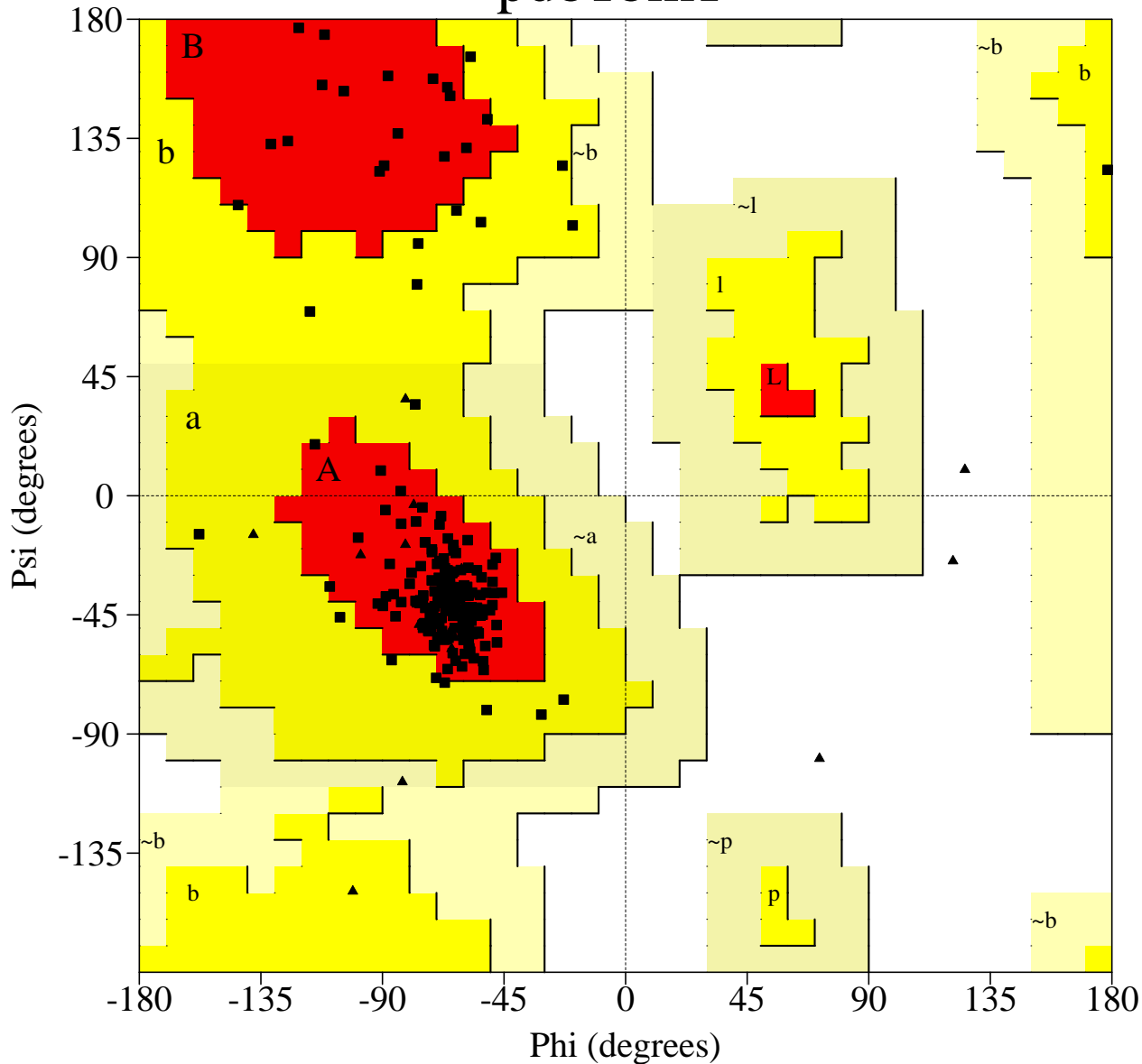


# Ramachandran Plot

## pdb1bm1



### Plot statistics

Residues in most favoured regions [A,B,L]	172	91.0%
Residues in additional allowed regions [a,b,l,p]	17	9.0%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	0	0.0%
Residues in disallowed regions	0	0.0%
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Number of non-glycine and non-proline residues	189	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	21	
Number of proline residues	9	
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Total number of residues	221	

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.