PHD

Structural and functional analysis of Staphylococcus aureus immune evasion proteins

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Link to publication
Based on an analysis of 118 structures of resolution of at least 2.0 Å and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Figure 5.2 Ramachandran Plots for Sbi IV – C3d models 1 and 2
Plot statistics are indicated and show that all non-glycine and non-proline residues fall within most favoured or additional allowed areas. Plots were generated using PROCHECK (Laskowski et al., 1993). Based on an analysis of 118 structures of resolution of at least 2.0 Å and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.