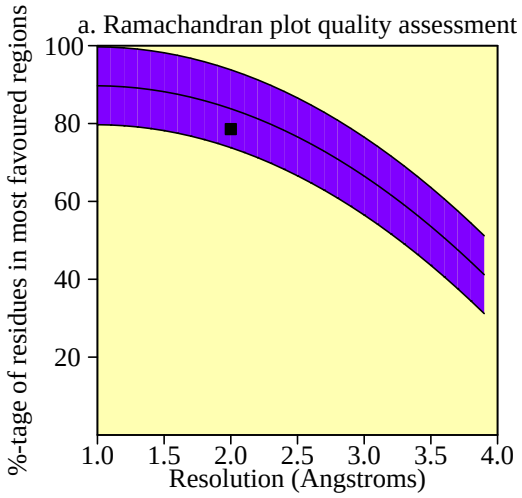
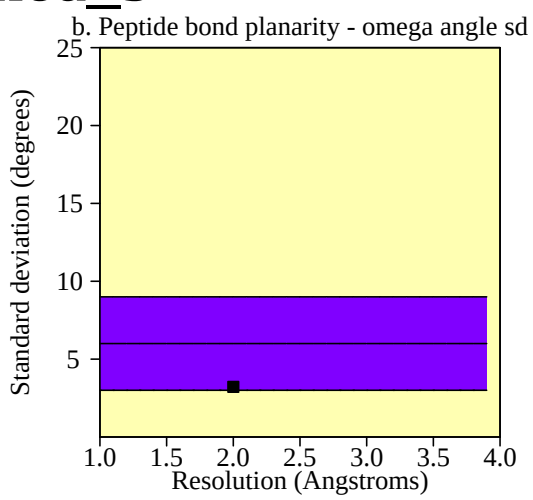
PROCHECK

Main-chain parameters
refined_5

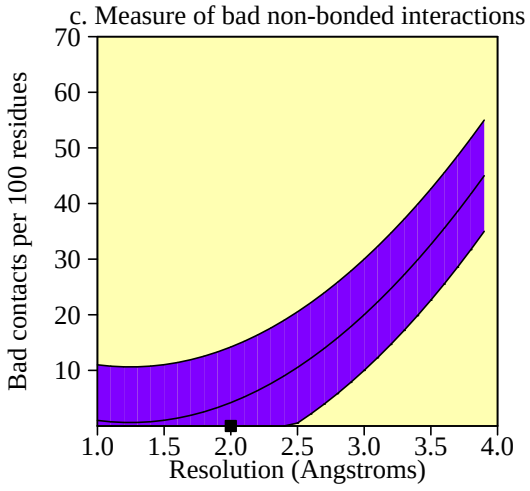
a. Ramachandran plot quality assessment



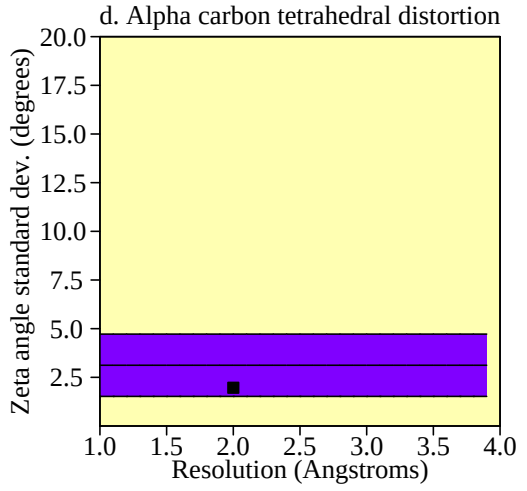
b. Peptide bond planarity - omega angle sd



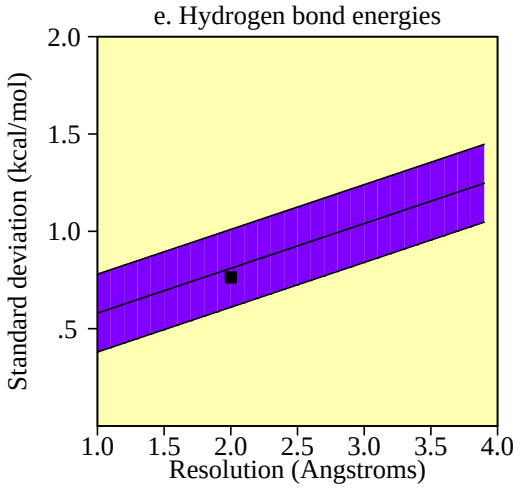
c. Measure of bad non-bonded interactions



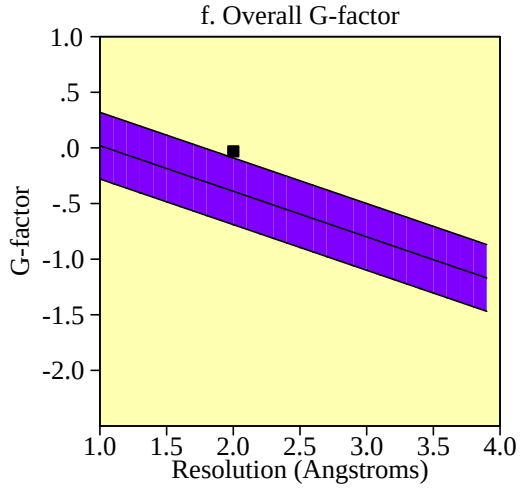
d. Alpha carbon tetrahedral distortion



e. Hydrogen bond energies



f. Overall G-factor



Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Comparison values Band width	No. of band widths from mean	
a. %-tage residues in A, B, L	56	78.6	83.8	10.0	-.5	Inside
b. Omega angle st dev	66	3.2	6.0	3.0	-.9	Inside
c. Bad contacts / 100 residues	0	.0	4.2	10.0	-.4	Inside
d. Zeta angle st dev	62	2.0	3.1	1.6	-.7	Inside
e. H-bond energy st dev	33	.8	.8	.2	-.2	Inside
f. Overall G-factor	67	.0	-.4	.3	1.2	BETTER

refined_5_04.ps