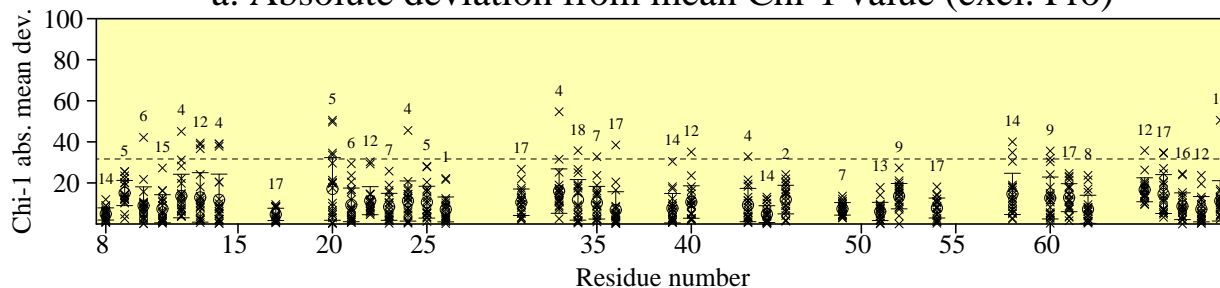


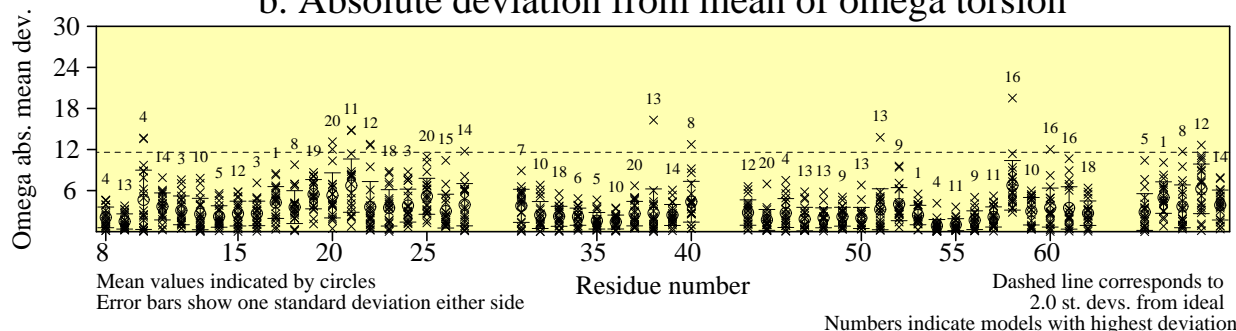
# Residue properties

## CTR107\_NMR\_em\_bcr3 (20 models)\*\*

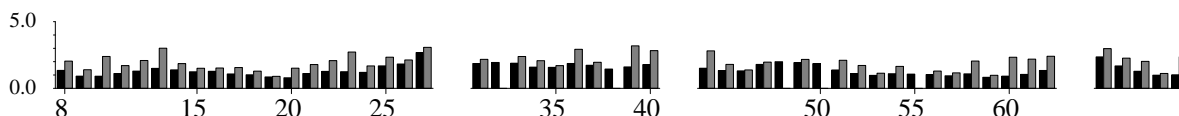
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



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



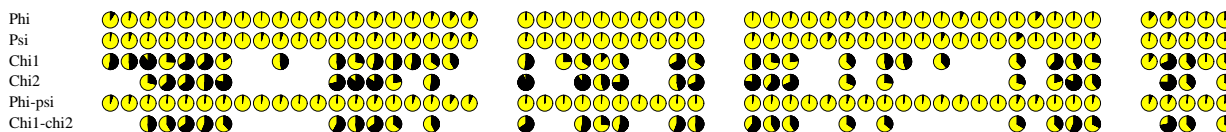
d. Secondary structure & average estimated accessibility



