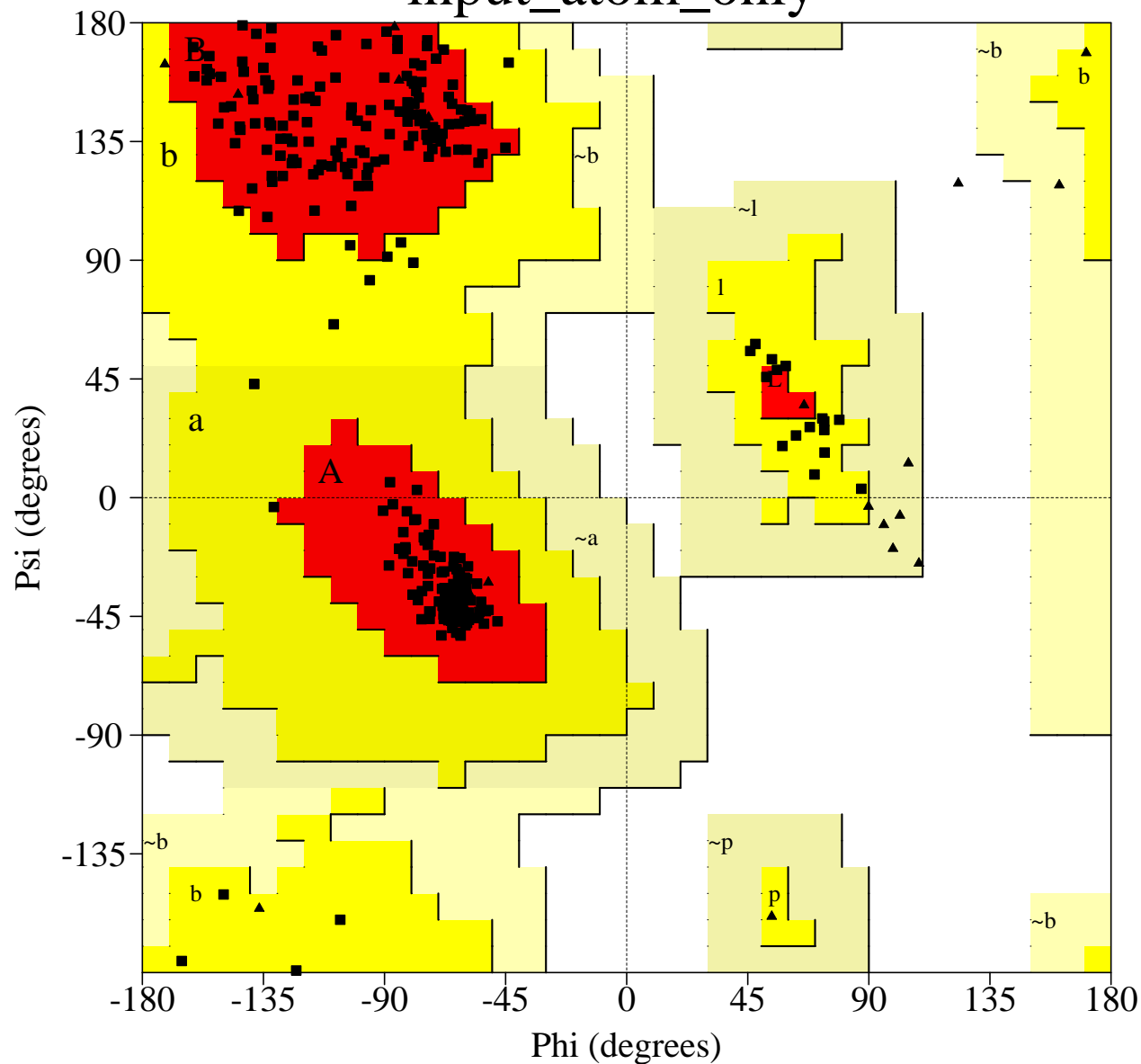


Ramachandran Plot

input_atom_only



Plot statistics

Residues in most favoured regions [A,B,L]	326	92.4%
Residues in additional allowed regions [a,b,l,p]	27	7.6%
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	353	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	22	
Number of proline residues	9	

Total number of residues	386	

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.