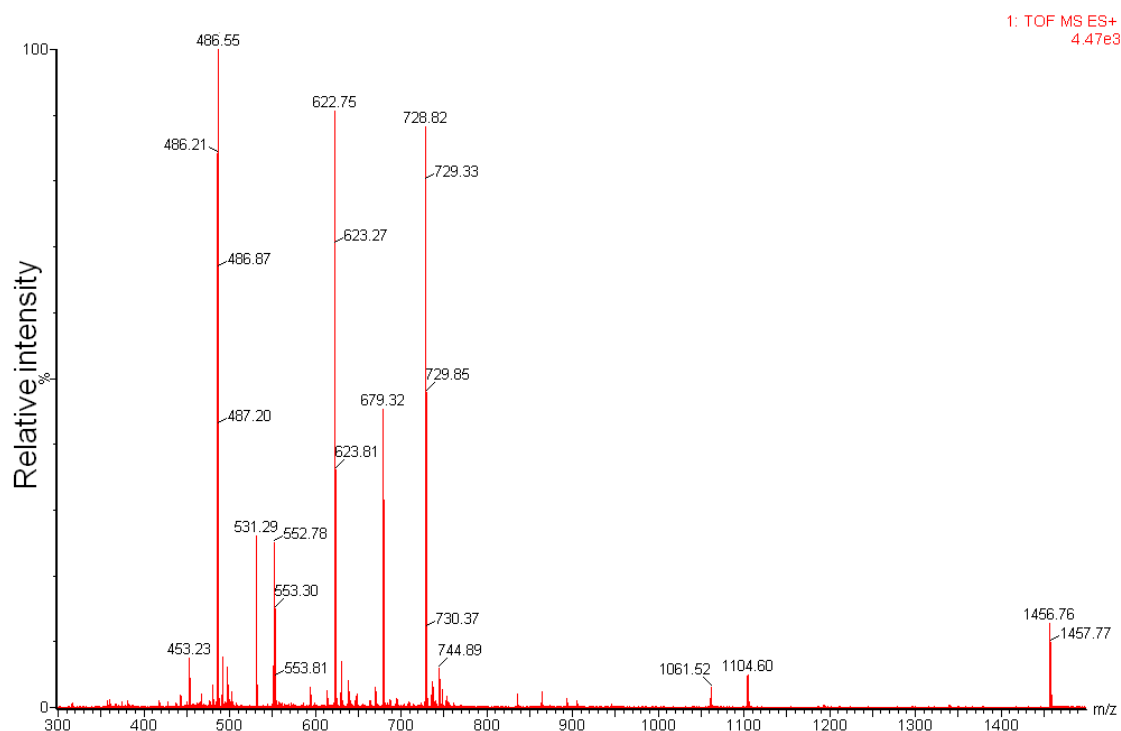
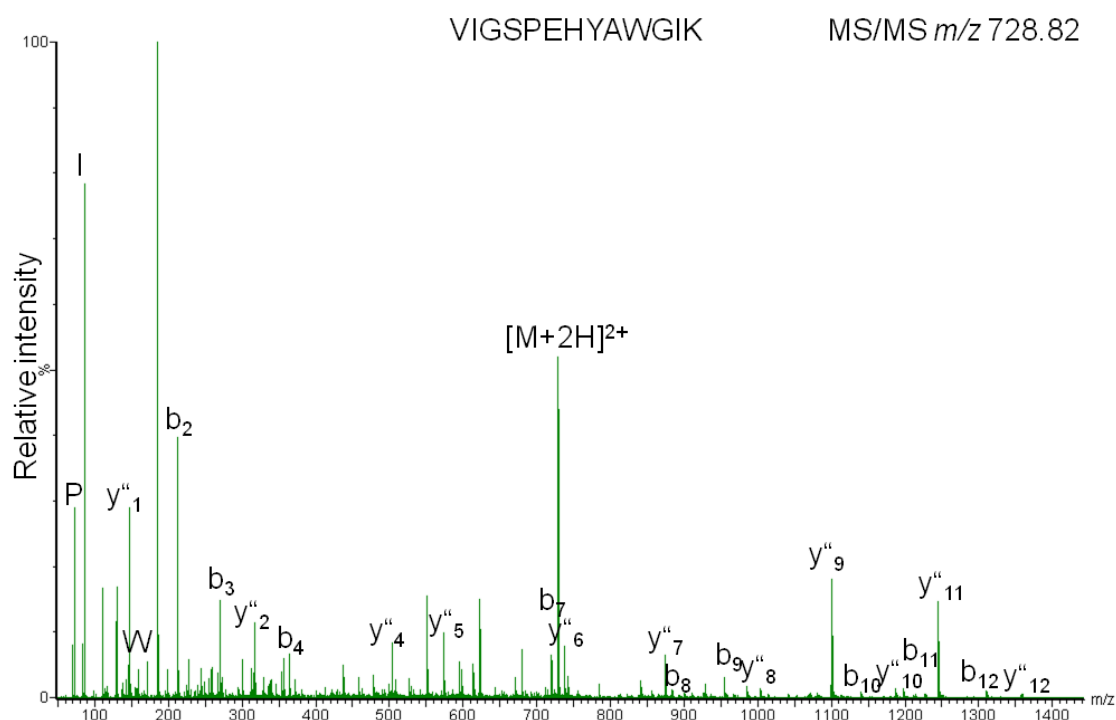


