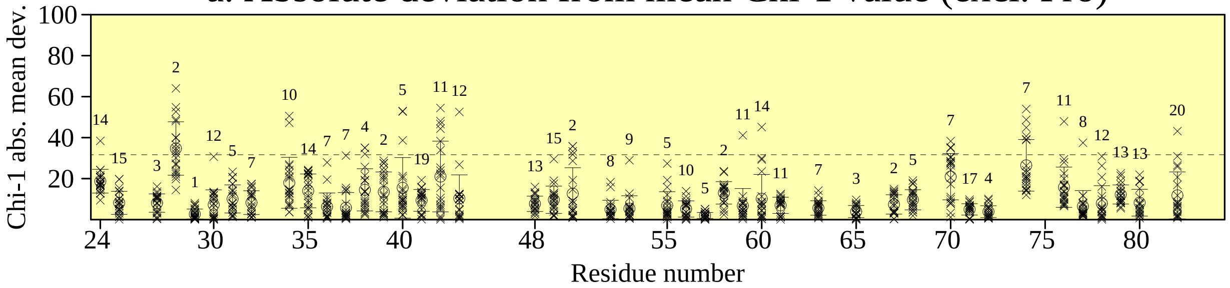
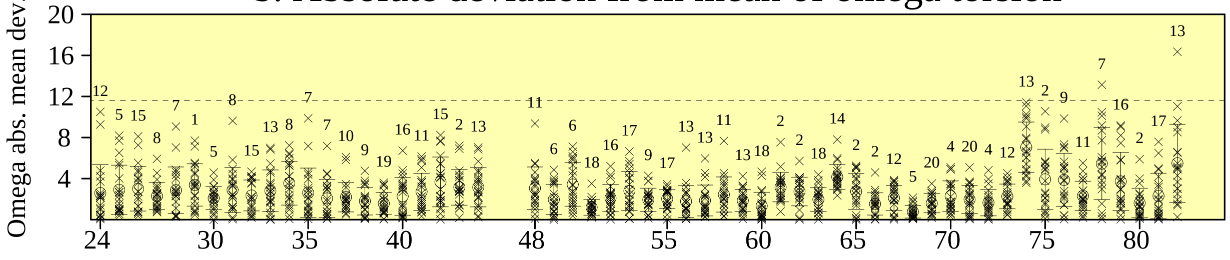
Residue properties

HR3646E_NMR_em_bcr3 (20 models)**

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



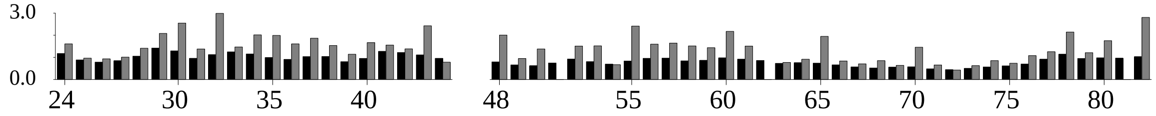
b. Absolute deviation from mean of omega torsion



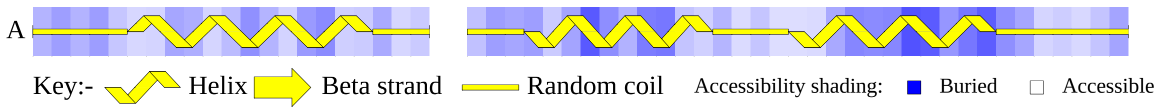
Mean values indicated by circles
Error bars show one standard deviation either side

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)

