin neutral loss: +

Peptide No.2107

SSPGYVGYSVKNK  
Confirmed sites:
Ambiguous sites: "@S:1orS:2orS:3orY:6, @S:1orS:2orS:3orY:6"

MS/MS Fragmentation of SSPGYVGYSVKNK  
Found in AT3G07810.1, heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative  

Match to Query: 2689: 1590.599670 from(796.307111,2+)  
Elution from: 36.158 to 36.158 scan no 3500 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1590.6004
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 30 Expect: 0.0051
Matched b ions: b(6)-98, b(6), b(7)-98, b(8)++, b(10)-98, b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

---

Peptide No.2108

SSSPNEDRGENQLVYDNLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSPNEDRGENQLVYDNLK
Found in AT5G35330.1, MBD02 (methyl-CpG-binding domain 2); DNA binding

Match to Query 4369: 2228.993373 from(744.005067,3+)
Elution from: 42.694 to 42.694 scan no 4322 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2107/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 2228.9950
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.013
Matched b ions: b(3), b(4)-98, b(5), b(6), b(6)+, b(7), b(7)-98, b(8)+, b(10), b(10)-98++, b(11)+, b(12)+, b(13)-98++, b(14)+, b(15)+, b(15)-98++, b(16)-98++, b(17)+, b(17)-98++
Matched y ions: y(2), y(3), y(5), y(7), y(8), y(9)+, y(9), y(12)+, y(13)+, y(14)+, y(15)+, y(16)+, y(17)-98++, y(17)+
Precursor origin neutral loss:

Peptide No.2109
SSSPNVFAAPPILQK
Confirmed sites: @S:1<br>S:2<br>S:3

MS/MS Fragmentation of SSSPNVFAAPPILQK
Found in AT4G20910.1, HEN1 (HUA ENHANCER 1)

Match to Query 2071: 1634.804998 from(818.409775,2+)
Elution from: 51.871 to 51.871 scan no 5283 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1634.8069  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 22 Expect: 0.048  
Matched b ions: b(6), b(7)-98, b(7), b(9)-98, b(12), b(14)-98++  
Matched y ions: y(6), y(7), y(8), y(9)  
Precursor origin neutral loss: +  

Peptide No.2110  
SSSPNVFAAPPILQK  
Confirmed sites: @S:3  
Ambigious sites:  
MS/MS Fragmentation of SSSPVFAAPPILQK  
Found in AT4G20910.1, HEN1 (HUA ENHANCER 1)  
Match to Query 2413: 1634.805474 from(818.410013,2+)  
Elution from: 51.853 to 51.853 scan no 5505 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1634.8069
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00024
Matched b ions: b(6), b(6)-98, b(7), b(9), b(9)-98, b(12), b(14), b(14)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(12), y(12)++, y(13)-98++
Precursor origin neutral loss:

Peptide No.2111

SSPPGNVDGFSIGK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of SSPPGNVDGFSIGK
Found in AT1G30480.1, DRT111 (DNA-damage-repair/toleration protein 111); nucleic acid binding / nucleotide binding

Match to Query 2034: 1527.660054 from(764.837303,2+)
Elution from: 42.369 to 42.369 scan no 4264 polarity:+

file:///C|/Documents%20and%20%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2110/2597) [2008/03/14 15:08:28]
Monoisotopic mass of neutral peptide Mr(calc): 1527.6606
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 9.6e-005
Matched b ions: b(7), b(8)++, b(8), b(8)-98, b(11)-98, b(13), b(13)-98, b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2112

SSSPPGNVDGFSIGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSPPGNVDGFSIGK
Found in AT1G30480.1, DRT111 (DNA-damage-repair/toleration protein 111); nucleic acid binding / nucleotide binding

Match to Query 2318: 1527.658520 from(764.836536,2+)
Elution from: 42.709 to 42.709 scan no 4325 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2111/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1527.6606
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.4e-005
Matched b ions: b(5)-98, b(7), b(7)-98, b(8)++, b(8)-98, b(9)-98, b(9), b(11)-98, b(13)++, b(14)-98, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13)-98++, y(13)++, y(14)-98++
Precursor origin neutral loss:

Peptide No.2113

SSPSAVPDLPK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of SSSPSAVPDLPK
Found in AT5G16280.1, binding

Match to Query 1427: 1263.573906 from(632.794229,2+)
Elution from: 35.227 to 35.227 scan no 3339 polarity:+

file:///C:/Documents%20and%20Settings/N.Sukunda/abi/result_v3/o0705103ppmGROUPmeadlist.htm (2112/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1263.5748  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 60 Expect: 6e-006  
Matched b ions: b(3)-98, b(3), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(9), b(9)+ +, b(10)-98, b(10), b(10)-98++  
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(9)++, y(11)-98++  
Precursor origin neutral loss:  

Peptide No.2114  
SSPSAVPDLPK  
Confirmed sites: @S:3  
Ambiguous sites:  

MS/MS Fragmentation of SSSPSAVPDLPK  
Found in AT5G16280.1, binding  

Match to Query 1432: 1263.572874 from(632.793713,2+)  
Elution from: 35.682 to 35.682 scan no 3302 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaodelist.htm (2113/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1263.5748  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 54 Expect: 2.8e-005  
Matched b ions: b(3)-98, b(3), b(4)-98, b(6), b(7), b(7)-98, b(8)-98, b(9), b(10)-98, b(10), b(10)-98++, b(11)-98  
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(9), y(9)+, y(10)-98++, y(10), y(10)+  
Precursor origin neutral loss: +

---

**Peptide No.2115**

**SSSPTREDVSVFR**  
Confirmed sites:  
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of **SSSPTREDVSVFR**  
Found in **AT5G46870.1**, RNA recognition motif (RRM)-containing protein

Match to Query 2664: 1545.680790 from(516.234206,3+)  
Elution from: 31.295 to 31.295 scan no 2882 polarity:+

---

---
Monoisotopic mass of neutral peptide Mr(calc): 1545.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00012
Matched b ions: b(2), b(3), b(6)+, b(6), b(7)+, b(8), b(8)+, b(8)-98++, b(9), b(9)-98++, b(9)-98++, b(10)+++, b(11)-98++, b(12)+++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)+, y(5), y(5)+, y(6), y(6)+, y(7)+, y(7), y(8)+, y(9), y(9)+, y(10)+
Precursor origin neutral loss:

Peptide No.2116

SSSPTRCEDSVSVFR
Confirmed sites: @S:1 or S:2

MS/MS Fragmentation of SSSPTRCEDSVSVFR
Found in AT5G46870.1, RNA recognition motif (RRM)-containing protein

Match to Query 2096: 1545.681453 from(516.234427,3+)
Elution from: 32.131 to 32.131 scan no 2898 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2115/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1545.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 2.4e-005
Matched b ions: b(2), b(3)-98, b(3), b(4), b(6), b(7)+, b(7)-98, b(8), b(8)+++, b(8)-98, b(8)-98 +++, b(9), b(9)-98++, b(9)-98, b(12)+++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)+, y(5), y(5)++, y(6), y(7)+, y(7)+, y(8)+, y(9), y(9) +++, y(10)+
Precursor origin neutral loss:

---

Peptide No.2117

SSSPTREDVSFVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSPTREDVSFVR
Found in AT5G46870.1, RNA recognition motif (RRM)-containing protein

Match to Query 2088: 1545.681507 from(516.234445,3+)
Elution from: 31.339 to 31.339 scan no 2828 polarity:+

file:///C:/Documents%20and%20Settings/N.Suabi/result_v3/o0705103ppmGROUPmeadlist.htm (2116/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1545.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 1.4e-006
Matched b ions: b(2), b(3)-98, b(3), b(5), b(6), b(6)+, b(7)-98++, b(7)+, b(8), b(8)+, b(8)-98++, b(9), b(9)-98++, b(9)-98, b(10)+, b(11)-98++, b(12)+, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4)+, y(5)+, y(5)+, y(6), y(6)+, y(7)+, y(7)+, y(8)+, y(8), y(9)+, y(10)+, y(11)+, y(11)-98++, y(12)-98++, y(12)+
Precursor origin neutral loss:

Peptide No.2118

SSSPTREDVSVFR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of SSSPTREDVSVFR
Found in AT5G46870.1, RNA recognition motif (RRM)-containing protein

Match to Query 2419: 1545.681838 from(773.848195,2+)
Elution from: 31.250 to 31.250 scan no 2830 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2117/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1545.6824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0066
Matched b ions: b(6), b(6)-98, b(7), b(7)-98, b(8)-98++, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(11)+, b(12), b(12)-98++, b(12)-98, b(12)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)+, y(9)-98++, y(9)+, y(10)-98, y(10)-98++, y(11), y(11)-98++, y(11)-98, y(11)+, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2119

SSSSGSDNTGGITFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SSSSGSDNTGGITFK
Found in AT5G25060.1, RNA recognition motif (RRM)-containing protein

Match to Query 2304: 1523.613456 from(762.814004,2+)
Elution from: 32.156 to 32.156 scan no 2921 polarity:+

file:///C%5C/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2118/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1523.6140
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0018
Matched b ions: b(7), b(8)-98, b(9)-98, b(12)-98, b(12), b(14)-98
Matched y ions: y(2), y(3), y(5)++, y(6), y(7), y(8), y(9), y(10), y(12), y(13)-98++, y(13)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2120

SSSVDREDVGGEAGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSVDREDVGGEAGK
Found in AT5G58040.1, ATFIP1[V] (ARABIDOPSIS HOMOLOG OF YEAST FIP1 [V]); RNA binding

Match to Query 1655: 1571.644306 from(786.829429,2+)
Elution from: 18.905 to 18.905 scan no 1138 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2119/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1571.6464
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.04
Matched b ions: b(8), b(8)-98, b(9)-98, b(14)++
Matched y ions: y(6), y(7), y(8), y(9), y(13)
Precursor origin neutral loss: +

Peptide No.2121

STAGTPEWMAPEVLRL
Confirmed sites:
Ambiguous sites: @S:1orT:2

MS/MS Fragmentation of STAGTPEWMAPEVLRL
Found in AT1G08720.1, EDR1 (ENHANCED DISEASE RESISTANCE 1); kinase/ protein threonine/tyrosine kinase

Match to Query 2838: 1723.763138 from(862.888845,2+)
Elution from: 54.966 to 54.966 scan no 5710 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2120/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1723.7640
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0032
Matched b ions: b(9)-98, b(10), b(11)-98, b(13)++
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(10)++, y(12)++
Precursor origin neutral loss: +

Peptide No.2122

STAGTPEWMAPEVLR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of STAGTPEWMAPEVLR
Found in AT1G08720.1, EDR1 (ENHANCED DISEASE RESISTANCE 1); kinase/ protein threonine/tyrosine kinase

Match to Query 2631: 1723.760456 from(862.887504,2+)
Elution from: 56.433 to 56.433 scan no 5907 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1723.7640
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.002
Matched b ions: b(10)-98, b(13)-98
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(10)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2123

STASLEYTMVDAFR
Confirmed sites: "@S:4,@Y:7"
Ambiguous sites:

MS/MS Fragmentation of STASLEYTMVDAFR
Found in AT4G01100.1, mitochondrial substrate carrier family protein

Match to Query 2202: 1806.691230 from(603.237686,3+)
Elution from: 36.457 to 36.457 scan no 3450 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2122/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1806.6936
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 23 Expect: 0.037
Matched b ions: b(5)-98, b(6)-98++, b(6)-98, b(7)-98
Matched y ions: y(5)+, y(8)+, y(9)+, y(10)+, y(11)+, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2124
STDDLSGFRK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of STDDLSGFRK
Found in AT1G33050.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G10470.1); similar to Subtilisin-like se

Match to Query 973: 1204.512120 from(603.263336,2+)
Elution from: 27.027 to 27.027 scan no 2242 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2123/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1204.5125  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 26 Expect: 0.014  
Matched b ions: b(4)-98, b(4)  
Matched y ions: y(4), y(5), y(6), y(6)+, y(7)+, y(7), y(8)+, y(9)+  
Precursor origin neutral loss: +

Peptide No.2125

STDDLSGFRK

Confirmed sites:  
Ambiguous sites: @S:1orT:2

MS/MS Fragmentation of STDDLSGFRK  
Found in AT1G33050.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G10470.1); similar to Subtilisin-like se

Match to Query 1278: 1204.512484 from(603.263518,2+)  
Elution from: 27.546 to 27.546 scan no 2337 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1204.5125
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.032
Matched b ions: b(3)-98, b(4), b(5)-98
Matched y ions: y(5), y(6), y(7)+, y(7), y(8)+
Precursor origin neutral loss: +

Peptide No.2126

STEGSSHASEISGSSPQEKL
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of STEGSSHASEISGSSPQEKL
Found in AT3G60240.2, EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G)

Match to Query 2878: 2070.835830 from(691.285866,3+)
Elution from: 18.491 to 18.491 scan no 1054 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2070.8378
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00087
Matched b ions: b(9)+, b(9), b(11), b(11)+, b(12)+, b(12), b(13)+, b(14)+, b(16)-98+,
b(16)+, b(18)+, b(19)+
Matched y ions: y(4), y(5), y(6), y(7), y(8)+, y(8), y(10)-98+, y(12)+, y(17)+
Precursor origin neutral loss:

Peptide No.2127

STEGSSHASSEISGSSPQEK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of STEGSSHASSEISGSSPQEK
Found in AT3G60240.2, EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G)

Match to Query 3188: 2070.834753 from(691.285527,3+)
Elution from: 18.044 to 18.044 scan no 1014 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea...
Monoisotopic mass of neutral peptide Mr(calc): 2070.8378
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0002
Matched b ions: b(8), b(11)++, b(12), b(12)++, b(13)++, b(14)++, b(16)-98+++, b(17)+++, b(18)+++, b(19)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)++, y(10)-98++, y(12)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.2128
STFISIPSMSPK
Confirmed sites: "@S:7,@S:11"
Ambiguous sites:

MS/MS Fragmentation of STFISIPSMSPK
Found in AT3G25500.1, AFH1 (FORMIN HOMOLOGY 1); actin binding

Match to Query 2637: 1540.628128 from(771.321340,2+)
Elution from: 53.491 to 53.491 scan no 5731 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2127/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1540.6285
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 8.5e-005
Matched b ions: b(4), b(5), b(10)-98
Matched y ions: y(3), y(5), y(6), y(7), y(7)-98, y(8), y(9), y(9)-196++, y(10), y(11)+, y(12)-196++
Precursor origin neutral loss: +

Peptide No.2129

STIDGCSDTELFER
Confirmed sites:
Ambiguous sites: @S:7 or T:9

MS/MS Fragmentation of STIDGCSDTELFER
Found in AT5G64930.1, CPR5 (CONSTITUTIVE EXPRESSION OF PR GENES 5)

Match to Query 2655: 1708.662846 from(855.338699,2+)
Elution from: 44.495 to 44.495 scan no 4579 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1708.6651  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 52 Expect: 2.7e-005  
Matched b ions:  
Matched y ions: y(2), y(3), y(4), y(5), y(8), y(10), y(11), y(11)++, y(12)++  
Precursor origin neutral loss: +  

Peptide No.2130  
STIESPFFQR  
Confirmed sites:  
Ambiguous sites: @S:1orT:2  

MS/MS Fragmentation of STIESPFFQR  
Found in AT1G09650.1, F-box family protein  

Match to Query 1236: 1290.562294 from(646.288423,2+)  
Elution from: 19.575 to 19.575 scan no 1254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1290.5645  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 24 Expect: 0.032  
Matched b ions: b(3), b(4), b(5), b(6)-98, b(9), b(9)-98  
Matched y ions: y(4), y(8)  
Precursor origin neutral loss: +

Peptide No.2131

STQDALIDRVPSGK  
Confirmed sites: @S:12  
Ambiguous sites:

MS/MS Fragmentation of STQDALIDRVPSGK  
Found in AT1G58250.1, SAB (SABRE)

Match to Query 2416: 1565.743954 from(783.879253,2+)  
Elution from: 33.521 to 33.521 scan no 3012 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1565.7450
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00016
Matched b ions: b(5), b(6), b(8), b(10), b(11)++ , b(12)-98, b(13)
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(6)-98, y(6), y(7)-98++, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(10)-98++, y(10)-98, y(11)++ , y(12)++ , y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.2132

STSAETIGD GDKDSPK
Confirmed sites: @S:14
Ambiguous sites:
MS/MS Fragmentation of STSAETIGD GDKDSPK
Found in AT5G21160.1, La domain-containing protein / proline-rich family protein

Match to Query 2587: 1686.697464 from(844.356008,2+)
Elution from: 18.966 to 18.966 scan no 1163 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1686.6985
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(6), b(7), b(11), b(13), b(13)++, b(14)-98, b(14), b(14)-98++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(9)-98, y(9), y(10), y(10)++, y(10)-98, y(10)-98++, y(11), y(11)-98, y(11)++, y(12), y(12)++, y(13)++, y(13)-98++, y(14)++, y(14), y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2133
STSAETIGDGDKDSPK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of STSAETIGDGDKDSPK
Found in AT5G21160.1, La domain-containing protein / proline-rich family protein

Match to Query 1923: 1686.696928 from(844.355740,2+)
Elution from: 18.883 to 18.883 scan no 1135 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaclist.htm (2132/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1686.6985  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 46 Expect: 0.00019  
Matched b ions: b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(10)-98, b(11), b(12)-98, b(13)-98, b(14)-98, b(14), b(15)-98  
Matched y ions: y(8), y(11), y(11)-98++, y(11)-98, y(11)+, y(12), y(13)+, y(14)-98++, y(14) ++  
Precursor origin neutral loss: +

Peptide No.2134

STSEIAMDR  
Confirmed sites:  
Ambiguous sites: @S:1orT:2orS:3

MS/MS Fragmentation of STSEIAMDR  
Found in AT1G03445.1, BSU1 (BRASSINOSTEROID INSENSITIVE 1 suppressor 1); protein serine/threonine phosphatase

Match to Query 689: 1088.419340 from(545.216946,2+)  
Elution from: 25.136 to 25.136 scan no 1954 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2133/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1088.4209
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.013
Matched b ions:
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss:

Peptide No.2135

STSGVDGNSPVSVCISPGER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of STSGVDGNSPVSVCISPGER
Found in AT2G44970.1, lipase-related

Match to Query 3645: 2083.885430 from(1042.949991,2+)
Elution from: 40.271 to 40.271 scan no 4024 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2083.8881
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 Expect: 3.2e-008
Matched b ions: b(5), b(6), b(8), b(9)-98, b(9), b(11), b(12), b(13), b(14)-98++, b(14), b(15), b(15)-98, b(16), b(18)+, b(19)-98, b(19)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(15), y(15)+, y(16)+, y(17)+, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2136

STTTTVSSVHSPTTDQDFS
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of STTTTVSSVHSPTTDQDFS
Found in AT2G17290.1, CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); anion channel/ calcium- and calmodulin-dependent protein

Match to Query 3942: 2204.946585 from(735.989471,3+)
Elution from: 27.729 to 27.729 scan no 2336 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2135/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2204.9474
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0026
Matched b ions: b(7)-98, b(8), b(9)-98, b(13)++
Matched y ions: y(13)++, y(14)++, y(15)-98++, y(15)+, y(16)++, y(17)+, y(18)+, y(18)-98++
Precursor origin neutral loss:

Peptide No.2137

SVAVQQPIDGSPR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SVAVQQPIDGSPR
Found in AT3G18230.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 1560: 1432.670078 from(717.342315,2+)
Elution from: 27.578 to 27.578 scan no 2271 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2136/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1432.6711
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 7e-009
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(8)+, b(9), b(10), b(11)-98
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(5)-98++, y(6), y(7), y(7)-98, y(7)+, y(8), y(8)-98, y(9), y(9)-98, y(9)+, y(10), y(10)+, y(10)-98, y(10)-98++, y(11), y(11)+, y(11)-98++, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2138
SVDADDSDVDIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SVDADDSDVDIK
Found in AT3G13200.1, Cwf15 / Cwc15 cell cycle control family protein

Match to Query 1271: 1357.526674 from(679.770613,2+)
Elution from: 28.867 to 28.867 scan no 2346 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1357.5286
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0002
Matched b ions: b(3), b(4), b(6)++, b(7), b(9)-98, b(10), b(11)-98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(7)-98, y(8), y(9), y(10)++, y(10), y(11)-98++, y (11)-98
Precursor origin neutral loss: +

Peptide No.2139
SVDKFEVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SVDKFEVK
Found in AT3G10020.1, similar to Os12g0147200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001066153.1); similar to Os

Match to Query 558: 1030.473488 from(516.244020,2+)
Elution from: 24.618 to 24.618 scan no 1873 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2138/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1030.4736
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0035
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(6)-98, b(6), b(6)+, b(7), b(7)-98, b(7)-98++
Matched y ions: y(2), y(5), y(5)+, y(6), y(6)+, y(7)+
Precursor origin neutral loss: +

Peptide No.2140

SVDQEEVVVGLEDADA
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SVDQEEVVVGLEDADA
Found in AT3G46530.1, RPP13 (RECOGNITION OF PERONOSPORA PARASITICA 13); ATP binding

Match to Query 2836: 1810.786242 from(906.400397,2+)
Elution from: 50.802 to 50.802 scan no 5282 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1810.7873
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 Expect: 1.8e-009
Matched b ions: b(3), b(4)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13)+, b(14), b(15)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)+, y(13)+, y(14), y(14)+
Precursor origin neutral loss: +

Peptide No.2141

SVEAGSNLTSPAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SVEAGSNLTSPAK
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G28770.1); similar to unnamed protein pr

Match to Query 1738: 1339.601256 from(670.807904,2+)
Elution from: 24.709 to 24.709 scan no 1919 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1339.6020
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 5e-006
Matched b ions: b(3), b(6), b(9), b(11)-98, b(12)
Matched y ions: y(3), y(4), y(4)-98, y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)+, y(12)-98+
y(12)+
Precursor origin neutral loss: +

Peptide No.2142

SVEAGSNLTSPAK
Confirmed sites: "@S:6,@S:10"
Ambiguous sites:

MS/MS Fragmentation of SVEAGSNLTSPAK
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G28770.1); similar to unnamed protein pr

Match to Query 1323: 1419.566708 from(710.790630,2+)
Elution from: 26.628 to 26.628 scan no 2152 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1419.5683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0015
Matched b ions: b(3), b(5), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-196, b(10)-98, b(10), b(11)-196, b(11)-98
Matched y ions: y(3), y(4), y(5), y(7), y(9)-98, y(9), y(9)-196, y(10)-98, y(10), y(10)-196, y(11)+, y(11), y(11)-98++, y(12)-98++, y(12)-196++
Precursor origin neutral loss: +

Peptide No.2143

SVEAGSNLTSPA
Confirmed sites: @S:10orT:9

MS/MS Fragmentation of SVEAGSNLTSPA
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G28770.1); similar to unnamed protein pr

Match to Query 1386: 1339.600520 from(670.807536,2+)
Elution from: 23.746 to 23.746 scan no 1801 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlelist.htm (2142/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1339.6020
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.038
Matched b ions: b(7), b(11)-98
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(11)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2144

SVEAGSNLTSPAK
Confirmed sites: "@T:9,@S:10"
Ambiguous sites:

MS/MS Fragmentation of SVEAGSNLTSPAK
Found in AT5G53440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT3G28770.1); similar to unnamed protein pr

Match to Query 1791: 1419.567276 from(710.790914,2+)
Elution from: 27.380 to 27.380 scan no 2257 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1419.5683
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.049
Matched b ions: b(4), b(9)-98, b(9), b(10), b(11)-98, b(11)-196, b(12)-98++
Matched y ions: y(3), y(4), y(5), y(8), y(9)-98, y(9), y(10), y(10)-98, y(11)-98++, y(11)+, y(12)-196++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2145

SVEDTAKPVSASSPEK
Confirmed sites:
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of SVEDTAKPVSASSPEK
Found in AT3G61670.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G46380.1); similar to unknown [Striga as

Match to Query 2594: 1710.769428 from(856.391990,2+)
Elution from: 20.634 to 20.634 scan no 1379 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1710.7713
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(6), b(11), b(13)-98, b(13)++, b(14)-98++
Matched y ions: y(3), y(6), y(8), y(9)-98, y(9), y(10), y(12)++, y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.2146
SVEEDCPSTSDAIELDGSEK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of SVEEDCPSTSDAIELDGSEK
Found in AT3G53030.1, SRPK4 (SER/ARG-RICH PROTEIN KINASE 4); kinase/ protein kinase

Match to Query 4133: 2246.874622 from(1124.444587,2+)
Elution from: 38.789 to 38.789 scan no 3790 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2145/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2246.8773
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 4.6e-005
Matched b ions: b(6), b(13), b(14), b(15), b(16), b(18)+, b(19)-98++, b(19)+
Matched y ions: y(4)-98, y(5)-98, y(5)-98, y(6)-98, y(6)-98, y(7)-98, y(7), y(8)-98, y(9), y(10), y(11), y(12), y(14)-98, y(14), y(15), y(15)-98, y(18)-98++, y(18)+, y(19)-98++
Precursor origin neutral loss: +

Peptide No.2147
SVENYPSSPSPR
Confirmed sites: @S:10
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of SVENYPSSPSPR
Found in AT1G11310.1, MLO2 (MILDEW RESISTANCE LOCUS O 2); calmodulin binding

Match to Query 1921: 1478.547368 from(740.280960,2+)
Elution from: 26.247 to 26.247 scan no 2104 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2146/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1478.5480
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0034
Matched b ions: b(5), b(8), b(8)-98, b(9)-98
Matched y ions: y(2), y(4)-98, y(4), y(6)-98, y(6), y(6)-196, y(7), y(7)-98, y(7), y(7)-196, y(8), y(9), y(9)-98++, y(10)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2148

SVETLSPFQQK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of SVETLSPFQQK
Found in AT1G07110.1, F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); fructose-2,6-bisphosphate 2-phosphatase

Match to Query 1399: 1342.616532 from(672.315542,2+)
Elution from: 38.662 to 38.662 scan no 3807 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2147/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1342.6170
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0023
Matched b ions: b(4), b(5), b(6)-98, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(10)+
Matched y ions: y(2), y(3), y(4)+, y(5), y(6), y(7), y(7)+, y(7)-98, y(8), y(8)+, y(9)-98++, y(9), y(9)+, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2149

SVETTLAELGVTLSNSAYK
Confirmed sites: "@S:16,@Y:18"
Ambiguous sites:

MS/MS Fragmentation of SVETTLAELGVTLSNSAYK
Found in AT1G06220.1, MEE5 (maternal effect embryo arrest 5); translation elongation factor/ translation factor, nucleic

Match to Query 3795: 2141.957628 from(714.993152,3+)
Elution from: 61.797 to 61.797 scan no 6609 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaList.htm (2148/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2141.9534  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Y18 : Phospho (Y)  
Ions Score: 28 Expect: 0.02  
Matched b ions: b(12)++, b(13)++, b(14)++, b(16)++, b(17)-98++, b(18)++  
Matched y ions: y(5), y(6), y(7), y(10)++, y(11)++  
Precursor origin neutral loss:

Peptide No.2150  
SVFCGCVQQPESP  
Confirmed sites: @S:12  
Ambiguous sites:

MS/MS Fragmentation of SVFCGCVQQPESP  
Found in AT4G02710.1, kinase interacting family protein  

Match to Query 2373: 1573.593002 from(787.803777,2+)  
Elution from: 41.594 to 41.594 scan no 3979 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1573.5942
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.001
Matched b ions: b(7), b(8), b(9), b(9)++, b(11), b(12), b(12)++
Matched y ions: y(4), y(5), y(6), y(7), y(10)
Precursor origin neutral loss: +

Peptide No.2151

SVFTEDLDPPETESESDSPK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of SVFTEDLDPPETESESDSPK
Found in AT1G03350.1, BSD domain-containing protein

Match to Query 4094: 2287.921948 from(1144.968250,2+)
Elution from: 46.586 to 46.586 scan no 4843 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2287.9257
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0027
Matched b ions: b(6), b(7), b(8), b(11), b(14)++, b(17)
Matched y ions: y(7), y(9), y(12)-98, y(12), y(13), y(14), y(14)-98++, y(15), y(16)++
Precursor origin neutral loss:

Peptide No.2152

SVGELPPELK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SVGELPPELK
Found in AT5G47430.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G17410.1); similar to hypothetical prote

Match to Query 858: 1147.550792 from(574.782672,2+)
Elution from: 40.641 to 40.641 scan no 4071 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2151/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1147.5526
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0087
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98
Matched y ions: y(4), y(5), y(6), y(8)
Precursor origin neutral loss: +

---

Peptide No.2153

SVGHVTPFGSR
Confirmed sites: "@S:1,@S:10"
Ambiguous sites:

MS/MS Fragmentation of SVGHVTPFGSR
Found in AT1G67630.1, DNA polymerase alpha subunit B family

Match to Query 1306: 1302.515038 from(652.264795,2+)
Elution from: 31.278 to 31.278 scan no 2820 polarity:+

---
Monoisotopic mass of neutral peptide Mr(calc): 1302.5159
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.023
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(8)-98, b(9)-98
Matched y ions: y(4), y(5), y(5)-98, y(6), y(7), y(7)-98, y(8)+, y(8)-98++, y(9)+, y(9)-98, y(9)-98++, y(10)-98++, y(10)+
Precursor origin neutral loss: +

Peptide No.2154

SVGHVTPEFSGR
Confirmed sites: "@S:1,@T:6"
Ambiguous sites:

MS/MS Fragmentation of SVGHVTPEFSGR
Found in AT1G67630.1, DNA polymerase alpha subunit B family

Match to Query 1590: 1302.515518 from(652.265035,2+)
Elution from: 32.559 to 32.559 scan no 2883 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2153/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1302.5159
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.0062
Matched b ions: b(4), b(4)-98, b(5)-98, b(5), b(6)-196, b(6)-98, b(6), b(8)-98, b(10), b(10)+
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(7)-98, y(8)+, y(9)+, y(10)-98++, y(10)+
Precursor origin neutral loss: +

Peptide No.2155
SVLDTPLSSAR
Confirmed sites: @S:1
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1508: 1304.540126 from(653.277339,2+)
Elution from: 42.201 to 42.201 scan no 4177 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1304.5414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0015
Matched b ions: b(5), b(6)-98, b(7)-98++
Matched y ions: y(5), y(6)+, y(6)-98, y(7), y(8), y(9), y(9)+, y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.2156

SVLDTPLSSAR
Confirmed sites: "@S:1,@T:5"
Ambiguous sites:

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1092: 1304.540006 from(653.277279,2+)
Elution from: 37.827 to 37.827 scan no 3627 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1304.5414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0002
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)-196, b(7)-98, b(7), b(8)-98++, b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(9)++, y(9), y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.2157

SVLDTPLSSAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1039: 1224.573986 from(613.294269,2+)
Elution from: 39.182 to 39.182 scan no 3879 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1224.5751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.00047
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8)-98, b(10)
Matched y ions: y(2), y(3), y(4)-98, y(4), y(4)+, y(5)-98, y(6), y(6)+, y(7), y(7)-98++, y(7)-98, y(7)+, y(8), y(8)-98++, y(8)-98, y(9)+, y(9), y(9)-98, y(9)-98++, y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.2158

SVLDTPLSSAR
Confirmed sites: "@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1584: 1304.539842 from(653.277197,2+)
Elution from: 44.126 to 44.126 scan no 4470 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1304.5414  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
Ions Score: 50 Expect: 5.3e-005  
Matched b ions: b(2), b(5), b(8)  
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(9)+, y(9)-98, y(9)-98++, y(10)-98++, y(10)-196++  
Precursor origin neutral loss: +

---

Peptide No.2159

SVLDTPLSSAR  
Confirmed sites:  
Ambiguous sites: @S:8 or S:9  

MS/MS Fragmentation of SVLDTPLSSAR  
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase  

Match to Query 1009: 1224.574548 from(613.294550,2+)  
Elution from: 39.140 to 39.140 scan no 3785 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2158/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1224.5751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.02
Matched b ions: b(2), b(5), b(7)
Matched y ions: y(4), y(5)-98, y(6), y(6)++, y(7)-98++, y(7)++, y(7), y(8), y(9)++, y(9), y(10)-98++
Precursor origin neutral loss: +

Peptide No.2160

SVLDTPLSSAR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase

Match to Query 1072: 1224.574312 from(613.294432,2+)
Elution from: 36.258 to 36.258 scan no 3487 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1224.5751  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 53 Expect: 4.2e-005  
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)-98, b(8), b(9), b(9)-98  
Matched y ions: y(2), y(3), y(4), y(5)+, y(5), y(6), y(7)-98++, y(7), y(7)-98, y(8), y(8)-98++, y(8)+, y(8)-98, y(9)+, y(9), y(9)-98++, y(9)-98, y(9)-98++, y(9)-98, y(10)-98++, y(10)-98, y(10)+  
Precursor origin neutral loss: +  

---

Peptide No.2161  
SVLDTPLSSAR  
Confirmed sites: "@T:5,@S:8"  
Ambiguous sites:  

MS/MS Fragmentation of SVLDTPLSSAR  
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase  

Match to Query 1585: 1304.540868 from(653.277710,2+)  
Elution from: 40.320 to 40.320 scan no 3811 polarity:+  

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2160/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1304.5414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.0002
Matched b ions: b(2), b(3), b(4), b(5)-98++, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(7)-98++, b(7)+, b(8)-98, b(8)-196, b(9)-98++, b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)+, b(10)-196
Matched y ions: y(2), y(3), y(4)-98, y(4), y(4)+, y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(7)-98++, y(7)-196++, y(7)+, y(7)-196, y(8), y(8)-98, y(8)-196, y(8)-98++, y(8)-196++, y(9)+, y(9), y(9)-98++, y(9)-98, y(9)-196++, y(9)-196, y(10)-98++, y(10)-196++, y(10)-98, y(10)-196, y(10)+
Precursor origin neutral loss: +

Peptide No.2162
SVLDTPLSSAR
Confirmed sites: @T:5
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of SVLDTPLSSAR
Found in AT1G35580.1, CINV1 (CYTOSOLIC INVERTASE 1); beta-fructofuranosidase
Match to Query 1089: 1304.538828 from(653.276690,2+)
Elution from: 40.223 to 40.223 scan no 3925 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1304.5414
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0025
Matched b ions: b(5), b(5)-98, b(6)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9)+, y(9), y(9)-98++, y(10)-98++, y(10)-196++, y(10)++
Precursor origin neutral loss: +

Peptide No.2163

SVNVNSGNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SVNVNSGNR
Found in AT1G31460.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G23270.1); similar to hypothetical prote

Match to Query 890: 1172.496730 from(587.255641,2+)
Elution from: 31.656 to 31.656 scan no 2867 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1172.4975
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 3.6e-005
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.2164

SVSAESLNSNVEELVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSAESLNSNVEELVK
Found in AT3G60380.1, similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT4G16790.1)

Match to Query 2839: 1783.822782 from(892.918667,2+)
Elution from: 51.497 to 51.497 scan no 5419 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1783.8240
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.022
Matched b ions: b(7)-98, b(11), b(11)-98, b(14)-98++
Matched y ions: y(4), y(9), y(10), y(11), y(12), y(14)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2165

SVSDSGCVDLLGQSR
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of SVSDSGCVDLLGQSR
Found in AT3G57200.1, similar to GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] (TAIR:AT2G)

Match to Query 2721: 1658.696682 from(830.355617,2+)
Elution from: 43.085 to 43.085 scan no 4286 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1658.6971
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0011
Matched b ions: b(7), b(8)-98, b(11)-98, b(13)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(13)-98++, y(13)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2166

SVSFGGIYNNK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSFGGIYNNK
Found in AT2G01980.1, SOS1 (SALT OVERLY SENSITIVE 1); sodium:hydrogen antiporter

Match to Query 1157: 1264.548290 from(633.281421,2+)
Elution from: 41.571 to 41.571 scan no 4192 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2165/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1264.5488
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 4.4e-006
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(8)-98, b(9), b(9)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)+, y(7), y(8), y(9)-98++, y(9), y(9)+, y(10)-98, y(10)-98++
Precursor origin neutral loss: +**

**Peptide No.2167**

SVSHKFEDLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSHKFEDLR
Found in AT4G36760.1, ATAP1 (aminopeptidase P1)

Match to Query 1801: 1296.586000 from(649.300276,2+)
Elution from: 25.754 to 25.754 scan no 2081 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1296.5863
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.018
Matched b ions: b(5)-98, b(5), b(7), b(8)-98, b(8)
Matched y ions: y(2), y(5), y(6), y(7)+, y(7), y(8), y(8)-98++, y(8)+, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2168

SVSMDSCFMGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSMDSCFMGK
Found in AT2G21230.1, bZIP family transcription factor

Match to Query 1664: 1327.464038 from(664.739295,2+)
Elution from: 41.298 to 41.298 scan no 4136 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1327.4648
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 84 Expect: 8.8e-009
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(7)-98, b(8)-98, b(9)-98, b(9)-98++, b(9), b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)-98++, y(9)++, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2169
SVSPGLCYR
Confirmed sites: "@S:1,@S:3"
Ambiguous sites:

MS/MS Fragmentation of SVSPGLCYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1205: 1197.428544 from(599.721548,2+)
Elution from: 35.569 to 35.569 scan no 3174 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2168/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1197.4290
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00013
Matched b ions: b(2), b(3)-98, b(3)-196, b(3), b(4)-196, b(5), b(5)-98, b(6)-98, b(6), b(6)-196, b(7), b(7)-98, b(8), b(8)-98, b(8)+
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)+, y(7)+, y(7)-98, y(7), y(7)-98++, y(8)-98++, y(8)-98, y(8)+
Precursor origin neutral loss: 

