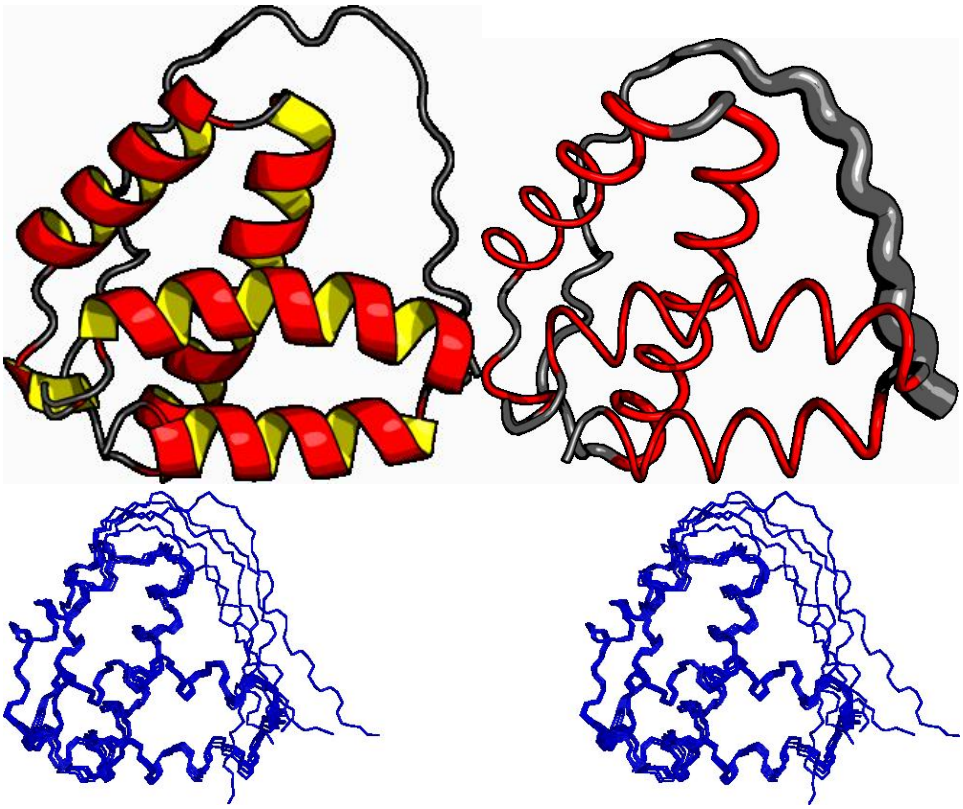
Structure Quality Analysis for NAME

Analyses performed for DAOP well-defined residues.

Procheck analysis, RMSD calculation and structure superimposition are based on DAOP with S(phi)+S(psi)>=1.8 : 2A-99A, 104A-106A

NESG ID:	NAME
PDB ID:	
Deposition date:	
Common Name:	
Class:	
Length (a.a.):	111
Organism:	
SwissProt / TrEMBL ID:	
# models:	5
Oligomerization:	monomer
Molecular weight:	13095



Secondary Structure Elements:
alpha helices: 3A-16A, 19A-36A, 46A-59A, 62A-81A
beta strands:

FIDs deposited in the BMRB? no

Comparison of core atoms:

DAOP > 1.8 Å : A:2..A:99, A:104..A:106
FindCore2 : A:1..A:96
CYRANGE : 1..91

RMSD	***All residues***	***Ordered residues[2]***	***Selected residues[3]***
All backbone atoms	1.5 Å	0.9 Å	0.9 Å
All heavy atoms	1.8 Å	1.0 Å	1.0 Å

Ramachandran Plot Summary for selected residues[3] from Procheck

Most favoured regions	*Additionally allowed regions*	*Generously allowed regions*	*Disallowed regions*
92.0%	7.8%	0.2%	0.0%

Ramachandran Plot Summary for selected residues[3] from Richardson Lab's Molprobity

Most favoured regions	*Allowed regions*	*Disallowed regions*	View plot	View model summary
95.4%	4.2%	0.4%		

