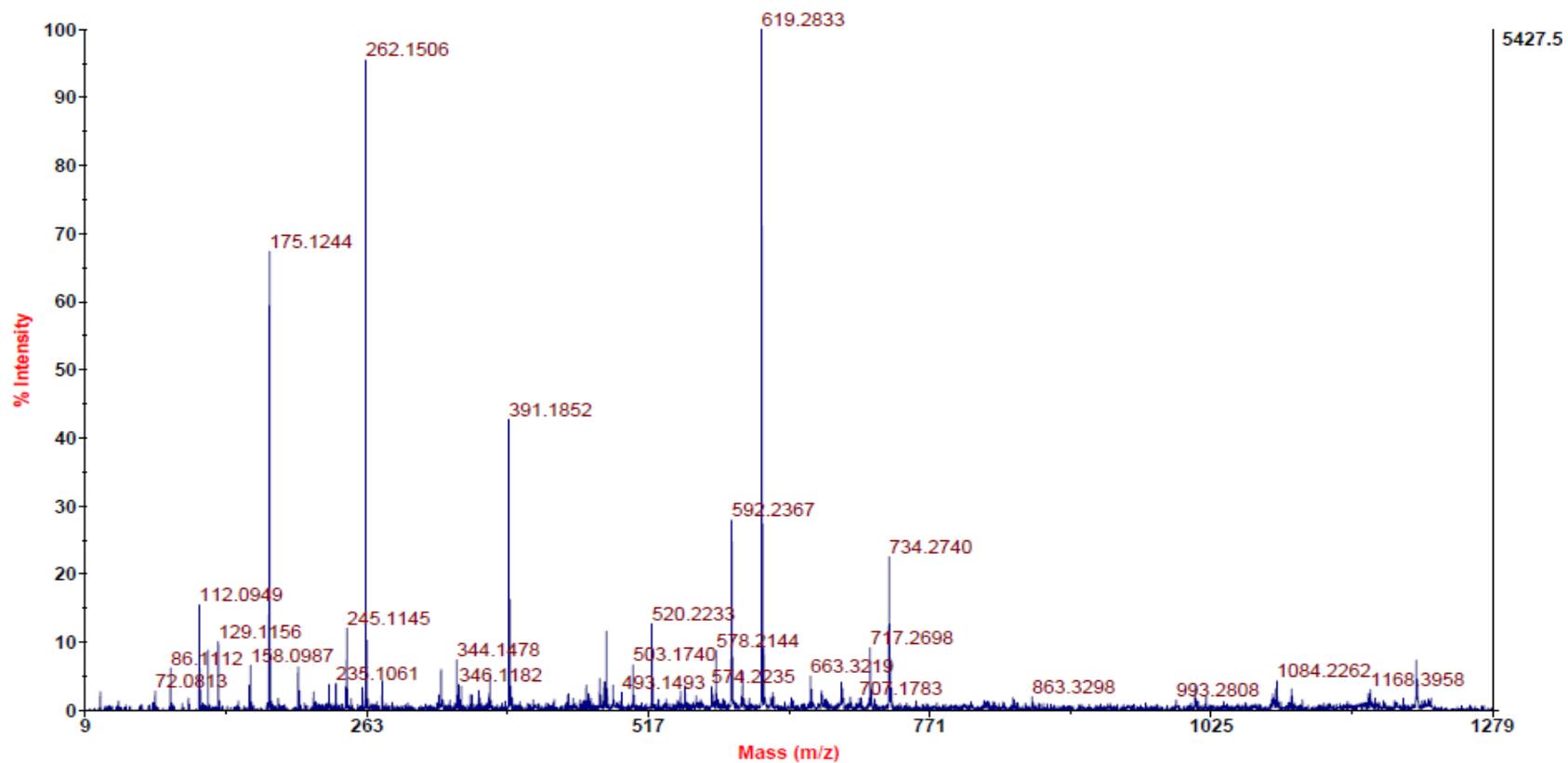


Supplementary Information

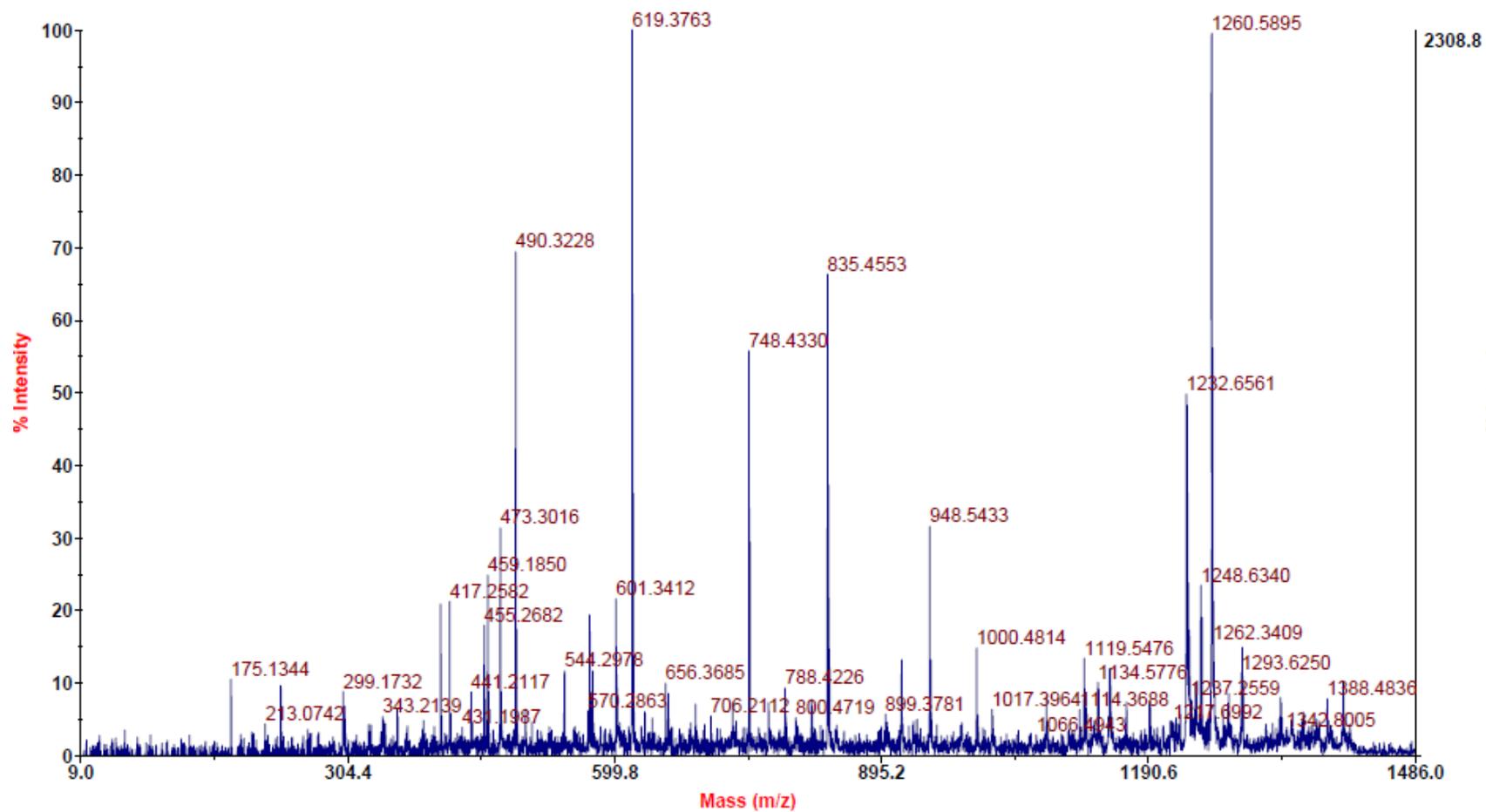
4700 MS/MS Precursor 1210.57 Spec #1 MC[BP = 619.3, 5427]