---

Peptide No.2170

SVSPGLCYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSPGLCYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 933: 1117.462618 from(559.738585,2+)
Elution from: 31.741 to 31.741 scan no 2772 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1117.4627  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 65 Expect: 1.1e-006  
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8)  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98++, y(7)-98, y(7), y(7)+, y(8)-98++, y(8)-98  
Precursor origin neutral loss: +

---

**Peptide No. 2171**

**SVSPSPQMAVPDVFK**

Confirmed sites: @S:3  
Ambiguous sites:

**MS/MS Fragmentation of SVSPSPQMAVPDVFK**

Found in **AT5G58950.1**, protein kinase family protein

Match to Query 2461: 1667.763044 from(834.888798,2+)

Elution from: 53.772 to 53.772 scan no 5740 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2170/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1667.7630
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0017
Matched b ions: b(5)++, b(6)-98++, b(9)-98, b(10)-98, b(10), b(13)-98
Matched y ions: y(5), y(6), y(8), y(10), y(10)+, y(11), y(12), y(12)+, y(13)-98++, y(13)+, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.2172
SVSSGNLSSMDMVEHK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSSGNLSSMDMVEHK
Found in AT4G27900.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G53420.1); similar to CCT [Medicago trun]

Match to Query 3022: 1786.724950 from(894.369751,2+)
Elution from: 38.993 to 38.993 scan no 3633 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2171/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1786.7266
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.7e-007
Matched b ions: b(3)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(14)++, b(14), b(14)-98, b(15)-98, b(15)-98++
Matched y ions: y(4)++, y(5), y(6), y(8), y(9), y(10), y(11), y(13), y(13)++, y(14)-98++, y(14)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2173
SVSSPFMNTASK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSSPFMNTASK
Found in AT1G77760.1, NIA1 (NITRATE REDUCTASE 1)

Match to Query 1419: 1334.557068 from(668.285810,2+)
Elution from: 36.000 to 36.000 scan no 3455 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2172/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1334.5577
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 1e-008
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)+, b(6)-98, b(7)-98, b(8)-98, b(8), b(10)-98, b(10)-98++, b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9), y(10)-98++, y(10)-98, y(10), y(10)+, y(11)-98, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2174
SVSSPFMNTASK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of SVSSPFMNTASK
Found in AT1G77760.1, NIA1 (NITRATE REDUCTASE 1)
Match to Query 1477: 1350.551578 from(676.283065,2+)
Elution from: 30.799 to 30.799 scan no 2718 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1350.5526
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 51 Expect: 3.8e-005
Matched b ions: b(3), b(4)-98, b(6)+, b(7)-98, b(10)-98, b(10)-98++, b(11)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8)+, y(8), y(9), y(10)-98++, y(10)-98, y(10)+, y(11)-98, y(11)-98++
Precursor origin neutral loss: +

---

Peptide No.2175

SVSSPFMNTASK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SVSSPFMNTASK
Found in AT1G77760.1, NIA1 (NITRATE REDUCTASE 1)

Match to Query 1748: 1350.552244 from(676.283398,2+)
Elution from: 31.339 to 31.339 scan no 2718 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1350.5526
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 Expect: 0.022
Matched b ions: b(3), b(4)-98, b(6)+, b(7)-98
Matched y ions: y(5), y(7), y(8), y(8)+, y(9), y(9)-98, y(10)-98++, y(10), y(10)+, y(11)-98, y (11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.2176

SVSTPFMNTTAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSTPFMNTTAK
Found in AT1G37130.1, NIA2 (NITRATE REDUCTASE 2)

Match to Query 2032: 1362.588504 from(682.301528,2+)
Elution from: 38.562 to 38.562 scan no 3812 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1362.5890
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.6e-007
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(7)-98, b(8)-98, b(9), b(9)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9), y(10)-98++, y(10)-98, y(10), y(10)+, y(11)-98, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2177
SVSTPFMNTTAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSTPFMNTTAK
Found in AT1G37130.1, NIA2 (NITRATE REDUCTASE 2)

Match to Query 1560: 1378.583196 from(690.298874,2+)
Elution from: 30.576 to 30.576 scan no 2725 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1378.5840  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 64 Expect: 2.6e-006  
Matched b ions: b(3), b(b)-98, b(b)-98, b(4), b(5)-98, b(7)-98, b(8)-98, b(9)-98, b(9), b(11)-98, b(11)  
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(8)+, y(9), y(9)+, y(10), y(10)-98++, y(10)+, y(10)-98, y(11)-98, y(11)-98++, y(11)+  
Precursor origin neutral loss: +  

Peptide No.2178  
SVSVDSCFMEK  
Confirmed sites: @S:3  
Ambiguous sites:  
MS/MS Fragmentation of SVSVDSCFMEK  
Found in AT4G38900.1, bZIP protein  

Match to Query 1530: 1367.513324 from(684.763938,2+)  
Elution from: 40.585 to 40.585 scan no 4028 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1367.5138
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 7.1e-005
Matched b ions: b(3)-98, b(4)-98, b(5), b(5)-98, b(5)+, b(6), b(6)-98, b(7)+, b(7)-98++, b(8)-98, b(8), b(9)-98, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(5)+, y(6), y(6)+, y(7), y(8), y(9)-98++, y(9), y(9)-98, y(9)+, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No. 2179

SVTDDELEELK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SVTDDELEELK
Found in AT4G33985.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G15590.2); similar to Os04g0282200 [Oryz]

Match to Query 1275: 1356.568994 from(679.291773,2+)
Elution from: 41.424 to 41.424 scan no 3967 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2178/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1356.5697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 2.2e-006
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98++, b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98
Matched y ions: y(2), y(3), y(4)+++, y(4), y(5), y(6), y(7), y(8), y(9), y(9)+
Precursor origin neutral loss: +

Peptide No.2180
SVVELTNGSSEDGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SVVELTNGSSEDGR
Found in AT1G54080.1, UB1A; mRNA 3'-UTR binding

Match to Query 1645: 1528.638898 from(765.326725,2+)
Elution from: 31.447 to 31.447 scan no 2682 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1528.6406  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 47 Expect: 9.4e-005  
Matched b ions: b(5), b(7), b(8), b(10)++  
Matched y ions: y(2), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9), y(10), y(11), y(12)++, y(13)-98++  
Precursor origin neutral loss:  

---  

Peptide No.2181  
SVVELTSGVSEDK  
Confirmed sites: @S:10  
Ambiguous sites:  

MS/MS Fragmentation of SVVELTSGVSEDK  
Found in AT1G17370.1, UBP1B (OLIGOURIDYLATE BINDING PROTEIN 1B); mRNA 3'-UTR binding  

Match to Query 1814: 1485.659664 from(743.837108,2+)  
Elution from: 35.875 to 35.875 scan no 3434 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1485.6599
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.006
Matched b ions: b(5), b(6), b(7), b(9), b(10)-98
Matched y ions: y(5), y(5)-98, y(6), y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)+, y(12)-98, y(12)-98++, y(12)+, y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.2182
SVVELTTGSSEDGK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of SVVELTTGSSEDGK
Found in AT3G14100.1, oligouridylate-binding protein, putative

Match to Query 2112: 1487.638538 from(744.826545,2+)
Elution from: 33.079 to 33.079 scan no 2839 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1487.6392
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.1e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)+, b(11), b(11)-98++, b(11)-98, b(12), b(12)+, b(12)-98++, b(13)
Matched y ions: y(3), y(4), y(5), y(6)-98, y(7), y(7)-98, y(8), y(9), y(10), y(10)+, y(11), y(12), y(12)+, y(12)-98, y(13)-98++
Precursor origin neutral loss:

Peptide No.2183
SVVFLCFGSMGGFSEEQVR
Confirmed sites: "@S:1,@S:9,@S:14"
Ambiguous sites:

MS/MS Fragmentation of SVVFLCFGSMGGFSEEQVR
Found in AT3G21780.1, UGT71B6 (UDP-glucosyl transferase 71B6); UDP-glucosyltransferase/ abscisic acid glucosyltransferase

Match to Query 4264: 2374.877418 from(792.633082,3+)
Elution from: 29.815 to 29.815 scan no 2679 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2182/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2374.8805
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0059
Matched b ions: b(4), b(5)++, b(6)++, b(8)++, b(9)++, b(10)-196, b(11)-98++, b(12)+, b(13)-98++, b(13)+, b(14)+, b(14)-196++, b(15)-98++, b(15)+, b(16)+, b(16)-98++, b(18)+
Matched y ions: y(6)-98, y(9)-98++, y(11)+, y(12)-196++, y(12)+
Precursor origin neutral loss:

Peptide No.2184

SVVSGDLGALQSPQK
Confirmed sites: @S:13
Ambiguous sites: @S:1orS:4

MS/MS Fragmentation of SVVSGDLGALQSPQK
Found in AT1G22060.1, similar to F-box family protein [Arabidopsis thaliana] (TAIR: AT1G22000.1); similar to putative myos

Match to Query 3036: 1731.746386 from(866.880469,2+)
Elution from: 48.128 to 48.128 scan no 5036 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1731.7481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00095
Matched b ions: b(6), b(7), b(7)-98, b(8)-98, b(8), b(10), b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-196
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y(12)+
Precursor origin neutral loss: +

Peptide No.2185

SVVSGDLSGLAQSPQK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of SVVSGDLSGLAQSPQK
Found in AT1G22060.1, similar to F-box family protein [Arabidopsis thaliana] (TAIR: AT1G22000.1); similar to putative myos

Match to Query 2333: 1651.780040 from(826.897296,2+)
Elution from: 40.074 to 40.074 scan no 3995 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2184/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1651.7818
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 4.3e-008
Matched b ions: b(4), b(8)++, b(8), b(10), b(11), b(12), b(13)++, b(13)-98, b(13), b(14)-98+, b(14)-98
Matched y ions: y(3), y(4), y(4)-98, y(5), y(6)-98, y(8), y(9), y(9)-98, y(10), y(11), y(12)+, y(12)-98, y(12), y(13), y(13)+, y(14)+, y(14)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2186

SVVSGDLGGLAQSPQK
Confirmed sites: "@S:4,@S:13"
Ambiguous sites:

MS/MS Fragmentation of SVVSGDLGGLAQSPQK
Found in AT1G22060.1, similar to F-box family protein [Arabidopsis thaliana] (TAIR: AT1G22000.1); similar to putative myos

Match to Query 3147: 1731.747372 from(866.880962,2+)
Elution from: 46.950 to 46.950 scan no 4928 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1731.7481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.064
Matched b ions: b(7)-98, b(7), b(10), b(10)-98, b(12)
Matched y ions: y(3), y(6)-98, y(6), y(8), y(9), y(9)-98, y(12)+, y(12), y(13)+, y(14)+, y(14)-98++, y(15)-98++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.2187

SWDNVDLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SWDNVDLK
Found in AT1G76720.1, translation initiation factor

Match to Query 598: 1055.431804 from(528.723178,2+)
Elution from: 39.717 to 39.717 scan no 3947 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2186/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1055.4325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0004
Matched b ions: b(2)-98, b(2), b(3), b(4), b(4)-98, b(5), b(5)-98, b(6)-98, b(7)-98, b(7)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)+
Precursor origin neutral loss: +

Peptide No.2188

SWEGNLDIR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SWEGNLDIR
Found in AT1G08760.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G13370.1); similar to Os09g0516700 [Oryz]

Match to Query 875: 1168.489856 from(585.252204,2+)
Elution from: 43.940 to 43.940 scan no 4502 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2187/2597) [2008/03/14 15:08:29]
Mascot Search Results: Peptide View

Monoisotopic mass of neutral peptide Mr(calc): 1168.4914
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00019
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4), b(5), b(6), b(7), b(7)-98, b(7)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)
Precursor origin neutral loss: +

Peptide No.2189

SWGITDPELQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SWGITDPELQR
Found in AT5G11970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G19460.1); similar to hypothetical prote

Match to Query 1888: 1380.607276 from(691.310914,2+)
Elution from: 48.772 to 48.772 scan no 5122 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea list.htm (2188/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1380.6075
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 1.6e-005
Matched b ions: b(2)-98, b(2), b(3), b(3)-98, b(4), b(4)-98, b(5), b(5)+, b(5)-98, b(6)-98, b(6), b(7)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)+
Precursor origin neutral loss: +

Peptide No.2190

SWGTVDLNLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SWGTVDLNLK
Found in AT1G76810.1, eukaryotic translation initiation factor 2 family protein / eIF-2 family protein

Match to Query 1026: 1211.558122 from(606.786337,2+)
Elution from: 51.746 to 51.746 scan no 5452 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2189/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1211.5587
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 2.2e-005
Matched b ions: b(2)-98, b(2), b(3)-98, b(3), b(4)+, b(4), b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9)+
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9)+
Precursor origin neutral loss: +

Peptide No.2191

SWGTVDLNLK
Confirmed sites: "@S:1,@T:4"
Ambiguous sites:

MS/MS Fragmentation of SWGTVDLNLK
Found in AT1G76810.1, eukaryotic translation initiation factor 2 family protein / eIF-2 family protein

Match to Query 1855: 1291.524138 from(646.769345,2+)
Elution from: 55.524 to 55.524 scan no 5904 polarity:+

file:///C/|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2190/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1291.5250
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0033
Matched b ions: b(4)-98, b(4), b(5)-196, b(5), b(5)-98, b(6)-196, b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.2192

SWSFGTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SWSFGTR
Found in AT4G23530.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G11300.1); similar to Protein of unknown

Match to Query 488: 919.359098 from(460.686825,2+)
Elution from: 40.667 to 40.667 scan no 4100 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 919.3589  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 19 Expect: 0.044  
Matched b ions: b(2), b(4)-98++, b(4)-98, b(5)-98++, b(6)-98  
Matched y ions: y(3), y(4), y(5)-98, y(5), y(5)-98++, y(6)+  
Precursor origin neutral loss: +

Peptide No.2193  

SWSHSSHASDVDSEDK  
Confirmed sites: @S:1  
Ambiguous sites: 

MS/MS Fragmentation of SWSHSSHASDVDSEDK  
Found in AT1G73200.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G17820.1); similar to unknown protein [O  

Match to Query 3322: 1852.689682 from(927.352117,2+)  
Elution from: 20.064 to 20.064 scan no 1336 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2192/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1852.6901
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.4e-005
Matched b ions: b(3)-98, b(7), b(10), b(10)-98, b(12), b(14)-98, b(15)-98++, b(15)++
Matched y ions: y(4), y(5), y(6), y(9), y(10), y(11), y(12), y(13)++, y(13), y(14)++
Precursor origin neutral loss: +

Peptide No.2194

SWSSSHASDVDSEDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SWSHSSHASDVDSEDK
Found in AT1G73200.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G17820.1); similar to unknown protein [O

Match to Query 2658: 1852.688168 from(927.351360,2+)
Elution from: 20.261 to 20.261 scan no 1304 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2193/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1852.6901
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0001
Matched b ions: b(7)-98, b(9), b(10), b(11), b(11)-98, b(12)-98, b(12), b(14), b(14)-98++, b(15)+++, b(15)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(11), y(12), y(13)++, y(13), y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.2195

SWSHSSHASDVDSEDK
Confirmed sites:
Ambiguous sites: @S:5

MS/MS Fragmentation of SWSHSSHASDVDSEDK
Found in AT1G73200.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G17820.1); similar to unknown protein [O

Match to Query 3321: 1852.688700 from(618.570176,3+)
Elution from: 20.049 to 20.049 scan no 1334 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2194/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1852.6901
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00073
Matched b ions: b(2), b(5)-98, b(7)-98, b(7)-98++, b(7)+, b(8)-98++, b(8)+, b(9)-98++, b(10)-98++, b(10)+, b(11)-98++, b(11)+, b(12)+, b(12)-98++, b(14)-98++, b(14)+, b(15)-98++, b(15)+
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10)+, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2196

SWSHSSHASDVDSDEKD
Confirmed sites: @S:6
Ambiguous sites: 

MS/MS Fragmentation of SWSHSSHASDVDSDEKD
Found in AT1G73200.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G17820.1); similar to unknown protein [O

Match to Query 2365: 1852.688145 from(618.569991,3+)
Elution from: 20.412 to 20.412 scan no 1282 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2195/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1852.6901
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00017
Matched b ions: b(5), b(7)-98++, b(7)-98, b(8)-98++, b(8)+, b(9)-98++, b(9)+, b(10)-98++, b(12)+, b(12)-98++, b(13)+, b(14)+, b(15)+, b(15)-98++
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(9), y(11)-98++, y(13)-98++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.2197
SYESDDEEPRK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SYESDDEEPRK
Found in AT2G07360.1, SH3 domain-containing protein

Match to Query 1618: 1433.533296 from(717.773924,2+)
Elution from: 17.894 to 17.894 scan no 995 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2196/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1433.5347
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 36 Expect: 0.001
Matched b ions: b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)-98++
Precursor origin neutral loss: +

Peptide No.2198

SYGDMTEMGGGGGGGR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SYGDMTEMGGGGGGGR
Found in AT2G25430.1, epsin N-terminal homology (ENTH) domain-containing protein

Match to Query 2608: 1624.563712 from(813.289132,2+)
Elution from: 33.424 to 33.424 scan no 2999 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1624.5646
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 Expect: 1.6e-08
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(14)-98++, b(15)-98, b(15)-98++, b(15)+
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)+, y(15)+, y(16) +
Precursor origin neutral loss: +

Peptide No.2199

SYGDMTEMGGGGGGGGR
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of SYGDMTEMGGGGGGGGR
Found in AT2G25430.1, epsin N-terminal homology (ENTH) domain-containing protein

Match to Query 2399: 1640.557734 from(821.286143,2+)
Elution from: 24.806 to 24.806 scan no 1907 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2198/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1640.5595
Fixed modifications: Carboxymethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 75 Expect: 8.1e-008
Matched b ions: b(4)-98, b(5)-98, b(7)-98, b(8)-98, b(9)-98, b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(15)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15)+
Precursor origin neutral loss: +

Peptide No.2200
SYGDMTEMGGGGGGGGGRDEK
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SYGDMTEMGGGGGGGGGRDEK
Found in AT2G25430.1, epsin N-terminal homology (ENTH) domain-containing protein
Match to Query 3406: 1996.727748 from(666.583192,3+)
Elution from: 28.387 to 28.387 scan no 2427 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1996.7291
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 1.1e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(8)-98, b(13)++, b(15)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(6)++, y(8)++, y(11)++, y(12)++, y(12), y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.2201
SYGDMTEMGGGGGGGRDEK
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of SYGDMTEMGGGGGGGRDEK
Found in AT2G25430.1, epsin N-terminal homology (ENTH) domain-containing protein

Match to Query 3011: 1996.728051 from(666.583293,3+)
Elution from: 28.382 to 28.382 scan no 2388 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1996.7291
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
Ions Score: 63 Expect: 2e-006
Matched b ions: b(2), b(3), b(4), b(5)
Matched y ions: y(6)+, y(7)+, y(8)+, y(11)+, y(12)+, y(13)+, y(14)+, y(15)+, y(16)+, y(17)+, y(18)+
Precursor origin neutral loss: +

Peptide No.2202
SYGSMDSLEPSK
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of SYGSMDSLEPSK
Found in AT5G14540.1, proline-rich family protein

Match to Query 1837: 1379.529280 from(690.771916,2+)
Elution from: 36.315 to 36.315 scan no 3386 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1379.5316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0045
Matched b ions: b(2), b(5)-98, b(6)-98, b(6), b(7)-98, b(8)+, b(8)-98, b(9)-98, b(9)
Matched y ions: y(3), y(4), y(6)+, y(6), y(7), y(8), y(10)
Precursor origin neutral loss: +

Peptide No.2203

SYGSMDSLEPSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SYGSMDSLEPSK
Found in AT5G14540.1, proline-rich family protein

Match to Query 1333: 1379.530470 from(690.772511,2+)
Elution from: 36.309 to 36.309 scan no 3339 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1379.5316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 6e-007
Matched b ions: b(5)-98, b(6)-98, b(8)++, b(8)-98, b(9)-98, b(9), b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.2204
SYGSMDSLEPSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SYGSMDSLEPSK
Found in AT5G14540.1, proline-rich family protein
Match to Query 1461: 1395.525044 from(698.769798,2+)
Elution from: 26.447 to 26.447 scan no 2119 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...v3/o0705103ppmGROUPmeadlist.htm (2203/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1395.5265
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 Expect: 0.0087
Matched b ions: b(5)-98, b(6)+, b(8)-98, b(9)-98, b(10)-98
Matched y ions: y(3), y(4), y(6)+, y(6), y(8)+, y(10)-98+
Precursor origin neutral loss: +

Peptide No.2205
SYGSMDSLEPSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SYGSMDSLEPSK
Found in AT5G14540.1, proline-rich family protein

Match to Query 1307: 1379.531006 from(690.772779,2+)
Elution from: 35.147 to 35.147 scan no 3287 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1379.5316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00012
Matched b ions: b(2), b(6), b(8)-98, b(9)-98, b(9), b(10)+, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(8)-98, y(10)-98++, y(10)-98, y(10)
Precursor origin neutral loss: +

Peptide No.2206

SYNSSSSSSSSSSSSRSDDLKLNGEHLK
Confirmed sites:
Ambiguous sites: "@S:1orY:2, @S:4orS:5orS:6, @S:5orS:6"

MS/MS Fragmentation of SYNSSSSSSSSSSSSRSDDLKLNGEHLK
Found in AT3G28770.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G76780.1); contains InterPro domain Prot

Match to Query 4752: 3144.236673 from(1049.086167,3+)
Elution from: 28.823 to 28.823 scan no 2543 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3144.2322
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.057
Matched b ions: b(6)-98, b(6), b(7)-196, b(8)+, b(8)-98, b(9)-294, b(11), b(13)-98, b(13)-294, b(15)-196++, b(16)+, b(17)-98++, b(18)-98++, b(18)+, b(19)-196++, b(19)-98++, b(21)-294++, b(24)+, b(24)-294++, b(24)-98++, b(27)+, b(27)-98++, b(27)-294++
Matched y ions: y(7)+, y(11), y(13)+, y(15)+, y(16)+, y(19)+, y(22)+, y(25)-196++, y(25)-98++, y(26)-196++, y(26)-98++
Precursor origin neutral loss: +

Peptide No.2207
SYSGSLYR
Confirmed sites: @5:3
Ambiguous sites:
MS/MS Fragmentation of SYSGSLYR
Found in AT5G14720.1, protein kinase family protein
Match to Query 753: 1011.405106 from(506.709829,2+)
Elution from: 29.361 to 29.361 scan no 2590 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1011.4062
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.033
Matched b ions: b(2), b(3), b(4)-98, b(5)+, b(5)-98, b(6)+, b(6)-98, b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)-98++, y(7)+
Precursor origin neutral loss: +

Peptide No.2208

SYSGSLYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SYSGSLYR
Found in AT5G14720.1, protein kinase family protein

Match to Query 503: 1011.406194 from(506.710373,2+)
Elution from: 29.320 to 29.320 scan no 2517 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1011.4062
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(Shown in table), 0.0000
Ions Score: 19 Expect: 0.056
Matched b ions: b(2), b(3), b(5)++, b(6)++, b(6)-98, b(6)
Matched y ions: y(1), y(2), y(3), y(5)++, y(5)-98, y(5), y(6)-98++, y(6)-98, y(6), y(7)++
Precursor origin neutral loss: +

Peptide No.2209
SYSHDHTGNLTLNR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of SYSHDHTGNLTLNR
Found in AT5G10270.1, CDKC1 (CYCLIN-DEPENDENT KINASE C;1); kinase

Match to Query 2187: 1580.635518 from(527.885782,3+)
Elution from: 17.261 to 17.261 scan no 942 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1580.6369  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:   
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 40 Expect: 0.0007  
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)+, b(7)+, b(8)+, b(9)+, b(10)+, b(11)-98++, b(12)-98++  
Matched y ions: y(2), y(3)-98, y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)+, y(7)-98, y(7)-98++, y(8)-98, y(8)+, y(8)-98++, y(9)-98++, y(9)+, y(10)-98++, y(10)+, y(11)-98++, y(11)+, y(12)-98++  
Precursor origin neutral loss: +  

Peptide No.2210  
SYSPGYEGAAAAAPDR  
Confirmed sites:  
Ambiguous sites: @S:1 or Y:2 or S:3  

MS/MS Fragmentation of SYSPGYEGAAAAAPDR  
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding  

Match to Query 2963: 1661.670874 from(831.842713,2+)  
Elution from: 31.121 to 31.121 scan no 2858 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2209/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1661.6722
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00019
Matched b ions: b(3), b(6), b(7)-98, b(9)-98, b(10), b(11)-98, b(12)-98, b(13), b(13)-98, b(15)++
Matched y ions: y(3), y(4), y(5), y(5)+, y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(13)+
Precursor origin neutral loss: +

Peptide No.2211

SYSPGYEGAAAAAPDR
Confirmed sites: @S:1
Ambiguous sites: @Y:2orS:3

MS/MS Fragmentation of SYSPGYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2869: 1741.638200 from(871.826376,2+)
Elution from: 34.461 to 34.461 scan no 3313 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1741.6385  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Y2 : Phospho (Y)  
Ions Score: 62 Expect: 2.6e-006  
Matched b ions: b(3)-98, b(6), b(7)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14)-98  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)+, y(10), y(13)+, y(13), y(15)+  
Precursor origin neutral loss: +

---

**Peptide No.2212**

**SYSPGYEGAAAAAPDR**  
Confirmed sites:  
Ambiguous sites: "@S:1orY:2, @S:3orY:6"

**MS/MS Fragmentation of SYSPGYEGAAAAAPDR**  
Found in **AT3G55460.1**, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3079: 1741.638022 from(871.826287,2+)  
Elution from: 35.307 to 35.307 scan no 3358 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1741.6385  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Y6 : Phospho (Y)  
Ions Score: 62 Expect: 2.7e-006  
Matched b ions: b(6)-98, b(6), b(7)+++, b(7)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(11), b(11)+++, b(12)-98, b(12), b(13)-98, b(13)  
Matched y ions: y(3), y(4), y(5), y(6)+++, y(7), y(8), y(9), y(9)+++, y(10), y(14), y(14)++  
Precursor origin neutral loss: +

Peptide No.2213

SYSPGYEGAAAAAPDR  
Confirmed sites: @S:3  
Ambiguous sites:

MS/MS Fragmentation of SYSPGYEGAAAAAPDR  
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2505: 1661.669758 from(831.842155,2+)  
Elution from: 31.152 to 31.152 scan no 2799 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1661.6722
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 5.9e-006
Matched b ions: b(2), b(3), b(4)-98, b(6)-98, b(6), b(7), b(7)-98, b(9)-98, b(9)-98++, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)+, y(13), y(14)-98++, y(14), y(14)+, y(14)-98, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2214

SYSPGYEGAAAAAPDR
Confirmed sites: @S:3
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of SYSPGYEGAAAAAPDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2671: 1741.638160 from(871.826356,2+)
Elution from: 35.372 to 35.372 scan no 3324 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2213/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1741.6385
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 4.8e-009
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(7)+, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(13)-98++, b(14)-98, b(15)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)+, y(9), y(10), y(11), y(13)+, y(13), y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2215
SYSPGYEAAAAAPDRDR
Confirmed sites: @S:1
Ambiguous sites:
MS/MS Fragmentation of SYSPGYEAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3288: 1932.798920 from(967.406736,2+)
Elution from: 28.652 to 28.652 scan no 2459 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1932.8003
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00068
Matched b ions: b(7)-98, b(9)-98, b(12)-98, b(13)-98, b(14)-98, b(15), b(17)-98, b(17)
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9)+, y(11), y(11)+, y(12), y(13)+, y(14)+, y(15)+, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.2216
SYSPGYEGAAAAAPDRDR
Confirmed sites: "@S:1,@S:3"
Ambiguous sites:

MS/MS Fragmentation of SYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3692: 2012.765016 from(671.928948,3+)
Elution from: 32.355 to 32.355 scan no 2948 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2215/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2012.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.4e-005
Matched b ions: b(2)-98, b(2), b(3)-196, b(3)-98, b(3), b(5), b(6), b(6)-98, b(7)-98, b(8)-196+ +, b(9)++, b(12)++, b(13)-196++, b(15)++, b(17)-98++
Matched y ions: y(4), y(5)++, y(6)++, y(7)++, y(8)++, y(8), y(10)++, y(11)++, y(12)++, y(13) +++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.2217
SYSPGYEGAAAAAPDRDR
Confirmed sites: "@S:1,@Y:2"
Ambiguous sites:

MS/MS Fragmentation of SYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3743: 2012.763840 from(1007.389196,2+)
Elution from: 31.248 to 31.248 scan no 2852 polarity:+

file://C/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2216/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2012.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y2 : Phospho (Y)
Ions Score: 65 Expect: 1.9e-006
Matched b ions: b(6)-98, b(7)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(15), b(15)+, b(17)-98, b(17), b(17)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(11), y(11)+, y(12)+, y(12), y(13)+, y(14)+, y(15)+, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.2218
SYSPGYEGAAAAAPDRDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SYSPGYEGAAAAAPDRDR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2543: 1932.800502 from(645.274110,3+)
Elution from: 28.561 to 28.561 scan no 2423 polarity:+

file://C:\Documents%20and%20Settings\N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2217/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1932.8003  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 55 Expect: 2.7e-005  
Matched b ions: b(2), b(3), b(3)-98, b(9)-98++, b(15)+, b(15)-98++  
Matched y ions: y(3)+, y(4), y(5)+, y(10)+, y(11)+, y(12)+, y(13)+, y(14)+, y(15)+, y(16)+, y(16)-98++, y(17)+  
Precursor origin neutral loss: +

Peptide No.2219

SYSPGYEAAAAPDRDR  
Confirmed sites: @S:3  
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of SYSPGYEAAAAPDRDR  
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 3734: 2012.763848 from(1007.389200,2+)  
Elution from: 31.303 to 31.303 scan no 2883 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2218/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2012.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 3.6e-007
Matched b ions: b(6)-98, b(7), b(7)-98, b(9)+, b(9)-98, b(9), b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(15), b(15)-98, b(15)+, b(17)-98, b(17)
Matched y ions: y(5), y(6), y(7), y(9), y(11), y(11)+, y(12)+, y(12), y(13)+, y(14)+, y(15)+, y(16)-98++, y(16)+
Precursor origin neutral loss: +

Peptide No.2220

SYSRSPSPVYER
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of SYSRSPSPVYER
Found in AT3G06480.1, DEAD box RNA helicase, putative

Match to Query 1752: 1586.616684 from(794.315618,2+)
Elution from: 23.966 to 23.966 scan no 1812 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1586.6167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.03
Matched b ions: b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(7)-196, b(8)+++, b(8)-196, b(9)-98+++, b(9)-196, b(11)
Matched y ions: y(3), y(5), y(6), y(7), y(7)-98, y(8)-196, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.2221
SYSRSPSVYER
Confirmed sites: @S:7
Ambiguous sites: @S:1orY:2orS:3

MS/MS Fragmentation of SYSRSPSVYER
Found in AT3G06480.1, DEAD box RNA helicase, putative

Match to Query 2175: 1586.616944 from(794.315748,2+)
Elution from: 24.782 to 24.782 scan no 1906 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2220/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1586.6167
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2: Phospho (Y)
S7: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0052
Matched b ions: b(5), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(10)
Matched y ions: y(2), y(3), y(5), y(7)-98, y(7), y(8)-98
Precursor origin neutral loss: +

Peptide No.2222

SYTPSPPR
Confirmed sites: "@T:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of SYTPSPPR
Found in AT1G55310.1, SR33 (SC35-like splicing factor 33); RNA binding

Match to Query 624: 1063.376640 from(532.695596,2+)
Elution from: 27.383 to 27.383 scan no 2176 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1063.3777
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.035
Matched b ions: b(2), b(3), b(3)-98, b(5)-196++, b(5)-98, b(5)-196, b(6)-196
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98++, y(6), y(6)-98
Precursor origin neutral loss: +

Peptide No.2223
SYTPSPPRGYGR
Confirmed sites: "@T:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of SYTPSPPRGYGR
Found in AT3G13570.1, SCL30a (SC35-like splicing factor 30a); RNA binding

Match to Query 2417: 1496.583762 from(499.868530,3+)
Elution from: 31.037 to 31.037 scan no 2798 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2222/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1496.5850
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.043
Matched b ions: b(2), b(3), b(5)-196++, b(5)-98, b(7)++
Matched y ions: y(3)++, y(7), y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(10)+, y(10)-196++
Precursor origin neutral loss: +

Peptide No.2224
TADSDKEETEDAKPLPKK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of TADSDKEETEDAKPLPKK
Found in AT4G24270.1, RNA recognition motif (RRM)-containing protein

Match to Query 3214: 2080.954290 from(694.658706,3+)
Elution from: 18.159 to 18.159 scan no 1028 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...result_v3/o0705103ppmgROUPmeadlist.htm (2223/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2080.9565
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.027
Matched b ions: b(4)-98, b(6)-98, b(8), b(8)-98, b(10)-98, b(11)-98, b(11)--, b(12)-98, b(12)-98++, b(16)-98++, b(16)--, b(17)-98++
Matched y ions: y(2), y(5), y(7)--, y(10)--, y(13)--, y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2225
TAGESDHSDLEASVVK
Confirmed sites: "@S:5,@S:8"
Ambiguous sites:

MS/MS Fragmentation of TAGESDHSDLEASVVK
Found in AT1G32640.1, ATMYC2 (JASMONATE INSENSITIVE 1); DNA binding / transcription factor

Match to Query 2256: 1803.694294 from(902.854423,2+)
Elution from: 33.510 to 33.510 scan no 2977 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaslist.htm (2224/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1803.6965  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 33 Expect: 0.0031  
Matched b ions: b(8), b(8)-98, b(9)-98, b(9), b(9)-196++, b(10), b(11)-98, b(11), b(12)-98, b(13)-196++, b(13), b(13)-98++, b(14), b(14)-98, b(14)-98++, b(14)+, b(15)-98, b(15), b(15)-196++, b(15)-98++  
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)-98, y(12)-98++, y(12), y(13)+, y(13)-98++, y(14)-196++, y(14)+, y(14)-98++  
Precursor origin neutral loss: +

Peptide No.2226

TAGESDHSDLEASVVK  
Confirmed sites: @S:8  
Ambiguous sites: @T:1orS:5

MS/MS Fragmentation of TAGESDHSDLEASVVK  
Found in AT1G32640.1, ATMYC2 (JASMONATE INSENSITIVE 1); DNA binding / transcription factor  
Match to Query 2994: 1803.695396 from(902.854974,2+)

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2225/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1803.6965
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0053
Matched b ions: b(6), b(7)-98, b(7), b(8)-196, b(8)-98, b(8), b(9)-196++, b(9)-98, b(9)-196, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(12)-196, b(13)-196++, b(13)+, b(14)-98, b(14)-98++, b(15)-98, b(15)-196, b(15)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)
Precursor origin neutral loss: +

Peptide No.2227

TASAIGAPCAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASAIGAPCAR
Found in AT5G02430.1, WD-40 repeat family protein

Match to Query 849: 1153.493848 from(577.754200,2+)
Elution from: 23.615 to 23.615 scan no 1779 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0185103ppmGROUPmeadlist.htm (2226/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1153.4951
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0043
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(4), y(6), y(7), y(8)-98++
Precursor origin neutral loss: +

Peptide No.2228
TASLDQSTQDLHK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASLDQSTQDLHK
Found in AT1G03445.1, BSU1 (BRASSINOSTEROID INSENSITIVE 1 suppressor 1); protein serine/threonine phosphatase

Match to Query 2054: 1522.665060 from(762.339806,2+)
Elution from: 24.270 to 24.270 scan no 1867 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1522.6665
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 9.1e-007
Matched b ions: b(3), b(4)-98, b(5)+, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(9), b(9)-98, b(10)-98, b(12)-98, b(12), b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)+, y(11)-98++, y(11)-98, y(11)+, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2229
TASLDQSTQDLHK
Confirmed sites: @T:1orS:3

MS/MS Fragmentation of TASLDQSTQDLHK
Found in AT1G03445.1, BSU1 (BRASSINOSTEROID INSENSITIVE 1 suppressor 1); protein serine/threonine phosphatase

Match to Query 1846: 1522.666232 from(762.340392,2+)
Elution from: 23.823 to 23.823 scan no 1777 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2228/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1522.6665
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 6e-006
Matched b ions: b(4)-98, b(5)++, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(10)-98, b(11)-98, b (12), b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.2230

TDKFGINGSMDLR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of TDKFGINGSMDLR
Found in AT1G79040.1, PSBR (photosystem II subunit R)

Match to Query 2391: 1629.720630 from(544.247486,3+)
Elution from: 43.294 to 43.294 scan no 4422 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1629.7222
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0074
Matched b ions: b(3), b(6), b(7), b(7)+, b(8)++, b(8), b(10)-98++, b(12)+
Matched y ions: y(2), y(3), y(5), y(6)-98++, y(6)++, y(6), y(7)+, y(7)-98++, y(8)+, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.2231

TDLAFR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TDLAFR
Found in AT2G40860.1, protein kinase family protein / protein phosphatase 2C ( PP2C) family protein

Match to Query 244: 801.341492 from(401.678022,2+)
Elution from: 28.789 to 28.789 scan no 2512 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 801.3422
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.028
Matched b ions: b(4)-98
Matched y ions: y(1), y(2), y(3), y(4)
Precursor origin neutral loss:

**Peptide No.2232**

**TDPIGLDNLSMDGESDPVYK**

Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **TDPIGLDNLSMDGESDPVYK**
Found in **AT4G30890.1**, UBP24 (UBIQUITIN-SPECIFIC PROTEASE 24); ubiquitin-specific protease

Match to Query 4212: 2347.972348 from(1174.993450,2+)
Elution from: 49.988 to 49.988 scan no 5251 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2347.9767
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 3.9e-008
Matched b ions: b(6), b(9), b(12)-98++, b(12), b(13), b(13)-98, b(14)-98++, b(14)-98, b(15)-98, b(15), b(16), b(17), b(17)-98, b(18)-98
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(13), y(14), y(15), y(15)-98, y(17), y(17)+, y(17)-98, y(18)+, y(19)+, y(19)-98++
Precursor origin neutral loss: +

