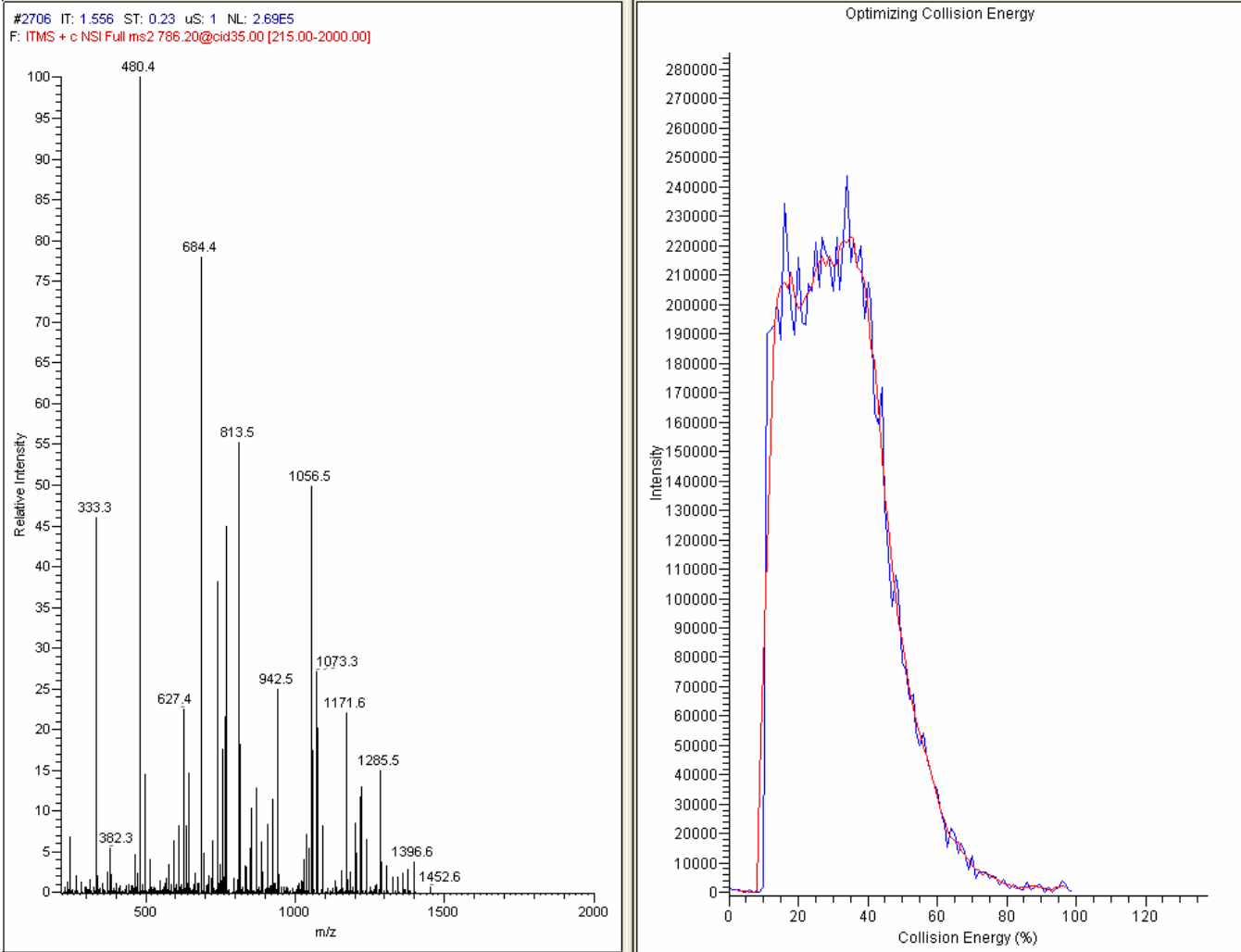


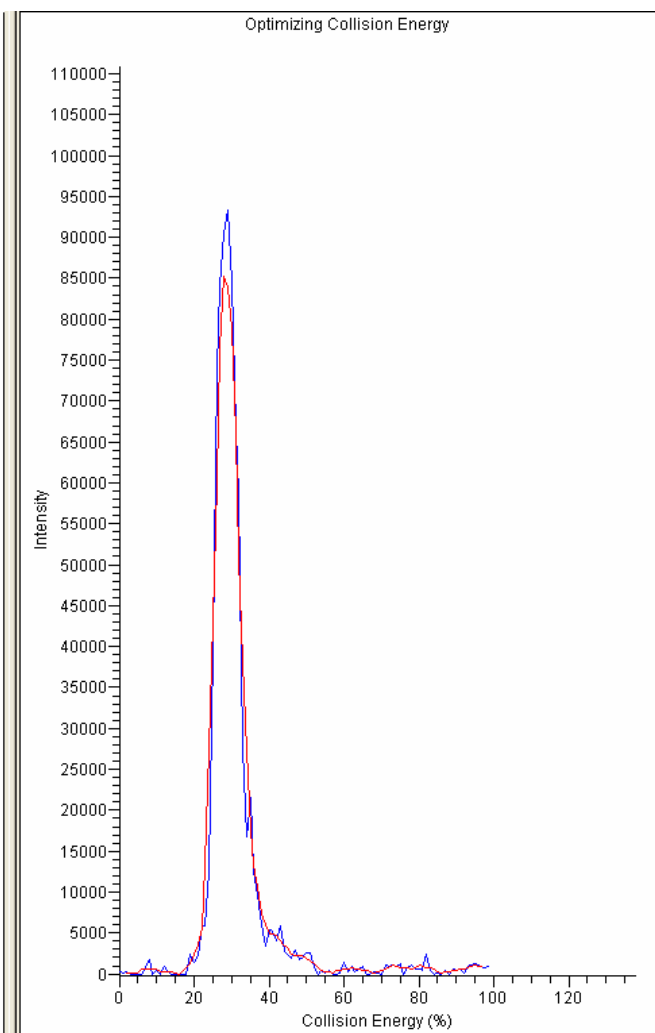
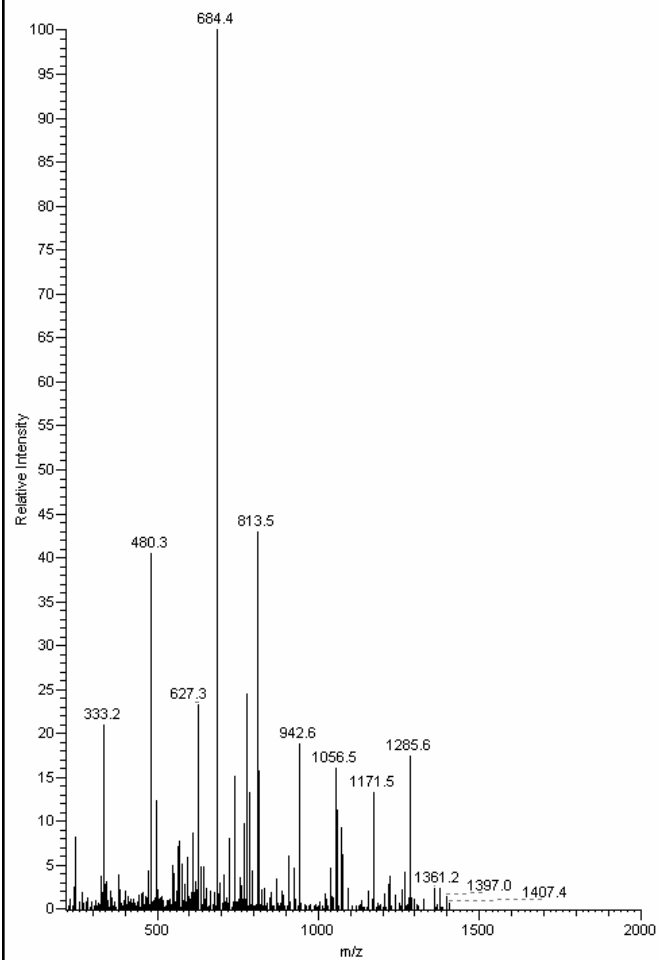
Supplemental Figure 1. The optimal CE range for Glu1-fibrinopeptide B [transition: 786.2 (+2) → 684.4 (+1, y6 ion)] under (a) CID and (b) PQD.

