

The inner membrane histidine kinase EnvZ senses osmolality via helix-coil transitions in the cytoplasm

Loo Chien Wang, Leslie K Morgan, Pahan Godakumbura, Linda J Kenney & Ganesh S Anand

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In the Supplementary Information section of the above paper, the mass/charge (m/z) values of peptides in Supplementary Tables S1 and S2 (for a subset of peptides with $z > 1$) were erroneously reported.

An equation $\frac{m}{z} = \frac{(M+m_{H^+})}{z}$ was incorrectly used for computing the m/z (Eqn. 1).

The correct equation is: $\frac{m}{z} = \frac{(M+zm_{H^+})}{z}$ (Eqn. 2), where M is the mass of the peptide, m_{H^+} is the mass of a proton (~1), and z is the charge state of the peptide.

Use of equation 1 or 2 does not alter the m/z values of the singly charged species ($z = 1$) reported. However for peptides with $z > 1$, the correct mass/charge would be marginally greater. For

instance, a peptide with a mass (M) of 1515.7212 Da and $z = 2$ will show a m/z value of 758.86 for the 2+ charged ion based on Eqn. 2, instead of 758.36 reported in Supplementary Table S1. This subtle shift in value of the mass/charge for a subset of the peptides due to the error is regretted.

In the Supplementary Information to this Corrigendum, we provide the corrected tables. These errors in computed m/z values do not alter any of the results, conclusions, or findings originally presented in the main paper or Supplementary Information. The subtle shift in m/z values does not change the peptide identification or alter the deuterium exchange values calculated for all the peptides across all m/z listed in the tables.