Peptide No.2233

TDPIGLDNSMDSGESDPVYK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of TDPIGLDNSMDSGESDPVYK
Found in AT4G30890.1, UBP24 (UBIQUITIN-SPECIFIC PROTEASE 24); ubiquitin-specific protease

Match to Query 4265: 2331.977550 from(1166.996051,2+)
Elution from: 55.198 to 55.198 scan no 5903 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2331.9817
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 6.5e-09
Matched b ions: b(4), b(7), b(9), b(10), b(12)-98, b(13)-98, b(13), b(15), b(15)-98, b(16)-98, b(17), b(17)-98, b(18)-98, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10)-98, y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98, y(15), y(15)-98, y(16), y(16)-98++, y(17)-98++, y(17), y(17)-98, y(17)++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.2234

TDQAILSNSSDLGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of TDQAILSNSSDLGR
Found in AT1G22280.1, protein phosphatase 2C, putative / PP2C, putative

Match to Query 2329: 1555.686658 from(778.850605,2+)
Elution from: 36.143 to 36.143 scan no 3251 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi_v3/o0705103ppmGROUPmeadlist.htm (2233/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1555.6879
Fixed modifications: Carboxyl methylation (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 2.3e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)+
+ , b(12), b(12)-98, b(12)-98++, b(12)+, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(8)-98++, y
(9), y(9)-98, y(9)+, y(10), y(10)-98, y(11)-98, y(11), y(11)+, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2235

TDQAILSNSSDLGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TDQAILSNSSDLGR
Found in AT1G22280.1, protein phosphatase 2C, putative / PP2C, putative

Match to Query 2035: 1555.686822 from(778.850687,2+)
Elution from: 34.665 to 34.665 scan no 3271 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2234/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1555.6879
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 8.5e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)+, b(8), b(9), b(9)-98, b(10), b(10)-98, b(10)+
+, b(11), b(12), b(12)-98++, b(12)-98, b(13), b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(7)-98++, y(8), y(8)-98, y(8)-
98++, y(8)+++, y(9), y(9)-98, y(9)+++, y(10)-98, y(10), y(10)+, y(11), y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2236
TDVPSNVTLTSNGSPSETK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TDVPSNVTLTSNGSPSETK
Found in AT3G23540.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G14290.1); similar to expressed protein

Match to Query 3637: 2012.892092 from(1007.453322,2+)
Elution from: 35.025 to 35.025 scan no 3101 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2235/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2012.8939  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 80 Expect: 1.1e-007  
Matched b ions: b(6), b(7), b(8), b(9), b(11), b(12), b(14)-98, b(14)-98++, b(17)  
Matched y ions: y(5), y(7)-98, y(7), y(8)-98, y(8), y(9), y(10), y(10)-98, y(11), y(12), y(12)-98, y(13), y(13)-98, y(15)+, y(15), y(16)-98++, y(16)+, y(16), y(17)-98++, y(17)+  
Precursor origin neutral loss: +

Peptide No.2237

TEALAEDAVSGSDLSDK  
Confirmed sites: @S:10  
Ambiguous sites: 

MS/MS Fragmentation of TEALAEDAVSGSDLSDK  
Found in AT5G42870.1, lipin family protein  

Match to Query 2196: 1786.750240 from(894.382396,2+)  
Elution from: 37.088 to 37.088 scan no 3540 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1786.7509
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00093
Matched b ions: b(6), b(10)-98, b(13)-98++, b(14), b(15)++
Matched y ions: y(5), y(7), y(8)-98, y(10), y(11), y(12), y(13), y(15)++
Precursor origin neutral loss: +

Peptide No.2238

TENETEPRKNK
Confirmed sites: "@T:1,@T:5"
Ambiguous sites:

MS/MS Fragmentation of TENETEPRKNK
Found in AT2G25625.1, similar to Os05g0575000 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001056395.1)

Match to Query 1972: 1504.597036 from(753.305794,2+)
Elution from: 60.001 to 60.001 scan no 6394 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1504.5960
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0039
Matched b ions: b(3), b(4), b(5), b(5)-98, b(6), b(6)-98, b(9)++, b(10), b(10)-98++
Matched y ions: y(5), y(8)-98, y(8)++
Precursor origin neutral loss: +

Peptide No.2239
TENLQFQADSFQR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of TENLQFQADSFQR
Found in AT3G54300.1, ATVAMP727 (Arabidopsis thaliana vesicle-associated membrane protein 727)

Match to Query 2376: 1662.704544 from(832.359548,2+)
Elution from: 40.469 to 40.469 scan no 4047 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2238/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1662.7039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 29 Expect: 0.011
Matched b ions: b(5), b(6), b(7)
Matched y ions: y(3), y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(8)-98, y(8), y(9)+, y(10)+, y(10)-98++, y(11), y(11)+, y(11)-98++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2240
TESAIFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TESAIFR
Found in AT3G49370.1, calcium-dependent protein kinase, putative / CDPK, putative

Match to Query 461: 902.389206 from(452.201879,2+)
Elution from: 31.931 to 31.931 scan no 2945 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2239/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 902.3899
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00044
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(6)-98
Precursor origin neutral loss: +

Peptide No.2241

TESSDDEICEKEVQPEMR
Confirmed sites: "@S:3,@S:4"
Ambiguous sites:

MS/MS Fragmentation of TESSDDEICEKEVQPEMR
Found in AT5G63700.1, zinc finger (C3HC4 type RING finger) family protein

Match to Query 4030: 2356.843844 from(1179.429198,2+)
Elution from: 25.249 to 25.249 scan no 1967 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...v3/o0705103ppmGROUPmeadlist.htm (2240/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2356.8477
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.0005
Matched b ions: b(7), b(10)+++, b(10)-196, b(12)-196, b(16)++
Matched y ions: y(4), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(15)-98, y(15)+++, y(16)-98++,
y(17)-196++
Precursor origin neutral loss: +
Monoisotopic mass of neutral peptide Mr(calc): 1989.7800
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 7.1e-009
Matched b ions: b(6), b(7), b(8), b(9)-98, b(10), b(11), b(11)+, b(11)-98, b(12), b(13), b(13)-98, b(13)+, b(15)-98, b(16)+, b(17), b(17)-98+
Matched y ions: y(3), y(4), y(5), y(6), y(7)+, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)+, y(14), y(14)-98++, y(15)+, y(16), y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2243

TFGSSLNNSGPR
Confirmed sites: "@S:7,@S:10"
Ambiguous sites:

MS/MS Fragmentation of TFGSSLNNSGPR
Found in AT1G50120.1, similar to Os06g0618600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001058085.1); similar to E

Match to Query 2356: 1481.594278 from(741.804415,2+)
Elution from: 46.036 to 46.036 scan no 4786 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1481.5952
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.025
Matched b ions: b(3), b(9)-98, b(10)-98
Matched y ions: y(4), y(5)+++, y(5), y(5)-98, y(6), y(7)-98, y(7), y(7)-196, y(8), y(8)-98, y(8)++, y(9), y(9)-98++, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.2244
TFSSMASEHPFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TFSSMASEHPFK
Found in AT2G05710.1, aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative

Match to Query 2040: 1447.583114 from(724.798833,2+)
Elution from: 41.602 to 41.602 scan no 4089 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1447.5843
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 3.9e-006
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)++, b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(9), b(11)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)+, y(10)-98++, y(10)-98, y(10), y(10)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2245
TFSSMASEHPFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TFSSMASEHPFK
Found in AT2G05710.1, aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative

Match to Query 2317: 1463.578916 from(732.796734,2+)
Elution from: 30.757 to 30.757 scan no 2760 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1463.5792
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 Expect: 0.0096
Matched b ions: b(3)-98, b(6)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(9)+', y(9), y(10)-98++, y(10)+
Precursor origin neutral loss: +

Peptide No.2246
TFTHEVVTLLWYR
Confirmed sites:
Ambiguous sites: @T:1orT:3

MS/MS Fragmentation of TFTHEVVTLLWYR
Found in AT3G48750.1, CDC2/CDC2A/CDC2AAT/CDK2/CDK;1 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/

Match to Query 2884: 1630.750858 from(816.382705,2+)
Elution from: 56.971 to 56.971 scan no 6082 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2245/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1630.7545
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00078
Matched b ions: b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(9), b(10), b(10)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.2247
TFTHEVVTLWYR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of TFTHEVVTLWYR
Found in AT3G48750.1, CDC2/CDC2A/CDC2AAT/CDK2/CDKA1 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/

Match to Query 2883: 1630.752788 from(816.383670,2+)
Elution from: 57.061 to 57.061 scan no 6050 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1630.7545
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 2.9e-007
Matched b ions: b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(9), b(10)-98, b(10)-98++, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)+, y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.2248

TFTICGNADYLAPEIVQGK
Confirmed sites:
Ambiguous sites: @T:1orT:3

MS/MS Fragmentation of TFTICGNADYLAPEIVQGK
Found in AT2G20040.1, kinase

Match to Query 4240: 2175.987636 from(1089.001094,2+)
Elution from: 61.481 to 61.481 scan no 6500 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2247/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2175.9911  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 43 Expect: 0.00059  
Matched b ions: b(9), b(11)-98, b(12)-98, b(12), b(13)-98, b(14)+, b(15)-98, b(16), b(17)  
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(14), y(15), y(15)+  
Precursor origin neutral loss: +

Peptide No.2249
TGGLLSDSEK  
Confirmed sites: @S:6  
Ambiguous sites:

MS/MS Fragmentation of TGGLLSDSEK  
Found in AT5G25150.1, nucleotide binding  
Match to Query 591: 1085.463528 from(543.739040,2+)  
Elution from: 29.055 to 29.055 scan no 2478 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2248/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1085.4641
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0029
Matched b ions: b(3), b(4), b(5), b(6)-98, b(7)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.2250
TGGLLDSEK
Confirmed sites:
Ambiguous sites: @S:6orS:8

MS/MS Fragmentation of TGGLLDSEK
Found in AT5G25150.1, nucleotide binding

Match to Query 655: 1085.463258 from(543.738905,2+)
Elution from: 30.185 to 30.185 scan no 2549 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1085.4641
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.01
Matched b ions: b(2), b(3), b(4), b(5)
Matched y ions: y(5), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(8)+, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2251

TGLSIQDHTP
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of TGLSIQDHTP
Found in AT1G02880.1, thiamin pyrophosphokinase, putative

Match to Query 782: 1147.490094 from(574.752323,2+)
Elution from: 31.963 to 31.963 scan no 2871 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1147.4911  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 35 Expect: 0.0026  
Matched b ions: b(9)++, b(9)  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)++  
Precursor origin neutral loss: +

Peptide No.2252

**TGLSNLSSPLK**  
Confirmed sites: @S:8  
Ambiguous sites: 

MS/MS Fragmentation of **TGLSNLSSPLK**  
Found in **AT1G54450.1**, calcium-binding EF-hand family protein

Match to Query 974: 1195.583988 from(598.799270,2+)  
Elution from: 40.092 to 40.092 scan no 3963 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1195.5849
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.021
Matched b ions: b(10)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.2253
TGRSSESDDLFAEK
Confirmed sites:
Ambiguous sites: @S:4 or S:5

MS/MS Fragmentation of TGRSSESDDLFAEK
Found in AT3G28180.1, ATCSLC04 (Cellulose synthase-like C4); transferase, transferring glycosyl groups

Match to Query 2828: 1689.757792 from(845.886172,2+)
Elution from: 45.977 to 45.977 scan no 4759 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2252/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide \( M_r(\text{calc}) \): 1689.7610  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 61 Expect: 8e-006  
Matched b ions: b(3), b(5)-98, b(6)-98, b(8), b(8)-98, b(10)-98, b(10), b(11)-98, b(11), b(11)-98++, b(12)-98, b(12), b(12)+, b(13), b(14)-98, b(14)+  
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(12)-98, y(12), y(13)+, y(14)-98++  
Precursor origin neutral loss: +  

Peptide No.2254  
TGSFVRPISPK  
Confirmed sites: @S:9  
Ambiguous sites:  

MS/MS Fragmentation of TGSFVRPISPK  
Found in AT2G38280.1, FAC1 (EMBRYONIC FACTOR1); AMP deaminase  

Match to Query 1661: 1267.631580 from(423.551136,3+)  
Elution from: 29.468 to 29.468 scan no 2605 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2253/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1267.6325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0028
Matched b ions: b(2), b(9)-98++, b(9)+, b(10)-98++, b(10)+
Matched y ions: y(2), y(3), y(4)+, y(5)+++, y(5), y(6)+++, y(7)+++, y(7)-98++, y(8)+++, y(8)-98++, y(9)+++, y(9)-98++, y(10)+++, y(10)-98++
Precursor origin neutral loss:

Peptide No.2255

TGVSLSDEDSSNLSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TGVSLSDEDSSNLSR
Found in AT1G31460.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G23270.1); similar to hypothetical prote

Match to Query 2507: 1732.715680 from(867.365116,2+)
Elution from: 32.946 to 32.946 scan no 3062 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2254/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1732.7152
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.054
Matched b ions:
Matched y ions: y(7), y(8), y(9), y(10), y(12)-98
Precursor origin neutral loss: +

Peptide No.2256
TGSVLSDEDSSNLSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TGSVLSDEDSSNLSR
Found in AT1G31460.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G23270.1); similar to hypothetical prote

Match to Query 2888: 1732.715768 from(867.365160,2+)
Elution from: 33.508 to 33.508 scan no 2896 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1732.7152
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 1.2e-009
Matched b ions: b(4), b(7)-98, b(8)-98, b(8), b(9), b(10)-98, b(10), b(11), b(14), b(14)-98, b(15)-98++, b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(12), y(12)-98++, y(13)+, y(13)-98, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.2257

THQENSPIHNFPGDGNRS
Confirmed sites: @S:6
Ambiguous sites:
Monoisotopic mass of neutral peptide Mr(calc): 1988.8126
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00013
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(8), b(8)-98, b(9)+, b(9)-98++, b(10)-98++, b(10)+, b(10)-98++, b(11)-98++, b(11)+, b(12)+, b(13)+, b(13)-98++, b(16)-98+
Matched y ions: y(4), y(5), y(6), y(7), y(8)+, y(8), y(9)+, y(9), y(10)+, y(11)+, y(12)-98+, y(13)-98++, y(13)+, y(14)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2258

THSFLGNGIASPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of THSFLGNGIASPK
Found in AT2G16640.1, ATTOC132/TOC132 (MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); transmembrane r

Match to Query 1649: 1407.653638 from(704.834095,2+)
Elution from: 34.377 to 34.377 scan no 3237 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1407.6547  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S11: Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769  
Ions Score: 27 Expect: 0.016  
Matched b ions: b(2), b(3), b(4), b(5), b(9), b(10), b(11)-98  
Matched y ions: y(4), y(6)-98++, y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(11)+, y(11)-98, y(11), y(12)++  
Precursor origin neutral loss: +

Peptide No.2259

TIDSPGQEETGMGTGVSK  
Confirmed sites: @S:4  
Ambiguous sites: 

MS/MS Fragmentation of TIDSPGQEETGMGTGVSK  
Found in AT2G32080.1, PUR ALPHA-1 (purin-rich alpha 1); nucleic acid binding  

Match to Query 2947: 1815.758438 from(908.886495,2+)  
Elution from: 32.615 to 32.615 scan no 2963 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2258/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1815.7597
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 5.7e-06
Matched b ions: b(7)+, b(7)-98, b(7), b(8)-98, b(9)-98, b(10)-98, b(11), b(12)-98, b(12), b(13), b(15), b(15)-98++, b(15)+, b(16)-98++
Matched y ions: y(4), y(5), y(7), y(8)+, y(8), y(10), y(12), y(13)+, y(13), y(14), y(14)+, y(14)-98++, y(15), y(15)+, y(15)-98
Precursor origin neutral loss: +

Peptide No.2260
TIDSPGQETGMTGVSK
Confirmed sites: @S:4
Ambiguous sites:
MS/MS Fragmentation of TIDSPGQETGMTGVSK
Found in AT2G32080.1, PUR ALPHA-1 (purin-rich alpha 1); nucleic acid binding

Match to Query 2364: 1831.752766 from(916.883659,2+)
Elution from: 25.761 to 25.761 scan no 1934 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2259/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1831.7546
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 Expect: 0.057
Matched b ions: b(8)-98, b(9), b(9)-98
Matched y ions: y(6), y(7), y(8), y(13), y(13)++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2261
TIEKEISDDDEEEEEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TIEKEISDDDEEEEEK
Found in AT5G56030.1, HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding

Match to Query 2712: 1901.765294 from(951.889923,2+)
Elution from: 30.410 to 30.410 scan no 2641 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2260/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1901.7666
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 1.8e-007
Matched b ions: b(5), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13)-98++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11)+, y(12)-98++, y(12)-98, y(12)+, y(13)-98++, y(13)+, y(13)-98
Precursor origin neutral loss: +

Peptide No.2262

TIFAKSDDEEEEGDTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TIFAKSDDEEEEGDTK
Found in AT2G20330.1, transducin family protein / WD-40 repeat family protein

Match to Query 2687: 1892.753598 from(947.384075,2+)
Elution from: 26.246 to 26.246 scan no 2092 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1892.7564
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 6.5e-005
Matched b ions: b(3), b(4), b(5), b(10)-98, b(11)-98, b(12), b(14)-98, b(14)
Matched y ions: y(3), y(4), y(5), y(9), y(10), y(11)-98, y(11), y(12)-98, y(14)+, y(14)-98+
Precursor origin neutral loss: +

Peptide No.2263
TIFAKSDDEEEEGDTKK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TIFAKSDDEEEEGDTKK
Found in AT2G20330.1, transducin family protein / WD-40 repeat family protein

Match to Query 2754: 2020.850788 from(1011.432670,2+)
Elution from: 22.824 to 22.824 scan no 1648 polarity:+

file:///C/\Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2262/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 2020.8514
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 2.6e-006
Matched b ions: b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(11), b(12)-98, b(12), b (13), b(14)-98, b(14), b(15)-98, b(16)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)-98++, y (14)-98++, y(15)-98++, y(15)-++
Precursor origin neutral loss: +

Peptide No.2264
TISVDEEESNPIHR
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of TISVDEEESNPIHR
Found in AT4G11680.1, zinc finger (C3HC4-type RING finger) family protein

Match to Query 2088: 1575.691426 from(788.852989,2+)
Elution from: 31.857 to 31.857 scan no 2894 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2263/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1575.6930  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 44 Expect: 0.00034  
Matched b ions: b(5), b(5)-98, b(6)-98, b(7), b(7)-98, b(11)++, b(11), b(12)-98, b(12)  
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(10), y(11)-98++, y(11)++  
Precursor origin neutral loss: +

Peptide No.2265

TKDELTEEESLSGK
Confirmed sites: @S:10  
Ambiguous sites:

MS/MS Fragmentation of TKDELTEEESLSGK
Found in AT2G39010.1, PIP2;6/PIP2E (plasma membrane intrinsic protein 2;6); water channel

Match to Query 1911: 1644.712228 from(823.363390,2+)  
Elution from: 29.176 to 29.176 scan no 2387 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1644.7131  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 23 Expect: 0.032  
Matched b ions: b(5), b(6), b(8)+, b(9), b(11)-98  
Matched y ions: y(5)-98, y(7)-98, y(8)-98, y(9)-98, y(9), y(10)+, y(10), y(10)-98, y(11)-98, y(12), y(12)-98, y(13)+  
Precursor origin neutral loss: +

Peptide No.2266

TKDELTEEESLS GK  
Confirmed sites:  
Ambiguous sites: @S:10orS:12

MS/MS Fragmentation of TKDELTEEESLS GK  
Found in AT2G39010.1, PIP2;6/PIP2E (plasma membrane intrinsic protein 2;6); water channel  

Match to Query 1831: 1644.711152 from(823.362852,2+)  
Elution from: 27.916 to 27.916 scan no 2324 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1644.7131
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0026
Matched b ions: b(5), b(6), b(8), b(8)+, b(9)
Matched y ions: y(5), y(5)-98, y(6)-98, y(7)-98, y(9), y(9)-98, y(10)+, y(10)-98, y(11)-98, y(11)-98++, y(12), y(12)-98
Precursor origin neutral loss: +

Peptide No.2267
TKDSPVMGLLTEENTSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of TKDSPVMGLLTEENTSK
Found in AT4G08310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G44780.2); similar to hypothetical prote

Match to Query 3546: 1928.878336 from(965.446444,2+)
Elution from: 44.327 to 44.327 scan no 4444 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2266/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1928.8802
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 5.8e-007
Matched b ions: b(3), b(4)-98, b(4), b(6)-98, b(6), b(7)-98, b(7), b(8)+, b(8), b(9)-98, b(9), b(10)-98++, b(10), b(10)-98, b(11), b(12)-98, b(12), b(13)+, b(13)-98, b(13), b(14), b(16)-98, b(16)-98++, b(16)+
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(14), y(14)-98, y(14)+, y(15)-98, y(15), y(15)-98++
Precursor origin neutral loss: +

Peptide No.2268

TKDSPVMGLLTEENTSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of TKDSPVMGLLTEENTSK
Found in AT4G08310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G44780.2); similar to hypothetical prote

Match to Query 3630: 1944.871911 from(649.297913,3+)
Elution from: 36.453 to 36.453 scan no 3515 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2267/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1944.8751
Fixed modifications: Carboxamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 Expect: 0.064
Matched b ions: b(4), b(5)-98, b(6), b(7), b(9)-98++, b(9)+, b(10)-98++, b(10)+, b(11)+, b(11)-98++, b(13)+, b(14)+, b(15)-98++
Matched y ions: y(5), y(6), y(7), y(8)+, y(8)++, y(11)+, y(15)-98++, y(16)+
Precursor origin neutral loss:

Peptide No.2269

TKDSPVMGLLTEENTSK
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TKDSPVMGLLTEENTSK
Found in AT4G08310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G44780.2); similar to hypothetical prote

Match to Query 3215: 1928.878449 from(643.966759,3+)
Elution from: 42.316 to 42.316 scan no 4337 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2268/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1928.8802
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 3.9e-005
Matched b ions: b(3), b(4), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98++, b(9), b(9)+, b(10)+,
+ b(10)-98++, b(11)+, b(11)-98++, b(12)+, b(12)+, b(13)+, b(14)+, b(16)+
Matched y ions: y(4), y(5), y(6), y(7), y(7)+, y(8), y(8)+, y(11)+
Precursor origin neutral loss:

Peptide No.2270

TKDSPVMGLLTEENTSK
Confirmed sites:
Ambiguous sites: @T:1orS:4

MS/MS Fragmentation of TKDSPVMGLLTEENTSK
Found in AT4G08310.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT1G44780.2); similar to hypothetical prote

Match to Query 3615: 1944.874962 from(649.298930,3+)
Elution from: 35.142 to 35.142 scan no 3379 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1944.8751
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 24 Expect: 0.051
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(9), b(9)-98++, b(10)-98++, b(10)+, b(11)-98++ , b(11)+++, b(12)+++, b(14)+++, b(15)-98++
Matched y ions: y(5), y(6), y(7), y(8)+, y(10), y(11)++
Precursor origin neutral loss:

Peptide No.2271

TLLSILRSAALAR
Confirmed sites: "@T:1,@S:4"
Ambiguous sites:

MS/MS Fragmentation of TLLSILRSAALAR
Found in AT4G02060.1, PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase

Match to Query 2427: 1656.868540 from(829.441546,2+)
Elution from: 59.162 to 59.162 scan no 6196 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1656.8728
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.023
Matched b ions: b(7)-98++, b(7), b(8), b(9), b(10)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(12)++
Precursor origin neutral loss:

Peptide No.2272
TLNPSAAAVA/SDDSE/EK
Confirmed sites: "@S:12,@S:15"
Ambiguous sites:

MS/MS Fragmentation of TLNPSAAAVA/SDDSE/EK
Found in AT4G00238.1, DNA-binding storekeeper protein-related

Match to Query 2842: 2065.810302 from(1033.912427,2+)
Elution from: 32.794 to 32.794 scan no 2971 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2065.8129  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 66 Expect: 1.8e-006  
Matched b ions: b(8), b(9), b(10), b(11), b(12)-98, b(13), b(14), b(14)-98, b(15)+, b(16)-98, b(17)-196++, b(18)-98++, b(18)-196++  
Matched y ions: y(3), y(5)-98, y(5), y(6)-98, y(6), y(7), y(8)-98, y(8), y(8)-196, y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(12), y(12)-98, y(13), y(13)-196, y(14), y(14)+, y(15)-98, y(15), y(15)-196, y(15)-98++, y(15)+, y(16), y(16)-98, y(16)-98++, y(17)+, y(17)-98++, y(18)+  
Precursor origin neutral loss: +  

---  

Peptide No.2273  
TLNSPSAAVAVSDDSEKEK  
Confirmed sites: "@S:12,@S:17"  
Ambiguous sites:  
MS/MS Fragmentation of TLNSPSAAVAVSDDSEKEK  
Found in AT4G00238.1, DNA-binding storekeeper protein-related  
Match to Query 3026: 2065.809888 from(1033.912220,2+)
Monoisotopic mass of neutral peptide Mr(calc): 2065.8129  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 87 Expect: 1.3e-008  
Matched b ions: b(7)++, b(9), b(10), b(11), b(14), b(18)-98++  
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)-98, y(8)-196, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(11), y(11)-196, y(11)-98, y(12), y(12)-98, y(13), y(14)++, y(14), y(15), y(15)-98, y(15)-98++, y(16), y(17)++, y(17)-98++  
Precursor origin neutral loss: +

Peptide No.2274

TLNSPSAAAVSDDSEKEK  
Confirmed sites:  
Ambiguous sites: "@S:12orS:15orS:17, @S:12orS:15orS:17"

MS/MS Fragmentation of TLNSPSAAAVSDDSEKEK  
Found in AT4G00238.1, DNA-binding storekeeper protein-related

Match to Query 3844: 2065.809764 from(1033.912158,2+)  
Elution from: 33.696 to 33.696 scan no 3131 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2065.8129
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0085
Matched b ions: b(7), b(9), b(10), b(11), b(17)++, b(18), b(18)-98++, b(18)-196++, b(18)++
Matched y ions: y(8), y(8)-98, y(8)-196, y(9)-98, y(9), y(9)-196, y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(14)++, y(15), y(15)-98++, y(16), y(16)-98++, y(16)++, y(17)+, y(17)-98++
Precursor origin neutral loss: +

Peptide No.2275

TLSDLNR
Confirmed sites: @5:3
Ambiguous sites:

MS/MS Fragmentation of TLSDLNR
Found in AT4G04210.1, PUX4 (LANT UBX DOMAIN-CONTAINING PROTEIN 4)

Match to Query 305: 897.395022 from(449.704787,2+)
Elution from: 28.635 to 28.635 scan no 2343 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 897.3957
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0012
Matched b ions: b(2), b(3), b(4), b(4)-98, b(5)-98, b(6)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(5)-98++, y(6)-98, y(6)+
Precursor origin neutral loss: +

Peptide No.2276

TLSDPFSNGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSDPFSNGK
Found in AT1G33990.1, hydrolase, alpha/beta fold family protein

Match to Query 843: 1144.479536 from(573.247044,2+)
Elution from: 39.597 to 39.597 scan no 3931 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2275/2597) [2008/03/14 15:08:29]
Monoisotopic mass of neutral peptide Mr(calc): 1144.4801
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.038
Matched b ions: b4-98, b4, b7-98
Matched y ions: y2, y6, y7, y8-98, y8, y8-98++
Precursor origin neutral loss: +

Peptide No.2277
TLSFMNNKFNFGSMPSVK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of TLSFMNNKFNFGSMPSVK
Found in AT3G20190.1, leucine-rich repeat transmembrane protein kinase, putative

Match to Query 2892: 1980.878283 from(661.300037,3+)
Elution from: 33.896 to 33.896 scan no 3105 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1980.8838
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.039
Matched b ions: b(7)+, b(10)+, b(11)+, b(13)+, b(13)-98+, b(14)-98+, b(14)+
+, b(15)+, b(16)-98+, b(16)+
Matched y ions: y(4), y(6)-98+, y(6)+, y(6)-98, y(7), y(7)-98, y(11)-98+, y(12)+, y
(15)-98+
Precursor origin neutral loss: +

Peptide No.2278
TLSLPPASPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TLSLPPASPR
Found in AT1G24267.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT1G24265.2); similar to bZIP transcription

Match to Query 722: 1117.552906 from(559.783729,2+)
Elution from: 33.476 to 33.476 scan no 3112 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1117.5533
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 
Ions Score: 22 Expect: 0.043
Matched b ions: b(2), b(3), b(4)
Matched y ions: y(4), y(6), y(7), y(8)
Precursor origin neutral loss: +

Peptide No.2279

TLSPKPPSPR
Confirmed sites: "@S:3,@S:8"
Ambiguous sites:

MS/MS Fragmentation of TLSPKPPSPR
Found in AT2G43680.1, IQD14; calmodulin binding

Match to Query 1631: 1238.544360 from(413.855396,3+)
Elution from: 24.756 to 24.756 scan no 1983 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1238.5461
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.024
Matched b ions: b(2), b(3), b(4)-98, b(5), b(5)-98++, b(5)+, b(6)-98++, b(6)+, b(7)-98++, b(7)+
Matched y ions: y(2), y(4)+, y(4)-98, y(5), y(5)-98++, y(5)+, y(6)+, y(7)+, y(7)-98++, y(8)-98++, y(8)+, y(9)+, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2280

TLSPKPSSPR
Confirmed sites: "@T:1,@S:8"
Ambiguous sites:

MS/MS Fragmentation of TLSPKPSSPR
Found in AT2G43680.1, IQD14; calmodulin binding

Match to Query 968: 1238.545120 from(620.279836,2+)
Elution from: 24.593 to 24.593 scan no 1895 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1238.5461
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.037
Matched b ions: b(2), b(5), b(5)-98, b(6)-98, b(8)-98, b(8), b(9)-196
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6), y(7)-98, y(7)
Precursor origin neutral loss: +

Peptide No.2281

TMIMFIGDGI\GKTV\IKANR
Confirmed sites: "\@T:1,\@T:13"
Ambiguous sites:

MS/MS Fragmentation of TMIMFIGDGI\GKTV\IKANR
Found in AT4G02300.1, pectinesterase family protein

Match to Query 4015: 2240.054769 from(747.692199,3+)
Elution from: 37.194 to 37.194 scan no 3611 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmealist.htm (2280/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2240.0499
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.061
Matched b ions: b(5), b(6)-98, b(6)-98++, b(6)+, b(7)+, b(8)+, b(8)-98++, b(9)+, b(9),
b(10)+, b(10), b(10)-98++, b(11)-98++, b(12)-98++, b(14)+, b(17)+, b(17)-98++, b(18)+
Matched y ions: y(6)+, y(7), y(9), y(9)+, y(9)-98, y(10), y(10)+, y(11)+, y(11)-98++, y
(13)-98++, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(15)+, y(18)+
Precursor origin neutral loss:

Peptide No.2282

TMRNSLNISMR
Confirmed sites: @5:5
Ambiguous sites:

MS/MS Fragmentation of TMRNSLNISMR
Found in AT4G35310.1, CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); calcium- and
calmodulin-dependent protein kinase/ kinase
Match to Query 2106: 1401.625434 from(701.819993,2+)
Elution from: 33.160 to 33.160 scan no 3099 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1401.6258
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.024
Matched b ions: b(4), b(5)-98, b(6)-98, b(8), b(8)+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)-98++
Precursor origin neutral loss: +

Peptide No.2283

TPDSPSCSEQSWSDK
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TPDSPSCSEQSWSDK
Found in AT1G31480.1, SGR2 (SHOOT GRAVITROPISM 2)

Match to Query 2358: 1830.675450 from(916.345001,2+)
Elution from: 28.880 to 28.880 scan no 2348 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1830.6768
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.0067
Matched b ions: b(3)-98, b(10)-98, b(10), b(14), b(14)-98++
Matched y ions: y(4), y(5), y(6), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.2284

TPEVNSPAKEIDVVPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TPEVNSPAKEIDVVPK
Found in AT5G63550.1, GTP binding / RNA binding

Match to Query 3568: 1930.928364 from(644.650064,3+)
Elution from: 36.248 to 36.248 scan no 3553 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2283/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1930.9288
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00016
Matched b ions: b(2), b(3), b(4), b(6)-98, b(8)-98, b(9), b(9)-98++, b(9)-98, b(10)+, b(10)-98++, b(11)+, b(11)-98++, b(12)+, b(12)-98++, b(13)+, b(13)-98++, b(14)+, b(14)-98++, b(15)-98++, b(15)+, b(15)-98++
Matched y ions: y(2), y(4), y(5)+, y(5), y(6), y(7), y(8), y(9)+, y(9)-98++, y(11)+, y(12)+, y(12)-98++, y(13)+, y(13)-98++, y(14)-98++, y(14)+, y(14)-98++, y(15)+, y(15)-98++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2285

TPFTSGLDLEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TPFTSGLDLEK
Found in AT1G48030.1, dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1)

Match to Query 1287: 1286.576718 from(644.295635,2+)
Elution from: 49.600 to 49.600 scan no 5223 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2284/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1286.5795
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0055
Matched b ions: b(6)-98, b(8)
Matched y ions: y(4), y(7)-98, y(7), y(8)-98, y(9)+, y(9)-98, y(9), y(10)-98++, y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.2286
TPKLGLGSIHLK
Confirmed sites: "@T:1,@S:8"
Ambiguous sites:

MS/MS Fragmentation of TPKLGLGSIHLK
Found in AT5G65950.1, binding

Match to Query 1538: 1422.700116 from(475.240648,3+)
Elution from: 36.902 to 36.902 scan no 3500 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2285/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1422.7037
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.018
Matched b ions: b(6)-98++, b(7)-98++, b(8)+, b(8)-98++, b(10)-196++, b(11)-196++
Matched y ions: y(5)+
Precursor origin neutral loss:

Peptide No.2287
TPLEVNNDGGLSLDDTMESR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of TPLEVNNDGGLSLDDTMESR
Found in AT3G47910.1, binding / nucleic acid binding / ubiquitin thiolesterase/ zinc ion binding

Match to Query 4058: 2128.859458 from(1065.437005,2+)
Elution from: 41.910 to 41.910 scan no 4130 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...o0705103ppmGROUPmeadlist.htm (2286/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2128.8620
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 4.4e-006
Matched b ions: b(4), b(7), b(8), b(13)-98, b(14)-98, b(17)-98
Matched y ions: y(4), y(6), y(8), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(13)+, y(13)-98, y(14)-98, y(14), y(15), y(15)-98, y(17)-98++
Precursor origin neutral loss: +

Peptide No.2288

TPNPFYVESDK
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TPNPFYVESDK
Found in AT3G07790.1, DGCR14-related

Match to Query 1544: 1375.567754 from(688.791153,2+)
Elution from: 40.198 to 40.198 scan no 3977 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1375.5697
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.053
Matched b ions: b(3)-98, b(6)-98, b(7)-98
Matched y ions: y(5), y(6), y(7)+, y(8), y(8)+, y(9)+, y(9), y(10)+
Precursor origin neutral loss: +

Peptide No.2289

TPSSLSPGNSGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of TPSLLSPGNSGR
Found in AT2G16405.1, transducin family protein / WD-40 repeat family protein

Match to Query 1792: 1351.612148 from(676.813350,2+)
Elution from: 33.280 to 33.280 scan no 3083 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2288/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1351.6133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00092
Matched b ions: b(5), b(9), b(10), b(11)-98++
Matched y ions: y(4), y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)
Precursor origin neutral loss: +

Peptide No.2290

TPSSLSPGNSGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TPSLLSPGNSGR
Found in AT2G16405.1, transducin family protein / WD-40 repeat family protein

Match to Query 1484: 1351.612620 from(676.813586,2+)
Elution from: 32.898 to 32.898 scan no 3001 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1351.6133
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0037
Matched b ions: b(5), b(7)+, b(7)-98, b(8)-98++, b(10), b(11)-98++
Matched y ions: y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)+, y(9), y(10), y(11), y(12)-98, y(12)+
Precursor origin neutral loss: +

Peptide No.2291

TPYHMMDDGSLSPR
Confirmed sites: "@S:12,@S:14"
Ambiguous sites:

MS/MS Fragmentation of TPYHMMDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3324: 2009.692410 from(670.904746,3+)
Elution from: 26.964 to 26.964 scan no 2193 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2009.6937
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0012
Matched b ions: b(4), b(6), b(8), b(8)+, b(9)+, b(10)+, b(11)+, b(12)+, b(13)-98++, b(14)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)+, y(6)-196, y(7)-98, y(7), y(8), y(8)-98, y(8)+ +, y(9)+, y(9)-98++, y(10)-98++, y(10)+, y(11)+, y(11)-196++, y(12)-98++, y(12)+, y(13)-98++, y(14)+, y(14)-98++, y(14)-196++, y(15)-98++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.2292

TPYHPMMDDDGSLSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor
Match to Query 3279: 1929.725988 from(644.249272,3+)
Elution from: 25.121 to 25.121 scan no 1982 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1929.7274
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.00000(shown in table), 63.9983
M7 : Oxidation (M), with neutral losses 0.00000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.00000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00097
Matched b ions: b(4), b(5), b(7)+, b(8)+, b(9)+, b(10), b(10)+, b(12)+, b(13)+, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(6), y(7), y(11)-98++, y(11)+, y(12)+, y(12)-98+ +, y(13)+, y(14)+, y(14)-98++, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2293

TPYHPMMDDDGSLSPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3168: 1913.732400 from(957.873476,2+)
Monoisotopic mass of neutral peptide Mr(calc): 1913.7325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.033
Matched b ions: b(4), b(9), b(10), b(13)+, b(14)-98
Matched y ions: y(6)-98, y(6), y(7), y(8), y(8)-98, y(11), y(12), y(12)-98, y(13)+, y(13)-98++, y(13), y(14)+, y(14)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2294

TPYHPMDDDGSLSPR
Confirmed sites: "@S:12,@S:14"
Ambiguous sites:

MS/MS Fragmentation of TPYHPMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3692: 1993.696686 from(665.572838,3+)
Elution from: 31.903 to 31.903 scan no 2965 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1993.6988
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6: Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 6.6e-005
Matched b ions: b(4), b(7), b(8)+, b(9)+, b(10), b(10)+, b(12)-98++, b(13)-98++, b(14)-196++, b(14)-98++, b(15)-196++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5)-98, y(5), y(6)-98++, y(6)-98, y(7), y(7)-98++, y(7)+, y(7)-98, y(8), y(8)-98++, y(8)-98, y(10)+, y(11)+, y(11)-196++, y(11)-98++, y(12)+, y(12)-98++, y(12)-196++, y(13)-196++, y(13)+, y(14)+, y(14)-98++, y(15)-98++, y(15)-196++, y(15)+
Precursor origin neutral loss: +

Peptide No.2295
TPYHPMMDDDGSLSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor
Match to Query 3237: 1913.730879 from(638.917569,3+)
Elution from: 31.288 to 31.288 scan no 2817 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1913.7325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.042
Matched b ions: b(4), b(6)++, b(8)++, b(9)++, b(10)+, b(14)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(9), y(9)-98 ++, y(10)++, y(11)-98++, y(11)+, y(12)+, y(12)-98++, y(14)-98++, y(14)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2296

TPYHPMMDDDGSLPR
Confirmed sites: "@S:12,@S:14"
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3651: 1993.698086 from(997.856319,2+)
Elution from: 32.559 to 32.559 scan no 3003 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1993.6988
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00063
Matched b ions: b(4), b(9), b(9)+, b(10), b(11), b(12)-98, b(13), b(13)-98, b(14)-98, b(14)-196, b(15)-196
Matched y ions: y(4)-98, y(4), y(5), y(6)-196, y(6)-98, y(6), y(7)-98, y(7), y(8)-98++, y(8), y(8)-98, y(8)-196, y(11), y(12), y(12)-98, y(13)+, y(13)-196++, y(13)-98++, y(13)-98++, y(14)-98++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2297
TPYHPMMDDDGSLSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3167: 1913.730063 from(638.917297,3+)
Monoisotopic mass of neutral peptide Mr(calc): 1913.7325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.002
Matched b ions: b(4), b(5), b(7), b(8)++, b(8), b(9)++, b(10), b(10)++, b(11), b(12)++, b(13)+ +, b(14)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(9), y(11)-98++, y(11)++, y(12)+++, y(12)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2298

TPYHPMMDDDGSLSPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3506: 1897.735538 from(949.875045,2+)
Monoisotopic mass of neutral peptide Mr(calc): 1897.7376
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.016
Matched b ions: b(4), b(8), b(9), b(12)++, b(13)++, b(14)-98
Matched y ions: y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(11), y(12)-98, y(12), y(12)++, y(13)-98++, y(13)+, y(13), y(14)-98++, y(14)+, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.2299

TPYHPMDDDDGSLPR
Confirmed sites: "@S:12,@S:14"
Ambiguous sites:

MS/MS Fragmentation of TPYHPMDDDDGSLPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor

Match to Query 3431: 1977.702816 from(660.241548,3+)
Elution from: 38.128 to 38.128 scan no 3736 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1977.7039
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769
Ions Score: 50 Expect: 3.8e-005
Matched b ions: b(4), b(5), b(6)+, b(6), b(7)+, b(7), b(8)+, b(8), b(9)+, b(9), b(10)+, b(10), b(11)+, b(12)-98++, b(13)-98++, b(14)-196++, b(14)-98++, b(15)-196++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5)-98, y(5)-98++, y(5)-196, y(5), y(6), y(6)-98++, y(6)+, y(6)-98, y(6)-196, y(7), y(7)-98, y(7)-98++, y(7)+, y(7)-196, y(8), y(8)-98++, y(8)-98, y(8)+, y(9)-98, y(9), y(9)-98++, y(9)+, y(10), y(10)+, y(10)-98++, y(11)+, y(11)-98++, y(11)-196++, y(12)+, y(12)-98++, y(12)-196++, y(13)+, y(14)+, y(14)-196++, y(14)-98++, y(15)-98++, y(15)+, y(15)-196++
Precursor origin neutral loss: +

Peptide No.2300
TPYHPMMDDDGSLSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TPYHPMMDDDGSLSPR
Found in AT5G52200.1, phosphatase inhibitor/ protein phosphatase inhibitor
Monoisotopic mass of neutral peptide Mr(calc): 1897.7376
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 3.8e-006
Matched b ions: b(4), b(4)+, b(5), b(6), b(6)+, b(7)+, b(7), b(8), b(8)+, b(9)+, b(9), b(10)+, b(10), b(11), b(12)+, b(13)+, b(14)-98++, b(15)+
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(4)+, y(5)-98++, y(5)-98, y(5)+, y(6), y(6)+, y(6)-98, y(7), y(7)+, y(7)-98, y(8), y(9), y(9)-98, y(9)-98++, y(10), y(10)-98++, y(10)+, y(11)+, y(11)-98++, y(12), y(12)+, y(12)-98++, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.2301

TQEESDAETPTGLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TQEESDAETPTGLK
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G19710.1); similar to MAPK activating pr
Match to Query 2258: 1584.654132 from (793.334342, 2+)
Elution from: 26.159 to 26.159 scan no 2090 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1584.6556
Fixed modifications: Carbamidomethyl (C)
Variable modifications: S5 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 48 Expect: 0.00011
Matched b ions: b(3), b(4), b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(11)-98, b(11)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(12)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.2302

TQRPPSPSLTAQR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TQRPPSPSLTAQR
Found in AT4G23040.1, UBX domain-containing protein

Match to Query 2576: 1517.734152 from (506.918660, 3+)
Elution from: 23.048 to 23.048 scan no 1749 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1517.7351
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 33 Expect: 0.0037
Matched b ions: b(2), b(3), b(6)-98++, b(6)+, b(6)-98, b(7)-98++, b(9)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)+, y(9), y(9)+, y(10)+, y(10)-98++, y(11)-98++, y(11)+
Precursor origin neutral loss: +

Peptide No.2303
TQTPGSTFLR
Confirmed sites: "@T:3,@S:6"
Ambiguous sites:

MS/MS Fragmentation of TQTPGSTFLR
Found in AT3G07790.1, DGCR14-related

Match to Query 1602: 1266.503616 from(634.259084,2+)
Elution from: 43.311 to 43.311 scan no 4414 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2302/2597) [2008/03/14 15:08:30]
Mascot Search Results: Peptide View

Monoisotopic mass of neutral peptide Mr(calc): 1266.5047
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.063
Matched b ions: b(2), b(3), b(5), b(6)-196
Matched y ions: y(4), y(6), y(7)-98, y(7), y(8)-98++, y(8), y(8)-196++, y(8)-98
Precursor origin neutral loss: +

Peptide No.2304

TQTPGSTFLR
Confirmed sites: "@T:3,@T:7"
Ambiguous sites:

MS/MS Fragmentation of TQTPGSTFLR
Found in AT3G07790.1, DGCR14-related

Match to Query 1754: 1266.503156 from(634.258854,2+)
Elution from: 43.169 to 43.169 scan no 4447 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1266.5047
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0005
Matched b ions: b(2), b(3)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.2305

TREESDSDEPQLGLR
Confirmed sites: "@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of TREESDSDEPQLGLR
Found in AT2G19710.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT4G29440.1); similar to MAPK activating pr

Match to Query 2630: 1977.770568 from(989.892560,2+)
Elution from: 33.586 to 33.586 scan no 3076 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1977.7718
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.049
Matched b ions: b(4), b(5), b(6)-98, b(7), b(8), b(8)-196, b(9)-196, b(10), b(10)-98, b(13)-98
Matched y ions: y(6), y(7), y(8), y(10), y(11), y(11)-98, y(12)-98++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2306

TRSFDDSPPAAAELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TRSFDDSPPAAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G22960.1); similar to hypothetical prote

Match to Query 2993: 1711.756204 from(856.885378,2+)
Elution from: 35.061 to 35.061 scan no 3325 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1711.7566  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 82 Expect: 5.9e-008  
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(10), b(11), b(12), b(13), b(13)-98, b(14)-98  
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(13)+  
Precursor origin neutral loss: +

Peptide No.2307

TRSFDDSPPAAELR  
Confirmed sites: "@S:3,@S:7"  
Ambiguous sites:

MS/MS Fragmentation of TRSFDDSPPAAELR  
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G22960.1); similar to hypothetical prote

Match to Query 3185: 1791.722354 from(896.868453,2+)  
Elution from: 38.474 to 38.474 scan no 3800 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2306/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1791.7230
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0017
Matched b ions: b(5), b(6)-98, b(6), b(7), b(7)-196, b(7)-98, b(10), b(11), b(13)-98++, b(13)-98, b(14)-98
Matched y ions: y(2), y(8), y(9), y(10), y(10)-98, y(11), y(12), y(13)-98, y(13)
Precursor origin neutral loss: +

Peptide No.2308

TRSFDDSPPAAELR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TRSFDDSPPAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G22960.1); similar to hypothetical prote

Match to Query 2422: 1711.754430 from(571.592086,3+)
Elution from: 34.814 to 34.814 scan no 3253 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2307/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1711.7566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0012
Matched b ions: b(7), b(7)+, b(7)-98, b(8)-98++, b(8)+, b(9)-98++, b(9)+, b(10)-98++, b(11)+, b(12)+
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)+, y(8), y(10)-98++, y(10)+, y(11)-98+, y(13)+
Precursor origin neutral loss:

Peptide No.2309

TRSFDDSPPAAAAELR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TRSFDDSPPAAAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G22960.1); similar to hypothetical prote

Match to Query 2805: 1711.755446 from(856.884999,2+)
Elution from: 33.794 to 33.794 scan no 3174 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1711.7566
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 Expect: 2e-006
Matched b ions: b(2), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(10), b(11), b(11)-98, b(13)-98, b(13), b(14), b(14)+
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)+
Precursor origin neutral loss: +

Peptide No.2310

TRSFDDSPPAAELR
Confirmed sites: @S:7
Ambiguous sites: @T:1orS:3

MS/MS Fragmentation of TRSFDDSPPAAELR
Found in AT4G11860.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G22960.1); similar to hypothetical prote

Match to Query 2968: 1791.721812 from(896.868182,2+)
Elution from: 37.339 to 37.339 scan no 3651 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1791.7230
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0037
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7), b(7)-196, b(7)-98, b(11), b(13)-98++, b(14)
Matched y ions: y(3), y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.2311

TRSFLGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TRSFLGR
Found in AT2G14120.1, dynamin-like protein 2b (ADL2b)

Match to Query 484: 915.431828 from(458.723190,2+)
Elution from: 23.369 to 23.369 scan no 1756 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2310/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 915.4327
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 Expect: 0.00021
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(5), b(5)-98, b(5)+
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6)-98++, y(6)+
Precursor origin neutral loss: +

Peptide No.2312
TRSSPETETHGEALLQSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TRSSPETETHGEALLQSR
Found in AT3G61690.1, nucleotidyltransferase

Match to Query 4020: 2191.023837 from(731.348555,3+)
Elution from: 34.752 to 34.752 scan no 3299 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2191.0270  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 39 Expect: 0.0013  
Matched b ions: b(4)-98, b(6)-98, b(7), b(7)-98, b(8), b(9)-98, b(11)-98++, b(11)+, b(12)+, b(12)-98++, b(13)-98++, b(13)+, b(14)+, b(15)+, b(16)-98++, b(17)-98++  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)+, y(9), y(10)+, y(10), y(11)+, y(12)+, y(15)+, y(16)+, y(17)-98++, y(17)+  
Precursor origin neutral loss: +

Peptide No.2313

TRSVKDVVDDAK  
Confirmed sites:  
Ambiguous sites: @T:1orS:3  

MS/MS Fragmentation of TRSVKDVVDDAK  
Found in AT1G67230.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G68790.1); similar to nuclear matrix con  

Match to Query 2052: 1411.668720 from(471.563516,3+)  
Elution from: 22.093 to 22.093 scan no 1634 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2312/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1411.6708
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0075
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)+, b(5)-98, b(6)+, b(6)-98++, b(7)-98++, b(7)+
+, b(8)-98++, b(8)+, b(9)+, b(9)-98++, b(10)+, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(7)
Precursor origin neutral loss: +

Peptide No.2314

TSCGSPNYAAPEVISGK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of TSCGSPNYAAPEVISGK
Found in AT3G01090.1, AKIN10 (Arabidopsis SNF1 kinase homolog 10, SNF1-RELATED PROTEIN KINASE 1.1); protein kinase

Match to Query 3326: 1816.769502 from(909.392027,2+)
Elution from: 37.011 to 37.011 scan no 3656 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2313/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1816.7702  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 83 Expect: 4.9e-008  
Matched b ions: b(3)-98, b(3), b(5)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(12), b(13)-98, b(13), b(14)-98, b(14)  
Matched y ions: y(3), y(4), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(13), y(14)++, y(15)++, y(16)-98++  
Precursor origin neutral loss: +  

Peptide No.2315  
TSCGSPNYAAPEVISGK  
Confirmed sites:  
Ambiguous sites: @T:1orS:2orS:5  

MS/MS Fragmentation of TSCGSPNYAAPEVISGK  
Found in AT3G01090.1, AKIN10 (Arabidopsis SNF1 kinase homolog 10, SNF1-RELATED PROTEIN KINASE 1.1); protein kinase  

Match to Query 2284: 1816.768176 from(909.391364,2+)  
Elution from: 38.298 to 38.298 scan no 3593 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1816.7702
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0041
Matched b ions: b(5)-98, b(5), b(9)-98, b(10)-98, b(11)-98, b(13), b(14)-98, b(14)
Matched y ions: y(7), y(8), y(9), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.2316
TSEPNSEDEAAGVGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TSEPNSEDEAAGVGK
Found in AT2G27100.1, SE (SERRATE); transcription factor

Match to Query 2145: 1569.618098 from(785.816325,2+)
Elution from: 20.627 to 20.627 scan no 1378 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1569.6195
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 6.8e-005
Matched b ions: b(6)-98, b(7)-98, b(9), b(10)-98, b(10), b(12)++, b(13)
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11)++, y(11), y(12)++, y(12)-98, y(12), y(12)-98++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2317
TSFSVPSPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TSFSVPSPK
Found in AT1G42550.1, PM11 (PLASTID MOVEMENT IMPAIRED1)

Match to Query 540: 1028.457168 from(515.235860,2+)
Elution from: 33.912 to 33.912 scan no 3138 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea list.htm (2316/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1028.4579  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 28 Expect: 0.0064  
Matched b ions: b(2), b(4)  
Matched y ions: y(2), y(3), y(4)-98, y(5), y(6), y(7), y(7)++  
Precursor origin neutral loss: +

Peptide No.2318

TSNDLEMVR  
Confirmed sites:  
Ambiguous sites: @T:1orS:2

MS/MS Fragmentation of TSNDLEMVR  
Found in AT2G45540.1, WD-40 repeat family protein / beige-related

Match to Query 1082: 1143.462400 from(572.738476,2+)  
Elution from: 33.036 to 33.036 scan no 3074 polarity:+

file:///C//Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2317/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1143.4631
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.036
Matched b ions: b(4)
Matched y ions: y(2), y(3), y(4), y(5)
Precursor origin neutral loss: +

Peptide No.2319

TSSAIHALK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSAIHALK
Found in AT5G47910.1, RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)

Match to Query 1022: 1077.520916 from(539.767734,2+)
Elution from: 22.487 to 22.487 scan no 1649 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1077.5219
Fixed modifications: Carboxymethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0027
Matched b ions: b(6)-98, b(7), b(7)-98, b(8), b(9), b(9)-98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(8)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2320
TSSEALVTIRGQSHSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSEALVTIRGQSHSR
Found in AT4G19510.1, disease resistance protein (TIR-NBS-LRR class), putative

Match to Query 3320: 1807.856502 from(603.626110,3+)
Elution from: 41.054 to 41.054 scan no 4172 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea
Monoisotopic mass of neutral peptide Mr(calc): 1807.8577
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.036
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(8)-98, b(8)-98++, b(8)++, b(10)-98++, b(10)++, b(10)-98, b(11)-98++, b(13)-98++, b(14)-98++, b(15)-98++
Matched y ions: y(7)++, y(8)++, y(9)++, y(10)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2321
TSSLSSSVASDTLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSLSSSVASDTLR
Found in AT5G35430.1, binding

Match to Query 2323: 1602.748948 from(802.381750,2+)
Elution from: 45.008 to 45.008 scan no 4647 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1602.7502
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(showed in table), 0.0000
Ions Score: 92 Expect: 5.8e-009
Matched b ions: b(4)-98, b(8)-98, b(9), b(12), b(13)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)-98++
Precursor origin neutral loss: +

Peptide No.2322

TSSLTLGSEEKEK
Confirmed sites: @
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of TSSLTLGSEEKEK
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 1512: 1359.579272 from(680.796912,2+)
Elution from: 29.252 to 29.252 scan no 2508 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1359.5806
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.012
Matched b ions: b(3)-98, b(4)-98, b(5), b(6)-98, b(7)++, b(7)-98, b(8), b(9)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(11)-98++
Precursor origin neutral loss: +

Peptide No.2323

TSSLTLGSEEEK
Confirmed sites: @S:8
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of TSSLTLGSEEEK
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 2128: 1439.545644 from(720.780098,2+)
Elution from: 31.812 to 31.812 scan no 2957 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2322/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1439.5470
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.06
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(6)-98, b(6), b(7)+, b(8)+, b(10)-98, b(11)-98, b(11)-196++, b(11)++
Matched y ions: y(5), y(6), y(6)-98, y(7), y(7)-98, y(7)+, y(8), y(8)-98, y(9), y(11)++
Precursor origin neutral loss: +

---

**Peptide No.2324**

**TSSLLTGSEEKEK**

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **TSSLLTGSEEKEK**

Found in **AT5G23080.1**, TGH (TOUGH); RNA binding

Match to Query 1209: 1359.580064 from(680.797308,2+)

Elution from: 28.565 to 28.565 scan no 2412 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1359.5806
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.00082
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(7)++, b(7)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(10)-98++, y(10), y(10)-98, y(10)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2325
TSSLTLGSEEKK
Confirmed sites: "@S:3,@S:8"
Ambiguous sites:

MS/MS Fragmentation of TSSLTLGSEEKEK
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 1370: 1439.546566 from(720.780559,2+)
Elution from: 31.757 to 31.757 scan no 2834 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1439.5470
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.00052
Matched b ions: b(3)-98, b(4)-98, b(5), b(7)++, b(8)++, b(8)-98, b(8)-196, b(11), b(11)-98
Matched y ions: y(2), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)-196+, y(10)-98++, y(10), y(11)++
Precursor origin neutral loss: +

Peptide No.2326
TSSLTGSEEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TSSLTGSEEK
Found in AT5G23080.1, TGH (TOUGH); RNA binding

Match to Query 1779: 1359.579862 from(680.797207,2+)
Elution from: 30.361 to 30.361 scan no 2681 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1359.5806
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 4e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(11)-98 ++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)-98, y(7), y(7)-98++, y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(10), y(10)-98++, y(10)-98, y(10)+, y(11)+
Precursor origin neutral loss: +

Peptide No.2327

TSVADGSSPHSHNIEMSK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of TSVADGSSPHSHNIEMSK
Found in AT3G52400.1, SYP122 (syntaxin 122); t-SNARE

Match to Query 3865: 2075.860398 from(692.960742,3+)
Elution from: 20.274 to 20.274 scan no 1317 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2326/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2075.8619  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 33 Expect: 0.0046  
Matched b ions: b(9), b(13)++, b(15)++  
Matched y ions: y(6)++, y(12)++, y(12)-98++, y(13)++, y(14)++, y(15)+++, y(15)-98++, y(16)++ y(16)-98++, y(17)-98++, y(17)++  
Precursor origin neutral loss: +

Peptide No.2328

TSVADGSSPHSHNIEMSK  
Confirmed sites:  
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of TSVADGSSPHSHNIEMSK  
Found in AT3G52400.1, SYP122 (syntaxin 122); t-SNARE  

Match to Query 3827: 2059.864300 from(1030.939426,2+)  
Elution from: 23.886 to 23.886 scan no 1800 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2059.8670
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.032
Matched b ions: b(8), b(11), b(13), b(15), b(16), b(16)+, b(17)+, b(17)-98++, b(18)+
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(11), y(11)+, y(14)+, y(14), y(14)-98++, y(15)-98++, y(16)+, y(17)-98++
Precursor origin neutral loss: +

Peptide No.2329

TSVADGSSPPHSHNIEMSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TSVADGSSPPHSHNIEMSK
Found in AT3G52400.1, SYP122 (syntaxin 122); t-SNARE

Match to Query 3078: 2059.865082 from(687.628970,3+)
Elution from: 22.431 to 22.431 scan no 1582 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2059.8670
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00047
Matched b ions: b(4), b(5), b(8)-98++, b(8), b(9)-98, b(13)-98++, b(13)+, b(17)+
Matched y ions: y(6)+, y(6), y(7)+, y(11)+, y(12)+, y(12)-98++, y(13)+, y(13)-98++,
y(14)+, y(14)-98++, y(15)+, y(15)-98++, y(16)+, y(16)-98++, y(17)-98++, y(17)+,
y(18)+
Precursor origin neutral loss:

Peptide No.2330

TSVADGSSPPHSHNIEMSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TSVADGSSPPHSHNIEMSK
Found in AT3G52400.1, SYP122 (syntaxin 122); t-SNARE

Match to Query 3709: 2075.859978 from(692.960602,3+)
Elution from: 19.583 to 19.583 scan no 1244 polarity:+

---

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2329/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2075.8619
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 36 Expect: 0.0024
Matched b ions: b(4), b(5), b(14)-98++
Matched y ions: y(8)+, y(11)+, y(11), y(12)-98++, y(12)+, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(15)+, y(15)-98++, y(16)+, y(16)-98++, y(17)-98++, y(17)+
Precursor origin neutral loss:

Peptide No.2331

TSVGGDDSNAANADMIK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TSVGGDDSNAANADMIK
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 2289: 1801.718702 from(901.866627,2+)
Elution from: 32.000 to 32.000 scan no 2756 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2330/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1801.7189  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 60 Expect: 6.6e-006  
Matched b ions: b(8), b(9)-98, b(11), b(12)-98, b(13)-98, b(14), b(17)  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(13), y(13)-98, y(14)-98, y(15)+, y(15), y(15)-98++, y(16)-98, y(16)-98++, y(16)++  
Precursor origin neutral loss: +

Peptide No.2332
TTCGTPNYVAPEVLSHK  
Confirmed sites: @T:1  
Ambiguous sites:

MS/MS Fragmentation of TTCGTPNYVAPEVLSHK  
Found in AT4G24400.1, CIPK8 (CBL-INTERACTING PROTEIN KINASE 8); kinase

Match to Query 3329: 1952.869674 from(977.442113,2+)  
Elution from: 38.884 to 38.884 scan no 3803 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1952.8703
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.014
Matched b ions: b(10)-98, b(15)++
Matched y ions: y(7), y(8), y(10), y(11), y(12), y(12)+, y(14), y(14)+, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.2333
TTEKEISDDEDEDEPKK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TTEKEISDDEDEDEPKK
Found in AT5G52640.1, HSP81-1 (HEAT SHOCK PROTEIN 81-1); ATP binding / unfolded protein binding

Match to Query 3895: 2086.845585 from(696.622471,3+)
Elution from: 20.602 to 20.602 scan no 1360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2086.8467
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.025
Matched b ions: b(8)-98, b(9)-98++, b(10)-98++, b(11)-98++, b(12)+, b(13)-98++, b(13)+, b(14)-98++
Matched y ions: y(3), y(4), y(6), y(6)+, y(7), y(8)+, y(9)+, y(11)-98++, y(12)+, y(14)-98+, y(14)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2334
TTESACVIIPPKIFR
Confirmed sites:
Ambiguous sites: @T:1orT:2orS:4
MS/MS Fragmentation of TTESACVIIPPKIFR
Found in AT5G24320.1, WD-40 repeat family protein

Match to Query 2638: 1810.908728 from(453.734458,4+)
Elution from: 18.262 to 18.262 scan no 1100 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1810.9052  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 22 Expect: 0.059  
Matched b ions: b(7)-98++, b(7)+, b(8)-98++, b(8)+, b(9)-98++, b(9)+, b(10)-98++  
Matched y ions: y(3), y(4), y(4)+, y(5), y(5)+, y(6)+, y(6), y(7)+  
Precursor origin neutral loss: +

---

Peptide No.2335

TTFGSQLR  
Confirmed sites: @S:5  
Ambiguous sites:

MS/MS Fragmentation of TTFGSQLR  
Found in AT5G49890.1, CLC-C (chloride channel C); anion channel/ voltage-gated chloride channel

Match to Query 866: 1101.521574 from(551.768063,2+)  
Elution from: 45.916 to 45.916 scan no 4751 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1101.5219
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.00071
Matched b ions: b(2), b(3)++, b(5)++, b(7)-98, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(6)-98, y(6), y(7)++, y(7)-98, y(7), y(7)-98++, y (8)-98++
Precursor origin neutral loss: +

Peptide No.2336

TTGRVSPAVDPPSPR
Confirmed sites: "@S:6,@S:13"
Ambiguous sites:

MS/MS Fragmentation of TTGRVSPAVDPPSPR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G80180.1); similar to Os06g0601100 [Oryz

Match to Query 3052: 1695.737739 from(566.253189,3+)
Elution from: 26.502 to 26.502 scan no 2201 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1695.7382
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0039
Matched b ions: b(2), b(4), b(5), b(6)-98, b(8)+, b(8), b(8)-98++, b(9)-98++, b(9), b(9)-98, b(9)+, b(10)+, b(10)-98++, b(11)-98++
Matched y ions: y(2), y(4), y(5)+, y(5), y(5)-98, y(6), y(6)+, y(7)-98, y(7), y(7)-98++, y(7)+, y(9)+, y(13)+, y(13)-98++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.2337

TTGRVSPAVDPSPR
Confirmed sites: @S:13
Ambiguous sites: @T:1orT:2orS:6

MS/MS Fragmentation of TTGRVSPAVDPSPR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT1G80180.1); similar to Os06g0601100 [Oryza

Match to Query 2764: 1695.737361 from(566.253063,3+)
Elution from: 26.590 to 26.590 scan no 2194 polarity:+

file:///C:/Documents%20and%20%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2336/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1695.7382
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0098
Matched b ions: b(6)-98, b(6)+, b(7)-98++, b(8)+, b(8)-98++, b(9)-98++, b(9), b(9)+
+, b(10)+, b(10), b(10)-98+, b(10)-98, b(11)-98++, b(13)-98++, b(14)-196++
Matched y ions: y(2), y(3)-98, y(3), y(4)+, y(4), y(4)-98, y(5)+, y(5), y(5)-98++, y(5)-98, y
(6), y(6)+, y(6)-98, y(6)-98, y(7)-98++, y(7), y(7)+, y(9), y(9)+
Precursor origin neutral loss: +

Peptide No.2338

TTGRVSPAVDPPSPR
Confirmed sites: @S:13
Ambiguous sites: @T:1orT:2orS:6

MS/MS Fragmentation of TTGRVSPAVDPPSPR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT1G80180.1); similar to Os06g0601100 [Oryz

Match to Query 2944: 1695.736348 from(848.875450,2+)
Elution from: 26.805 to 26.805 scan no 2225 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2337/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1695.7382
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0081
Matched b ions: b(6)-98, b(9), b(10)-98, b(10), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(9)
Precursor origin neutral loss: +

Peptide No.2339

TTSIGDGGEEGVDDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TTSIGDGGEEGVDDK
Found in AT4G26130.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT5G56980.1); similar to cDNA-5-encoded pro

Match to Query 1674: 1558.602068 from(780.308310,2+)
Elution from: 23.660 to 23.660 scan no 1771 polarity:+

file:///C/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2338/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1558.6035
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 1.7e-007
Matched b ions: b(3)-98, b(4)-98, b(6), b(8)+, b(8)-98, b(9)-98, b(12), b(13)
Matched y ions: y(2), y(3), y(5), y(6), y(8), y(8)+, y(9), y(10), y(11), y(11)+, y(12), y(12)+, y(13)-98++, y(13), y(13)+
Precursor origin neutral loss: +

Peptide No.2340

TTSIGDGGEEGVDDK
Confirmed sites:
Ambiguous sites: @T:1orT:2orS:3

MS/MS Fragmentation of TTSIGDGGEEGVDDK
Found in AT4G26130.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G56980.1); similar to cDNA-5-encoded pro

Match to Query 1952: 1558.601512 from(780.308032,2+)
Elution from: 23.600 to 23.600 scan no 1747 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1558.6035
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 7.6e-007
Matched b ions: b(3)-98, b(4)-98, b(6), b(8)++, b(12)
Matched y ions: y(2), y(3), y(5), y(6), y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.2341
TTSLGSNDFQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TTSLGSNDFQK
Found in AT5G43310.1, COP1-interacting protein-related

Match to Query 1192: 1276.533402 from(639.273977,2+)
Elution from: 28.328 to 28.328 scan no 2418 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1276.5336
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.00065
Matched b ions: b(4)-98, b(10)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9)-98++, y(9), y(9)-98, y(9)++
Precursor origin neutral loss: +

Peptide No.2342

TVCVVHLLNK
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TVCVVHLLNK
Found in AT5G24950.1, CYP71A15 (cytochrome P450, family 71, subfamily A, polypeptide 15); oxygen binding

Match to Query 1635: 1261.627776 from(421.549868,3+)
Elution from: 19.596 to 19.596 scan no 1275 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1261.6254
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0036
Matched b ions: b(3)+, b(4)-98++, b(5)+, b(6)+, b(7)-98++, b(8)+, b(9)-98++
Matched y ions: y(5), y(5)+, y(7)+
Precursor origin neutral loss: +

Peptide No.2343

TVDGETENLPNGDSSPK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of TVDGETENLPNGDSSPK
Found in AT4G28080.1, binding

Match to Query 3341: 1838.755724 from(920.385138,2+)
Elution from: 28.105 to 28.105 scan no 2382 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2342/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1838.7571
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 7.2e-09
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11)+, b(11), b(13), b(15)-98
Matched y ions: y(3), y(4)-98, y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)+, y(9), y(9)-98, y(10), y(10)-98++, y(10), y(12)+, y(12), y(13)+, y(14)-98++, y(14), y(14)+, y(15), y(15)+, y(16)-98++
Precursor origin neutral loss:

Peptide No.2344

TVGDVETVGFQSPYAVSR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TVGDVETVGFQSPYAVSR
Found in AT5G58350.1, WNK4 (Arabidopsis WNK kinase 4); kinase

Match to Query 3440: 1990.905084 from(996.459818,2+)
Elution from: 50.597 to 50.597 scan no 5306 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1990.9037  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 72 Expect: 7.1e-007  
Matched b ions: b(6)-98, b(8)-98, b(9), b(9)-98, b(11)-98, b(12), b(12)-98, b(15), b(16)-98  
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)  
Precursor origin neutral loss: +  

Peptide No.2345  
TVGILEGPKVTTTPDGR  
Confirmed sites:  
Ambiguous sites: @T:11orT:12  

MS/MS Fragmentation of TVGILEGPKVTTTPDGR  
Found in AT1G05890.1, zinc finger protein-related  

Match to Query 2597: 1689.832230 from(845.923391,2+)  
Elution from: 46.709 to 46.709 scan no 4863 polarity:+  

file:///C:/Documents%20and%20Settings/N.Su_...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2344/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1689.8338
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00024
Matched b ions: b(10), b(12)-98, b(14)
Matched y ions: y(4), y(6), y(7), y(7)-98, y(9)-98, y(9), y(10), y(11), y(12), y(12)+, y(14)+, y (15)-98++
Precursor origin neutral loss:

Peptide No.2346
TVGILEGPVVTTPDGR
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of TVGILEGPVVTTPDGR
Found in AT1G05890.1, zinc finger protein-related

Match to Query 2290: 1689.831832 from(845.923192,2+)
Elution from: 46.814 to 46.814 scan no 4724 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1689.8338
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 3.5e-006
Matched b ions: b(6), b(9), b(10), b(11), b(12)++, b(12)-98, b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(12), y(12)++, y(12)-98++, y(13)++, y(14)++, y(14), y(15)-98++
Precursor origin neutral loss:

Peptide No.2347

TVMSPPSSPPR
Confirmed sites: @S:4
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of TVMSPPSSPPR
Found in AT1G61850.1, patatin family protein

Match to Query 1314: 1314.506796 from(658.260674,2+)
Elution from: 32.968 to 32.968 scan no 3043 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2346/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1314.5080
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0017
Matched b ions: b(2), b(4)-98++, b(4)-98, b(4), b(8)-196, b(8)+, b(8), b(8)-98, b(9)-98++, b(9)-98, b(10)-196++
Matched y ions: y(2), y(3), y(6), y(7), y(8), y(8)-98, y(9)-98++, y(9)-98, y(9), y(9)+, y(10)-196++, y(10)-98++, y(10)-196, y(10)-98
Precursor origin neutral loss: +

Peptide No.2348

TVQFVDWCPTGFK
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of TVQFVDWCPTGFK
Found in AT5G19770.1, TUA3 (tubulin alpha-3)

Match to Query 2753: 1663.705702 from(832.860127,2+)
Elution from: 59.875 to 59.875 scan no 6435 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2347/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1663.7105  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 48 Expect: 0.00012  
Matched b ions: b(5), b(6), b(7), b(8)  
Matched y ions: y(4), y(4)+, y(5)-98, y(5), y(6)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(11)+, y(11)-98++, y(12)-98++  
Precursor origin neutral loss:

---

Peptide No. 2349

TVSGTSSSSPEDI  
Confirmed sites: @S:10  
Ambiguous sites:

MS/MS Fragmentation of TVSGTSSSSPEDI  
Found in AT5G52200.1, phosphatase inhibitor/protein phosphatase inhibitor

Match to Query 1998: 1430.617016 from(716.315784,2+)  
Elution from: 41.617 to 41.617 scan no 4179 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1430.6178
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 5.5e-005
Matched b ions: b(3), b(5), b(6), b(7), b(9), b(12), b(13)+, b(13), b(13)-98++
Matched y ions: y(4), y(5), y(7), y(8), y(9)
Precursor origin neutral loss:

Peptide No.2350

TVTIVELIKRR
Confirmed sites: "@T:1,@T:3"
Ambiguous sites:

MS/MS Fragmentation of TVTIVELIKRR
Found in AT1G76010.1, nucleic acid binding

Match to Query 2246: 1486.769394 from(744.391973,2+)
Elution from: 48.852 to 48.852 scan no 5133 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1486.7673
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.033
Matched b ions: b(2), b(7), b(8), b(9)
Matched y ions: y(2), y(4)
Precursor origin neutral loss:

Peptide No.2351

TVSYIQSR
Confirmed sites: @Y:5
Ambiguous sites:

MS/MS Fragmentation of TVSYIQSR
Found in AT5G35980.1, protein kinase family protein

Match to Query 1116: 1195.526454 from(598.770503,2+)
Elution from: 34.379 to 34.379 scan no 3192 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1195.5274
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y5 : Phospho (Y)
Ions Score: 54 Expect: 2.6e-005
Matched b ions: b(2), b(5), b(6), b(7), b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)++, y(7)
Precursor origin neutral loss:

Peptide No.2352

TYMVSPGRQDDDLYSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TYMVSPGRQDDDLYSR
Found in AT2G32910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G61910.3); similar to expressed protein

Match to Query 3630: 1981.822392 from(991.918472,2+)
Elution from: 37.784 to 37.784 scan no 3707 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1981.8241
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0021
Matched b ions: b(5), b(6)-98, b(9), b(10), b(11), b(12)-98, b(12)
Matched y ions: y(4), y(5), y(6), y(7), y(10)+, y(11)+, y(11), y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.2353
TYMVSPGRQDDDLYSR
Confirmed sites:
Ambiguous sites: @T:1orY:2orS:5

MS/MS Fragmentation of TYMVSPGRQDDDLYSR
Found in AT2G32910.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT5G61910.3); similar to expressed protein

Match to Query 3328: 1981.820582 from(991.917567,2+)
Elution from: 36.617 to 36.617 scan no 3598 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2352/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1981.8241
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.026
Matched b ions: b(5), b(6)-98, b(9)-98, b(10), b(11)-98, b(11)
Matched y ions: y(4), y(5), y(6), y(7), y(11)++, y(11)
Precursor origin neutral loss: +

Peptide No.2354

TYTMLGTMENPGVMVLAIKDLFAK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of TYTMLGTMENPGVMVLAIKDLFAK
Found in AT1G18550.1, kinesin motor protein-related

Match to Query 4226: 2754.300468 from(919.107432,3+)
Elution from: 41.118 to 41.118 scan no 4023 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2754.3083
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 Expect: 0.0044
Matched b ions: b(6), b(8)-98, b(10)-98, b(11), b(11)++, b(12)++, b(13)++, b(13)-98+ +, b(14)++, b(15)-98++, b(15)++, b(17)++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(23)+ +
Matched y ions: y(10), y(11)++, y(11), y(13), y(13)++, y(16)++, y(18)++, y(20)-98++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

---

**Peptide No.2355**

**VAEEESSEDDEDSVDR**

Confirmed sites: 
Ambiguous sites: @S:6orS:7

**MS/MS Fragmentation of** **VAEEESSEDDEDSVDR**

Found in **AT1G30960.1**, GTP-binding protein (ERG)

