Corrigendum

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

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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.