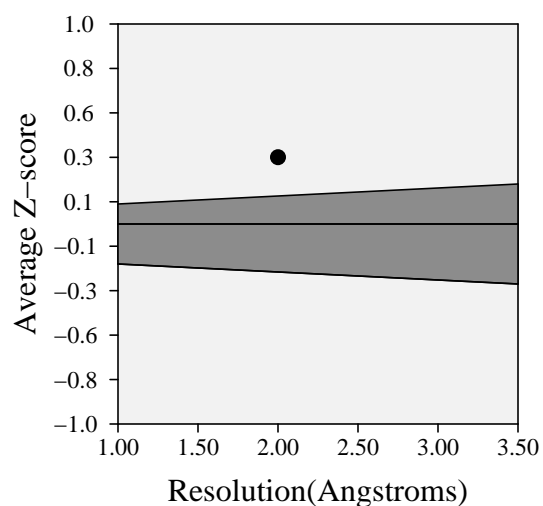


PROVE

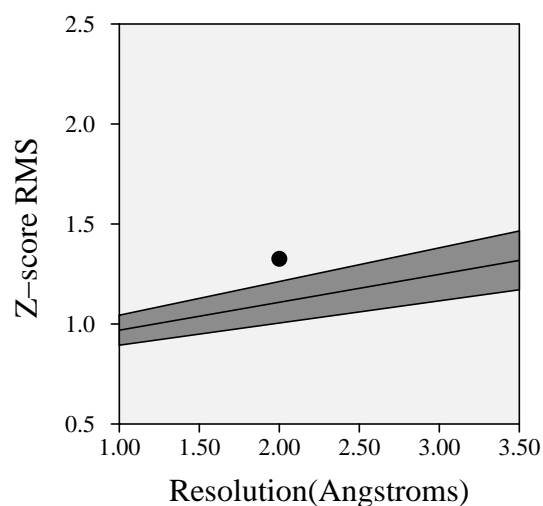
model1.pdb

Analysis of entire structure

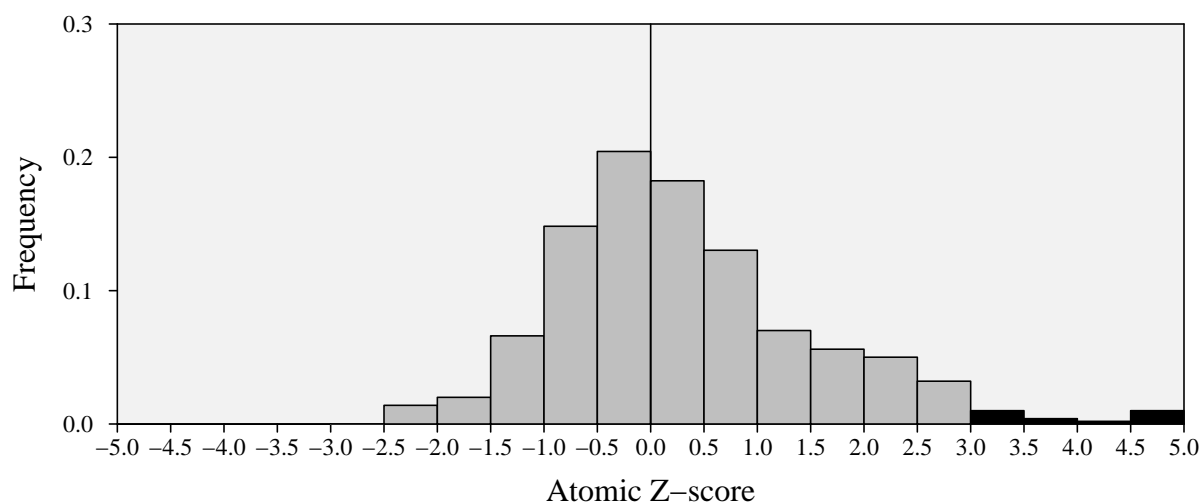
Average Z-score



Z-score RMS



Distribution of atomic Z-scores

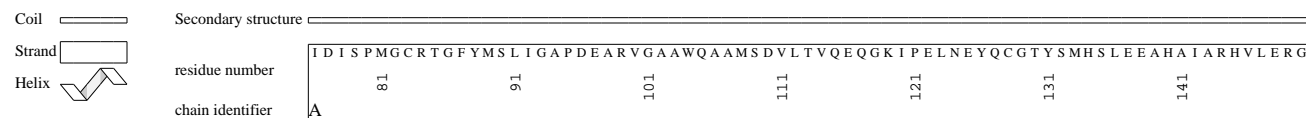