Match to Query 3486: 1889.668108 from(945.841330,2+)
Monoisotopic mass of neutral peptide Mr(calc): 1889.6687
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00028
Matched b ions: b(5), b(8)-98, b(9), b(11), b(12), b(13), b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(11), y(11)-98, y(13)+, y(14)+, y(15)+
Precursor origin neutral loss: +

Peptide No.2356

VAEEESSEDDEDSVDR
Confirmed sites: "@S:6,@S:7"
Ambiguous sites:

MS/MS Fragmentation of VAEEESSEDDEDSVDR
Found in AT1G30960.1, GTP-binding protein (ERG)

Match to Query 3306: 1969.633826 from(985.824189,2+)
Elution from: 22.995 to 22.995 scan no 1756 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1969.6350
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 3.2e-006
Matched b ions: b(5), b(7)-196, b(8)-196, b(9)-98, b(9), b(10), b(11)-196, b(11), b(11)-98, b (12), b(12)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)-98, y(11)-196, y(11)-98, y(11), y(12)++, y(13)-98++, y(13)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2357

VAEEESEDDEDSVDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VAEEESEDDEDSVDR
Found in AT1G30960.1, GTP-binding protein (ERG)

Match to Query 2780: 1889.665224 from(945.839888,2+)
Elution from: 21.123 to 21.123 scan no 1415 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1889.6687
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 1.3e-005
Matched b ions: b(5), b(9), b(10), b(11), b(12), b(14), b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8)+, y(9), y(10), y(11), y(13)+, y(15)+
Precursor origin neutral loss: +

Peptide No.2358
VAIASVFGNDSDED
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VAIASVFGNDSDED
Found in AT5G26610.1, D111/G-patch domain-containing protein

Match to Query 1532: 1517.591036 from(759.802794,2+)
Elution from: 56.629 to 56.629 scan no 5661 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2357/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1517.5922
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 Expect: 0.06
Matched b ions: b(4), b(6), b(9)++
Matched y ions: y(5)-98++, y(7), y(7)++, y(8), y(9), y(10), y(13)++
Precursor origin neutral loss:

Peptide No.2359
VALTSLQSLPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VALTSLQSLPR
Found in AT1G76850.1, SEC5A (EXOCYST COMPLEX COMPONENT SEC5)

Match to Query 1177: 1263.658200 from(632.836376,2+)
Elution from: 46.271 to 46.271 scan no 4806 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1263.6588  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 59 Expect: 8.4e-006  
Matched b ions: b(4), b(7), b(8), b(9)-98, b(9)  
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9)+, y(10)+  
Precursor origin neutral loss: +

---

**Peptide No.2360**

VAPEYIGGSDSESGK  
Confirmed sites:  
Ambiguous sites: @S:11orS:13orS:9

MS/MS Fragmentation of VAPEYIGGSDSESGK  
Found in AT3G15120.1, AAA-type ATPase family protein

Match to Query 2379: 1574.649196 from(788.331874,2+)  
Elution from: 29.699 to 29.699 scan no 2379 polarity:+

---
Monoisotopic mass of neutral peptide Mr(calc): 1574.6501
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0088
Matched b ions: b(6), b(7), b(13)-98, b(14)++
Matched y ions: y(8)++, y(8), y(8)-98, y(9), y(10), y(12)++, y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.2361
VAPTVLMTSPSSPQR
Confirmed sites:
Ambiguous sites: "@S:11orS:12orS:15, @S:12orS:15"

MS/MS Fragmentation of VAPTVLMTSPSSPQR
Found in AT2G33620.1, DNA-binding family protein / AT-hook protein 1 (AHP1)

Match to Query 3389: 1873.802974 from(937.908763,2+)
Elution from: 39.134 to 39.134 scan no 3890 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2360/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1873.8046
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.048
Matched b ions: b(6), b(7), b(8), b(9), b(12)-196++, b(14)-196++, b(14)-196
Matched y ions: y(6), y(7), y(7)-98, y(8), y(9), y(10), y(10)-98, y(13)+, y(14)+, y(14)-98++, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.2362

VAPTQVLMTPSSPQSR
Confirmed sites: @S:15
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of VAPTQVLMTPSSPQSR
Found in AT2G33620.1, DNA-binding family protein / AT-hook protein 1 (AHP1)

Match to Query 3377: 1873.803934 from(937.909243,2+)
Elution from: 39.095 to 39.095 scan no 3892 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1873.8046
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00064
Matched b ions: b(6), b(7), b(8), b(9), b(14)
Matched y ions: y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(11), y(11)-98, y(12)-98++, y(13)+, y(14)+, y(14)-98++, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2363
VAPTQVLMTPSSPQSR
Confirmed sites: @S
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of VAPTQVLMTPSSPQSR
Found in AT2G33620.1, DNA-binding family protein / AT-hook protein 1 (AHP1)

Match to Query 2713: 1777.843368 from(889.928960,2+)
Elution from: 38.855 to 38.855 scan no 3833 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2362/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1777.8434
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 5.3e-006
Matched b ions: b(6), b(7), b(8), b(9)
Matched y ions: y(4), y(6), y(7), y(8), y(8)-98, y(9)-98++, y(9), y(10), y(11), y(13)++, y(14)++, y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2364
VAPTQLMTTPSSPQSR
Confirmed sites: @S:15
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of VAPTQLMTTPSSPQSR
Found in AT2G33620.1, DNA-binding family protein / AT-hook protein 1 (AHP1)

Match to Query 3017: 1857.807858 from(929.911205,2+)
Elution from: 43.457 to 43.457 scan no 4442 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1857.8097
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 5.8e-005
Matched b ions: b(7), b(8)
Matched y ions: y(4), y(4)-98, y(6), y(7)-98, y(7), y(8), y(8)-196, y(9), y(10), y(11), y(14)+, y(15)++
Precursor origin neutral loss: +

Peptide No.2365

VAPTQVLMTPSSPQSR
Confirmed sites:
Ambiguous sites: @S:11orS:12orS:15

MS/MS Fragmentation of VAPTQVLMTPSSPQSR
Found in AT2G33620.1, DNA-binding family protein / AT-hook protein 1 (AHP1)

Match to Query 3153: 1777.840528 from(889.927540,2+)
Elution from: 39.894 to 39.894 scan no 3991 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2364/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1777.8434  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 32 Expect: 0.0054  
Matched b ions: b(8), b(9)  
Matched y ions: y(7), y(8), y(9), y(10), y(11)-98, y(14)++, y(15)++  
Precursor origin neutral loss:

Peptide No.2366

VASPENGAVR  
Confirmed sites: @S:3  
Ambiguous sites:

MS/MS Fragmentation of VASPENGAVR  
Found in AT5G52040.1, ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding

Match to Query 624: 1078.479794 from(540.247173,2+)  
Elution from: 18.766 to 18.766 scan no 1137 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2365/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1078.4808
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 2.2e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)+, b(5), b(5)-98, b(6)-98, b(6)+, b(8)-98, b(9)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)+, y(8)-98++, y(8), y(8)-98, y(8)+, y(9)+, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2367

VAVNMAAPQVSDSV
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VAVNMAAPQVSDSV
Found in AT5G09620.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 2115: 1466.646160 from(734.330356,2+)
Elution from: 45.958 to 45.958 scan no 4657 polarity:+

file:///C/Document%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2366/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1466.6476  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 65 Expect: 2.8e-006  
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(12), b(13)++  
Matched y ions: y(4), y(5), y(7), y(7)-98, y(8), y(9), y(9)-98, y(11), y(12)-98, y(13)++, y(13)-98++  
Precursor origin neutral loss: +

Peptide No.2368

VCDSCYVKLSKVSEINDTNR  
Confirmed sites: "@S:4,@Y:6,@S:10"  
Ambiguous sites:

MS/MS Fragmentation of VCDSCYVKLSKVSEINDTNR  
Found in AT1G76950.1, zinc finger protein (PRAF1) / regulator of chromosome condensation (RCC1) family protein

Match to Query 4122: 2626.026210 from(1314.020381,2+)  
Elution from: 37.463 to 37.463 scan no 3667 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2367/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2626.0246
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.047
Matched b ions: b(3), b(6)+, b(6), b(7)-98, b(7), b(10), b(10)-196, b(12)-196, b(13)-196
Matched y ions: y(5), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(16)-98, y(16)-98++, y(19)+, y(19)-98++
Precursor origin neutral loss: +

---

Peptide No.2369

VCVEVPLESSS
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VCVEVPLESSS
Found in AT5G47680.1, RNA binding / tRNA methyltransferase

Match to Query 1279: 1284.530418 from(643.272485,2+)
Elution from: 47.053 to 47.053 scan no 4908 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1284.5308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.1e-005
Matched b ions: b(3), b(4), b(5), b(7), b(8), b(10)
Matched y ions: y(6), y(7), y(8), y(10)++
Precursor origin neutral loss: +

Peptide No.2370
VDAASRSQSPYAAE
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VDAASRSQSPYAAE
Found in AT5G64200.1, ATSC35 ("Arabidopsis thaliana arginine-serine-rich splicing factor 35, 35 kDa protein"); RNA bindin

Match to Query 2217: 1610.600438 from(806.307495,2+)
Elution from: 23.989 to 23.989 scan no 1799 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2369/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1610.6014
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.012
Matched b ions: b(6), b(7), b(7)-98, b(9)-98, b(11), b(11)-196++, b(11)-98++, b(11)++,
b(12)-196++, b(12), b(12)-98++, b(12)++, b(12)-98, b(13)-98++, b(13)+, b(13)-196++
Matched y ions: y(5), y(6), y(8)+, y(9)-98, y(9)+, y(10), y(11), y(11)-98++, y(12)+, y(13)+
Precursor origin neutral loss: +

Peptide No.2371
VDDGNESEGDESPEFSFLFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VDDGNESEGDESPEFSFLFK
Found in AT5G64070.1, phosphatidylinositol 4-kinase (PI4K)

Match to Query 3744: 2179.844130 from(1090.929341,2+)
Elution from: 58.549 to 58.549 scan no 6131 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2370/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2179.8470
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00021
Matched b ions: b(8), b(10)-98, b(11)-98, b(12)-98, b(14), b(15)-98
Matched y ions: y(5), y(7), y(8), y(10), y(11), y(12), y(13), y(14), y(16)-98++, y(16)++, y(18)++
Precursor origin neutral loss: +

Peptide No.2372

VDKSMPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VDKSMPK
Found in AT1G35940.1, AT hook motif-containing protein-related

Match to Query 360: 899.381712 from(450.698132,2+)
Elution from: 31.299 to 31.299 scan no 2788 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2371/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 899.3823
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.012
Matched b ions: b(3), b(5), b(6)-98, b(6)
Matched y ions: y(4), y(5)+, y(6)+
Precursor origin neutral loss: +

Peptide No.2373
VDLNKLPDPETSDDDD
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VDLNKLPDPETSDDDD
Found in AT4G36900.1, RAP2.10 (related to AP2 10); DNA binding / transcription factor

Match to Query 2752: 1751.712966 from(876.863759,2+)
Elution from: 44.100 to 44.100 scan no 4491 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1751.7139
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.00056
Matched b ions: b(5), b(6), b(7), b(8), b(10), b(11), b(14)++
Matched y ions: y(7), y(9), y(10), y(14)++
Precursor origin neutral loss: +

Peptide No.2374

VDMEVETATPK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of VDMEVETATPK
Found in AT5G62440.1, similar to defective chloroplasts and leaves protein-related / DCL protein-related [Arabidopsis thab]

Match to Query 1127: 1298.544820 from(650.279686,2+)
Elution from: 29.131 to 29.131 scan no 2499 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1298.5465
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 1.1e-007
Matched b ions: b(4), b(5), b(8)
Matched y ions: y(2), y(3), y(3)-98, y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98++, y(9)+, y(9), y(10)+, y(10)
Precursor origin neutral loss: +

---

Peptide No.2375

VDSEGVLCGANFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VDSEGVLCGANFK
Found in AT4G27450.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G15450.1); similar to unknown [Glycine m

Match to Query 2142: 1474.614910 from(738.314731,2+)
Elution from: 42.898 to 42.898 scan no 4350 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1474.6163
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 Expect: 1.3e-009
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4)+, b(4), b(5)-98, b(5)+, b(6)-98, b(6), b(7)+, b(7)-98, b(7), b(7)-98++, b(8)+, b(8)-98, b(8), b(9)-98, b(9)-98++, b(9), b(10)-98, b(10), b(11)-98, b(11), b(11)+, b(12)-98, b(12), b(12)+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)+, y(8), y(8)+, y(9), y(10), y(10)+, y(11)-98, y(11)-98++, y(11), y(11)+, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2376

VDSFDVEALEVPGAPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VDSFDVEALEVPGAPR
Found in AT5G09400.1, KUP7 (K+ uptake permease 7); potassium ion transporter

Match to Query 2860: 1779.806618 from(890.910585,2+)
Elution from: 57.603 to 57.603 scan no 6168 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1779.8080
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 Expect: 1.1e-005
Matched b ions: b(7)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(14), b(15)++, b(15)-98
Matched y ions: y(5), y(6), y(7), y(10)
Precursor origin neutral loss:

Peptide No.2377

VDSHMSSFLTTGK
Confirmed sites:
Ambiguous sites: @T:10orT:11orS:6orS:7

MS/MS Fragmentation of VDSHMSSFLTTGK
Found in AT2G04270.1, glycoside hydrolase starch-binding domain-containing protein

Match to Query 2256: 1488.636194 from(745.325373,2+)
Elution from: 52.542 to 52.542 scan no 5479 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1488.6320
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.059
Matched b ions: b(11)-98++
Matched y ions: y(8)++, y(10)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.2378
VDSSGDVCAGTFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VDSSGDVCAGTFK
Found in AT5G43830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G22850.1); similar to aluminum-induced p

Match to Query 2174: 1421.552498 from(711.783525,2+)
Elution from: 30.843 to 30.843 scan no 2791 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1421.5534
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 5.6e-010
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5)-98++, b(5), b(6)-98, b(6), b(7)+, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11), y(11)-98, y(11)+, y(12)+, y(12), y(12)-98, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2379
VDSSGEVCGVTFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VDSSGEVCGVTFK
Found in AT3G22850.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G43830.1); similar to aluminum-induced p

Match to Query 2307: 1463.598900 from(732.806726,2+)
Elution from: 38.694 to 38.694 scan no 3838 polarity:+

200 400 600 800 1000 1200 1400
y(2) b(2), b(5)-98++

200 400 600 800 1000 1200 1400
b(3) y(2), b(4)-98, b(5)-98++, b(5), b(6)-98, b(6), b(7)+, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12)

200 400 600 800 1000 1200 1400
y(3) y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11), y(11)-98, y(11)+, y(12)+, y(12), y(12)-98, y(12)-98++
Monoisotopic mass of neutral peptide Mr(calc): 1463.6003
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(should in table), 0.0000
Ions Score: 95 Expect: 1.8e-009
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5)-98++, b(5), b(6)-98, b(6), b(7)-98, b(7), b(7)+, b(8)-98, b(8), b(8)+, b(9)-98, b(9)+, b(10)-98, b(10), b(10)-98++, b(10)+, b(11)-98, b(11), b(11)+, b(12), b(12)-98, b(12)-98++, b(12)+
Matched y ions: y(2), y(3), y(4), y(5), y(5)+, y(6), y(6)+, y(7), y(8), y(8)+, y(9), y(9)+, y(10), y(10)+, y(11)-98, y(11), y(11)-98++, y(11)+, y(12)+, y(12), y(12)-98, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2380

VDSSGEVCVTFK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VDSSGEVCVTFK
Found in AT3G22850.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G43830.1); similar to aluminum-induced p

Match to Query 1956: 1463.598552 from(732.806552,2+)
Elution from: 38.699 to 38.699 scan no 3817 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abib/9739/2597/2008/03/14 15:08:30
Monoisotopic mass of neutral peptide Mr(calc): 1463.6003
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 7.4e-008
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)+, b(12)-98, b(12), b(12)-98+
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9), y(9)+, y(10)-98++, y(11)-98, y(11), y(11)-98++, y(11)+, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2381

VDSSQNWAGHI
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VDSSQNWAGHI
Found in AT5G43830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G22850.1); similar to aluminum-induced p

Match to Query 1299: 1292.517662 from(647.266107,2+)
Elution from: 41.042 to 41.042 scan no 4089 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1292.5186
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 1.4e-006
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(7)-98++, b(8)-98, b(8), b(9)-98, b(10)++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9), y(9)-98, y(9)++, y(10)+, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2382
VDSSQNWAGHI
Confirmed sites: @S:3orS:4
Ambiguous sites: 
MS/MS Fragmentation of VDSSQNWAGHI
Found in AT5G43830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G22850.1); similar to aluminum-induced p
Match to Query 1206: 1292.517212 from(647.265882,2+)
Elution from: 40.242 to 40.242 scan no 3891 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1292.5186  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 39 Expect: 0.00064  
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(10)-98++, b(10)++  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(9)-98++, y(9), y(9)-98, y(10)+, y(10)-98++  
Precursor origin neutral loss: +

---

**Peptide No.2383**

**VDSSVEWEPLR**  
Confirmed sites:  
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of **VDSSVEWEPLR**  
Found in **AT1G27100.1**, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G69890.1); similar to Cytosolic fatty-ac

Match to Query 1648: 1395.605758 from(698.810155,2+)  
Elution from: 47.700 to 47.700 scan no 4992 polarity:+

---

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2382/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1395.6071
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0023
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(7)+, b(8)-98, b(8), b(9)-98
Matched y ions: y(3), y(4), y(6), y(7), y(9)-98++, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2384

VEASGSDDEPEDALQATIDK
Confirmed sites: @S:4orS:6

MS/MS Fragmentation of VEASGSDDEPEDALQATIDK
Found in AT3G01180.1, glycogen synthase, putative

Match to Query 3295: 2283.926100 from(1142.970326,2+)
Elution from: 48.807 to 48.807 scan no 4875 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2283.9267
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000
Ions Score: 52 Expect: 4.8e-005
Matched b ions: b(9), b(10)-98, b(10), b(11)-98, b(13)-98, b(14), b(15)-98, b(15), b(16)-98, b(17)-98, b(18)+, b(19)-98++
Matched y ions: y(7), y(10), y(11), y(12), y(13), y(14), y(18)-98++, y(19)+, y(19)-98++, y(20)+, y(20)-98++
Precursor origin neutral loss: +

Peptide No.2385
VEDLWDEQKPQLSPNEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VEDLWDEQKPQLSPNEK
Found in AT3G48530.1, CBS domain-containing protein

Match to Query 3002: 2133.959934 from(712.327254,3+)
Elution from: 41.791 to 41.791 scan no 4117 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2133.9619
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 1.5e-006
Matched b ions: b(3), b(4), b(5), b(8), b(9), b(13)-98++, b(16)+
Matched y ions: y(4), y(5)+, y(5), y(6)-98, y(7)+, y(8)+, y(8)-98++, y(9)+, y(11)+, y(12)-98++, y(12)+, y(13)+, y(13)-98++, y(14)+, y(14)-98++, y(15)+, y(15)-98+++, y(16)+
Precursor origin neutral loss: +

Peptide No.2386
VEEVKDESSDDAGMMGLFD
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)
Match to Query 3976: 2152.820312 from(1077.417432,2+)
Elution from: 59.053 to 59.053 scan no 6244 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2152.8217
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.014
Matched b ions: b(7), b(8), b(12), b(13), b(14), b(15), b(18)-98++, b(18)++
Matched y ions: y(9), y(18)++
Precursor origin neutral loss: +

Peptide No. 2387

VEEVKDESSDDAGMMGLFD
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 3913: 2168.813060 from(1085.413806,2+)
Elution from: 51.316 to 51.316 scan no 5396 polarity:+

file:///C/\Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2386/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2168.8166
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 Expect: 0.0039
Matched b ions: b(6), b(7), b(8)-98, b(10), b(12)-98, b(14), b(14)+, b(14), b(15)+, b(17)-98++, b(17)+, b(18)+, b(18)-98++
Matched y ions: y(5), y(7), y(8), y(9), y(12), y(13), y(14), y(14)-98++, y(15), y(15)+, y(16)+, y(16)-98++, y(17)-98++, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2388

VEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4376: 2232.785038 from(1117.399795,2+)
Elution from: 67.149 to 67.149 scan no 7163 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2387/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2232.7880
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 1.6e-006
Matched b ions: b(4), b(5), b(7), b(8)-98, b(9)+, b(9)-196, b(9)-98, b(10), b(10)-98, b(11), b(11)-196, b(11)-98, b(12), b(12)-196, b(12)-98, b(13), b(13)-98++, b(13)-98, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(16), b(16)-196++, b(16)+, b(16)-98, b(16)-98++, b(16)-196, b(16)-98++, b(17), b(17)-196++, b(17)-98, b(17)+, b(18)-98++, b(18)-196++, b(18)+
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12)-196, y(12), y(13), y(14)-98, y(14), y(14)-196, y(15), y(15)-196, y(15)+, y(16), y(16)-196++, y(17)-196++, y(17)-98++, y(17)+, y(18)-98++, y(18)+
Precursor origin neutral loss: +

Peptide No.2389

VEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)
Match to Query 4073: 2248.780292 from(1125.397422,2+)  
Elution from: 55.818 to 55.818 scan no 5908 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2248.7829  
Fixed modifications: Carbamidomethyl (C) 
Variable modifications:  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 65 Expect: 6.8e-007  
Matched b ions: b(4), b(6), b(7), b(8)-98, b(9)++, b(10), b(11), b(12), b(12)-98, b(13), b(14)-196++, b(14)-98++, b(14), b(14)-98, b(15), b(15)-98, b(16), b(16)-98++, b(16)++, b(17)-196++, b(17), b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(18)-196++  
Matched y ions: y(5), y(7), y(8), y(11), y(12)-196, y(14)-98, y(14), y(15), y(15), y(16), y(16)-98++, y(18)-98++, y(18)++  
Precursor origin neutral loss: +

Peptide No.2390

VEEVKDESSDDAGMMGLFD  
Confirmed sites: "@S:8,@S:9"  
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD  
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)
Match to Query 3894: 2264.772874 from (1133.393713, 2+)
Elution from: 46.824 to 46.824 scan no 4795 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2264.7779
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 Expect: 0.018
Matched b ions: b(7), b(8)-98, b(10), b(11), b(11)-98, b(12), b(12)-196, b(12)-98, b(14), b(17)-196++, b(17)-98++, b(17)+, b(18)-98++, b(18)-196++, b(18)+
Matched y ions: y(7), y(8), y(9), y(12), y(12)-196, y(14), y(15), y(17)-98++, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2391

VEEVKDESSDDAGMMGLFD
Confirmed sites: "@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)
Match to Query 4115: 2248.780192 from (1125.397372, 2+)  
Elution from: 56.730 to 56.730 scan no 6019 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2248.7829  
Fixed modifications: Carbamidomethyl (C)

Variable modifications:
  S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
  S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
  M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 56 Expect: 6.3e-006
Matched b ions: b(4), b(6), b(7), b(8), b(10), b(11), b(12)-98, b(12)-96, b(13), b(13)-98, b(14)-196++, b(14), b(15), b(15)-98, b(17)-98++, b(17), b(17)-196++, b(17)-98, b(17)-98++, b(18)-98++, b(18)-196++, b(18)++  
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(12)-196, y(12), y(14), y(14)-98, y(15)++, y(16), y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++

Precursor origin neutral loss: +

Peptide No.2392

VEEVKDESSDDAGMMGLFD

Confirmed sites: @S:9

Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Mascot Search Results: Peptide View

Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 3916: 2152.816210 from(1077.415381,2+)
Elution from: 60.242 to 60.242 scan no 6367 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2152.8217
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.018
Matched b ions: b(7), b(12)-98, b(12), b(14), b(15), b(16)-98++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(7), y(8), y(11), y(12), y(14), y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2393

VEEVKDESSDDAGMMGLFD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4208: 2168.812508 from(1085.413530,2+)

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2392/2597) [2008/03/14 15:08:30]
Elution from: 49.398 to 49.398 scan no 5196 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2168.8166  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
Ions Score: 35 Expect: 0.0011  
Matched b ions: b(7), b(8), b(11), b(12), b(12)-98, b(13), b(14), b(15), b(15)-98, b(17)-98++, b(17)++, b(18)++  
Matched y ions: y(8), y(14), y(15)++, y(16)-98++  
Precursor origin neutral loss:

---

Peptide No.2394

VEEVKDESSDDAGMMGLFD  
Confirmed sites: @S:9  
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDDAGMMGLFD  
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4288: 2184.807724 from(1093.411138,2+)  
Elution from: 42.020 to 42.020 scan no 4232 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2184.8115
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 1.1e-005
Matched b ions: b(6), b(7), b(8), b(9)-98, b(10), b(11), b(12), b(14), b(15), b(15)+, b(16), b(16)+, b(17)+, b(18)+
Matched y ions: y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(18)+
Precursor origin neutral loss: +

Peptide No.2395

VEEVKDESSDAGMMGLFD
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VEEVKDESSDAGMMGLFD
Found in AT3G28500.1, 60S acidic ribosomal protein P2 (RPP2C)

Match to Query 4209: 2168.812630 from(1085.413591,2+)
Elution from: 51.505 to 51.505 scan no 5450 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea...
Monoisotopic mass of neutral peptide Mr(calc): 2168.8166
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 Expect: 0.00011
Matched b ions: b(4), b(7), b(8), b(11)-98, b(11), b(12), b(12)-98, b(13), b(14), b(14)+, b(15), b(17)+, b(17), b(17)-98++, b(18)+, b(18)-98++
Matched y ions: y(5), y(7), y(8), y(11), y(14), y(14)+, y(15)+, y(16)-98++, y(17)+, y(18)+, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2396

VEFENSDSDPDSPSDLR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSDPDSPSDLR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2725: 1862.719802 from(932.367177,2+)
Elution from: 35.392 to 35.392 scan no 3304 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2395/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1862.7207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 1.1e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(10), b(11)-98, b(12)+, b(12)-98, b(13), b(13)-98, b(14), b(15), b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98+, y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)-98+, y(12), y(12)-98, y(13), y(13)-98, y(14)-98+, y(14)+, y(14)-98, y(14), y(15)+, y(15)-98+
Precursor origin neutral loss: +

Peptide No.2397

VEFENSDDSPSDLR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of VEFENSDDSPSDLR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 3380: 1862.719782 from(932.367167,2+)
Elution from: 37.554 to 37.554 scan no 3552 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2396/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1862.7207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 1.9e-08
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(12), b(13), b(13)-98, b(13)++, b(14), b(15)
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(9), y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(13)++, y(14)-98++, y(14), y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2398

VEFENSDSDSPSDSLR
Confirmed sites: "@S:6,@S:10"
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSDSPSDSLR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 3302: 1942.683892 from(972.349222,2+)
Elution from: 39.829 to 39.829 scan no 3928 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.6870
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 3.3e-007
Matched b ions: b(3), b(5), b(6)-98, b(7), b(9), b(10)-98, b(11)-196, b(13), b(13)-98, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(10), y(11)-98, y(11), y(12), y(12)-98, y(12)++, y(13), y(13)-98, y(13)+, y(14)-196++, y(14)+, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2399
VEFENSDSDPSDSLRL
Confirmed sites: "@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSDPSDSLRL
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 3243: 1942.684508 from(972.349530,2+)
Elution from: 40.266 to 40.266 scan no 4074 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2398/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1942.6870
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 6.8e-007
Matched b ions: b(5), b(7), b(8)-196, b(9)-98, b(9), b(10)-98, b(10), b(11)-196, b(13), b(13)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(9)-98, y(10), y(11), y(11)-98, y(12), y(12)-196, y(12)-98, y(13), y(14)-98++, y(14)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2400

VEFENSDSDSPSDSLR
Confirmed sites: "@S:6,@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSDSPSDSLR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2756: 2022.649442 from(1012.331997,2+)
Elution from: 44.565 to 44.565 scan no 4419 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2022.6534
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0033
Matched b ions: b(7)-98, b(7), b(8)-98++, b(9), b(10)-98, b(11)-196, b(13)-98, b(13), b(14)
Matched y ions: y(6), y(7), y(8), y(9), y(12)+, y(13), y(14)-98++, y(14)-196++, y(14)+, y(15)+, y(15)-98++, y(15)-294
Precursor origin neutral loss: +

Peptide No.2401

VEFENSDSDSPSDSLRL
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSDSPSDSLRL
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 3432: 1862.718424 from(932.366488,2+)
Elution from: 35.479 to 35.479 scan no 3448 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1862.7207
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 1.4e-09
Matched b ions: b(7), b(8), b(10)-98, b(10), b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14)-98+, y(15)++
Precursor origin neutral loss: +

Peptide No.2402
VEFENSDSPDSPSDLR
Confirmed sites: "@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of VEFENSDSPDSPSDLR
Found in AT5G11110.1, ATSPS2F (sucrose phosphate synthase 2F); sucrose-phosphate synthase

Match to Query 2541: 1942.685858 from(972.350205,2+)
Elution from: 39.858 to 39.858 scan no 3880 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.6870
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 3.7e-005
Matched b ions: b(3), b(5), b(7), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11)-196, b(13)-98, b(13), b(15)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8)-98, y(9)-98, y(9), y(9)-196, y(10)+, y(10), y(10)-98, y(11)-98, y(11), y(11)-196, y(12)-98, y(12), y(13), y(13)-98, y(14)+, y(14)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.2403
VELNNDGLCEGSPNK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VELNNDGLCEGSPNK
Found in AT5G16680.1, PHD finger family protein

Match to Query 2059: 1724.704046 from(863.359299,2+)
Elution from: 31.896 to 31.896 scan no 2862 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2402/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1724.7076
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.002
Matched b ions: b(12)-98
Matched y ions: y(5), y(9), y(10), y(11), y(12)++, y(13)++, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.2404

VEPEESESDDVIIVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of VEPEESESDDVIIVR
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 3223: 1794.791180 from(898.402866,2+)
Elution from: 43.151 to 43.151 scan no 4383 polarity:+

file:///C//Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2403/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1794.7924
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 8.6e-06
Matched b ions: b(9), b(10), b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(10)-98, y(12)+, y(13)-98++, y(13)+, y
(13), y(13)-98, y(14)+
Precursor origin neutral loss: +

Peptide No.2405

VEPEESESDDVIIVR
Confirmed sites:
Ambiguous sites: @S:6orS:8

MS/MS Fragmentation of VEPEESESDDVIIVR
Found in AT1G19870.1, IQD32 (IQ-domain 32); calmodulin binding

Match to Query 2901: 1794.792042 from(898.403297,2+)
Elution from: 41.853 to 41.853 scan no 4232 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2404/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1794.7924  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 40 Expect: 0.00078  
Matched b ions: b(5), b(10)++, b(10), b(11)-98++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(14)  
Matched y ions: y(3), y(4), y(5), y(6), y(10), y(12), y(12)++, y(13)++, y(13)-98, y(13)-98++, y(14)++  
Precursor origin neutral loss: +  

Peptide No.2406  
VFCSQVSNLSTEMAR  
Confirmed sites: "@S:7,@S:10"  
Ambiguous sites:  
MS/MS Fragmentation of VFCSQVSNLSTEMAR  
Found in AT3G13300.1, VCS (VARICOSE); nucleotide binding  
Match to Query 3035: 1887.727916 from(944.871234,2+)  
Elution from: 45.735 to 45.735 scan no 4734 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1887.7297  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 39 Expect: 0.00094  
Matched b ions: b(6), b(7)+, b(8)-98, b(9), b(11), b(12)-98, b(13)-98, b(13)-98++, b(14)-98, b(14), b(14)-196++  
Matched y ions: y(3), y(4), y(5), y(6)-98, y(7), y(7)-98, y(9)-98, y(9), y(9)-196, y(10), y(10)-98, y(12), y(13)-98, y(13)-98++, y(14)-98++, y(14)+  
Precursor origin neutral loss: +

Peptide No.2407

VFCSQVSNL Stevens  
Confirmed sites: @S:7  
Ambiguous sites: @S:10 or T:11  

MS/MS Fragmentation of VFCSQVSNLSTE MAR  
Found in AT3G13300.1, VCS (VARICOSE); nucleotide binding  

Match to Query 3482: 1887.727094 from(944.870823,2+)  
Elution from: 45.724 to 45.724 scan no 4774 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2406/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1887.7297
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.015
Matched b ions: b(6), b(7), b(9)-98, b(9), b(12)-98, b(12)-196++, b(13)-98, b(13), b(13)-98+ +, b(14)-98
Matched y ions: y(6)-98, y(6), y(7), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(13)-98, y(13), y (13)-98++, y(14)+++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2408
VFDLEDLLRASAEVLGK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VFDLEDLLRASAEVLGK
Found in AT1G48480.1, RKL1 (Receptor-like kinase 1); ATP binding / kinase/ protein serine/threonine kinase

Match to Query 3361: 1953.977956 from(977.996254,2+)
Elution from: 68.804 to 68.804 scan no 7279 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2407/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1953.9812
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0048
Matched b ions: b(9), b(10), b(11)-98, b(13)-98++, b(13)-98, b(13), b(13)+, b(14), b(14)-98++ , b(15), b(15)-98
Matched y ions: y(3), y(6), y(7)-98, y(8)-98, y(9), y(14)+, y(16)+
Precursor origin neutral loss: +

Peptide No.2409
VGADLDSDSEK
Confirmed sites: @5:7
Ambiguous sites:

MS/MS Fragmentation of VGADLDSDSEK
Found in AT4G02510.1, TOC159 (translocon outer membrane complex 159)

Match to Query 1272: 1214.469398 from(608.241975,2+)
Elution from: 23.022 to 23.022 scan no 1692 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1214.4704
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 2.2e-09
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9)-98++, b(10)-98, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(6)+, y(7)-98, y(7), y(7)+, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)+, y(10)+, y(10), y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2410
VGEADIVISHIQKPESPK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of VGEADIVISHIQKPESPK
Found in AT5G43560.1, meprin and TRAF homology domain-containing protein / MATH domain-containing protein

Match to Query 3718: 2026.014237 from(676.345355,3+)
Elution from: 41.505 to 41.505 scan no 4211 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2409/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2026.0135
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(showed in table), 97.9769
Ions Score: 28 Expect: 0.012
Matched b ions: b(6)
Matched y ions: y(5), y(8)-98, y(11)-98++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.2411

VGEDIRSDSEDDDD
Confirmed sites: "@S:7,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VGEDIRSDSEDDDD
Found in AT3G19260.1, LAG1 HOMOLOG 2 (LONGEVITY ASSURANCE GENE1 HOMOLOG 2)

Match to Query 3133: 1725.530052 from(863.772302,2+)
Elution from: 24.029 to 24.029 scan no 1861 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1725.5291
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.011
Matched b ions: b(7)-98, b(10)-98, b(11)+, b(12)+, b(13)-98++, b(13)-196++, b(13)+
Matched y ions: y(8), y(10), y(13)-98++, y(13)+
Precursor origin neutral loss: +

Peptide No.2412

VGFPGasR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VGFPGasR
Found in AT5G13540.1, Stone et al. (Plant Cell, 2007, PubMed ID 17194765) suggested that this locus is misannotated, with

Match to Query 263: 869.378648 from(435.696600,2+)
Elution from: 30.456 to 30.456 scan no 2694 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 869.3796
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0007
Matched b ions: b(3), b(4), b(6)
Matched y ions: y(1), y(3), y(4)+, y(4), y(5)-98++, y(5)-98, y(5), y(5)++, y(6), y(6)++, y(6)-98+++, y(6)-98, y(7)++, y(7)
Precursor origin neutral loss: +

Peptide No.2413
VGSGMIVAIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VGSGMIVAIK
Found in AT4G35600.1, CONNEXIN 32; kinase

Match to Query 907: 1053.529668 from(527.772110,2+)
Elution from: 45.396 to 45.396 scan no 4710 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2412/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1053.5293
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0026
Matched b ions: b(3), b(7)-98, b(7), b(8)-98, b(9)-98
Matched y ions: y(5), y(7), y(8)-98++, y(8)-98, y(8), y(9)+, y(9)
Precursor origin neutral loss: +

Peptide No.2414
VGSLESDQTLSMATLIEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VGSLESDQTLSMATLIEK
Found in AT1G43710.1, EMB1075 (EMBRYO DEFECTIVE 1075); carboxy-lyase

Match to Query 3298: 2000.935394 from(1001.474973,2+)
Elution from: 60.882 to 60.882 scan no 6360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2000.9377
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 5e-007
Matched b ions: b(8), b(10)-98, b(10), b(11)-98, b(12)-98, b(13)
Matched y ions: y(3), y(6), y(7), y(8), y(10), y(11), y(13), y(14), y(16)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.2415

VGSTEEIEDESMK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VGSTEEIEDESMK
Found in AT3G04820.1, pseudouridylate synthase

Match to Query 1869: 1532.594196 from(767.304374,2+)
Elution from: 31.947 to 31.947 scan no 2848 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.5953  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S3 : Phospho (ST), with neutral losses 97.9769 (shown in table), 0.0000  
Ions Score: 51 Expect: 3.1e-005  
Matched b ions: b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(10)++  
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(12)++, y(12)-98++  
Precursor origin neutral loss: +

Peptide No.2416

VGSTEEIEDESMTK  
Confirmed sites:  
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of VGSTEEIEDESMTK  
Found in AT3G04820.1, pseudouridylate synthase  

Match to Query 2085: 1532.594012 from(767.304282,2+)  
Elution from: 32.102 to 32.102 scan no 2927 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1532.5953
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 3.4e-005
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(10)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2417

VGSVQNWSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VGSVQNWSK
Found in AT3G22850.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G43830.1); similar to aluminum-induced p

