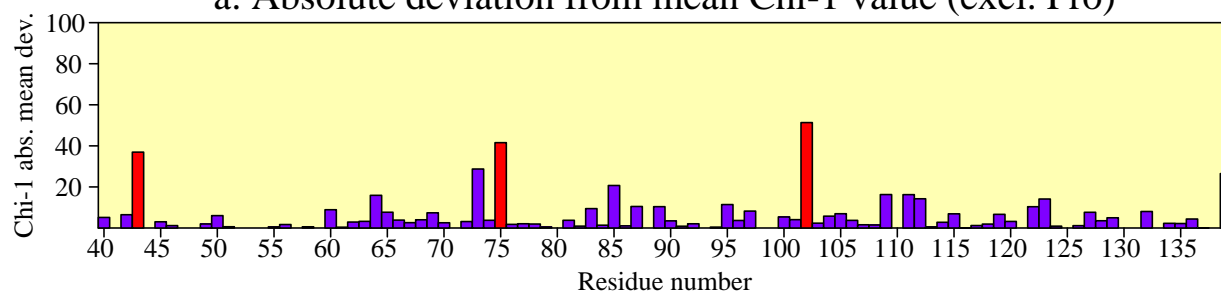


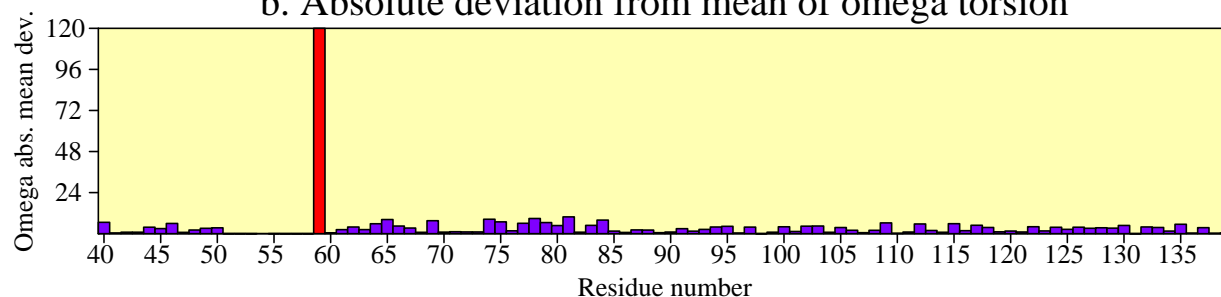
Residue properties

Model_12

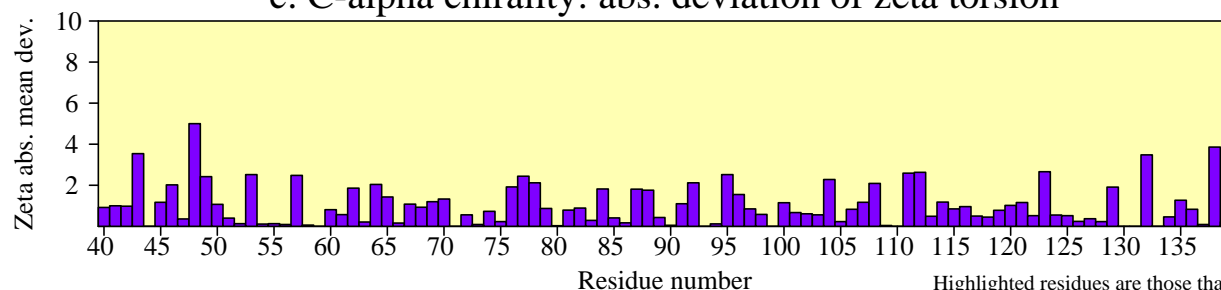
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion



c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



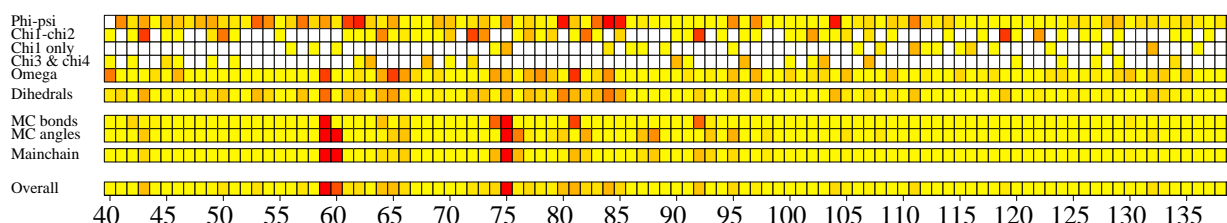
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

