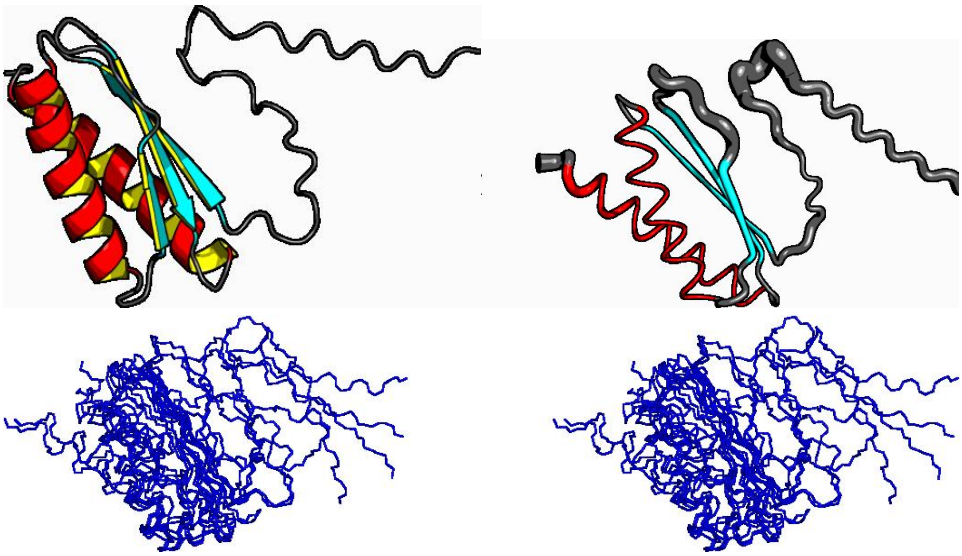
Structure Quality Analysis for NAME

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 : 5A-14A, 17A-23A, 25A-27A, 30A-107A

NESG ID:	NAME
PDB ID:	
Deposition date:	
Common Name:	
Class:	
Length (a.a.):	108
Organism:	
SwissProt / TrEMBL ID:	
# models:	5
Oligomerization:	monomer
Molecular weight:	12037



Secondary Structure Elements:
alpha helices: 41A-58A, 85A-104A
beta strands: 31A-37A, 75A-81A, 63A-66A

FIDs deposited in the BMRB? no

Comparison of core atoms:

DAOP > 1.8 Å : A:6..A:7, A:9..A:14, A:18..A:23, A:25..A:27, A:30..A:107
FindCore2 : A:26..A:108**Selected
CYRANGE : 3..23 , 30..95

RMSD	***All residues***	***Ordered residues[2]***	***Selected residues[3]***
All backbone atoms	9.0 Å	8.1 Å	8.1 Å
All heavy atoms	8.9 Å	8.4 Å	8.4 Å

Ramachandran Plot Summary for selected residues[3] from Procheck

Most favoured regions	*Additionally allowed regions*	*Generously allowed regions*	*Disallowed regions*
84.9%	15.1%	0.0%	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

90.8% 8.6% 0.6%

Global quality scores

Program	*Verify3D*	*ProsaII (-ve)*	*Procheck (phi-psi)*[3]	*Procheck (all)*[3]	*MolProbity Clashscore*
Raw score	0.11	N/A	-0.22	-0.10	0.00
Z-score[1]	-5.62	N/A	-0.55	-0.59	1.53