(a)

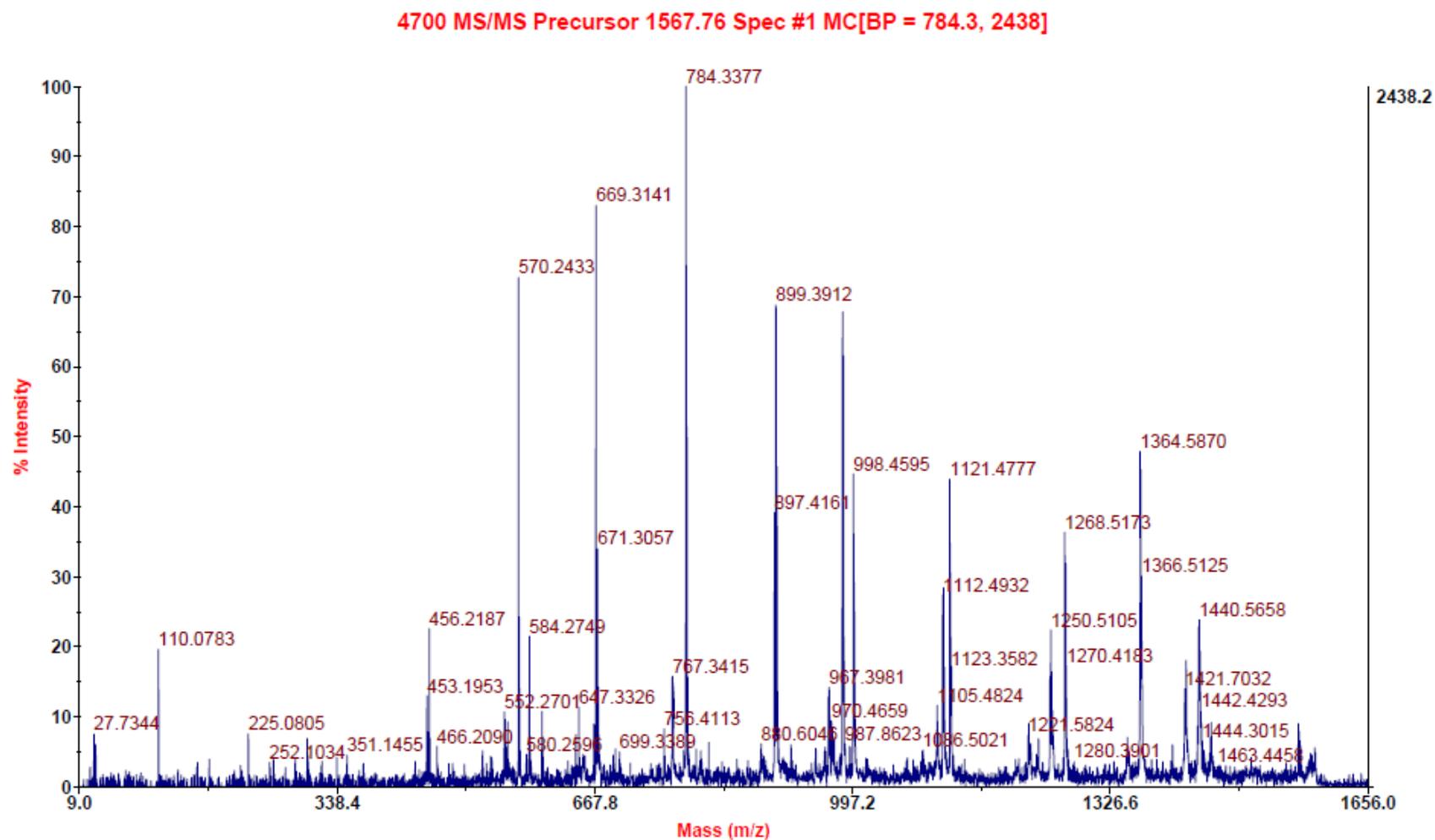
Figure S1. Cont.

