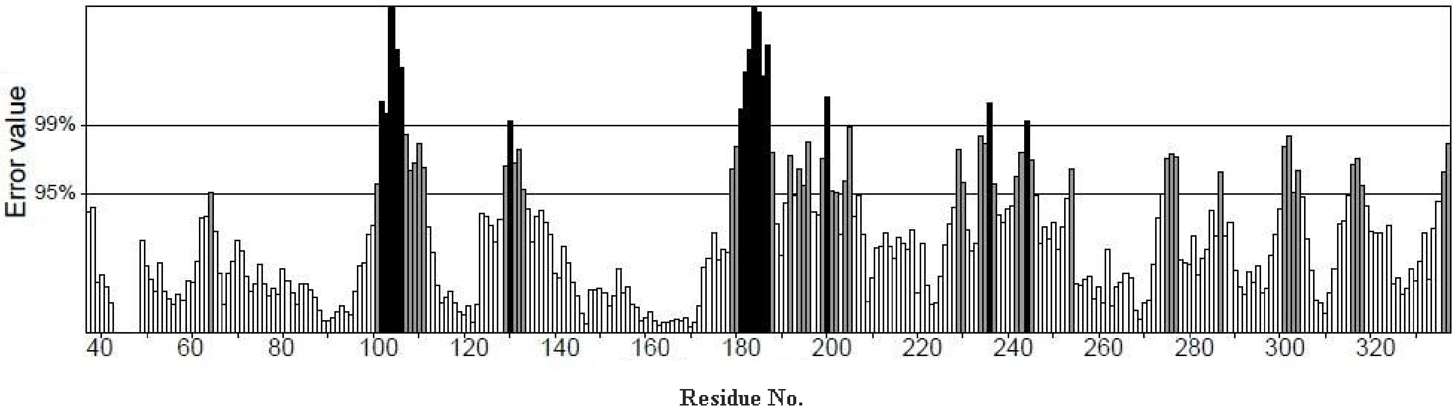
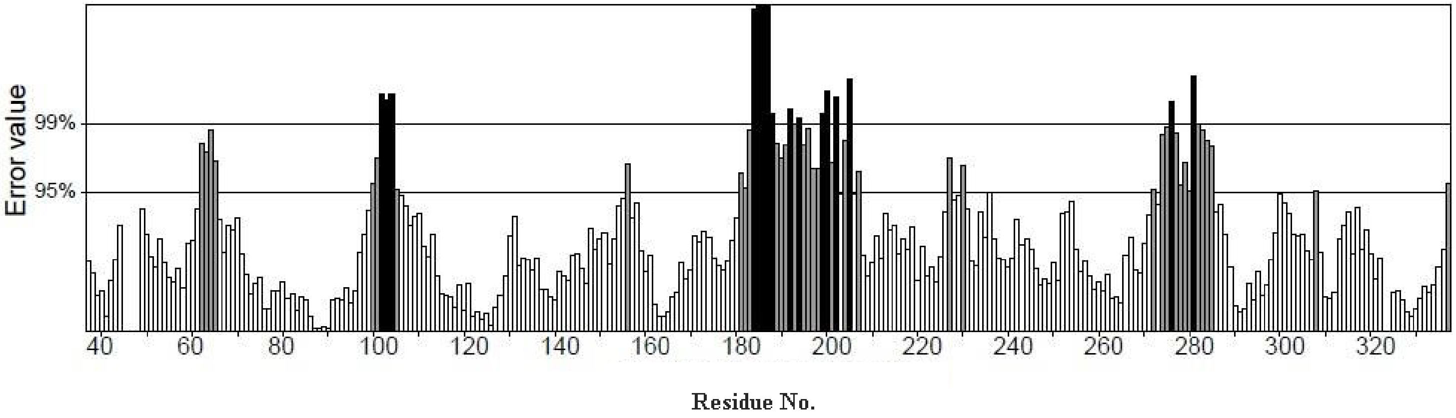
**(A)** **Overall quality factor: 78.778**



**(B)** **Overall quality factor: 82.051**



**Supplementary Fig. 8.** The overall quality of non-bonded interactions between atoms of wild type kir6.2 (A) and mutant kir6.2 (B) models are depicted residue wise along X-axis with respect to error function along Y-axis. Two lines drawn on error axis to indicate the confidence percentage with which it is possible to reject regions that exceed that error value.