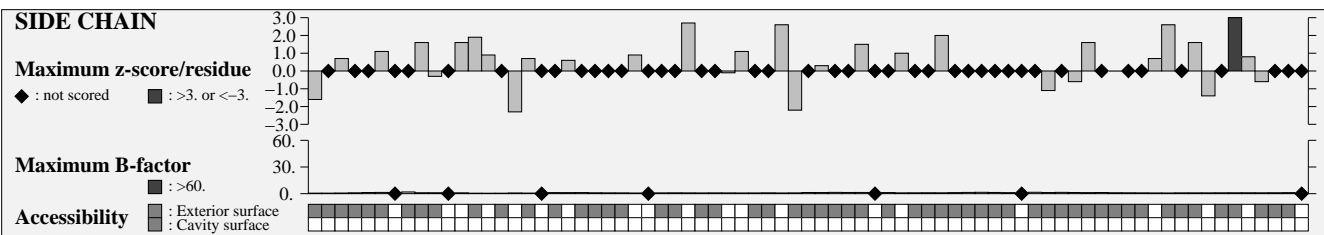
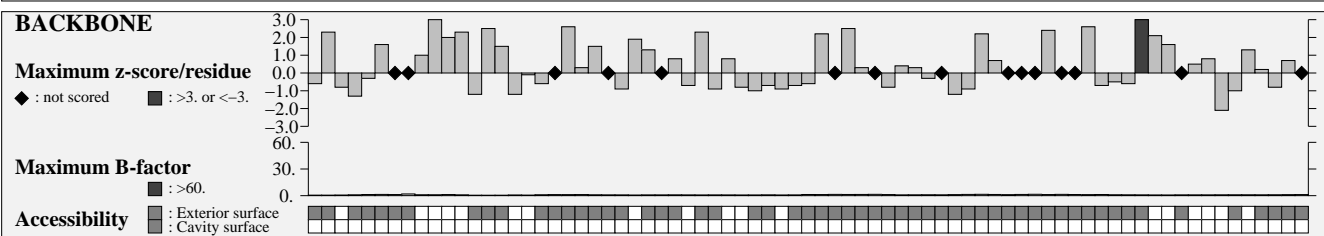
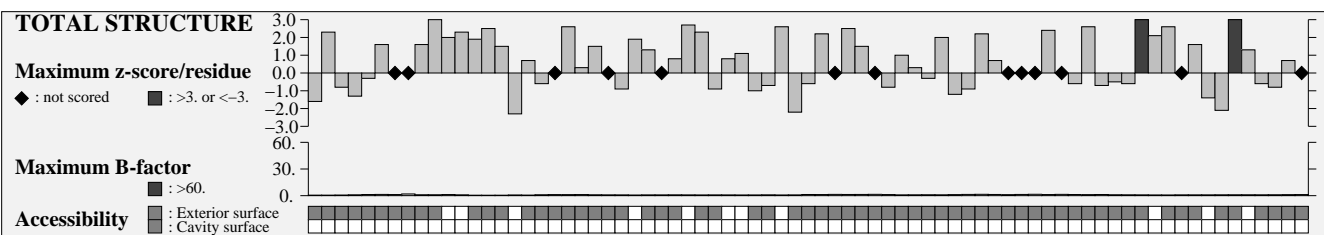
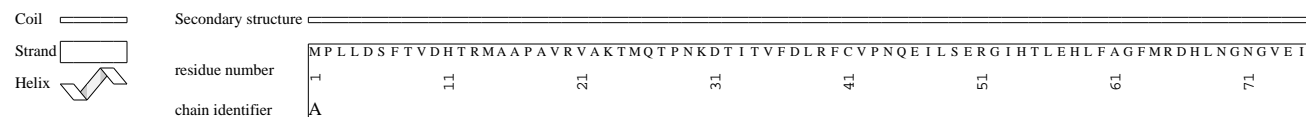
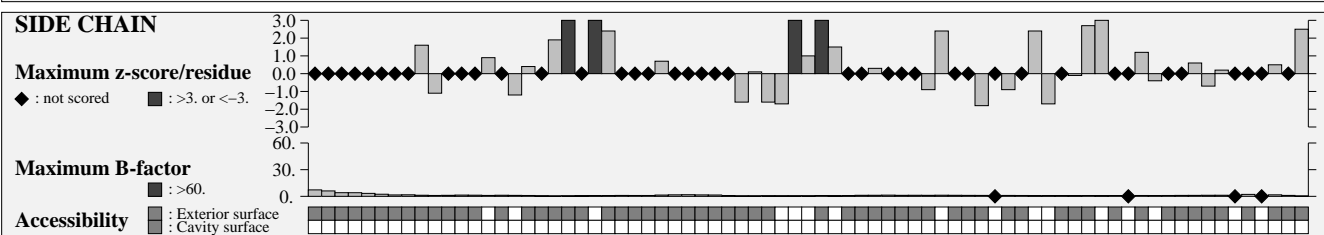
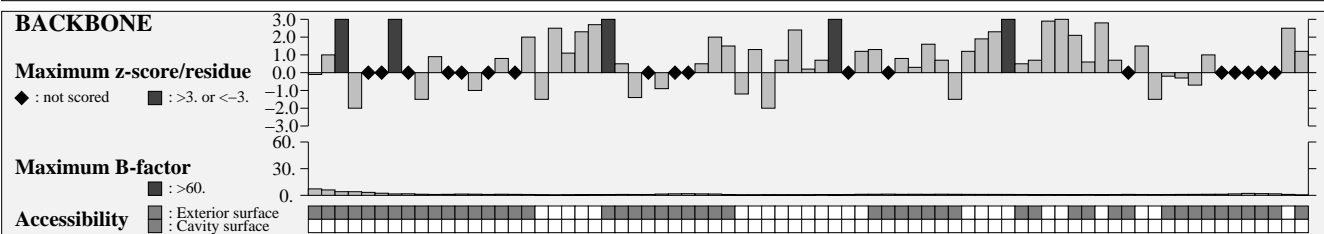
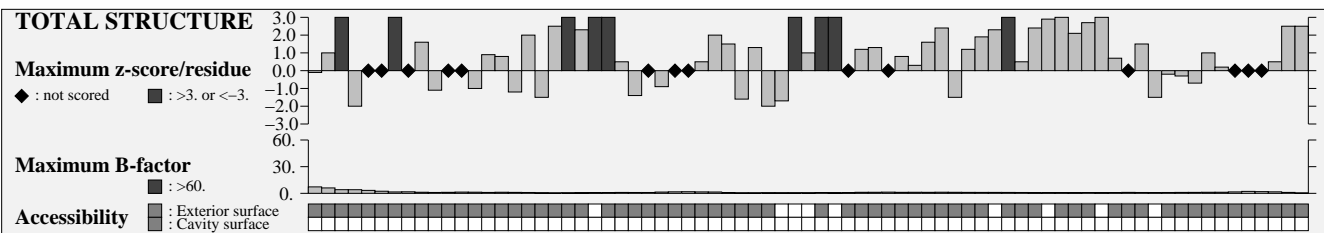