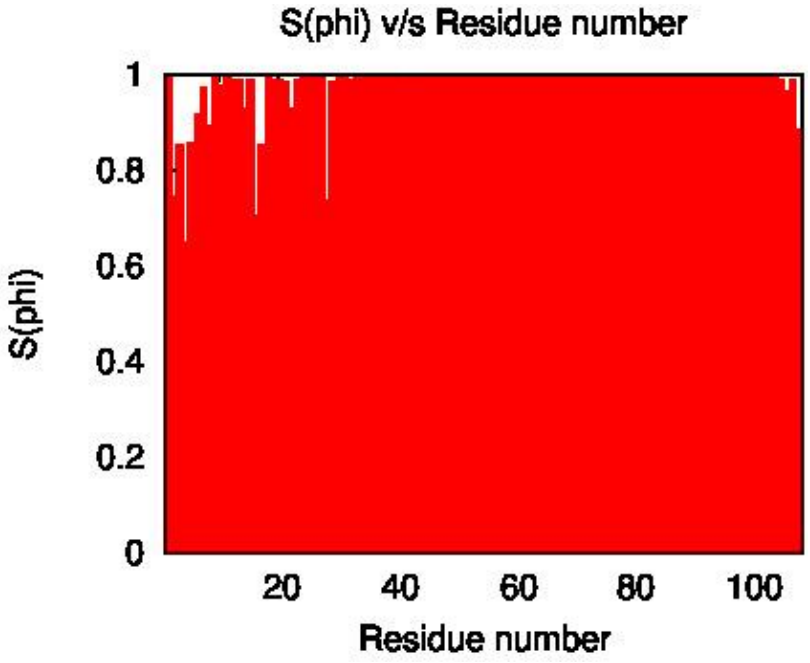
Close Contacts and Deviations from Ideal Geometry (from PDB validation software)

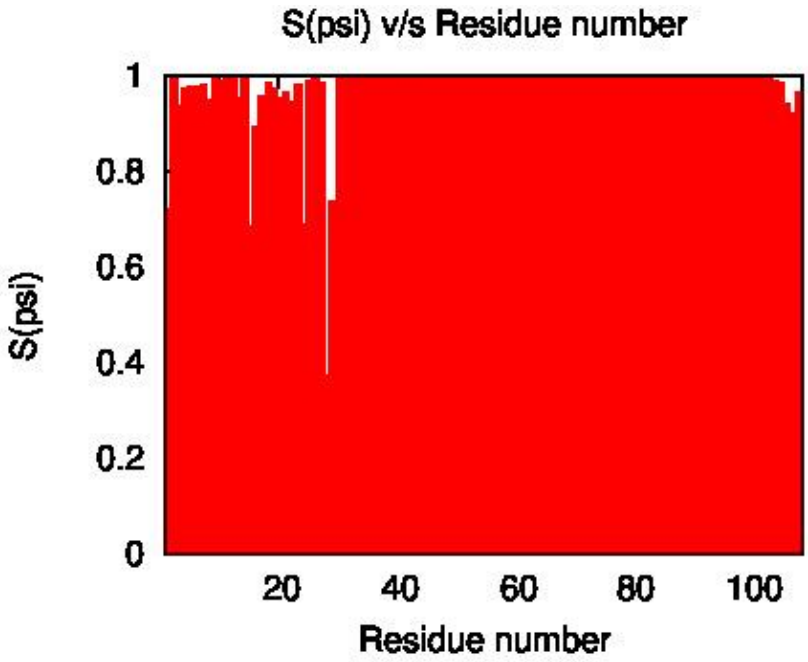
Number of close contacts (within 1.6 &Aring for H atoms, 2.2 &Aring for heavy atoms):	0
RMS deviation for bond angles:	1.9 °
RMS deviation for bond lengths:	0.012 Å

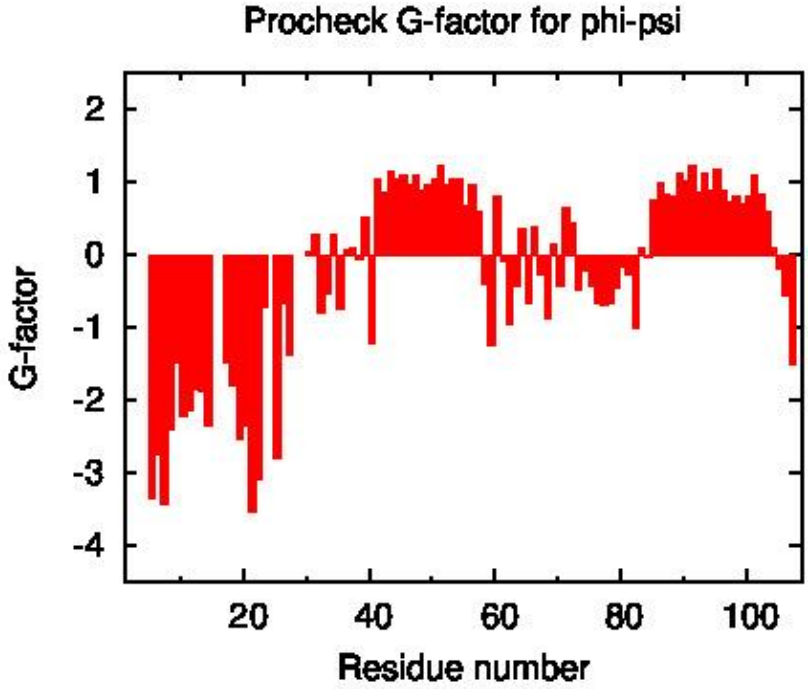
[1] With respect to mean and standard deviation for a set of 252 X-ray structures < 500 residues, of resolution <= 1.80 Å, R-factor <= 0.25 and R-free <= 0.28; a positive value indicates a 'better' score

