



Supplemental Fig. 2. MS/MS spectra of the peptide containing residues 560-587 of Fusion Protein C. (A) the wild type peptide; (B) the peptide with an Asn→Ser substitution. The sequence of the peptide, the fragmentation pattern, and the detected fragment ions are shown at the top of each panel. “y” and “b” ions are as described for Figure 4. Calculated m/z values are $y_3 = 301.19$ and $y_4 = 415.23$ when residue 584 is Asn, and $y_3 = 301.19$ and $y_4 = 388.22$ when residue 584 in Ser. The MS/MS spectra clearly show Ser substitution at Asn-584 [the difference in m/z value between y_4 (388.21) and y_3 (301.18) in Supplemental Fig. 2B is 87.03, not 114.04]