

In the article, "A Collision Cross-Section Database of Singly-Charged Peptide Ions" by Lei Tao, Janel R. McLean, John A. McLean, and David H. Russell which was published in the July issue, Vol. 18, No. 7, pages 1232-1238, [Figures 1 and 2](#) failed to print in color. The publisher regrets the error. The corrected figures are shown below, with their corresponding figure legends.

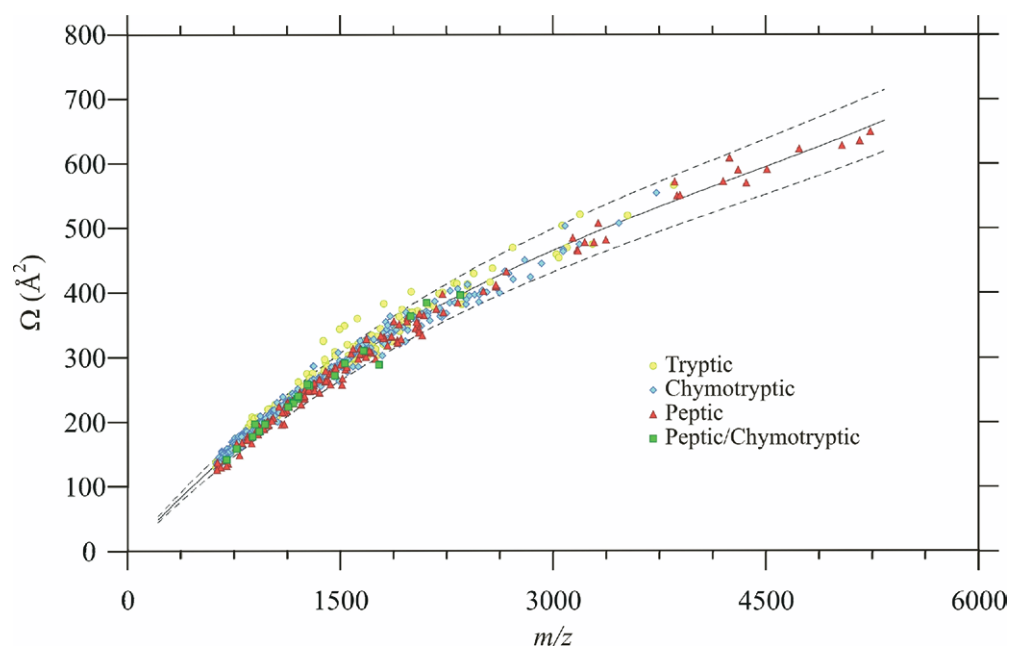


Figure 1. Plot of ion-neutral collision cross-sections versus m/z for 607 $[M + H]^+$ peptide ions. The solid line corresponds to a third-order polynomial fit to the data ($R^2 = 0.988$) and corresponds to the average mobility-mass correlation ($y = 2.81 \cdot 10^{-9}x^3 - 3.55 \cdot 10^{-5}x^2 + 2.32 \cdot 10^{-1}x + 41.91$, $R^2 = 0.988$). The dashed lines represent $\pm 7\%$ deviation from the fit.

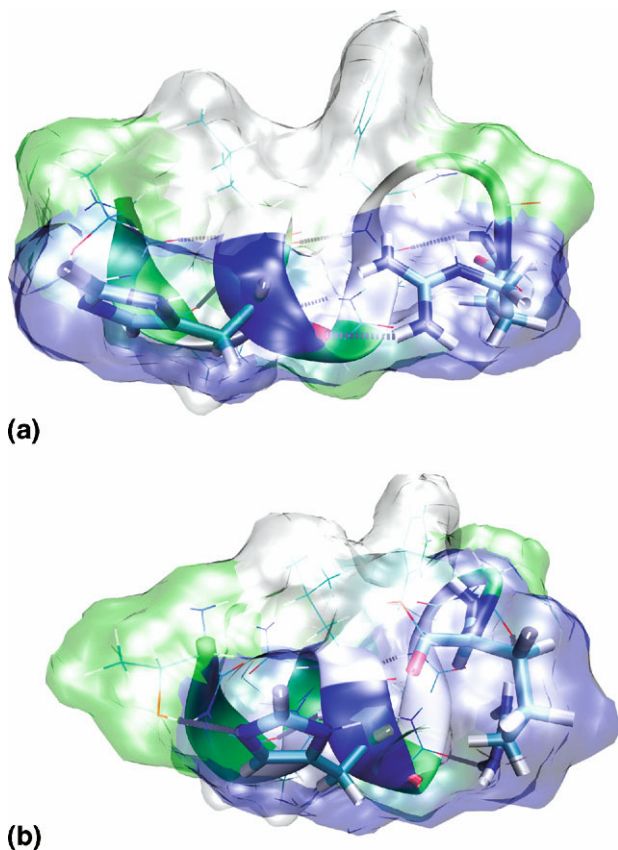


Figure 2. Proposed structures for TGPNLHGLFGR $[M + H]^+$ ions consistent with the ion-neutral collision cross-sections measured by (a) MALDI and reported for (b) ESI [18], respectively. The images are produced using VMD (UIUC, Urbana-Champaign, IL). The colors represent different types of residues; white denotes nonpolar residues, green denotes polar residues, blue denotes basic residues, and red denotes acidic residues. α -helical regions are given as coiled ribbons.