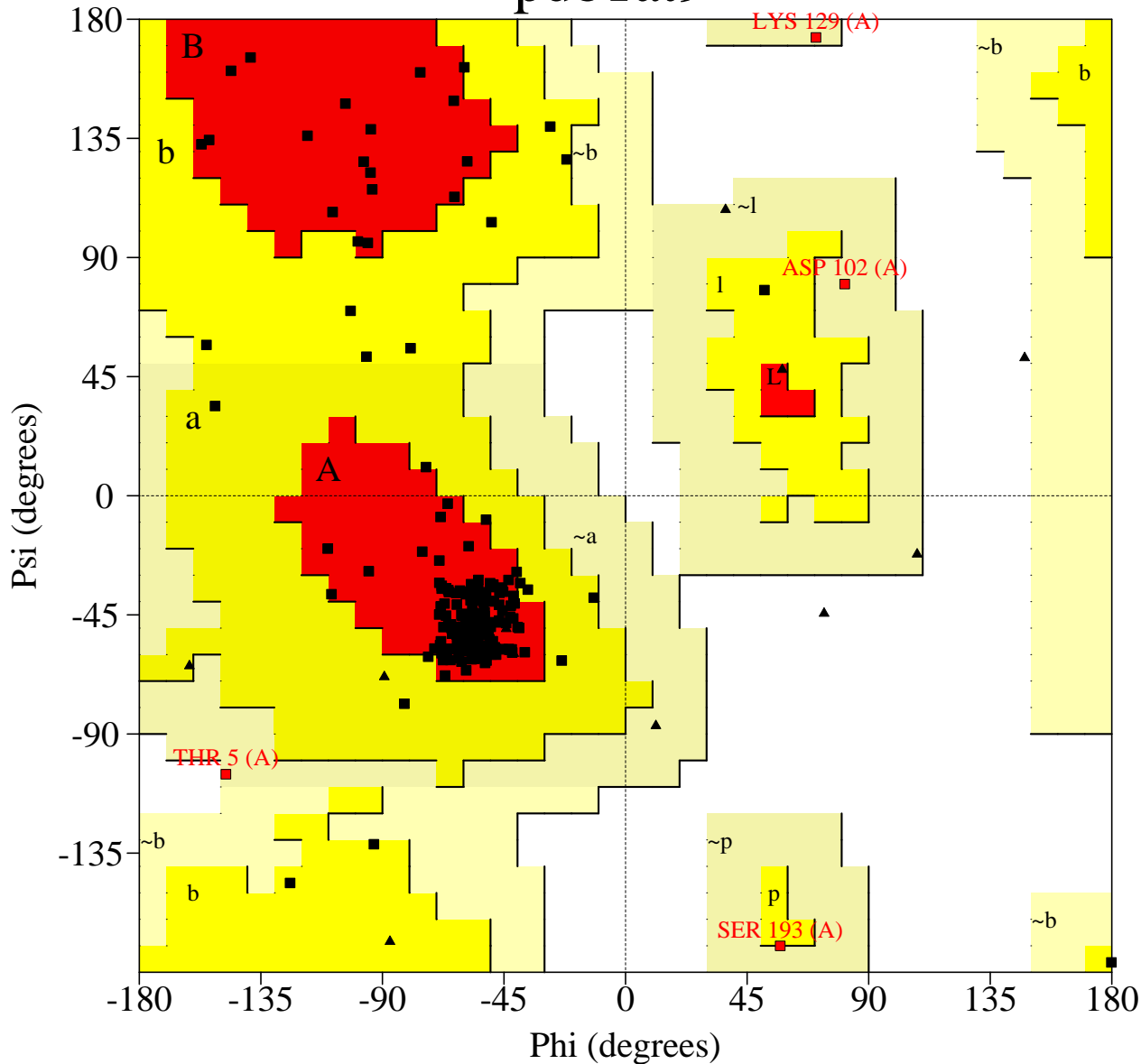


Ramachandran Plot

pdb1at9



Plot statistics

Residues in most favoured regions [A,B,L]	174	88.3%
Residues in additional allowed regions [a,b,l,p]	19	9.6%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	4	2.0%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	197	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	23	
Number of proline residues	9	

Total number of residues	230	

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.