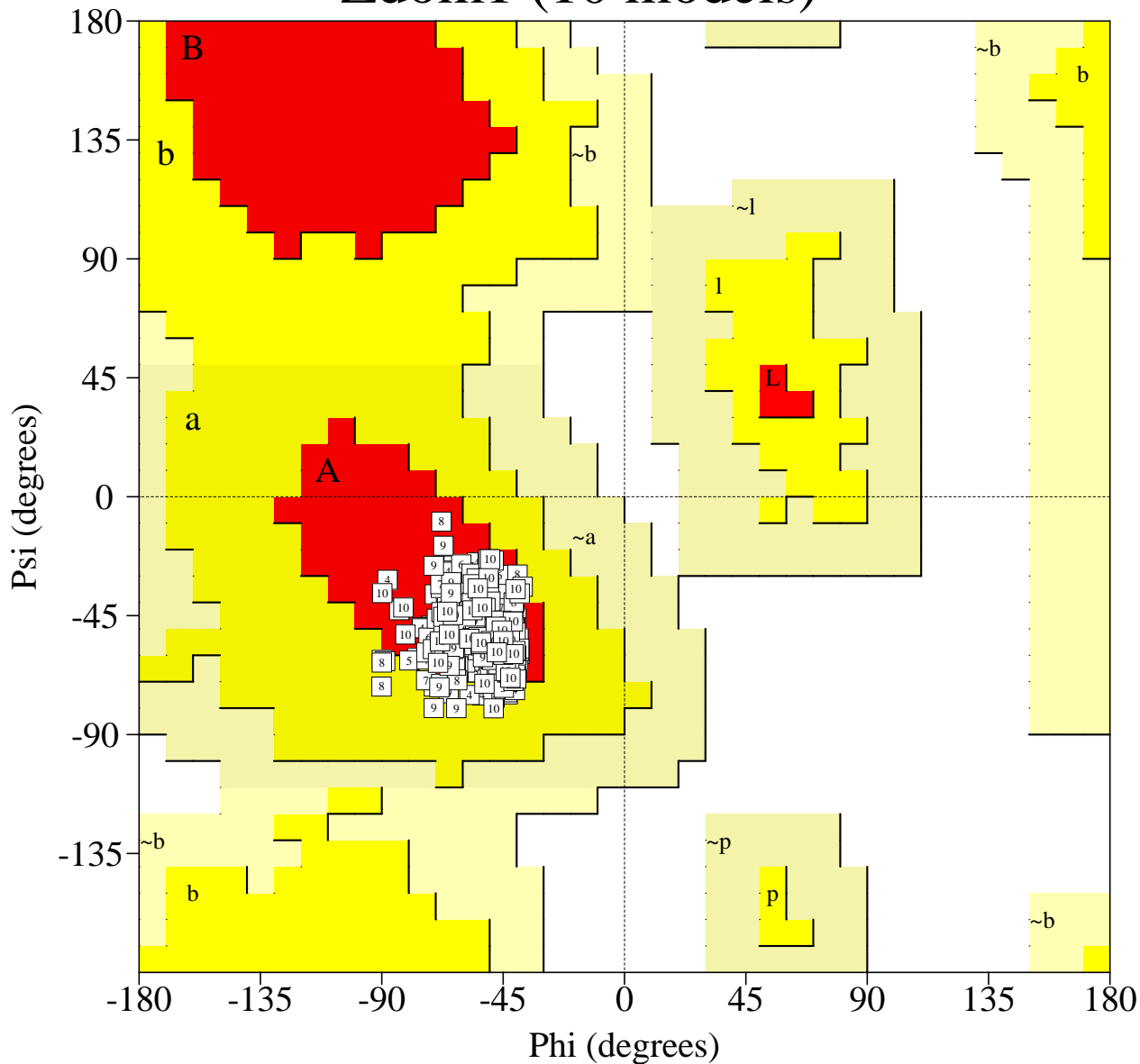


Ramachandran Plot

Zdom1 (10 models)**



Plot statistics

Residues in most favoured regions [A,B,L]	363	93.1%
Residues in additional allowed regions [a,b,l,p]	27	6.9%
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	390	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	0	
Number of proline residues	0	

Total number of residues	390	

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.