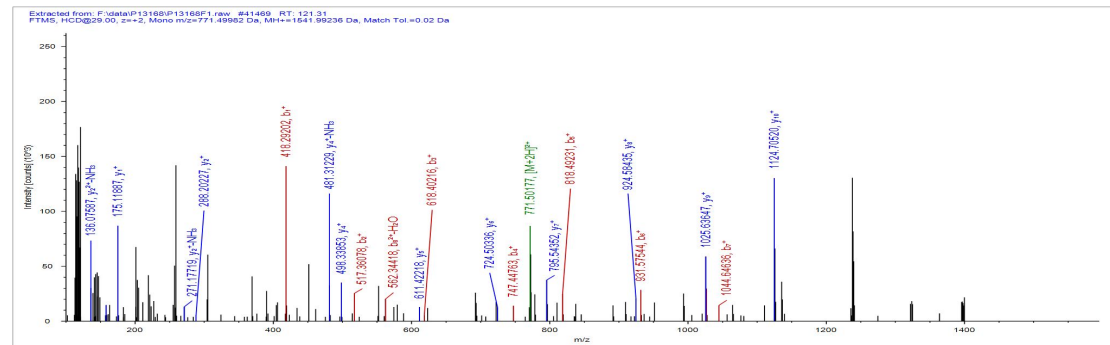


Supplemental Figure S3 The annotated tandem mass spectra of the identified proteins based on a single high-confidence peptide assignment with 95% confidence of false discovery rate (FDR)≤1% in leaves of Hg-stressed wheat seedlings

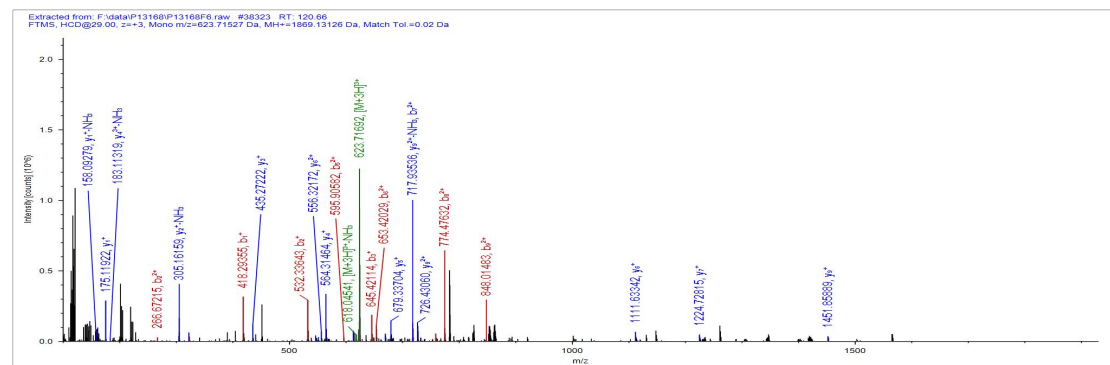
(1) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 771.50 with score 1.65

Protein description: Short-chain dehydrogenase/reductase 2 OS=Aegilops tauschii GN=F775_14029 PE=4 SV=1-[M8BRJ0_AEGTA]



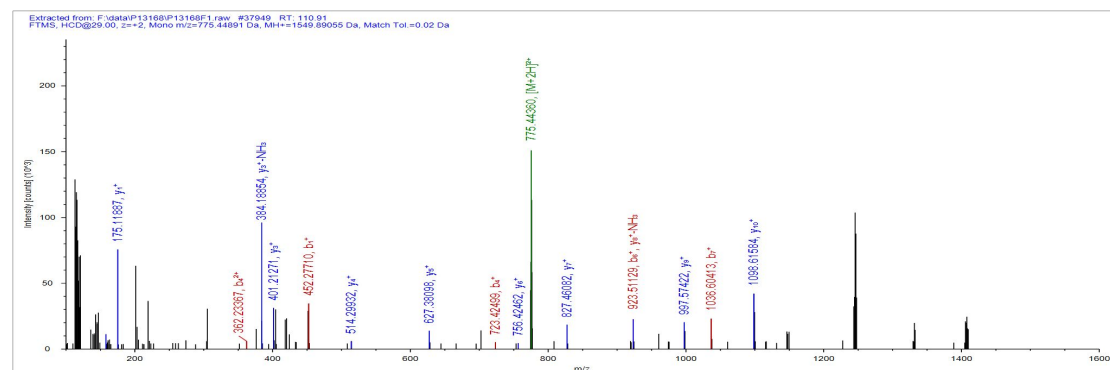
(2) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 623.72 with score 13.70

Protein description: ADP-ribosylation factor-like protein 5 OS=Aegilops tauschii GN=F775_28541 PE=4 SV=1-[M8C0H6_AEGTA]



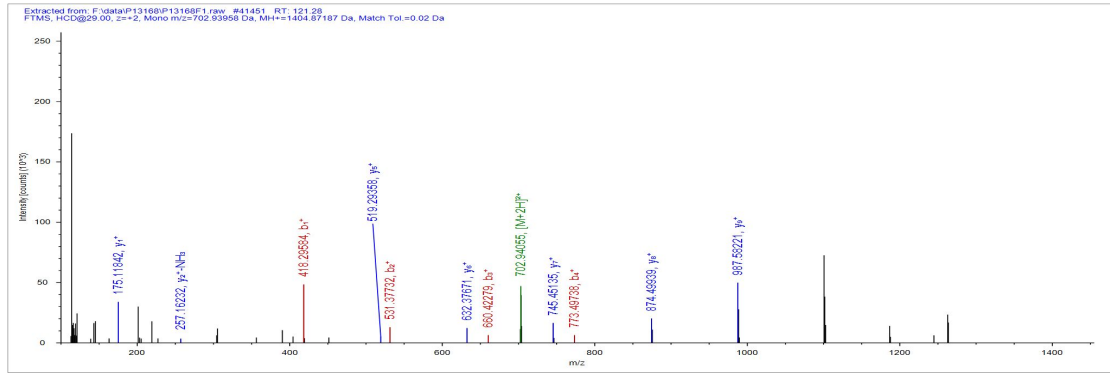
(3) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 775.45 with score 23.91

Protein description: BTB/POZ domain-containing protein OS=Aegilops tauschii GN=F775_19312 PE=4 SV=1-[M8BIF8_AEGTA]



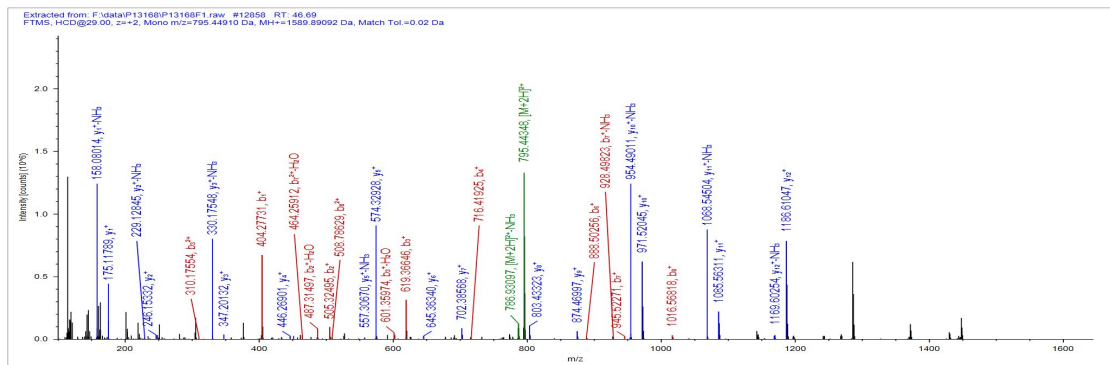
(4) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 702.94 with score 27.99

