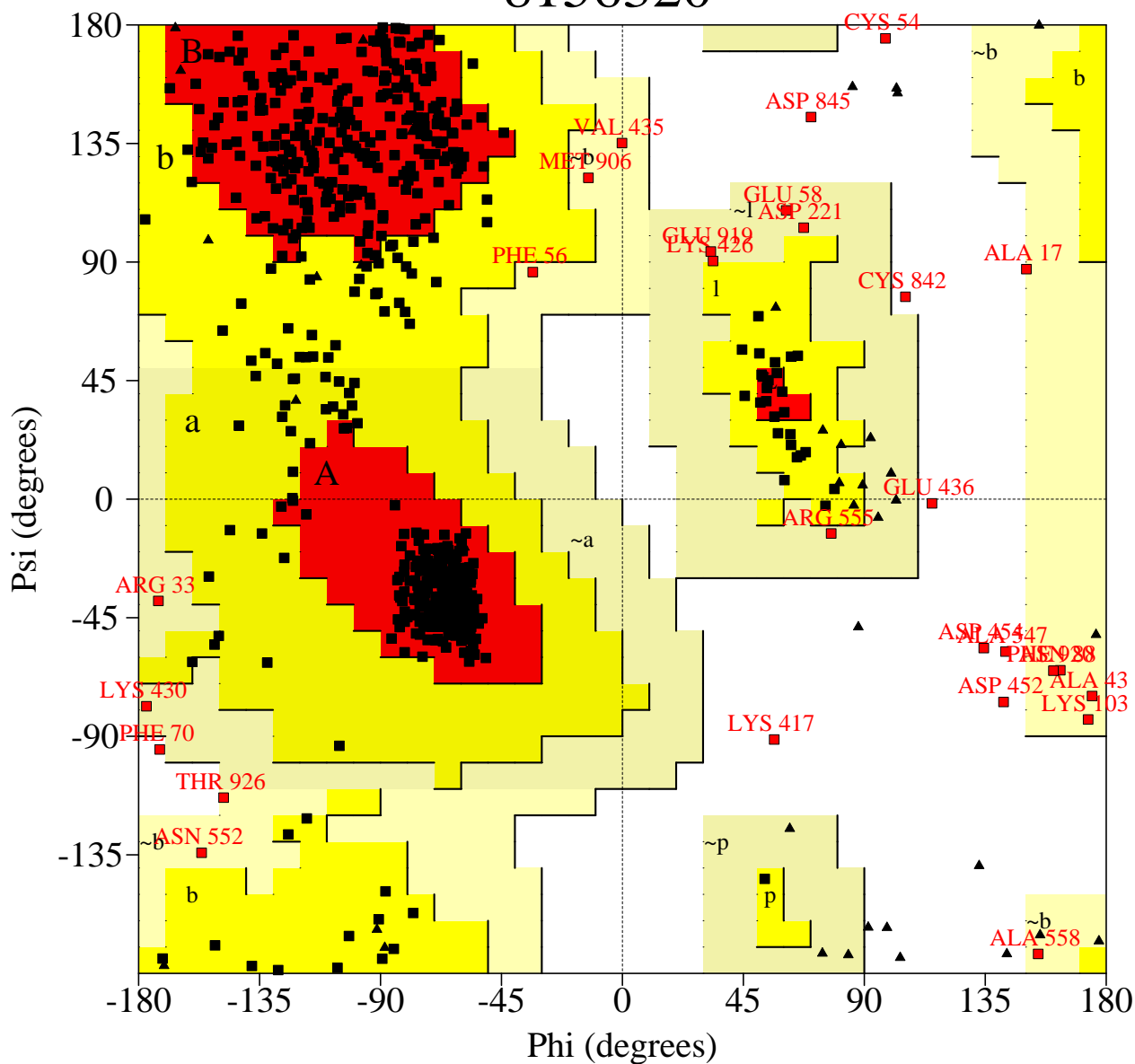


# Ramachandran Plot

## 8156320



### Plot statistics

Residues in most favoured regions [A,B,L]	730	85.4%
Residues in additional allowed regions [a,b,l,p]	98	11.5%
Residues in generously allowed regions [~a,~b,~l,~p]	18	2.1%
Residues in disallowed regions	9	1.1%
-----		
Number of non-glycine and non-proline residues	855	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	45	
Number of proline residues	30	
-----		
Total number of residues	932	

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.