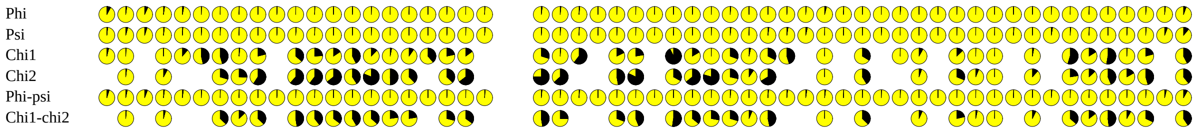


d. Secondary structure & average estimated accessibility

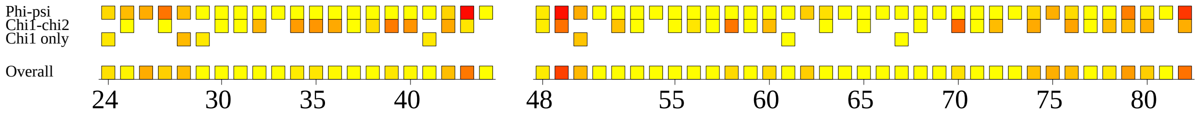


e. Sequence & average estimated accessibilities

f. Circular variances



g. G-factors

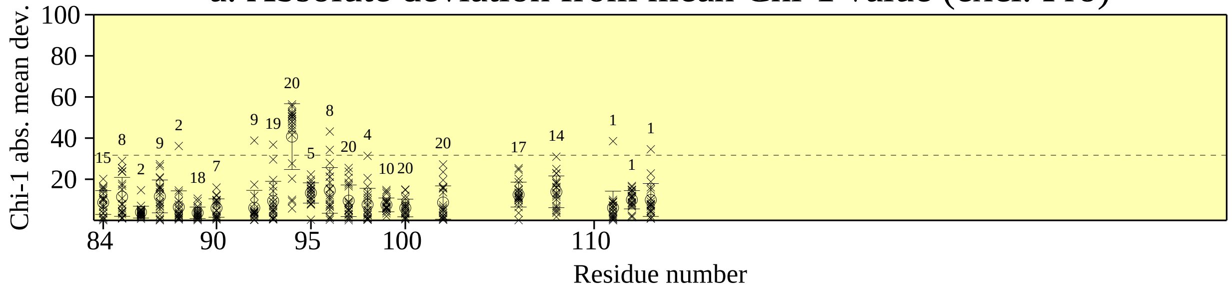


** Selected residues only

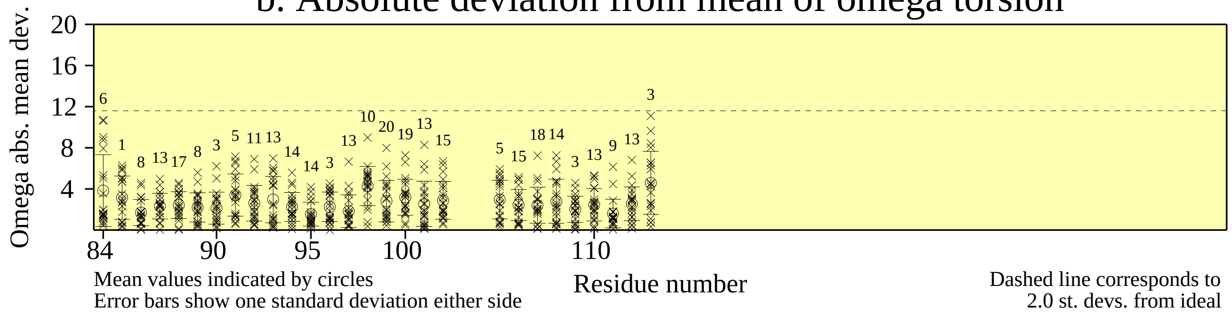
Residue properties

HR3646E_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
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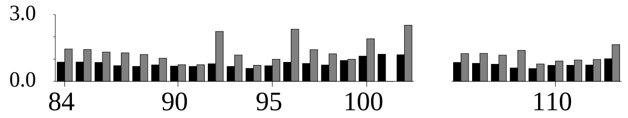
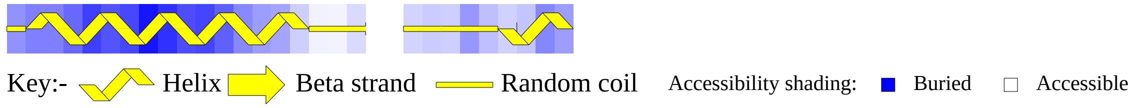
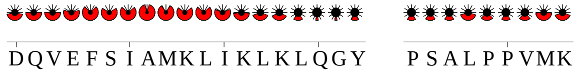


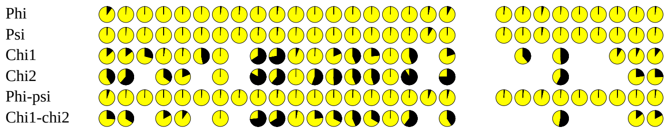
d. Secondary structure & average estimated accessibility



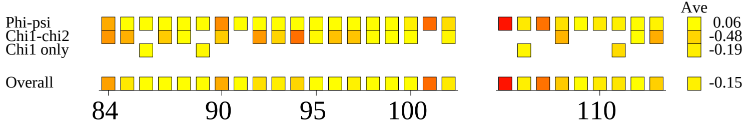
e. Sequence & average estimated accessibilities



f. Circular variances



g. G-factors



** Selected residues only