Protein description: Obtusifolios 14-alpha demethylase OS=Aegilops tauschii GN=F775_29557 PE=4 SV=1-[M8BK79_AEGTA]



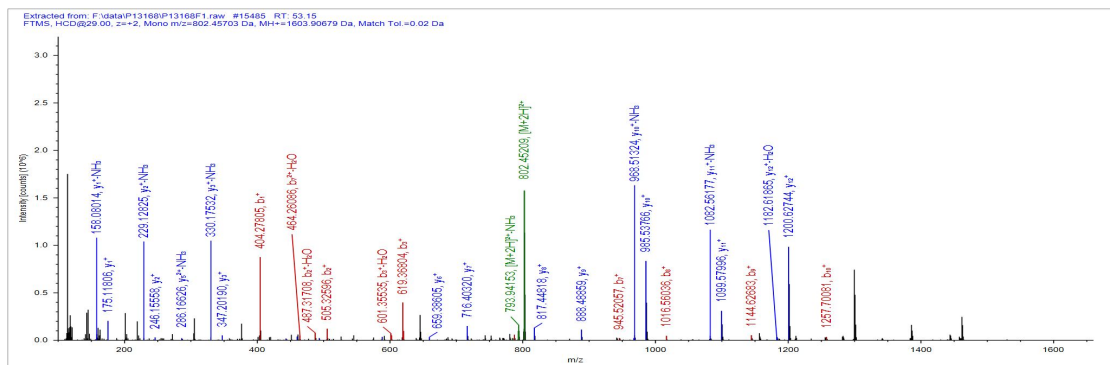
(5) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 795.45 with score 40.42

Protein description: Pathogenesis-related protein 4 (Fragment) OS=Triticum aestivum GN=PR4 PE=2 SV=1- [Q9SQG8_WHEAT]



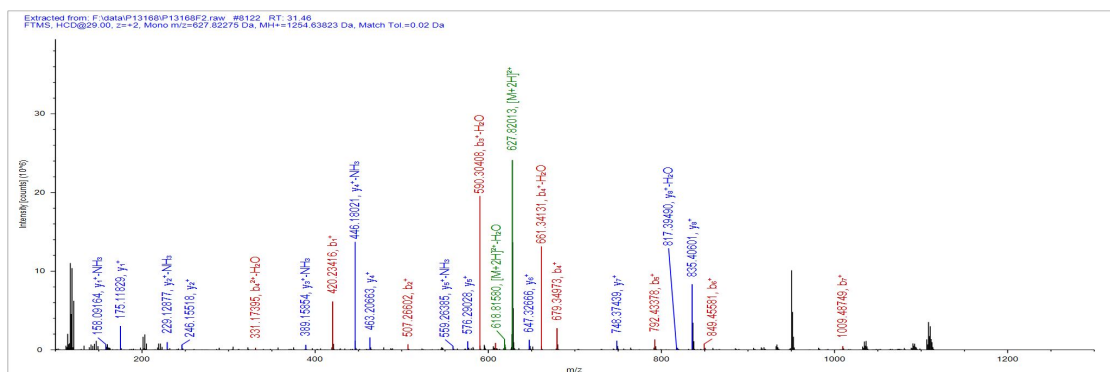
(6) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 802.46 with score 49.65

Protein description: PR-4 (Fragment) OS=Triticum aestivum PE=2 SV=1- [Q9SQG3_WHEAT]



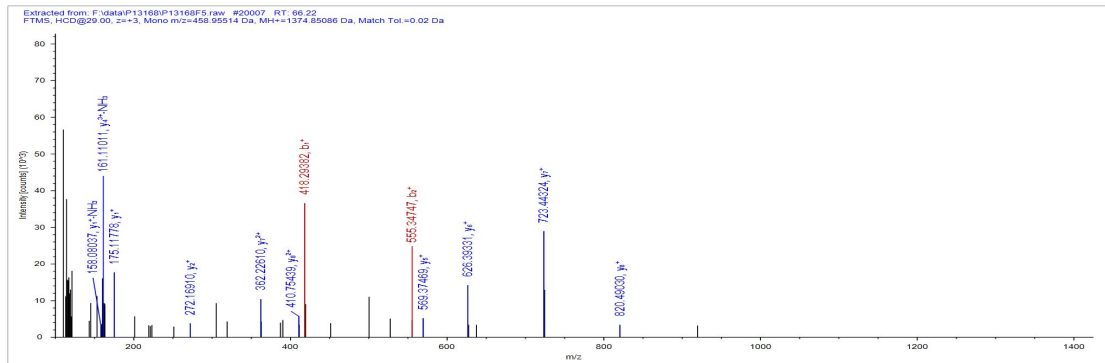
(7) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 627.82 with score 19.13

Protein description: Pathogenesis-related protein 1 OS=Aegilops tauschii GN=F775_31533 PE=4 SV=1- [N1QT70_AEGTA]



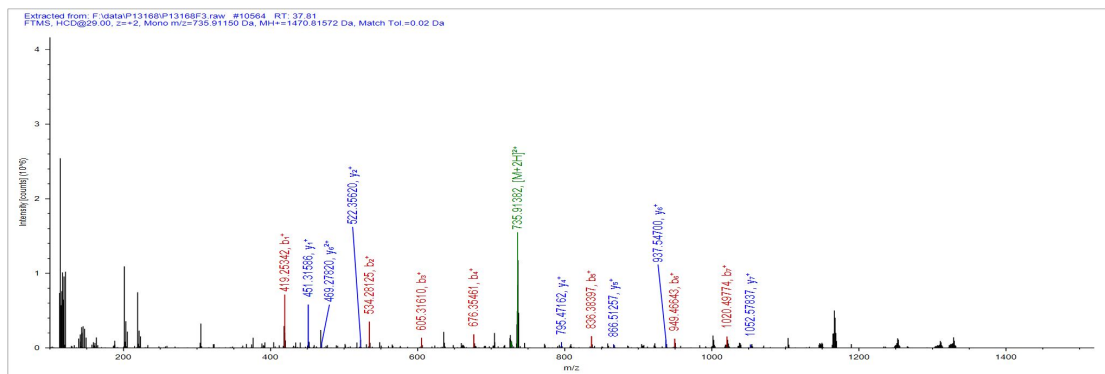
(8) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 458.96 with score 27.68

Protein description: Cytochrome P450 71D7 OS=Aegilops tauschii GN=F775_26289 PE=4 SV=1-
[N1R399_AEGTA]



