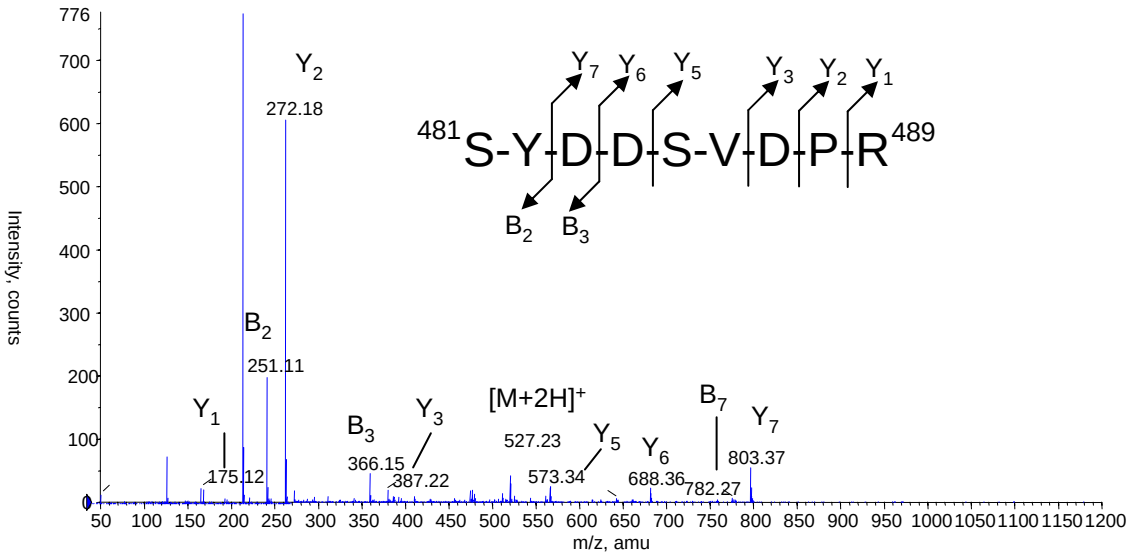
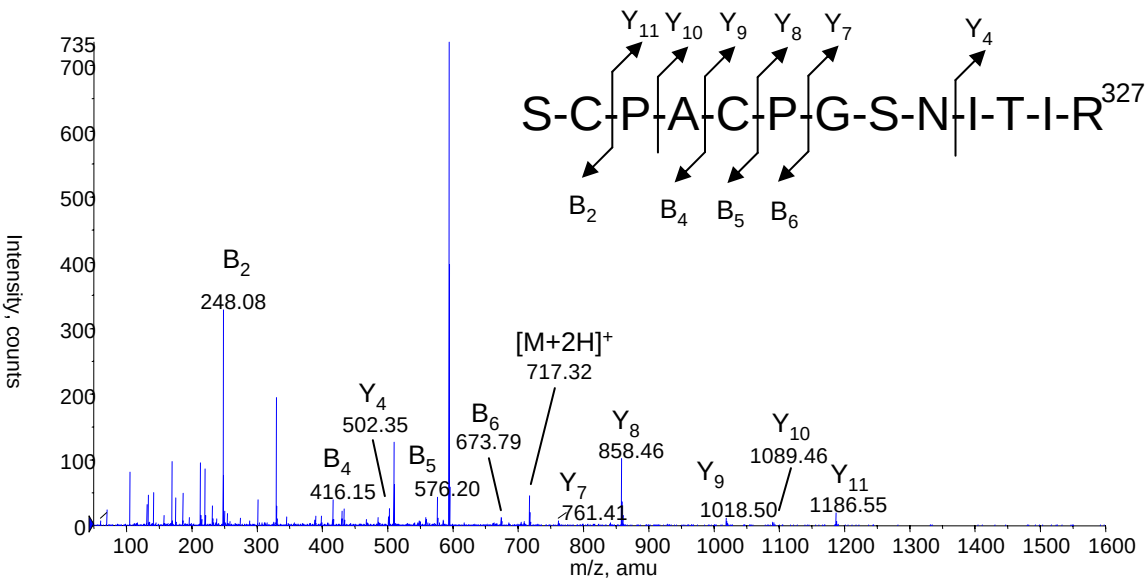
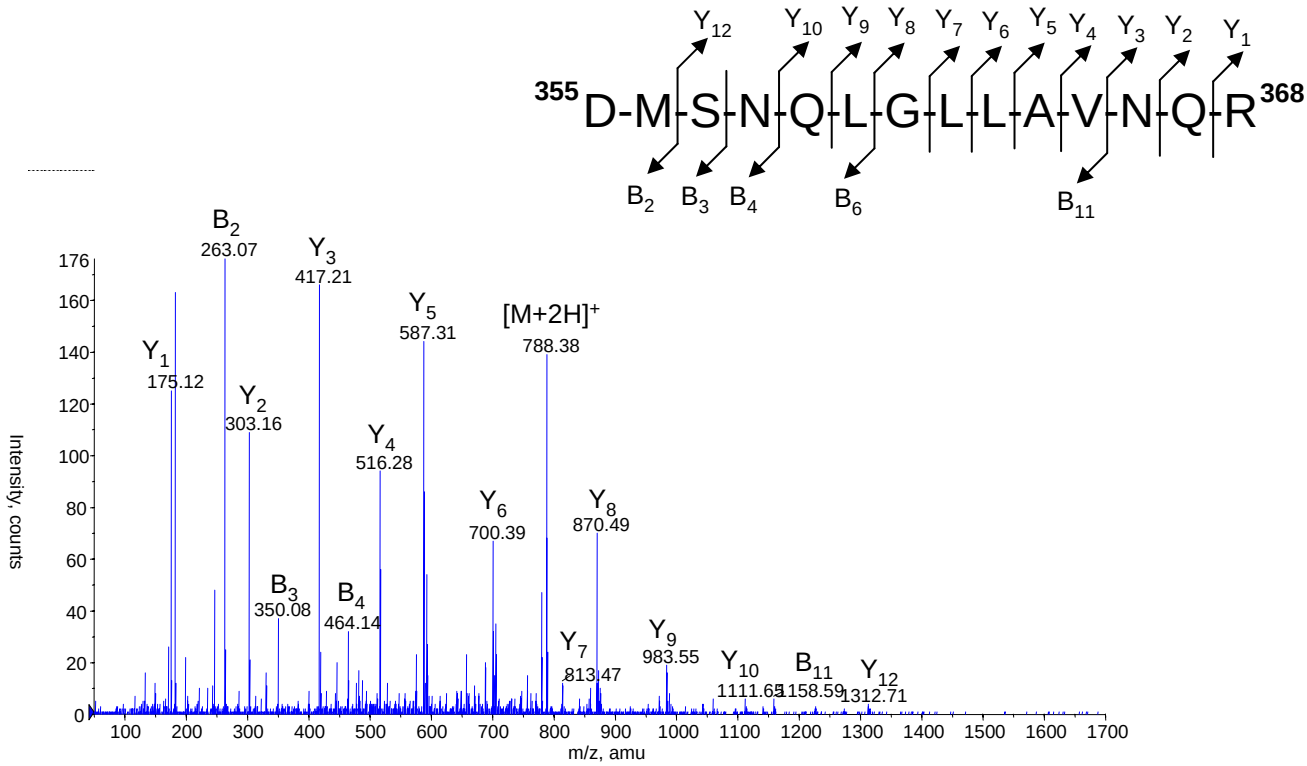
SEQUENCING SPECTRA OF HUMAN MPO



