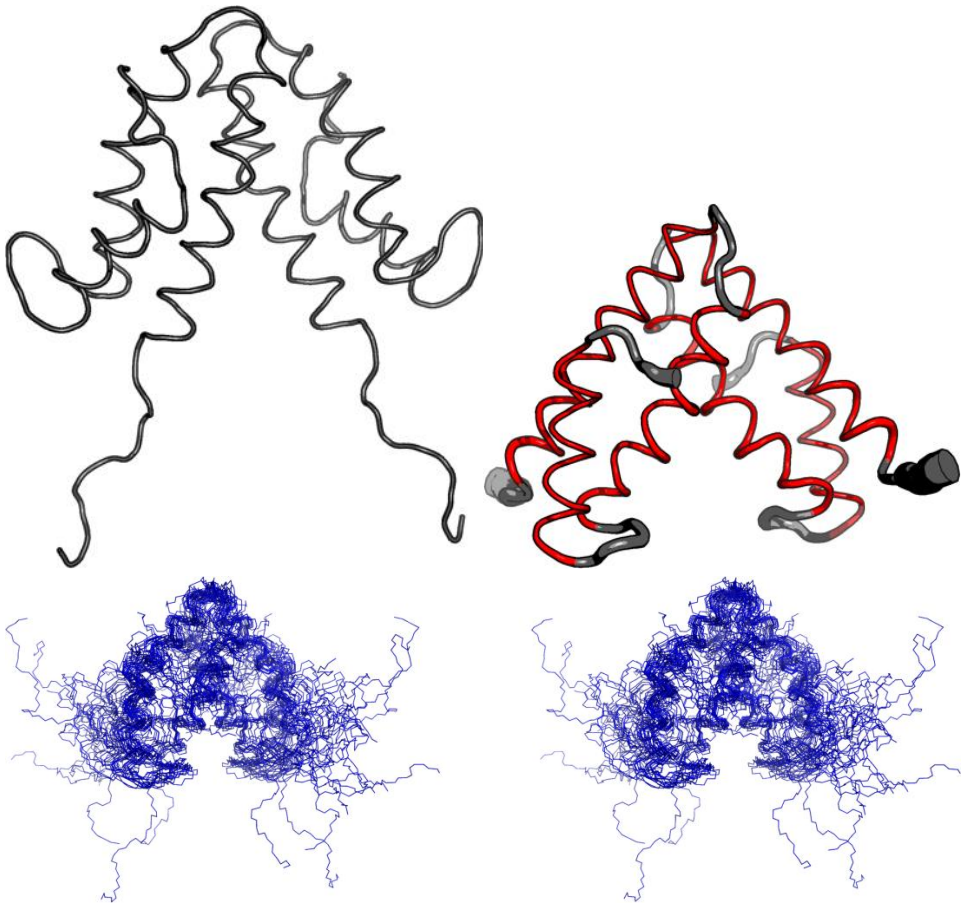
Structure Quality Analysis for NAME

Analyses performed for user defined residues.
The constraints analysis is based on the following files: NOE distance constraints file. Angular constraints file.
Procheck analysis,RMSD calculation and structure superimposition are based on: User defined residues

NESG ID:	NAME
PDB ID:	
Deposition date:	
Common Name:	
Class:	
Length (a.a.):	160
Organism:	
SwissProt / TrEMBL ID:	
# models:	20
Oligomerization:	dimer
Molecular weight:	19055



Secondary Structure Elements:
Inter-chain break(s) between 80 & 91
alpha helices: 7A-19A, 27A-43A, 49A-68A, 7B-19B, 27B-43B, 49B-68B
beta strands:

Total number of restricting constraints per restrained residue:	13.2
Restricting long range constraints per restrained residue:	2.5

Distance violations per model
Calculated using sum over r^-6

0.1 - 0.2 Å	0.2 - 0.5 Å	> 0.5 Å
16.6	16.3	2.5

Dihedral angle violations per model

1 - 10 °	> 10 °
0.3	0

FIDs deposited in the BMRB? no

RPF Scores

Recall	Precision	F-measure	DP-score
0.748	0.644	0.692	0.585

RMSD	*All residues*	*Ordered residues*[2]	*Selected residues*[3]
All backbone atoms	4.8 Å	2.9 Å	3.4 Å
All heavy atoms	5.4 Å	3.2 Å	3.8 Å

