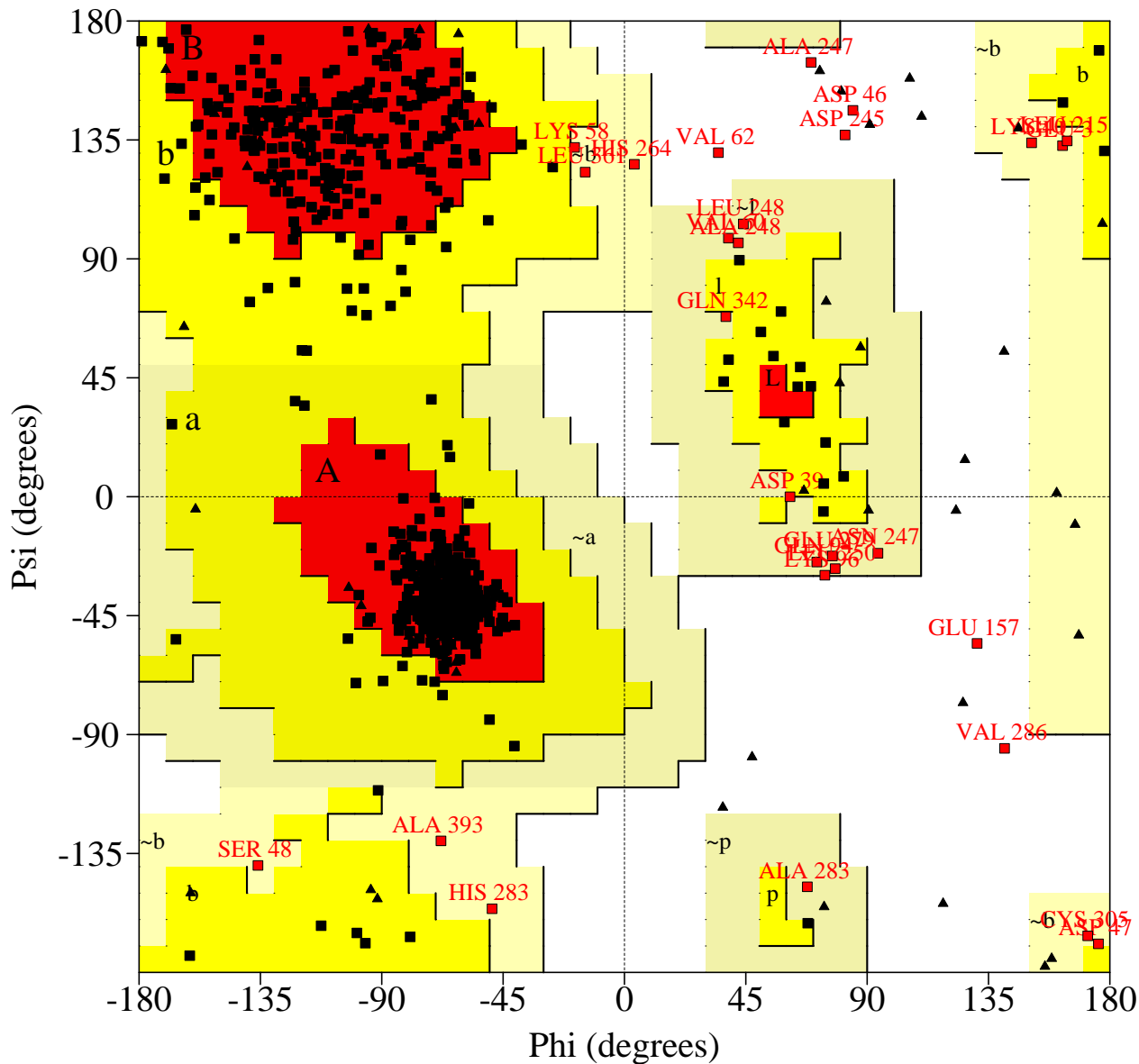


# Ramachandran Plot



### Plot statistics

Residues in most favoured regions [A,B,L]	664	87.8%
Residues in additional allowed regions [a,b,l,p]	64	8.5%
Residues in generously allowed regions [-a,-b,-l,-p]	22	2.9%
Residues in disallowed regions	6	0.8%
-----		
Number of non-glycine and non-proline residues	756	100.0%
Number of end-residues (excl. Gly and Pro)	4	
Number of glycine residues (shown as triangles)	67	
Number of proline residues	41	
-----		
Total number of residues	868	

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.