

Supplemental FIGURE S2. Hyp location within the Pro-rich domain of AGP31
using MALDI-TOF/TOF MS/MS.

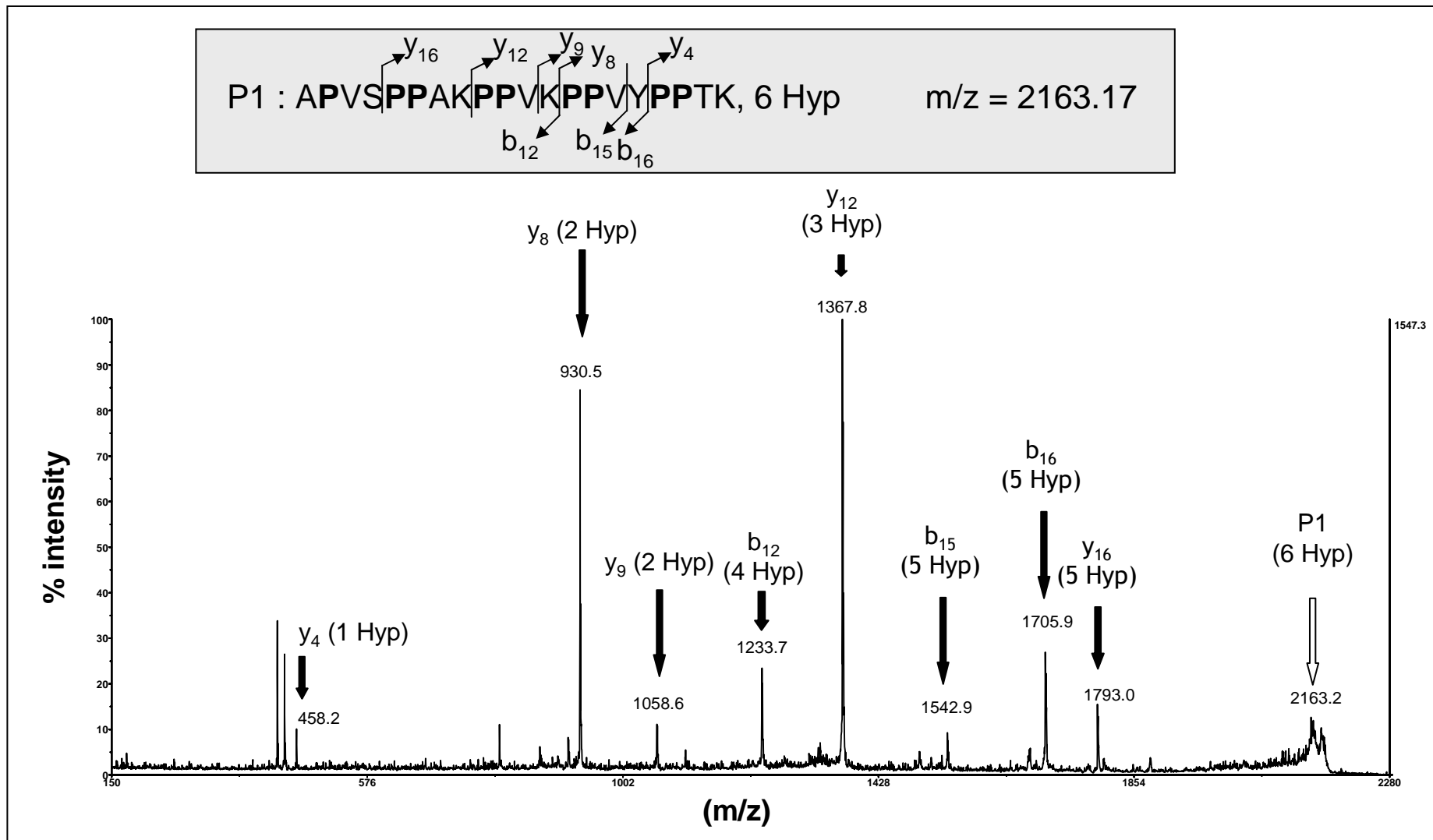


Figure S2A. MALDI-TOF/TOF MS/MS spectrum of the P1 peptide (m/z 2163.17, white arrow) of the AGP31 Pro-rich domain.

Fragmentation was carried out on the deglycosylated AGP31 P1 tryptic peptide obtained following gel excision of an HF sample (see Fig. 3B). Peaks corresponding to b and y fragment ions are labeled with black arrows and the number of Hyp predicted from the fragment masses is indicated. The fragmentation pattern is reported onto the sequence in which Pro residues possibly hydroxylated are in bold (in frame). The number of Hyp residues predicted within each fragment allowed partial Hyp location. Non-assigned peaks mostly corresponded to internal fragments.

