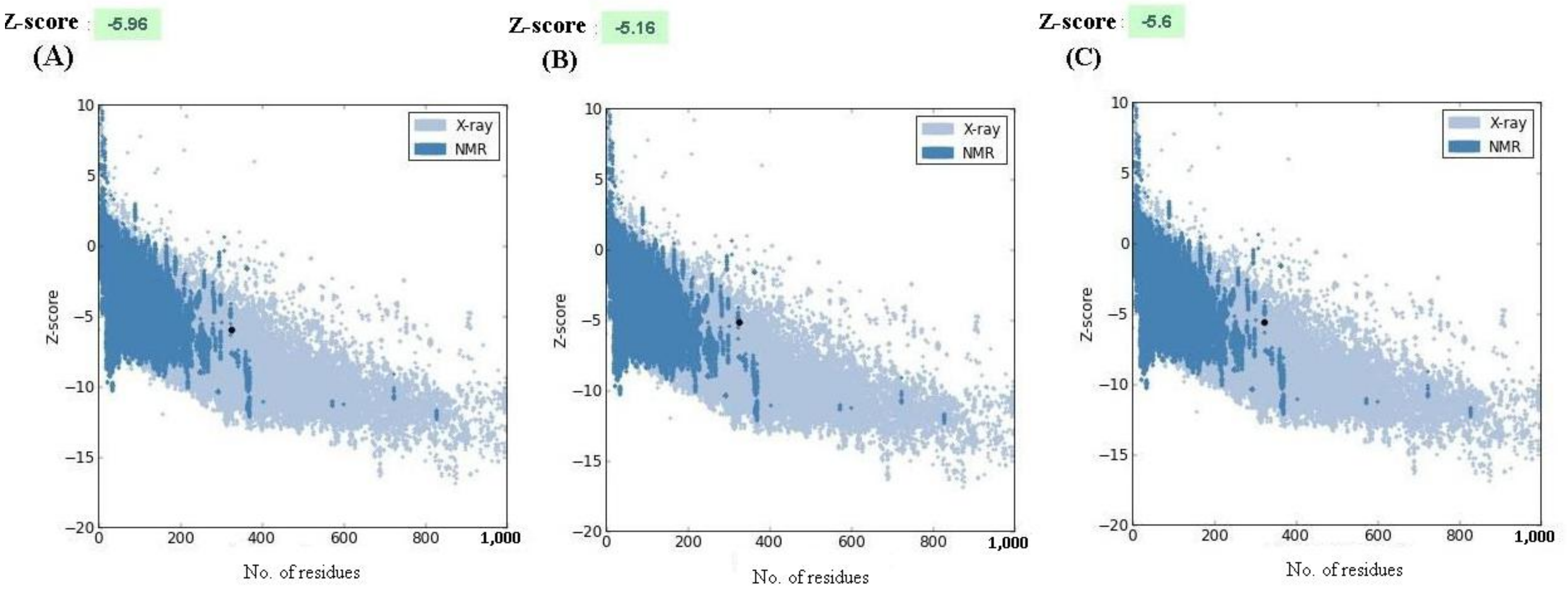

**Supplementary Fig. 2.**The Z-score are plotted for kir6.2 current model (A), second existing model of kir6.2 models (B), and third existing model of kir6.2 (C) indicate overall model quality. The black dot spot in the picture specifies the current predicted kir6.2 model is in the range of Z-scores of all experimentally determined protein chains in current PDB.