Ramachandran Plot Summary for selected residues[3] from Procheck

Most favoured regions	*Additionally allowed regions*	*Generously allowed regions*	*Disallowed regions*
90.9%	6.9%	2.2%	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
93.3%	5.1%	1.6%		

Global quality scores

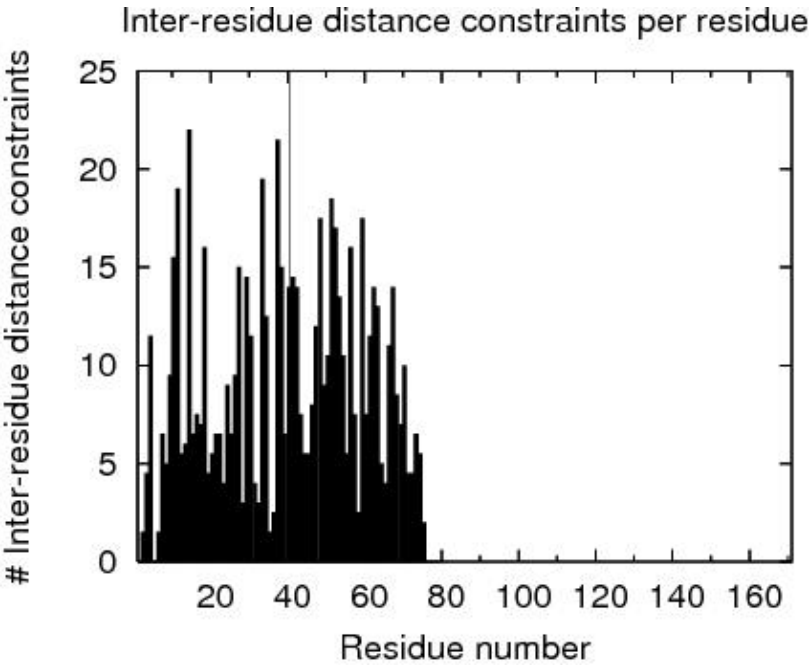
Program	*Verify3D*	*ProsaII (-ve)*	*Procheck (phi-psi)*[3]	*Procheck (all)*[3]	*MolProbity Clashscore*
-Raw score	0.30	0.30	0.54	0.42	15.63
Z-score[1]	-2.57	-1.45	2.44	2.48	-1.16

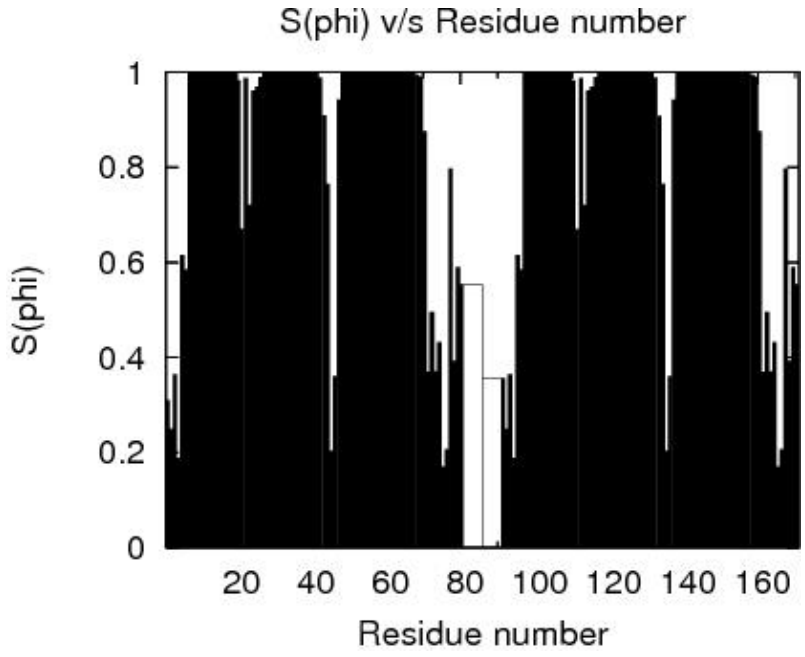
Generalized linear model RMSD prediction: 2.01

