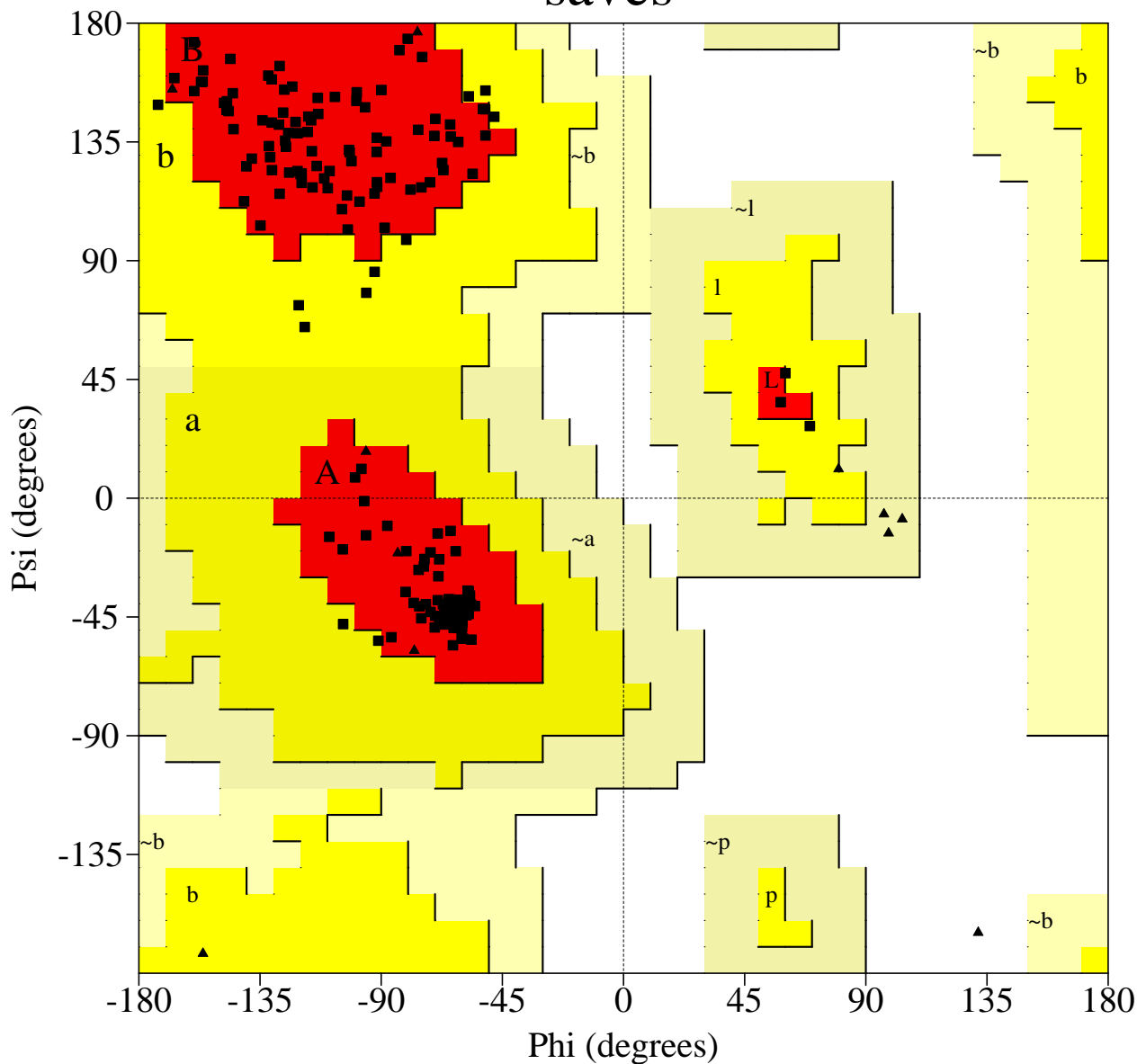


# Ramachandran Plot

saves



### Plot statistics

|  |     |        |
|--|-----|--------|
| Residues in most favoured regions [A,B,L]            | 156 | 94.0%  |
| Residues in additional allowed regions [a,b,l,p]     | 10  | 6.0%   |
| 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       | 166 | 100.0% |
| Number of end-residues (excl. Gly and Pro)           | 3   |        |
| Number of glycine residues (shown as triangles)      | 11  |        |
| Number of proline residues                           | 10  |        |
| -----  |     |        |
| Total number of residues                             | 190 |        |

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.