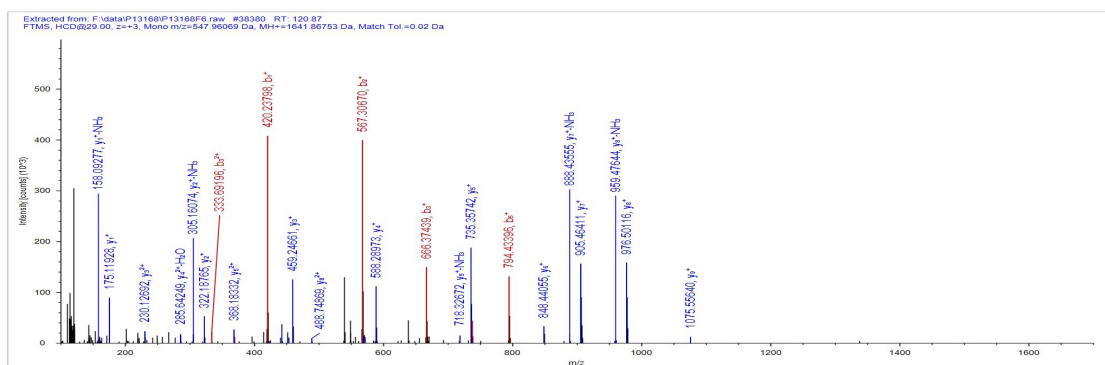
(9) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 735.91 with score 11.39

Protein description: 31.7 kDa class I endochitinase-antifreeze protein OS=Secale cereale PE=2 SV=1-
[Q9AXR9_SECCE]



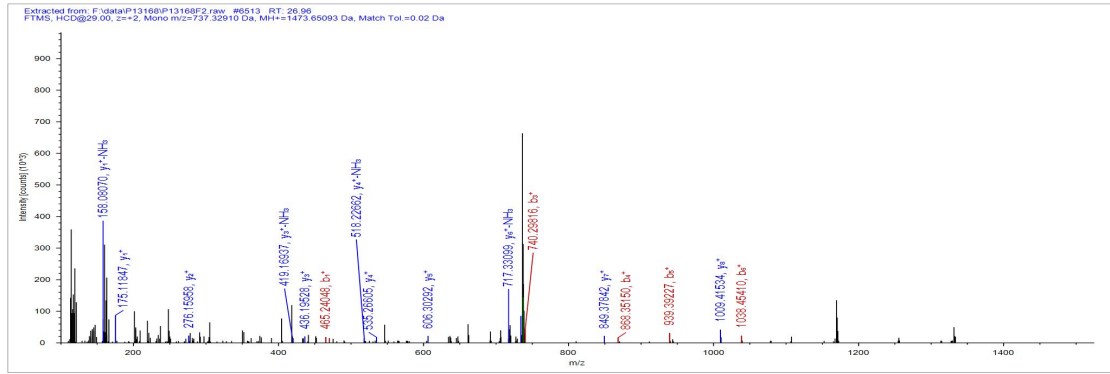
(10) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 547.96 with score 64.75

Protein description: Protein SRG1 OS=Aegilops tauschii GN=F775_05007 PE=4 SV=1- [M8BPR9_AEGTA]



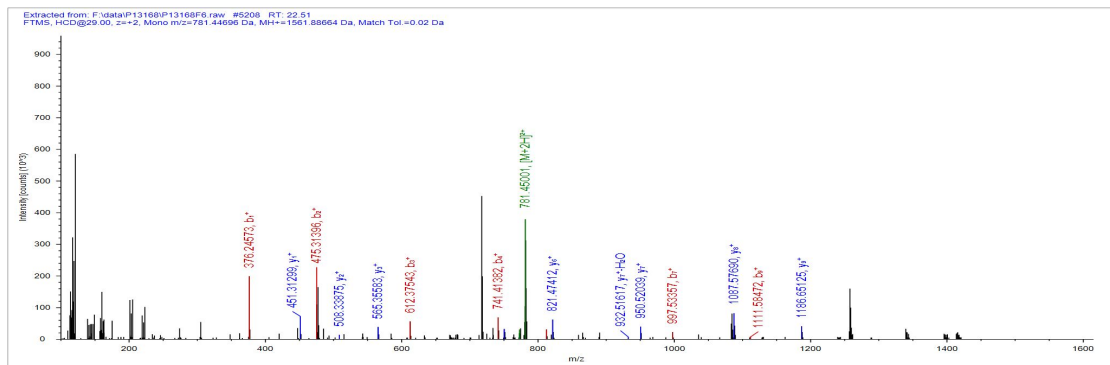
(11) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 737.33 with score 6.44

Protein description: Bowman-Birk type proteinase inhibitor I-2B (Fragment) OS=Triticum aestivum PE=1 SV=1-
[IBB1_WHEAT]



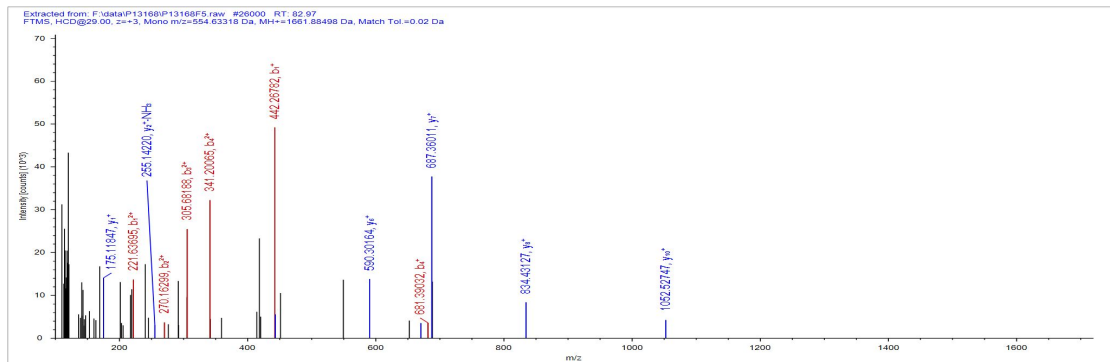
(12) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 781.45 with score 21.25

Protein description: Cytochrome P450 99A2 OS=Aegilops tauschii GN=F775_31064 PE=4SV=1-[R7WC43_AEGTA]



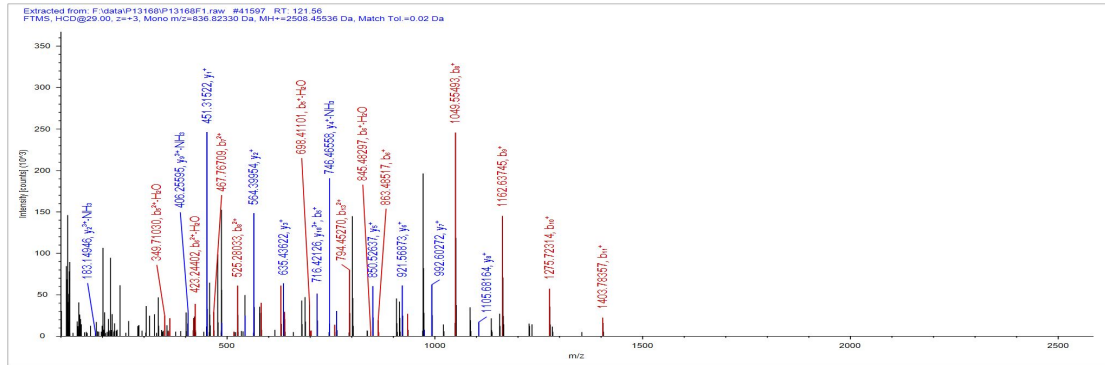
(13) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 554.63 with score 27.85

