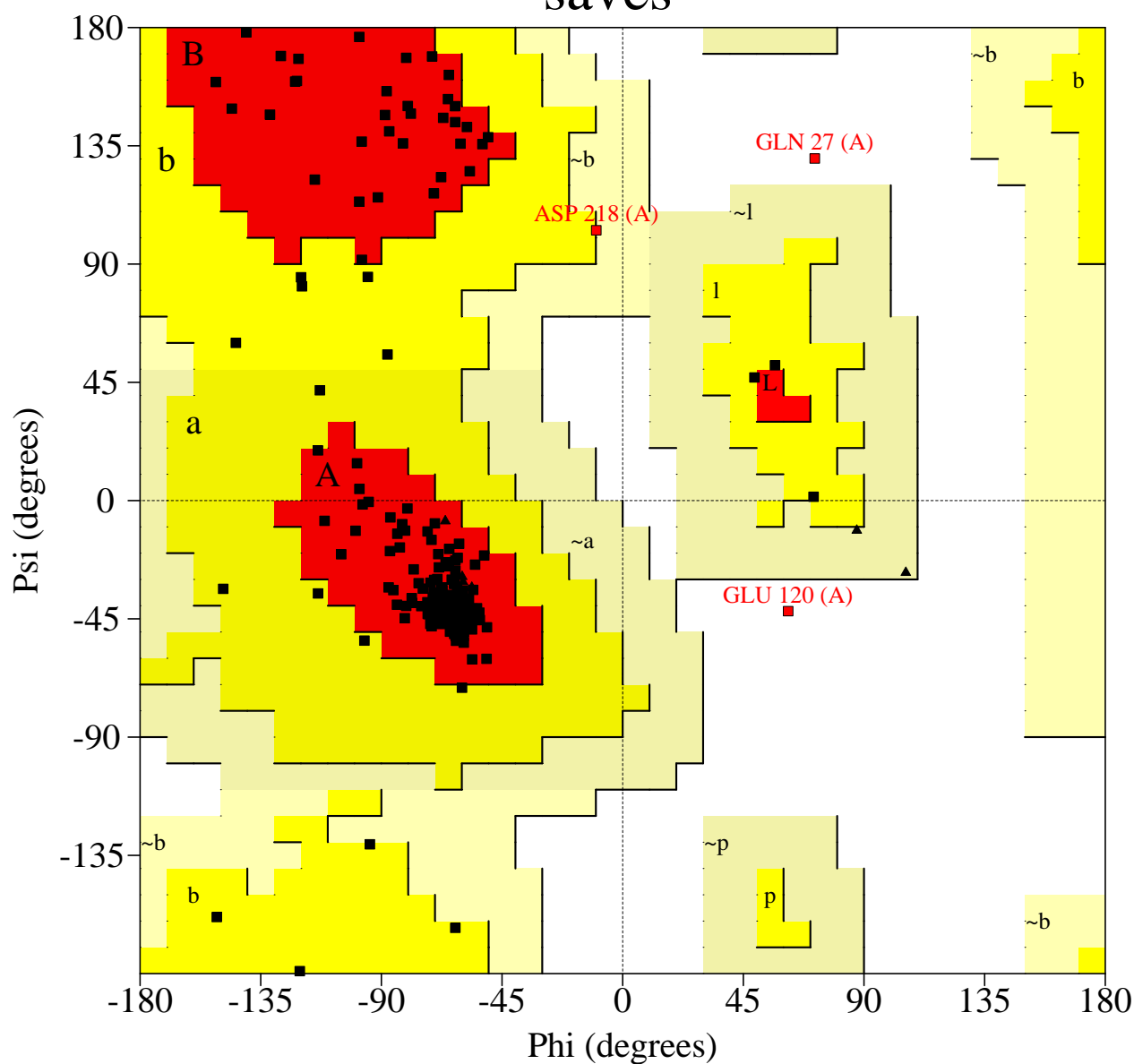


Ramachandran Plot

saves



Plot statistics

Residues in most favoured regions [A,B,L]	194	91.1%
Residues in additional allowed regions [a,b,l,p]	16	7.5%
Residues in generously allowed regions [~a,~b,~l,~p]	1	0.5%
Residues in disallowed regions	2	0.9%

Number of non-glycine and non-proline residues	213	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	7	
Number of proline residues	10	

Total number of residues	232	

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.