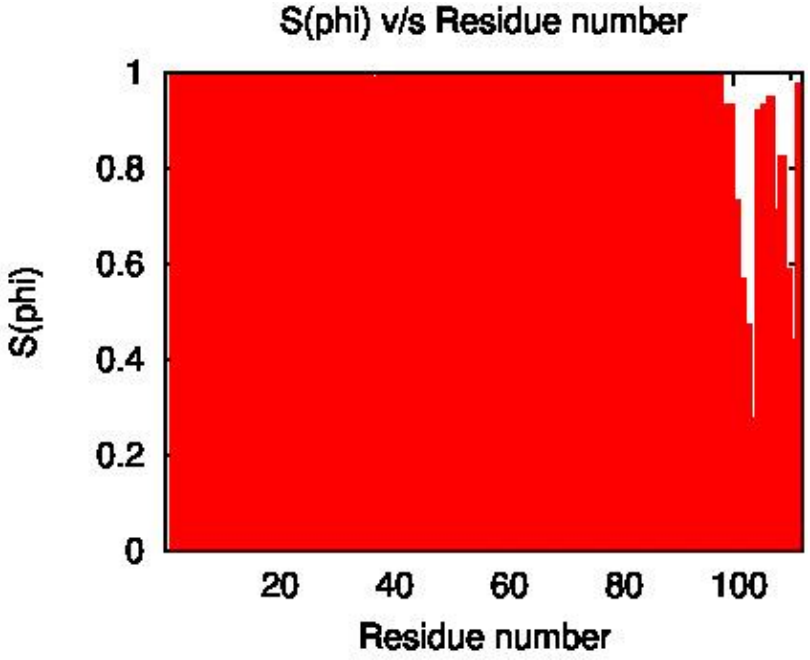
Global quality scores

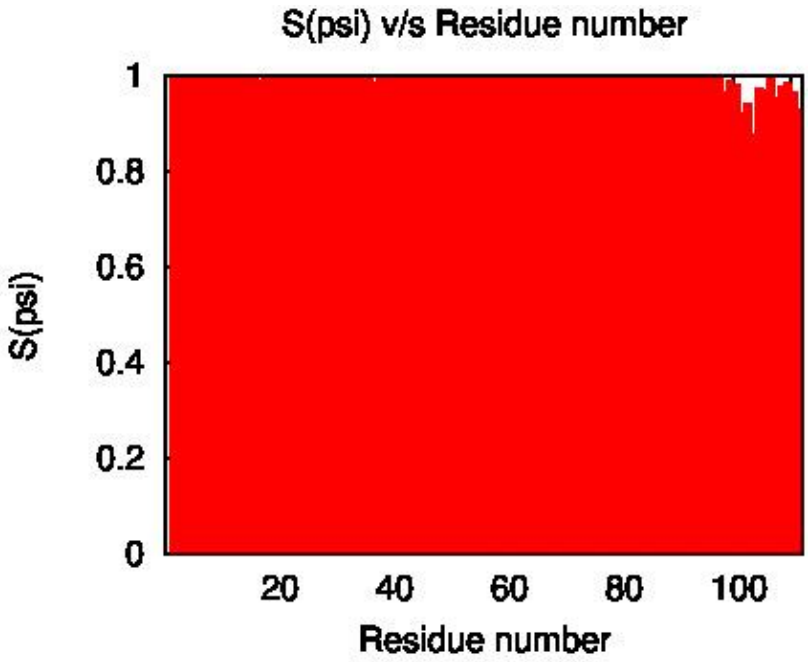
Program	*Verify3D*	*ProsaII (-ve)*	*Procheck (phi-psi)[3]*	*Procheck (all)[3]*	*MolProbity Clashscore*
Raw score	0.13	N/A	0.26	0.33	1.94
Z-score[1]	-5.30	N/A	1.34	1.95	1.19

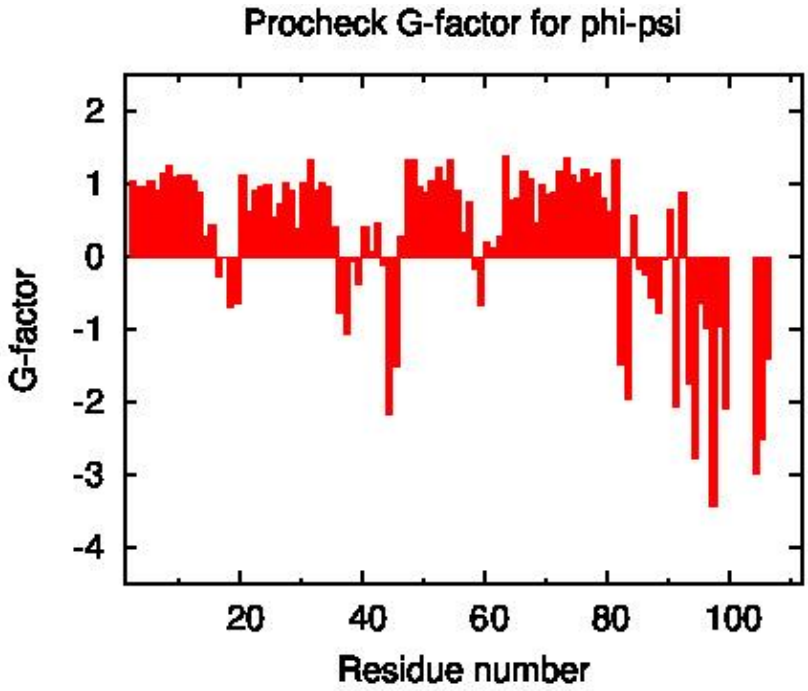
Close Contacts and Deviations from Ideal Geometry (from PDB validation software)