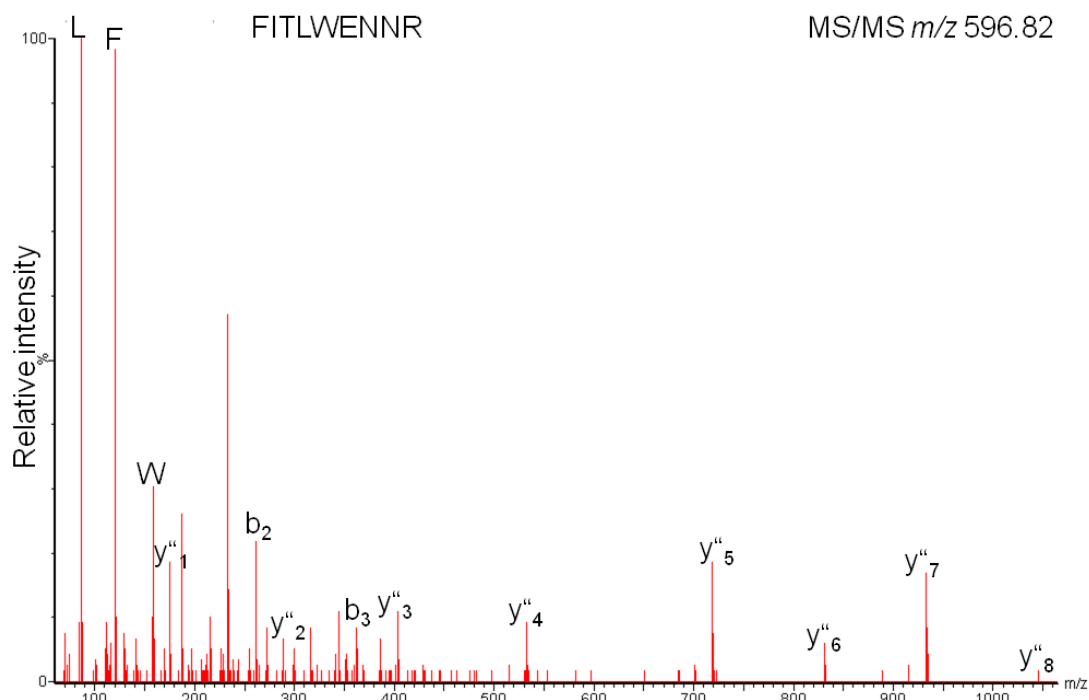
Additional file 18 - Exemplary spectra for peptides derived from LP2, LP4 and LP5 found in the purified lipoprotein (fraction 60, Fig. 5).