KAQIGKEAPEFKAPAYCPCGS I KE ID INEYRGKYVLLFYPLDWTFCPTMIGYSELGQLKE INCEVIGVSVDSVYCHQAWCEADKSKGGVGKLTFL

f. Max. deviation_r (see listing)



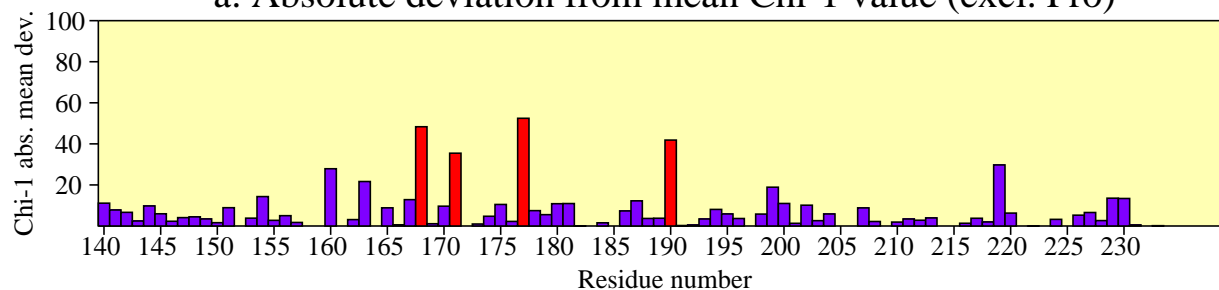
g. G-factors



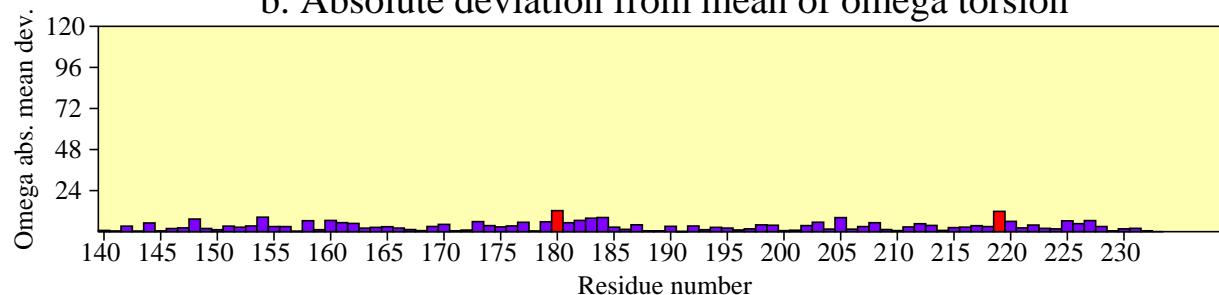
Residue properties

Model_12

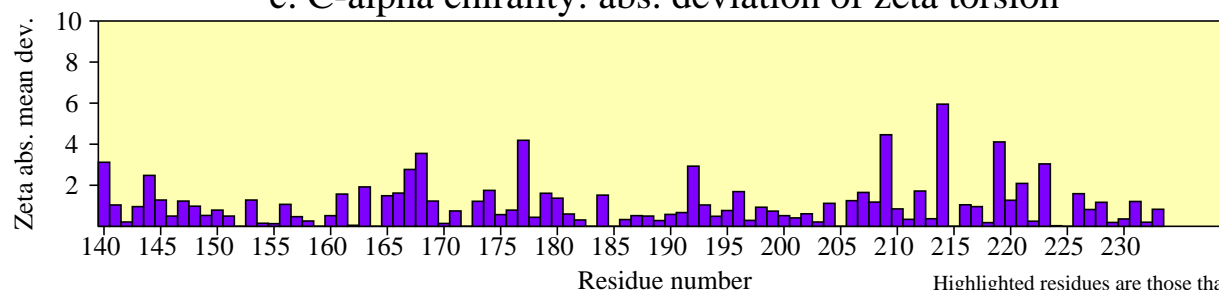
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

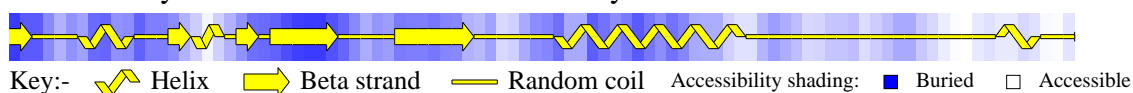


c. C-alpha chirality: abs. deviation of zeta torsion



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed



f. Max. deviation (see listing)



g. G-factors