(a) CID:

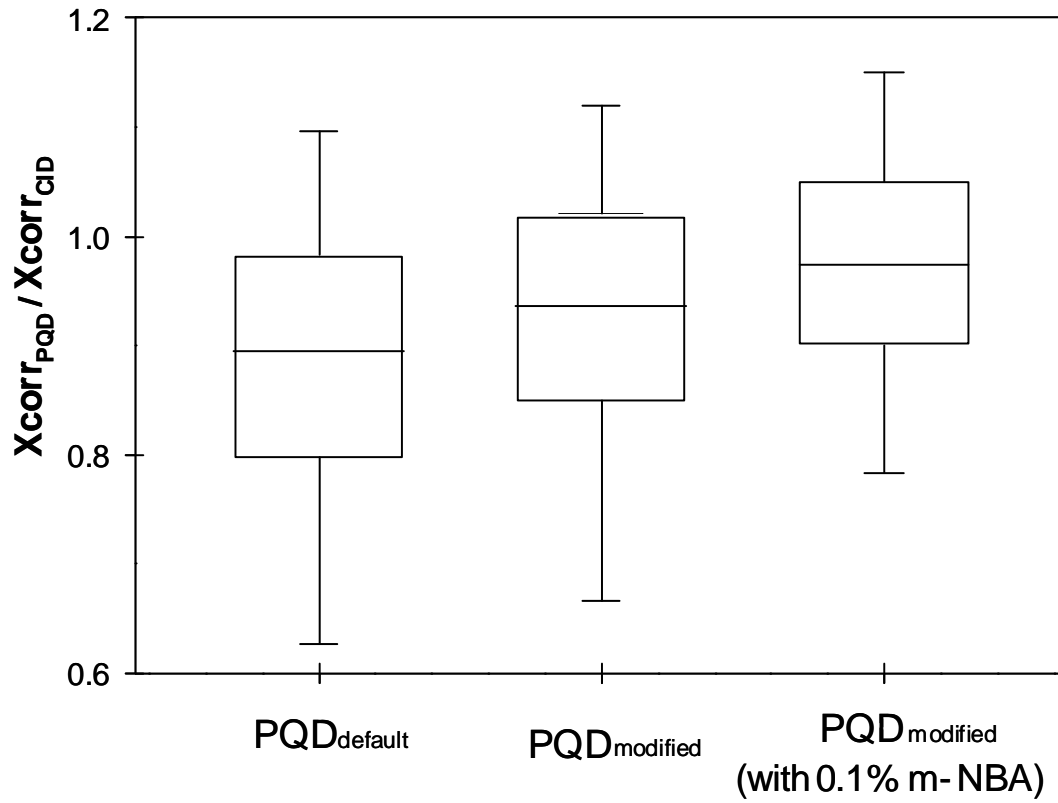


(b) PQD:

#5093 IT: 1.689 ST: 0.20 uS: 1 NL: 9.18E4
F: ITMS + c NSI Full ms2 786.20@pqd30.00 [215.00-2000.00]