Protein description: Secologanin synthase OS=Triticum urartu GN=TRIUR3_25996 PE=4 SV=1-[M8A608_TRIUA]



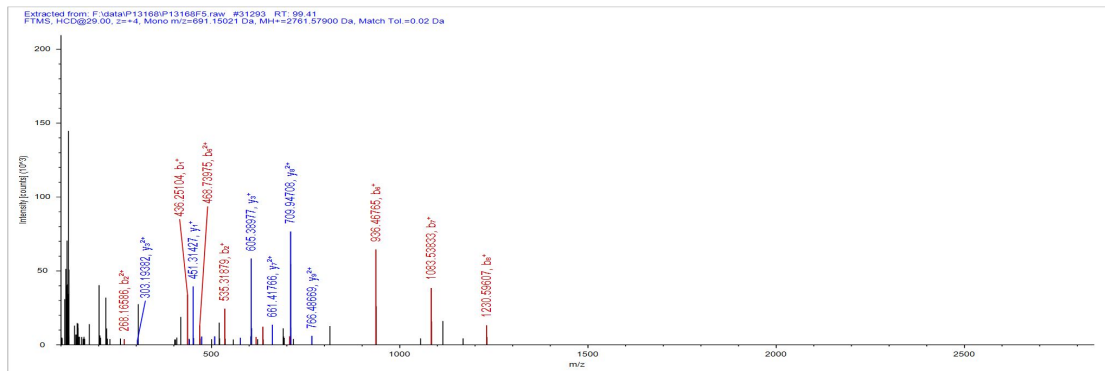
(14) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 836.82 with score 250.85

Protein description: Putative L-ascorbate peroxidase, chloroplastic OS=Aegilops tauschii GN=F775_29816 PE=4 SV=1-[M8BMC6_AEGTA]



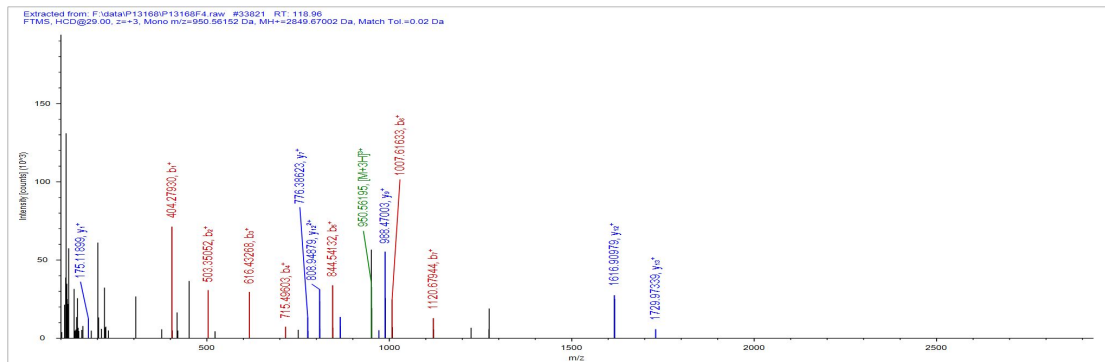
(15) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 691.15 with score 23.06

Protein description: Germin-like protein 4-1 OS=Aegilops tauschii GN=F775_29467 PE=4 SV=1-
[N1QYL9_AEGTA]



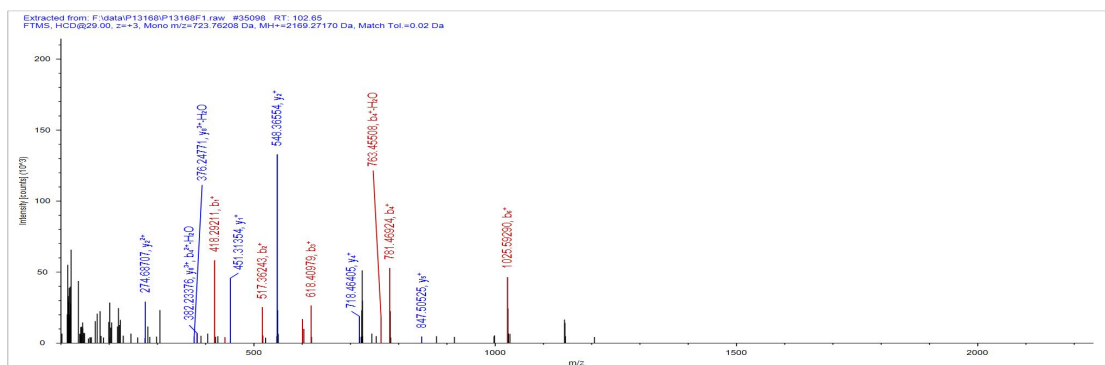
(16) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 950.56 with score 39.06

Protein description: Caffeic acid 3-O-methyltransferase OS=Aegilops tauschii GN=F775_26154 PE=4 SV=1-
[M8C7H1_AEGTA]



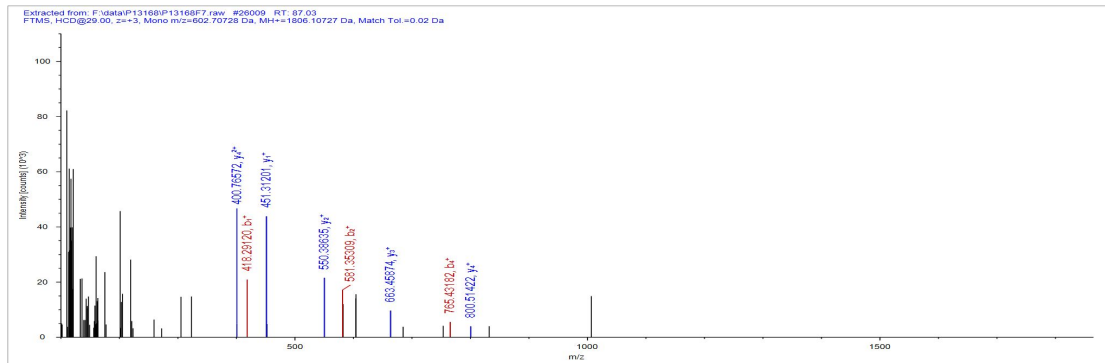
(17) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 723.76 with score 30.94

Protein description: UDP-glucosyltransferase OS=Triticum aestivum PE=2 SV=1- [D2KPG7_WHEAT]



