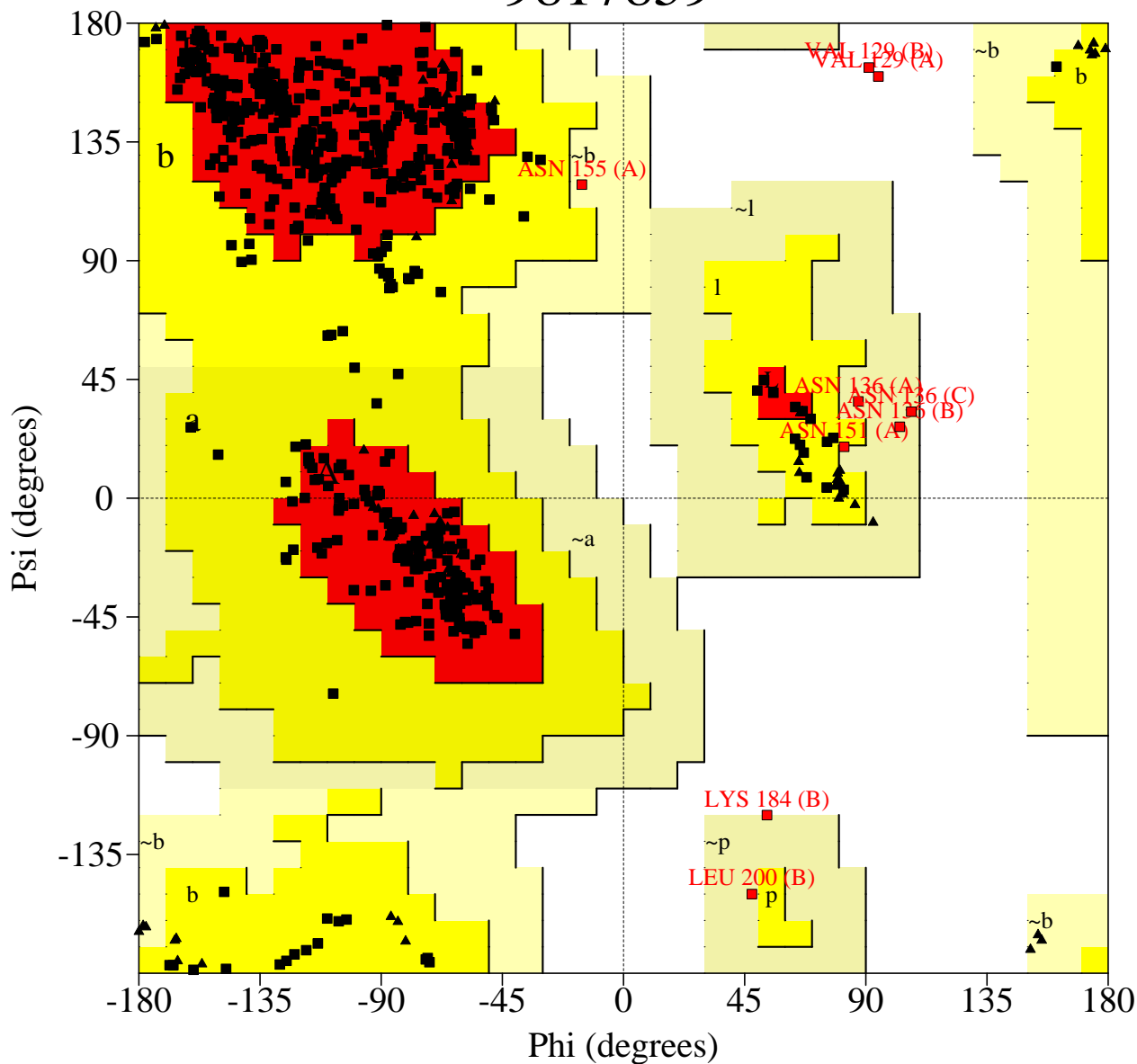


# Ramachandran Plot

## 9817859



### Plot statistics

Residues in most favoured regions [A,B,L]	571	88.1%
Residues in additional allowed regions [a,b,l,p]	68	10.5%
Residues in generously allowed regions [~a,~b,~l,~p]	7	1.1%
Residues in disallowed regions	2	0.3%
-----		
Number of non-glycine and non-proline residues	648	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	75	
Number of proline residues	30	
-----		
Total number of residues	753	

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.