



Supplementary Fig. 3. The overall quality of non-bonded interactions between atoms of current model of kir6.2 (A), second existing kir6.2 model (B), and third existing kir6.2 model (C) 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.