Match to Query 641: 1083.474112 from(542.744332,2+)
Elution from: 27.620 to 27.620 scan no 2321 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1083.4750
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 9.2e-007
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98++, b(8)-98, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98++, y(7)-98, y(7), y(7)+, y(8)+, y(8), y(8)-98, y(8)-98++
Precursor origin neutral loss: +

Peptide No.2418

VGVEEELPVSESLK
Confirmed sites:
Ambiguous sites: @S:11orS:13

MS/MS Fragmentation of VGVEEELPVSESLK
Found in AT4G02510.1, TOC159 (translocon outer membrane complex 159)

Match to Query 2838: 1692.821118 from(847.417835,2+)
Elution from: 51.121 to 51.121 scan no 5311 polarity:+

file:///C|/Documents%20and%20%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2417/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1692.8222
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0044
Matched b ions: b(7), b(9), b(10)
Matched y ions: y(5), y(5)-98, y(6), y(7)-98, y(8), y(10), y(14)+
Precursor origin neutral loss: +

Peptide No.2419

VGVGAESPAAATDCSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VGVGAESPAAATDCSK
Found in AT3G54760.1, dentin sialophosphoprotein-related

Match to Query 2633: 1598.662714 from(800.338633,2+)
Elution from: 25.608 to 25.608 scan no 2041 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1598.6647
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 6e-009
Matched b ions: b(3), b(4), b(5), b(6), b(6)+, b(7)-98, b(7)+, b(8)-98, b(8), b(9)-98, b(9)+, b(9), b(9)-98+, b(10), b(10)-98, b(10)-98+, b(11)+, b(11)-98, b(11), b(11)-98++, b(12)-98, b(12), b(13), b(13)+, b(13)-98, b(13)-98+, b(14)-98, b(14), b(14)-98+, b(15), b(15)-98, b(15)+
Matched y ions: y(3), y(4), y(5), y(6), y(6)+, y(7), y(7)+, y(8), y(9), y(10), y(10)-98+, y(10)-98, y(11)-98, y(11), y(11)-98++, y(11)+, y(12), y(12)-98, y(12)-98++, y(12)+, y(13)-98, y(13), y(13)-98++, y(13)+, y(14)-98++, y(14)-98, y(14)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2420

VHACVGGSVVR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of VHACVGGSVVR
Found in AT1G54270.1, ELF4A-2 (eukaryotic translation initiation factor 4A-2); ATP-dependent helicase
Match to Query 1282: 1221.531478 from(611.773015,2+)
Elution from: 19.385 to 19.385 scan no 1211 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1221.5325
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 2.3e-005
Matched b ions: b(2), b(3), b(4), b(5), b(5)+, b(6), b(7), b(7)+, b(8)-98, b(8), b(9)-98, b(10), b(10)-98, b(10)-98++
Matched y ions: y(1), y(2), y(3), y(4)-98++, y(5)-98++, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2421

VHEGAPDTEVLLASPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of VHEGAPDTEVLLASPR
Found in AT4G31160.1, transducin family protein / WD-40 repeat family protein

Match to Query 2992: 1769.834319 from(590.952049,3+)
Elution from: 38.586 to 38.586 scan no 3579 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1769.8349
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00051
Matched b ions: b(9), b(9)+, b(10)+, b(10), b(11)+, b(12)+, b(13)+, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(9)+, y(10)-98++, y(13)+
Precursor origin neutral loss:

---

Peptide No.2422

VHLSESPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VHLSESPK
Found in AT4G17720.1, RNA recognition motif (RRM)-containing protein

Match to Query 533: 975.441014 from(488.727783,2+)
Elution from: 19.101 to 19.101 scan no 1060 polarity:+

file:///C:/Documents%20and%20Settings/N.Su.../abi/result_v3/o0705103ppmGROUPmeadlist.htm (2421/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 975.4426  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
lons Score: 32 Expect: 0.004  
Matched b ions: b(2), b(3), b(5)-98, b(6)-98  
Matched y ions: y(2), y(5), y(6), y(6)-98, y(7)+, y(7)-98++  
Precursor origin neutral loss: +

Peptide No.2423

VHLSESPK  
Confirmed sites: @S:6  
Ambiguous sites:

MS/MS Fragmentation of VHLSESPK  
Found in AT4G17720.1, RNA recognition motif (RRM)-containing protein

Match to Query 628: 975.441600 from(488.728076,2+)  
Elution from: 18.261 to 18.261 scan no 1070 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 975.4426
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.016
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6)
Matched y ions: y(2), y(3), y(4), y(4)-98++, y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7)+, y(7), y(7)-98++
Precursor origin neutral loss: +

Peptide No.2424

VHLSPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VHLSPR
Found in AT3G24180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G49900.1); similar to unknown protein [A

Match to Query 218: 787.373656 from(394.694104,2+)
Elution from: 18.727 to 18.727 scan no 1142 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 787.3742
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0054
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98
Matched y ions: y(2), y(3)++, y(3)-98, y(4)-98, y(4), y(5)++, y(5)-98, y(5)-98++
Precursor origin neutral loss: +

Peptide No.2425

VHSDNNLVELGEVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VHSDNNLVELGEVK
Found in AT2G34410.1, O-acetyltransferase family protein

Match to Query 2736: 1631.754542 from(816.884547,2+)
Elution from: 38.926 to 38.926 scan no 3850 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2424/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1631.7555
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 Expect: 1e-007
Matched b ions: b(2), b(4), b(4)-98, b(5), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)+, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)+, b(12), b(12)+, b(13), b(13)-98, b(13)-98+, b(13)+
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)+, y(13)-98 +
Precursor origin neutral loss: +

Peptide No.2426

VIADKPSDEEDDRQR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VIADKPSDEEDDRQR
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 3374: 1851.798294 from(618.273374,3+)
Elution from: 18.808 to 18.808 scan no 1135 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...ibi/result_v3/o0705103ppmGROUPmeadlist.htm (2425/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1851.8000  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 76 Expect: 2.1e-007  
Matched b ions: b(2), b(3), b(4), b(5), b(7)-98, b(7), b(8), b(8)++, b(8)-98, b(10), b(11), b(11)-98, b(11)-98++, b(12), b(14)-98++  
Matched y ions: y(2), y(3)++, y(3), y(4)++, y(4), y(5)++, y(6)++, y(7)++, y(7), y(8)++, y(9)-98++, y(10), y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)+, y(14)-98++  
Precursor origin neutral loss: +  

---

**Peptide No.2427**

VIDASPKRGSYDYGSPK  
Confirmed sites: "@S:5,@S:10,@S:15"  
Ambiguous sites:

MS/MS Fragmentation of VIDASPKRGSYDYGSPK  
Found in AT3G53500.1, RSZ32; nucleic acid binding  
Match to Query 2996: 2030.777448 from(677.933092,3+)  
Elution from: 23.271 to 23.271 scan no 1703 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2030.7788
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.011
Matched b ions: b(2), b(3), b(5)-98, b(6), b(7)+, b(7)-98, b(7), b(8)+, b(9)-98++, b(9)+, b(10)-98, b(10)-196++, b(10)+, b(10)-98++, b(11)-98++, b(11)+, b(11)-196++, b(12)-196++, b(12)+, b(12)-98++, b(13)-196++, b(13)+, b(15)-196++, b(15)-98++, b(15)-294++, b(16)-294++, b(16)-196++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-196, y(9)-98, y(9)+, y(10)+, y(10)-98++, y(11)+, y(11)-98++, y(12)+, y(12)-98++, y(12)-196++, y(13)+, y(13)-196++, y(13)-196++, y(14)-98++, y(14)+, y(14)-294++, y(14)-196++, y(15)-196++, y(15)-98++, y(15)+, y(15)-294++, y(16)-98++, y(16)+, y(16)-294++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.2428
VIDASPKRGSDYDGSPK
Confirmed sites: "@S:5,/@S:10,/@Y:12"
Ambiguous sites:
MS/MS Fragmentation of **VIDASPKRGSDYDGSPK**

Found in **AT3G53500.1**, RSZ32; nucleic acid binding

Match to Query 3108: 2030.777824 from(1016.396188,2+)
Elution from: 22.302 to 22.302 scan no 1573 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2030.7788
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y12 : Phospho (Y)
Ions Score: 26 Expect: 0.02
Matched b ions: b(5)-98, b(10)-98, b(11)-98, b(11), b(13)-98, b(15)-196, b(15)-98, b(15), b(15)-98++, b(16)-196, b(16)-98, b(16)-196++
Matched y ions: y(6), y(7), y(9)-98, y(10), y(11), y(11)+, y(12), y(12)-98, y(12)+, y(12)-98+, y(13)-98++, y(13)-196++, y(13)+, y(14)-196++, y(14)-98++, y(14)+, y(15)-98++, y(15)+, y(15)-196++, y(16)-196++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

---

**Peptide No.2429**

**VIDASPKRGSDYDGSPK**
Confirmed sites: "@S:5,@Y:12,@S:15"
Ambiguous sites:
MS/MS Fragmentation of \textbf{VIDASPKRGSDYDGSPK}
Found in \textbf{AT3G53500.1}, RSZ32; nucleic acid binding

Match to Query 3521: 2030.776712 from(1016.395632,2+)
Elution from: 22.518 to 22.518 scan no 1632 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2030.7788
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y12 : Phospho (Y)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.024
Matched b ions: b(5)-98, b(7)-98, b(12), b(12)-98++, b(13)-98, b(14), b(15)-196, b(15)-98, b(15)-98++, b(16)-196++, b(16)+
Matched y ions: y(4), y(4)-98, y(7)-98, y(8)-98, y(9)-98, y(11)+, y(12), y(12)-98, y(12)-98++, y(14)-196++, y(14)-98++, y(14)+, y(15)-98++, y(15)+, y(16)-196++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

\textbf{Peptide No.2430}
\textbf{VISETDSSSSPVSTKQPDDR}
Confirmed sites: 
Ambiguous sites: @S:10orS:9

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2429/2597) [2008/03/14 15:08:30]
MS/MS Fragmentation of **VISETDSSSPVSTKPQDR**
Found in **AT5G58220.1**, steroid binding

Match to Query 3840: 2098.940700 from(700.654176,3+)
Elution from: 23.896 to 23.896 scan no 1605 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2098.9419
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.059
Matched b ions: b(2), b(6), b(12)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(4), y(9)++, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++
Precursor origin neutral loss: +

---

**Peptide No.2431**

**VISETDSSSPVSTKPQDR**
Confirmed sites:
Ambiguous sites: @S:8orS:9

MS/MS Fragmentation of **VISETDSSSPVSTKPQDR**
Found in **AT5G58220.1**, steroid binding
Match to Query 3717: 2098.941507 from(700.654445,3+)
Elution from: 22.931 to 22.931 scan no 1655 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2098.9419
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0014
Matched b ions: b(9)-98, b(13)-98++
Matched y ions: y(4), y(5), y(7)+, y(9)+, y(9), y(12)+, y(13)+, y(14)+, y(15)+, y(15)-98+, y(16)+, y(17)+, y(17)-98++
Precursor origin neutral loss: +

Peptide No.2432

VIVQDVANSVTSDDNDSSK
Confirmed sites:
Ambiguous sites: @S:12

MS/MS Fragmentation of VIVQDVANSVTSDDNDSSK
Found in AT1G67440.1, EMB1688 (EMBRYO DEFECTIVE 1688); GTP binding / GTPase

Match to Query 3907: 2186.918658 from(1094.466605,2+)
Elution from: 37.836 to 37.836 scan no 3697 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2186.9216
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 5e-005
Matched b ions: b(6), b(10), b(14), b(17), b(18)
Matched y ions: y(9), y(10), y(10)-98, y(11), y(12), y(13), y(14), y(15), y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.2433

VLDGLVSSPSR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VLDGLVSSPSR
Found in AT1G16170.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G79660.1); similar to Os08g0266200 [Oryz]

Match to Query 983: 1208.580268 from(605.297410,2+)
Elution from: 40.008 to 40.008 scan no 3986 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2432/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1208.5802
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0044
Matched b ions: b(5)
Matched y ions: y(3), y(4), y(5)-98, y(6), y(8), y(9), y(10)++
Precursor origin neutral loss: +

Peptide No.2434

VLEFLESPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VLEFLESPK
Found in AT5G63550.1, GTP binding / RNA binding

Match to Query 808: 1140.545462 from(571.280007,2+)
Elution from: 48.853 to 48.853 scan no 5126 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1140.5467
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.013
Matched b ions: b(6), b(7)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8)+
Precursor origin neutral loss: +

---

Peptide No.2435

VLGNRSPSRSPVR
Confirmed sites: "@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of VLGNRSPSRSPVR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 3208: 1754.796084 from(585.939304,3+)
Elution from: 18.701 to 18.701 scan no 1137 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea.html (2434/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1754.7978
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.043
Matched b ions: b(2), b(5), b(6), b(8)+, b(8)-98++, b(8)-98, b(8), b(9)-98++, b(10)-98++, b(11)-98++, b(11)-196++, b(12)-98++, b(12)-196++, b(12)+, b(13)-196++, b(13)+, b(14)+, b(14)-196++, b(14)-98++
Matched y ions: y(3), y(5)+, y(6)+, y(6)-98, y(7)+, y(7)-98++, y(7)-98, y(7), y(8)+, y(9)+, y(9)-196++, y(9)-98++, y(10)-98++, y(10)-196++, y(11)+, y(11)-98++, y(12)-98++, y(12)+, y(13)-98++, y(13)-196++, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2436

VLGNRNRSRSRSRPR
Confirmed sites: "@S:8,@S:10,@S:12"
Ambiguous sites:

MS/MS Fragmentation of VLGNRNRSRSRPR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 3055: 1834.763442 from(918.388997,2+)
Monoisotopic mass of neutral peptide Mr(calc): 1834.7641
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.06
Matched b ions: b(7), b(8), b(8)-98, b(11), b(12)-98, b(13)++, b(14)-294
Matched y ions: y(3), y(5), y(6)-98, y(6), y(7), y(7)-98, y(9), y(13)-98++, y(13)++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2437

VLGNNRSPSRSPVR
Confirmed sites: "@S:8,@S:12"
Ambiguous sites:

MS/MS Fragmentation of VLGNNRSPSRSPVR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 3107: 1754.795331 from(585.939053,3+)
Elution from: 19.021 to 19.021 scan no 1199 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2436/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1754.7978
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.001
Matched b ions: b(2), b(7)+, b(8)+, b(8)-98, b(8), b(8)-98++, b(9)-98++, b(10)-98++, b (11)+, b(12)-98++, b(12)-196++, b(12)+, b(13)-196++, b(13)+, b(14)+, b(14)-98++, b (14)-196++
Matched y ions: y(1), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)+, y(6), y(6)-98, y(7)+, y(7)-98, y (7), y(7)-98++, y(9)-98++, y(9)+, y(10)-196++, y(10)-196++, y(10)+, y(11)+, y(11)-98++, y(12)+, y(12)-98++, y(13)+, y(13)-98++, y(13)-196++, y(14)-98++, y(14)+
Precursor origin neutral loss: +

Peptide No.2438
VLIAEAGNCGSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VLIAEAGNCGSPR
Found in AT4G24620.1, PGI1 (CHLOROPLASTIC PHOSPHOGLUCOSE ISOMERASE)

Match to Query 1478: 1351.594412 from(676.804482,2+)
Mascot Search Results: Peptide View

Elution from: 27.768 to 27.768 scan no 2342 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1351.5955
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 1.3e-07
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8), b(9), b(10)-98, b(10), b(11)-98
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(8)+, y(9), y(9)+, y(9)-98, y(10)+, y(10), y(10)-98++, y(10)-98, y(11)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2439

VLISESEDEILIK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of VLISESEDEILIK
Found in AT4G30480.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 2782: 1782.852150 from(892.433351,2+)
Elution from: 52.400 to 52.400 scan no 5455 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2438/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1782.8539
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 0.00011
Matched b ions: b(9)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13), b(14), b(14)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(10), y(11)-98, y(11), y(12)+, y(12)-98, y(12), y(13)-98++, y(13)+, y(14)+
Precursor origin neutral loss: +

Peptide No.2440
VLISESSEDEILIK
Confirmed sites: "@S:5,@S:6,@S:8"
Ambiguous sites:

MS/MS Fragmentation of VLISESSEDEILIK
Found in AT4G30480.1, tetraticopeptide repeat (TPR)-containing protein

Match to Query 2861: 1942.781460 from(972.398006,2+)
Elution from: 66.993 to 66.993 scan no 6406 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.7866  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 35 Expect: 0.0033  
Matched b ions: b(4), b(7)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-196, b(14)-98, b(14)  
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(11)-196, y(11)-98, y(11), y(13)-196++, y(13)-98+, y(14)+++, y(14)-98++  
Precursor origin neutral loss: +

Peptide No.2441

VLISESSEDEILIK  
Confirmed sites: "@S:5,@S:8"  
Ambiguous sites: 

MS/MS Fragmentation of VLISESSEDEILIK  
Found in AT4G30480.1, tetraticopeptide repeat (TPR)-containing protein  

Match to Query 3358: 1862.819108 from(932.416830,2+)  
Elution from: 58.772 to 58.772 scan no 6216 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1862.8203
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00036
Matched b ions: b(4), b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98, b(10)+, b(11)-98, b(11), b(11)-98+, b(12)-98, b(12), b(12)-196, b(12)+, b(13), b(13)-196, b(13)+, b(13), b(14), b(14)-98, b(14)+, b(14)-196+
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(10), y(11)-98, y(11)-196, y(11), y(12)-196++, y(12)-196, y(12), y(12)-98++, y(12)-98, y(12)+, y(13)-98++, y(13)+, y(13), y(13)-196++, y(13)-98, y(13)-196, y(14)-98++, y(14)+
Precursor origin neutral loss:

Peptide No.2442
VLLSESEDEILIK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of VLLSESEDEILIK
Found in AT4G30480.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 3010: 1782.852806 from(892.433679,2+)
Elution from: 52.967 to 52.967 scan no 5411 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 1782.8539  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 28 Expect: 0.018  
Matched b ions: b(11), b(12), b(12)-98, b(13), b(13)++, b(14)  
Matched y ions: y(7), y(8), y(9), y(10), y(13)++  
Precursor origin neutral loss:

Peptide No.2443  

VLISESSEDEILIK  
Confirmed sites: "@S:6,@S:8"  
Ambiguous sites:

MS/MS Fragmentation of VLISESSEDEILIK  
Found in AT4G30480.1, tetratricopeptide repeat (TPR)-containing protein

Match to Query 3089: 1862.817830 from(932.416191,2+)  
Elution from: 57.837 to 57.837 scan no 6159 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1862.8203
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.011
Matched b ions: b(4), b(7)-98, b(11), b(12), b(12)-98, b(13)-196, b(13), b(14), b(14)+, b(14)-98
Matched y ions: y(6), y(7), y(8), y(10)-98, y(10), y(11), y(11)-98, y(13)+, y(13), y(13)-98, y(14)+
Precursor origin neutral loss: +

Peptide No.2444

VLISSSEDEILIK
Confirmed sites: @S:8  
Ambiguous sites:

MS/MS Fragmentation of VLISSSEDEILIK
Found in AT4G30480.1, tetratrico peptide repeat (TPR)-containing protein

Match to Query 3194: 1782.852296 from(892.433424,2+)
Elution from: 52.533 to 52.533 scan no 5584 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1782.8539
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 2.7e-005
Matched b ions: b(4), b(6), b(7), b(8)-98, b(9)-98, b(9), b(10), b(11)-98, b(11), b(12), b(12)-
98, b(12)++, b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y
(12)++, y(12), y(13)-98++, y(13)++, y(13)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.2445

VLPPVEQESDVELETK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VLPPVEQESDVELETK
Found in AT3G10530.1, transducin family protein / WD-40 repeat family protein

Match to Query 3182: 1890.884198 from(946.449375,2+)
Elution from: 41.371 to 41.371 scan no 4168 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1890.8863  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 59 Expect: 1.4e-005  
Matched b ions: b(6), b(8), b(10), b(11), b(11)-98, b(12), b(13), b(13)-98, b(14), b(14)-98  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12)+, y(13)+, y(13)-98++, y(13), y(14)+, y(14), y(14)-98++, y(14)-98, y(15)+, y(15)-98++  
Precursor origin neutral loss: +

---

**Peptide No.2446**

**VLPPVEQESDVELETK**  
Confirmed sites: @T:15  
Ambiguous sites:

MS/MS Fragmentation of **VLPPVEQESDVELETK**  
Found in **AT3G10530.1**, transducin family protein / WD-40 repeat family protein

Match to Query 2781: 1890.883758 from(946.449155,2+)  
Elution from: 41.292 to 41.292 scan no 4046 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1890.8863
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.062
Matched b ions: b(9)++, b(13)++, b(14)++
Matched y ions: y(13)++, y(14)++, y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2447
VLQEEMSVDSADAPSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of VLQEEMSVDSADAPSK
Found in AT2G19930.1, RNA-dependent RNA polymerase family protein

Match to Query 2895: 1810.768532 from(906.391542,2+)
Elution from: 35.114 to 35.114 scan no 3336 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2446/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1810.7696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 1.8e-005
Matched b ions: b(3), b(4), b(9), b(11), b(12)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.2448

VLSHAVSEDSVSVHSTFASR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VLSHAVSEDSVSVHSTFASR
Found in AT5G17330.1, GAD (Glutamate decarboxylase 1); calmodulin binding

Match to Query 4074: 2194.003628 from(1098.009090,2+)
Elution from: 35.353 to 35.353 scan no 3365 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeablist.htm (2447/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2194.0055
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00022
Matched b ions: b(6), b(8)-98, b(8), b(10)-98, b(11), b(13)-98
Matched y ions: y(4), y(5), y(7), y(9), y(12), y(13), y(14)-98, y(14), y(15)-98, y(17)-98++, y(18)++ , y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.2449

VLHAVSESDVSVHSTFASR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VLVHAVSESDVSVHSTFASR
Found in AT5G17330.1, GAD (Glutamate decarboxylase 1); calmodulin binding

Match to Query 4026: 2194.003281 from(732.341703,3+)
Elution from: 36.171 to 36.171 scan no 3440 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2448/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2194.0055
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 1.4e-006
Matched b ions: b(5), b(6), b(7), b(9)++, b(10)-98, b(10), b(10)-98++, b(11)-98, b(11), b(12)-98++, b(12)++, b(13)-98++, b(13)+++, b(14)-98++, b(14)+++, b(15)-98++, b(18)-98++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)+++, y(10), y(12)-98, y(12)-98++, y(13)-98++, y(14)+++, y(14)-98++, y(15)-98++, y(15)+++, y(15)-98++, y(16)+++, y(17)+++, y(17)-98++, y(18)+++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.2450
VLSMSNSPEAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VLSMSNSPEAR
Found in AT1G67310.1, calmodulin binding / transcription regulator

Match to Query 1175: 1269.540462 from(635.777507,2+)
Elution from: 30.789 to 30.789 scan no 2750 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1269.5424
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 1.1e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(9), b(10)-98++, b(10)-98
Matched y ions: y(2), y(4), y(4)+, y(5), y(6), y(7), y(8), y(9)-98++, y(9)-98, y(9), y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2451

VLVSPTNRGNSNSVRK
Confirmed sites: "@T:6,@S:10,@S:12"
Ambiguous sites:

MS/MS Fragmentation of VLVSPTNRGNSNSVRK
Found in AT3G05330.1, ATN (A. THALIANA TAN1)

Match to Query 3323: 1852.801254 from(618.607694,3+)
Elution from: 18.492 to 18.492 scan no 1112 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2450/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1852.7998
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.011
Matched b ions: b(6)-98, b(8)+, b(9)-98, b(10)+, b(12)-294++, b(13)-98++
Matched y ions: y(5)-98, y(7)-98, y(9)+, y(10)+, y(11)-98++, y(11)+, y(12)+, y(13)-98+
y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2452

VMSESEMVSGAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VMSESEMVSGAR
Found in AT1G52780.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G21700.1); similar to hypothetical prote

Match to Query 1762: 1361.535294 from(681.774923,2+)
Elution from: 35.627 to 35.627 scan no 3182 polarity:+

file:///C|/Documents%20and%20Settings/N.Su_...abi_v3/o0705103ppmGROUPmeadlist.htm (2451/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1361.5356
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 2.6e-005
Matched b ions: b(2), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2453

VMYDMDSDEQCLLR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VMYDMDSDEQCLLR
Found in AT4G32620.1, nucleic acid binding

Match to Query 3373: 1968.729164 from(985.371858,2+)
Elution from: 50.886 to 50.886 scan no 5341 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2452/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1968.7304
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 2.2e-005
Matched b ions: b(8), b(9), b(11), b(12), b(13)-98, b(14)-98, b(14)
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(11), y(12), y(13)-98++, y(13), y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2454
VNDETSEGTMEER
Confirmed sites: @S:6
Ambiguous sites:
MS/MS Fragmentation of VNDETSEGTMEER
Found in AT1G20370.1, tRNA pseudouridine synthase family protein
Match to Query 2188: 1676.622276 from(839.318414,2+)
Elution from: 22.403 to 22.403 scan no 1578 polarity:+

file:///C|/Documents%20and%20%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2453/2597) (2008/03/14 15:08:30)
Monoisotopic mass of neutral peptide Mr(calc): 1676.6236  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 86 Expect: 1.2e-008  
Matched b ions: b(4), b(9)-98++  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(12), y(12)++, y(13)+, y(13)-98++  
Precursor origin neutral loss: +

Peptide No.2455

VNEDVPDETPLTPK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of VNEDVPDETPLTPK
Found in AT3G17460.1, PHD finger family protein

Match to Query 2335: 1632.726056 from(817.370304,2+)
Elution from: 34.801 to 34.801 scan no 3294 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2454/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1632.7284
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0014
Matched b ions: b(4), b(5), b(8), b(9), b(12)-98
Matched y ions: y(3), y(5), y(6), y(7)-98, y(9), y(10)-98, y(10)-98++, y(11), y(13)+
Precursor origin neutral loss: +

Peptide No.2456
VNNNDSEVETSKPSSPK
Confirmed sites: @T:11
Ambiguous sites: @S:12

MS/MS Fragmentation of VNNNDSEVETSKPSSPK
Found in AT5G55640.1, similar to Os03g0412200 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001050353.1); similar to ex

Match to Query 2804: 2024.866836 from(675.962888,3+)
Elution from: 17.921 to 17.921 scan no 1035 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.8687
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.044
Matched b ions: b(5), b(12)-98++
Matched y ions: y(6), y(10)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.2457
VNNNDSEVETSKPSSPK
Confirmed sites:
Ambiguous sites: @S:15orS:16

MS/MS Fragmentation of VNNNDSEVETSKPSSPK
Found in AT5G55640.1, similar to Os03g0412200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050353.1); similar to ex

Match to Query 2795: 2024.867571 from(675.963133,3+)
Elution from: 18.266 to 18.266 scan no 1032 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2024.8687  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 40 Expect: 0.0013  
Matched b ions:  
Matched y ions: y(5), y(6), y(6)-98, y(9)+, y(10)-98++, y(10)+, y(11)+, y(13)+, y(14)+, y(15)+, y(16)+, y(17)+, y(17)-98++  
Precursor origin neutral loss: +

Peptide No.2458

VPDLGGSDTEDIQSATK  
Confirmed sites: @S:7  
Ambiguous sites:

MS/MS Fragmentation of VPDLGGSDTEDIQSATK  
Found in AT5G19490.1, repressor protein-related

Match to Query 1953: 1698.696952 from(850.355752,2+)  
Elution from: 28.336 to 28.336 scan no 2381 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1698.6985
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 8e-007
Matched b ions: b(5), b(8)-98, b(10), b(11)-98++, b(11)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98, y(12)-98, y(12), y(13)-98++, y(13)-98, y(14)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2459
VPEAQITNSATPTTTPR
Confirmed sites: "@S:9,@T:15"
Ambiguous sites:

MS/MS Fragmentation of VPEAQITNSATPTTTPR
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 3251: 1942.839868 from(972.427210,2+)
Elution from: 30.689 to 30.689 scan no 2806 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.8438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.0002
Matched b ions: b(8), b(10), b(11)-98, b(15), b(15)-98
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7), y(8)-98, y(8), y(9), y(11), y(11)+, y(12), y(15)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.2460
VPEAQITNSATPTTTPR
Confirmed sites: "@T:11, @T:15"
Ambiguous sites:

MS/MS Fragmentation of VPEAQITNSATPTTTPR
Found in AT4G39680.1, SAP domain-containing protein

Match to Query 3603: 1942.842700 from(972.428626,2+)
Elution from: 30.698 to 30.698 scan no 2800 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1942.8438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0012
Matched b ions: b(7), b(8), b(11)-98, b(14), b(15)-98, b(15)-196++, b(15)-196, b(16)-196
Matched y ions: y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(12), y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2461

VPFFTVFIYLK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of VPFFTVFIYLK
Found in AT5G06710.2, HAT14 (homeobox-leucine zipper protein 14); DNA binding

Match to Query 1673: 1452.745464 from(485.255764,3+)
Elution from: 34.150 to 34.150 scan no 3140 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2460/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1452.7458
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T5: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.034
Matched b ions: b(7)-98++, b(8)-98++, b(9)-98++, b(10)-98++
Matched y ions:
Precursor origin neutral loss: +

Peptide No.2462
VPSPCLTPIGSGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **VPSPCLTPIGSGR**
Found in **AT2G29140.1**, APUM3 (ARABIDOPSIS PUMILIO 3); RNA binding

Match to Query 2293: 1419.657596 from(710.836074,2+)
Elution from: 38.151 to 38.151 scan no 3786 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1419.6581
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.007
Matched b ions: b(6)-98++, b(6)-98, b(8)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11)-98++, y(11)+, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2463
VQEIVSEIFGKSPCK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VQEIVSEIFGKSPCK
Found in AT4G37910.1, MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding

Match to Query 3198: 1799.850798 from(900.932675,2+)
Elution from: 50.352 to 50.352 scan no 5302 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1799.8528
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 7.3e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9), b(10), b(12)-98
Matched y ions: y(3), y(4)-98, y(4), y(6)-98, y(6), y(7)-98, y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)+, y(13)-98, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2464
VQEIVSEIFGKSPCK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of VQEIVSEIFGKSPCK
Found in AT4G37910.1, MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding

Match to Query 3232: 1799.850945 from(600.957591,3+)
Elution from: 50.809 to 50.809 scan no 5360 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1799.8528
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0099
Matched b ions: b(2), b(4), b(5), b(9)++, b(14)-98++
Matched y ions: y(3), y(10)+, y(10)-98++, y(11)+, y(11)-98++, y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss:

Peptide No.2465

VQETSEGSQLEFQSSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of VQETSEGSQLEFQSSR
Found in AT1G13220.2, nuclear matrix constituent protein-related

Match to Query 3685: 1977.830746 from(989.922649,2+)
Elution from: 37.718 to 37.718 scan no 3574 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2464/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1977.8316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 2.8e-009
Matched b ions: b(3), b(4), b(5), b(5)+, b(6), b(6)-98, b(7)-98++, b(8)-98, b(8), b(9)-98, b(10), b(10)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98, b(15), b(15)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)+, y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(13)-98++, y(14), y(14)-98, y(15)-98++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2466
VQETSEQLSEFQSSR
Confirmed sites: "@S:5,@S:8"
Ambiguous sites:
MS/MS Fragmentation of VQETSEQLSEFQSSR
Found in AT1G13220.2, nuclear matrix constituent protein-related

Match to Query 3663: 2057.795782 from(1029.905167,2+)
Elution from: 39.418 to 39.418 scan no 3907 polarity:+
 Monoisotopic mass of neutral peptide Mr(calc): 2057.7980  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 77 Expect: 1.6e-007  
Matched b ions: b(6)-98, b(8)-98, b(9)-196, b(10), b(10)-98, b(12), b(12)-98, b(13)-98, b(14), b(15)-196  
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)+, y(8), y(9), y(10)+, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13), y(14), y(14)-196++, y(16)-98++, y(16)+  
Precursor origin neutral loss: +  

---  

**Peptide No.2467**  
VQETSEGSQLSEFQSSR  
Confirmed sites:  
Ambiguous sites: @T:4orS:5  

**MS/MS Fragmentation of VQETSEGSQLSEFQSSR**  
Found in AT1G13220.2, nuclear matrix constituent protein-related  

Match to Query 3607: 1977.829798 from(989.922175,2+)  
Elution from: 37.578 to 37.578 scan no 3659 polarity:+

---
Monoisotopic mass of neutral peptide Mr(calc): 1977.8316
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 2.1e-007
Matched b ions: b(3), b(5), b(5)-98, b(6), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98++, b(13)-98, b(14), b(14)-98, b(14)-98++, b(15)-98++, b(15)+, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)+, y(8), y(9), y(10), y(11), y(12), y(14)-98, y(14), y(15)-98++, y(15)+, y(16)+
Precursor origin neutral loss: +

Peptide No.2468

VQETSEGSQLSEFQSSR
Confirmed sites: @S:8
Ambiguous sites: @T:4orS:5

MS/MS Fragmentation of VQETSEGSQLSEFQSSR
Found in AT1G13220.2, nuclear matrix constituent protein-related

Match to Query 3817: 2057.794704 from(1029.904628,2+)
Elution from: 40.057 to 40.057 scan no 3992 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2467/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 2057.7980
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00044
Matched b ions: b(5), b(8)-98, b(9)-196, b(10), b(10)-98, b(12)-98, b(12), b(13)-196, b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(8)+, y(8), y(9), y(10)+, y(10)-98, y(11), y(12)-98, y(14)-196++, y(14), y(15)+, y(15)-98++, y(16)+, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2469

VQGEVASQSCAVSPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VQGEVASQSCAVSPR
Found in AT4G00930.1, CIP4.1 (CIP4.1)

Match to Query 2805: 1653.717066 from(827.865809,2+)
Elution from: 23.816 to 23.816 scan no 1799 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1653.7181  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications: 
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 81 Expect: 6.1e-008  
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(11), b(12), b(12)++, b(13)-98  
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(11), y(13)-98++, y(13)++, y(14)++  
Precursor origin neutral loss: +

Peptide No.2470

VQIESGVMTAETGTYR  
Confirmed sites: @T:9  
Ambiguous sites:

MS/MS Fragmentation of VQIESGVMTAETGTYR  
Found in AT2G17700.1, protein kinase family protein

Match to Query 3004: 1836.795584 from(919.405068,2+)  
Elution from: 34.807 to 34.807 scan no 3258 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2469/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1836.7964  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 98 Expect: 1.8e-009  
Matched b ions: b(4), b(7), b(8), b(9)-98, b(10)-98, b(11)-98, b(11), b(14)  
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y(12), y(12)-98, y(13), y(14)+, y(14), y(15)+  
Precursor origin neutral loss: +

Peptide No.2471

VQIESGVMTAETGT YR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of VQIESGVMTAETGT YR
Found in AT2G17700.1, protein kinase family protein

Match to Query 3355: 1820.799974 from(911.407263,2+)
Elution from: 40.593 to 40.593 scan no 4111 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2470/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1820.8015  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 93 Expect: 5.7e-009  
Matched b ions: b(7), b(8), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(14), b(14)-98, b(15)  
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(12), y(13), y(14), y(14)-98++, y(14), y(14)-98++, y(15)+, y(15)-98++  
Precursor origin neutral loss: +

Peptide No.2472

VRADTSSDEEDDLK  
Confirmed sites: "@S:6,@S:7"  
Ambiguous sites:

MS/MS Fragmentation of VRADTSSDEEDDLK  
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 2089: 1738.631866 from(870.323209,2+)  
Elution from: 22.757 to 22.757 scan no 1652 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1738.6335  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 31 Expect: 0.0037  
Matched b ions: b(4), b(5), b(6)-98, b(8)-98, b(9), b(10)-196, b(10), b(11), b(11)-196, b(11)-98, b(12)+, b(12), b(12)-196, b(13), b(13)-196+, b(13)-98+, b(13)+  
Matched y ions: y(4), y(6), y(8)-98, y(10)-196, y(10), y(12), y(13)+, y(13)-98+  
Precursor origin neutral loss: +

Peptide No.2473

VREDDLYSPR  
Confirmed sites: @S:8  
Ambiguous sites:

MS/MS Fragmentation of VREDDLYSPR  
Found in AT5G18810.1, SCL28 (SC35-like splicing factor 28); RNA binding  

Match to Query 1302: 1328.574952 from(665.294752,2+)  
Elution from: 25.774 to 25.774 scan no 2028 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2472/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1328.5762
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 5.3e-005
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(9)++
Precursor origin neutral loss: +

Peptide No.2474

VRSIQFGQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VRSIQFGQK
Found in AT2G17360.1, 40S ribosomal protein S4 (RPS4A)

Match to Query 1198: 1141.563528 from(571.789040,2+)
Elution from: 25.237 to 25.237 scan no 2028 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2473/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1141.5645
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.019
Matched b ions: b(5)++, b(5), b(6), b(7)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++
Precursor origin neutral loss: +

Peptide No.2475

VVRDSMTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of VVRDSMTK
Found in AT5G20890.1, chaperonin, putative

Match to Query 751: 1014.456254 from(508.235403,2+)
Elution from: 19.751 to 19.751 scan no 1268 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1014.4569
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.016
Matched b ions: b(4), b(5)-98, b(6)-98, b(7)-98, b(7), b(7)-98++
Matched y ions: y(2), y(3), y(4)-98, y(7)++
Precursor origin neutral loss: +

Peptide No.2476

VRVSDDEDRK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VRVSDDEDRK
Found in AT1G80930.1, MIF4G domain-containing protein / MA3 domain-containing protein

Match to Query 1884: 1297.563879 from(433.528569,3+)
Elution from: 15.408 to 15.408 scan no 763 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2475/2597) [2008/03/14 15:08:30]
Monoisotopic mass of neutral peptide Mr(calc): 1297.5663
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0015
Matched b ions: b(4)-98, b(5)-98, b(6)-98++
Matched y ions: y(2)+, y(4)+, y(5)+, y(6)+, y(7)-98++, y(8)-98++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2477
VSADFDADSDDEIVLVPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VSADFDADSDDEIVLVPK
Found in AT4G17060.1, similar to transcription factor [Arabidopsis thaliana] (TAIR: AT2G44730.1); contains domain Origin o

