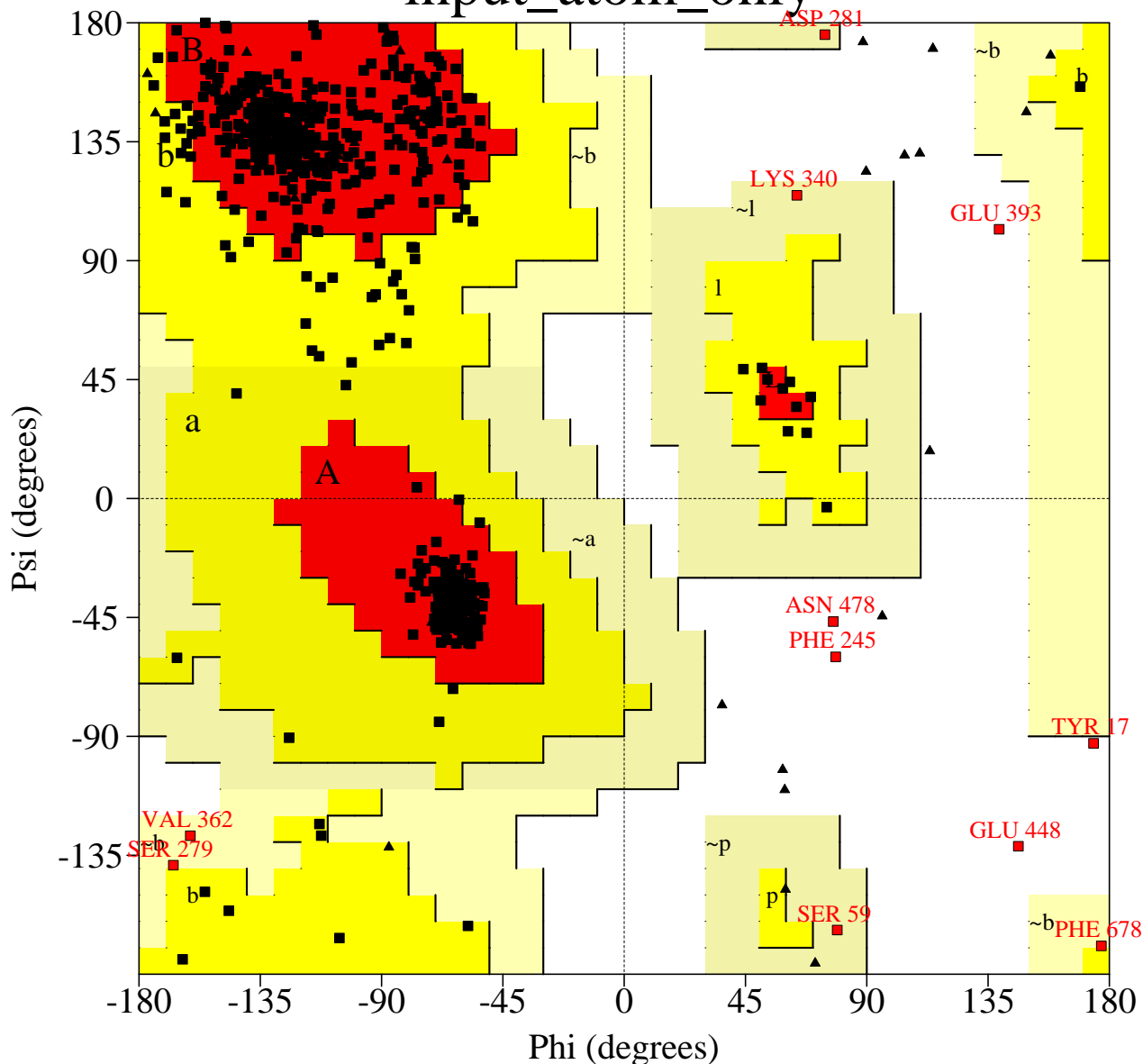


# Ramachandran Plot

input\_atom\_only



### Plot statistics

Residues in most favoured regions [A,B,L]	605	89.1%
Residues in additional allowed regions [a,b,l,p]	63	9.3%
Residues in generously allowed regions [-a,-b,-l,-p]	6	0.9%
Residues in disallowed regions	5	0.7%
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Number of non-glycine and non-proline residues	679	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	35	
Number of proline residues	19	
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Total number of residues	735	

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.