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The impact of chromatography and mass spectrometry on the analysis of protein phosphorylation sites

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The following passage on page 901 contains minor printing errors. The correct text is:

The example of the phosphoprotein standard β -casein demonstrates some of the difficulties one might have to expect in phosphorylation site analysis. Only the smaller phosphopeptide (amino acid residues 33–48, FQpSEEQ-QQTEDELQDK, m/z 2061.8290; SwissProt P02666) was detected, but was then missed by data-dependent HPLC-MS/MS in positive ion mode. Only SIM on the pre-determined m/z finally produced a suitable spectrum (Fig. 2). MALDI-MS is often used to identify phosphopeptide candidates for such specific fragmentation experiments [82]. The larger peptide (1–25, RELEELNVPGEIVEpSLpSpSpSEESITR, m/z 3122.2662) apparently stuck to the column material [60, 83], but even if eluted it would have been too large to be efficiently fragmented within the timeframe of a chromatographic peak.

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