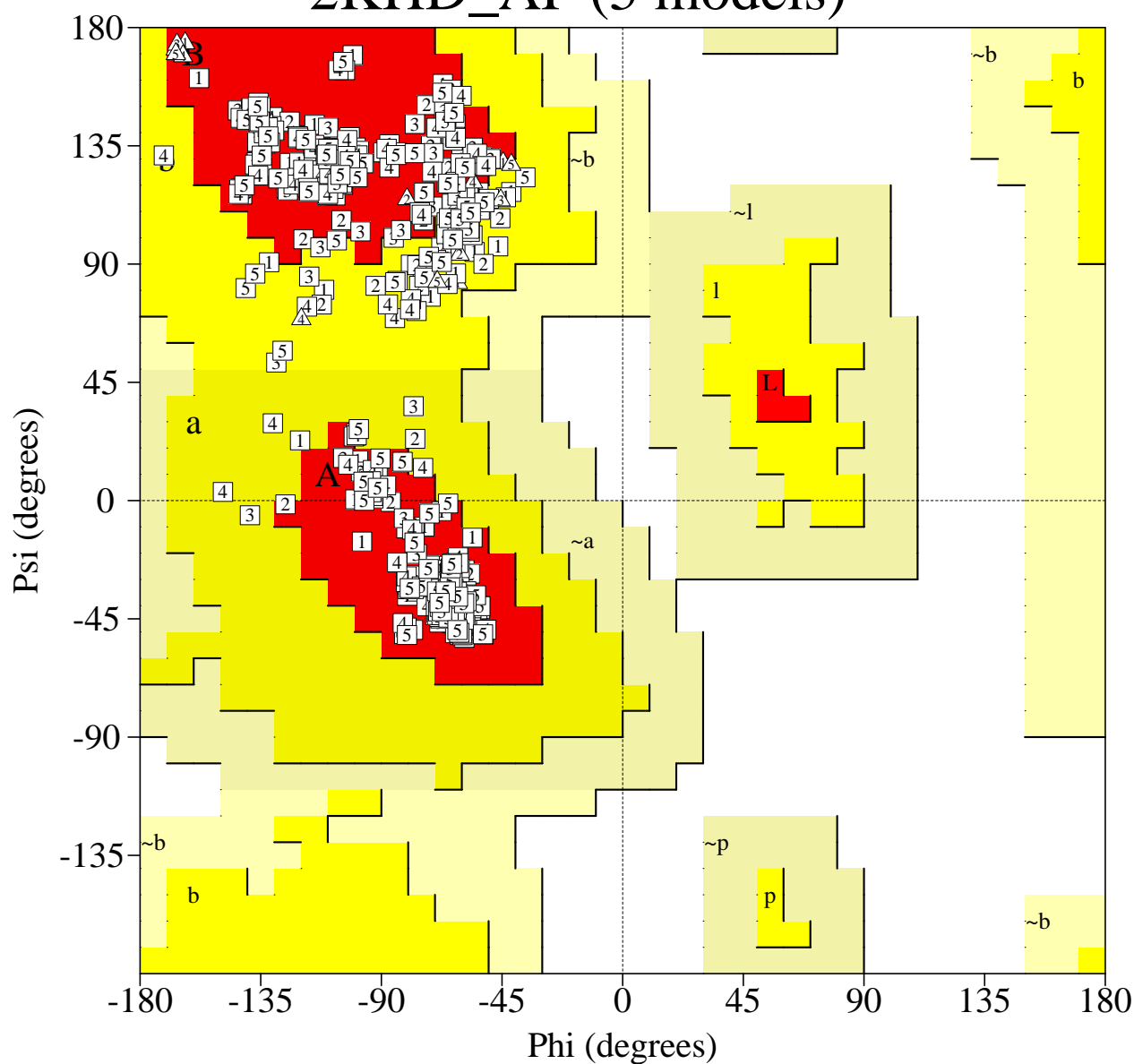


Ramachandran Plot

2KHD_AF (5 models)**



Plot statistics

Residues in most favoured regions [A,B,L]	395	84.9%
Residues in additional allowed regions [a,b,l,p]	70	15.1%
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	465	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	20	
Number of proline residues	5	

Total number of residues	490	

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.