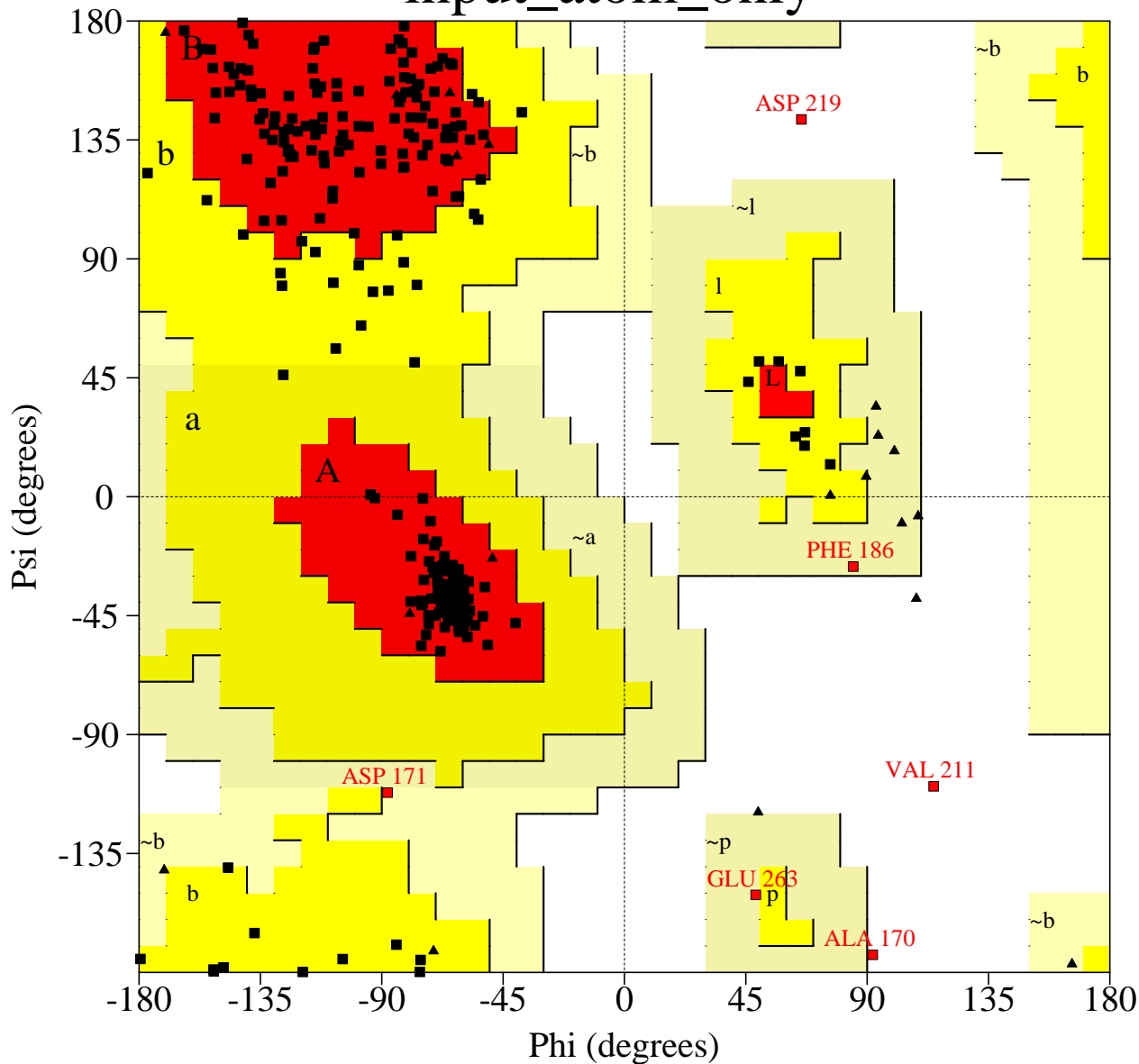


Ramachandran Plot

input_atom_only



Plot statistics

| | | |
|--|-----|--------|
| Residues in most favoured regions [A,B,L] | 297 | 86.1% |
| Residues in additional allowed regions [a,b,l,p] | 42 | 12.2% |
| Residues in generously allowed regions [-~a,-~b,-~l,-~p] | 3 | 0.9% |
| Residues in disallowed regions | 3 | 0.9% |
| ---- | | |
| Number of non-glycine and non-proline residues | 345 | 100.0% |
| Number of end-residues (excl. Gly and Pro) | 1 | |
| Number of glycine residues (shown as triangles) | 21 | |
| Number of proline residues | 9 | |
| ---- | | |
| Total number of residues | 376 | |

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.