4700 MS/MS Precursor 1406.7 Spec #1 MC[BP = 619.4, 2309]



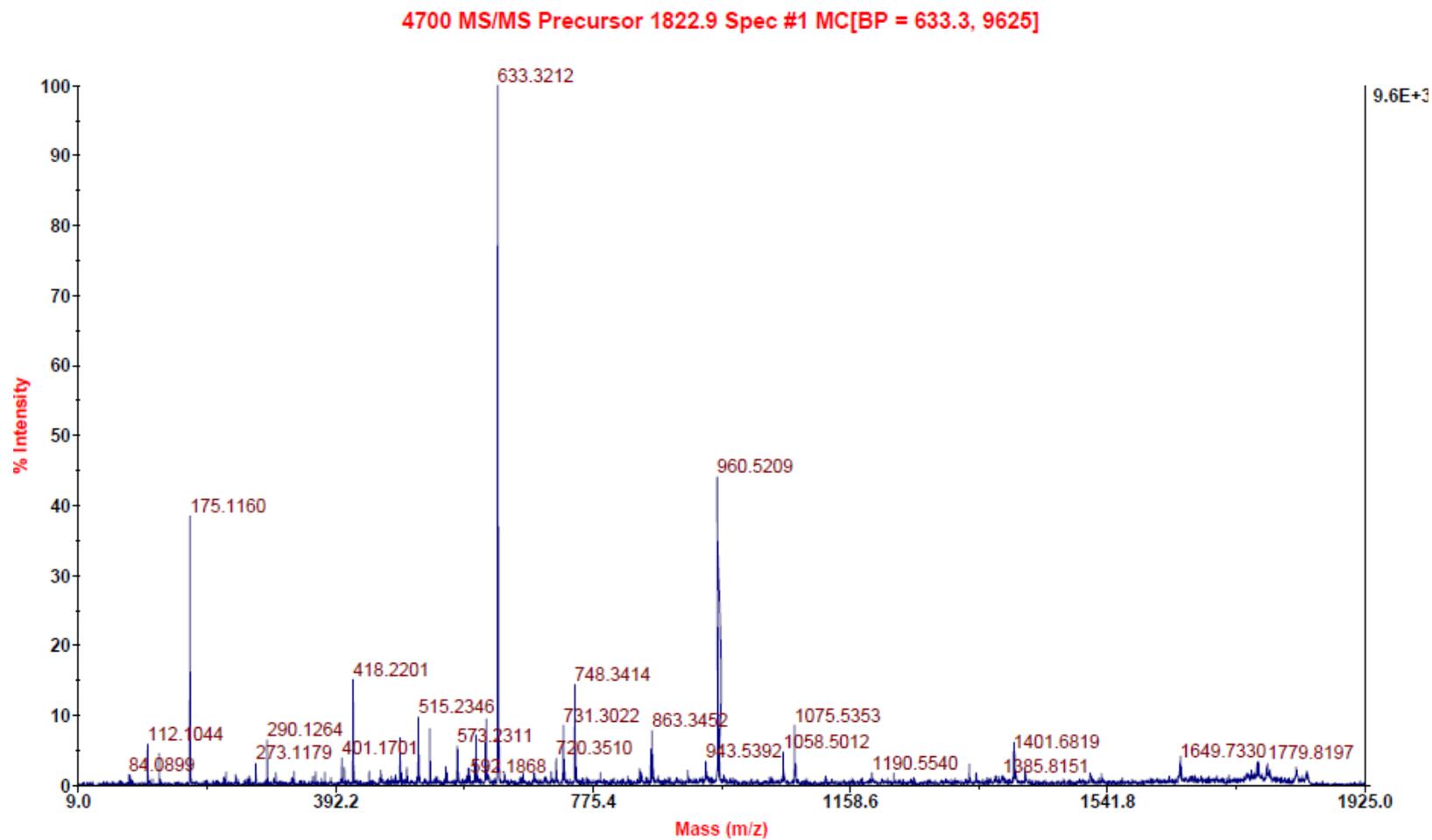
(b)

Figure S1. Cont.



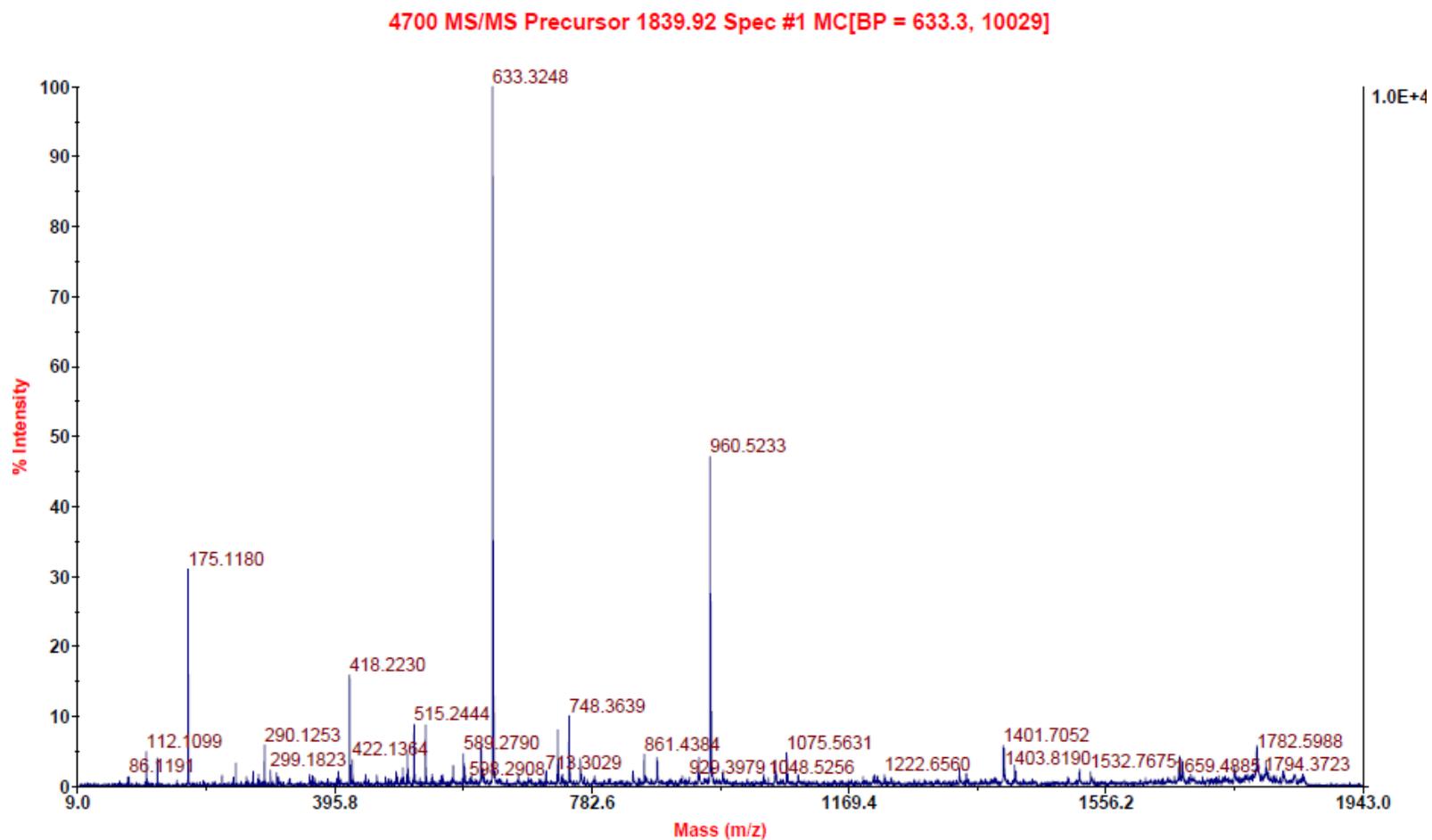
(c)

Figure S1. Cont.



