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Corrigendum: Computational analysis of Ayurvedic metabolites for potential treatment of drug-resistant *Candida auris*

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A Corrigendum on

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In the published article, there was an error in [Figure 8](#) as published. [A part of the figure was not labeled]. The corrected [Figure 8](#) and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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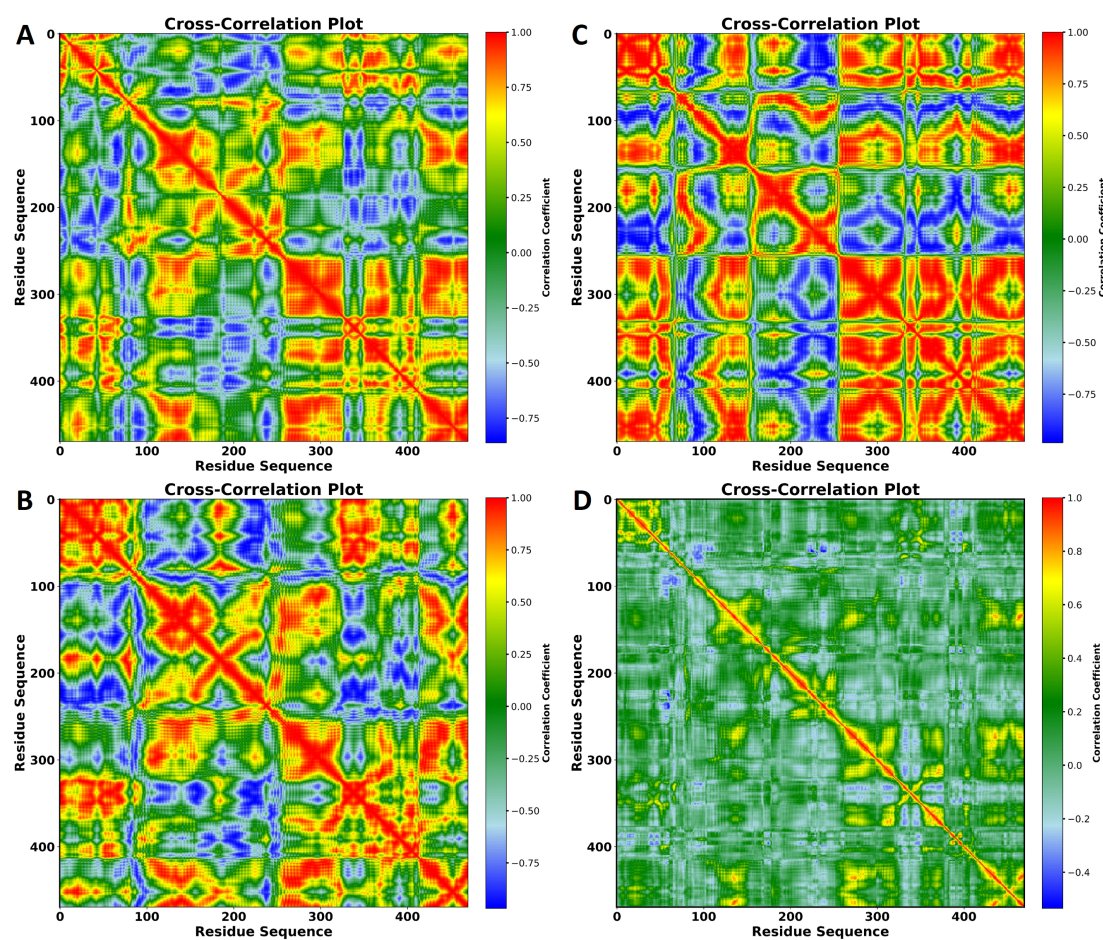


FIGURE 8

Cross-correlation plots of residue motions in the protein in complexes with (A) VNI, (B) trans-p-coumaric acid, (C) MCPHB, and (D) Cross-correlation plot of residue motions in the apoprotein. The x- and y-axes represent the residue sequence, and the color scale on the right indicates the correlation coefficients, ranging from -1 (anti-correlated, blue) to +1 (positively correlated, red). These plots show the degree of correlated and anti-correlated motions between residues throughout the 100 ns MD simulation.