Comparative genomics and proteomics analysis of phages infecting multi-drug resistant *Escherichia coli* O177 isolated from cattle faeces

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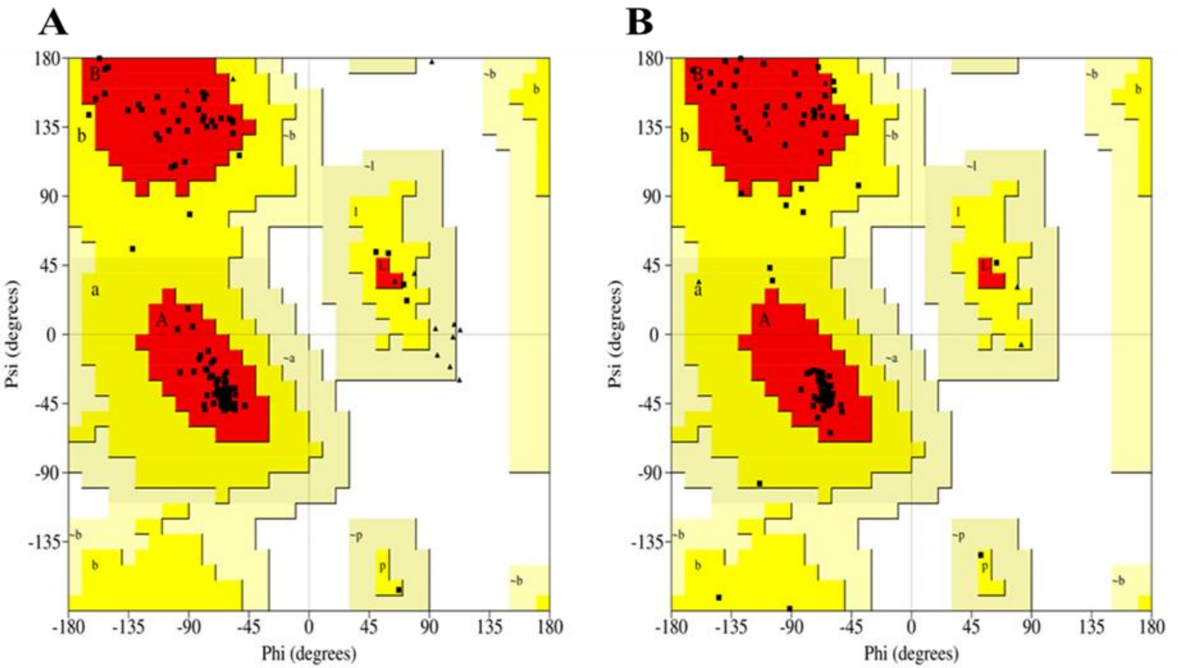
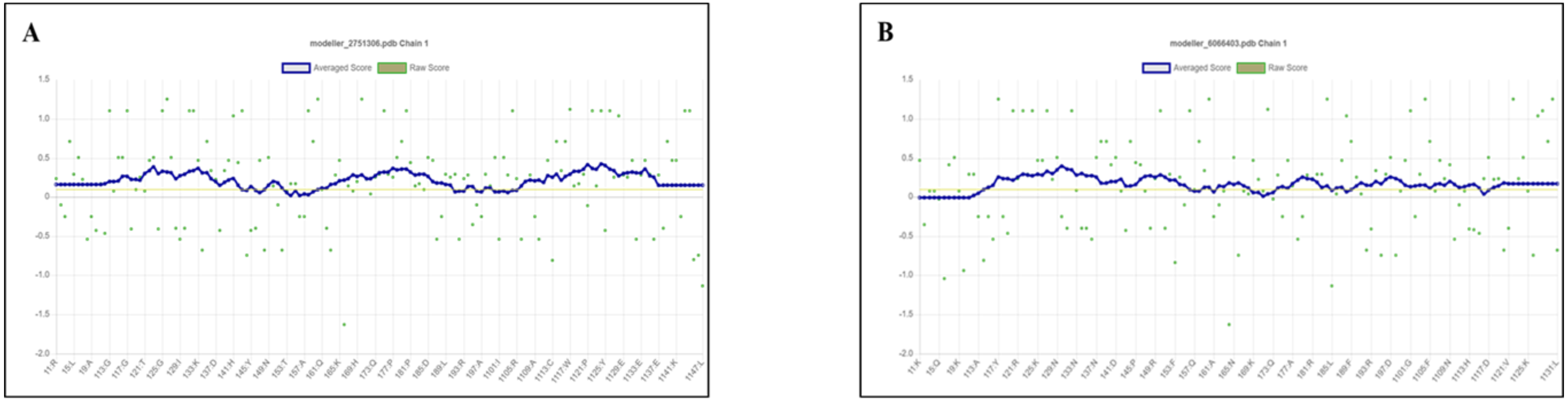
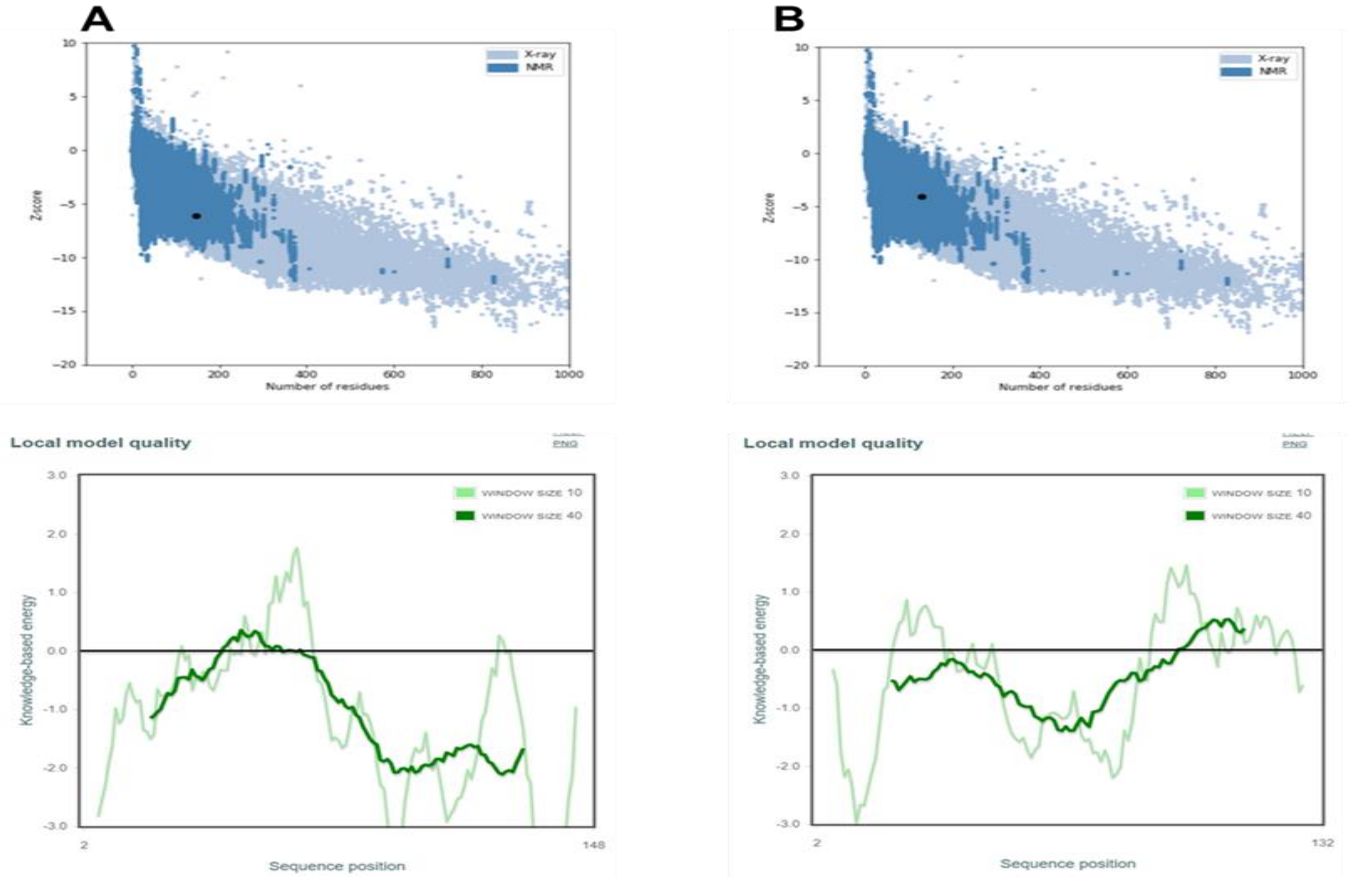


Supplementary Figure 1: Ramachandran plot depicting the phi-psi torsion angles for all the residues of the models (**A** = lysozyme, and **B** = endolysin proteins) predicted by PROCHECK. Red colour represents the most favoured region while yellow colour represents the allowed region, and white colour represents disallowed region. The A, B, L: Most favoured regions; a, b, l: additional allowed regions; ~a, ~b, ~l, ~p: generously allowed regions.



Supplementary Figure 2: The VERIFY_3D plot showing the models (**A** = lysozyme, and **B** = endolysin proteins). The blue line represents the average score, which is the standard to judge the quality of the structure; it is considered as a high-quality model when more than 80 % of the residues have 3D-D score of higher than 0.2.

The VERIFY_3D plot for.



Supplementary Figure 3: ProSA sever Z-score of the final models (**A** = lysozyme, **B** = endolysin and, **C**= tail fiber proteins). The Z-score plots (Upper part) shows the Z-score (black dots). The energy plot (lower part) as computed by PROSA server.