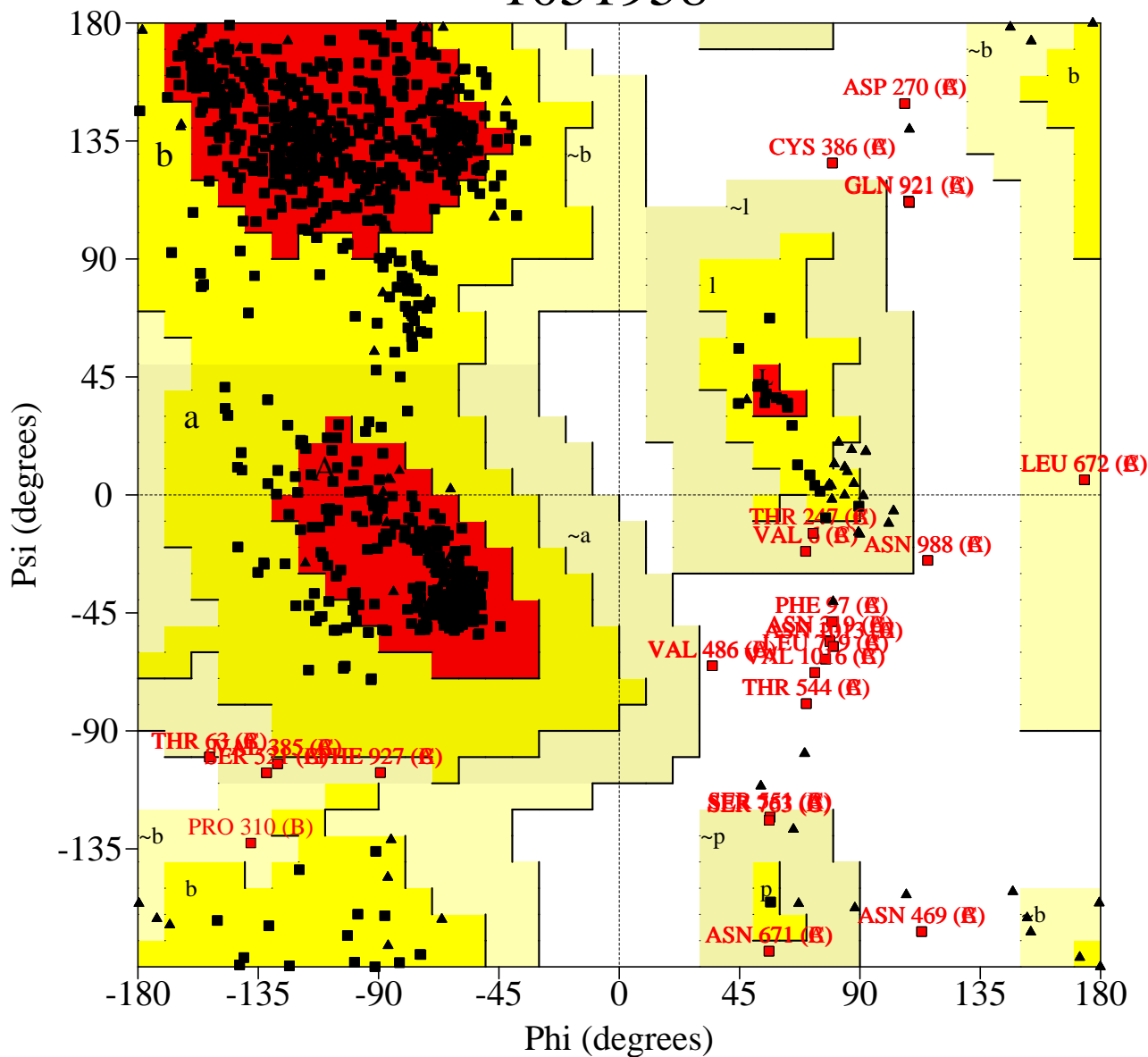


Ramachandran Plot

1051958



Plot statistics

Residues in most favoured regions [A,B,L]	2378	85.1%
Residues in additional allowed regions [a,b,l,p]	352	12.6%
Residues in generously allowed regions [~a,~b,~l,~p]	30	1.1%
Residues in disallowed regions	36	1.3%

Number of non-glycine and non-proline residues	2796	100.0%
Number of end-residues (excl. Gly and Pro)	6	
Number of glycine residues (shown as triangles)	228	
Number of proline residues	99	

Total number of residues	3129	

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.