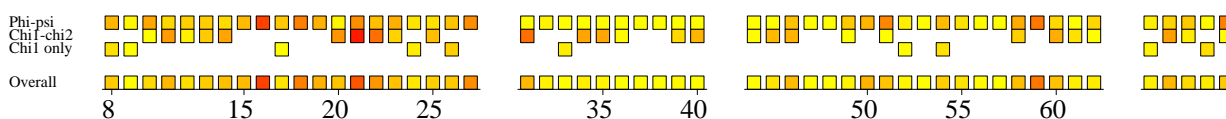
e. Sequence & average estimated accessibilities



f. Circular variances



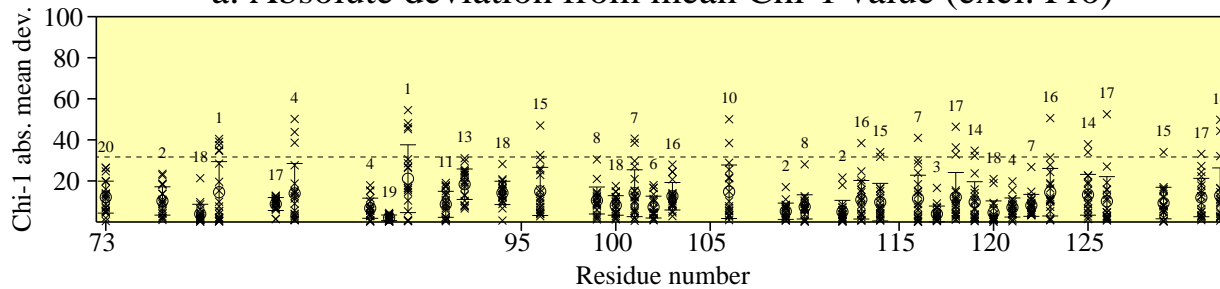
g. G-factors



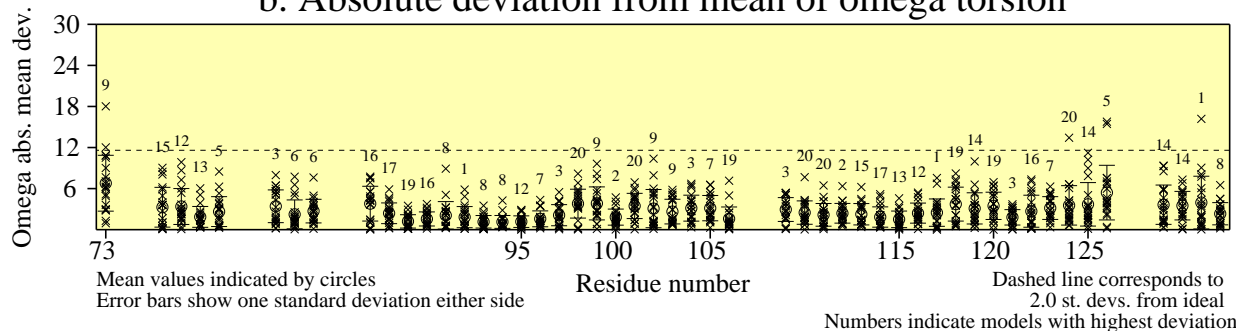
# Residue properties

## CTR107\_NMR\_em\_bcr3 (20 models)\*\*

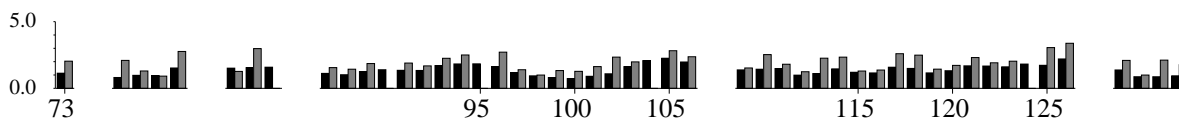
a. Absolute deviation from mean Chi-1 value (excl. Pro)



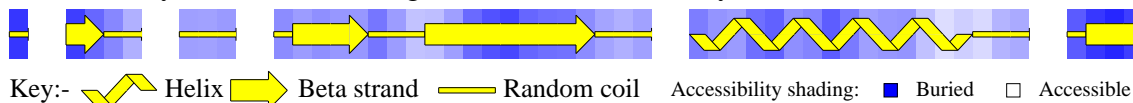
b. Absolute deviation from mean of omega torsion



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



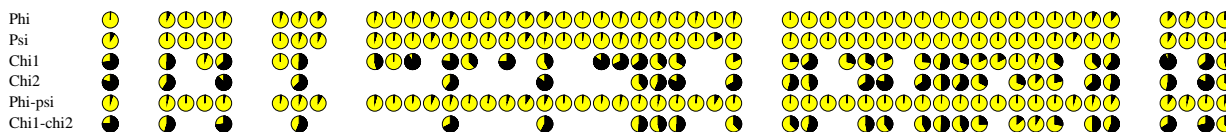
d. Secondary structure & average estimated accessibility