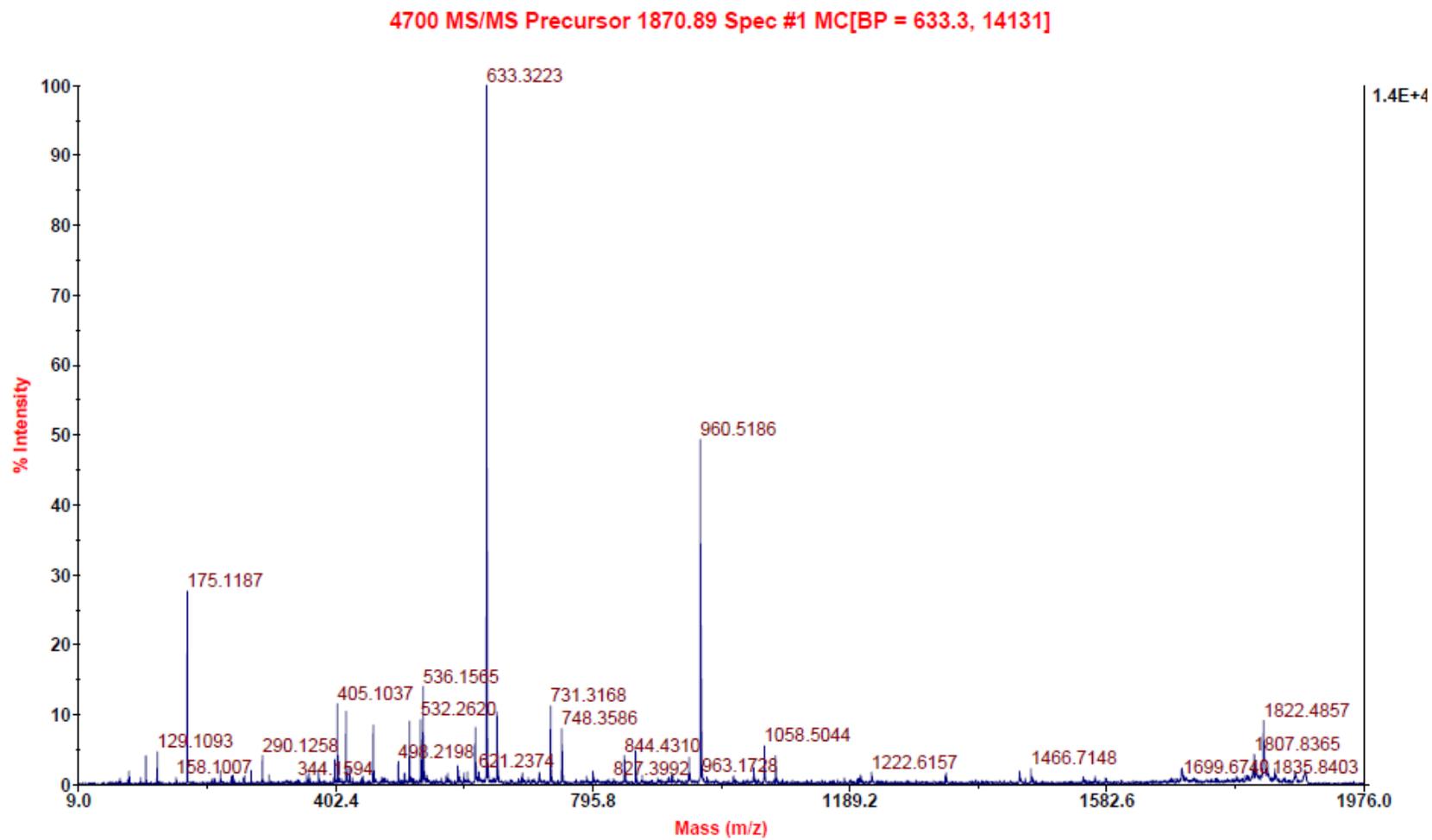
(d)

Figure S1. Cont.



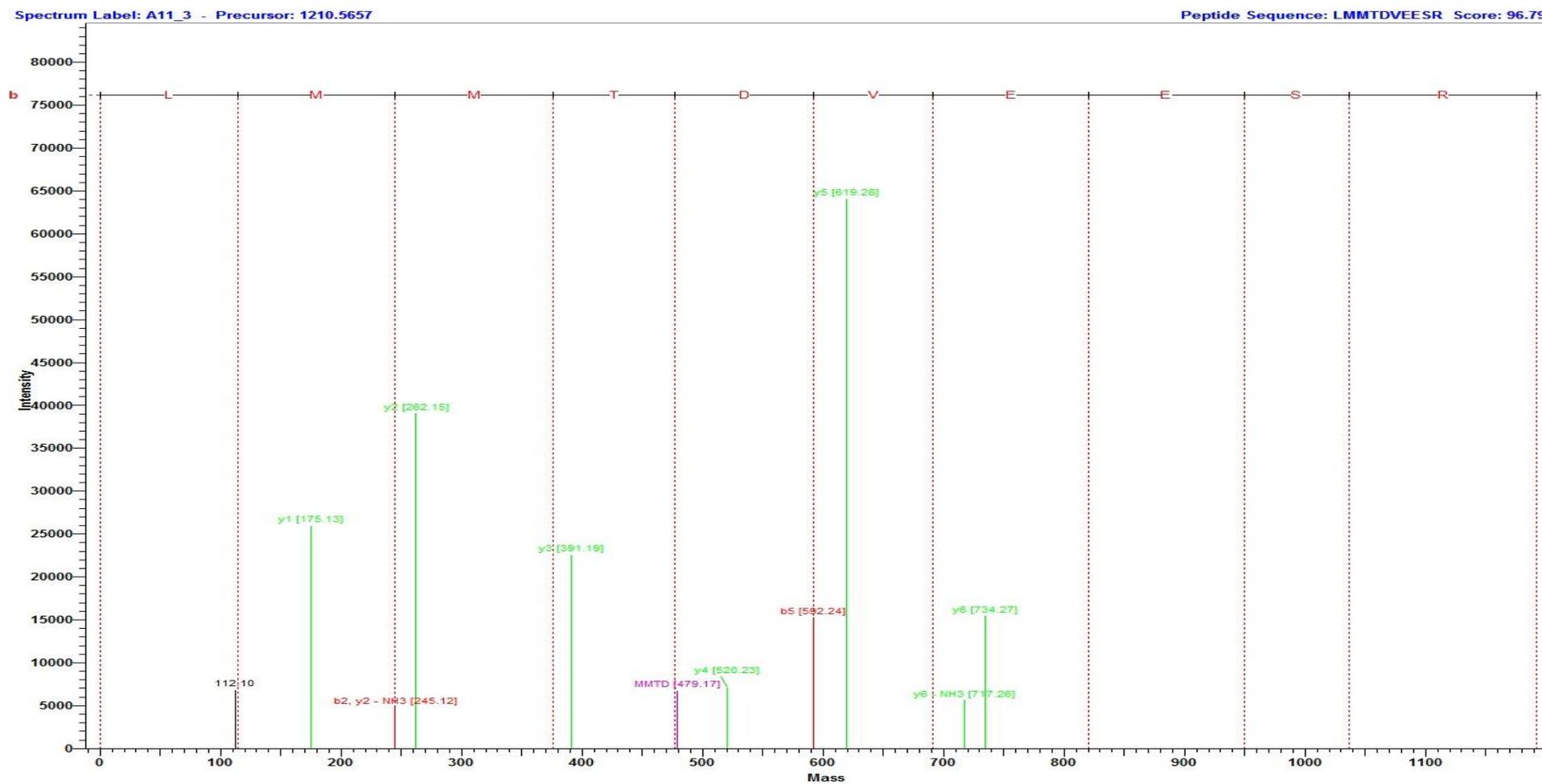
(e)

Figure S1. Cont.



