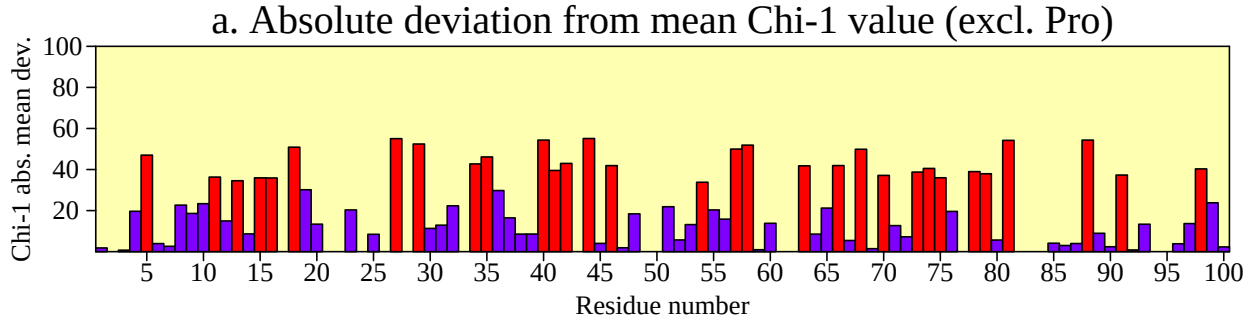
PROCHECK

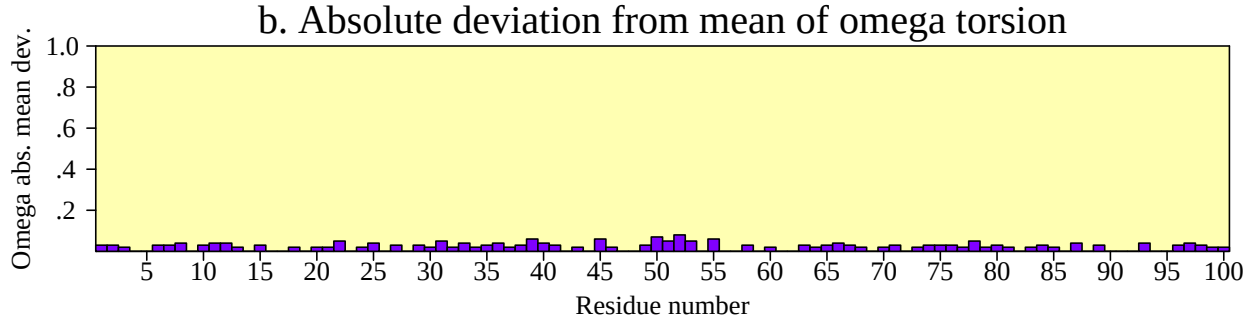
Residue properties

analyzed_7

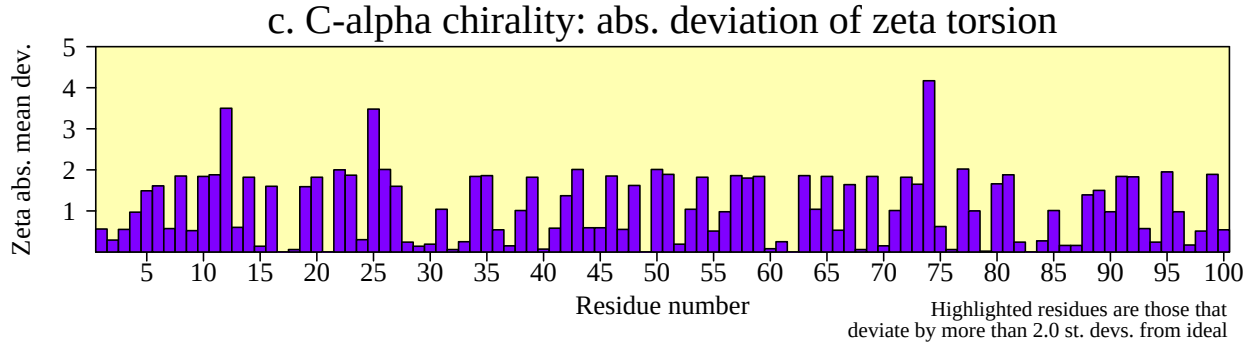
a. Absolute deviation from mean Chi-1 value (excl. Pro)



