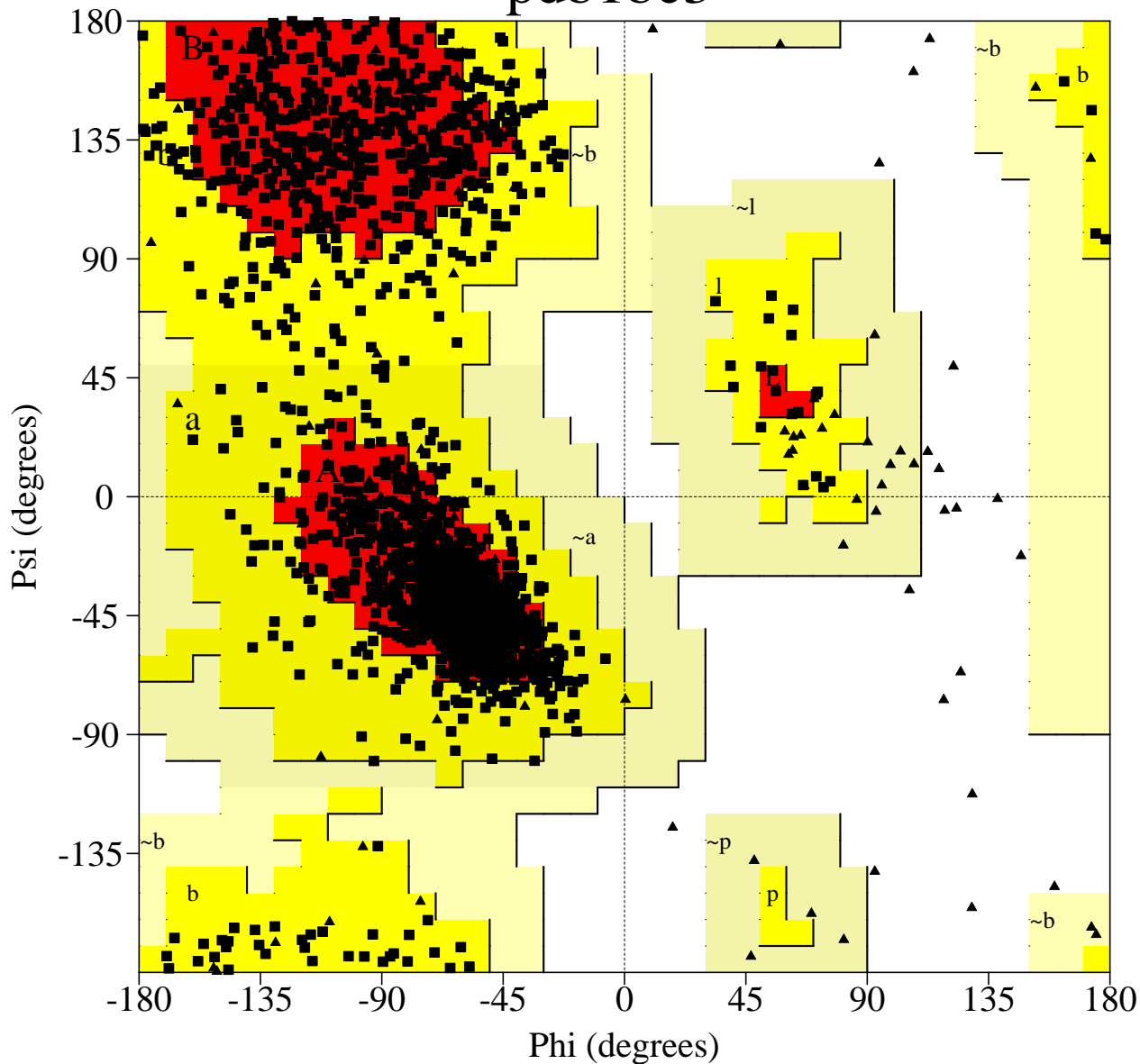


Ramachandran Plot

pdb1be3



Plot statistics

Residues in most favoured regions [A,B,L]	1474	82.3%
Residues in additional allowed regions [a,b,l,p]	318	17.7%
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	1792	100.0%
Number of end-residues (excl. Gly and Pro)	19	
Number of glycine residues (shown as triangles)	136	
Number of proline residues	102	

Total number of residues	2049	

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.