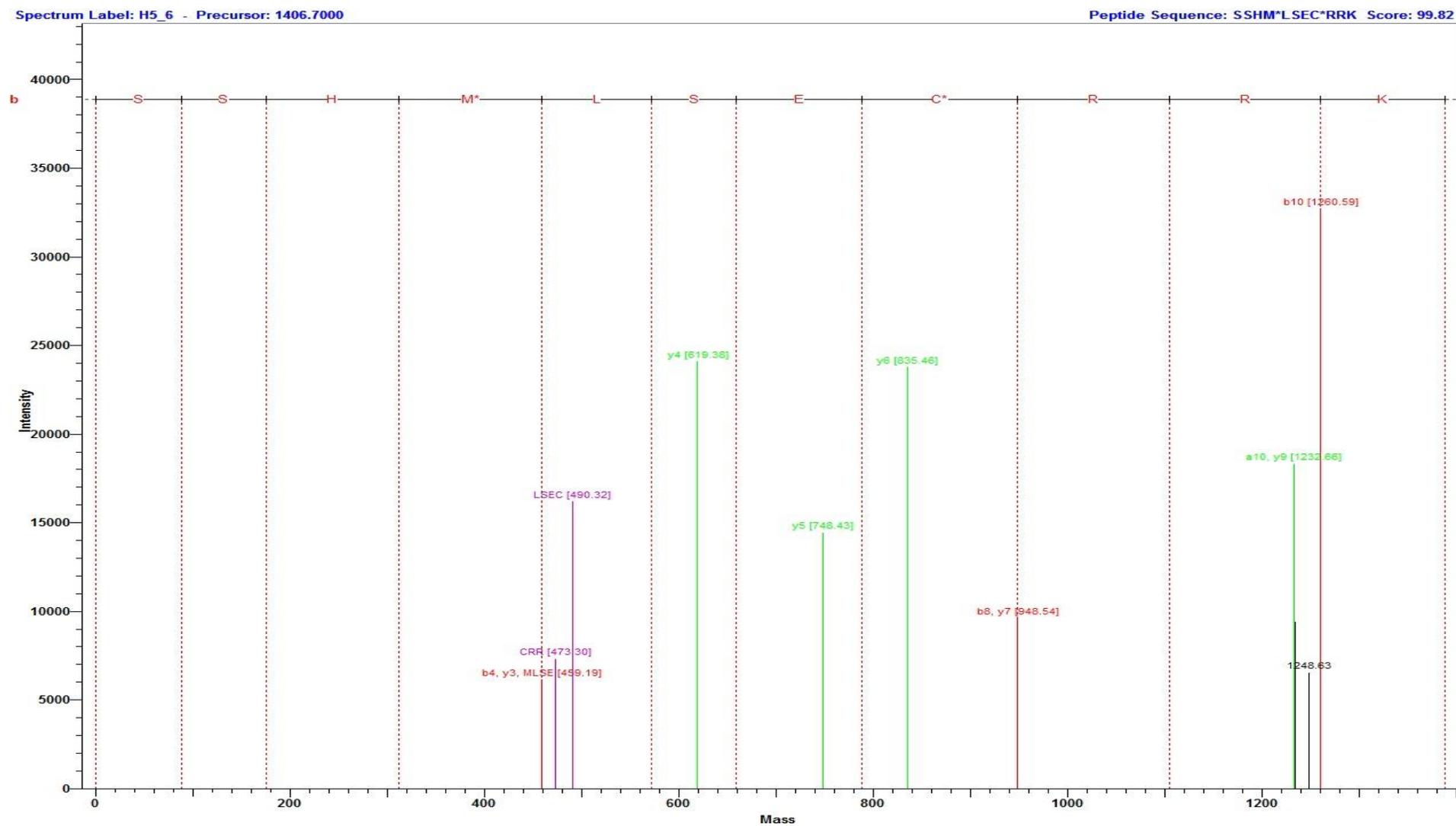
(f)

Figure S1. Cont.



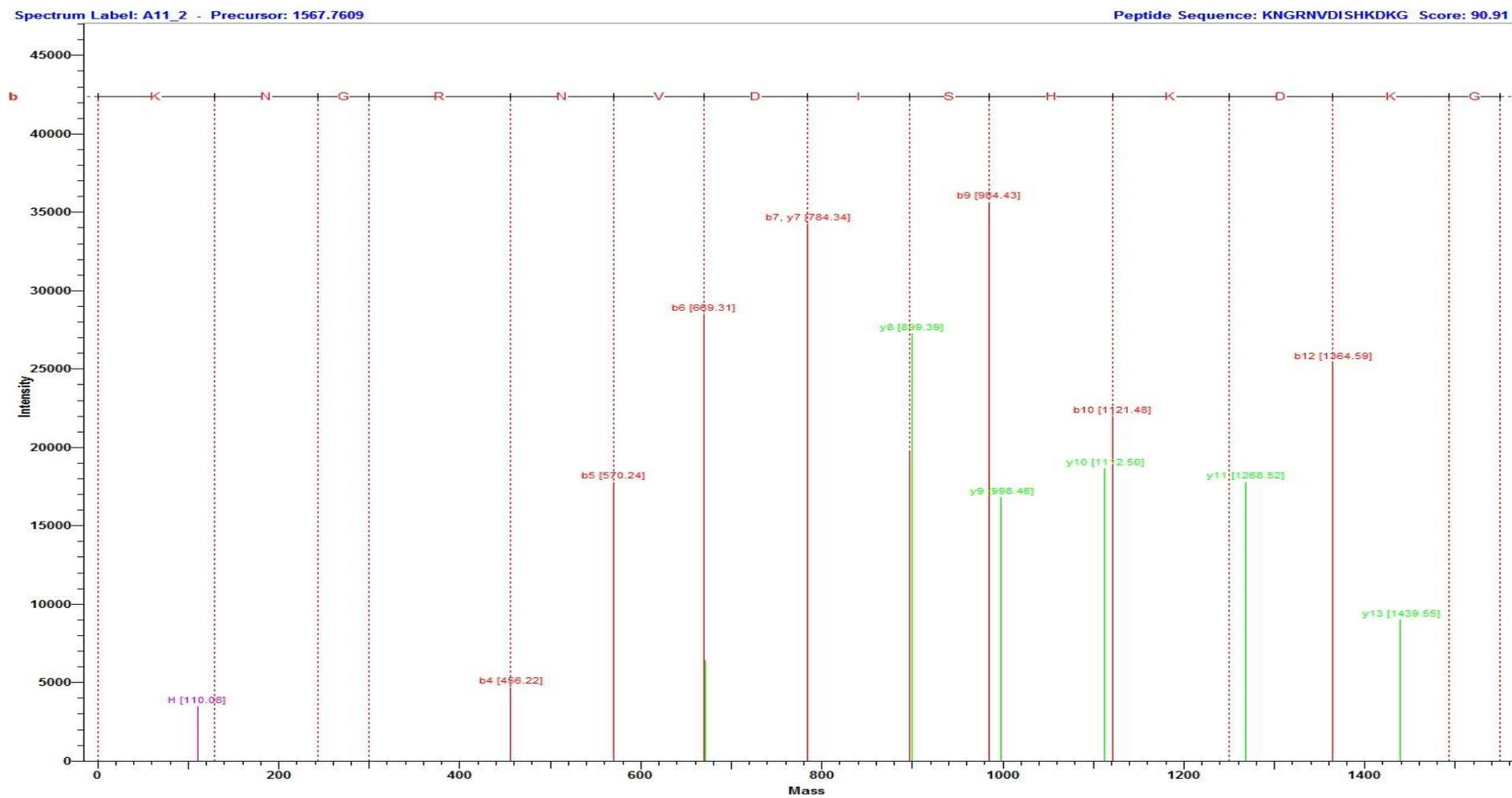
(g)

