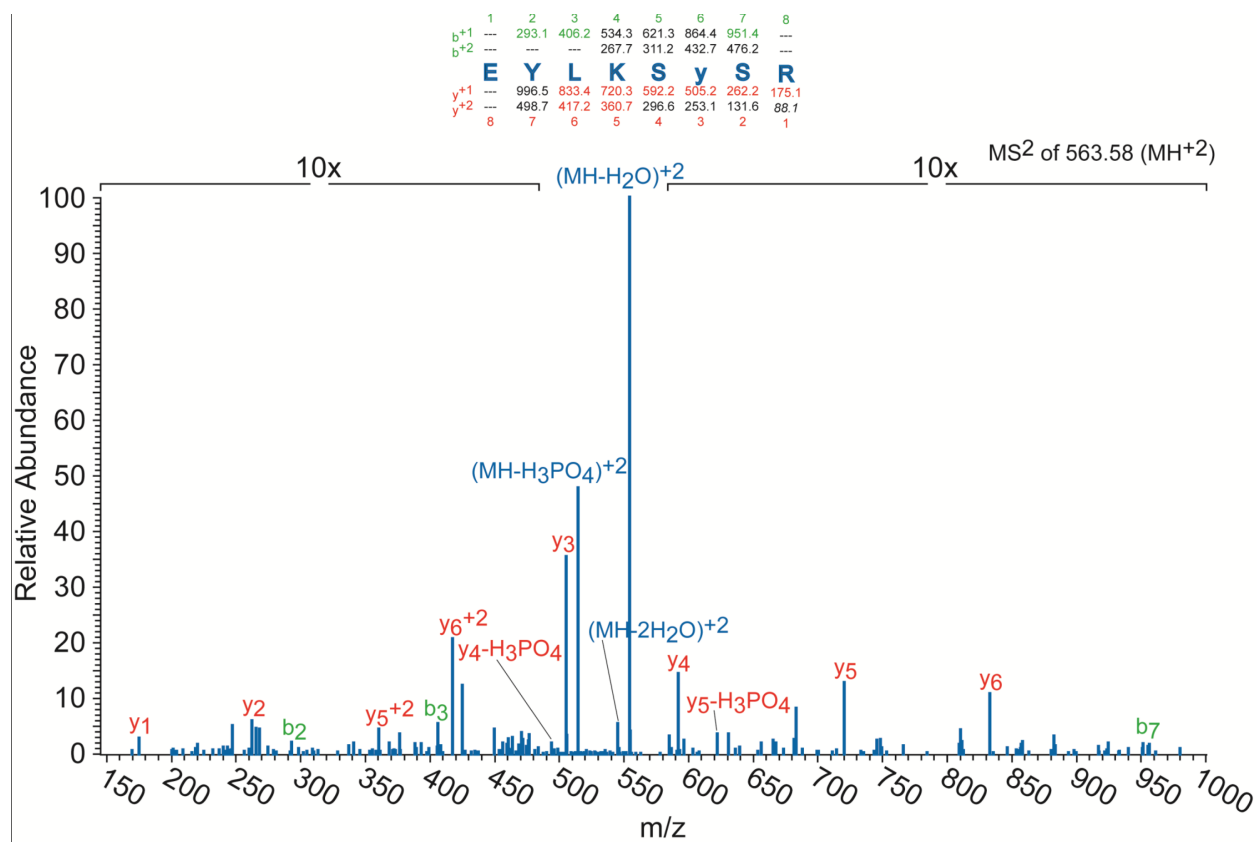


**Fig. S1**

MS<sup>2</sup> CID fragmentation pattern of the E<sub>9</sub>YLKs/ySR<sub>16</sub> peptide containing the newly identified phosphorylation site; the “/” indicates that, based upon the MS<sup>2</sup> CID fragmentation spectra displayed here and in Figure 2B, it cannot be determined if the single phosphorylation is located on Ser13 or Tyr14. The peptide sequence with its theoretical “b” and “y” ions are located above the spectra, with the ions that were used for identification denoted with colored highlights in the sequence and corresponding labels in the spectrum. Though it is ambiguous from the two fragmentation spectra whether the phosphorylation site is at Ser13 or Tyr14, the ion fragment masses listed above the spectra are for the phosphorylation to be at Tyr14 for the sake of simplicity in the display.