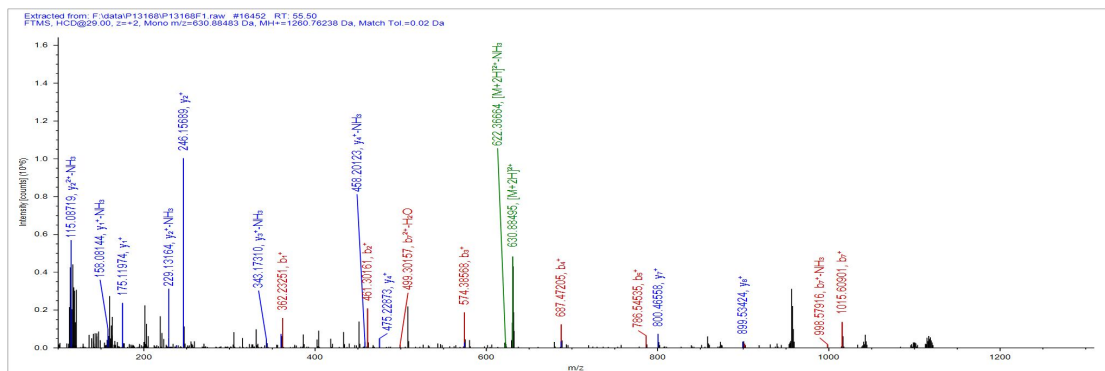
(18) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 602.71 with score 14.43

Protein description: Putative NADH dehydrogenase OS=*Oryza sativa* subsp. *japonica* GN=P0473D02.16 PE=2 SV=1- [Q6YZ09_ORYSJ]



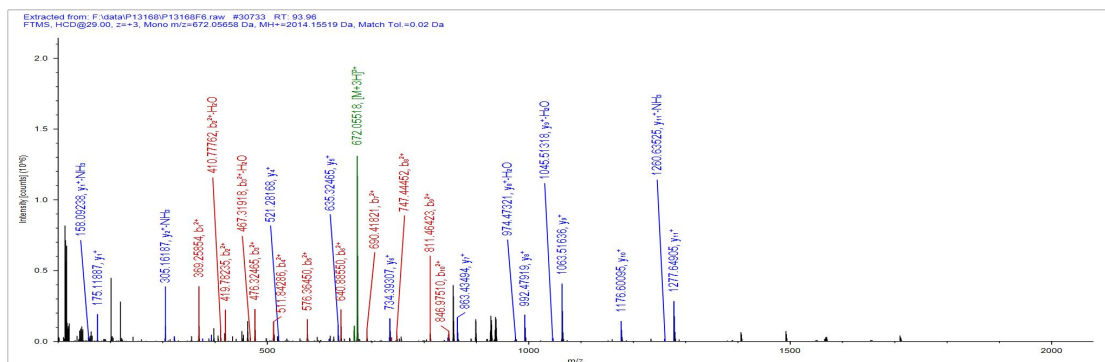
(19) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 630.88 with score 30.62

Protein description: Mitochondrial formate dehydrogenase 1 (Fragment) OS=*Oryza sativa* subsp. *indica* PE=2 SV=1- [A6N0B2_ORYSJ]



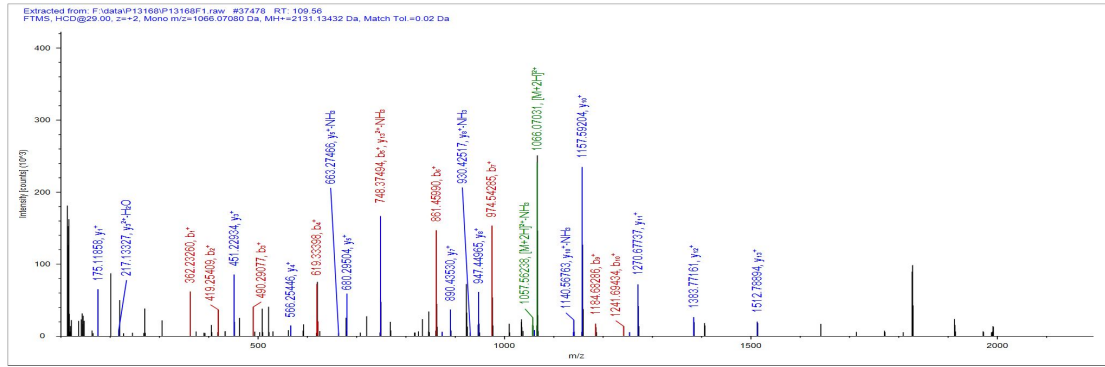
(20) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 672.06 with score 472.17

Protein description: Glyceraldehyde-3-phosphate dehydrogenase-like protein (Fragment) OS=*Miscanthus sinensis* PE=2 SV=1- [H9B8E3_MISSI]



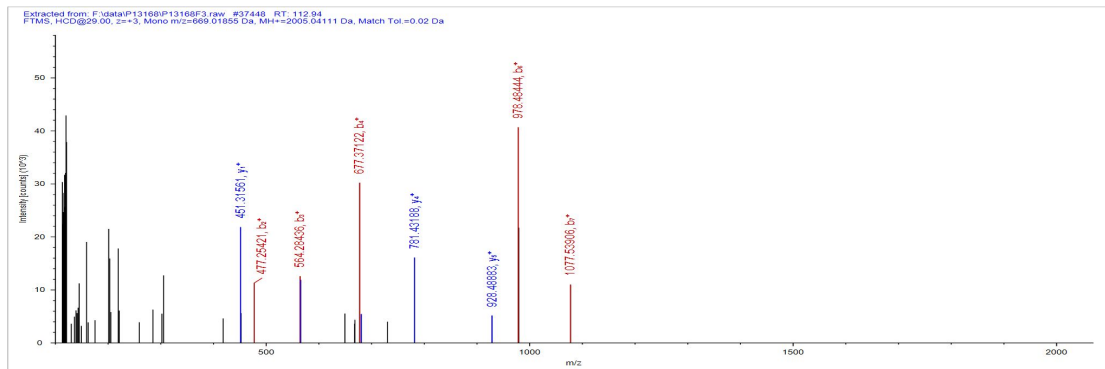
(21) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 1066.07 with score 262.86

Protein description: Malate dehydrogenase, glyoxysomal OS=*Aegilops tauschii* GN=F775_30777 PE=4 SV=1- [R7W1Q1_AEGTA]



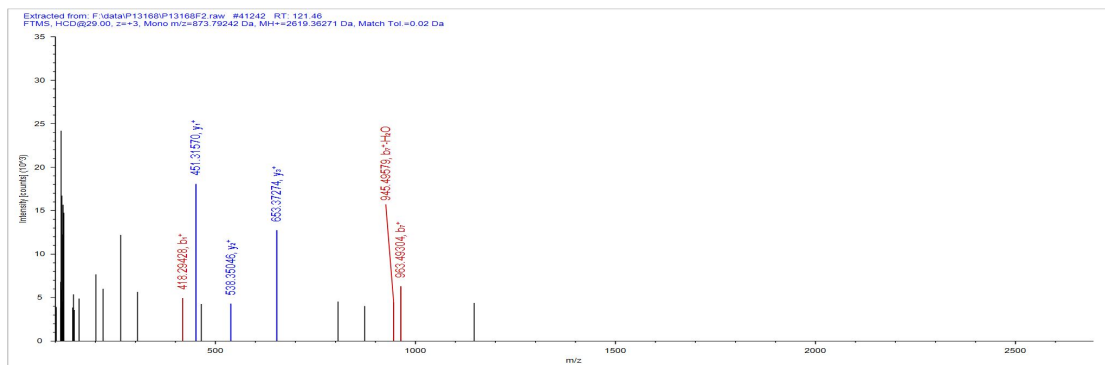
(22) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 669.02 with score 33.57

