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Author Correction: Antimicrobial Peptide Potency is Facilitated by Greater Conformational Flexibility when Binding to Gram-negative Bacterial Inner Membranes

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This Article contains errors in the C and D panels of Figure 5 and in Supplementary Figures S9 and S10 where mislabelling occurred. The correct Figures 5, S9 and S10 appear below as Figures 1, 2 and 3 respectively.

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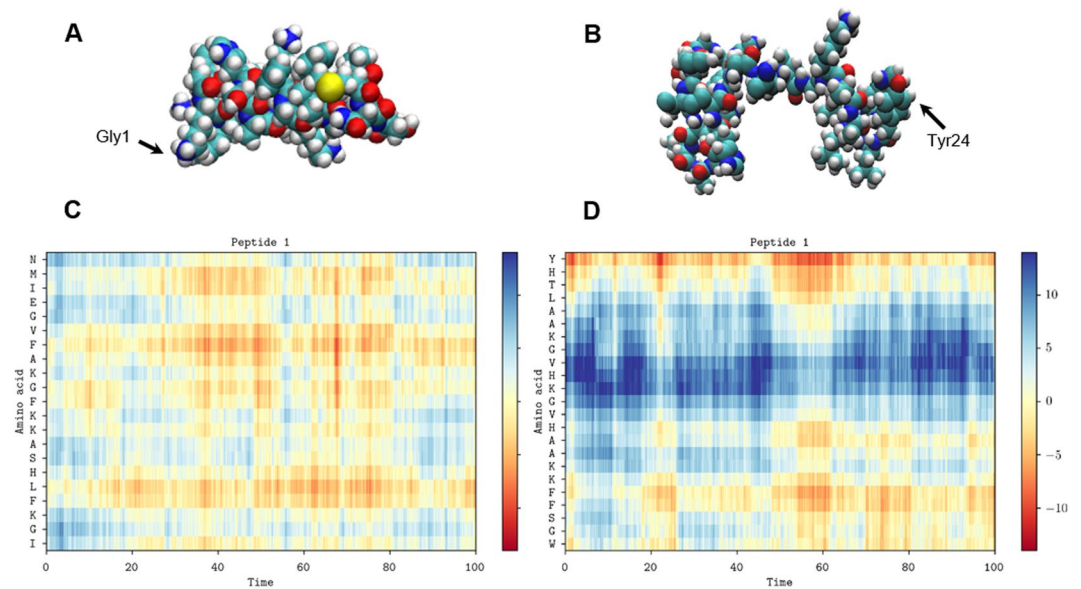


Figure 1. Conformational flexibility and alignment. Space-filling models of magainin 2 (A) and pleurocidin (B) showing representative conformations in the membrane of one of eight peptides in each simulation at 100 ns. The distance (Å) to the upper membrane leaflet phosphate plane of each amino acid in the representative peptide is plotted over 100 ns for magainin 2 (C) and pleurocidin (D).

