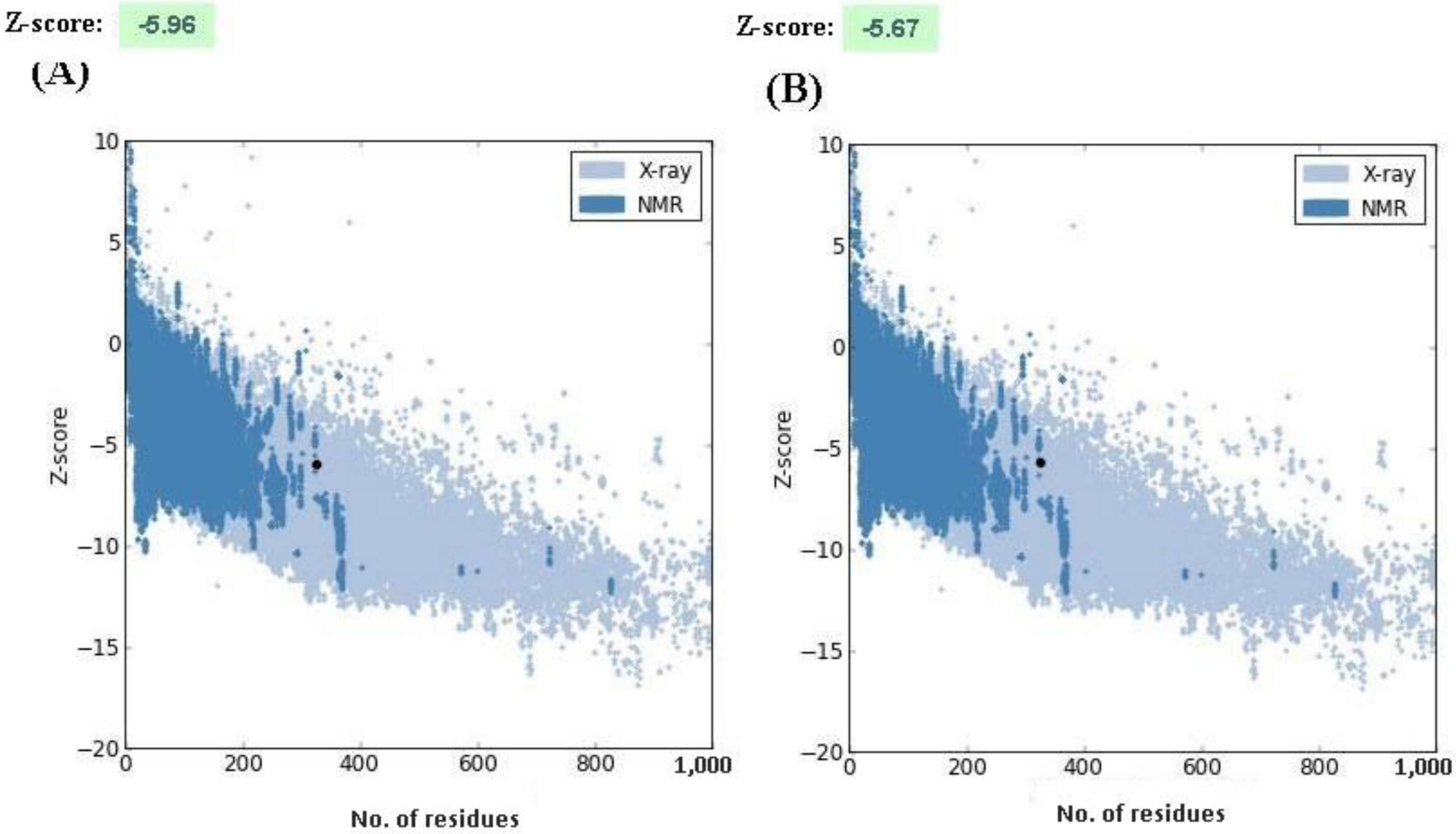

Supplementary Fig. 6. The z-score are plotted for wild type kir6.2 (A) and mutant type kir6.2 (B) models indicate overall model quality. The black dot spot in the picture specifies the kir6.2 model is in the range of z-scores of all experimentally determined protein chains in current PDB.