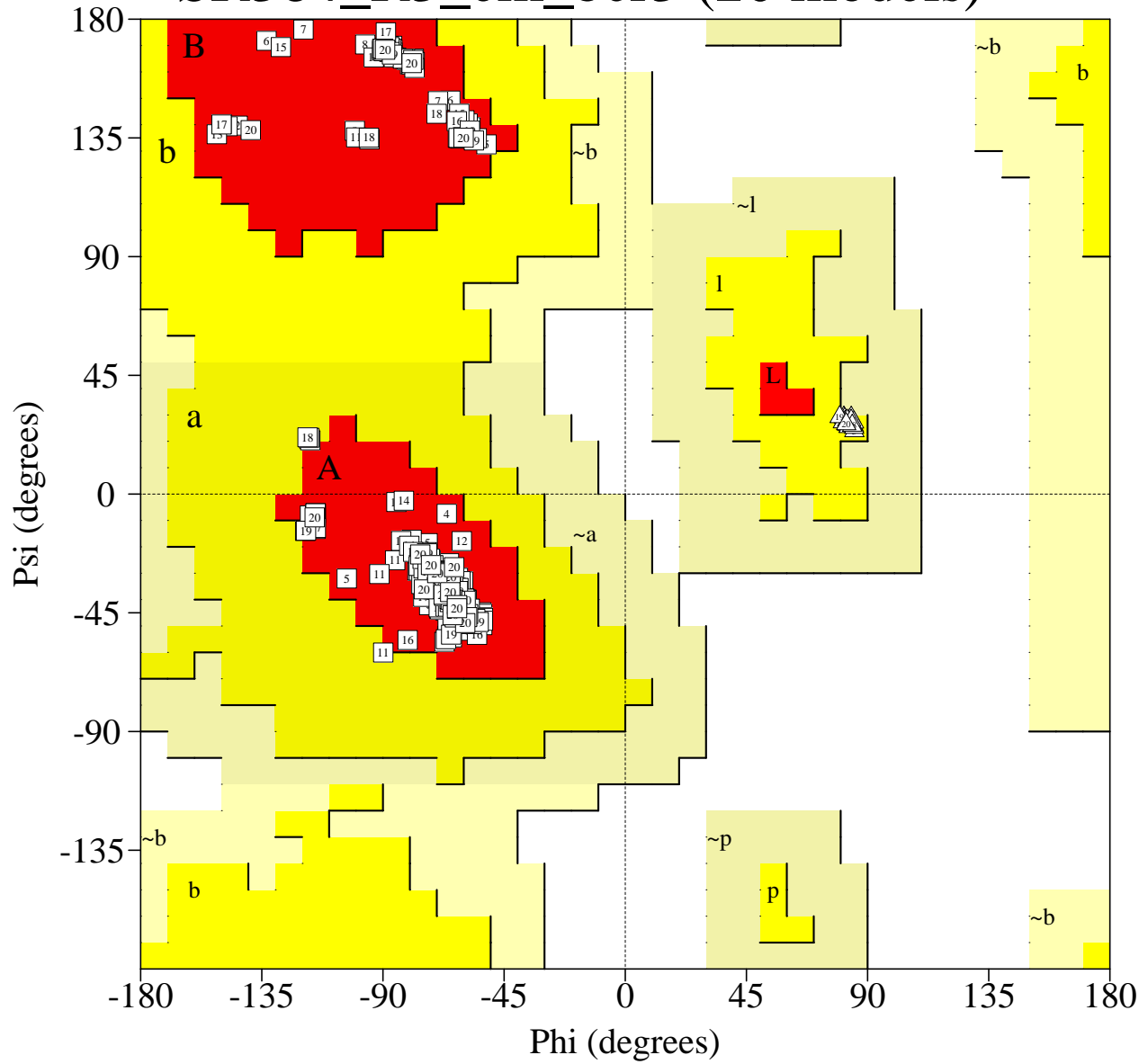


Ramachandran Plot

SR384_R3_em_bcr3 (20 models)**



Plot statistics

| | | |
|--|-----|--------|
| Residues in most favoured regions [A,B,L] | 715 | 99.3% |
| Residues in additional allowed regions [a,b,l,p] | 5 | 0.7% |
| Residues in generously allowed regions [-a,-b,-l,-p] | 0 | 0.0% |
| Residues in disallowed regions | 0 | 0.0% |
| ---- | | |
| Number of non-glycine and non-proline residues | 720 | 100.0% |
| Number of end-residues (excl. Gly and Pro) | 0 | |
| Number of glycine residues (shown as triangles) | 20 | |
| Number of proline residues | 0 | |
| ---- | | |
| Total number of residues | 740 | |

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.
Model numbers shown inside each data point.