Figure S1. Cont.



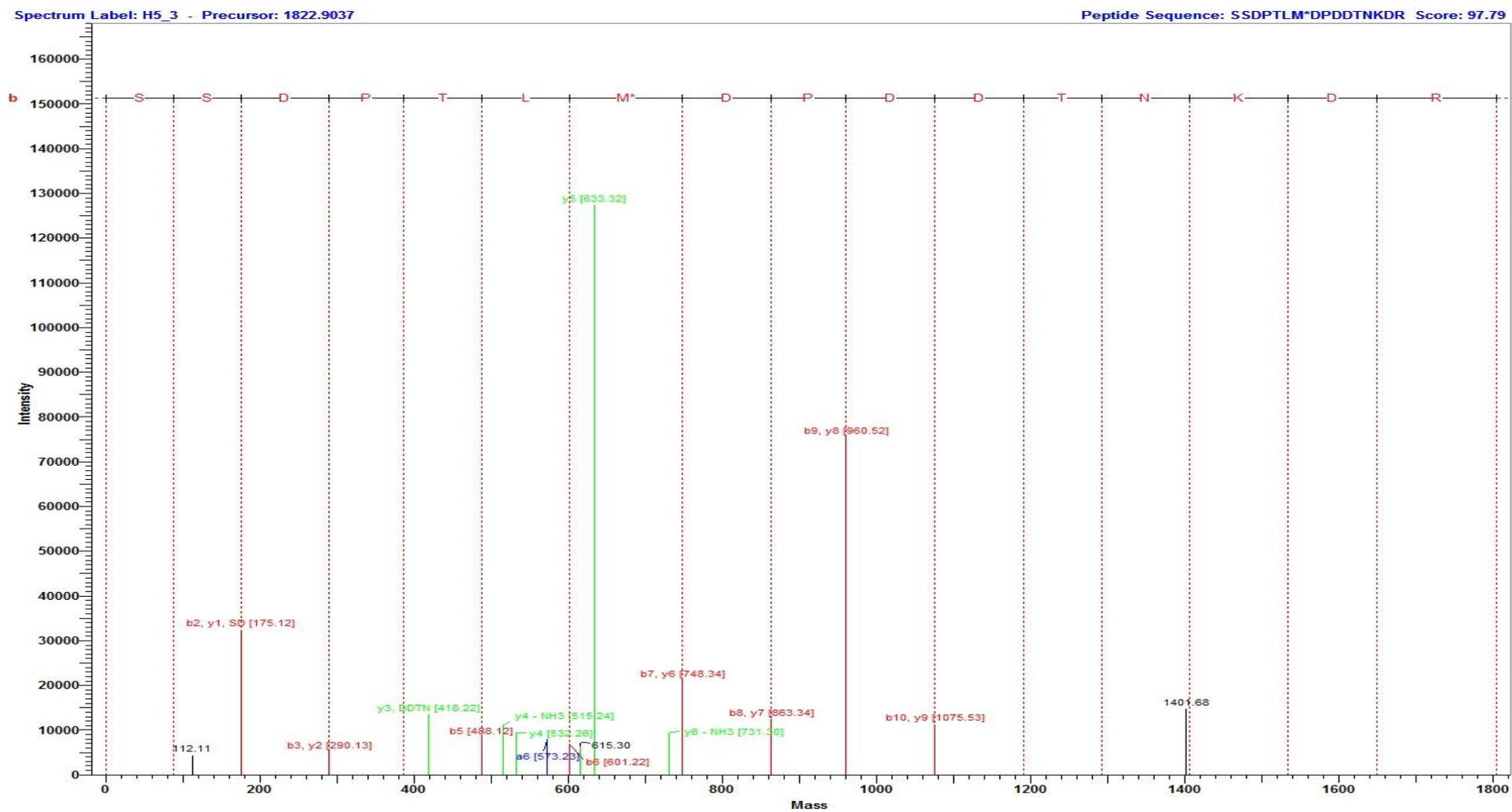
(h)

Figure S1. Cont.