Protein description: Beta-glucosidase 4 OS=Triticum urartu GN=TRIUR3_09534 PE=4 SV=1-
[M8APV4_TRIUA]



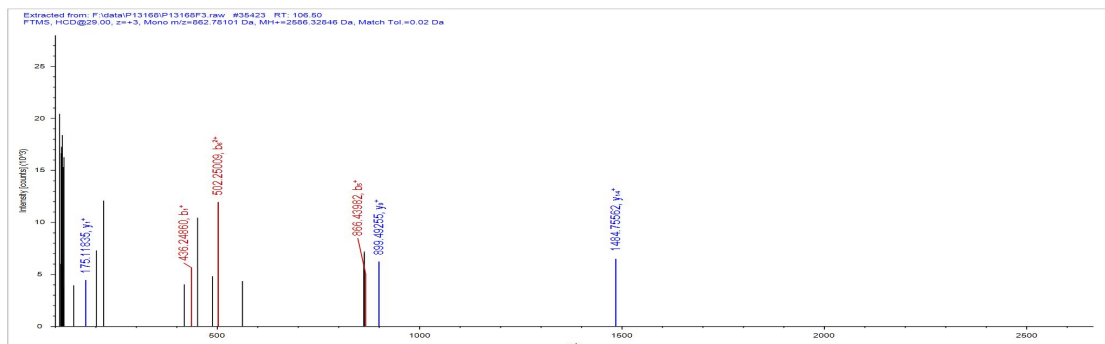
(23) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 873.79 with score 5.73

Protein description: Serine carboxypeptidase-like 51 OS=Triticum urartu GN=TRIUR3_23998 PE=4 SV=1-
[M7ZA68_TRIUA]



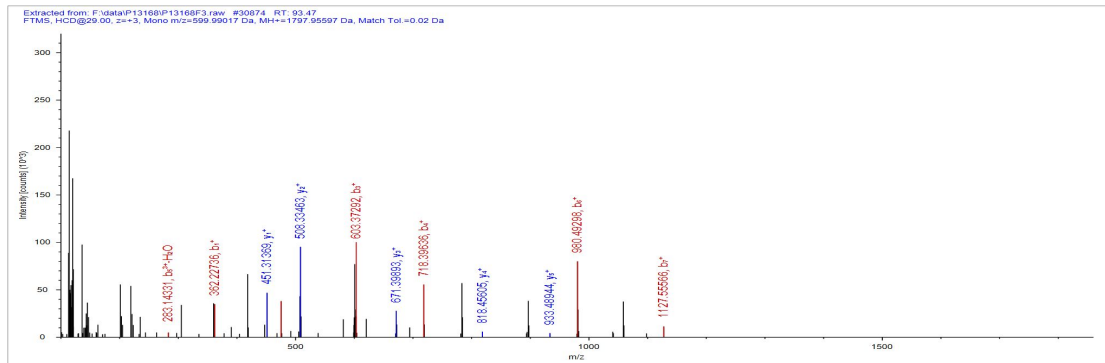
(24) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 862.78 with score 2.43

Protein description: Alanine--glyoxylate aminotransferase 2-like protein 3, mitochondrial OS=Triticum urartu
GN=TRIUR3_23613 PE=4 SV=1- [M7YW64_TRIUA]



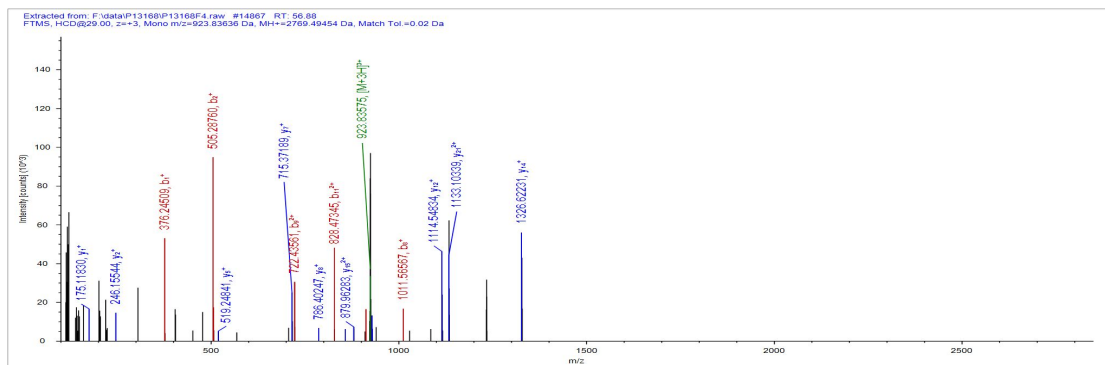
(25) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 599.99 with score 16.30

Protein description: U2 small nuclear ribonucleoprotein B OS=Aegilops tauschii GN=F775_07762 PE=4 SV=1-[M8BQC8_AEGTA]



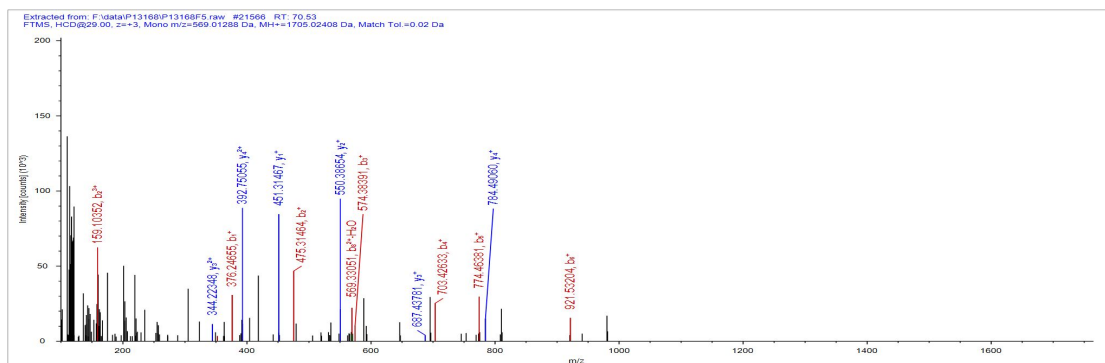
(26) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 923.84 with score 25.16

Protein description: Protein TIME FOR COFFEE OS=Aegilops tauschii GN=F775_26481 PE=4 SV=1-[M8CBH0_AEGTA]