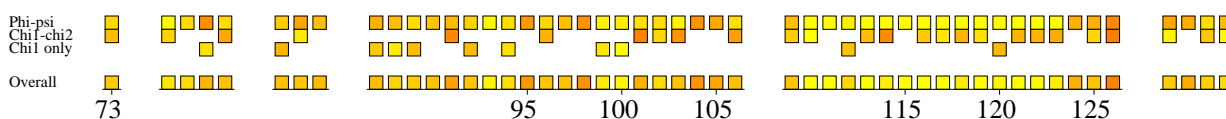
e. Sequence & average estimated accessibilities



f. Circular variances



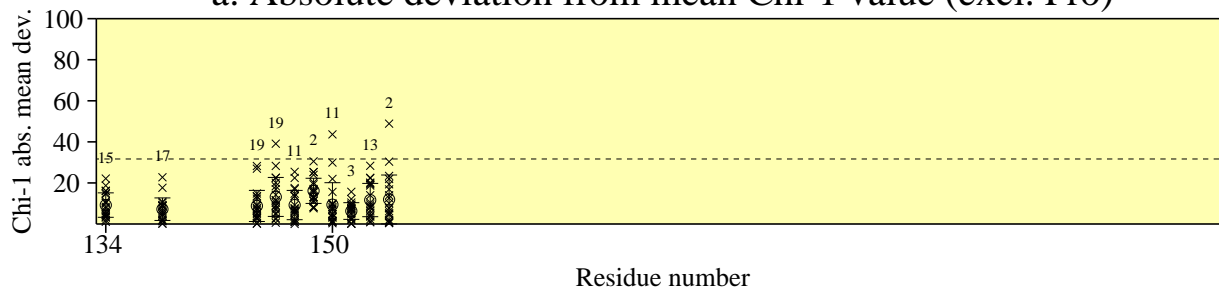
g. G-factors



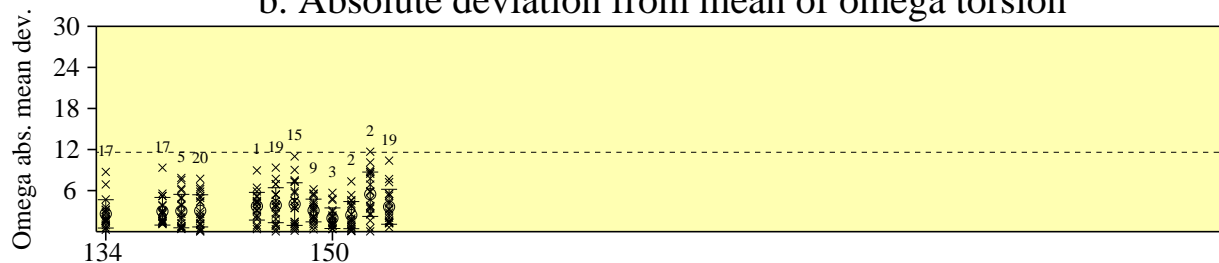
# Residue properties

## CTR107\_NMR\_em\_bcr3 (20 models)\*\*

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

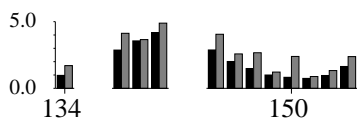


b. Absolute deviation from mean of omega torsion

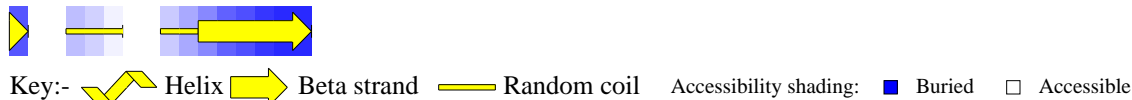


Mean values indicated by circles  
 Error bars show one standard deviation either side  
 Dashed line corresponds to 2.0 st. devs. from ideal  
 Numbers indicate models with highest deviation

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



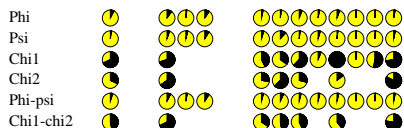
d. Secondary structure & average estimated accessibility



e. Sequence & average estimated accessibilities



f. Circular variances



g. G-factors

