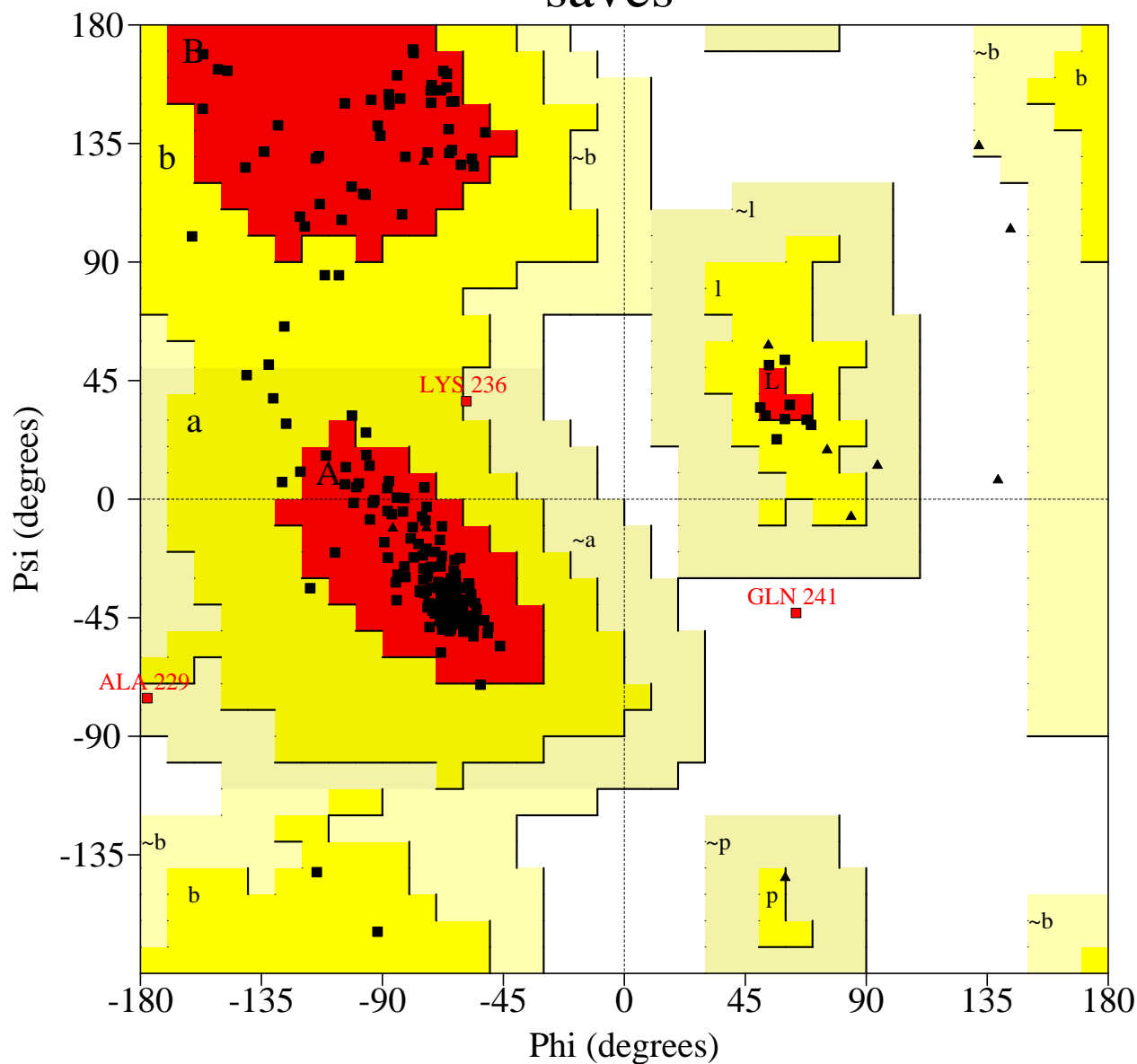


# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	221	90.6%
Residues in additional allowed regions [a,b,l,p]	20	8.2%
Residues in generously allowed regions [~a,~b,~l,~p]	2	0.8%
Residues in disallowed regions	1	0.4%
-----		
Number of non-glycine and non-proline residues	244	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	13	
Number of proline residues	10	
-----		
Total number of residues	269	

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.