Ramachandran Plot

![Ramachandran Plot](final_apo_ece_01.ps)

**Plot statistics**

- Residues in most favoured regions \([A,B,L]\)          503 86.3%
- Residues in additional allowed regions \([a,b,l,p]\)  72 12.3%
- Residues in generously allowed regions \([-a,-b,-l,-p]\) 6 1.0%
- Residues in disallowed regions                              2 0.3%

- Number of non-glycine and non-proline residues          583 100.0%
- Number of end-residues (excl. Gly and Pro)                6
- Number of glycine residues (shown as triangles)          35
- Number of proline residues                               36

- Total number of residues                                660

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.