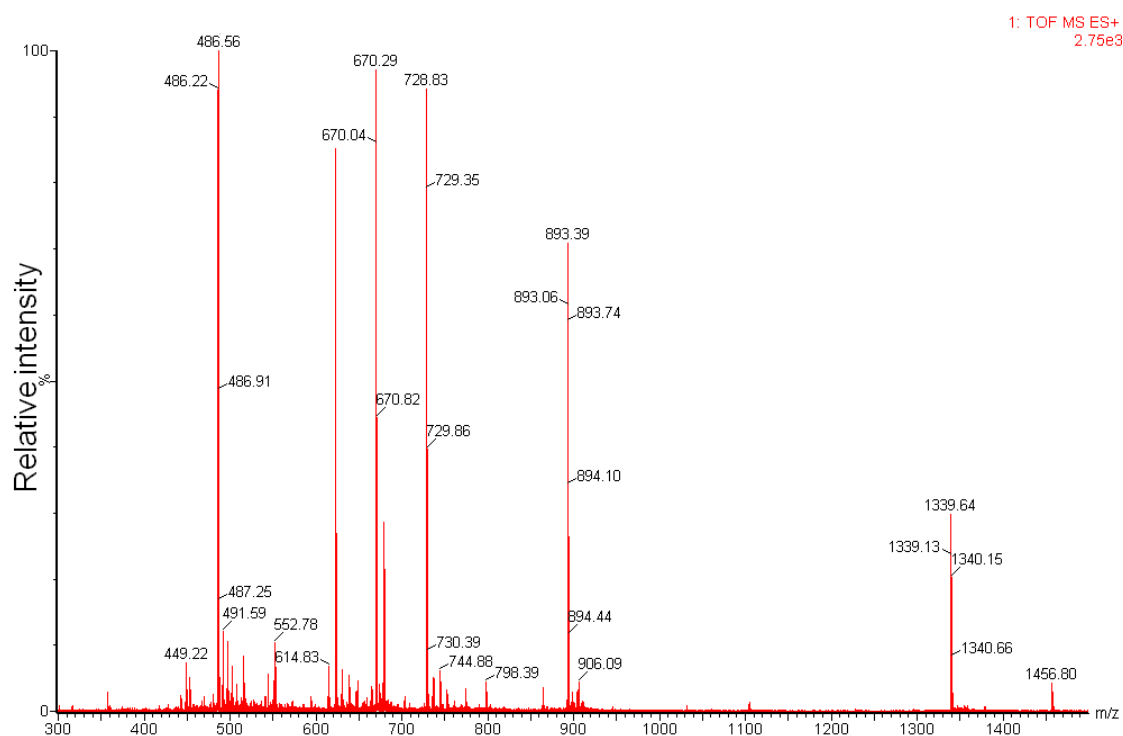
MS spectrum showing the scan with the most intense ion at m/z 728.82 subjected to MS/MS fragmentation.



MS/MS of the ion at m/z 728.82. All ions of the y-series were observed as well as b and immonium ions. The peptide is unique to LP3/L301.

