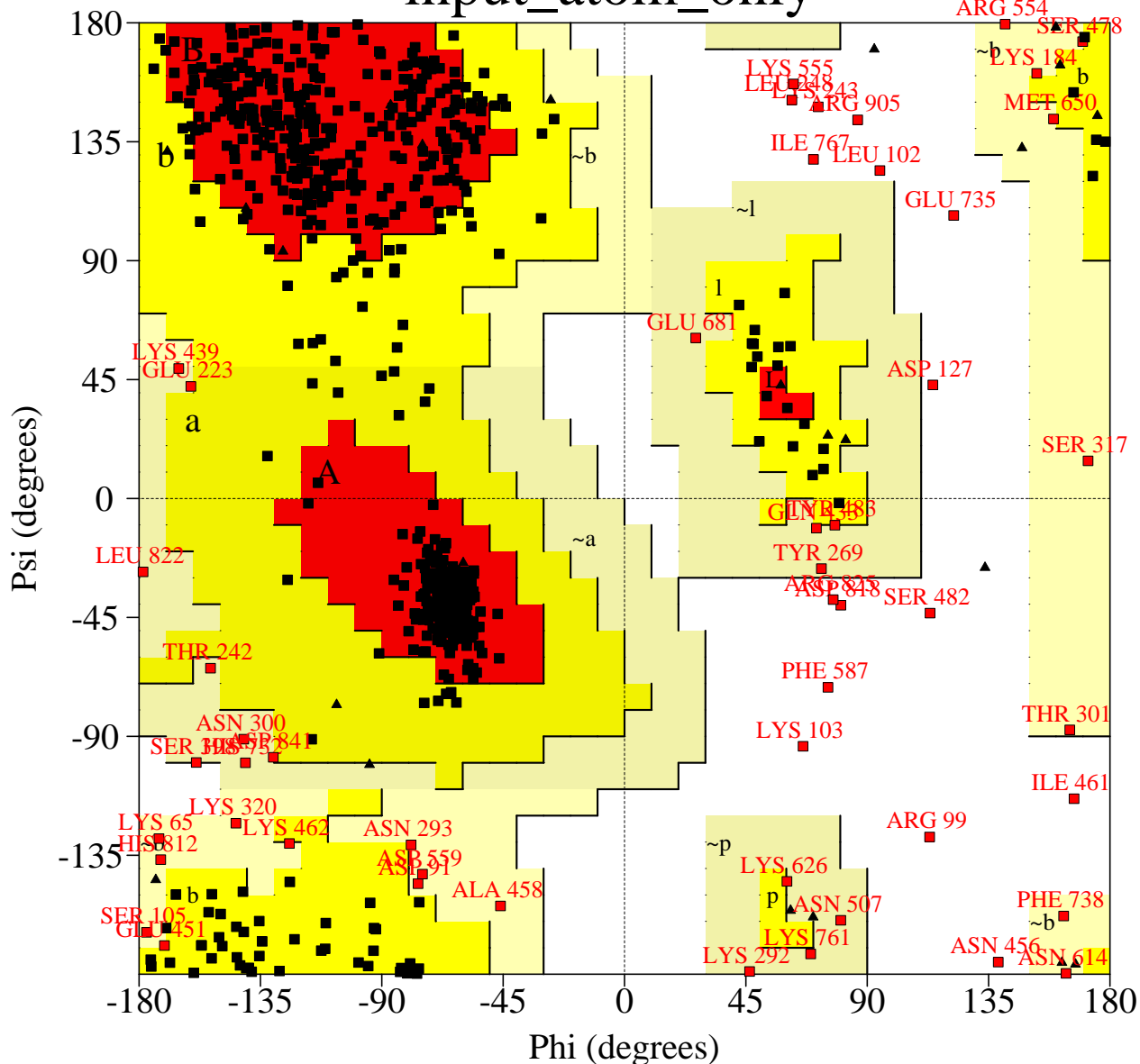


Ramachandran Plot

input_atom_only



Plot statistics

Residues in most favoured regions [A,B,L]	700	79.6%
Residues in additional allowed regions [a,b,l,p]	129	14.7%
Residues in generously allowed regions [-a,-b,-l,-p]	34	3.9%
Residues in disallowed regions	16	1.8%
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Number of non-glycine and non-proline residues	879	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	30	
Number of proline residues	10	
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Total number of residues	921	

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.