[2] Ordered residues (DAOP): 5A-14A, 17A-23A, 25A-27A, 30A-107A

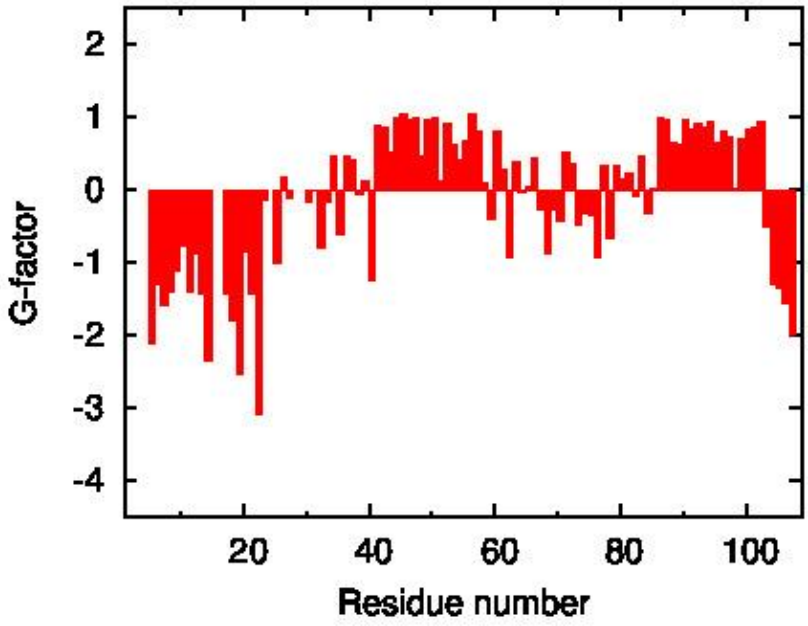
[3] Selected residues DAOP with S(phi)+S(psi)>=1.8 : 5A-14A, 17A-23A, 25A-27A, 30A-107A