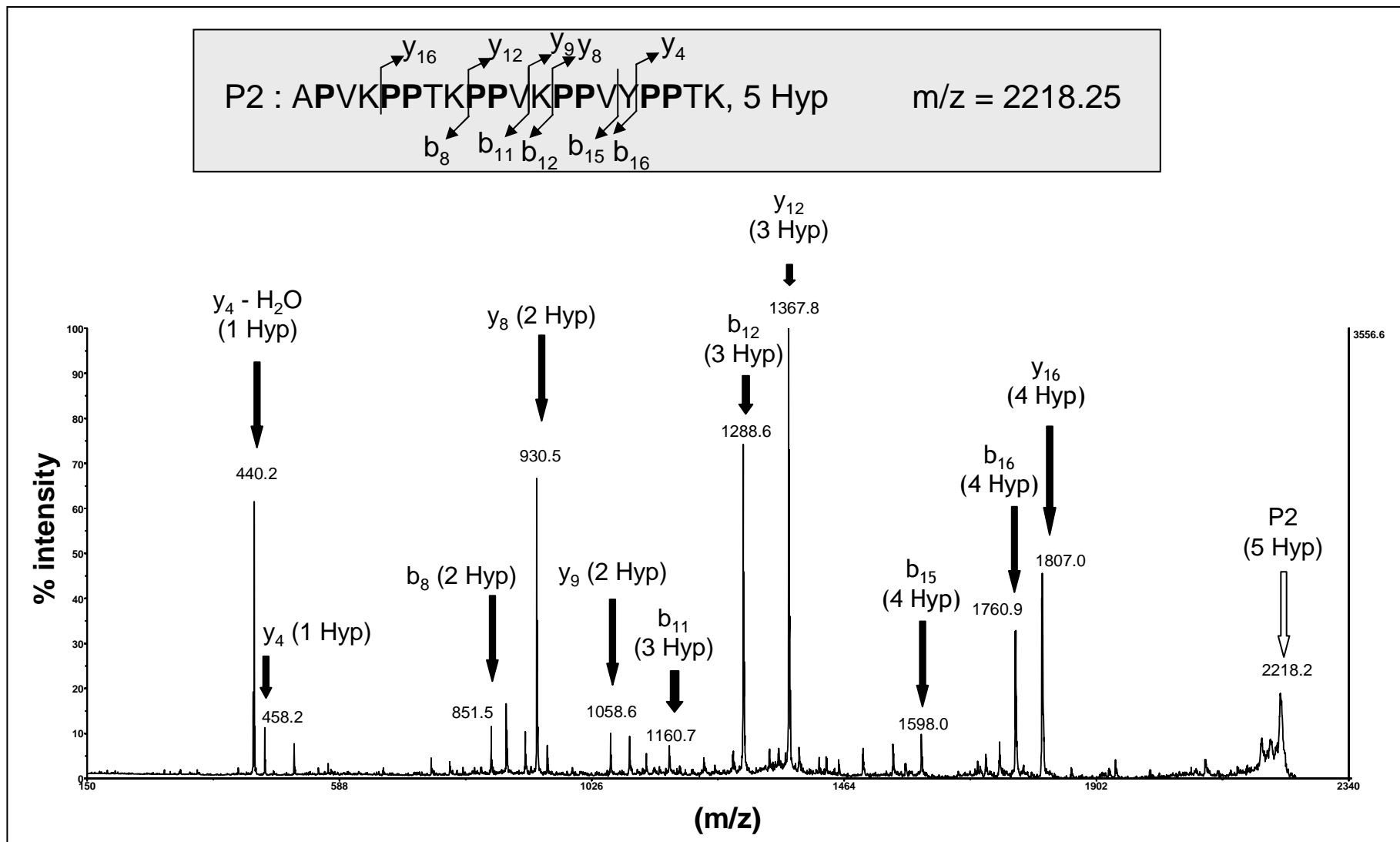


Figure S2B. MALDI-TOF/TOF MS/MS spectrum of the P2 peptide (m/z 2218.25, white arrow) of the AGP31 Pro-rich domain.

Fragmentation was carried out on the deglycosylated AGP31 P2 tryptic peptide obtained following gel excision of an HF sample (see Fig. 3B). Peaks corresponding to b and y fragment ions are labeled with black arrows and the number of Hyp predicted from the fragment masses is indicated. The fragmentation pattern is reported onto the sequence in which Pro residues possibly hydroxylated are in bold (in frame). The number of Hyp residues predicted within each fragment allowed partial Hyp location. Non-assigned peaks mostly corresponded to internal fragments.

