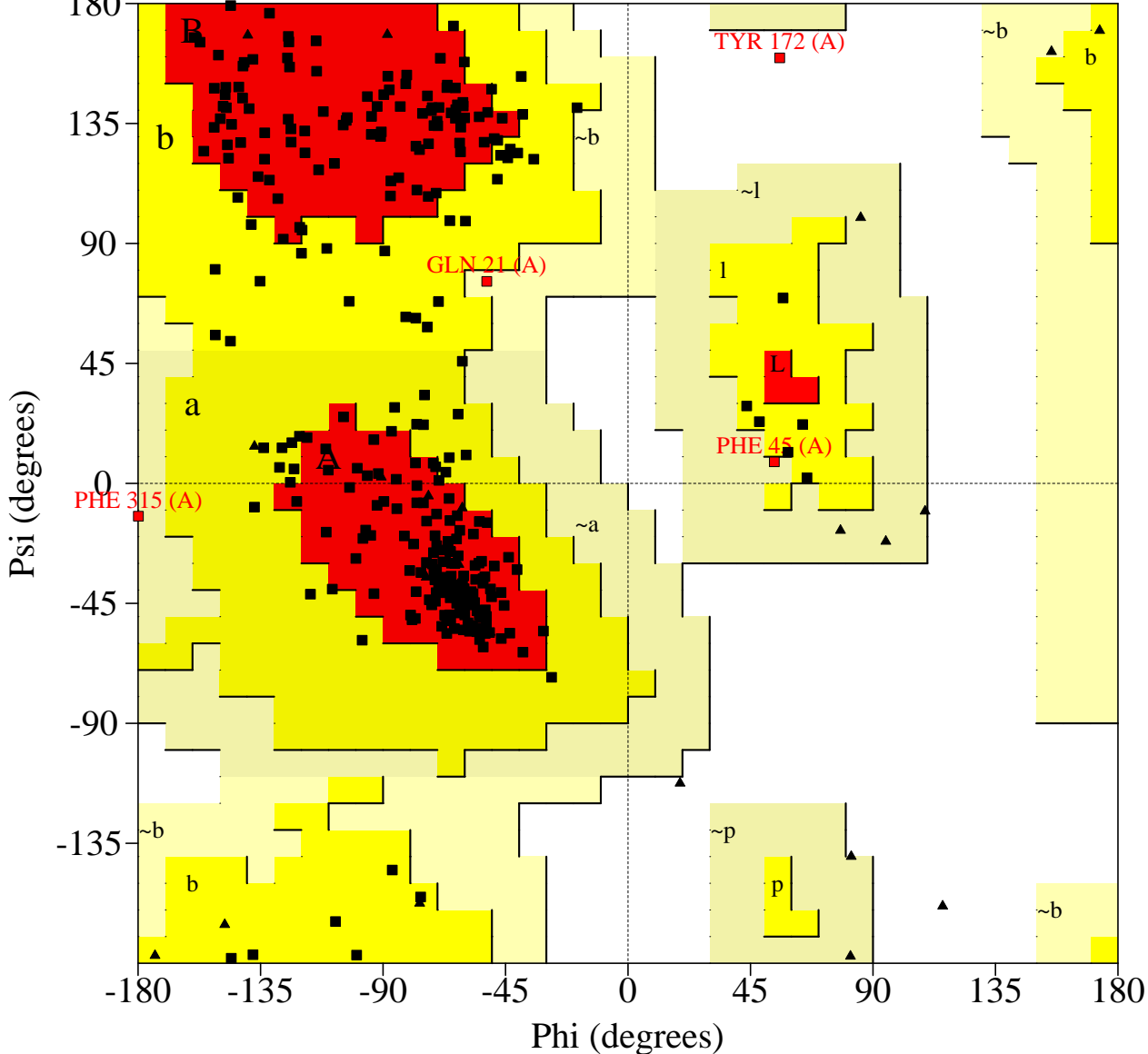


Plot statistics

Residues in most favoured regions [A,B,L]	199	65.7%
Residues in additionally allowed regions [a,b,l,p]	80	26.4%
Residues in generously allowed regions [~a,~b,~l,~p]	16	5.3%
Residues in disallowed regions	8	2.6%
-----		
Number of non-glycine and non-proline residues	303	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	15	
Number of proline residues	25	
-----		
Total number of residues	345	

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.

FIGURE S1A



Residues in most favoured regions [A,B,L]	235	79.9%
Residues in additional allowed regions [a,b,l,p]	55	18.7%
Residues in generously allowed regions [~a,~b,~l,~p]	3	1.0%
Residues in disallowed regions	1	0.3%
-----		
Number of non-glycine and non-proline residues	294	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	24	
Number of proline residues	23	
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Total number of residues	343	

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.

**FIGURE S1B**