Match to Query 3697: 2013.880226 from(1007.947389,2+)
Elution from: 56.267 to 56.267 scan no 6030 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2038.819
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 9.4e-006
Matched b ions: b(5), b(6), b(8), b(12), b(13)-98, b(13), b(14), b(14)-98, b(14)+, b(15)+, b(15)-98, b(15), b(16)-98++, b(16)-98, b(16), b(17)-98
Matched y ions: y(3), y(4), y(5), y(7), y(8)+, y(9), y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)+, y(17)+
Precursor origin neutral loss: +

Peptide No.2478
VSDLGGDDDPSR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VSDLGGDDDPSR
Found in AT1G04780.1, ankyrin repeat family protein

Match to Query 1838: 1454.591968 from(728.303260,2+)
Elution from: 34.827 to 34.827 scan no 3294 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.5926
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 3.1e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)+, b(10)-98++, b(10), b(10)-98, b(12), b(12)+
Matched y ions: y(3), y(4), y(4)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(7)-98++, y(8), y(8)-98+, y(8)-98, y(9), y(9)-98, y(9)+, y(10)-98++, y(10), y(10)+, y(11), y(11)-98++, y(11)+, y(12)+
Precursor origin neutral loss: +

Peptide No.2479
VSDLLGDDDPSR
Confirmed sites: @S:10orS:12
Ambiguous sites: 
MS/MS Fragmentation of VSDLLGDDDPSR
Found in AT1G04780.1, ankyrin repeat family protein
Match to Query 1934: 1454.591874 from(728.303213,2+)
Elution from: 35.672 to 35.672 scan no 3419 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1454.5926
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.2e-007
Matched b ions: b(4), b(5), b(7), b(12)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(8)-98, y(9), y(10)-98++, y(10), y(11), y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2480
VSDSSDDLRSQMK
Confirmed sites:
Ambiguous sites: @S:20rS:4

MS/MS Fragmentation of VSDSSDDLRSQMK
Found in AT1G78240.1, dehydration-responsive protein-related

Match to Query 2735: 1661.658590 from(831.836571,2+)
Elution from: 24.303 to 24.303 scan no 1773 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2479/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1661.6604  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 33 Expect: 0.0032  
Matched b ions: b(6)-98, b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)+, b(12)-98, b(12), b(12)-98++, b(12)+, b(13)-98, b(13)-98++, b(13)+  
Matched y ions: y(4), y(6), y(7), y(8), y(10), y(13)-98++, y(13)+  
Precursor origin neutral loss: +

Peptide No.2481

VSDSSDLRDSQMK
Confirmed sites: @S:4  
Ambiguous sites: 

MS/MS Fragmentation of VSDSSDLRDSQMK  
Found in AT1G78240.1, dehydration-responsive protein-related

Match to Query 2142: 1661.659026 from(831.836789,2+)  
Elution from: 22.730 to 22.730 scan no 1621 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2480/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1661.6604
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00012
Matched b ions: b(4)-98, b(6), b(7), b(7)-98, b(8)-98, b(10)-98, b(10), b(10)++, b(11)++, b(12)-98, b(13)-98, b(13)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11)-98++, y(11)++, y(12)-98, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.2482

VSDTSELSEDGEVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VSDTSELSEDGEVK
Found in AT4G02860.1, catalytic

Match to Query 2039: 1444.596396 from(723.305474,2+)
Elution from: 28.027 to 28.027 scan no 2363 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2481/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1444.5970
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 2.1e-005
Matched b ions: b(4), b(5)++, b(6), b(8)-98, b(10)-98, b(11)++, b(11)-98, b(11), b(12)-98++, b(12)-98, b(12)
Matched y ions: y(2), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)++, y(11)-98, y(11), y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2483
VSEEDDGSEEEERVR
Confirmed sites: "@S:8,@S:10"
Ambiguous sites:

MS/MS Fragmentation of VSEEDDGSEEEERVR
Found in AT1G32490.1, EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); ATP-dependent RNA helicase

Match to Query 3329: 2010.708240 from(1006.361396,2+)
Elution from: 22.941 to 22.941 scan no 1654 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2482/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2010.7092
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.018
Matched b ions: b(5), b(6), b(8), b(11)-98, b(12)-98, b(12)+, b(12)-196++, b(12)-98++, b(14), b(14)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(10)-98++, y(10)-98, y(10), y(10)-196++, y(11)-98, y(11), y(11)+, y(11)-196++, y(11)-98++, y(12)-98++, y(12)+, y(15)+, y(15)-98++
Precursor origin neutral loss: +

Peptide No.2484

VSFDDESSPPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VSFDDESSPPK
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G19710.1); similar to MAPK activating pr

Match to Query 997: 1213.489218 from(607.751885,2+)
Elution from: 30.866 to 30.866 scan no 2702 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1213.4904
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 6.1e-005
Matched b ions: b(2), b(4), b(6), b(7)-98, b(9)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)+, y(9)+, y(9)
Precursor origin neutral loss: +

Peptide No.2485
VSLAVDDEKSDEAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VSLAVDDEKSDEAK
Found in AT1G03530.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G66540.1); similar to unnamed protein pr

Match to Query 2010: 1699.718040 from(850.866296,2+)
Elution from: 26.403 to 26.403 scan no 2135 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2484/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1699.7189
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 6.8e-007
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(13)-98, b(13), b(14), b(14)+
Matched y ions: y(4), y(5)-98, y(6)-98, y(6), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9)-98, y(9), y(9)+, y(10), y(10)-98, y(11)-98, y(11)+, y(12)-98++, y(12)+, y(13)-98++, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

---

Peptide No.2486

VSPAVDPPSPR
Confirmed sites: "@S:2,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VSPAVDPPSPR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G80180.1); similar to Os06g0601100 [Oryz]

Match to Query 1712: 1280.520130 from(641.267341,2+)
Elution from: 29.301 to 29.301 scan no 2582 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeandlist.htm (2485/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1280.5203
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.00000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.00000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00014
Matched b ions: b(2), b(4), b(5)-98, b(5)+, b(5), b(6)-98, b(9)-196, b(9)+, b(10)-98+
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(7)-98, y(7), y(8)+, y(9), y(9)+, y(9)-98++, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2487

VSPAVDPPSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VSPAVDPPSPR
Found in AT1G15400.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G80180.1); similar to Os06g0601100 [Oryz]

Match to Query 1222: 1200.553804 from(601.284178,2+)
Elution from: 26.832 to 26.832 scan no 2208 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...v3/o0705103ppmGROUPmeadlist.htm (2486/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1200.5540
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 2.1e-005
Matched b ions: b(4), b(5), b(6), b(8), b(9)-98
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(5)-98++, y(5)++, y(5)-98, y(6), y(7), y(7)-98, y(8), y(8)++, y(9)++, y(9), y(9)-98++, y(10)++
Precursor origin neutral loss:

---

Peptide No.2488

VSSFEALQPATR
Confirmed sites: @S:2
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of VSSFEALQPATR
Found in AT1G74910.1, ADP-glucose pyrophosphorylase family protein

Match to Query 1435: 1384.637894 from(693.326223,2+)
Elution from: 37.466 to 37.466 scan no 3573 polarity:+

file:///C/...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2487/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1384.6387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 9.7e-005
Matched b ions: b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++
Precursor origin neutral loss: +

Peptide No.2489

VSSFEALQPATR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VSSFEALQPATR
Found in AT1G74910.1, ADP-glucose pyrophosphorylase family protein

Match to Query 1852: 1384.637720 from(693.326136,2+)
Elution from: 38.986 to 38.986 scan no 3743 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1384.6387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 9.8e-008
Matched b ions: b(4)-98, b(5), b(5)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10)+, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10)-98++, y(10)+, y(11)+, y(11)-98++
Precursor origin neutral loss:

Peptide No.2490

VSSFLSSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VSSFLSSK
Found in AT4G33400.1, dem protein-related / defective embryo and meristems protein-related

Match to Query 522: 1020.452212 from(511.233382,2+)
Elution from: 32.420 to 32.420 scan no 2937 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1020.4529
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0022
Matched b ions: b(2), b(3)
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98++, y(7)-98, y(7), y(8)+, y(8), y(8)-98++
Precursor origin neutral loss: +

Peptide No.2491
VSSFSLSSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of VSSFSLSSK
Found in AT4G33400.1, dem protein-related / defective embryo and meristems protein-related

Match to Query 637: 1020.452800 from(511.233676,2+)
Elution from: 32.794 to 32.794 scan no 3008 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2490/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1020.4529
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.031
Matched b ions: b(2)
Matched y ions: y(2), y(3), y(4), y(6)++, y(7)-98++, y(7)-98, y(7), y(7)++, y(8)++, y(8), y(8)-98++
Precursor origin neutral loss: +

---

**Peptide No.2492**

**VSSPPKPVSAAPK**

Confirmed sites: @S:3

Ambiguous sites:

**MS/MS Fragmentation of VSSPPKPVSAAPK**

Found in AT1G16610.1, SR45 (arginine-serine-rich 45); RNA binding

Match to Query 1963: 1343.683740 from(448.901856,3+)
Elution from: 21.356 to 21.356 scan no 1485 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1343.6850
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0036
Matched b ions: b(2), b(3), b(4)+, b(5)-98++, b(6)+, b(7)+, b(7)-98++, b(8)+, b(9)-98++,
  b(11)+, b(12)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)+, y(8)+, y(10)+, y(11)-98++, y(11)+, y(12)-98++, y(12)+
Precursor origin neutral loss:

Peptide No.2493
VSSPRVPNPAIQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VSSPRVPNPAIQK
Found in AT1G52320.1, similar to unknown protein [Arabidopsis thaliana] (TAIR:
AT5G25590.1); similar to Spectrin repeat [M

Match to Query 2618: 1568.805315 from(523.942381,3+)
Elution from: 30.771 to 30.771 scan no 2762 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2492/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1568.8075
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.051
Matched b ions: b(4), b(7), b(9)++, b(9)-98++, b(10)-98++, b(10)++
Matched y ions: y(4), y(5), y(6)++, y(7)++, y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y (13)++, y(13)-98++
Precursor origin neutral loss:

Peptide No.2494

VSYVESEDSEDIDDGK
Confirmed sites: "@S:6,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VSYVESEDSEDIDDGK
Found in AT2G13370.1, CHR5 (chromatin remodeling 5); ATP binding / DNA binding / chromatin binding / helicase

Match to Query 3261: 1945.674732 from(973.844642,2+)
Elution from: 34.695 to 34.695 scan no 3296 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2493/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1945.6754
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 3.6e-006
Matched b ions: b(3), b(4), b(7)-98, b(8)-98, b(10)-98, b(10)-196, b(11), b(12), b(12)-196, b(12)-98, b(13), b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(11)-98, y(11), y(12)+, y(12)-98, y(12), y(13), y(13)-98++, y(13)-196, y(14)-98++, y(14)+, y(15)-98++, y(15)+
Precursor origin neutral loss: +

Peptide No.2495

VSYVESEDSEDIDDGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VSYVESEDSEDIDDGK
Found in AT2G13370.1, CHR5 (chromatin remodeling 5); ATP binding / DNA binding / chromatin binding / helicase

Match to Query 2401: 1865.707808 from(933.861180,2+)
Elution from: 31.673 to 31.673 scan no 2833 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v%3/o0705103ppmGROUPmeadlist.htm (2494/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1865.7091
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 6.7e-006
Matched b ions: b(5), b(7), b(8), b(10)-98, b(10), b(11), b(12), b(12)-98, b(13), b(14)
Matched y ions: y(4), y(6), y(8), y(9), y(10)-98++, y(11)-98, y(11), y(12)-98, y(12), y(13), y(14) ++, y(15)+
Precursor origin neutral loss: +

Peptide No.2496
VTEIEPK
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of VTEIEPK
Found in AT5G26667.1, uridylate kinase / uridine monophosphate kinase / UMP kinase (PYR6)

Match to Query 304: 894.409516 from(448.212034,2+)
Elution from: 31.048 to 31.048 scan no 2654 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 894.4099
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0007
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4), b(4)-98, b(5), b(5)-98, b(6)-98
Matched y ions: y(2), y(3), y(4)+, y(4), y(5), y(6)+
Precursor origin neutral loss: +

Peptide No.2497

VTSADLSPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VTSADLSPK
Found in AT5G14720.1, protein kinase family protein

Match to Query 507: 996.452350 from(499.233451,2+) Elution from: 22.650 to 22.650 scan no 1530 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 996.4529
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0012
Matched b ions: b(2)
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.2498

VTSESDFMTEYVVTR
Confirmed sites: @Y:11
Ambiguous sites:

MS/MS Fragmentation of VTSESDFMTEYVVTR
Found in AT2G43790.1, ATMPK6 (MAP KINASE 6); MAP kinase/ kinase

Match to Query 3014: 1842.774782 from(922.394667,2+)
Elution from: 48.033 to 48.033 scan no 4998 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2497/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1842.7746
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y11 : Phospho (Y)
Ions Score: 70 Expect: 9.8e-007
Matched b ions: b(6), b(7), b(8), b(11), b(12), b(13), b(14)
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(12)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.2499

VTSESDFMTEYVVTR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of VTSESDFMTEYVVTR
Found in AT2G43790.1, ATMPK6 (MAP KINASE 6); MAP kinase/ kinase

Match to Query 2896: 1842.772500 from(922.393526,2+)
Elution from: 47.061 to 47.061 scan no 4902 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1842.7746  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 59 Expect: 1.2e-005  
Matched b ions: b(6), b(7), b(8), b(9), b(9)-98, b(10), b(11), b(12), b(13)  
Matched y ions: y(3), y(6), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(13)+, y(14)+, y(14)-98++  
Precursor origin neutral loss: +

Peptide No.2500  
VTSIIDSVPESPQRP  
Confirmed sites: @S:11  
Ambiguous sites:  
MS/MS Fragmentation of VTSIIDSVPESPQRP  
Found in AT3G08710.1, ATH9 (thioredoxin H-type 9); thiol-disulfide exchange intermediate  
Match to Query 2579: 1703.810804 from(852.912678,2+)  
Elution from: 41.611 to 41.611 scan no 4202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1703.8131
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.002
Matched b ions: b(8), b(10), b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(9), y(10), y(14)++
Precursor origin neutral loss: +

Peptide No.2501
VTTLDCSEPSEAGR
Confirmed sites: @S:11
Ambiguous sites:
MS/MS Fragmentation of VTTLDCSEPSEAGR
Found in AT5G65770.1, nuclear matrix constituent protein-related

Match to Query 2017: 1687.674510 from(844.844531,2+)
Elution from: 27.051 to 27.051 scan no 2104 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 1.5e-005
Matched b ions: b(5), b(8), b(11)-98, b(11)-98++, b(12)
Matched y ions: y(3), y(4), y(6), y(7)-98, y(7), y(8)-98, y(9), y(9)-98, y(10), y(10)+, y(10)-98+
y(11), y(11)-98, y(12), y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2502
VTTLDCSEPSEAGR
Confirmed sites: @5:7
Ambiguous sites:

MS/MS Fragmentation of VTTLDCSEPSEAGR
Found in AT5G65770.1, nuclear matrix constituent protein-related

Match to Query 2213: 1687.675726 from(844.845139,2+)
Elution from: 25.706 to 25.706 scan no 2019 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2501/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1687.6760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.0052
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(11)-98++, b(11)+, b(11)-98, b(12)-98++, b(13)-98
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10), y(11), y(12)-98++, y(13)+, y(14)+
Precursor origin neutral loss: +

Peptide No.2503

VTTLDCSESPSEAGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VTTLDCSESPSEAGR
Found in AT5G65770.1, nuclear matrix constituent protein-related

Match to Query 2519: 1687.674900 from(844.844726,2+)
Elution from: 25.929 to 25.929 scan no 2093 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1687.6760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00013
Matched b ions: b(6), b(7), b(8), b(9)-98, b(11)-98, b(12), b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10)-98, y(10), y(11), y(12), y(13)+, y(13)-98++, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2504

VTVMDTLSR
Confirmed sites:
Ambiguous sites: @T:6orS:8

MS/MS Fragmentation of VTVMDTLSR
Found in AT4G28470.1, AtRPN1b/RPN1B (26S proteasome regulatory subunit S2 1B); binding

Match to Query 727: 1100.493262 from(551.253907,2+)
Elution from: 34.796 to 34.796 scan no 3290 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2503/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1100.4937
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.026
Matched b ions: b(4)
Matched y ions: y(5), y(6), y(6)+, y(7), y(7)-98, y(8)+, y(8)
Precursor origin neutral loss: +

Peptide No.2505

VVDEVAIVHLTESPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VVDEVAIVHLTESPK
Found in AT5G46870.1, RNA recognition motif (RRM)-containing protein

Match to Query 2539: 1714.852422 from(858.433487,2+)
Elution from: 44.649 to 44.649 scan no 4593 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2504/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1714.8542
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 8.1e-005
Matched b ions: b(5), b(7), b(8), b(9)+, b(9), b(10), b(12), b(14)-98++
Matched y ions: y(3), y(5), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(11), y(11)+, y(12)-98, y(13)-98, y(13)-98++, y(13)+, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2506

VVEKPASPEPVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VVEKPASPEPVK
Found in AT5G35200.1, epsin N-terminal homology (ENTH) domain-containing protein

Match to Query 1900: 1487.726114 from(744.870333,2+)
Elution from: 20.333 to 20.333 scan no 1340 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1487.7272
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.00012
Matched b ions: b(4), b(5), b(8)-98, b(10)-98, b(10), b(10)+, b(11)-98, b(11)-98++, b(12)-98, b(12)
Matched y ions: y(3), y(5), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(9)+, y(10)-98, y(10)-98++, y(11)-98, y(11)-98++, y(11)+, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2507
VVFSDRVSSGESR
Confirmed sites: "@S:8,@S:9"
Ambiguous sites:

MS/MS Fragmentation of VVFSDRVSSGESR
Found in AT1G01540.1, protein kinase family protein

Match to Query 2590: 1583.637016 from(792.825784,2+)
Elution from: 31.266 to 31.266 scan no 2808 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2506/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1583.6381
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.054
Matched b ions: b(5), b(6), b(8)-98, b(9)-196, b(9)-98, b(11)-98, b(11), b(11)-196, b(12)++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-196, y(8)++, y(8), y(8)-196++, y(8)-196, y(8)-98, y(11)-196++, y(11)-98++, y(11)++, y(12)-196++, y(12)+, y(12)-98++
Precursor origin neutral loss: +

Peptide No.2508
VVFSDRVSSGESR
Confirmed sites: "@S:9,@S:12"
Ambiguous sites:

MS/MS Fragmentation of VVFSDRVSSGESR
Found in AT1G01540.1, protein kinase family protein

Match to Query 1771: 1583.636454 from(528.886094,3+)
Elution from: 31.529 to 31.529 scan no 2693 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1583.6381
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.02
Matched b ions: b(2), b(6)
Matched y ions: y(2)++, y(4)-98, y(5), y(5)-196, y(6)-98, y(7)-196, y(8)+, y(9)+, y(10)+, y(10)-98++, y(11)-98++, y(11)+, y(11)-196++, y(12)-196++, y(12)-98++, y(12)+
Precursor origin neutral loss: +

Peptide No.2509

VVGAFMEGGSGDENK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VVGAFMEGGSGDENK
Found in AT3G52880.1, ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); monodehydroascorbate reductase (NADH)

Match to Query 2181: 1575.625708 from(788.820130,2+)
Elution from: 36.291 to 36.291 scan no 3456 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1575.6275
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 3.4e-006
Matched b ions: b(5), b(6), b(7), b(12), b(13)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(5), y(6), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)+, y(11)-98++, y(13)-98, y(13)-98++, y(13), y(13)+, y(14)+, y(14)-98, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2510

VVLKPVSHSPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VVLKPVSHSPK
Found in AT1G62390.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-contain

Match to Query 1228: 1269.683460 from(424.235096,3+)
Elution from: 19.277 to 19.277 scan no 1177 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2509/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1269.6846
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.018
Matched b ions: b(2), b(3), b(5), b(8)+, b(9)+, b(10)-98+
Matched y ions: y(2), y(5)-98, y(7), y(8)+, y(9)+, y(9)-98+, y(10)-98+, y(10)+
Precursor origin neutral loss:

Peptide No.2511
VVLKPVSHSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VVLKPVSHSPK
Found in AT1G62390.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetraciclopeptide repeat (TPR)-contain

Match to Query 1758: 1269.683406 from(424.235078,3+)
Elution from: 18.548 to 18.548 scan no 1144 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2510/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1269.6846
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00021
Matched b ions: b(2), b(5), b(6), b(6)+, b(9)-98++, b(9)+, b(10)-98++
Matched y ions: y(2), y(3), y(4)-98++, y(4), y(4)+, y(5)-98, y(5), y(5)+, y(6)-98, y(6), y(6)-98++,
y(7)-98, y(7), y(7)+, y(8)+, y(9)+, y(9)-98++, y(10)-98++, y(10)+
Precursor origin neutral loss: +

Peptide No.2512

VVRTKTSSETTMNTNISVILEK
Confirmed sites:
Ambiguous sites: "@T:4orT:6orS:7, @T:4orT:6orS:7, @S:8orS:9"

MS/MS Fragmentation of VVRTKTSSETTMNTNISVILEK
Found in AT2G34150.1, WAVE1 (Wiskott-Aldrich syndrome protein)-family
verprolin homologous protein 1)

Match to Query 5034: 2777.244093 from(926.755307,3+)
Elution from: 44.797 to 44.797 scan no 4619 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPEadlist.htm (2511/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2777.2360
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0061
Matched b ions: b(7), b(9), b(10), b(13)+, b(14), b(14)+, b(15)+, b(15)-98++, b(17)+, b(20)+, b(21)+, b(22)+
Matched y ions: y(4), y(9), y(17)-196++, y(19)-294++
Precursor origin neutral loss:

Peptide No.2513

VVSLDPARDSTELK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VVSLDPARDSTELK
Found in AT3G10190.1, calmodulin, putative

Match to Query 2665: 1608.774546 from(805.394549,2+)
Elution from: 35.568 to 35.568 scan no 3393 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2512/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1608.7760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00019
Matched b ions: b(4), b(5), b(8), b(9), b(10)-98, b(10), b(12)-98, b(12), b(13)-98
Matched y ions: y(2), y(4), y(5), y(6), y(8)+, y(8), y(9)-98++, y(9)-98, y(9), y(9)+, y(10)-98, y(10)+, y(12)-98, y(12)-98++, y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss: +

---

Peptide No.2514
VVSLDPARDSTELK
Confirmed sites:
Ambiguous sites: @S:10orT:11

MS/MS Fragmentation of VVSLDPARDSTELK
Found in AT3G10190.1, calmodulin, putative

Match to Query 2194: 1608.774962 from(805.394757,2+)
Elution from: 34.396 to 34.396 scan no 3235 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1608.7760
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0077
Matched b ions: b(4), b(5), b(8), b(9), b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(2), y(5), y(5)-98, y(6), y(6)-98, y(8), y(8)+, y(9)-98, y(9), y(9)+, y(9)-98+
y(10), y(10)-98, y(12)-98++, y(12)-98, y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2515
VVYVAPPRPPSPVVR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VVVAPPYPPSPVVR
Found in AT2G45140.1, vesicle-associated membrane protein, putative / VAMP, putative

Match to Query 2845: 1612.847788 from(807.431170,2+)
Elution from: 35.467 to 35.467 scan no 3423 polarity:+

file:///C/|\Documents%20and%20Settings/N.Su...abi\result_v3/o0705103ppmGROUPmeadlist.htm (2514/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1612.8490
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.0051
Matched b ions: b(6), b(11), b(11)-98, b(12)-98
Matched y ions: y(3), y(6), y(7)-98, y(8)+, y(8), y(9)+, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10)-98++, y(10), y(12)-98++, y(12), y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2516
VWSGGVAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VWSGGVAK
Found in AT5G31787.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G32312.1)

Match to Query 248: 882.399198 from(442.206875,2+)
Elution from: 43.411 to 43.411 scan no 4436 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 882.4000
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 Expect: 0.058
Matched b ions: b(3), b(4), b(4)-98++
Matched y ions: y(3)+, y(4)+, y(5)+, y(7)+
Precursor origin neutral loss:

Peptide No.2517

VYGPHFASPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VYGPHFASPK
Found in AT2G30860.1, ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase

Match to Query 912: 1181.527312 from(591.770932,2+)
Elution from: 28.228 to 28.228 scan no 2404 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...v3/o0705103ppmGROUPmeadlist.htm (2516/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1181.5270
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.0093
Matched b ions: b(2), b(8)-98
Matched y ions: y(2), y(3), y(4)-98, y(5), y(6)++, y(6), y(7)-98++, y(7), y(7)-98, y(8), y(8)-98+ +, y(8)++, y(8)-98, y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.2518

VYHSDDDEQGQVDK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VYHSDDDEQGQVDK
Found in AT2G28130.1, similar to Os01g0241100 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001042551.1)

Match to Query 2056: 1713.651382 from(857.832967,2+)
Elution from: 18.037 to 18.037 scan no 1012 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1713.6519
Fixed modifications: Carbamidomethyl (C)
Variable modifications: 
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.045
Matched b ions: b(6), b(8)-98, b(11)++, b(12)-98++, b(12)++, b(12)-98, b(13)+
Matched y ions: y(7), y(11)-98, y(11), y(12)-98++, y(12)++, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2519

VYNLVEEEGSLESDDDK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VYNLVEEEGSLESDDDK
Found in AT3G17740.1, similar to Os02g0772500 [Oryza sativa (japonica cultivar-group)]
(GB:NP_001048265.1); similar to Un

Match to Query 3062: 2019.816380 from(1010.915466,2+)
Elution from: 45.307 to 45.307 scan no 4541 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2019.8197
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 5.3e-007
Matched b ions: b(4), b(6), b(7), b(8), b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(14), b(14)-98, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98, y(15)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.2520

VYNLVEEGSLESDDDK
Confirmed sites: "@S:10, @S:13"
Ambiguous sites:

MS/MS Fragmentation of VYNLVEEGSLESDDDK
Found in AT3G17740.1, similar to Os02g0772500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048265.1); similar to Un

Match to Query 3826: 2099.784402 from(1050.899477,2+)
Elution from: 49.561 to 49.561 scan no 5213 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2519/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2099.7860
Fixed modifications: Carboxamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00023
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(11)-98, b(12)-98, b(12)-98++, b(12), b(13)++ , b(13)-196, b(14)
Matched y ions: y(5)-98, y(5), y(6)-98, y(7), y(8)-98, y(9), y(9)-98, y(10)-98, y(12)-196++, y(12)-98, y(12), y(13)+++, y(13), y(13)-98, y(14), y(16)-98++, y(16)+
Precursor origin neutral loss: +

Peptide No.2521

VYSDDERSDHGVQAGYR
Confirmed sites: "@S:3,@S:8"
Ambiguous sites:

MS/MS Fragmentation of **VYSDDERSDHGVQAGYR**
Found in **AT2G01190.1**, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 3901: 2112.791724 from(705.271184,3+)
Elution from: 25.015 to 25.015 scan no 2018 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmealdlist.htm (2520/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2112.7939
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.0052
Matched b ions: b(3)-98, b(4), b(5)-98, b(6)-98, b(7), b(9)-196, b(9), b(9)-196++, b(9)+ +, b(10)-196++, b(10)-98++, b(10)+++, b(11)-196++, b(11)-98++, b(11)+++, b(12)+++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)-98++, b(14)-98++, b(15)+++
Matched y ions: y(4), y(5), y(6), y(7), y(8)+, y(10)+, y(11)-98, y(11)-98++, y(11)+, y(12)-98++, y(12)+, y(13)+, y(13)-98++, y(14)-98++, y(14)+, y(15)-98++, y(15)-196++, y(15)+++, y(16)-98++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.2522

VYSDDERSDHGVQAGYR
Confirmed sites: "@S:3,@Y:16"
Ambiguous sites:

MS/MS Fragmentation of VYSDDERSDHGVQAGYR
Found in AT2G01190.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 2950: 2112.791080 from(1057.402816,2+)
Elution from: 26.149 to 26.149 scan no 2014 polarity:+

Monoisotopic mass of neutral peptide Mr(calc): 2112.7939
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y16 : Phospho (Y)
Ions Score: 21 Expect: 0.053
Matched b ions: b(9), b(13)-98++
Matched y ions: y(8), y(12)++, y(13)+, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2523
VYSDDERSDHGVQAGYR
Confirmed sites: @S:8
Ambiguous sites: @Y:2orS:3

MS/MS Fragmentation of VYSDDERSDHGVQAGYR
Found in AT2G01190.1, octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

Match to Query 3903: 2112.791910 from(1057.403231,2+)
Elution from: 25.188 to 25.188 scan no 2019 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2522/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2112.7939
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y2 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0032
Matched b ions: b(7)++, b(7), b(9)-98, b(9), b(10), b(10)-98, b(12)-98, b(12), b(13)-98, b(13)-98++, b(13)+, b(15)
Matched y ions: y(5), y(7), y(8), y(10), y(11)-98, y(12)-98++, y(12)+, y(13)-98++, y(13)+, y(14)+, y(14)-98++, y(16)-98++, y(16)+
Precursor origin neutral loss: +

Peptide No.2524
VYSTATSPSPSEISVK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VYSTATSPSPSEISVK
Found in AT5G41970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G49320.1); similar to LOC496075 protein

Match to Query 2651: 1731.795852 from(866.905202,2+)
Elution from: 34.114 to 34.114 scan no 3202 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2523/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1731.7968
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.1e-005
Matched b ions: b(4), b(7)-98, b(8)-98, b(11)-98, b(12), b(13), b(14), b(14)+, b(15)
Matched y ions: y(3), y(7), y(9), y(10), y(10)-98, y(11), y(12), y(13), y(13)+, y(14), y(14)+, y(15)+
Precursor origin neutral loss: +

Peptide No.2525

VYSTATSPSPSEISVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of VYSTATSPSPSEISVK
Found in AT5G41970.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G49320.1); similar to LOC496075 protein

Match to Query 2582: 1731.795796 from(866.905174,2+)
Elution from: 34.208 to 34.208 scan no 3210 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2524/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1731.7968
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0041
Matched b ions: b(5), b(10)+, b(11)-98, b(13)
Matched y ions: y(3), y(4), y(7), y(8)-98, y(9), y(10), y(10)-98, y(11)-98++, y(11), y(11)-98, y(12), y(13)+, y(14), y(14)+, y(15)+
Precursor origin neutral loss:

Peptide No.2526
WAAENGVSGDYDALCQNEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of WAAENGVSGDYDALCQNEK
Found in AT4G23850.1, long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase

Match to Query 4326: 2205.865456 from(1103.940004,2+)
Elution from: 45.826 to 45.826 scan no 4735 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2525/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2205.8674
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 4.1e-006
Matched b ions: b(4), b(10)-98, b(12)-98, b(12), b(14)-98, b(15)-98, b(16), b(17)-98++, b (18)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(15)-98, y(16)-98++, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No. 2527
WAAGNSSPTDEVEIVEEVGEK
Confirmed sites:
Ambiguous sites: @S:6orS:7orT:9

MS/MS Fragmentation of WAAGNSSPTDEVEIVEEVGEK
Found in AT1G67580.1, protein kinase family protein

Match to Query 4533: 2325.001548 from(776.007792,3+)
Elution from: 57.072 to 57.072 scan no 6034 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2526/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2325.0049
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 2.4e-006
Matched b ions: b(11), b(11)+, b(12), b(12)-98++, b(13)+, b(15)+, b(16)+, b(17)+, b(18)+, b(18)-98++, b(19)+, b(20)+
Matched y ions: y(5), y(6)
Precursor origin neutral loss:

Peptide No.2528

WELLEDTSADEDK
Confirmed sites:
Ambiguous sites: @T:8orS:9

MS/MS Fragmentation of WELLEDTSADEDK
Found in AT1G80810.1, binding

Match to Query 2110: 1744.669058 from(873.341805,2+)
Elution from: 49.973 to 49.973 scan no 5004 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1744.6716
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.00096
Matched b ions: b(3), b(12)
Matched y ions: y(8), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.2529
WENEQGFLDCQSDK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of WENEQGFLDCQSDK
Found in AT4G16310.1, amine oxidase family protein / SWIRM domain-containing protein

Match to Query 3161: 1834.685522 from(918.350037,2+)
Elution from: 44.174 to 44.174 scan no 4314 polarity:+

file:///C/|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea|list.htm (2528/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1834.6869
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.023
Matched b ions: b(4), b(5), b(9), b(12)-98, b(13)-98
Matched y ions: y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9)
Precursor origin neutral loss: +

---

Peptide No.2530

WGVGVAAGSDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of WGVGVAAGSDK
Found in AT3G16830.1, TPR2 (TOPLESS-RELATED 2)

Match to Query 751: 1125.484842 from(563.749697,2+)
Elution from: 34.532 to 34.532 scan no 3253 polarity:+

file:///C/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2529/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1125.4855
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 6.5e-06
Matched b ions: b(2), b(3), b(4), b(5), b(7)++, b(7), b(10)-98
Matched y ions: y(2), y(4)-98, y(4)++, y(4), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.2531
WHSCSEDVEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of WHSCSEDVEVR
Found in AT5G25070.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT5G16730.1); similar to Os08g0516000 [Oryz]

Match to Query 2244: 1482.558378 from(742.286465,2+)
Elution from: 25.618 to 25.618 scan no 2061 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2530/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1482.5599
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0018
Matched b ions: b(2), b(6), b(7), b(8)-98, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(8), y(9), y(9)-98, y(10)+, y(10)-98++
Precursor origin neutral loss: +

Peptide No.2532

WPAEVQSPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of WPAEVQSPK
Found in AT3G05090.1, transducin family protein / WD-40 repeat family protein

Match to Query 731: 1120.494862 from(561.254707,2+)
Elution from: 32.127 to 32.127 scan no 2930 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1120.4954
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0014
Matched b ions: b(7)-98
Matched y ions: y(2), y(3), y(4)-98++, y(4), y(5), y(6), y(7), y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.2533

WSQALNDVNIAGEHFLNWDKESK
Confirmed sites: @S:23
Ambiguous sites:

MS/MS Fragmentation of WSQALNDVNIAGEHFLNWDKESK
Found in AT1G63730.1, disease resistance protein (TIR-NBS-LRR class), putative

Match to Query 3952: 2837.273148 from(946.764992,3+)
Elution from: 52.648 to 52.648 scan no 5089 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2532/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2837.2809
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S23 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.045
Matched b ions: b(8), b(11), b(12), b(19)+, b(20)+, b(21)+
Matched y ions: y(6), y(15)-98++, y(16)-98++, y(18)+, y(18)-98++, y(19)-98++, y(20)-98++,
y(21)-98++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.2534
WSSEEDSDGNLQAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of WSSEEDSDGNLQAK
Found in AT1G55930.1, CBS domain-containing protein / transporter associated domain-containing protein

Match to Query 2604: 1644.631350 from(823.322951,2+)
Elution from: 28.392 to 28.392 scan no 2202 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1644.6304
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.031
Matched b ions: b(10), b(10)-98, b(11), b(12)-98
Matched y ions: y(3), y(6), y(8), y(9)-98, y(10)-98++, y(10)-98, y(11)-98, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.2535
WSVSLKSPK
Confirmed sites: @S:8
Ambiguous sites:
MS/MS Fragmentation of WSVSLKSPK
Found in AT1G67900.1, phototropic-responsive NPH3 family protein

Match to Query 1295: 1167.567296 from(584.790924,2+)
Elution from: 33.256 to 33.256 scan no 3112 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1167.5689
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0041
Matched b ions: b(8)-98
Matched y ions: y(2), y(3)-98, y(4), y(5), y(6), y(7), y(8), y(8)+
Precursor origin neutral loss: +

Peptide No.2536

WWKDAQDSMPSESVEKR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of WWKDAQDSMPSESVEKR
Found in AT5G22035.1, ubiquitin-specific protease-related

Match to Query 3240: 2173.918082 from(1087.966317,2+)
Elution from: 40.850 to 40.850 scan no 4080 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2173.9139
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.032
Matched b ions: b(4), b(10), b(11), b(13), b(14), b(14)-98
Matched y ions: y(3), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(9)-98, y(10)-98, y(13)-98, y(13)-98 ++
Precursor origin neutral loss: +

Peptide No.2537

WYLTGERNSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of WYLTGERNSPR
Found in AT1G32090.1, early-responsive to dehydration protein-related / ERD protein-related

Match to Query 2304: 1457.643914 from(729.829233,2+)
Elution from: 33.785 to 33.785 scan no 3169 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1457.6452
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0014
Matched b ions: b(3), b(4), b(7), b(8), b(9)-98, b(9), b(10)-98, b(10)++
Matched y ions: y(2), y(4)-98, y(5)-98, y(5), y(7), y(8)+, y(9)-98++, y(9)+, y(9), y(10)-98++
Precursor origin neutral loss: +

Peptide No.2538
YAGTEVEFNDVK
Confirmed sites: @Y:1
Ambiguous sites:

MS/MS Fragmentation of YAGTEVEFNDVK
Found in AT5G20720.1, CPN20 (CHAPERONIN 20); calmodulin binding

Match to Query 1489: 1450.600330 from(726.307441,2+)
Elution from: 36.352 to 36.352 scan no 3345 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaclid.htm (2537/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1450.6017
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y: Phospho (Y)
Ions Score: 92 Expect: 3.9e-09
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)+
Precursor origin neutral loss:

Peptide No.2539

YAPANSPPLPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of YAPANSPPLPR
Found in AT4G28990.1, RNA-binding protein-related

