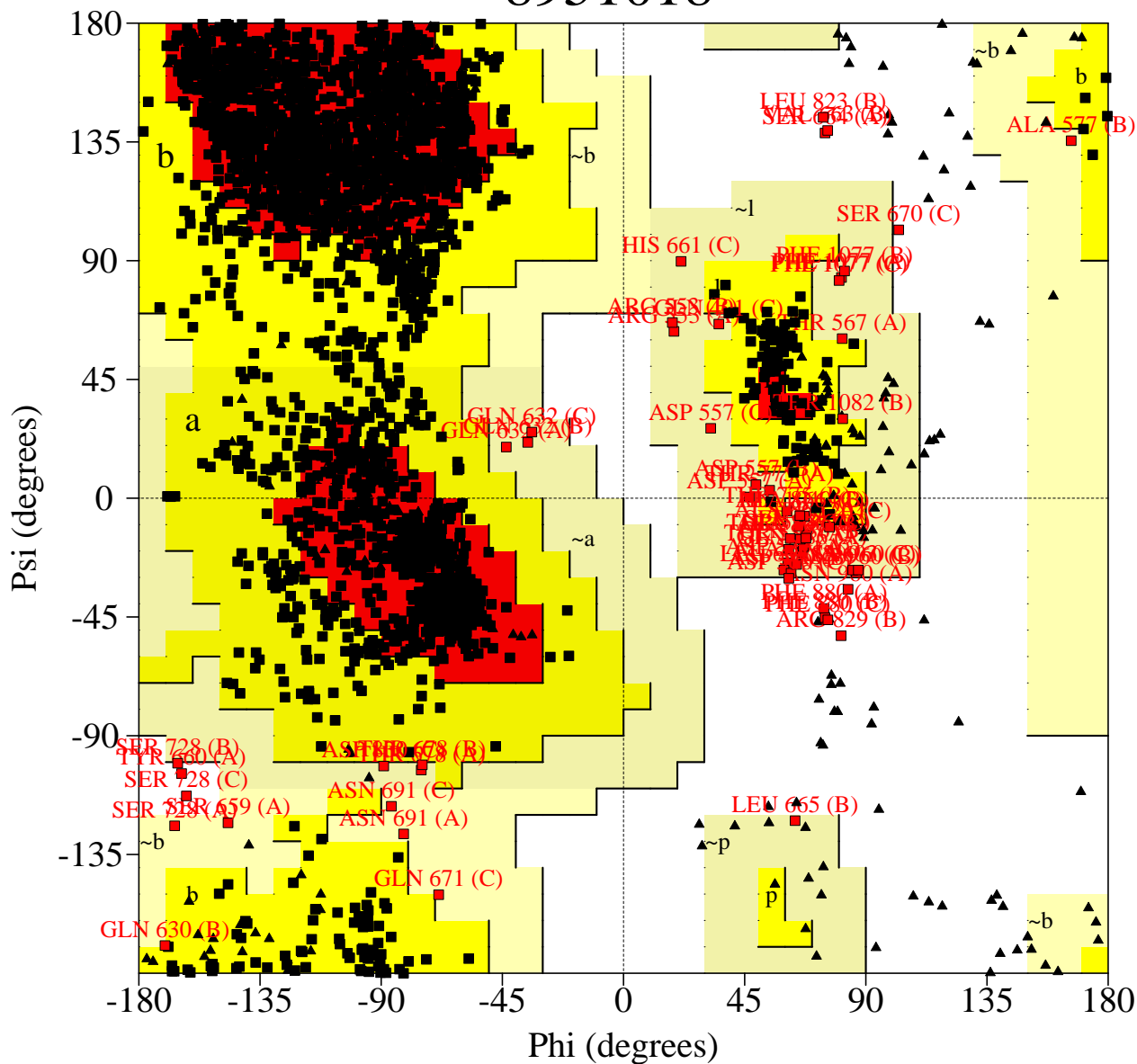


# Ramachandran Plot

## 8951018



### Plot statistics

Residues in most favoured regions [A,B,L]	2299	78.4%
Residues in additional allowed regions [a,b,l,p]	576	19.6%
Residues in generously allowed regions [~a,~b,~l,~p]	46	1.6%
Residues in disallowed regions	13	0.4%
Number of non-glycine and non-proline residues	2934	100.0%
Number of end-residues (excl. Gly and Pro)	6	
Number of glycine residues (shown as triangles)	210	
Number of proline residues	156	
Total number of residues	3306	

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.