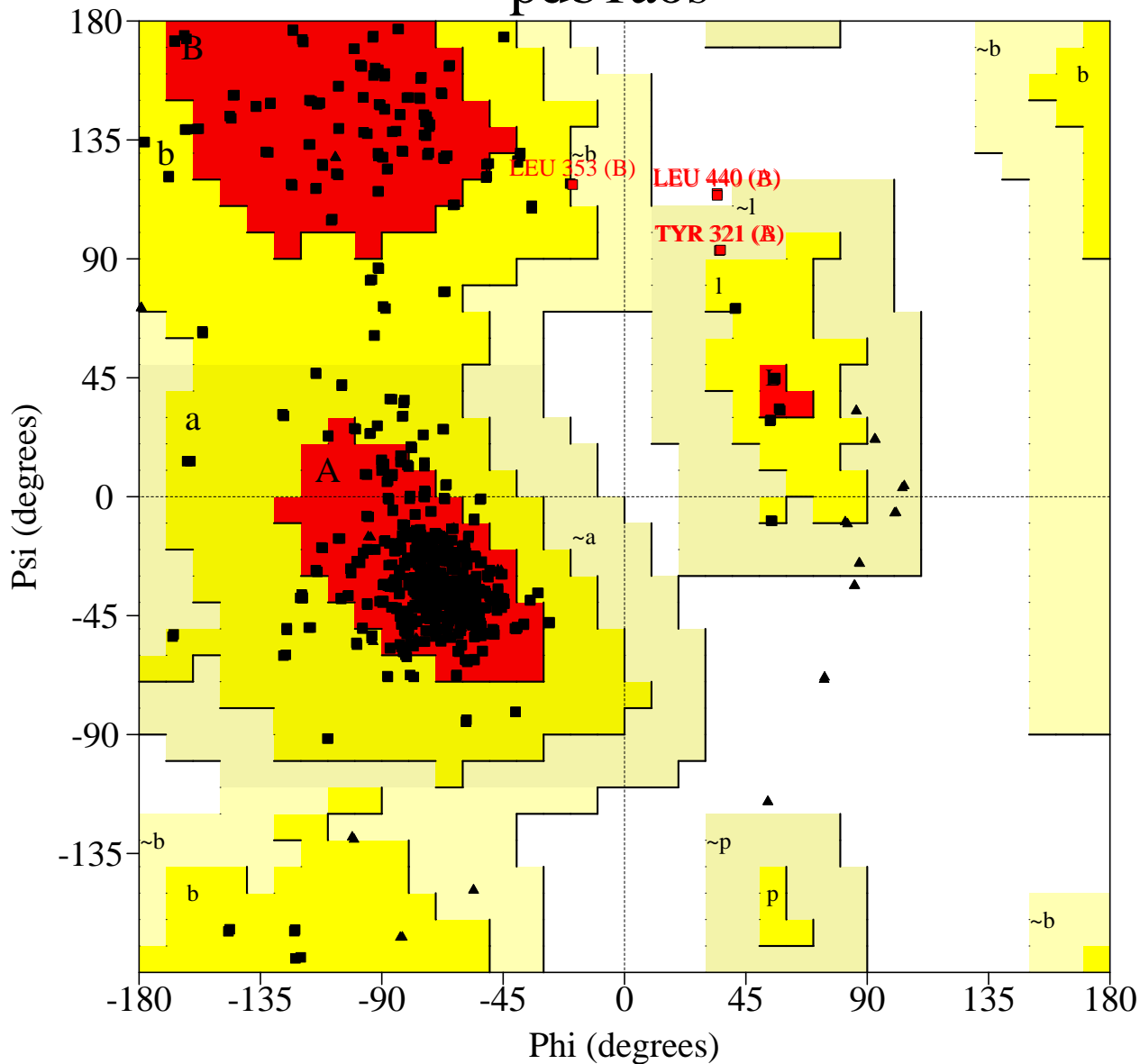


# Ramachandran Plot

pdb1aos



### Plot statistics

Residues in most favoured regions [A,B,L]	676	86.2%
Residues in additional allowed regions [a,b,l,p]	103	13.1%
Residues in generously allowed regions [-~a,-~b,-~l,-~p]	3	0.4%
Residues in disallowed regions	2	0.3%
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Number of non-glycine and non-proline residues	784	100.0%
Number of end-residues (excl. Gly and Pro)	8	
Number of glycine residues (shown as triangles)	56	
Number of proline residues	20	
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Total number of residues	868	

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.