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Example of Results Section from a Published Paper

The following information is excerpted from Mattapalli, H.; Monteith, W. B.; Burns, C. S.; Danell, A. S. *J. Am. Soc. Mass Spectrom.*, **2009**, *20*, 2199-2205. Notice information regarding the figure is written in paragraph form, and the figure is explicitly referred to in the paragraph. Results calculated from data in the figures also are presented in this paragraph; the text refers to an equation presented in a separate part of the paper, but you would tabulate your relevant data and show equations in the results section.

A 10 μM PC4 solution with one equivalent of zinc added was analyzed with nanoESI, shown in Figure 5(a). The average and standard deviation for the fraction of total peptide signal (Equation 1) arising from the PC4:Zn^{2+} pair was 43(±2)%. Using the estimated dissociation constant of 0.7 μM to calculate the fraction of peptide expected in the bound form, we arrive at the value of 77%. A 0.250 mL aliquot of that same PC4:Zn^{2+} solution was infused through the ESI emitter at a flow rate of 0.250 mL/hr for one hour with no ESI potential applied and no nebulizer or dry gas flowing. Sample was collected as described for the AAS experiments. This sample was then analyzed with nanoESI (Figure 5(b)), and the PC4:Zn^{2+} signal comprised only 17(±3)% of the total peptide signal in the mass spectra.

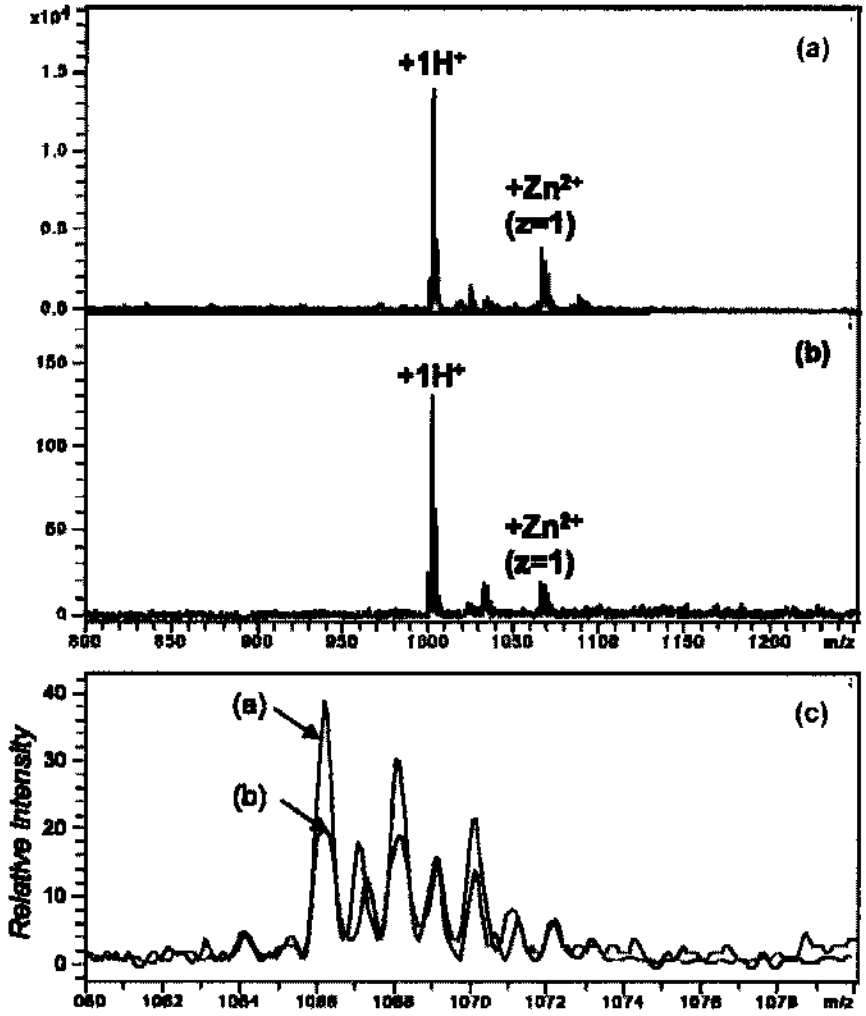

Figure 5. Mass spectra of 1:1 (10 μM each) PC4:Zn^{2+} using nanoESI (a) before infusion through the ESI emitter and (b) after infusion. A magnified view of the +Zn^{2+} peaks from (a) and (b) is shown in (c).