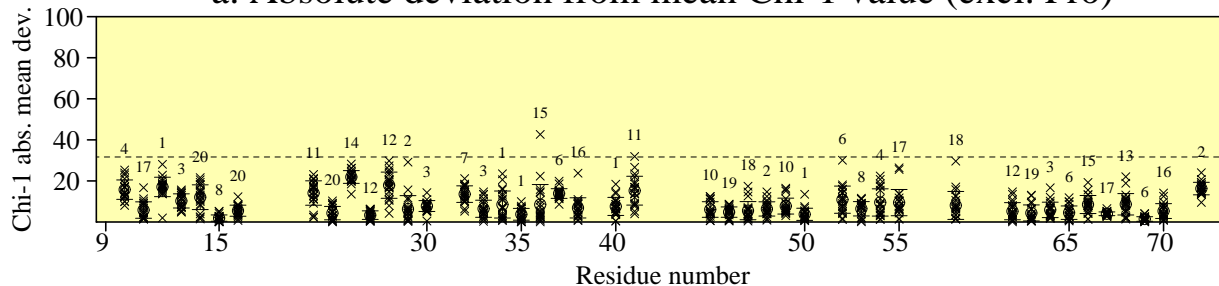


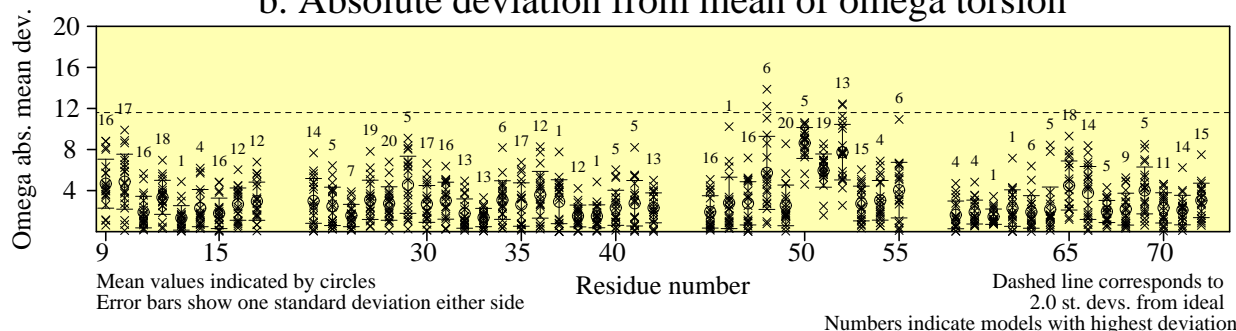
Residue properties

DHR29B_NMR_em_bcr3 (20 models)**

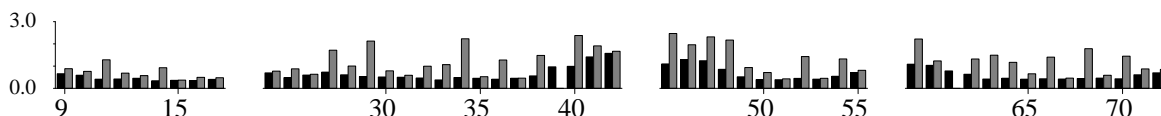
a. Absolute deviation from mean Chi-1 value (excl. Pro)



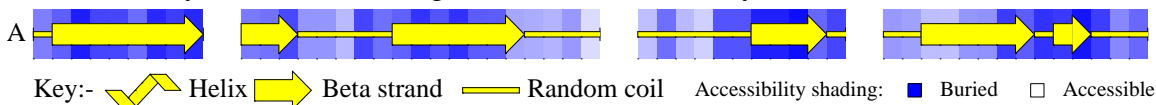
b. Absolute deviation from mean of omega torsion



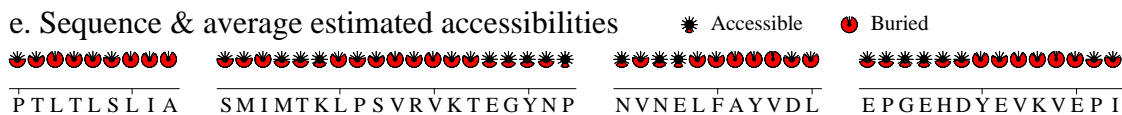
c. RMS devs from mean coords: main-chain (black) and side-chain (grey)