Match to Query 1187: 1261.585840 from(631.800196,2+)
Elution from: 31.938 to 31.938 scan no 2872 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2538/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1261.5856
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00036
Matched b ions: b(6), b(6)-98, b(8), b(9)
Matched y ions: y(2), y(5), y(6), y(7), y(8)+, y(8), y(9)-98++, y(9)+, y(9)
Precursor origin neutral loss: +

Peptide No.2540

YARTDAHYLLIADSLTELK
Confirmed sites: "@Y:1,@Y:11,@S:15"
Ambiguous sites:

MS/MS Fragmentation of YARTDAHYLLIADSLTELK
Found in AT2G32415.1, 3'-5' exonuclease/ nucleic acid binding

Match to Query 4849: 2696.156673 from(899.726167,3+)
Elution from: 40.217 to 40.217 scan no 4017 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2539/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2696.1577
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
Y11 : Phospho (Y)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.015
Matched b ions: b(8)++, b(8), b(9)++, b(11)++, b(12)++, b(17)++, b(18)-98++, b(19)-98++
Matched y ions: y(6), y(9)+++, y(9), y(9)-98++, y(10)++, y(10), y(12)++, y(13)++, y(20)++
Precursor origin neutral loss:

Peptide No.2541

YCHSDPYPSSSTSTSPEK
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of YCHSDPYPSSSTSTSPEK
Found in AT1G53180.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT3G15115.1)

Match to Query 4025: 2195.834229 from(732.952019,3+)
Elution from: 23.022 to 23.022 scan no 1708 polarity:+

file://C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmea clandest.htm (2540/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2195.8354
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 41 Expect: 0.00042
Matched b ions: b(3), b(5), b(7), b(7)++, b(9)++, b(10)++, b(11)++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.2542
YCVPNTSDADTSPDQSK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of YCVPNTSDADTSPDQSK
Found in AT2G47390.1, serine-type peptidase

Match to Query 3508: 1963.748532 from(982.881542,2+)
Elution from: 30.253 to 30.253 scan no 2455 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2541/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1963.7507
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 Expect: 3e-007
Matched b ions: b(3), b(10), b(11), b(12)-98, b(14), b(15)
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(9)-98, y(10), y(11), y(11)-98, y(13), y(14)+, y(14), y(14)-98, y(15)-98++, y(15), y(15)-98, y(15)+
Precursor origin neutral loss: +

Peptide No.2543
YCVPTSDADTSPDQSK
Confirmed sites:
Ambiguous sites: @S:12orS:16

MS/MS Fragmentation of YCVPTSDADTSPDQSK
Found in AT2G47390.1, serine-type peptidase

Match to Query 3677: 1963.750460 from(982.882506,2+)
Elution from: 29.816 to 29.816 scan no 2616 polarity:+

file:///C|/Documents%20and%20Settings/N.Suu...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2542/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1963.7507
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00014
Matched b ions: b(2), b(3), b(8)
Matched y ions: y(6), y(7), y(8), y(10), y(12), y(13), y(14)+, y(14), y(15)-98++, y(15)+, y(15)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.2544

YLDIKSPNK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of YLDIKSPNK
Found in AT2G29560.1, enolase, putative

Match to Query 1233: 1271.578534 from(636.796543,2+)
Elution from: 31.909 to 31.909 scan no 2868 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1271.5798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.00096
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(8), b(8)+, b(9)
Matched y ions: y(3), y(4)-98, y(4), y(5), y(5)-98, y(6), y(7), y(7)-98++, y(7)-98, y(8)+, y(8), y(8)-98++, y(8)-98, y(9)+
Precursor origin neutral loss: +

Peptide No.2545
YSDSSLVR
Confirmed sites: @5:3
Ambiguous sites:

MS/MS Fragmentation of YSDSSLVR
Found in AT2G34260.1, transducin family protein / WD-40 repeat family protein

Match to Query 662: 1120.443168 from(561.228860,2+)
Elution from: 26.471 to 26.471 scan no 2131 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1120.4438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.00012
Matched b ions: b(2), b(3)-98++, b(3), b(4)-98, b(5), b(8)+, b(8)-98
Matched y ions: y(1), y(2), y(4), y(6), y(7)-98, y(7), y(7)-98++, y(8), y(8)-98++, y(8)-98
Precursor origin neutral loss: +

Peptide No.2546
YDSDDLVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YDSDDLVR
Found in AT2G34260.1, transducin family protein / WD-40 repeat family protein

Match to Query 955: 1120.442654 from(561.228603,2+)
Elution from: 27.122 to 27.122 scan no 2222 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2545/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1120.4438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.00091
Matched b ions: b(2), b(4), b(8)+
Matched y ions: y(2), y(3), y(4), y(5)-98, y(6)-98++, y(7)-98++, y(7)-98, y(7)
Precursor origin neutral loss: +

Peptide No.2547

YDSSSLVR
Confirmed sites:
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of YDSSSLVR
Found in AT2G34260.1, transducin family protein / WD-40 repeat family protein

Match to Query 1103: 1120.442638 from(561.228595,2+)
Elution from: 27.046 to 27.046 scan no 2274 polarity:+

file:///C/ Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2546/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1120.4438
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 Expect: 0.043
Matched b ions: b(2), b(8)-98
Matched y ions: y(5)-98, y(6)-98, y(7)-98++, y(7)-98, y(7), y(8), y(8)-98
Precursor origin neutral loss: +

Peptide No.2548

YFFPSDTEDQGDDSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YFFPSDTEDQGDDSK
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G19710.1); similar to MAPK activating pr

Match to Query 2986: 1829.664842 from(915.839697,2+)
Elution from: 44.880 to 44.880 scan no 4593 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1829.6669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 4.1e-005
Matched b ions: b(2), b(3), b(8)-98, b(9), b(10)-98, b(13)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11)+, y(11), y(12)-98, y(12), y(12)-98++, y(12)+, y(13)+, y(13), y(13)-98++
Precursor origin neutral loss: +

Peptide No.2549
YFFPSDTEDQGDDSK
Confirmed sites:
Ambiguous sites: @S:5orT:7

MS/MS Fragmentation of YFFPSDTEDQGDDSK
Found in AT4G29440.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT2G19710.1); similar to MAPK activating pr

Match to Query 2861: 1829.662988 from(915.838770,2+)
Elution from: 43.933 to 43.933 scan no 4501 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1829.6669
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0019
Matched b ions: b(2), b(3), b(9), b(10)-98, b(12), b(13)
Matched y ions: y(5), y(6), y(7), y(11)++, y(11), y(12)++, y(12)-98, y(12), y(12)-98++, y(13)+
+, y(13)-98++, y(13)-98, y(13)
Precursor origin neutral loss: +

Peptide No.2550
YFPDQIAGVAMVAPMINPYEPSMTK
Confirmed sites: "@Y:1,@Y:19"
Ambiguous sites: @S:22orT:24

MS/MS Fragmentation of YFPDQIAGVAMVAPMINPYEPSMTK
Found in AT3G09690.1, hydrolase, alpha/beta fold family protein

Match to Query 3777: 3009.217962 from(1004.079930,3+)
Elution from: 40.401 to 40.401 scan no 3958 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 3009.2205
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
Y19 : Phospho (Y)
T24 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.031
Matched b ions: b(3), b(5), b(8)+, b(8), b(24)-98++
Matched y ions: y(6)-98, y(9), y(13)+, y(14)-98++, y(15)-98++, y(17)-98++, y(20)-98++, y(20)+, y(21)-98++, y(22)+, y(22)-98++, y(23)-98++, y(24)+, y(24)-98++
Precursor origin neutral loss: +

Peptide No.2551

YGAGIGPGVYDIHSPR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of YGAGIGPGVYDIHSPR
Found in AT5G17920.1, ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroylglutamate-homocyste

Match to Query 2708: 1737.787662 from(580.269830,3+)
Elution from: 39.936 to 39.936 scan no 3942 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2550/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1737.7875
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S14: Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 6.4e-005
Matched b ions: b(2), b(4), b(5), b(6)
Matched y ions: y(5)-98++, y(5)-98, y(9)++, y(10)-98++, y(10)+++, y(11)+++, y(11)-98++, y(12)+++, y(13)+++, y(13)-98++, y(14)+++, y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.2552
YGAGIGPGVYDIHSPR
Confirmed sites: @Y:10
Ambiguous sites:

MS/MS Fragmentation of YGAGIGPGVYDIHSPR
Found in AT5G17920.1, ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroyltriglutamate-homocyste

Match to Query 2594: 1737.786930 from(580.269586,3+)
Elution from: 39.122 to 39.122 scan no 3868 polarity:+

file:///C/|Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2551/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1737.7875
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y10 : Phospho (Y)
Ions Score: 41 Expect: 0.00071
Matched b ions: b(2), b(5)
Matched y ions: y(2), y(6), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss:

---

Peptide No.2553

YGDGQTQQTEGIPR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of YGDGQTQQTEGIPR
Found in AT3G15500.1, ATNAC3 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 55); transcription factor

Match to Query 2815: 1685.703606 from(562.908478,3+)
Elution from: 27.451 to 27.451 scan no 2193 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1685.7046
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.021
Matched b ions: b(2), b(3)
Matched y ions: y(3)+, y(4)+, y(6)+, y(11)+, y(12)+, y(13)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2554

YGSFKGTPPSEK
Confirmed sites: "@Y:1,@T:7"
Ambiguous sites:

MS/MS Fragmentation of YGSFKGTPPSEK
Found in AT4G31540.1, ATEX070G1 (exocyst subunit EXO70 family protein G1); protein binding

Match to Query 1511: 1456.566194 from(729.290373,2+)
Elution from: 28.195 to 28.195 scan no 2256 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2553/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1456.5676
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 0.05
Matched b ions: b(5), b(7)-98, b(7), b(8)-98, b(10)-98++, b(11)-98
Matched y ions: y(5), y(6)-98, y(7), y(7)-98, y(9)+, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2555
YHGHSMSDPGSTYR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGSTYR
Found in AT1G24180.1, IAR4 (IAA-conjugate-resistant 4); pyruvate dehydrogenase (acyl-transferring)

Match to Query 3000: 1673.627523 from(558.883117,3+)
Elution from: 20.208 to 20.208 scan no 1364 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2554/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1673.6293
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.049
Matched b ions: b(2), b(8)++, b(8), b(8)-98++, b(9)-98++, b(9)+, b(10)-98++
Matched y ions: y(3), y(4), y(5), y(6)+, y(6), y(9)-98++, y(9)-98, y(9)+, y(12)+
Precursor origin neutral loss: +

Peptide No.2556
YHTSPERSPR
Confirmed sites: "@S:5,@S:9"
Ambiguous sites:

MS/MS Fragmentation of YHTSPERSPR
Found in AT3G63400.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 1741: 1582.631830 from(792.323191,2+)
Elution from: 21.137 to 21.137 scan no 1439 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2555/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1582.6330
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.0078
Matched b ions: b(2), b(3), b(7), b(9)-98
Matched y ions: y(3), y(4), y(5)-98, y(6), y(7), y(8)+, y(8), y(9)+, y(9), y(9)-98++, y(9)-98, y(10)-98++, y(10)-98
Precursor origin neutral loss: +

Peptide No.2557

YIEYDSTFDEEEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of YIEYDSTFDEEEK
Found in AT5G48570.1, peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative

Match to Query 2684: 1746.654080 from(874.334316,2+)
Elution from: 42.582 to 42.582 scan no 4254 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1746.6549
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.0067
Matched b ions: b(7)-98, b(8)-98, b(9), b(10), b(11)-98, b(11)+
Matched y ions: y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.2558
YIEYDSTFDEEEEK
Confirmed sites:
Ambiguous sites: @S:6orT:7

MS/MS Fragmentation of YIEYDSTFDEEEEK
Found in AT5G48570.1, peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative

Match to Query 2128: 1746.655880 from(874.335216,2+)
Elution from: 42.621 to 42.621 scan no 4109 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2557/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1746.6549
Fixed modifications: Carboxymethyl (C)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00026
Matched b ions: b(2), b(5), b(9), b(10), b(10)-98, b(11), b(12)
Matched y ions: y(4), y(6), y(8), y(9)-98, y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)+
Precursor origin neutral loss: +

Peptide No.2559

YKLEAEIEGSGERK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of YKLEAEIEGSGERK
Found in AT5G62390.1, ATBAG7 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 7); calmodulin binding

Match to Query 2823: 1687.780170 from(563.600666,3+)
Elution from: 29.538 to 29.538 scan no 2569 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2558/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1687.7817  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 26 Expect: 0.026  
Matched b ions: b(2), b(3), b(4), b(5)+ , b(5), b(6), b(7), b(8), b(8)+ , b(12)-98++, b(12)+ , b(13)-98++  
Matched y ions: y(2), y(4)+ , y(4), y(5)+ , y(6)-98++, y(6)-98, y(6), y(7), y(7)-98, y(8)-98++, y(8)+ , y(9)+ , y(10)-98++, y(11)+ , y(11)-98++, y(12)-98++, y(12)+ , y(13)+ , y(13)-98++  
Precursor origin neutral loss: +  

---

Peptide No.2560

YLAQQQGEGADSV  
Confirmed sites: @S:12  
Ambiguous sites:  

MS/MS Fragmentation of YLAQQQGEGADSV  
Found in AT4G21450.1, vesicle-associated membrane family protein / VAMP family protein  

Match to Query 1446: 1444.586256 from(723.300404,2+)  
Elution from: 30.334 to 30.334 scan no 2655 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1444.5871
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 9.5e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11), b(12)++, b(12)-98++
Matched y ions: y(3), y(5), y(6), y(7)-98, y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.2561

YLQSGSEDDDDDTDTK
Confirmed sites: "@S:4,@S:6"
Ambiguous sites:

MS/MS Fragmentation of YLQSGSEDDDDDTDTK
Found in AT3G56150.1, EIF3C (EUkaryotic Translation Initiation Factor 3)

Match to Query 2397: 1847.599562 from(924.807057,2+)
Elution from: 24.508 to 24.508 scan no 1772 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2560/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1847.6023  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 36 Expect: 0.00061  
Matched b ions: b(6)-98, b(7)-98, b(7)-196, b(8), b(8)-98, b(9), b(10), b(11), b(12)-98++, b(13)-98, b(13)  
Matched y ions: y(4), y(5), y(6), y(7), y(11), y(12), y(13)-196++, y(13)+, y(13)-98++  
Precursor origin neutral loss: +  

Peptide No.2562  
YLQSGSEDDDDTDTK  
Confirmed sites: @S:6  
Ambiguous sites:  
MS/MS Fragmentation of YLQSGSEDDDDTDTK  
Found in AT3G56150.1, EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3)  
Match to Query 3161: 1767.634596 from(884.824574,2+)  
Elution from: 22.289 to 22.289 scan no 1593 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1767.6360
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 1.6e-009
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)+, y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(11)-98++, y(12)-98, y(12), y(13)+, y(13)-98++, y(13)-98, y(14)+, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2563

YLSGSEDDDDDTDTK
Confirmed sites: 
Ambiguous sites: "@Y:1orS:4orS:6, @Y:1orS:4orS:6"

MS/MS Fragmentation of YLSGSEDDDDDTDTK
Found in AT3G56150.1, EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3)

Match to Query 3272: 1847.601394 from(924.807973,2+)
Elution from: 24.777 to 24.777 scan no 1919 polarity:+

file:///C|/Documents%20and%20%Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2562/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1847.6023  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
Y1 : Phospho (Y)  
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000  
Ions Score: 34 Expect: 0.0011  
Matched b ions: b(7)-98, b(8), b(9), b(9)-98, b(10), b(11), b(12)-98++, b(12)-98, b(13)-98, b(13)  
Matched y ions: y(4), y(5), y(6), y(7), y(9)  
Precursor origin neutral loss: +

Peptide No.2564

YLQSGSEDDDDDTDTK  
Confirmed sites: "@Y:1,@S:6"  
Ambiguous sites:  

MS/MS Fragmentation of YLQSGSEDDDDDTDTK  
Found in AT3G56150.1, EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3)  

Match to Query 2348: 1847.600518 from(924.807535,2+)  
Elution from: 23.862 to 23.862 scan no 1798 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2563/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1847.6023
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 1e-005
Matched b ions: b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98++, b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)+, y(7), y(9), y(10)-98, y(10)-98++, y(10), y(11)-98, y(11), y(11)+, y(13)-98++
Precursor origin neutral loss: +

Peptide No.2565

YMEYAVTVETYTLSK
Confirmed sites:
Ambiguous sites: @T:12

MS/MS Fragmentation of YMEYAVTVETYTLSK
Found in AT5G49460.1, ACLB-2 (ATP-citrate lyase B-2)

Match to Query 3418: 1876.825728 from(626.615852,3+)
Elution from: 37.584 to 37.584 scan no 3556 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2564/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1876.8205
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 Expect: 0.04
Matched b ions: b(2), b(4), b(5)+, b(6), b(8)+, b(9)+, b(10)+, b(12)+, b(12)-98++, b(13)+, b(13)-98++
Matched y ions: y(4), y(5)-98++, y(6)-98++, y(7)-98, y(8)+, y(10)+, y(11)-98++, y(12)-98+, y(13)-98++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.2566
YMVKKEGSAK
Confirmed sites: "@Y:1,@S:8"
Ambiguous sites:

MS/MS Fragmentation of YMVKKEGSAK
Found in AT4G25730.1, FtsJ-like methyltransferase family protein

Match to Query 1825: 1299.531440 from(650.772996,2+)
Elution from: 25.387 to 25.387 scan no 2031 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmgROUPmeadlist.htm (2565/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1299.5335
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.039
Matched b ions: b(4), b(7)+++, b(7), b(8)-98++, b(8)-98, b(8), b(8)+++, b(9), b(9)-98, b(9)++
Matched y ions: y(2), y(6)-98
Precursor origin neutral loss: +

Peptide No.2567

YPTTPIVCSGNR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of YPTTPIVCSGNR
Found in AT1G20630.1, CAT1 (CATALASE 1); catalase

Match to Query 1766: 1443.620090 from(722.817321,2+)
Elution from: 32.182 to 32.182 scan no 2905 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2566/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1443.6217
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.0048
Matched b ions: b(4)-98, b(4), b(5)-98, b(6)-98, b(7)-98, b(7)+++, b(7)
Matched y ions: y(4), y(5), y(6), y(8), y(9)+++, y(9)-98++, y(10)-98, y(10)+++, y(10)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.2568

YQVSEDDGNSG DENLEAN
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of YQVSEDDGNSG DENLEAN
Found in AT3G45830.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT1G02290.1); similar to unknown protein [Or

Match to Query 2904: 2076.789690 from(1039.402121,2+)
Elution from: 30.491 to 30.491 scan no 2676 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2076.7909
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 3.4e-009
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(10), b(12), b(13)-98, b(14)-98, b(14), b(15), b(16), b(16)-98, b(17)-98++, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)-98, y(9), y(11)-98, y(11), y(12), y(12)-98, y(13), y(13)-98, y(15)+, y(15)-98, y(15), y(16)-98++, y(16), y(16)-98, y(16)+, y(17)+
Precursor origin neutral loss: +

Peptide No.2569
YRSRSPVPR
Confirmed sites: "@S:3,@S:5"
Ambiguous sites:

MS/MS Fragmentation of YRSRSPVPR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPlicing FACTOR 31); RNA binding

Match to Query 1255: 1276.547223 from(426.523017,3+)
Elution from: 17.362 to 17.362 scan no 962 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeaIst.htm (2568/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1276.5478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.065
Matched b ions: b(2), b(3)-98, b(4)-98++, b(5)-196++, b(5)-98, b(5)-98++, b(5)+, b(6)-196++, b(6)+, b(6)-98++, b(7)-98++, b(7)-196++, b(7)+, b(8)-196+
Matched y ions: y(2)+, y(2), y(4)+, y(4), y(6)+, y(7)-196++, y(7)+
Precursor origin neutral loss: +

Peptide No.2570
YRSRSPVPR
Confirmed sites: "@Y:1,@S:3"
Ambiguous sites:

MS/MS Fragmentation of YRSRSPVPR
Found in AT3G61860.1, ATRSP31 (ARGININE/SERINE-RICH SPlicing FACTOR 31); RNA binding

Match to Query 1364: 1276.546334 from(639.280443,2+)
Elution from: 17.338 to 17.338 scan no 936 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1276.5478
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00086
Matched b ions: b(3)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98
Matched y ions: y(2), y(4), y(7)-98, y(8)-98++
Precursor origin neutral loss: +

Peptide No.2571
YRSRSYSPAPR
Confirmed sites: "@S:3,@S:5,@S:7"
Ambiguous sites:

MS/MS Fragmentation of YRSRSYSPAPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2234: 1578.576477 from(527.199435,3+)
Elution from: 19.673 to 19.673 scan no 1229 polarity:+

file:///C|/Documents%20and%20% Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2570/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1578.5782
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.029
Matched b ions: b(2), b(3), b(3)-98, b(4)-98++, b(5)-98++, b(5)-196++, b(6)+, b(6)-196++, b(6)-98++, b(7)-196++, b(7)-294++, b(8)-294++, b(9)-98++, b(9)-196++, b(10)-294++
Matched y ions: y(2), y(4), y(5), y(5)-98, y(8)-196++
Precursor origin neutral loss: +

Peptide No.2572

YRSRSYSPAPR
Confirmed sites: "@Y:1,@S:3,@S:7"
Ambiguous sites:

MS/MS Fragmentation of YRSRSYSPAPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 2257: 1578.577203 from(527.199677,3+)
Elution from: 19.511 to 19.511 scan no 1204 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2571/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1578.5782
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.021
Matched b ions: b(3)-98, b(5)-98++, b(6)-98++, b(6)+, b(7)-196++, b(9)-98++, b(9)-196+
+, b(10)-196++
Matched y ions: y(2), y(4)+, y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)+
Precursor origin neutral loss: +

Peptide No.2573

YRTSPSPDRSPYR
Confirmed sites: "@S:4,@Y:12"
Ambiguous sites:

MS/MS Fragmentation of YRTSPSPDRSPYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 3174: 1740.700548 from(581.240792,3+)
Elution from: 21.224 to 21.224 scan no 1477 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2572/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1740.7022
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S4: Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y12: Phospho (Y)
Ions Score: 25 Expect: 0.02
Matched b ions: b(2), b(3), b(4)-98, b(4), b(6), b(6)-98, b(7)+, b(7)-98, b(8)-98, b(9)-98++, b(9)+, b(10)-98++, b(10)+, b(11)+, b(11)-98++, b(12)-98++, b(12)+
Matched y ions: y(3)+, y(3), y(4)+, y(4), y(6)+, y(8)+, y(10)-98++, y(10)+, y(11)-98+, y(11)+, y(12)-98+
Precursor origin neutral loss: +

Peptide No.2574

YRTSPSPDRSPYR
Confirmed sites: @S:6
Ambiguous sites: @Y:1orT:3

MS/MS Fragmentation of YRTSPSPDRSPYR
Found in AT4G32420.1, peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein

Match to Query 3066: 1740.701428 from(871.357990,2+)
Elution from: 21.869 to 21.869 scan no 1574 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1740.7022
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
  Y1 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.018
Matched b ions: b(4), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)+, y(8), y(9), y(9)-98, y(10)
Precursor origin neutral loss: +

Peptide No.2575

YSGENLDALGLQVFK
Confirmed sites:
Ambiguous sites: @Y:1orS:2

MS/MS Fragmentation of YSGENLDALGLQVFK
Found in AT2G43320.1, similar to unknown protein [Arabidopsis thaliana] (TAIR: AT4G14000.1); similar to At2g43320/T1O24.6

Match to Query 3134: 1732.804330 from(867.409441,2+)
Elution from: 63.198 to 63.198 scan no 6632 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1732.8072
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0035
Matched b ions: b(13)-98
Matched y ions: y(6), y(7), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.2576

YSLDNNPSSVLSPR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of YSLDNNPSSVLSPR
Found in AT4G00752.1, UBX domain-containing protein

Match to Query 2252: 1627.722398 from(814.868475,2+)
Elution from: 42.116 to 42.116 scan no 4262 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2575/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1627.7243
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 6.4e-006
Matched b ions: b(6), b(10), b(11), b(12), b(12)-98
Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y(12)+
Precursor origin neutral loss: +

Peptide No.2577
YSLVLDPNLDAGTPR
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of YSLVLDPNLDAGTPR
Found in AT3G03570.1, similar to signal transducer [Arabidopsis thaliana] (TAIR: AT4G40050.1); similar to unknown protein

Match to Query 2524: 1709.799860 from(855.907206,2+)
Elution from: 53.051 to 53.051 scan no 5620 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1709.8025  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications:  
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769  
Ions Score: 71 Expect: 6.9e-007  
Matched b ions: b(3), b(6), b(10)  
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9)-98, y(9), y(10), y(11), y(12), y(13)++  
Precursor origin neutral loss:

Peptide No.2578

YSPPYYSPPR  
Confirmed sites: @S:7  
Ambiguous sites: @Y:1orS:2  

MS/MS Fragmentation of YSPPYYSPPR  
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding  

Match to Query 2060: 1385.508704 from(693.761628,2+)  
Elution from: 41.688 to 41.688 scan no 4235 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1385.5094
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.017
Matched b ions: b(2), b(3)-98, b(5)-98, b(6)-98, b(7)-98, b(7)-196, b(8)-196
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(6), y(7), y(7)++, y(7)-98, y(8)++, y(8)-98, y(8), y(8)-98++
Precursor origin neutral loss: +

Peptide No. 2579

YSPPYYSPPR
Confirmed sites:
Ambiguous sites: "@Y:1orS:2, @Y:5orY:6orS:7"

MS/MS Fragmentation of YSPPYYSPPR
Found in AT3G55460.1, SCL30 (SC35-like splicing factor 30); RNA binding

Match to Query 1687: 1385.508958 from(693.761755,2+)
Elution from: 41.749 to 41.749 scan no 4157 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2578/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1385.5094
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 24 Expect: 0.012
Matched b ions:
Matched y ions: y(3), y(6), y(7), y(8)++, y(8)
Precursor origin neutral loss: +

Peptide No.2580

YSPSIAYSPSNAR
Confirmed sites:
Ambiguous sites: "@Y:1orS:2, @S:10orS:8"

MS/MS Fragmentation of YSPSIAYSPSNAR
Found in AT4G35800.1, NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase

Match to Query 2623: 1571.605260 from(786.809906,2+)
Elution from: 37.993 to 37.993 scan no 3735 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6058
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0043
Matched b ions: b(2), b(3)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(11)-98++, b(12)-196++, b(12)++
Matched y ions: y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)+, y(10)+, y(11), y(11)+, y(11)-98++
Precursor origin neutral loss: +

**Peptide No.2581**

YSPSIAYSPSNAR
Confirmed sites: @S:8
Ambiguous sites: @Y:1orS:2

MS/MS Fragmentation of YSPSIAYSPSNAR
Found in AT4G35800.1, NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase

Match to Query 2533: 1571.604356 from(786.809454,2+)
Elution from: 38.156 to 38.156 scan no 3746 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1571.6058
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0033
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(12)-196++, b(12)++
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)++, y(10)++, y(11), y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.2582

YSPSIAYSPSAR
Confirmed sites:
Ambiguous sites: "@Y:1orS:2, @Y:7orS:8"

MS/MS Fragmentation of YSPSIAYSPSAR
Found in AT4G35800.1, NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase

Match to Query 2448: 1571.603300 from(786.808926,2+)
Elution from: 38.091 to 38.091 scan no 3728 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2581/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1571.6058
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 23 Expect: 0.019
Matched b ions: b(5)-98, b(5), b(6)-98, b(8)-98
Matched y ions: y(5), y(7), y(8), y(9), y(9)+, y(10)+, y(11), y(11)+
Precursor origin neutral loss: +

Peptide No.2583
YSSESEENLNVSQK
Confirmed sites: @
Ambiguous sites: @Y:1orS:2orS:3

MS/MS Fragmentation of YSSESEENLNVSQK
Found in AT3G02260.1, BIG (DARK OVER-EXPRESSION OF CAB 1); binding / ubiquitin-protein ligase/ zinc ion binding

Match to Query 2248: 1806.731838 from(904.373195,2+)
Elution from: 26.341 to 26.341 scan no 2127 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2582/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1806.7308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00011
Matched b ions: b(4)-98, b(10), b(11), b(12), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.2584
YSSESEENLNVSQK
Confirmed sites: @S:3
Ambiguous sites:
MS/MS Fragmentation of YSSESEENLNVSQK
Found in AT3G02260.1, BIG (DARK OVER-EXPRESSION OF CAB 1); binding / ubiquitin-protein ligase/ zinc ion binding
Match to Query 2302: 1806.729726 from(904.372139,2+)
Elution from: 27.503 to 27.503 scan no 2164 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1806.7308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.00072
Matched b ions: b(4)-98, b(7), b(11)-98, b(12), b(12)-98
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10), y(11), y(13)-98++, y(14)
Precursor origin neutral loss:

---

Peptide No.2585

YSSESEENNLNVSQK
Confirmed sites:
Ambiguous sites: @Y:1orS:2orS:3

MS/MS Fragmentation of YSSESEENNLNVSQK
Found in AT3G02260.1, BIG (DARK OVER-EXPRESSION OF CAB 1); binding / ubiquitin-protein ligase/ zinc ion binding

Match to Query 2795: 1806.732234 from(904.373393,2+)
Elution from: 26.375 to 26.375 scan no 2153 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1806.7308
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
Ions Score: 46 Expect: 0.00015
Matched b ions: b(10), b(12), b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.2586
YSVDMSVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of YSVDMSPVK
Found in AT3G26560.1, ATP-dependent RNA helicase, putative

Match to Query 740: 1120.451258 from(561.232905,2+)
Elution from: 25.776 to 25.776 scan no 1936 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2585/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1120.4511
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.002
Matched b ions: b(4)
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7)+, y(7), y(7)-98, y(8)
Precursor origin neutral loss: +

Peptide No.2587
YSVDMPVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of YSVDMPVK
Found in AT3G26560.1, ATP-dependent RNA helicase, putative

Match to Query 733: 1104.455444 from(553.234998,2+)
Elution from: 34.287 to 34.287 scan no 3158 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2586/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1104.4562
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00015
Matched b ions: b(2), b(4), b(4)+, b(6)-98, b(8)-98, b(8)
Matched y ions: y(3), y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)+, y(7)-98, y(8), y(8)-98
Precursor origin neutral loss: +

Peptide No.2588

YTYGKHIVSRLEIQPSIEGMK
Confirmed sites: "@Y:1,@T:2,@Y:3,@S:15"
Ambiguous sites:

MS/MS Fragmentation of YTYGKHIVSRLEIQPSIEGMK
Found in AT4G25880.3, APUM6 (ARABIDOPSIS PUMILIO 6); RNA binding

Match to Query 4069: 2655.057507 from(886.026445,3+)
Elution from: 55.753 to 55.753 scan no 5703 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2587/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2655.0647
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y1 : Phospho (Y)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y3 : Phospho (Y)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.0083
Matched b ions: b(3)+, b(5), b(6), b(9)-98, b(10)+, b(11)+, b(12)+, b(13)+, b(13)-98+, b(15)+, b(16)+, b(17)+, b(18)+, b(19)+, b(19)-98++
Matched y ions: y(3), y(15)-98++, y(16)-98++, y(16)+
Precursor origin neutral loss: +

Peptide No.2589

YTYGKHIVSRLEQPSIEMK
Confirmed sites: "@T:2,@Y:3,@S:15"
Ambiguous sites:

MS/MS Fragmentation of YTYGKHIVSRLEQPSIEMK
Found in AT4G25880.3, APUM6 (ARABIDOPSIS PUMILIO 6); RNA binding

Match to Query 4664: 2575.091460 from(859.371096,3+)
Elution from: 52.482 to 52.482 scan no 5581 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2575.0983
Fixed modifications: Carboxymethyl (C)
Variable modifications:
  T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
  Y3 : Phospho (Y)
  S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.024
Matched b ions: b(6)-98, b(7)+, b(7)-98, b(8), b(8)-98+, b(10)+, b(11)+, b(12)+, b(12)-98+, b(14)+, b(15)-98+, b(15)+, b(16)+, b(17)+, b(18)+, b(19)+
Matched y ions: y(4), y(7), y(9)-98, y(10)-98, y(11)+, y(14)-98+, y(16)-98+, y(19)+
Precursor origin neutral loss:

Peptide No.2590

YVEDLESGFSSDVESK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of YVEDLESGFSSDVESK
Found in AT3G18480.1, CCAAT displacement protein-related / CDP-related

Match to Query 2406: 1869.752384 from(935.883468,2+)  
Elution from: 45.491 to 45.491 scan no 4539 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2589/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1869.7557
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 Expect: 5.7e-008
Matched b ions: b(4), b(6), b(9), b(10)
Matched y ions: y(4), y(6), y(7)-98, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15)-98
Precursor origin neutral loss: +

Peptide No.2591

YVEEWVGPGSPMNSPR
Confirmed sites: "@S:10,@S:14"
Ambiguous sites:

MS/MS Fragmentation of YVEEWVGPGSPMNSPR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB: XP_001055538.1)]; similar to Os02g0750

Match to Query 3681: 1979.750860 from(990.882706,2+)
Elution from: 44.123 to 44.123 scan no 4570 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1979.7525
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0036
Matched b ions: b(4), b(5), b(6), b(7), b(10)-98, b(14)-98++, b(14)-98, b(15)-196++, b(15)-196
Matched y ions: y(6), y(7), y(9), y(10), y(11), y(11)-98
Precursor origin neutral loss: +

Peptide No.2592
YVEEVVGPGSPMNSPR
Confirmed sites: "@S:10,@S:14"
Ambiguous sites:

MS/MS Fragmentation of YVEEVVGPGSPMNSPR
Found in AT1G36310.1, similar to PREDICTED: similar to CG17807-PA [Rattus norve (GB: XP_001055538.1); similar to Os02g0750

Match to Query 3241: 1963.754348 from(982.884450,2+)
Elution from: 48.204 to 48.204 scan no 5043 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2591/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1963.7576  
Fixed modifications: Carbamidomethyl (C) 
Variable modifications:  
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 
Ions Score: 59 Expect: 7.3e-006  
Matched b ions: b(5), b(6), b(7), b(10)-98, b(12)+, b(13)++  
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12), y(13)+, y(14)+, y(15)-98++  
Precursor origin neutral loss: +  

Peptide No.2593  
YVSEYYRGSMSMCSK  
Confirmed sites:  
Ambiguous sites: @Y:5orY:6  

MS/MS Fragmentation of YVSEYYRGSMSMCSK  
Found in AT1G28110.1, SCPL45; serine carboxypeptidase  

Match to Query 3042: 2029.766043 from(677.595957,3+)  
Elution from: 34.150 to 34.150 scan no 3220 polarity:+

file:///C:/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2592/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 2029.7620
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y6 : Phospho (Y)
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 Expect: 0.032
Matched b ions: b(2), b(3), b(6), b(6)++, b(8)++, b(10)++, b(14)++, b(15)++
Matched y ions: y(2), y(4)++, y(6)++, y(8), y(10)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss:

Peptide No.2594

YYAAESMLILDPETGEYSEEK
Confirmed sites: "@S:6,@T:14,@Y:17,@S:18"
Ambiguous sites:

MS/MS Fragmentation of YYAAESMLILDPETGEYSEEK
Found in AT5G18660.1, DVR (PALE-GREEN AND CHLOROPHYLL B REDUCED 2); 3,8-divinyl protochlorophyllide a 8-vinyl reductase

Match to Query 3946: 2772.943767 from(925.321865,3+)
Elution from: 41.366 to 41.366 scan no 4066 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 2772.9484
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y17 : Phospho (Y)
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.027
Matched b ions: b(15)-196++, b(15)-98++, b(19)-294++
Matched y ions: y(6)-98, y(11)++, y(12)++, y(13)++, y(15)-196++, y(18)++
Precursor origin neutral loss: +

Peptide No.2595
YYMESEMSDGSSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of YYMESEMSDGSSR
Found in AT2G27880.1, argonaute protein, putative / AGO, putative

Match to Query 1980: 1709.555888 from(855.785220,2+)
Elution from: 20.242 to 20.242 scan no 1310 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2594/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide \( \text{Mr(calc)}: 1709.5586 \)
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21  Expect: 0.0084
Matched b ions: b(11)-98
Matched y ions: y(5), y(6), y(7), y(7)-98, y(9)-98, y(10), y(12)-98++, y(12)++
Precursor origin neutral loss: +

---

**Peptide No.2596**

**YYMESEMSDGSSR**

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of **YYMESEMSDGSSR**
Found in **AT2G27880.1**, argonaute protein, putative / AGO, putative

Match to Query 2028: 1709.555906 from(855.785229,2+)
Elution from: 20.105 to 20.105 scan no 1308 polarity:+
Monoisotopic mass of neutral peptide Mr(calc): 1709.5586
Fixed modifications: Carboxylmethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 14 Expect: 0.038
Matched b ions: b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(4), y(5), y(8)+, y(10), y(12)+, y(13)+
Precursor origin neutral loss: +

Peptide No.2597

YUMESEMSDGSSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of YUMESEMSDGSSR
Found in AT2G27880.1, argonaute protein, putative / AGO, putative

Match to Query 1982: 1677.568464 from(839.791508,2+)
Elution from: 34.778 to 34.778 scan no 3142 polarity:+

file:///C|/Documents%20and%20Settings/N.Su...abi/result_v3/o0705103ppmGROUPmeadlist.htm (2596/2597) [2008/03/14 15:08:31]
Monoisotopic mass of neutral peptide Mr(calc): 1677.5687
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 9.8e-009
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98++, b(9)-98, b(9), b(10)-98, b(11)-98, b(12), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(8), y(8)+++, y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12)-98++, y(12), y(12)+++, y(12)-98, y(13)-98, y(13)++
Precursor origin neutral loss: +