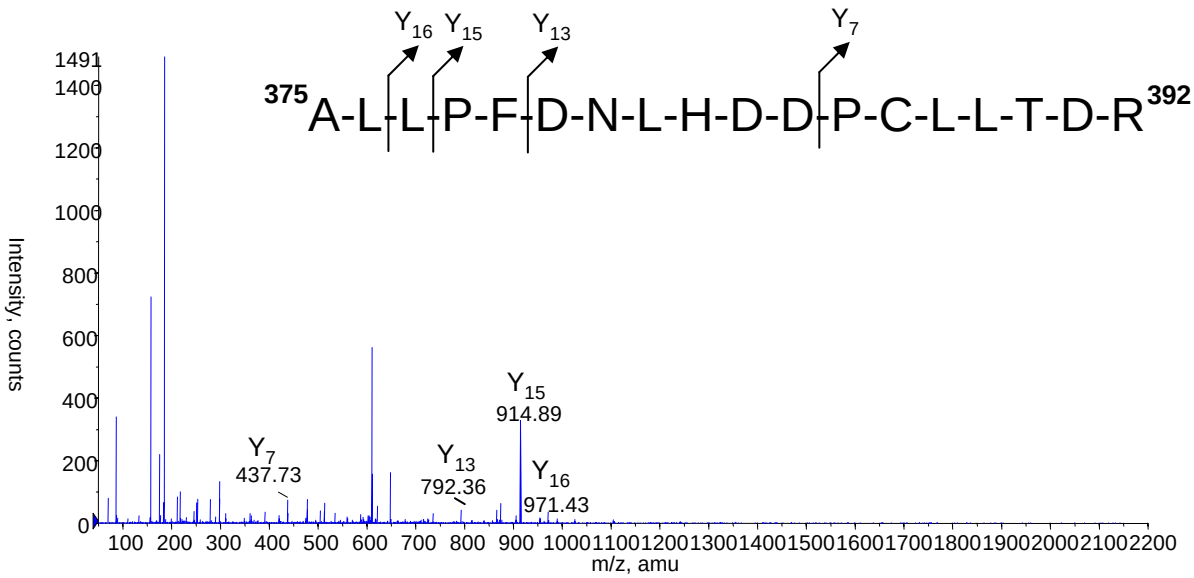
CID-MS/MS mass spectrum of the parent ion at m/z 1052.4 ([M+2H]$^+$, 527.16), all fragments ions are one charged, correspondingto the fraction 28.
After tryptic digest and LC, the glycopeptide was deglycosylated using PNGase F. The peptidic aglycone was then purified on C18 Zip-tip and analyzed by nanoESI-MS/MS. The parent ion corresponds to the predicted mass of the tryptic peptide ^{481}SYDDSVDPR^{489} containing the N^{483} glycosylation site.
The N^{483} residue was transformed in aspartic residue after PNGase treatment.