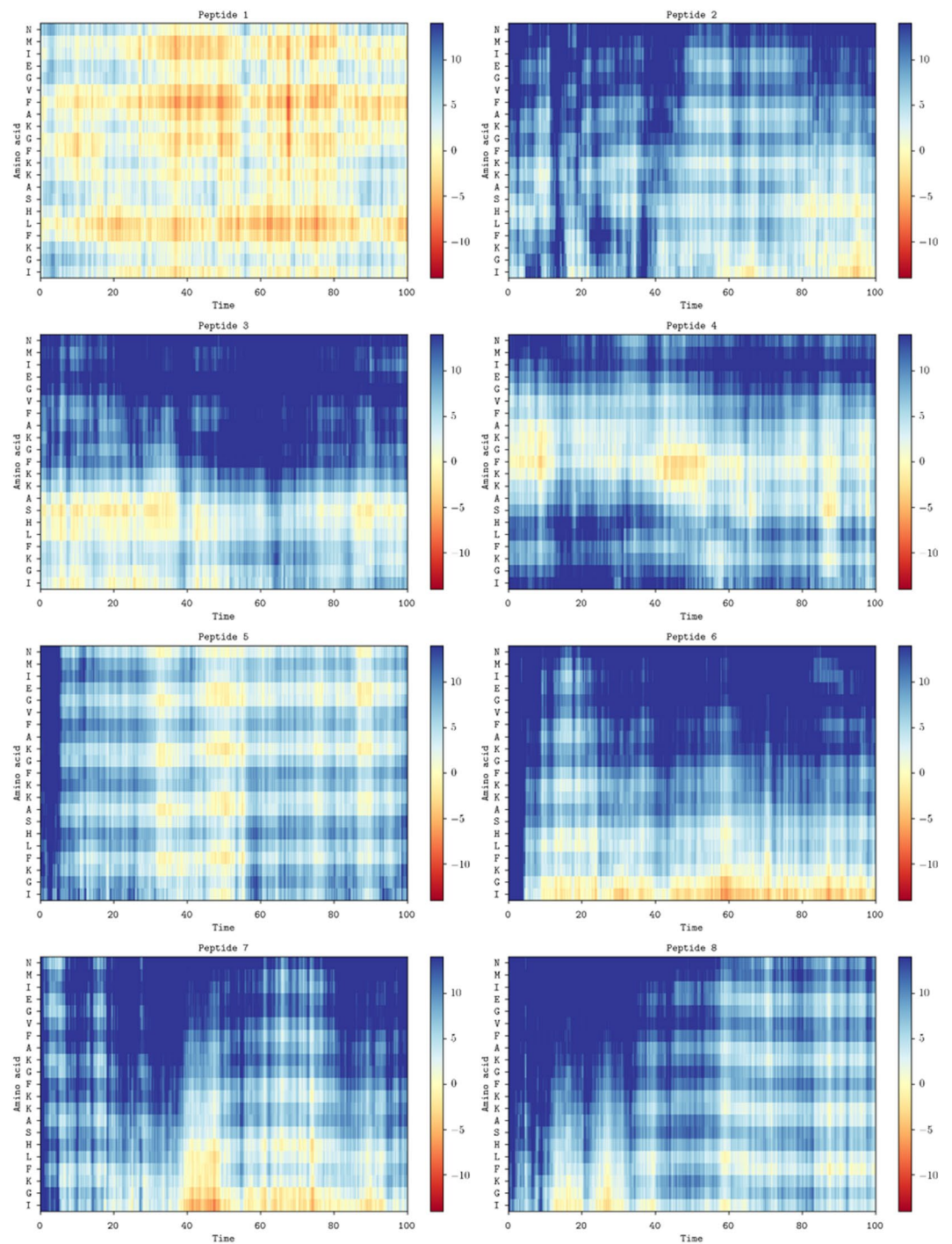


Figure 2.

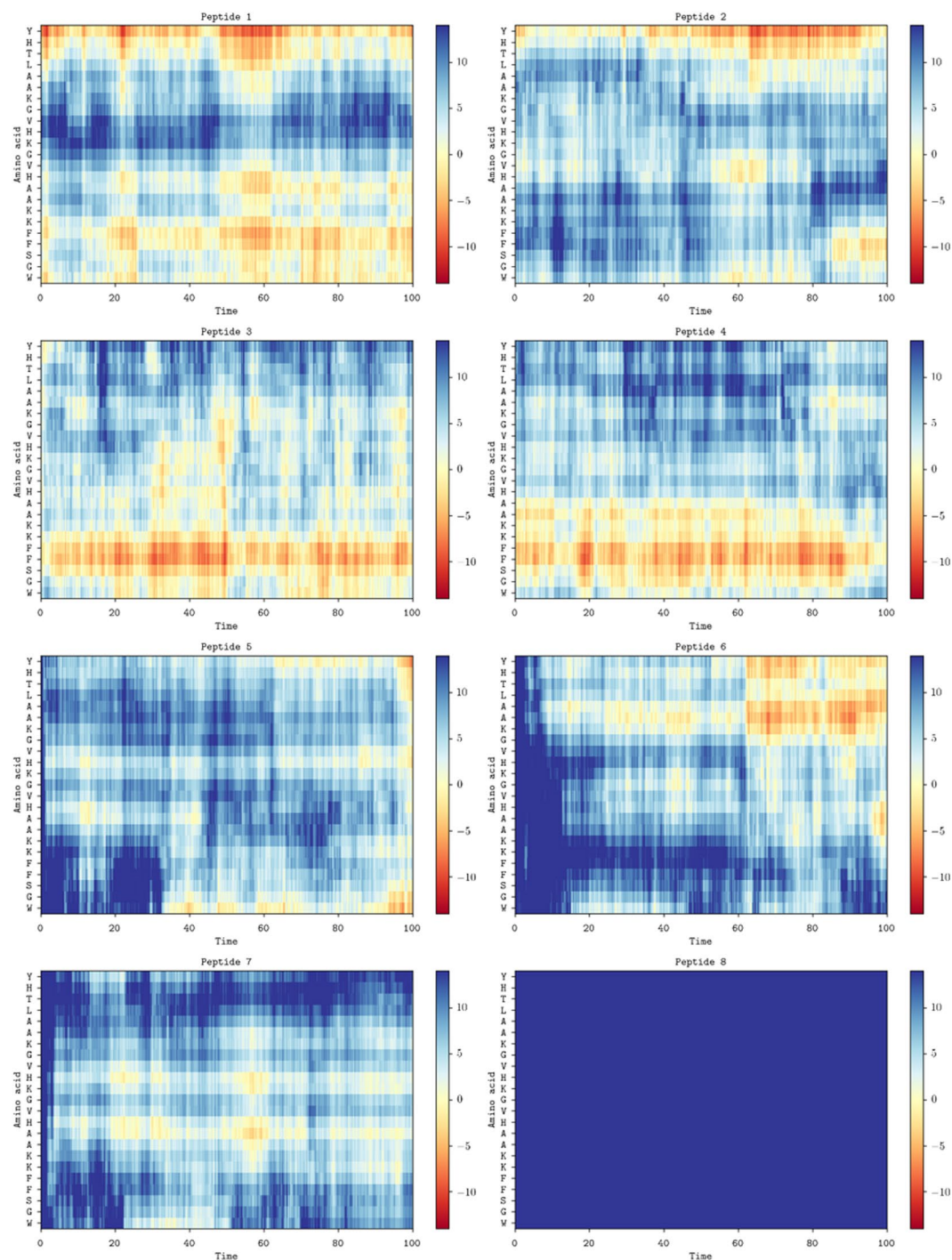


Figure 3.

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