Z-score mean	0.334
Z-score stddev	1.284
Z-score RMS	1.326
# scored atoms	552
# outliers	13
% outliers	2.400

PROVE

model1.pdb

Analysis of residues



PROVE

model1.pdb

Analysis of residues (2)

TOTAL STRUCTURE

Maximum z-score/residue

◆ : not scored ■ : >3, or <-3.

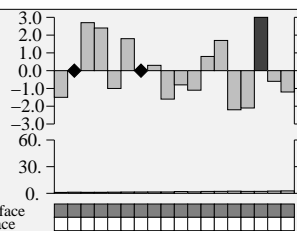
Maximum B-factor

■ : >60.

Accessibility

■ : Exterior surface

■ : Cavity surface



BACKBONE

Maximum z-score/residue

◆ : not scored ■ : >3, or <-3.

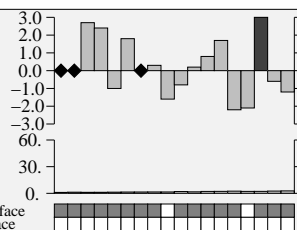
Maximum B-factor

■ : >60.

Accessibility

■ : Exterior surface

■ : Cavity surface



SIDE CHAIN

Maximum z-score/residue

◆ : not scored ■ : >3, or <-3.

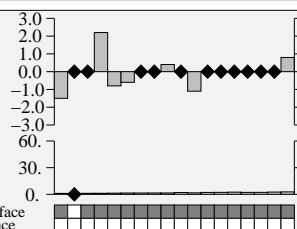
Maximum B-factor

■ : >60.


Accessibility


■ : Exterior surface


■ : Cavity surface



Coil 

Secondary structure 

Strand 

Helix 

residue number

chain identifier

I G V N R N D E L A L P E E K L K S
151 161
A