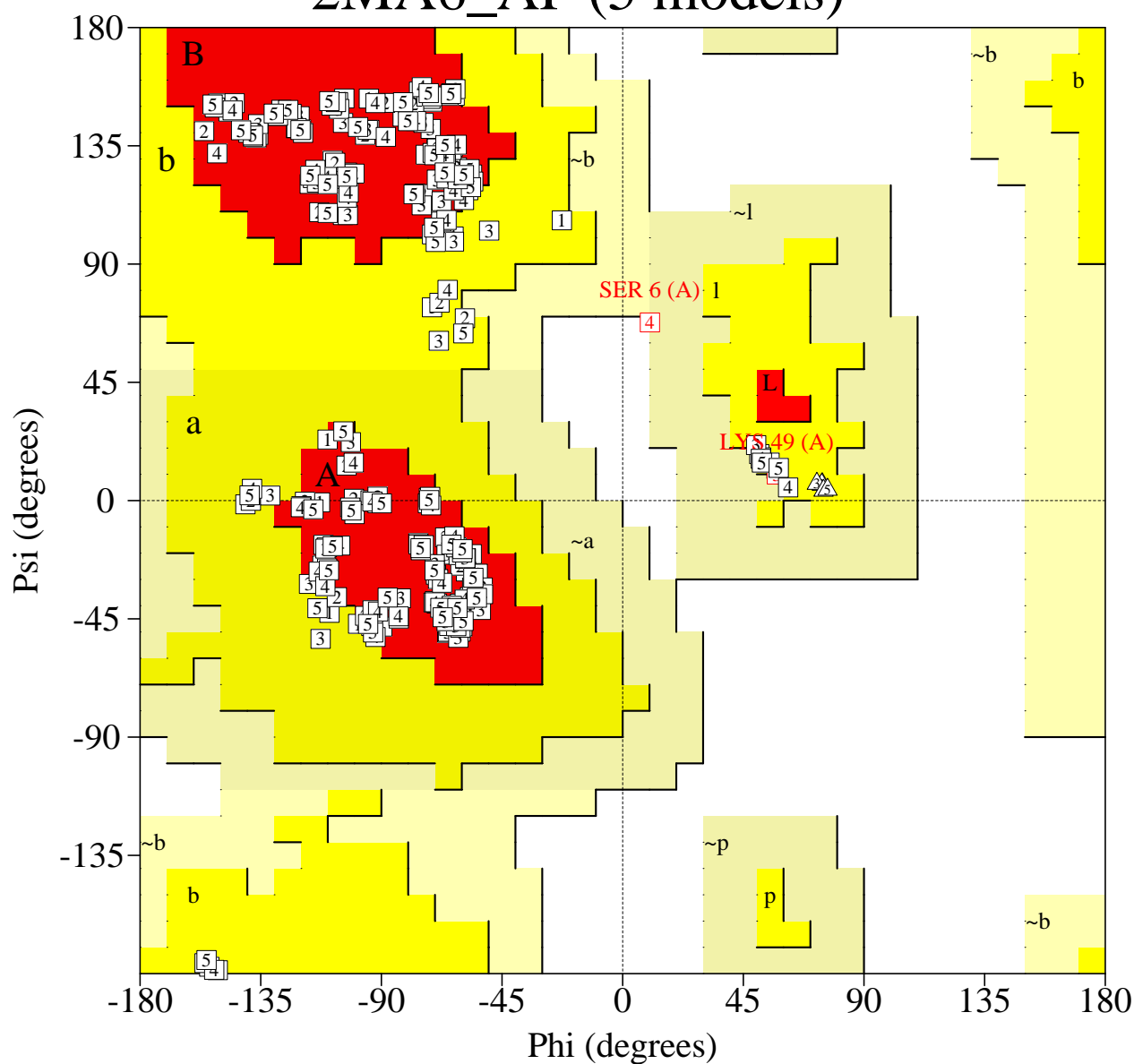


Ramachandran Plot

2MA6_AF (5 models)**



Residues in most favoured regions [A,B,L]	219	84.2%
Residues in additional allowed regions [a,b,l,p]	39	15.0%
Residues in generously allowed regions [~a,~b,~l,~p]	2	0.8%
Residues in disallowed regions	0	0.0%
	----	----
Number of non-glycine and non-proline residues	260	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	5	
Number of proline residues	20	

Total number of residues	285	

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.