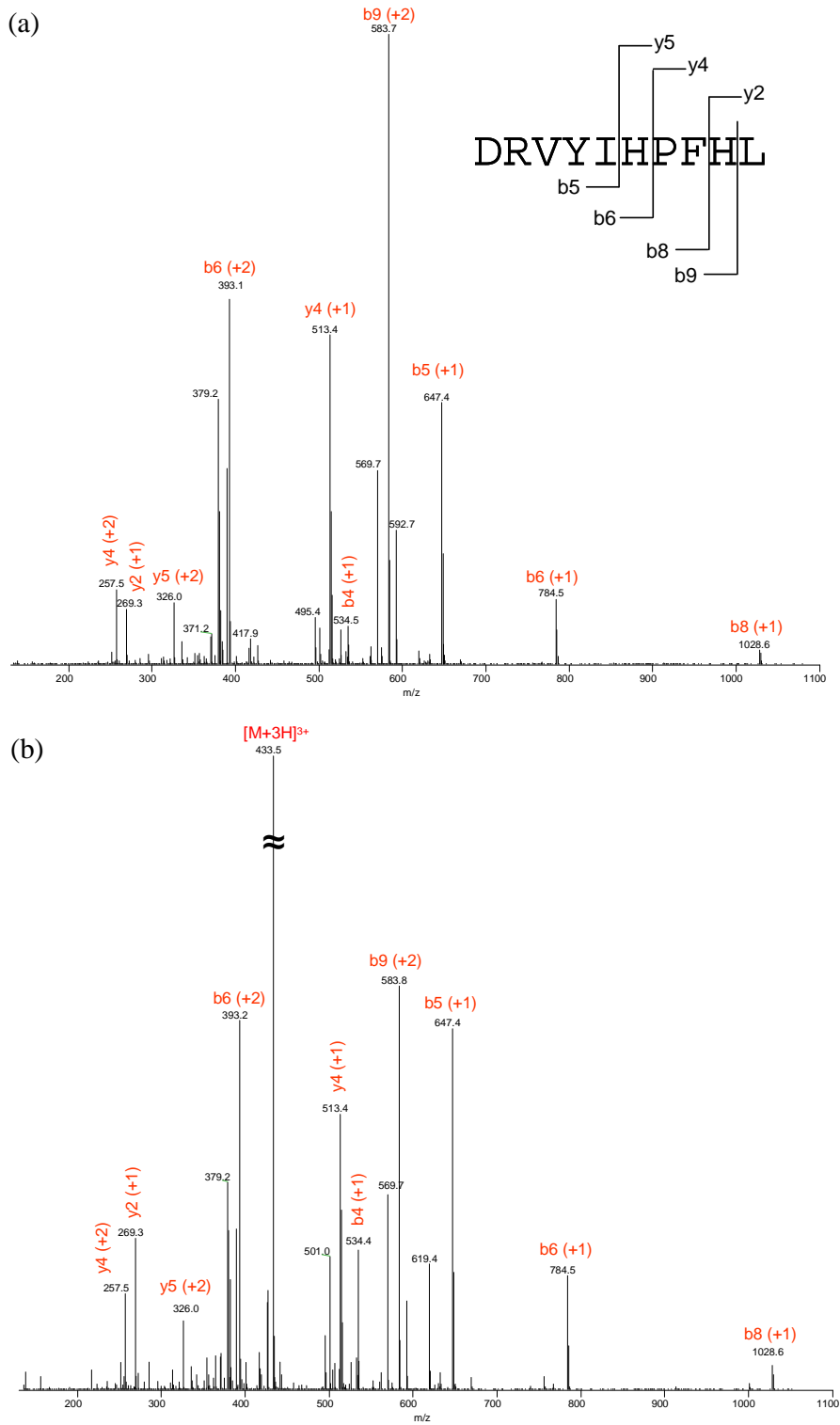


Supplemental Figure 2. Box and whisker plot of relative Xcorr scores ($X_{\text{corr}}^{\text{PQD}}/X_{\text{corr}}^{\text{CID}}$) of the 6-protein mixture, using settings of $\text{PQD}_{\text{default}}$, $\text{PQD}_{\text{modified}}$ (standard mobile phases*), and $\text{PQD}_{\text{modified}}$ (with 0.1% m-NBA in the standard mobile phases).



