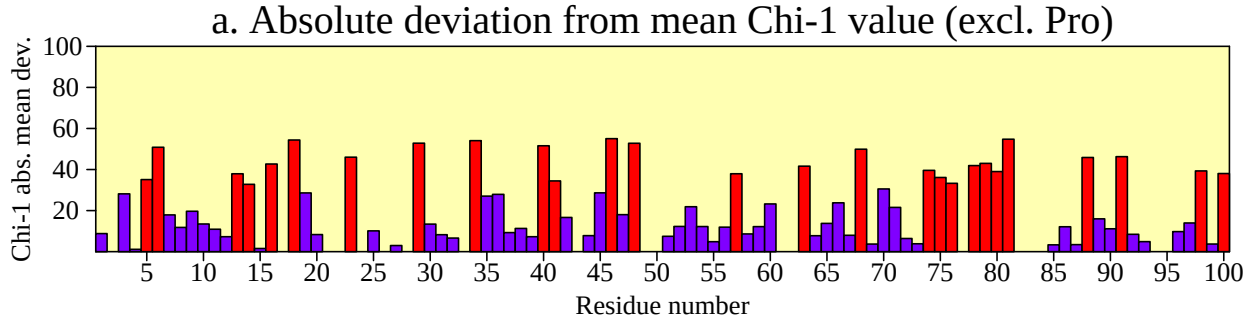
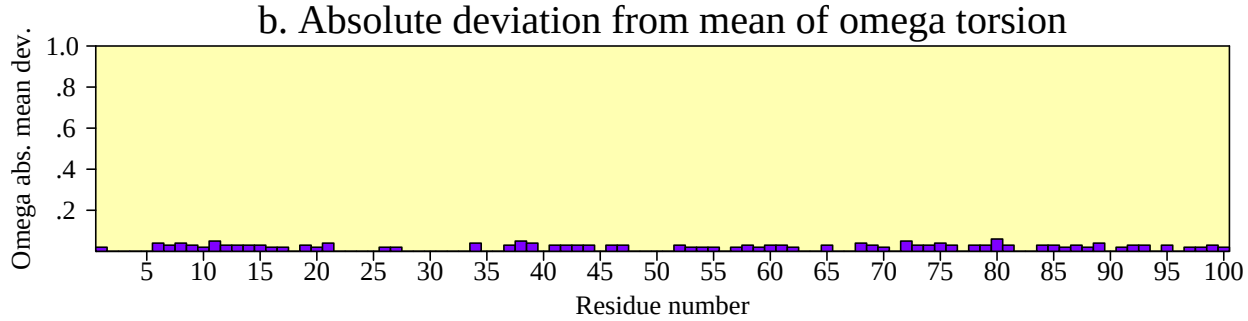
PROCHECK

Residue properties
analyzed_8

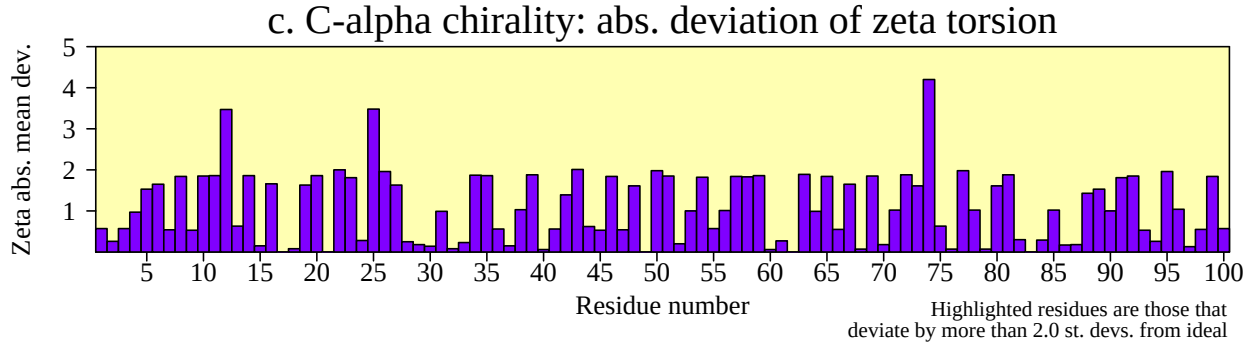
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