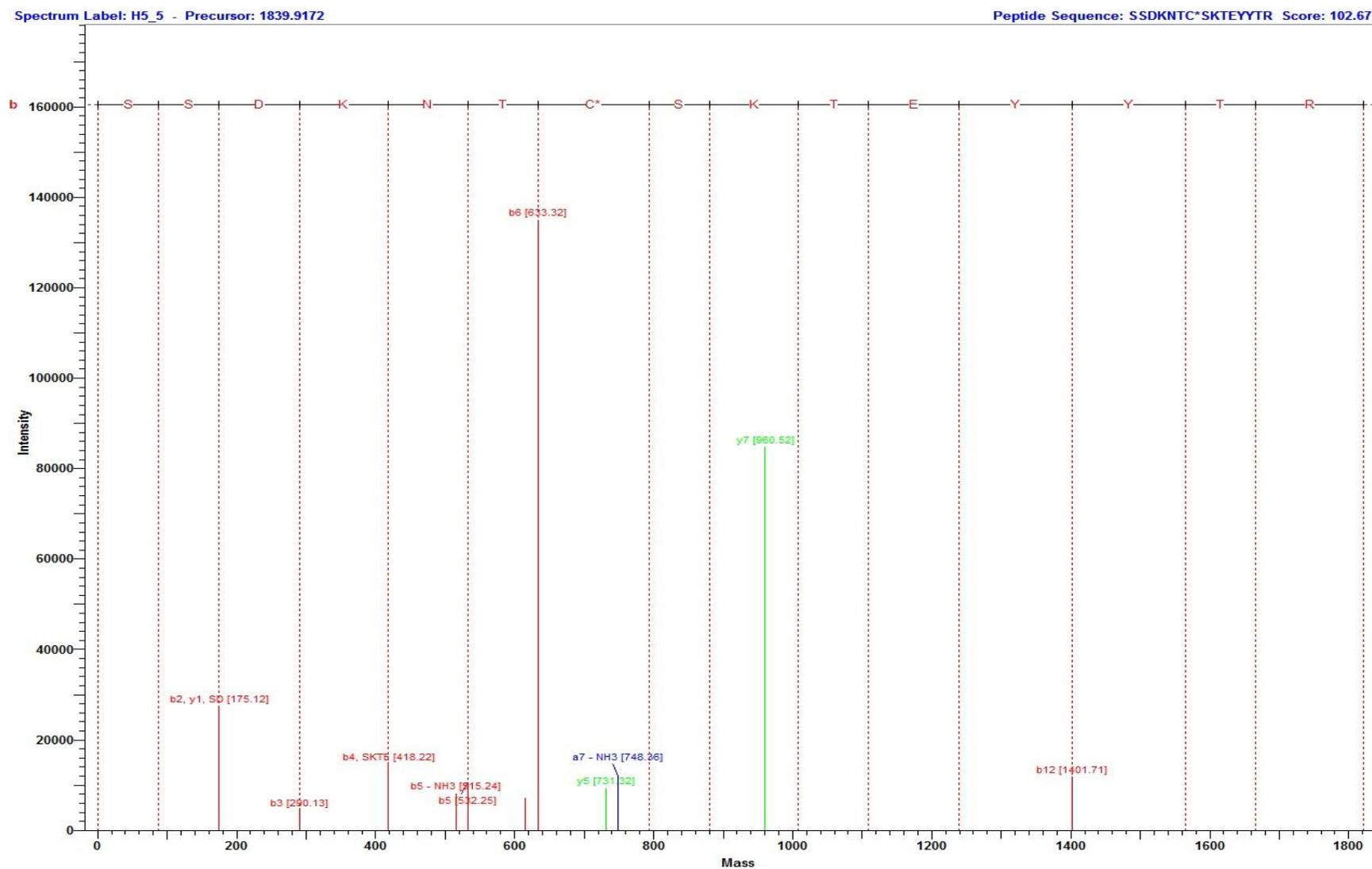
(i)

Figure S1. Cont.



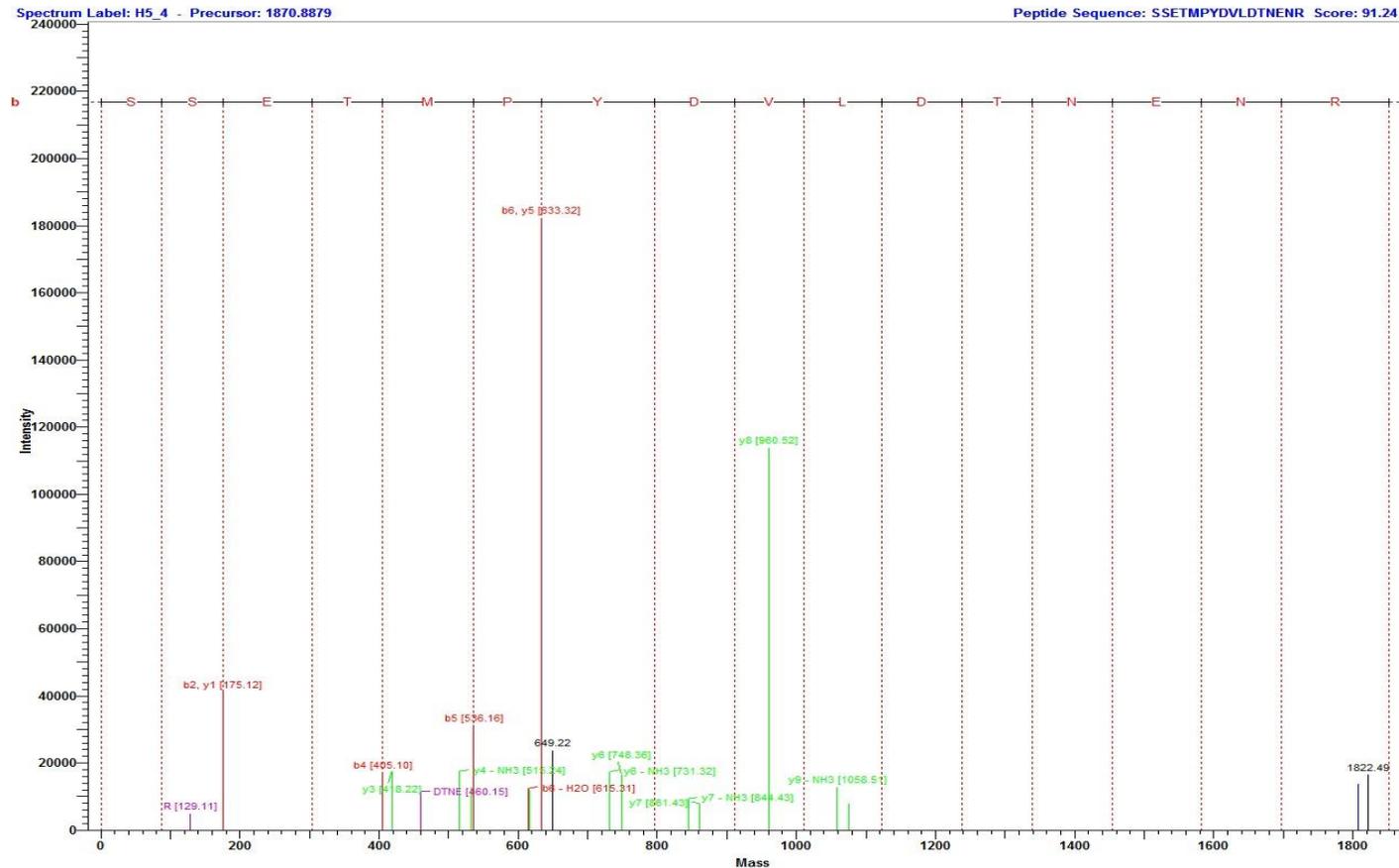
(j)

Figure S1. Cont.



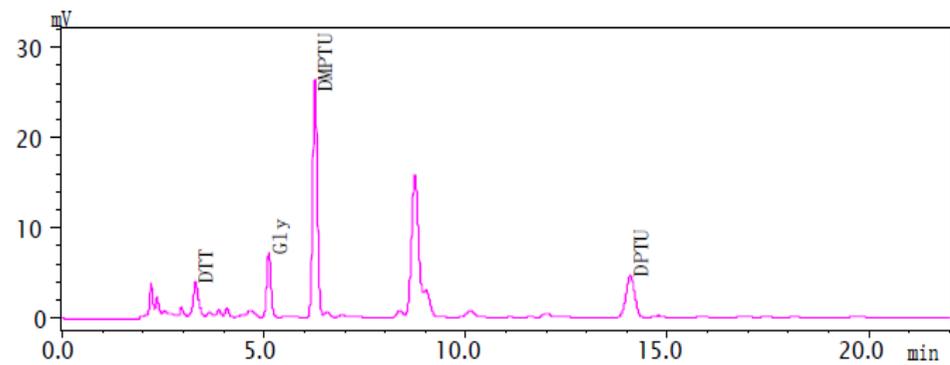
(k)

Figure S1. Cont.