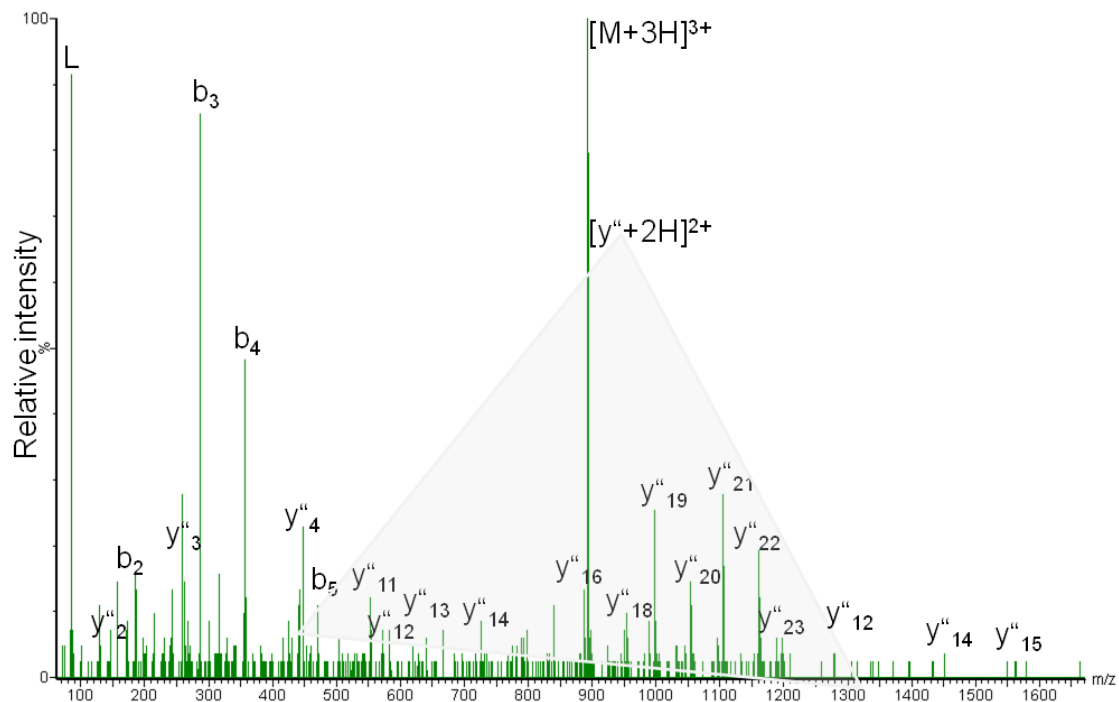


MS/MS spectrum of m/z 596.82. Peptide present in LP2, LP4, LP5 and L302 but not in LP3/L301. All ions of the y-series were observed as well as b and immonium ions.

