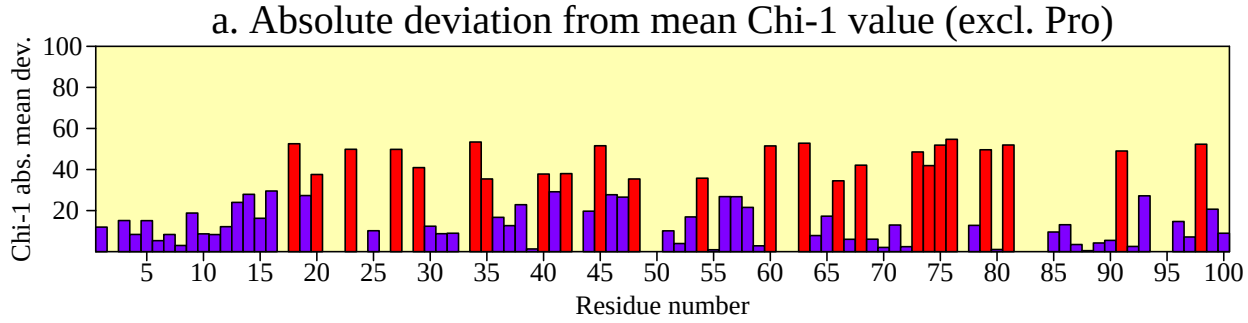
PROCHECK

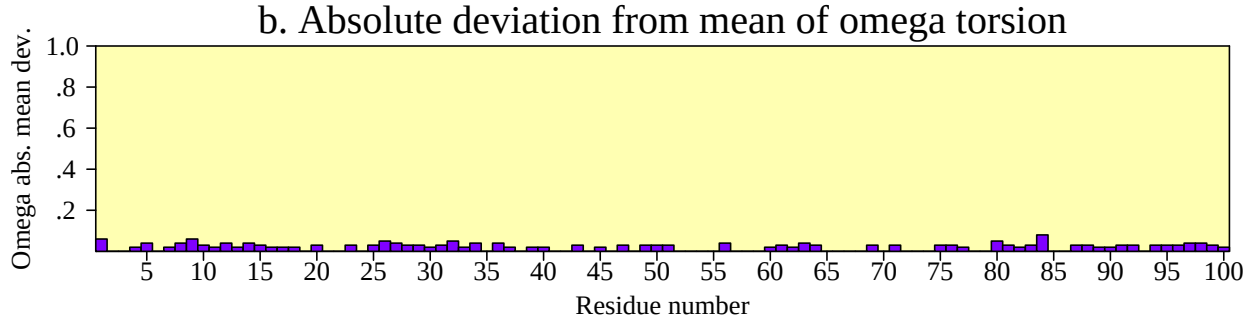


# Residue properties
## analyzed_6

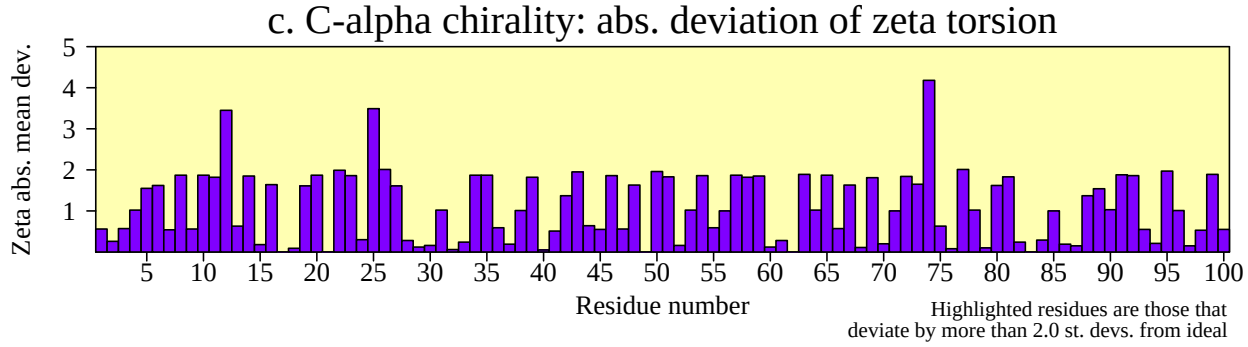
a. Absolute deviation from mean Chi-1 value (excl. Pro)