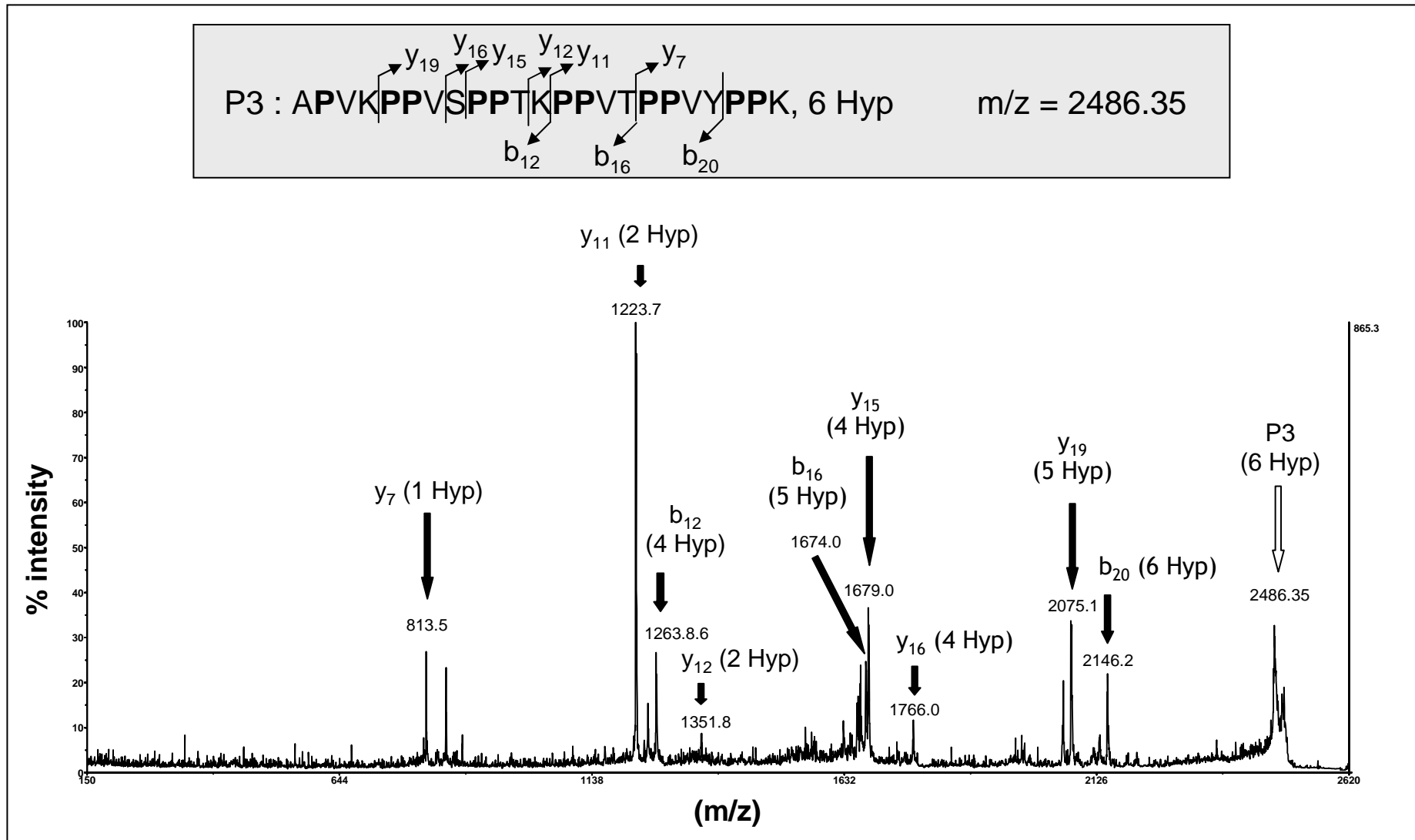


Figure S2C. MALDI-TOF/TOF MS/MS spectrum of the P3 peptide (m/z 2486.35, white arrow) of the AGP31 Pro-rich domain.

Fragmentation was carried out on the deglycosylated AGP31 P3 tryptic peptide obtained following gel excision of an HF sample (see Fig. 3B). Peaks corresponding to b and y fragment ions are labeled with black arrows and the number of Hyp predicted from the fragment masses is indicated. The fragmentation pattern is reported onto the sequence in which Pro residues possibly hydroxylated are in bold (in frame). The number of Hyp residues predicted within each fragment allowed partial Hyp location. Non-assigned peaks mostly corresponded to internal fragments.

