



Figure S1. Ramachandran plot analysis of modeled Human  $\beta$ -tubulin (TBB5\_HUMAN) using MODELLER. Here, red region indicates favored region, yellow region for allowed and light yellow shows generously allowed region and white for disallowed region. Phi and Psi angles determine torsion angles.

Table S2. Ramachandran plot statistics of modeled Human  $\beta$ -tubulin using MODELLER.

Plot statistics		
Residues in most favoured regions [A,B,L]	337	87.1%
Residues in additional allowed regions [a,b,l,p]	45	11.6%
Residues in generously allowed regions [ $\sim$ a, $\sim$ b, $\sim$ l, $\sim$ p]	4	1.0%
Residues in disallowed regions	1	0.3%
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Number of non-glycine and non-proline residues	387	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	35	
Number of proline residues	20	
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Total number of residues	444	