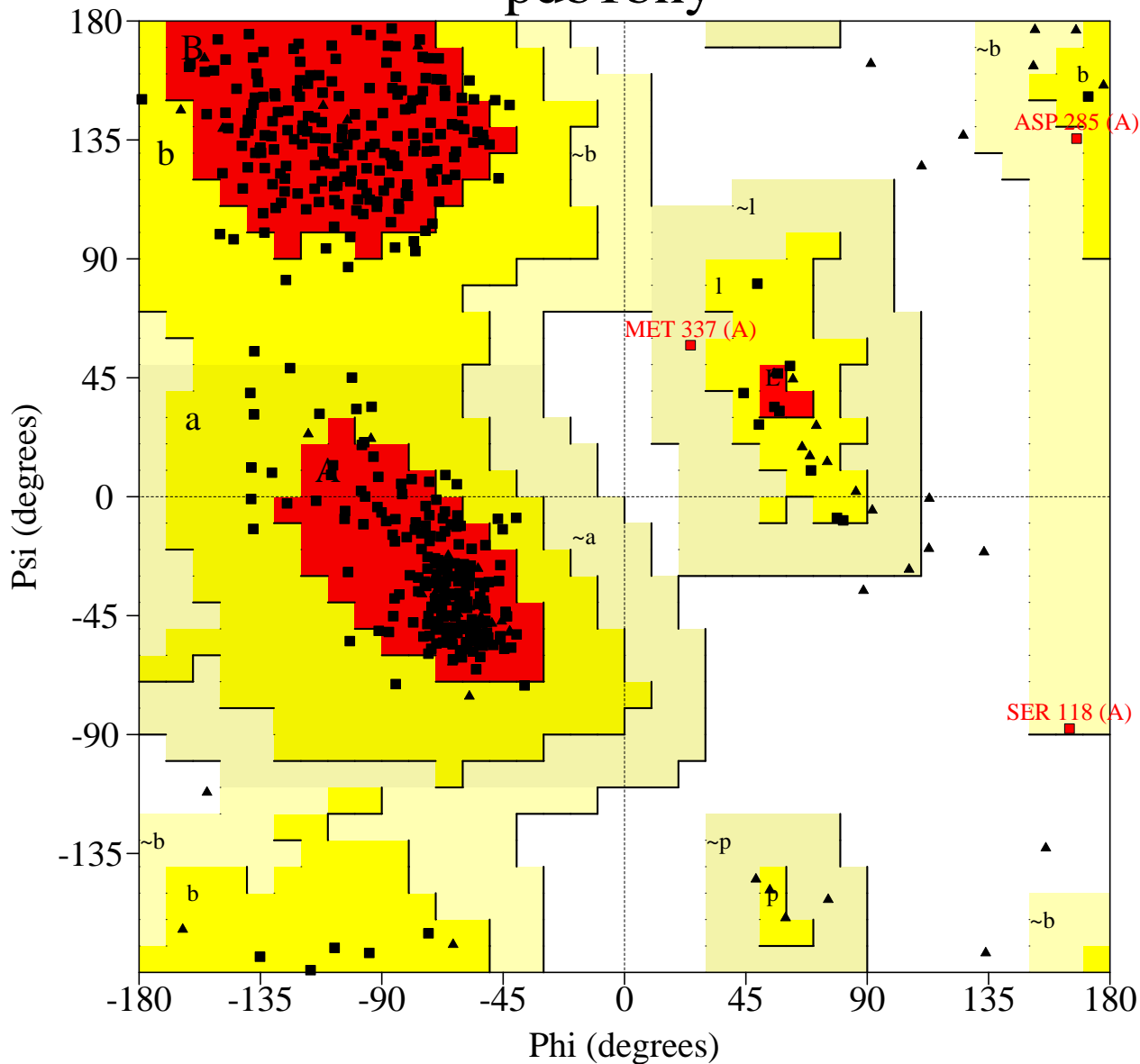


# Ramachandran Plot

## pdb1bhy



### Plot statistics

Residues in most favoured regions [A,B,L]	349	87.5%
Residues in additional allowed regions [a,b,l,p]	47	11.8%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	3	0.8%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	399	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	57	
Number of proline residues	25	
-----		
Total number of residues	482	

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.