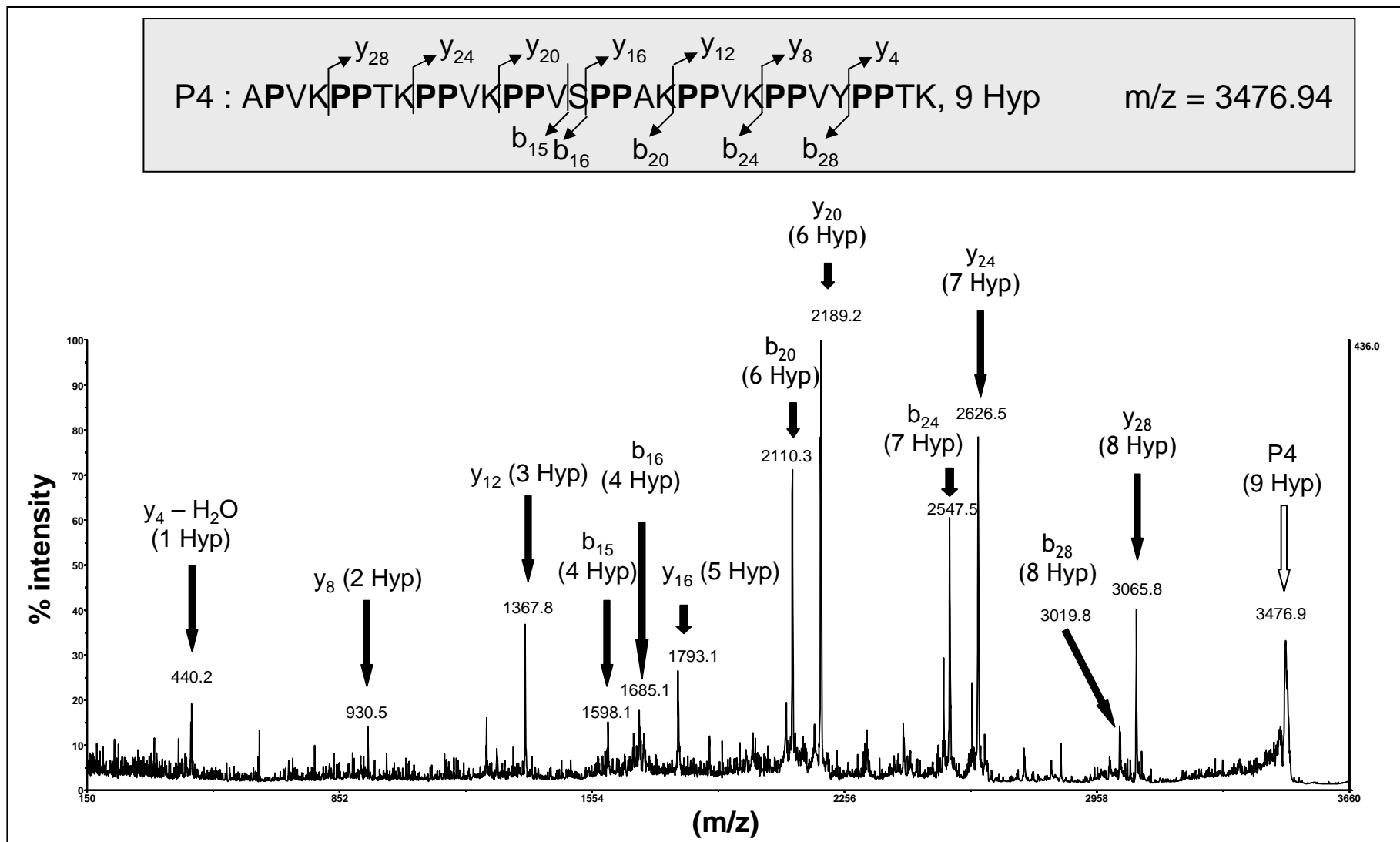


Figure S2D. MALDI-TOF/TOF MS/MS spectrum of the P4 peptide (m/z 3476.94, white arrow) of the AGP31 Pro-rich domain.

Fragmentation was carried out on the deglycosylated AGP31 P4 tryptic peptide obtained following gel excision of an HF sample (see Fig. 3B). Peaks corresponding to b and y fragment ions are labeled with black arrows and the number of Hyp predicted from the fragment masses is indicated. The fragmentation pattern is reported onto the sequence in which Pro residues possibly hydroxylated are in bold (in frame). The number of Hyp residues predicted within each fragment allowed partial Hyp location. Non-assigned peaks mostly corresponded to internal fragments.