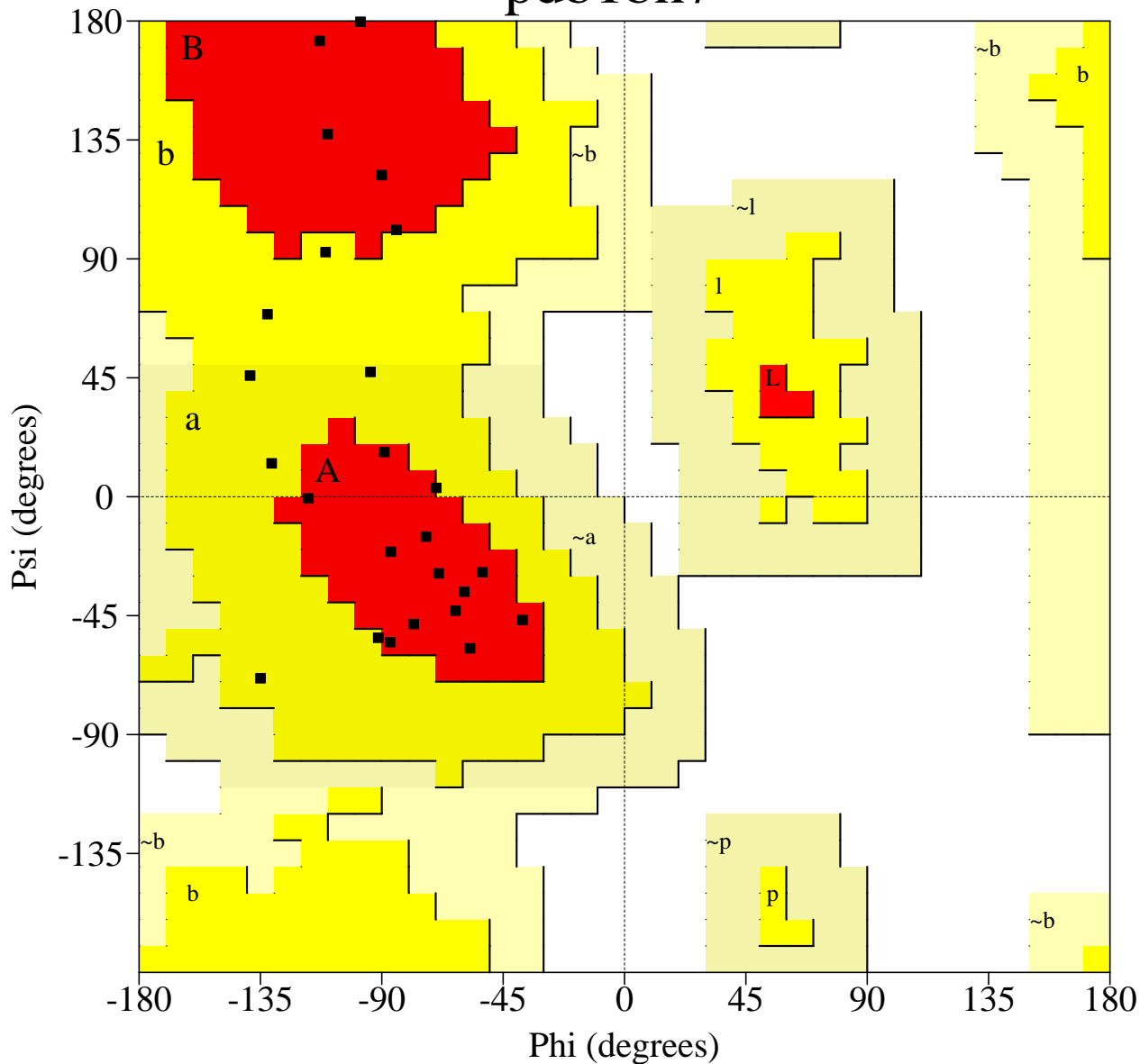


Ramachandran Plot

pdb1bh7



Plot statistics

Residues in most favoured regions [A,B,L]	14	63.6%
Residues in additional allowed regions [a,b,l,p]	8	36.4%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	0	0.0%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	22	100.0%
Number of end-residues (excl. Gly and Pro)	5	
Number of glycine residues (shown as triangles)	0	
Number of proline residues	4	

Total number of residues	31	

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.