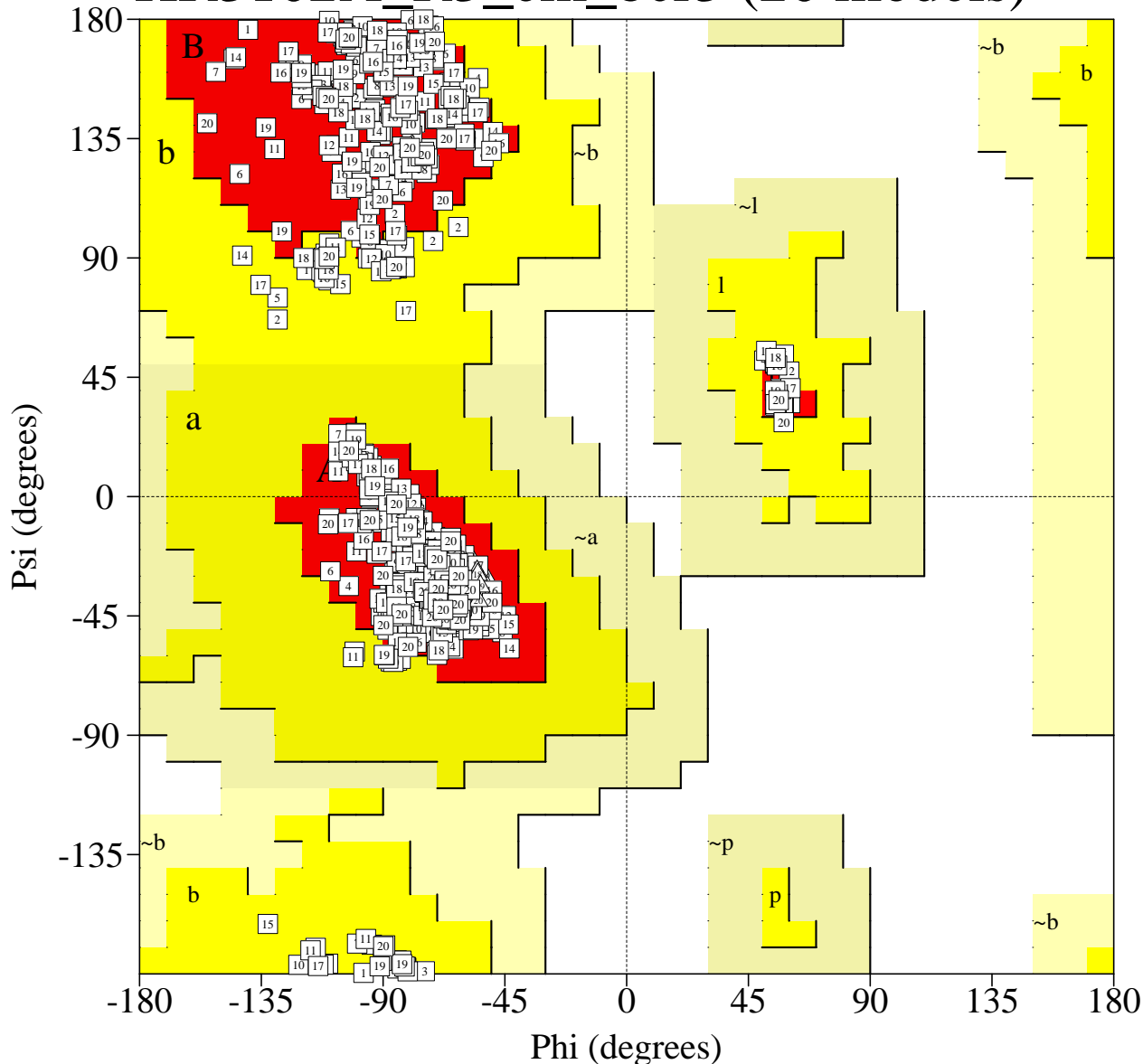


# Ramachandran Plot

## HR3102A\_R3\_em\_bcr3 (20 models)\*\*



### Plot statistics

Residues in most favoured regions [A,B,L]	1194	93.3%
Residues in additional allowed regions [a,b,l,p]	86	6.7%
Residues in generously allowed regions [-a,-b,-l,-p]	0	0.0%
Residues in disallowed regions	0	0.0%
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Number of non-glycine and non-proline residues	1280	100.0%
Number of end-residues (excl. Gly and Pro)	0	
Number of glycine residues (shown as triangles)	60	
Number of proline residues	20	
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Total number of residues	1360	

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.