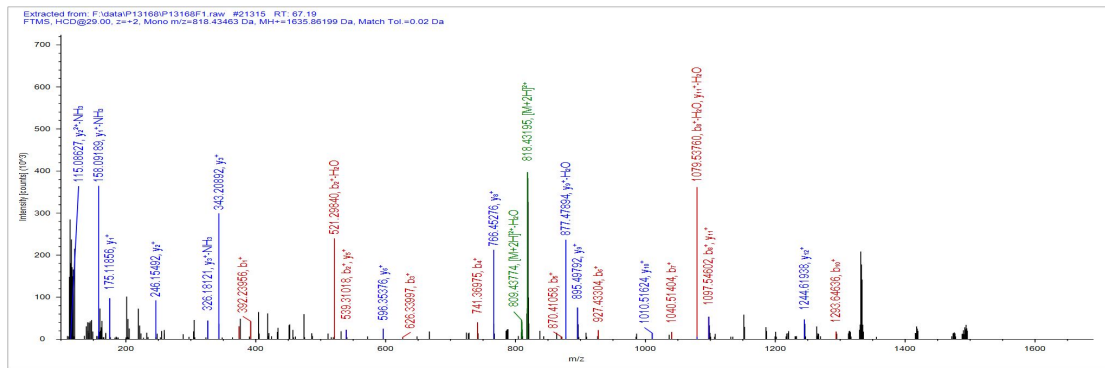
(27) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 569.01 with score 16.26

Protein description: O-methyltransferase ZRP4 OS=Aegilops tauschii GN=F775_20740 PE=4 SV=1-[M8AJF8_AEGTA]



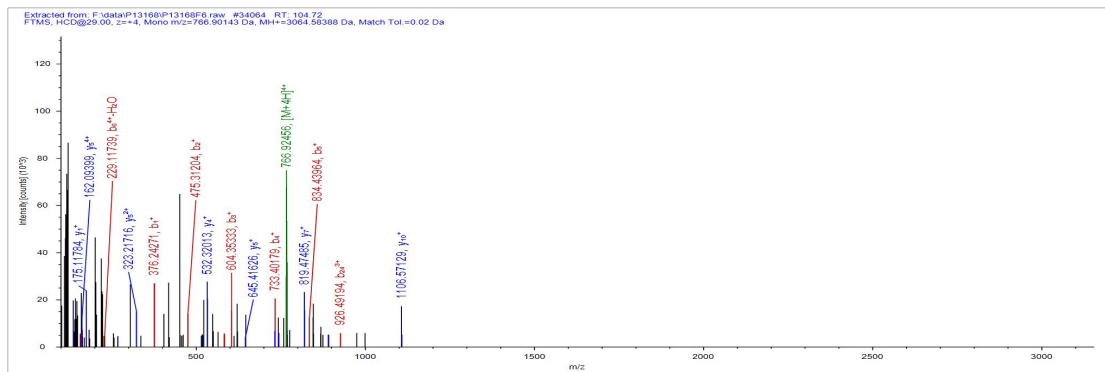
(28) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 818.43 with score 18.48

Protein description: Subtilisin-like protease OS=Aegilops tauschii GN=F775_02353 PE=4 SV=1-[R7W7E1_AEGTA]



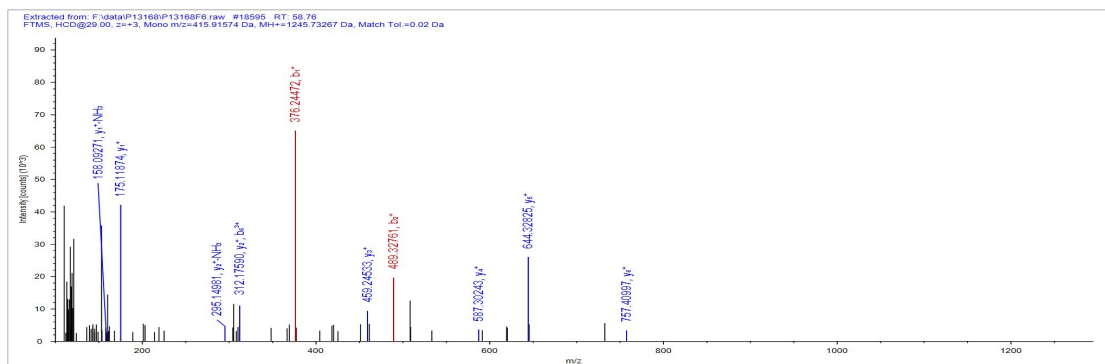
(29) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 766.90 with score 6.80

Protein description: Protein fluG OS=Triticum urartu GN=TRIUR3_22350 PE=4 SV=1- [M7ZP85_TRIUA]



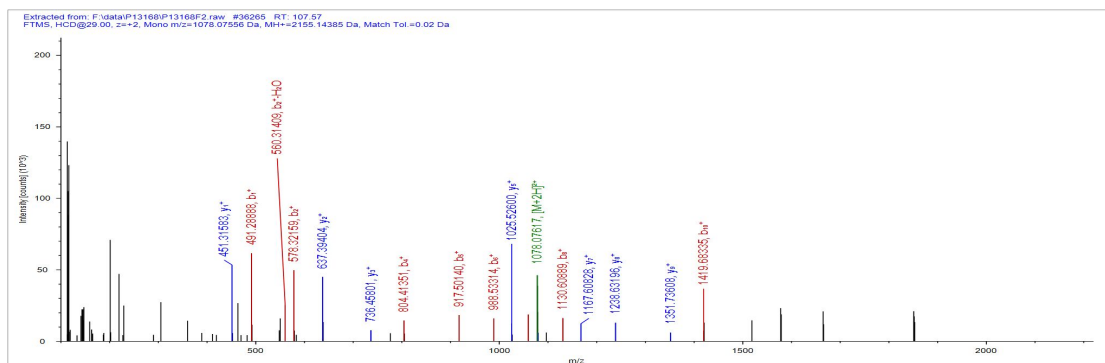
(30) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 415.92 with score 30.48

Protein description: Ribosomal protein L16 OS=Bambusa oldhamii GN=rp116 PE=3 SV=1- [B8Q6P4_BAMOL]



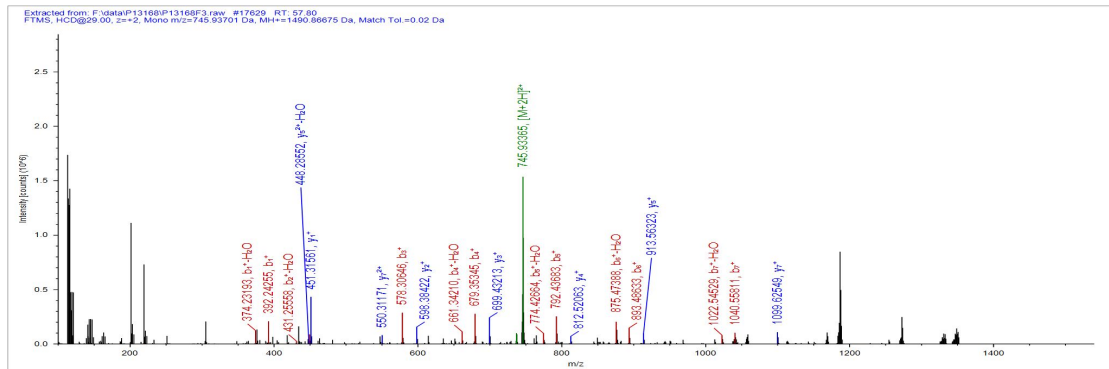
(31) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 1078.08 with score 871.41