Number of close contacts (within 1.6 &Aring for H atoms, 2.2 &Aring for heavy atoms):	0
RMS deviation for bond angles:	1.9 °
RMS deviation for bond lengths:	0.012 Å

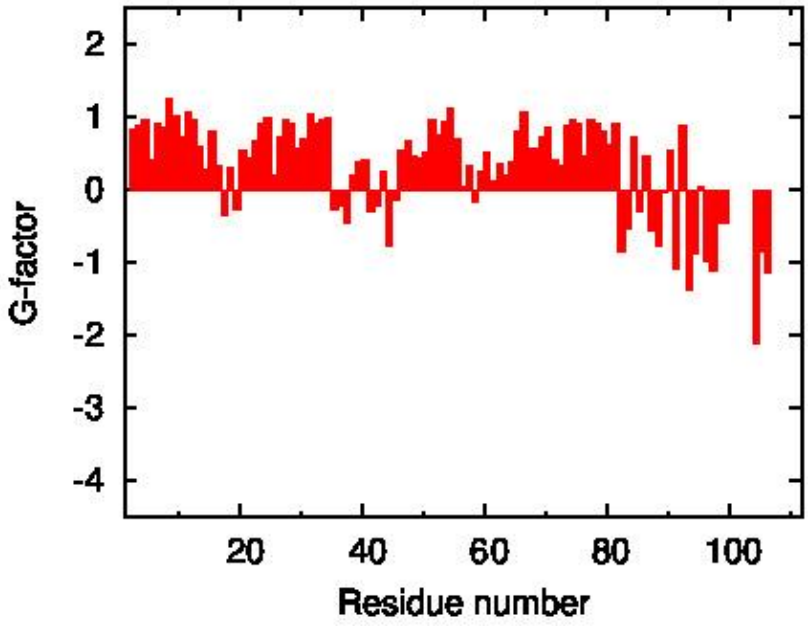
[1] With respect to mean and standard deviation for a set of 252 X-ray structures < 500 residues, of resolution <= 1.80 Å, R-factor <= 0.25 and R-free <= 0.28; a positive value indicates a 'better' score
[2] Ordered residues (DAOP): 2A-99A, 104A-106A
[3] Selected residues DAOP with S(phi)+S(psi)>=1.8 : 2A-99A, 104A-106A

