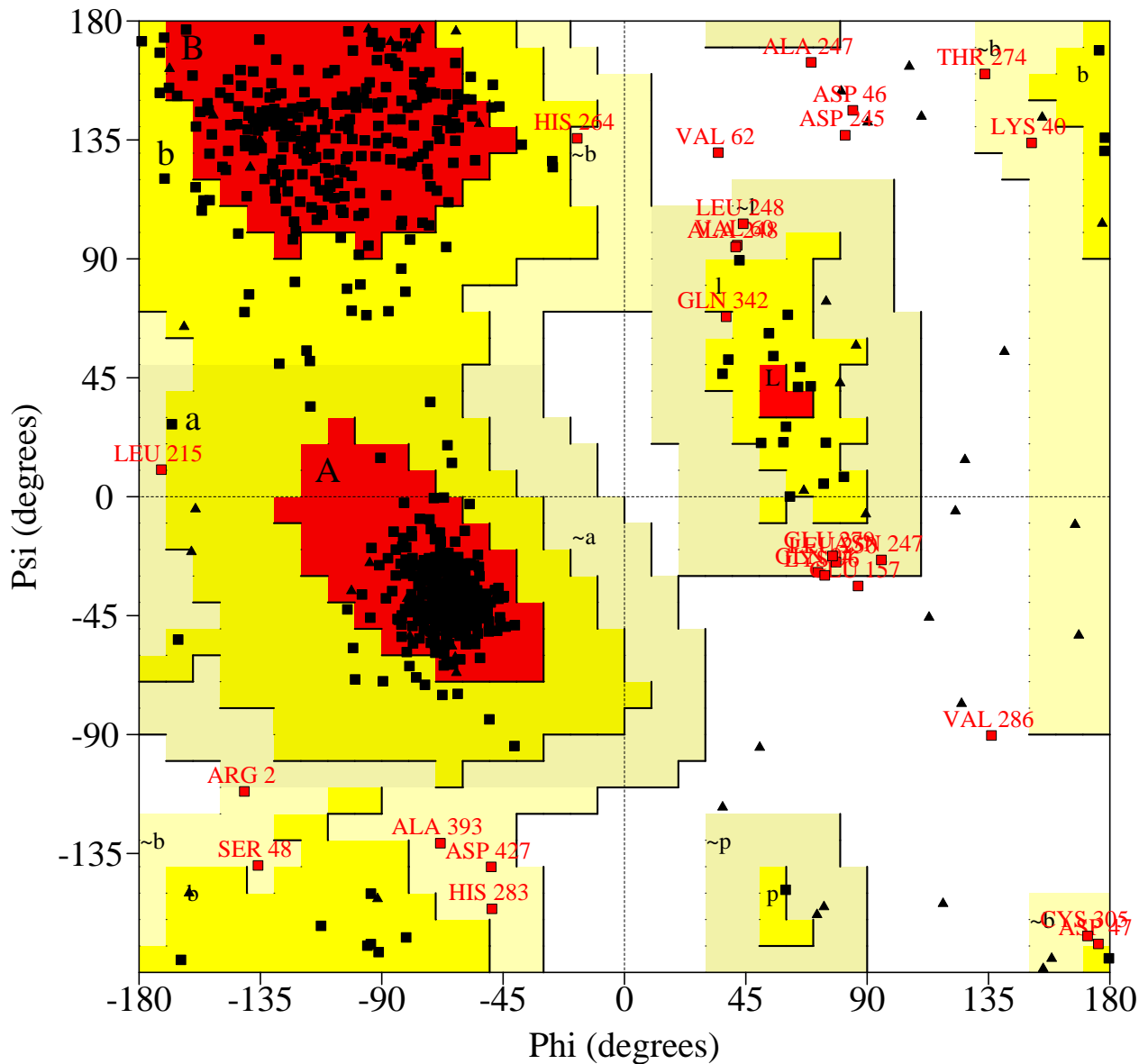


# Ramachandran Plot



### Plot statistics

Residues in most favoured regions [A,B,L]	656	86.8%
Residues in additional allowed regions [a,b,l,p]	74	9.8%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	20	2.6%
Residues in disallowed regions	6	0.8%
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Number of non-glycine and non-proline residues	756	100.0%
Number of end-residues (excl. Gly and Pro)	8	
Number of glycine residues (shown as triangles)	68	
Number of proline residues	40	
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Total number of residues	872	

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.