b. Absolute deviation from mean of omega torsion

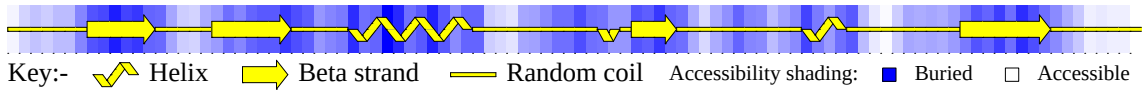



c. C-alpha chirality: abs. deviation of zeta torsion



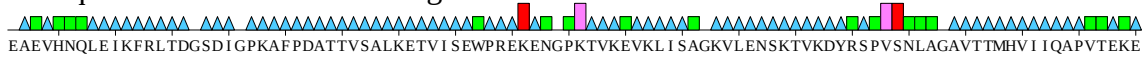

Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



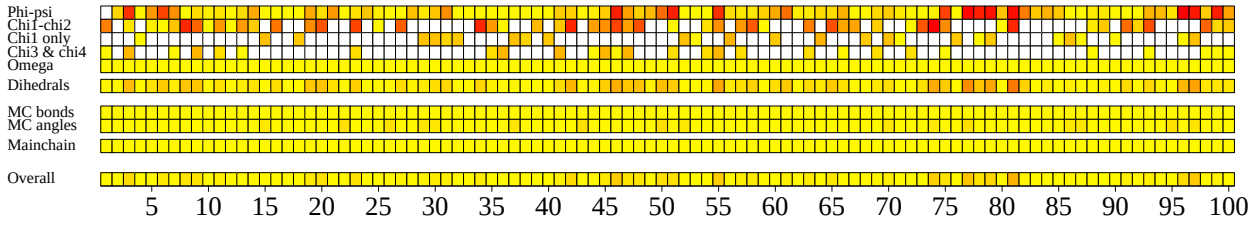
Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed




f. Max. deviation (see listing)

g. G-factors

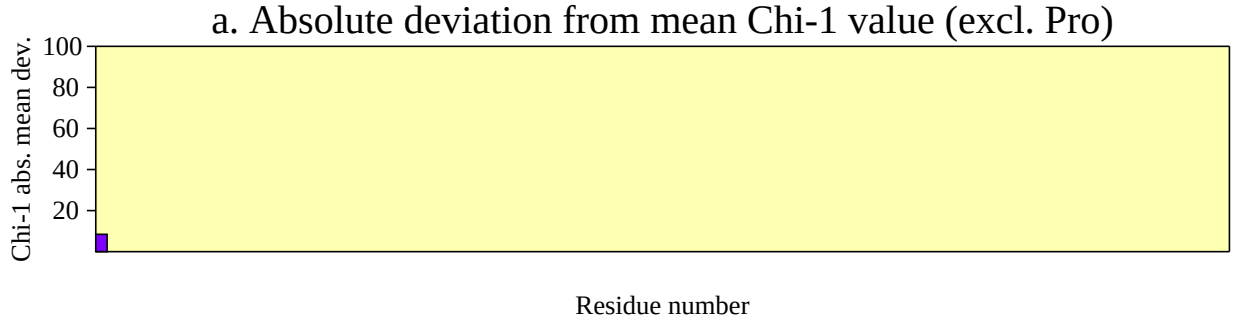



analyzed_6_06.ps

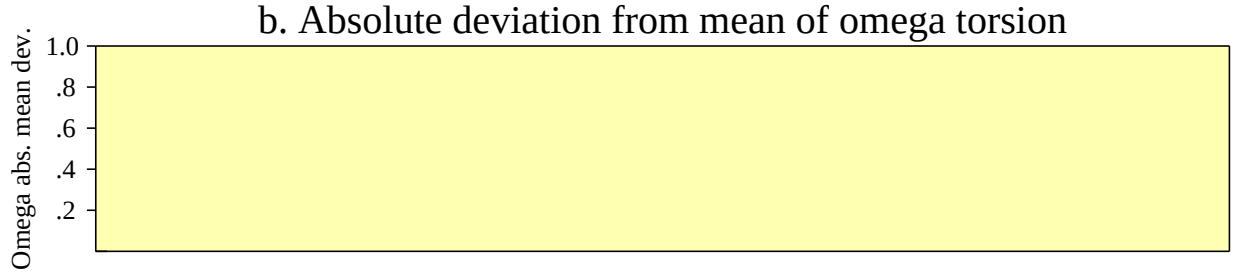
# Residue properties

## analyzed_6

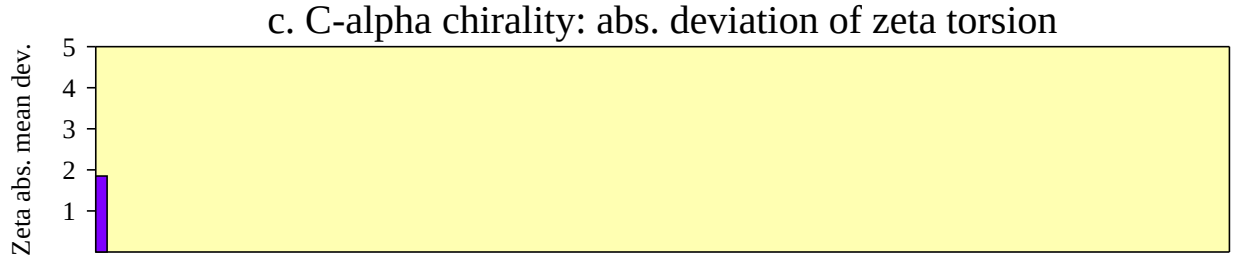
a. Absolute deviation from mean Chi-1 value (excl. Pro)




b. Absolute deviation from mean of omega torsion




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

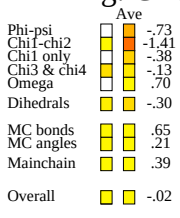



Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility

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

e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

f. Max. deviation (see listing)

g. G-factors