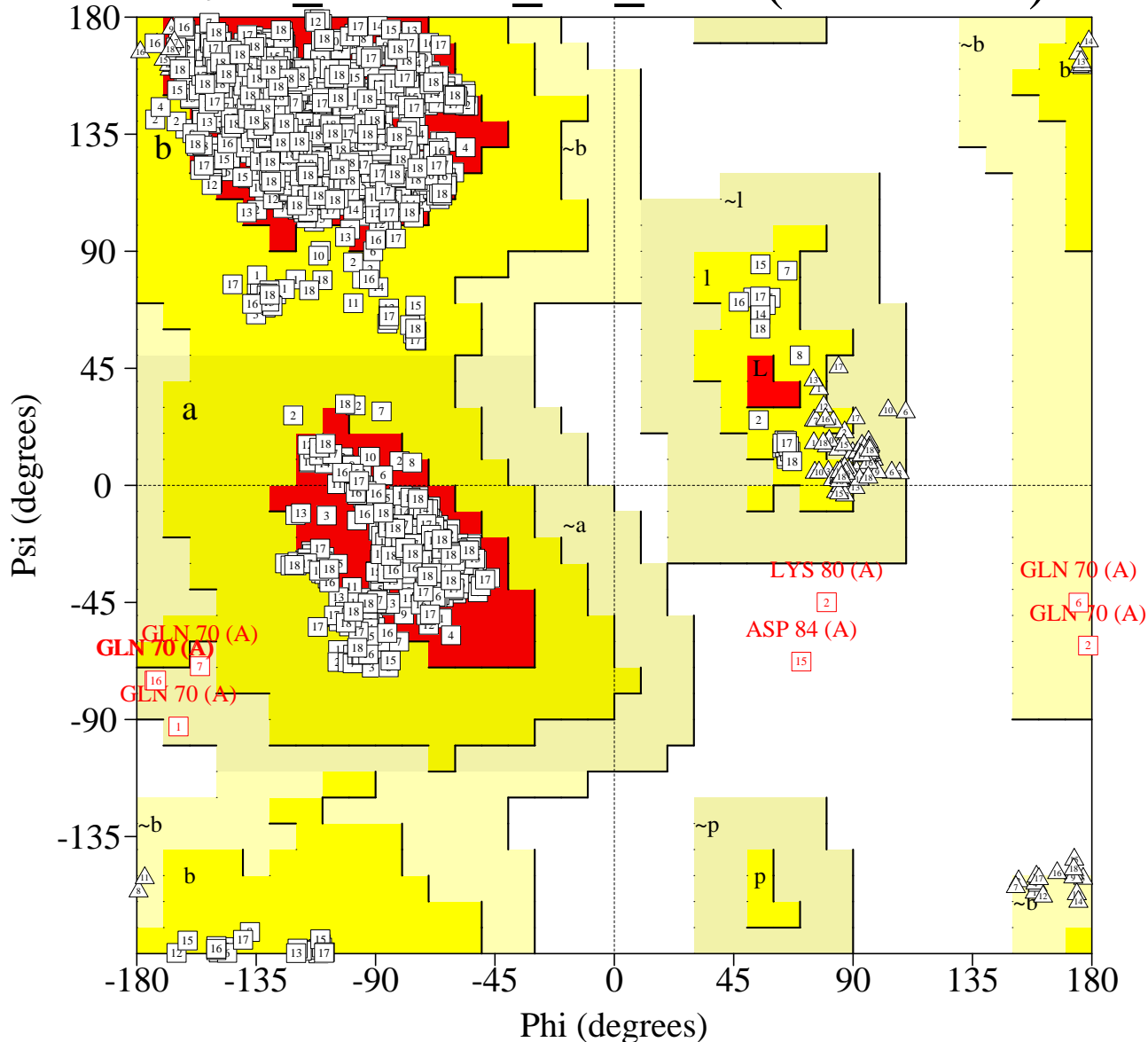


Ramachandran Plot

HR1958_R3Cons_em_bcr3 (18 models)**



Plot statistics

Residues in most favoured regions [A,B,L]	1950	91.0%
Residues in additional allowed regions [a,b,l,p]	184	8.6%
Residues in generously allowed regions [-a,-b,-l,-p]	6	0.3%
Residues in disallowed regions	2	0.1%
	----	-----
Number of non-glycine and non-proline residues	2142	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	108	
Number of proline residues	90	
	----	-----
Total number of residues	2340	

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.