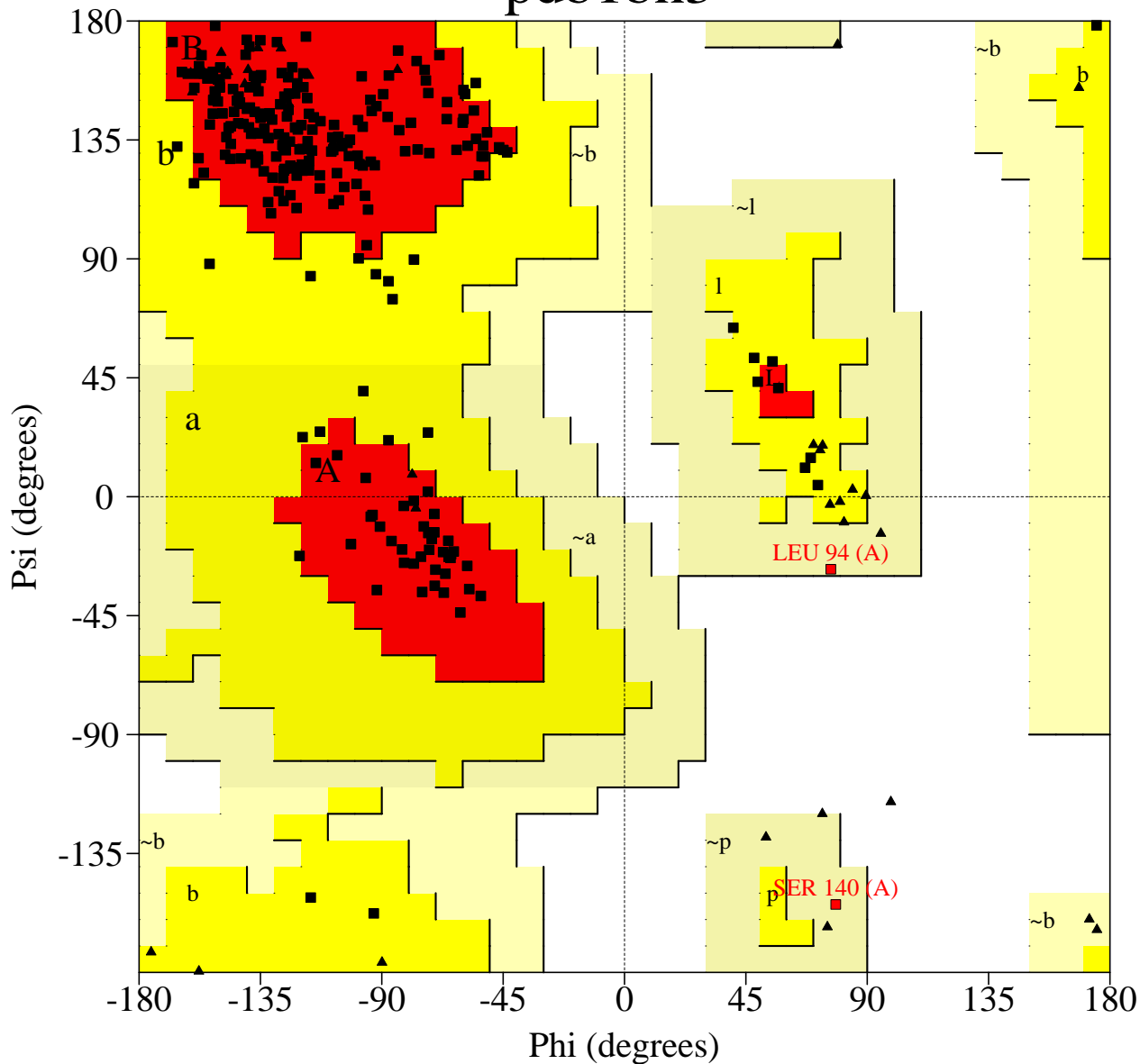


Ramachandran Plot

pdb1bh3



Plot statistics

Residues in most favoured regions [A,B,L]	222	88.4%
Residues in additional allowed regions [a,b,l,p]	27	10.8%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	2	0.8%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	251	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	35	
Number of proline residues	1	

Total number of residues	289	

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.