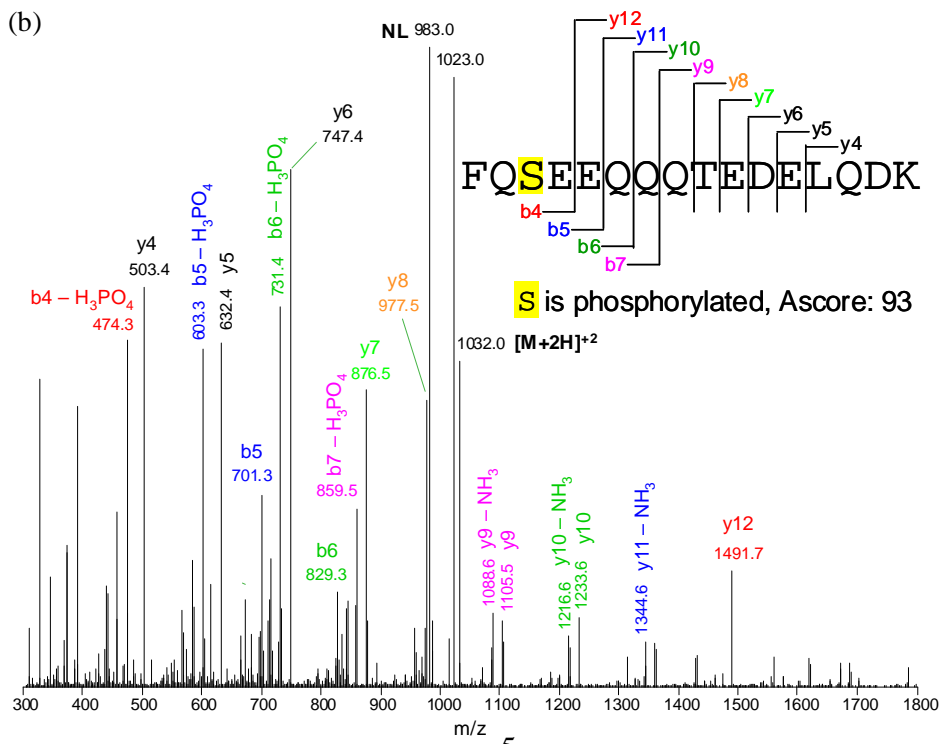
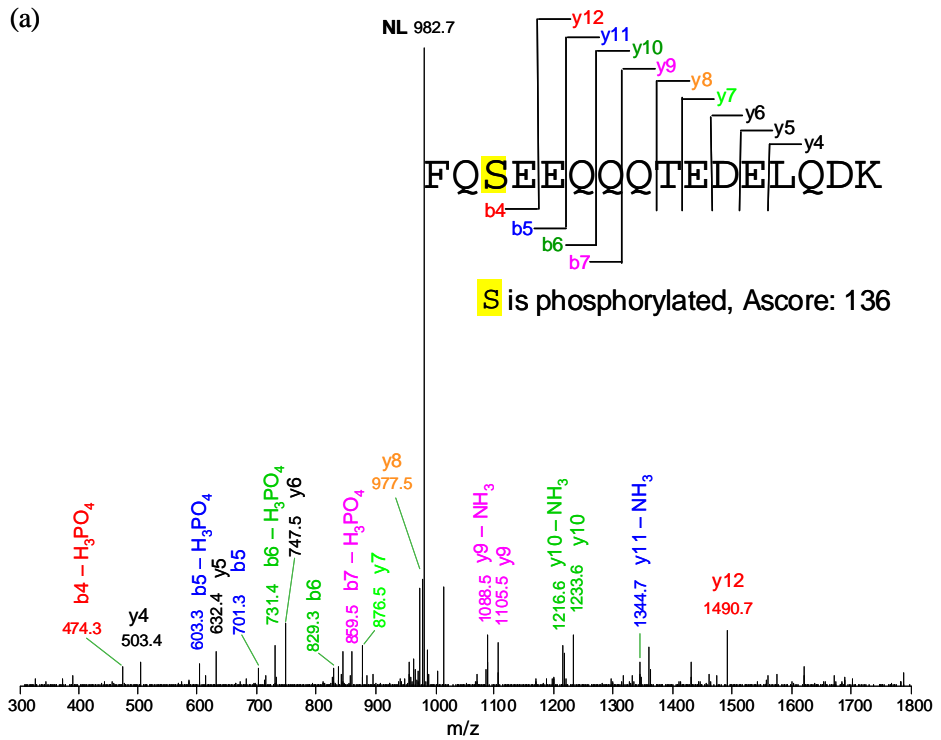
* Water with 0.1% formic acid (mobile phase A); acetonitrile with 0.1% formic acid (mobile phase B).

