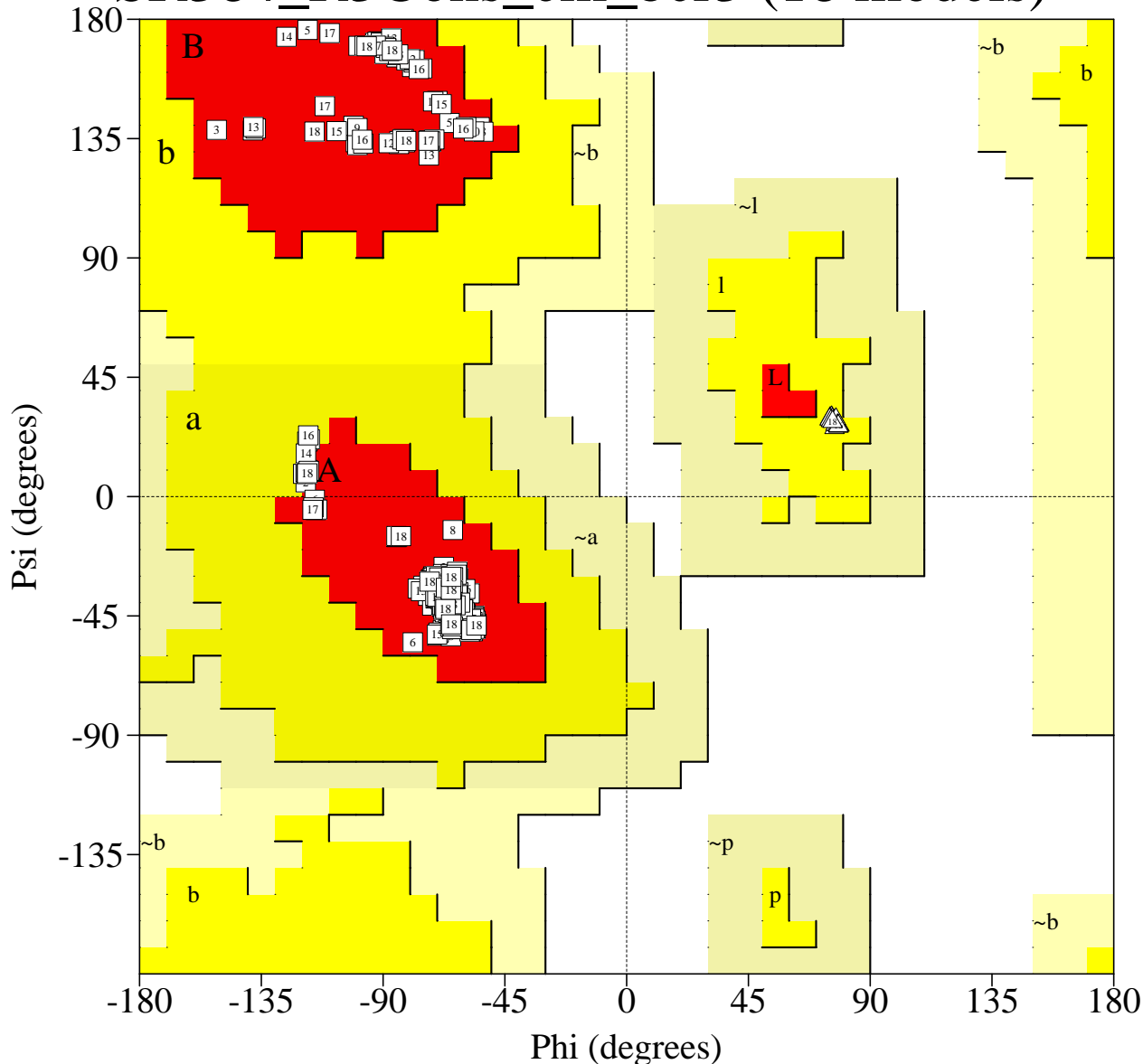


Ramachandran Plot

SR384_R3Cons_em_bcr3 (18 models)**



Plot statistics

Residues in most favoured regions [A,B,L]	645	99.5%
Residues in additional allowed regions [a,b,l,p]	3	0.5%
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	648	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	18	
Number of proline residues	0	

Total number of residues	666	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.
Model numbers shown inside each data point.