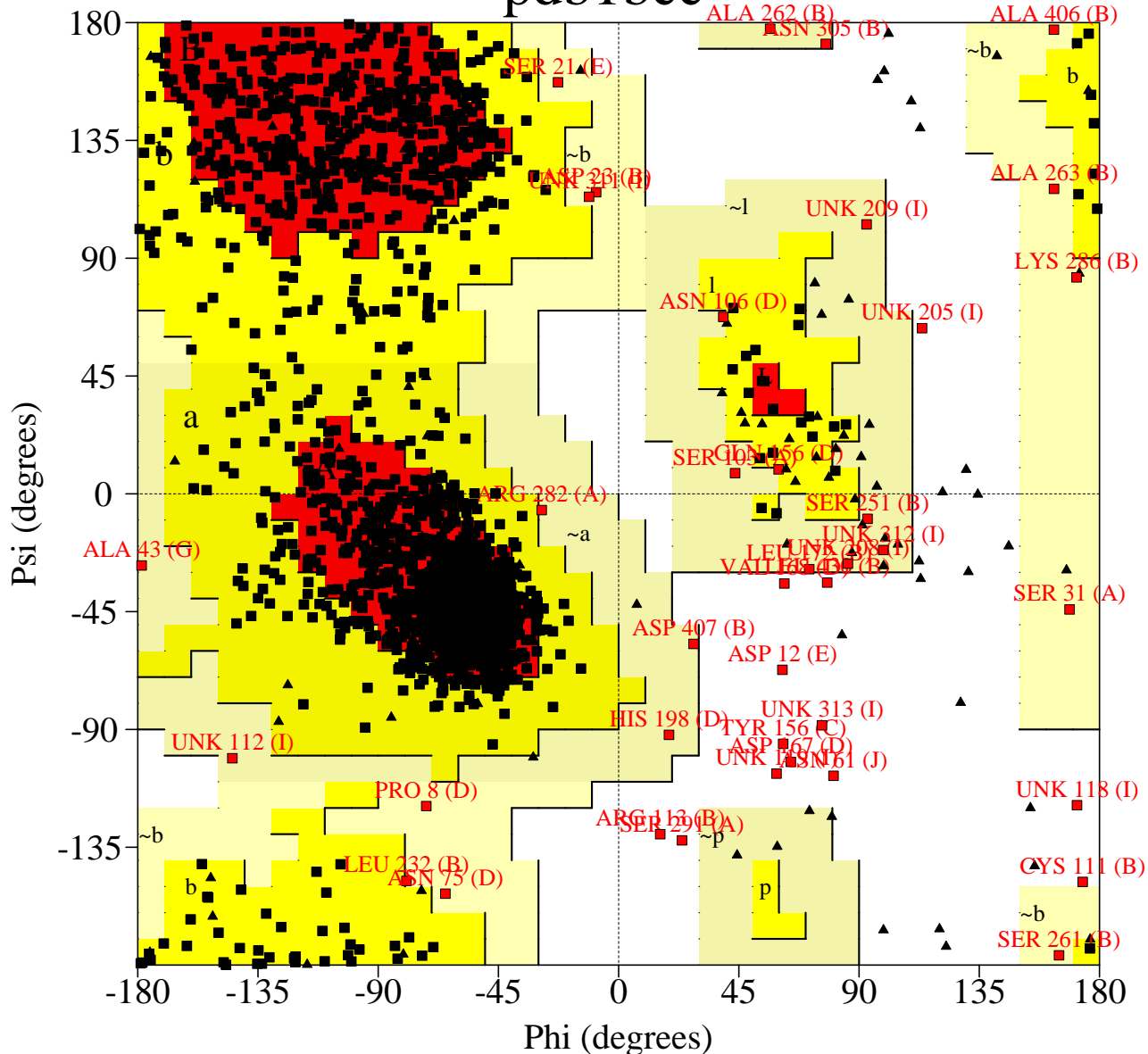


Ramachandran Plot

pdb1bcc



Plot statistics

| | | |
|--|------|--------|
| Residues in most favoured regions [A,B,L] | 1368 | 78.4% |
| Residues in additional allowed regions [a,b,l,p] | 338 | 19.4% |
| Residues in generously allowed regions [-a,-b,-l,-p] | 25 | 1.4% |
| Residues in disallowed regions | 13 | 0.7% |
| Number of non-glycine and non-proline residues | 1744 | 100.0% |
| Number of end-residues (excl. Gly and Pro) | 22 | |
| Number of glycine residues (shown as triangles) | 127 | |
| Number of proline residues | 107 | |
| Total number of residues | 2000 | |

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.