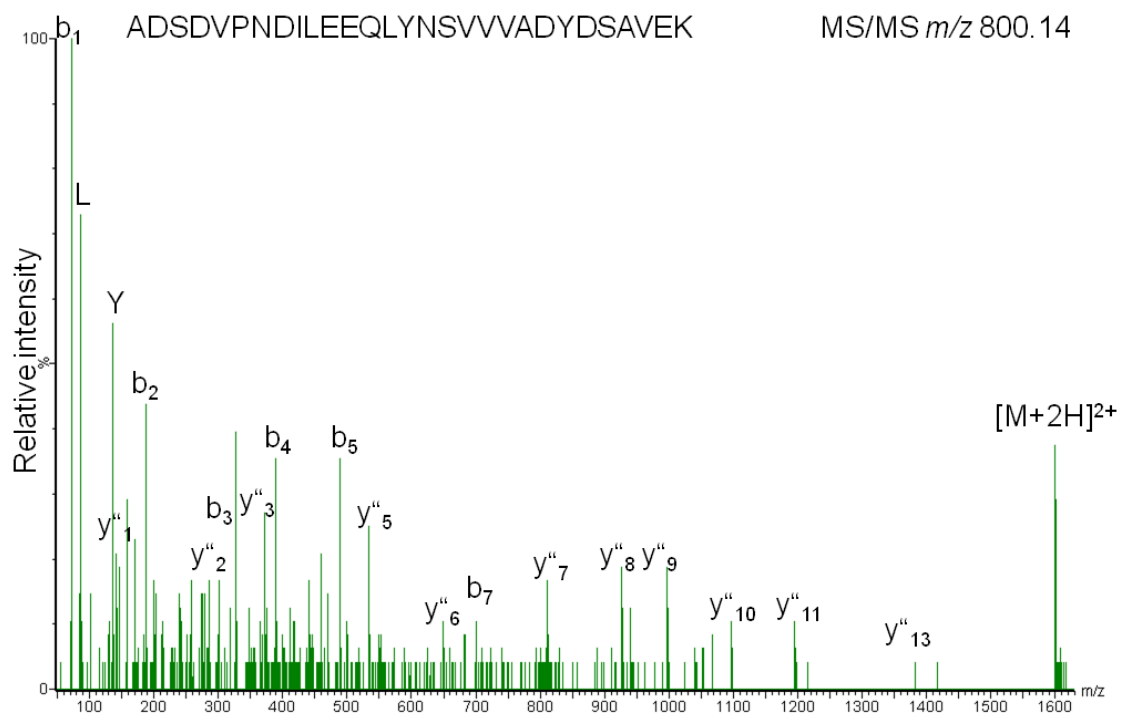


MS spectrum showing the scan with the most intense ion at m/z 893.06 subjected to MS/MS fragmentation.

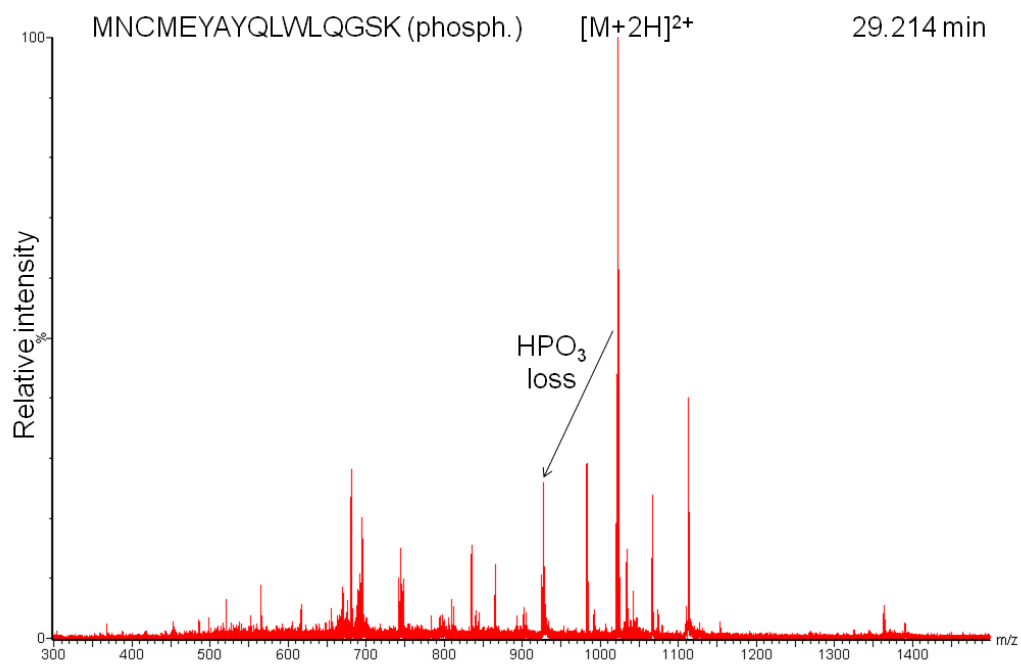
DGLALTLSNDVQGDDGRPAYGDGKDK

MS/MS m/z 893.06

MS/MS of the ion at m/z 893.06. All ions of the y-series were observed as well as b and immonium ions. The peptide is unique to C7A8A3.



MS/MS of the ion at m/z 800.14. All ions of the y-series were observed as well as b and immonium ions. The peptide is N-terminal in Q6Q0S8.



Overview scan (top) and MS/MS spectrum for the phosphorylated (or O-sulfonated) form of a peptide unique in LP3/L301. The peptide easily loses 80 Da. No modified fragment ions can be observed so that the phosphorylation/O-sulfonation site remains ambiguous.