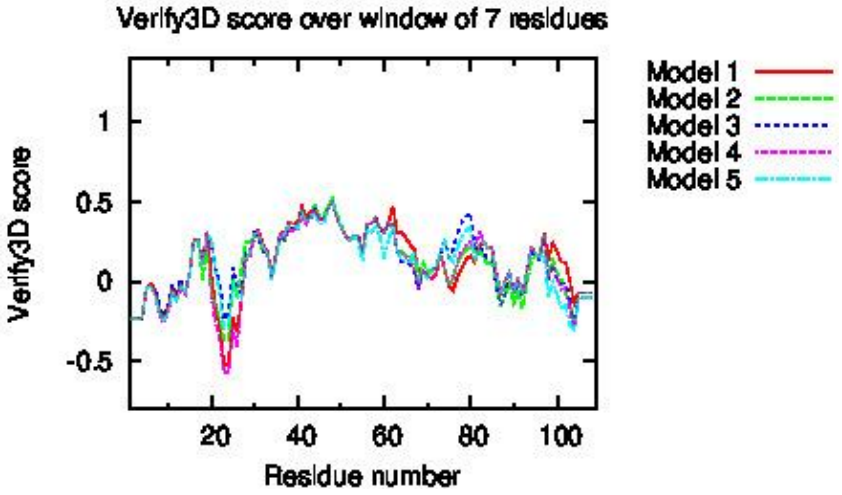


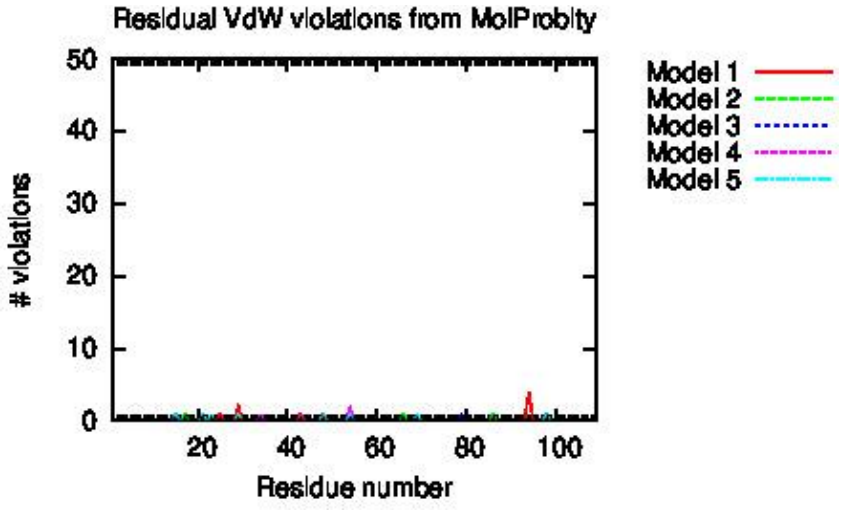

S(psi) v/s Residue number
S(psi)
1
0.8
0.6
0.4
0.2
0
20
40
60
80
100
Residue number

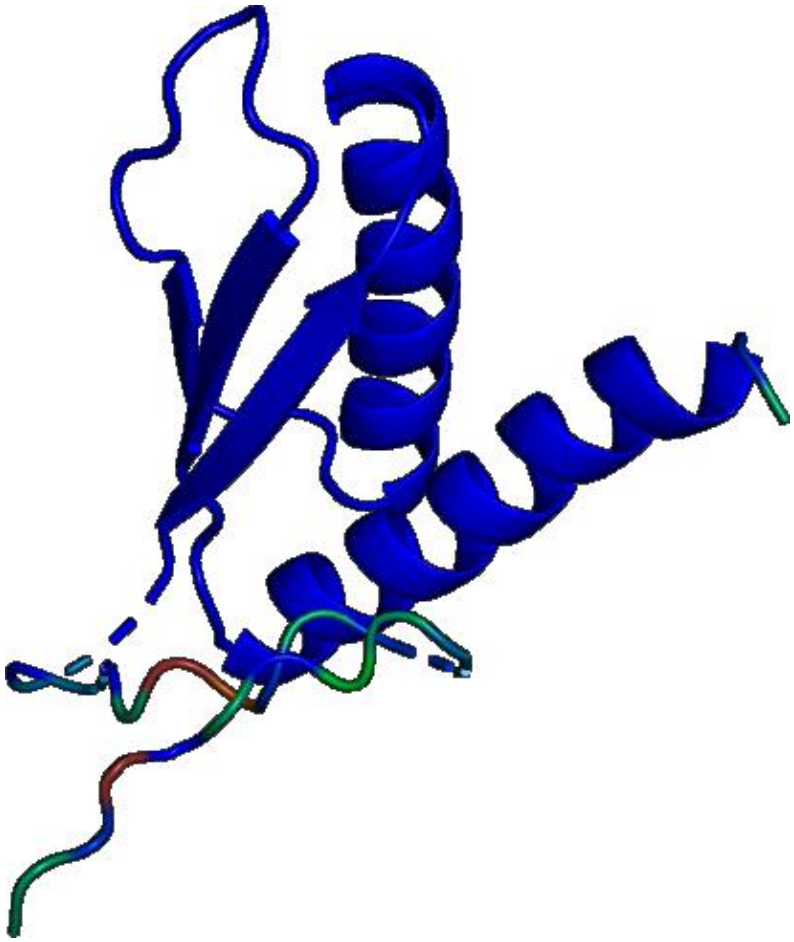

Procheck G-factor for phi-psi
G-factor
2
1
0
-1
-2
-3
-4
20
40
60
80
100
Residue number

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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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

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