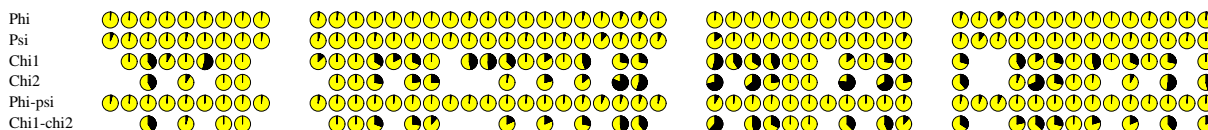
d. Secondary structure & average estimated accessibility



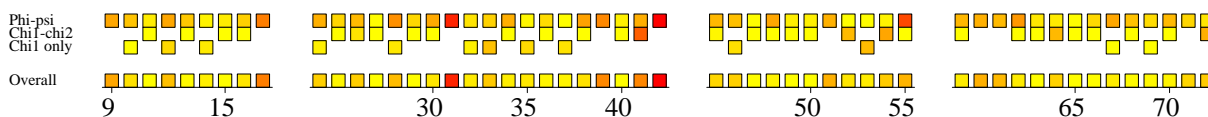
e. Sequence & average estimated accessibilities



f. Circular variances

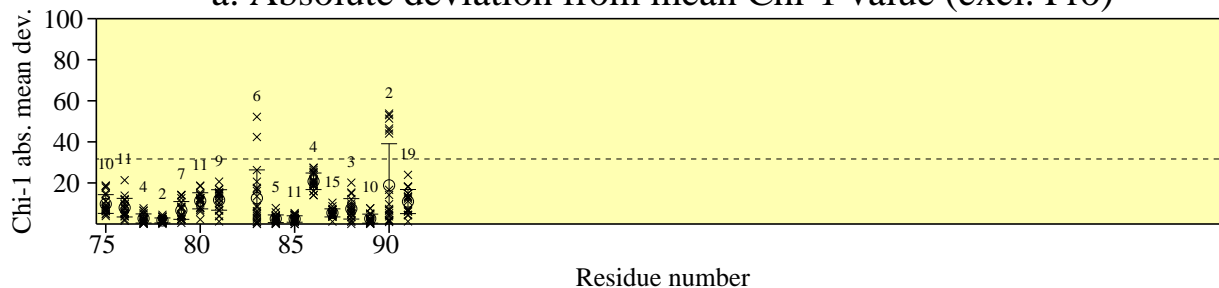


g. G-factors

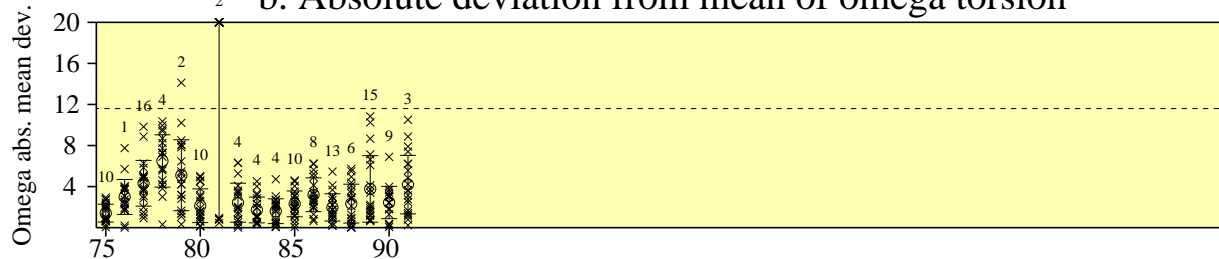


Residue properties DHR29B_NMR_em_bcr3 (20 models)**

a. Absolute deviation from mean Chi-1 value (excl. Pro)

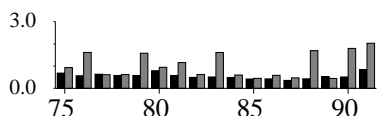


b. Absolute deviation from mean of omega torsion



Mean values indicated by circles
 Error bars show one standard deviation either side
 Dashed line corresponds to 2.0 st. devs. from ideal
 Numbers indicate models with highest deviation

c. RMS devs from mean coords: main-chain (black) and side-chain (grey)



d. Secondary structure & average estimated accessibility



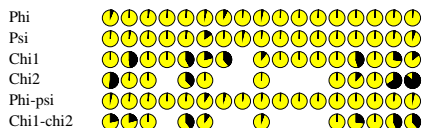
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & average estimated accessibilities

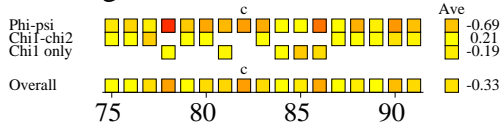


* Accessible Buried

f. Circular variances



g. G-factors



c = cis-peptide