PROCHECK Page 1

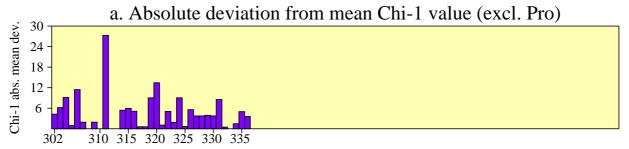
Residue properties 4555558

a. Absolute deviation from mean Chi-1 value (excl. Pro) 30 Chi-1 abs. mean dev. 24 18 12 265 270 275 280 Residue number b. Absolute deviation from mean of omega torsion Omega abs. mean dev. 15 12 9 6 265 270 275 280 285 Residue number c. C-alpha chirality: abs. deviation of zeta torsion 5 Zeta abs. mean dev. 4 3 2 230 235 240 245 250 255 260 265 270 Residue number Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal d. Secondary structure & estimated accessibility Beta strand — Random coil Accessibility shading: e. Sequence & Ramachandran regions △ Most favoured ■ Allowed □ Generous ■ Disallowed f. Max. deviation (see listing) g. G-factors

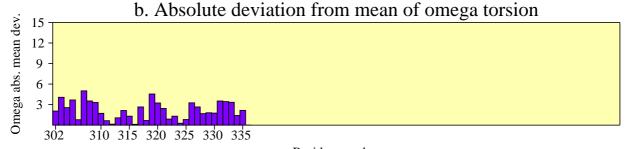
210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300

PROCHECK Page 2

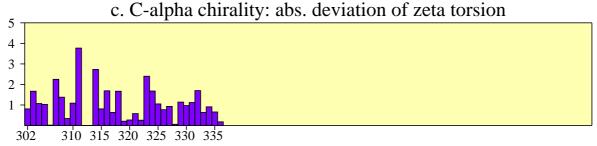
Residue properties 4555558



Residue number



Residue number



Residue number

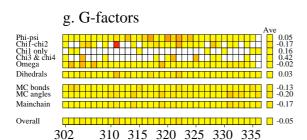
Highlighted residues are those that deviate by more than 2.0 st. devs. from ideal

d. Secondary structure & estimated accessibility



e. Sequence & Ramachandran regions △ Most favoured ■ Allowed □ Generous ■ Disallowed

f. Max. deviation (see listing)



Zeta abs. mean dev.