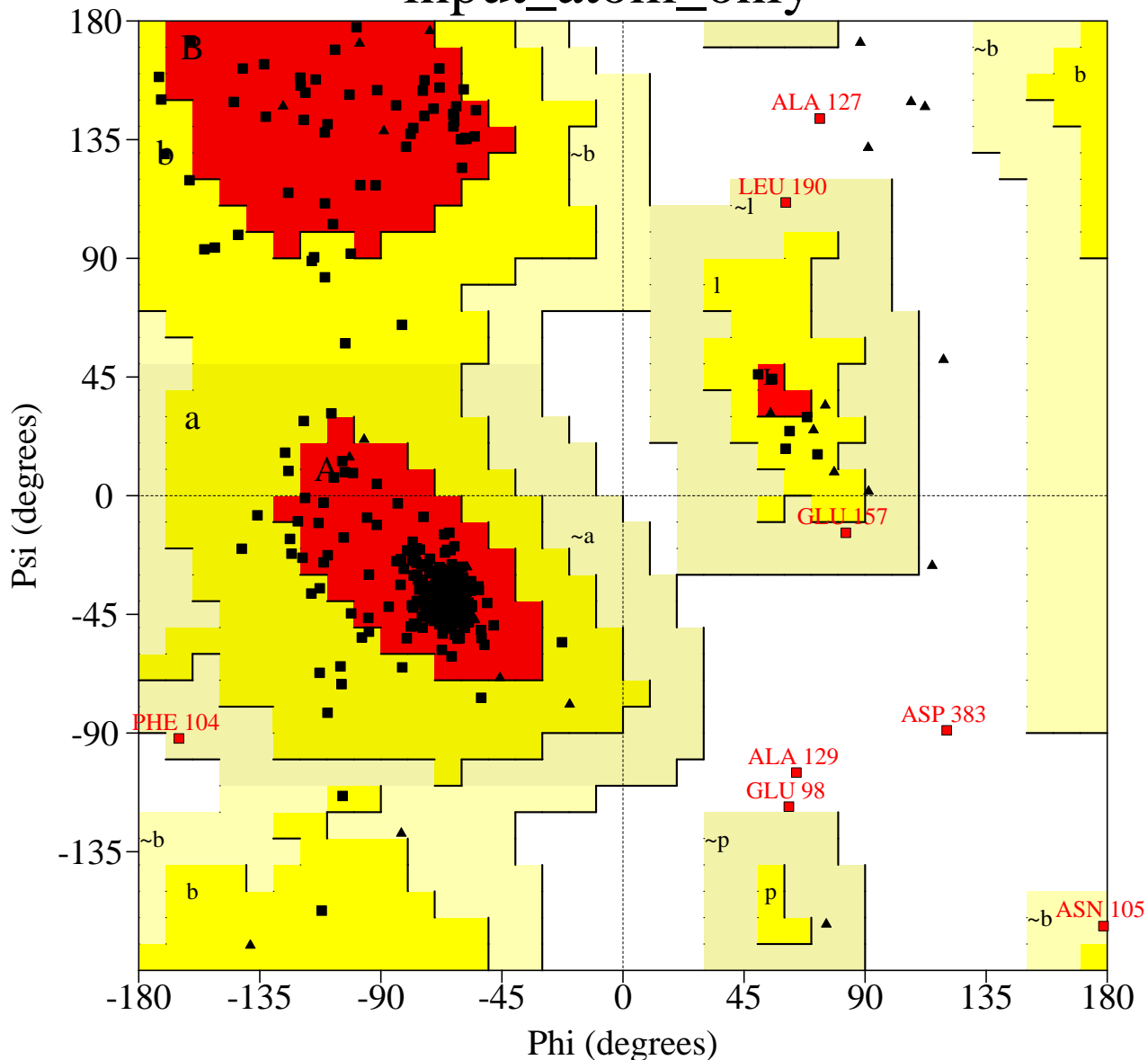


# Ramachandran Plot

## input\_atom\_only



### Plot statistics

Residues in most favoured regions [A,B,L]	304	86.6%
Residues in additional allowed regions [a,b,l,p]	39	11.1%
Residues in generously allowed regions [-a,-b,-l,-p]	4	1.1%
Residues in disallowed regions	4	1.1%
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Number of non-glycine and non-proline residues	351	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	51	
Number of proline residues	12	
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Total number of residues	415	

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.