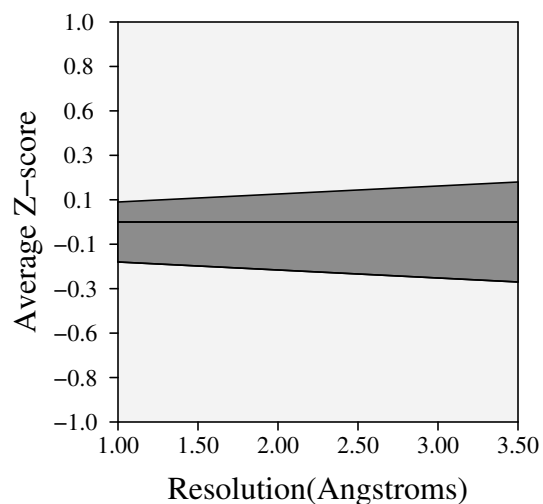


PROVE

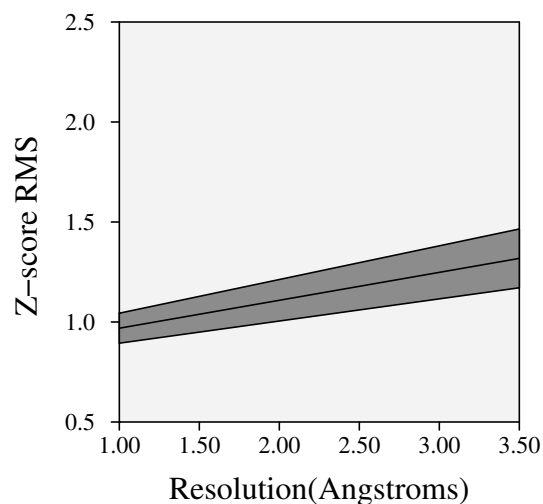
Model_12.pdb

Analysis of entire structure

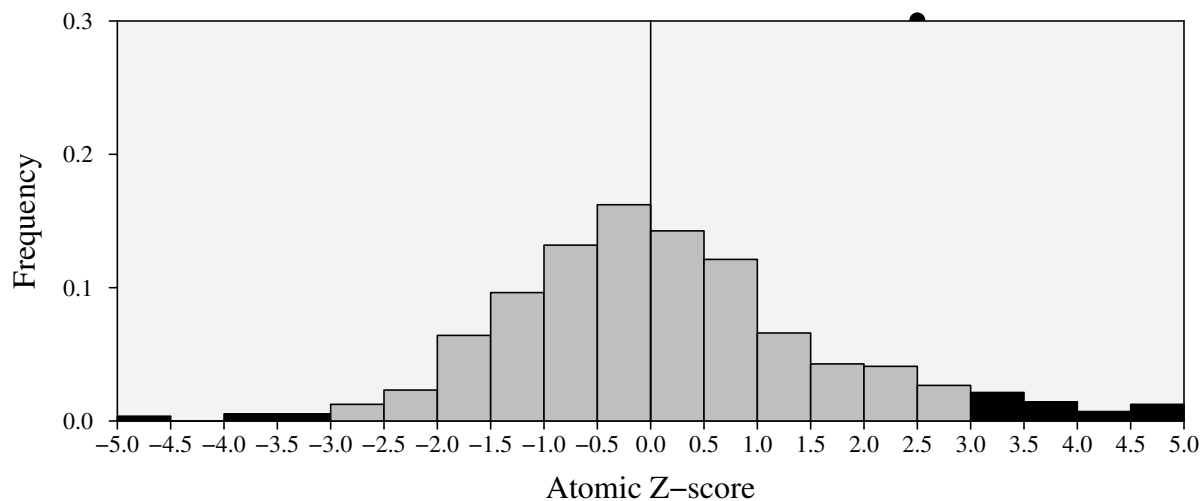
Average Z-score



Z-score RMS



Distribution of atomic Z-scores



Z-score mean	6.446
Z-score stddev	79.103
Z-score RMS	79.303
# scored atoms	635
# outliers	42
% outliers	6.600

PROVE

Model_12.pdb

Analysis of residues

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

KAQIGKEAPEFKAPAYCPCGSIKEIDINEYRGKYVLLFYPLDWTFCPTMIGYSELAGQLKEINCEVIGVSVD
E 40 50 60 70 80 90 100 110

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

SVYCHQAWCEADKSKGGVGKLTFLVSDIKRCISIKYGMNLNVEAGIARRGYVIIDDKGKVRVYIQMNDGIGRSTE
E 120 130 140 150 160 170 180

PROVE

Model_12.pdb

Analysis of residues (2)