b. Absolute deviation from mean of omega torsion

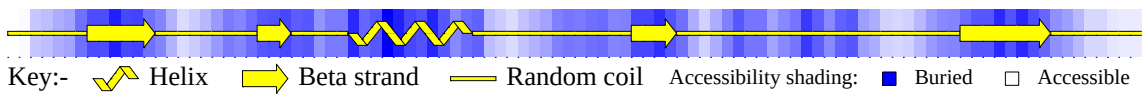


c. C-alpha chirality: abs. deviation of zeta torsion



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

d. Secondary structure & estimated accessibility

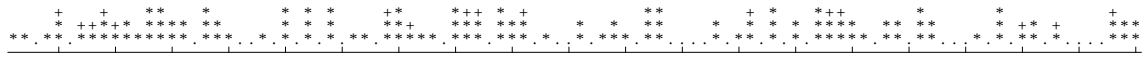


Key:- Helix Beta strand Random coil Accessibility shading: Buried Accessible

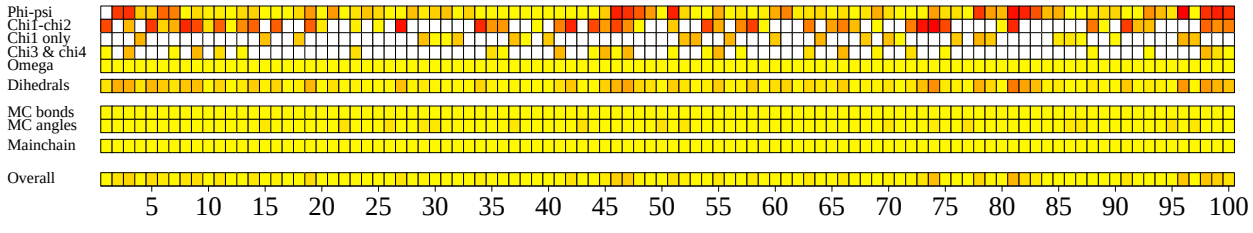
e. Sequence & Ramachandran regions Most favoured Allowed Generous Disallowed

EAEVHNQLEIKFRLTDGSDIGPKAFPDATTVSALKETVISEWPREKENGPKTVKEVKLISAGKVLENSKTVKDYRSPVSNLAGAVTTMHVIIQAPVTEKE

f. Max. deviation (see listing)



g. G-factors

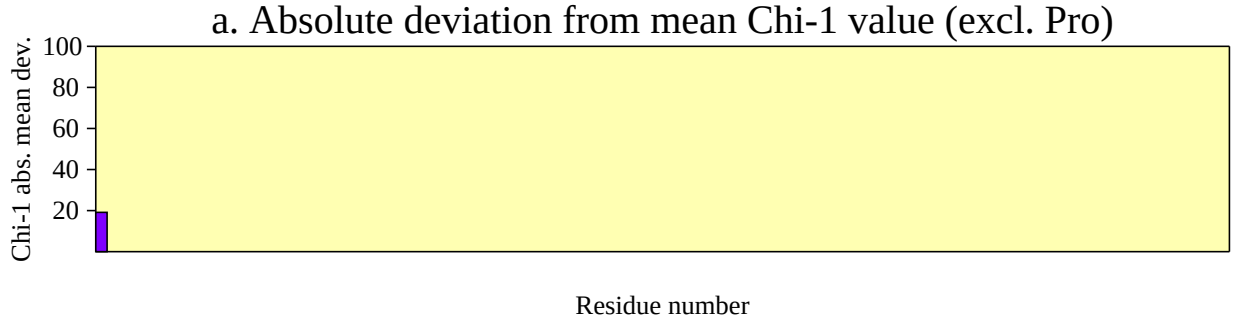


analyzed_7_06.ps

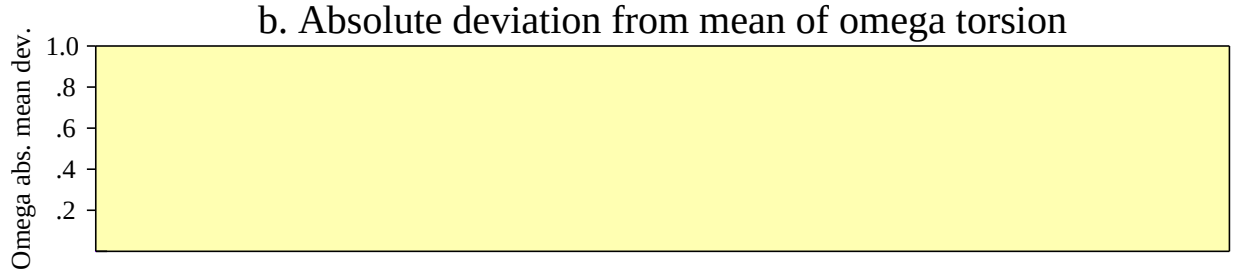
Residue properties

analyzed_7

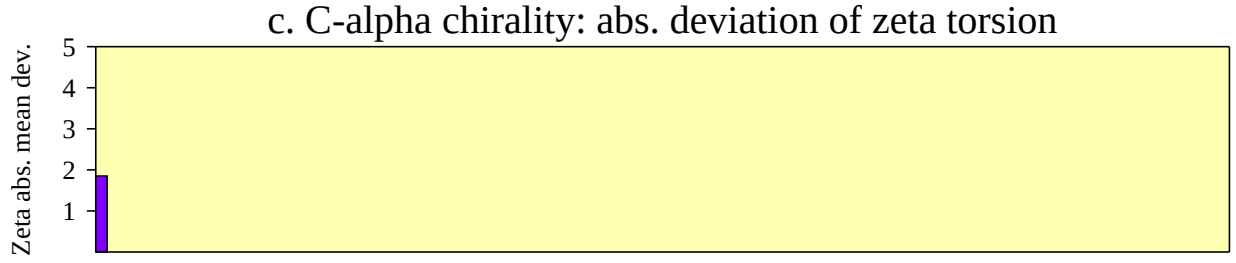
a. Absolute deviation from mean Chi-1 value (excl. Pro)



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

K

f. Max. deviation (see listing)

*

g. G-factors

	Ave
Phi-psi	-.69
Chi1-chi2	-1.73
Chi1 only	-.53
Chi3 & chi4	-.03
Omega	.70
Dihedrals	-.33
MC bonds	.65
MC angles	.21
Mainchain	.39
Overall	-.04