**Fig. S2**

MS<sup>2</sup> CID fragmentation pattern of the shorter synthetic peptide mimicking 212-228 amino acid region of P protein with phosphorylation at Ser226 residue. Corresponding ions were denoted as mentioned in the Fig. S1.

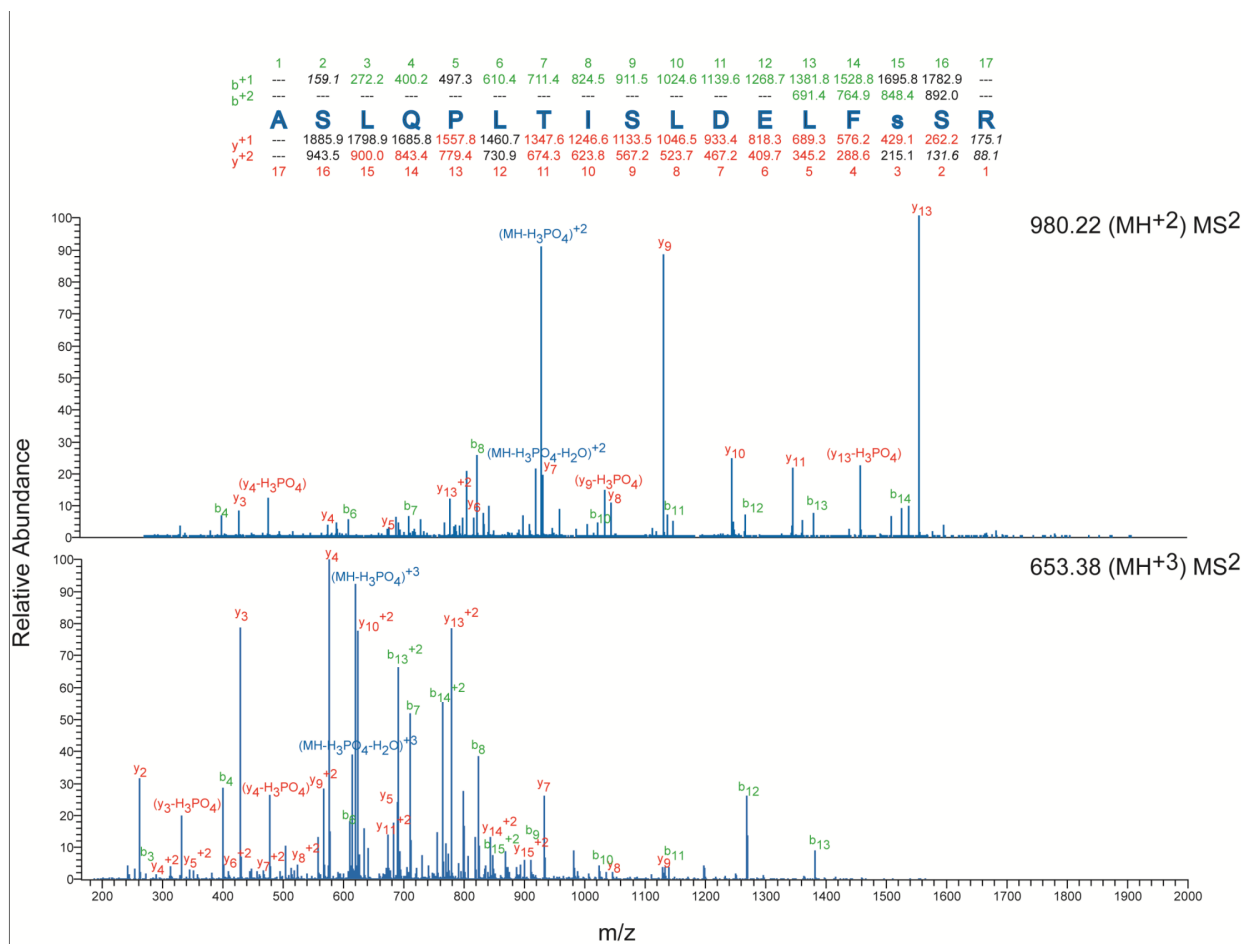


Fig. S3

MS<sup>2</sup> CID fragmentation pattern of the longer synthetic peptide mimicking 212-239 amino acid region of P protein with phosphorylation at Ser226 residue. Corresponding ions were denoted as mentioned in the Fig. S1.