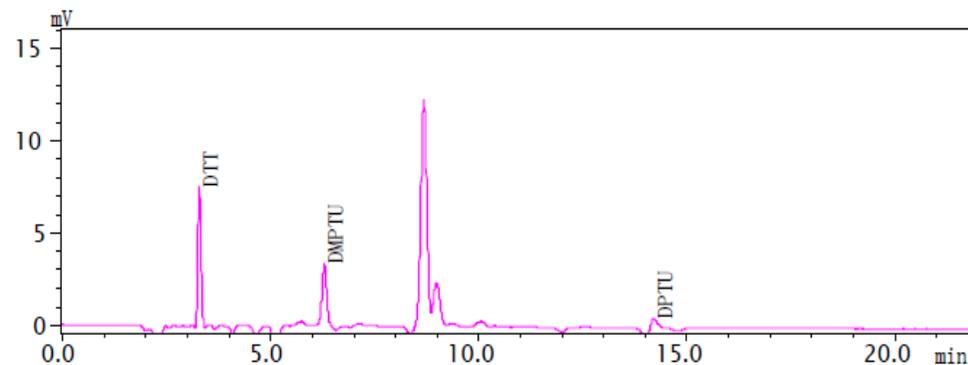


(I)

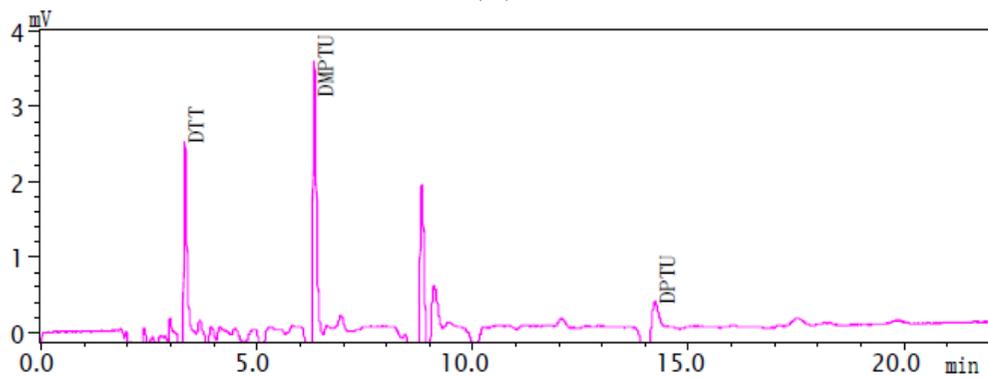
Figure S1. Peptide mass fingerprinting (PMF) and amino acid sequence of D2-3. (a) The MS spectrum of peptide fragmentation 1210.57 Da; (b) The MS spectrum of peptide fragmentation 1406.70 Da; (c) The MS spectrum of peptide fragmentation 1567.76 Da; (d) The MS spectrum of peptide fragmentation 1822.90 Da; (e) The MS spectrum of peptide fragmentation 1839.92 Da; (f) The MS spectrum of peptide fragmentation 1870.89 Da; (g) The amino acid sequence of the peptide 1210.57 Da; (h) The amino acid sequence of the peptide 1406.70 Da; (i) The amino acid sequence of the peptide 1567.76 Da; (j) The amino acid sequence of the peptide 1822.90 Da; (k) The amino acid sequence of the peptide 1839.92 Da; (l) The amino acid sequence of the peptide 1870.89 Da.



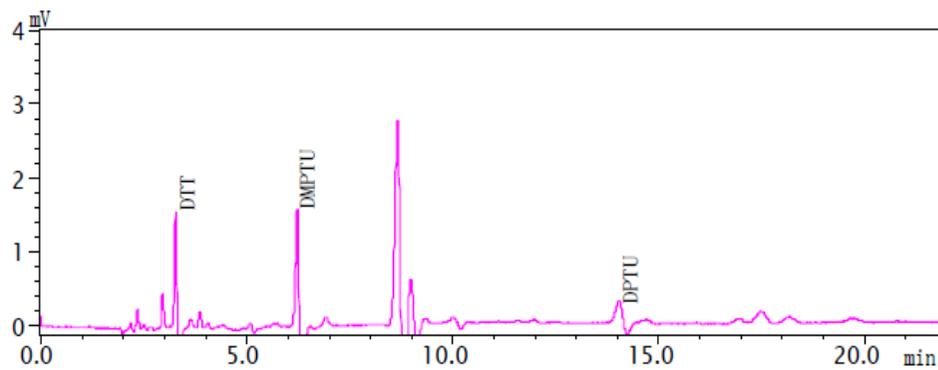
(A)



(B)

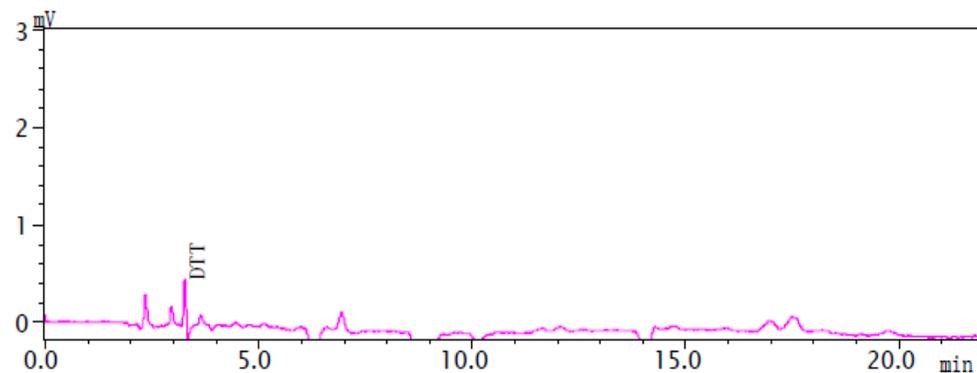


(C)



(D)

Figure S2. Cont.



(E)

Figure S2. *N*-terminal sequencing by Edman degradation. (A) The HPLC chromatogram of Gly. (B) The HPLC chromatogram of Pro. (C) The HPLC chromatogram of Tyr. (D) The HPLC chromatogram of Tyr. (E) The HPLC chromatogram of Tyr. (No effective signal peaks were available in the Figure. Five amino acid residues (Gly-Pro-Tyr-Tyr-Tyr) were analyzed, but their amount yield (pmol) and evaluated values were very low. Therefore, we suppose that the *N*-terminus of the purified protein (D2-3) was blocked.)

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