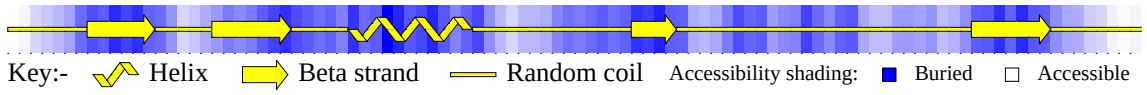


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility

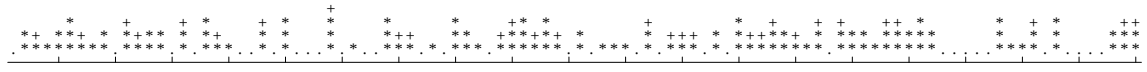


Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

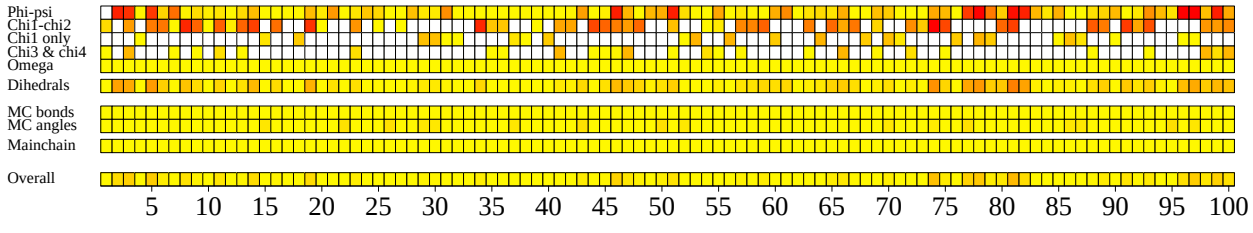
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

EAEVHNQLEIKFRLTDGSDIGPKAFPDATTVSALKETVISEWPREKENGPKTVKEVKLISAGKVLENSKTVKDYRSPVSNLAGAVTTMHVIIQAPVTEKE

f. Max. deviation (see listing)



g. G-factors

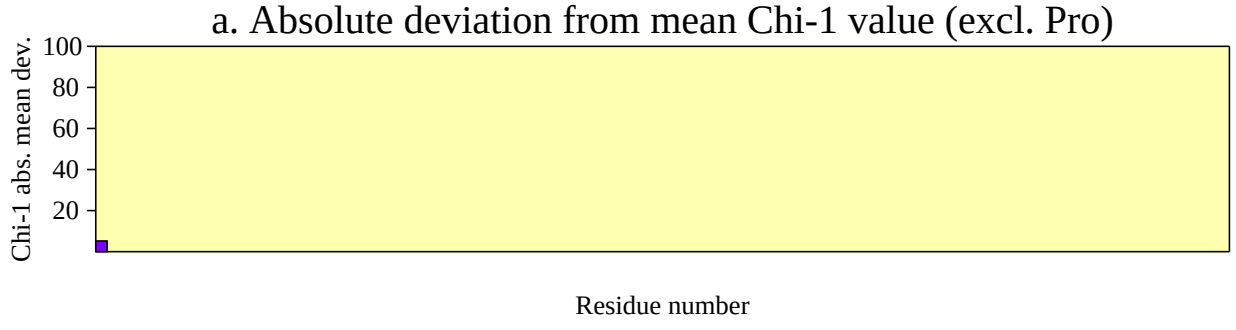


analyzed_8_06.ps

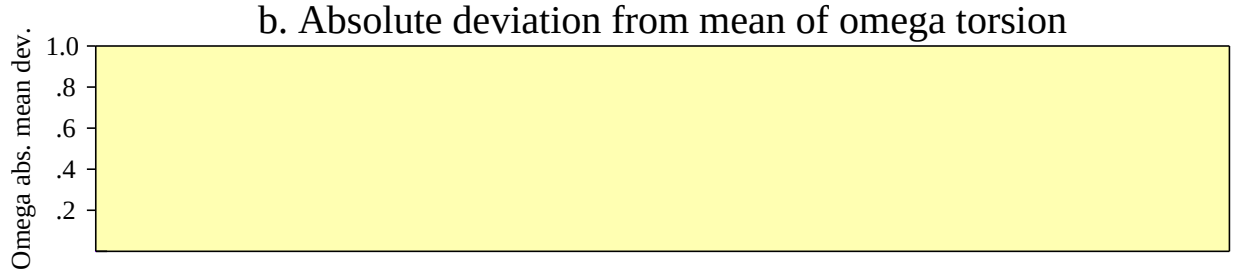
Residue properties

analyzed_8

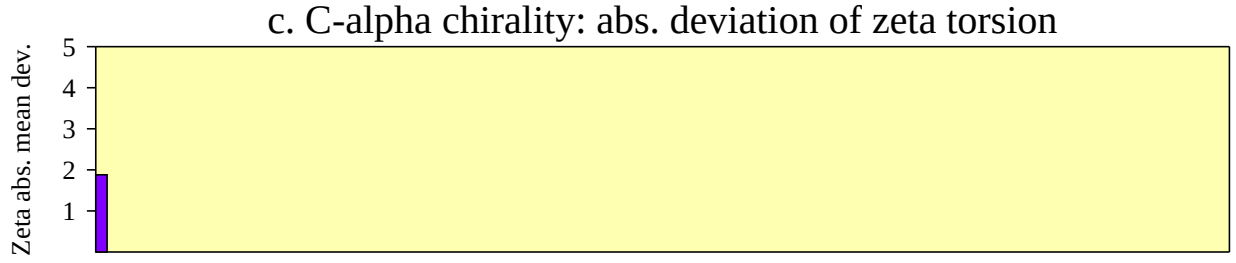
a. Absolute deviation from mean Chi-1 value (excl. Pro)



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

	Ave
Phi-psi	-.68
Chi1-chi2	-1.67
Chi1 only	-.35
Chi3 & chi4	.03
Omega	.70
Dihedrals	-.30
MC bonds	.65
MC angles	.21
Mainchain	.39
Overall	-.02