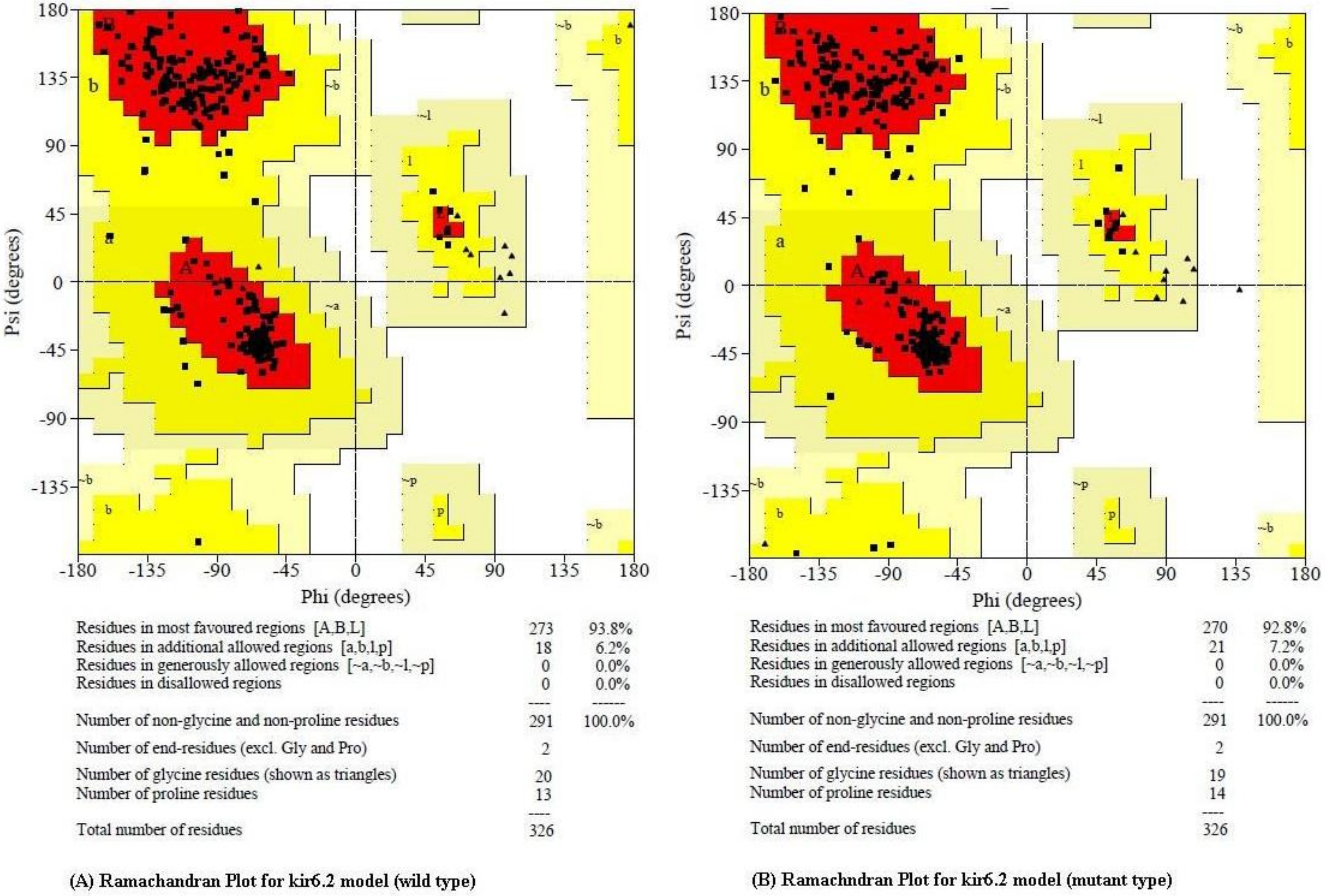

Residues in most favoured regions [A,B,L]	273	93.8%
Residues in additional allowed regions [a,b,l,p]	18	6.2%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	291	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	20	
Number of proline residues	13	

Total number of residues	326	

(A) Ramachandran Plot for kir6.2 model (wild type)

Residues in most favoured regions [A,B,L]	270	92.8%
Residues in additional allowed regions [a,b,l,p]	21	7.2%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
	----	------
Number of non-glycine and non-proline residues	291	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	19	
Number of proline residues	14	

Total number of residues	326	

(B) Ramachndran Plot for kir6.2 model (mutant type)

Supplementary Fig. 7. The backbone folding patterns plotted for wild type kir6.2 (A) and mutant type kir6.2 (B) models. Each black dot spot corresponds to one amino acid residue of kir6.2 chain. On the plot most favoured regions, additional allowed regions, generously allowed regions and disallowed regions are shown in red, yellow, light yellow and white color respectively.