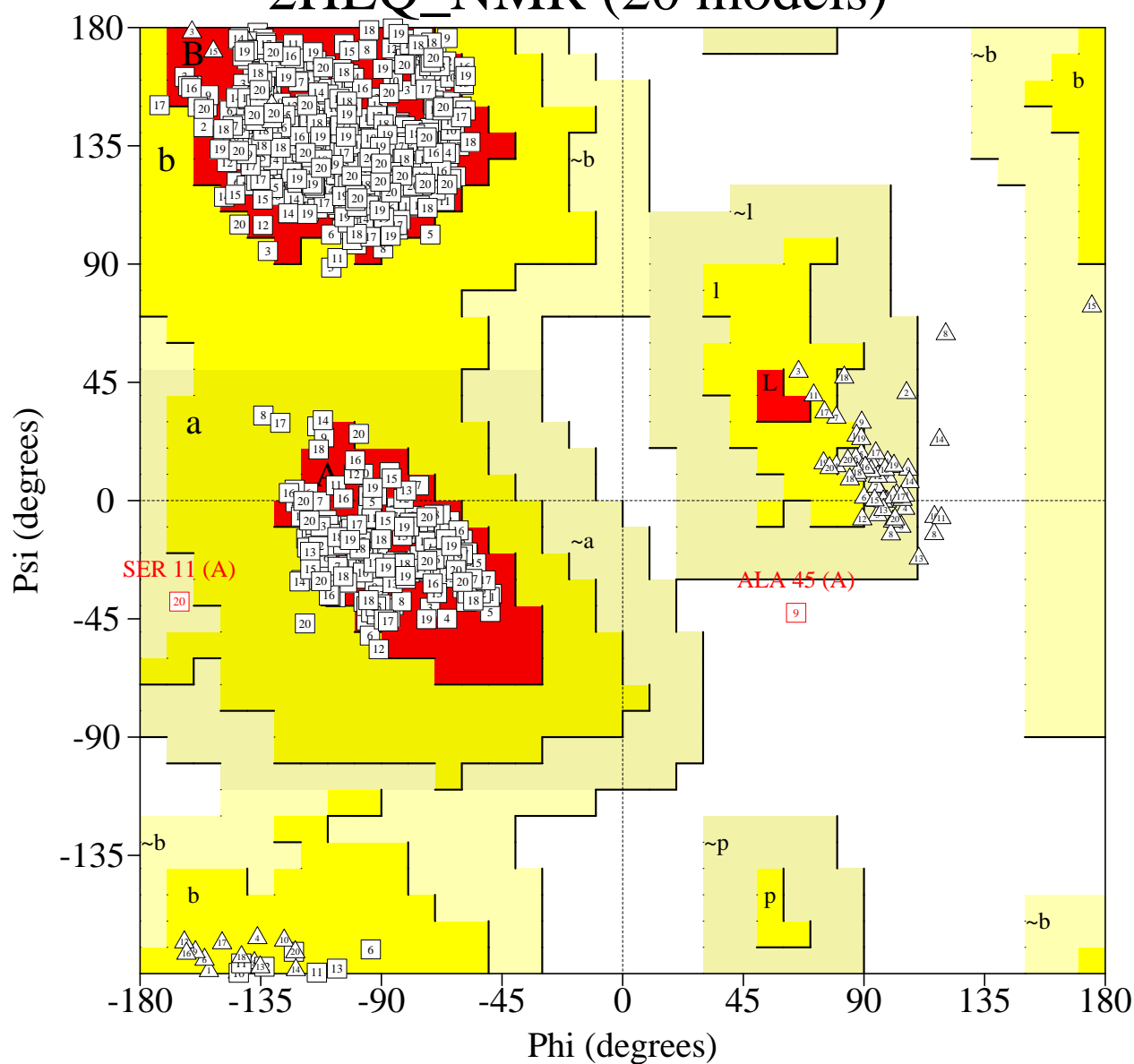


Ramachandran Plot

2HEQ_NMR (20 models)**



Plot statistics

| | | |
|--|-----|--------|
| Residues in most favoured regions [A,B,L] | 724 | 95.3% |
| Residues in additional allowed regions [a,b,l,p] | 34 | 4.5% |
| Residues in generously allowed regions [~a,~b,~l,~p] | 1 | 0.1% |
| Residues in disallowed regions | 1 | 0.1% |
| ----- | | |
| Number of non-glycine and non-proline residues | 760 | 100.0% |
| Number of end-residues (excl. Gly and Pro) | 0 | |
| Number of glycine residues (shown as triangles) | 80 | |
| Number of proline residues | 40 | |
| ----- | | |
| Total number of residues | 880 | |

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.