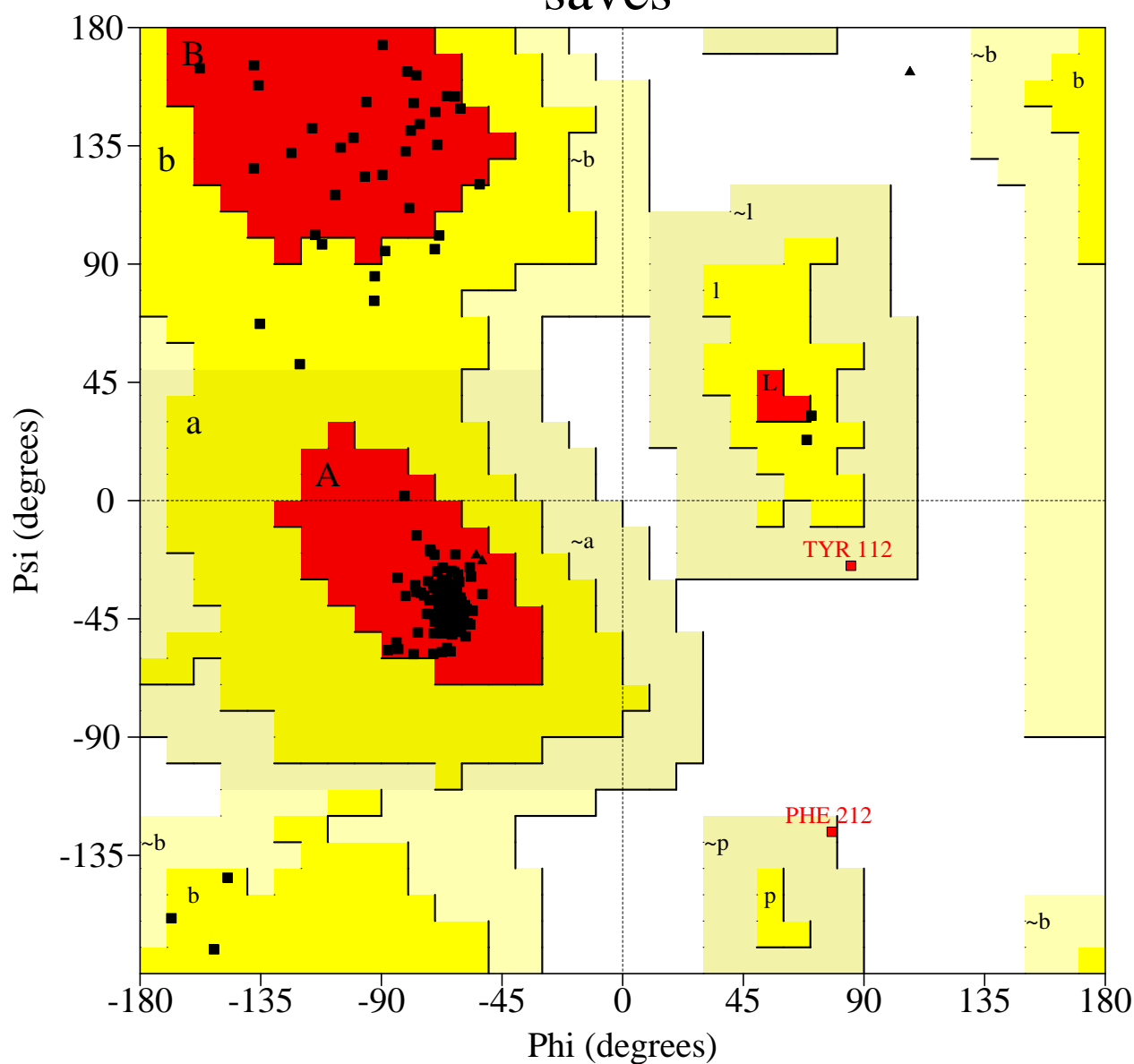


# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	250	94.3%
Residues in additional allowed regions [a,b,l,p]	13	4.9%
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	265	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	11	
Number of proline residues	11	
-----		
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.