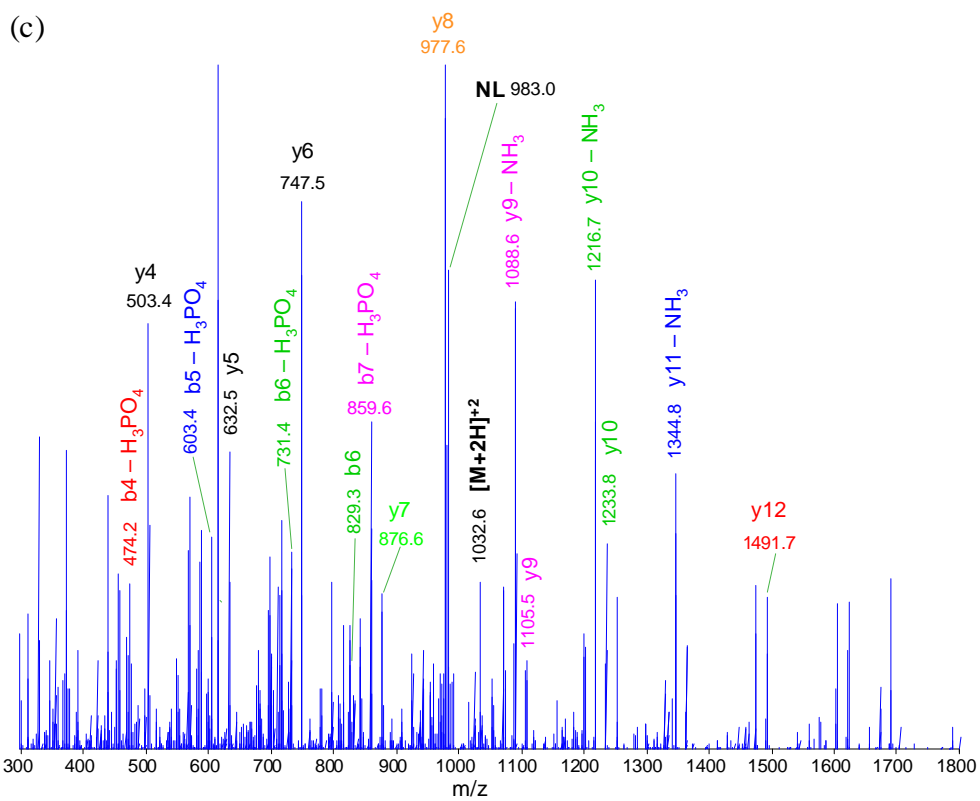
Supplemental Figure 3. (a) CID and (b) PQD mass spectra of triply charged DRVYIHPFHL (angiotensin I) acquired at collision energy of 35% on an LTQ.



Supplemental Figure 4. Tandem mass spectra of (a) conventional CID, (b) PQD, and (c) triple quadrupole-type collision, respectively, of FQS(phos)EEQQQTEDELQDK, with some fragment ions indicated.

The collision energy were 35%, 30%, and 50 (based on rolling collision energy of Qtrap 4000), for CID, PQD, and QqQ, respectively.





Supplemental Figure 5. Tandem mass spectra of (a) CID, (b) default PQD, and (c) triple quadrupole-type collision, respectively, of TRDIY(phos)ETDYRK with some fragment ions indicated. (collision energy: 35%, 25%, and 34 based on rolling collision energy, respectively).