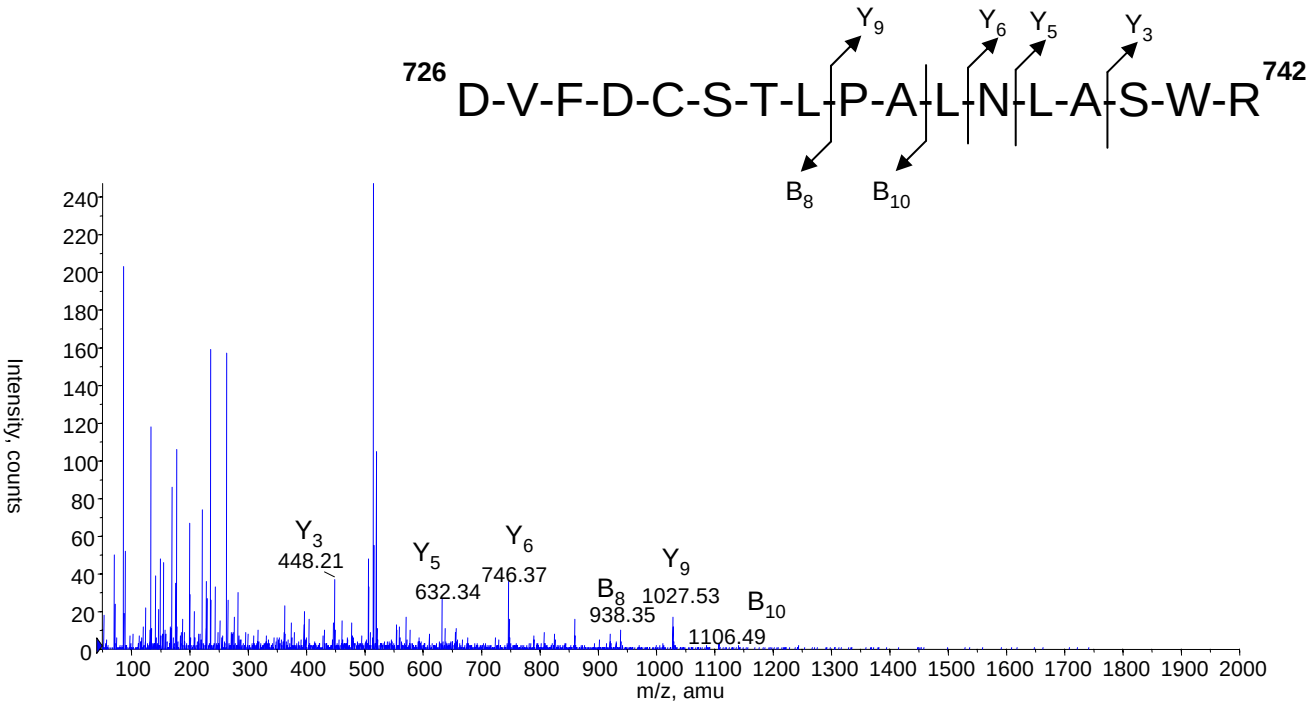
CID-MS/MS mass spectrum of the parent ion at m/z 1432 ([M+2H]$^+$, 717.23), all fragments ions are one charged and cysteine residues are carbamidomethylated, corresponding to fraction 38. The parent ion corresponds to the predicted mass of the tryptic peptide ^{315}SCPACPGSNITIR^{327} containing the N^{323} glycosylation site.



CID-MS/MS mass spectrum of the parent ion at m/z 1573.8 ([M+2H]$^+$, 788.29), all fragments ions are one charged and cysteine residues are carbamidomethylated, corresponding to the fraction 50. The parent ion corresponds to the predicted mass of the tryptic peptide ^{355}DMSNQLGLLAVNQR^{368} containing the N^{355} glycosylation site.



CID-MS/MS mass spectrum of the parent ion at m/z 2124.05 ([M+3H]$^{+}$, 709.3), cysteine residues are carbamidomethylated, corresponding to the fraction 64.
The parent ion corresponds to the predicted mass of the tryptic peptide ^{375}ALLPFDNLHDDPCLLTDR^{392} containing the N^{391} glycosylation site.



CID-MS/MS mass spectrum of the parent ion at m/z 1963.9 ([M+2H]$^{+}$, 983.3), all fragments ions are one charged and cysteine residues are carbamidomethylated, corresponding to the fraction 70. The parent ion corresponds to the predicted mass of the tryptic peptide ^{726}DVFDCSTLPALNLASWR^{742} containing the N^{729} glycosylation site.