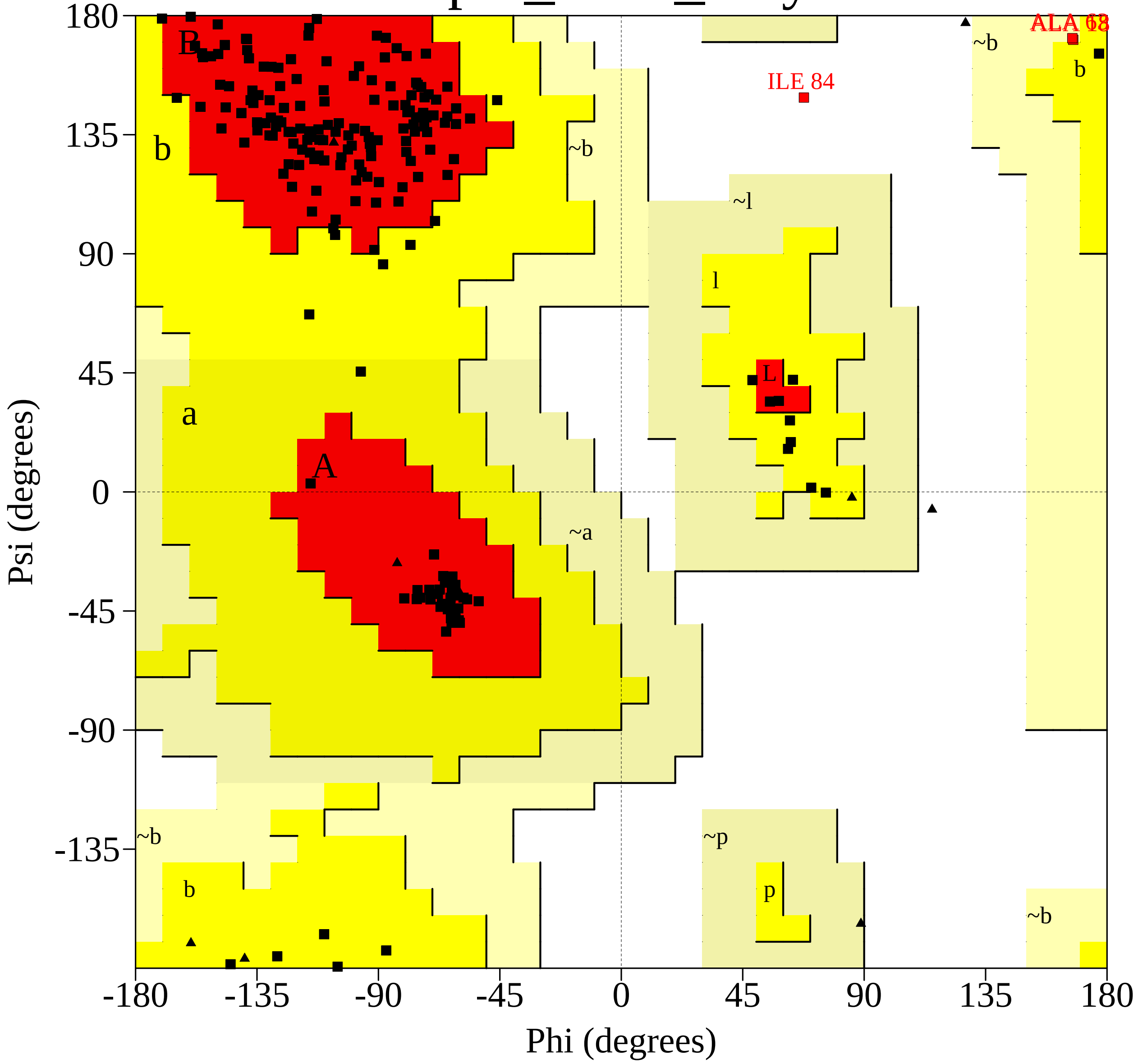
PROCHECK

Ramachandran Plot

input_atom_only



Plot statistics

Residues in most favoured regions [A,B,L]	178	87.3%
Residues in additional allowed regions [a,b,l,p]	23	11.3%
Residues in generously allowed regions [~a,~b,~l,~p]	2	1.0%
Residues in disallowed regions	1	0.5%
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Number of non-glycine and non-proline residues	204	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	9	
Number of proline residues	5	

Total number of residues	220	

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.