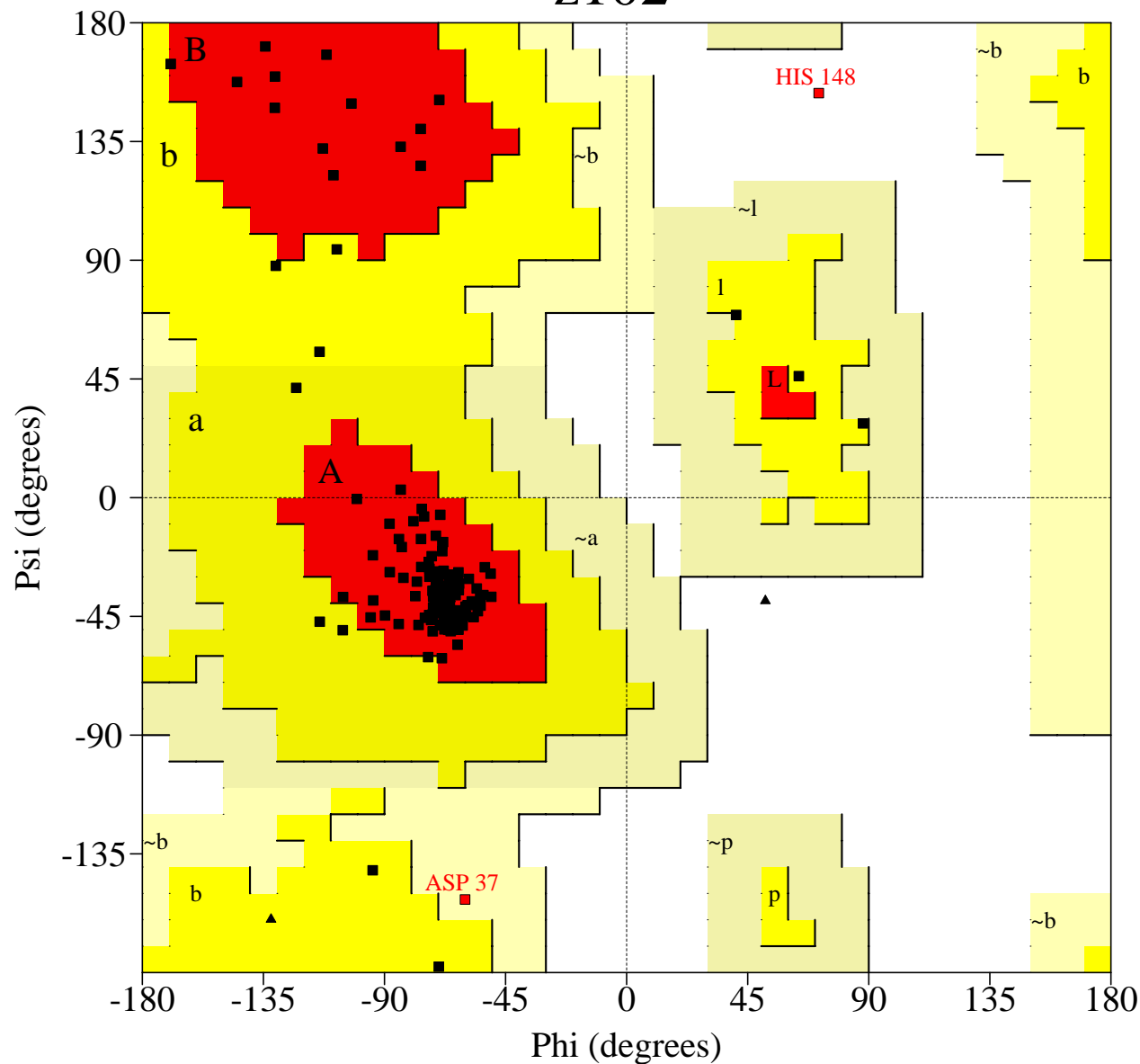


Ramachandran Plot

z102



Plot statistics

Residues in most favoured regions [A,B,L]	136	91.3%
Residues in additional allowed regions [a,b,l,p]	11	7.4%
Residues in generously allowed regions [~a,~b,~l,~p]	1	0.7%
Residues in disallowed regions	1	0.7%

Number of non-glycine and non-proline residues	149	100.0%
Number of end-residues (excl. Gly and Pro)	4	
Number of glycine residues (shown as triangles)	3	
Number of proline residues	3	

Total number of residues	159	

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.