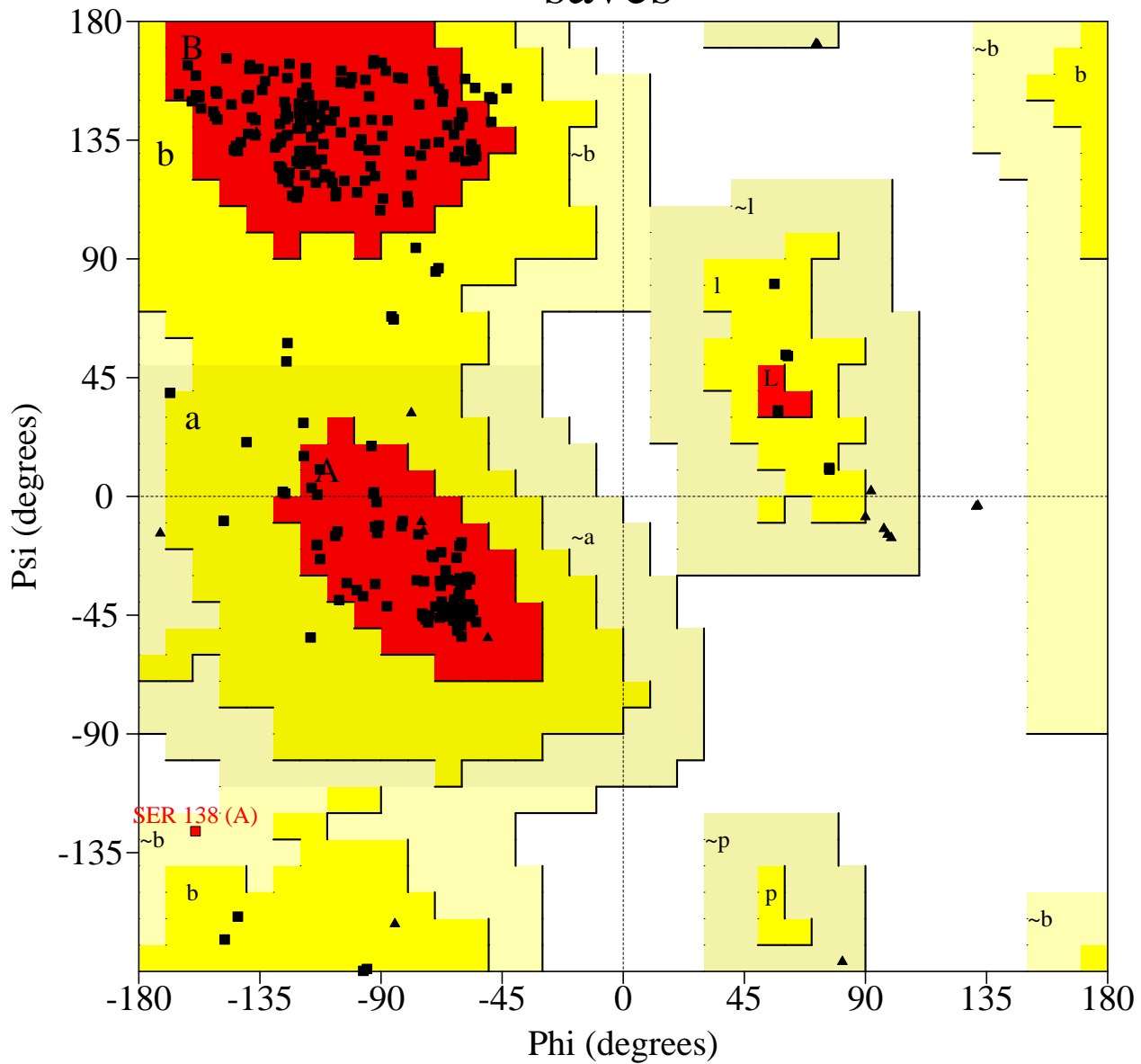


# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	253	91.0%
Residues in additional allowed regions [a,b,l,p]	24	8.6%
Residues in generously allowed regions [~a,~b,~l,~p]	1	0.4%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	278	100.0%
Number of end-residues (excl. Gly and Pro)	5	
Number of glycine residues (shown as triangles)	17	
Number of proline residues	17	
-----		
Total number of residues	317	

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.