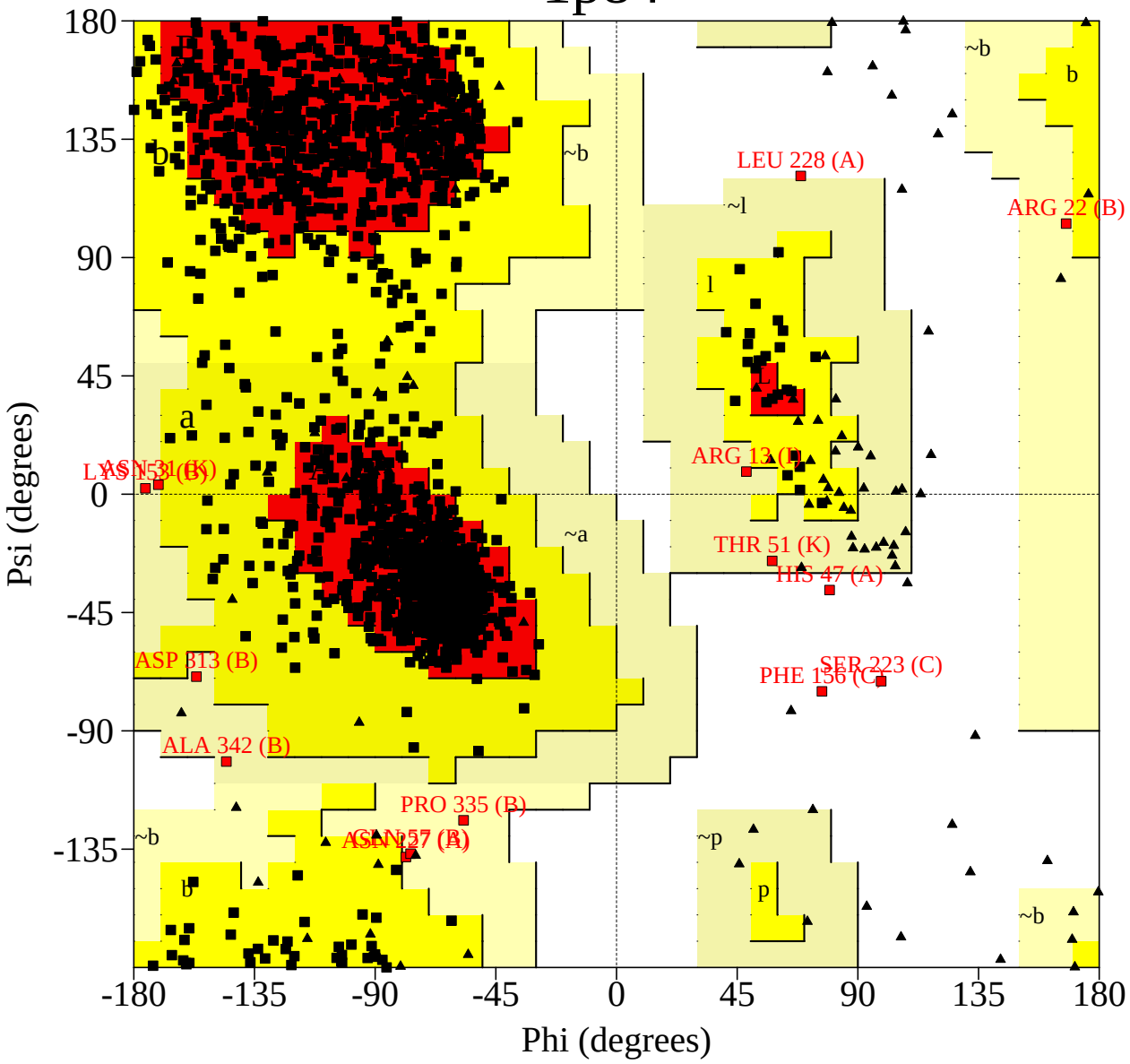
PROCHECK

Ramachandran Plot

1p84



Plot statistics

Residues in most favoured regions [A,B,L]	1655	86.8%
Residues in additional allowed regions [a,b,l,p]	239	12.5%
Residues in generously allowed regions [~a,~b,~l,~p]	9	0.5%
Residues in disallowed regions	4	0.2%
	----	------
Number of non-glycine and non-proline residues	1907	100.0%
Number of end-residues (excl. Gly and Pro)	20	
Number of glycine residues (shown as triangles)	141	
Number of proline residues	100	

Total number of residues	2168	

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.