Protein description: Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment) OS=Alloteropsis sp. Hodkinson 230 GN=rbcL PE=3 SV=1- [B0YIC3_9POAL]



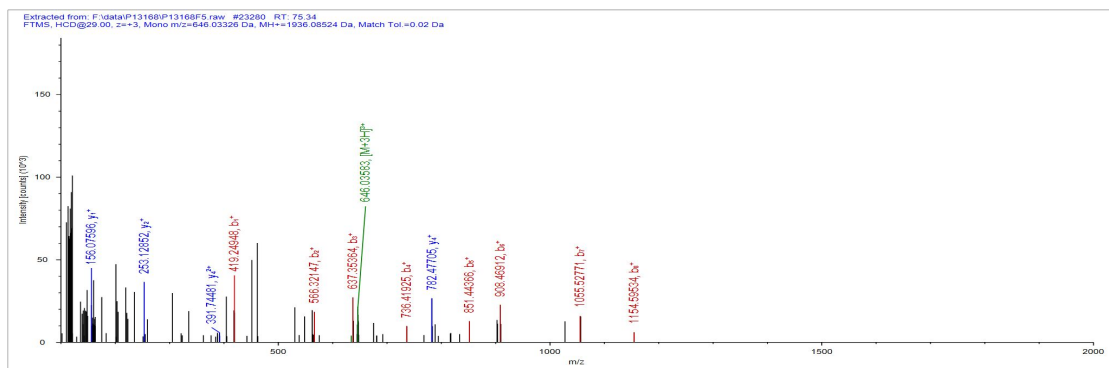
(32) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 745.94 with score 74.93

Protein description: Plastocyanin, chloroplastic OS=Aegilops tauschii GN=F775_26065 PE=4 SV=1-
[M8C4F9_AEGTA]



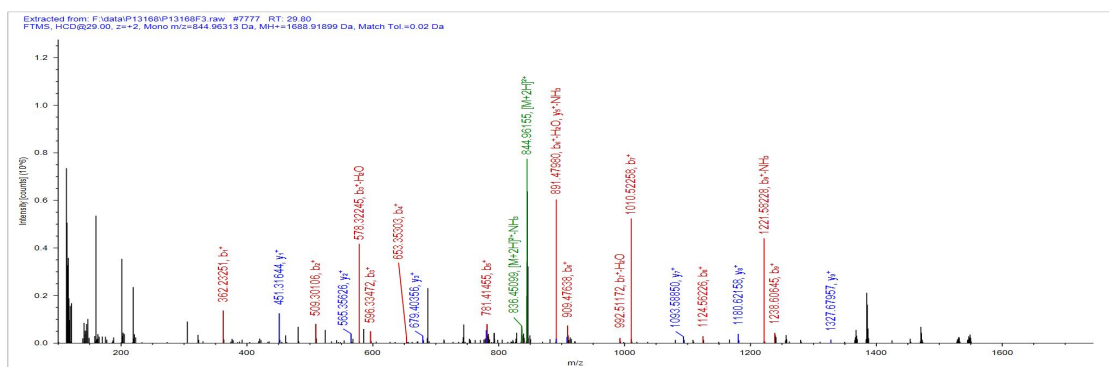
(33) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 646.03 with score 25.78

Protein description: Putative ferredoxin OS=Oryza sativa subsp. japonica GN=OJ1567_G09.131-2 PE=2 SV=1-
[Q7XIU1_ORYSJ]



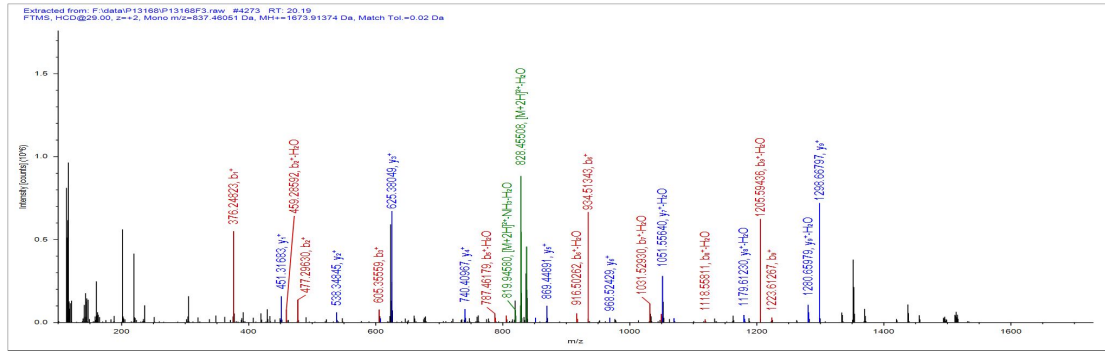
(34) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 844.96 with score 23.81

Protein description: Rpl32 (Fragment) OS=Aegilops geniculata GN=rpl32 PE=4 SV=1- [B3SYV1_9POAL]



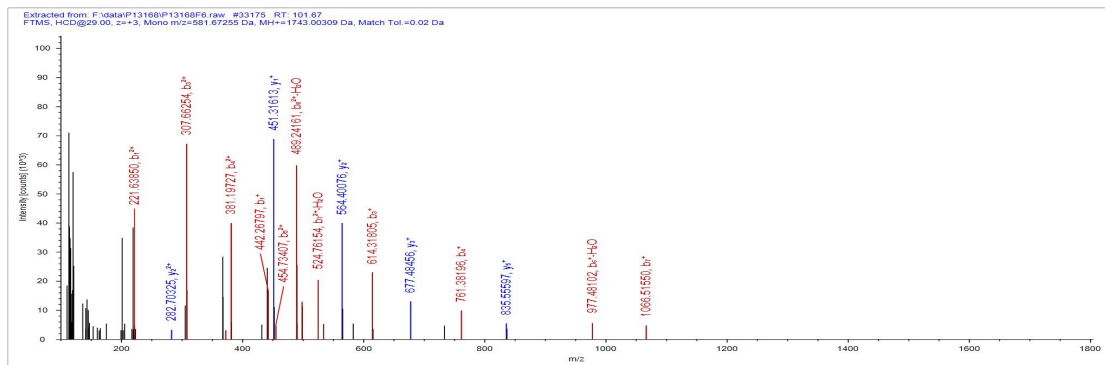
(35) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 837.46 with score 11.73

Protein description: Photosystem II subunit H (Fragment) OS=Danthonia californica PE=4 SV=1-
[B3SHF8_9POAL]



(36) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 581.67 with score 25.86

Protein description: Putative Mg-protoporphyrin IX monomethyl ester cyclase (Fragment) OS=Dactylis glomerata
GN=At103 PE=4 SV=1- [A7WMU4_DACGL]



(37) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 700.89 with score 4.56

Protein description: Metal transporter Nramp2 OS=Triticum urartu GN=TRIUR3_32667 PE=4 SV=1-
[M7ZWB1_TRIUA]