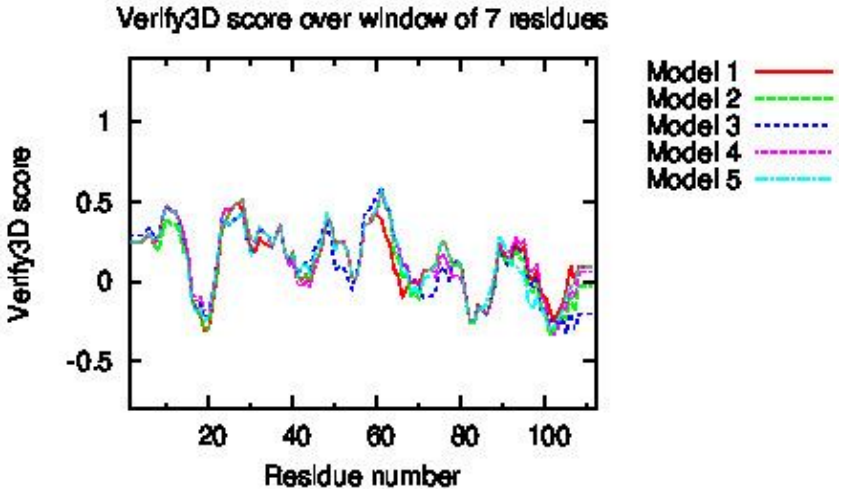


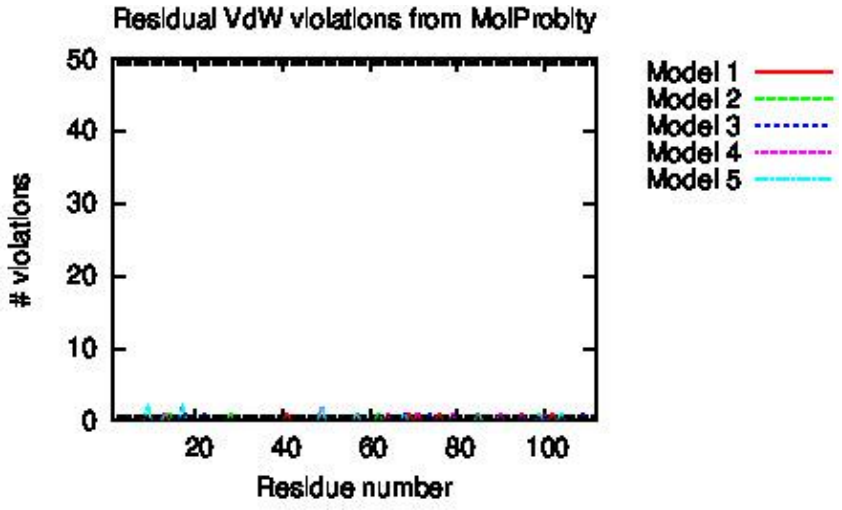

S(psi) v/s Residue number
S(psi)
1
0.8
0.6
0.4
0.2
0
20
40
60
80
100
Residue number

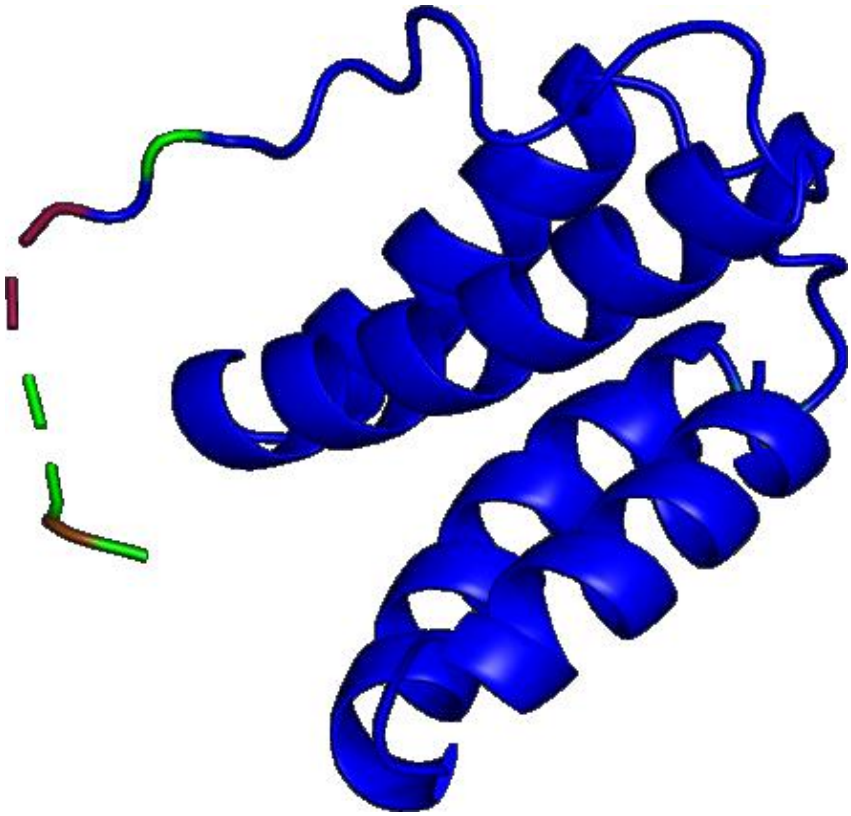

Procheck G-factor for phi-psi
G-factor
2
1
0
-1
-2
-3
-4
20
40
60
80
100
Residue number

Procheck G-factor for all dihedral angles









Residue Plot of Ramachandran anlysis(based on data from Richardson Lab's Molprobity)

References:
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Protein Structure Validation Suite (PSVS)

Software Environment

Software for structure quality evaluation:

DSSP	DsspCMBI-April-2000
pdbstat	PdbStat-5.20.8 Version
AutoAssign	Version 2.4.0 (uses only AVS scripts)
RPF analysis	ASDP-2.3
PDB validation	Version 8.061
Verify3D	Version 1.0 corrected by Aneerban
ProsaII	Prosa2003
PROCHECK	Version 3.5.4

MolProbity programs:

cluster	1999
clashlistcluster	1999 (corrected by Aneerban)
mage	Version 6.35.040409
prekin	Version 6.35.040406
reduce	Version 2.14
probe	Version 2.6

Other Software:

PERL	Version 5.16.3
convert	ImageMagick 6.7.8
ps2pdf	Ghostscript 9.25
htmldoc	v1.8.28
gnuplot	Version 4.6.2
jpegtopnm	netpbm-progs 10.79.00
pnmcrop	netpbm-progs 10.79.00
pnmtojpeg	netpbm-progs 10.79.00

Information updated on October, 2021. RTT