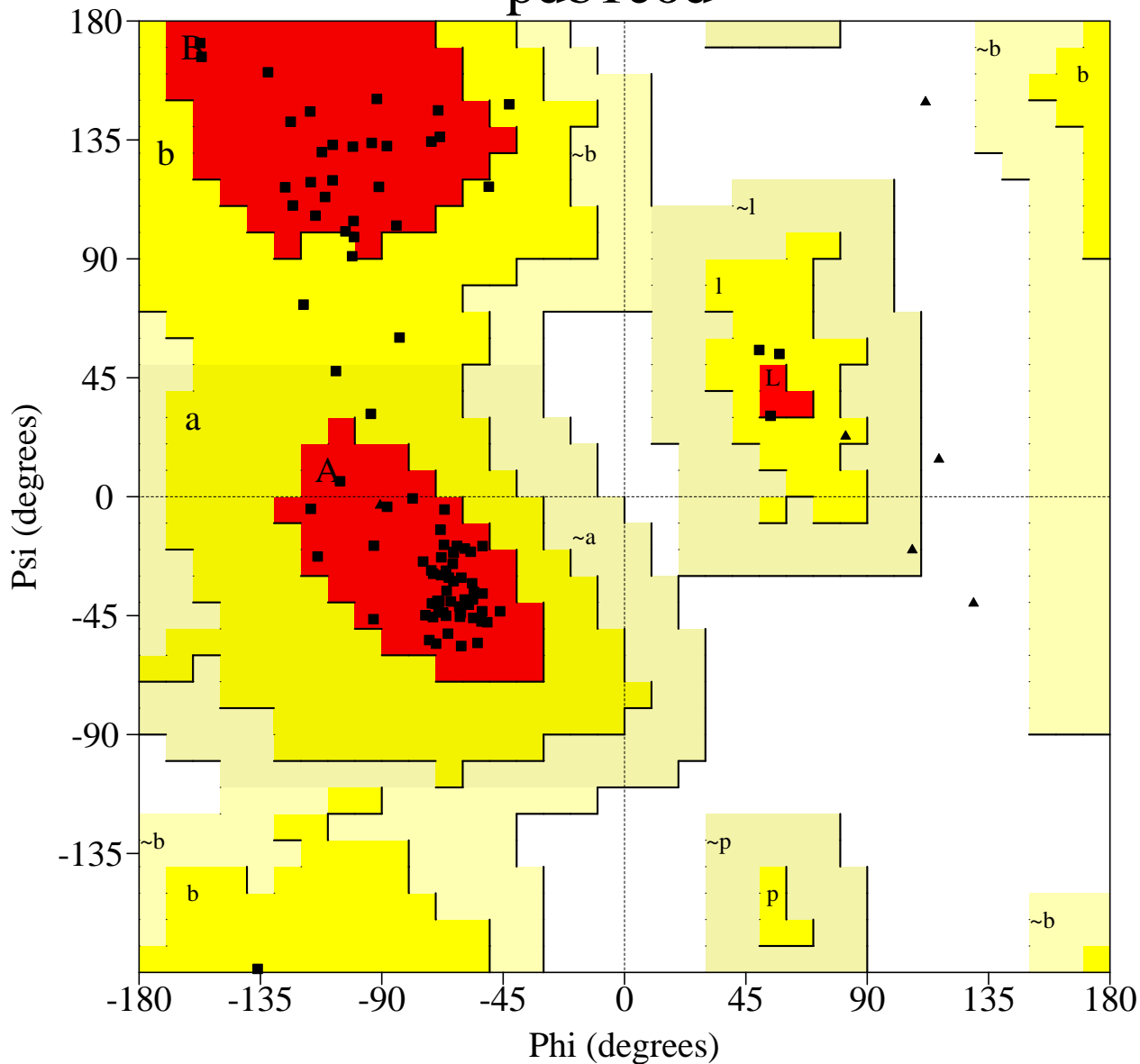


# Ramachandran Plot

pdb1eod



### Plot statistics

|  |     |        |
|--|-----|--------|
| Residues in most favoured regions [A,B,L]                | 76  | 88.4%  |
| Residues in additional allowed regions [a,b,l,p]         | 10  | 11.6%  |
| 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           | 86  | 100.0% |
| Number of end-residues (excl. Gly and Pro)               | 2   |        |
| Number of glycine residues (shown as triangles)          | 6   |        |
| Number of proline residues                               | 6   |        |
| -----  |     |        |
| Total number of residues                                 | 100 |        |

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.