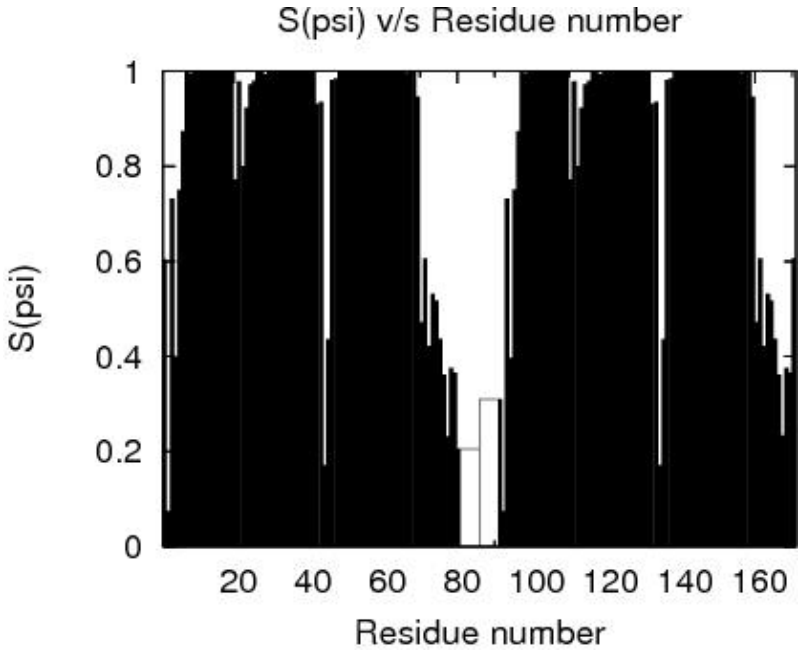
Close Contacts and Deviations from Ideal Geometry (from PDB validation software)

Number of close contacts (within 1.6 &Aring for H atoms, 2.2 &Aring for heavy atoms):	16
RMS deviation for bond angles:	0.8 °
RMS deviation for bond lengths:	0.010 Å

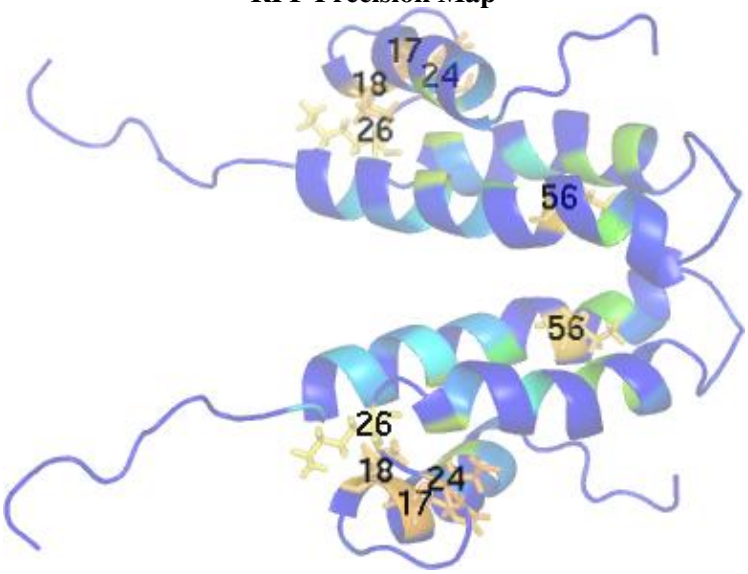
[1] With respect to mean and standard deviation for a set of 252 X-ray structures < 500 residues, of resolution <= 1.80 Å, R-factor <= 0.25 and R-free <= 0.28; a positive value indicates a 'better' score
[2]Order residues: 7A-19A,24A-43A,47A-69A,7B-19B,24B-43B,47B-69B
[3]Selected residues: 7A-20A,24A-42A,47A-69A,7B-19B,22B-42B,47B-68B


Inter-residue distance constraints per residue
Inter-residue distance constraints
25
20
15
10
5
0
20
40
60
80
100
120
140
160
Residue number

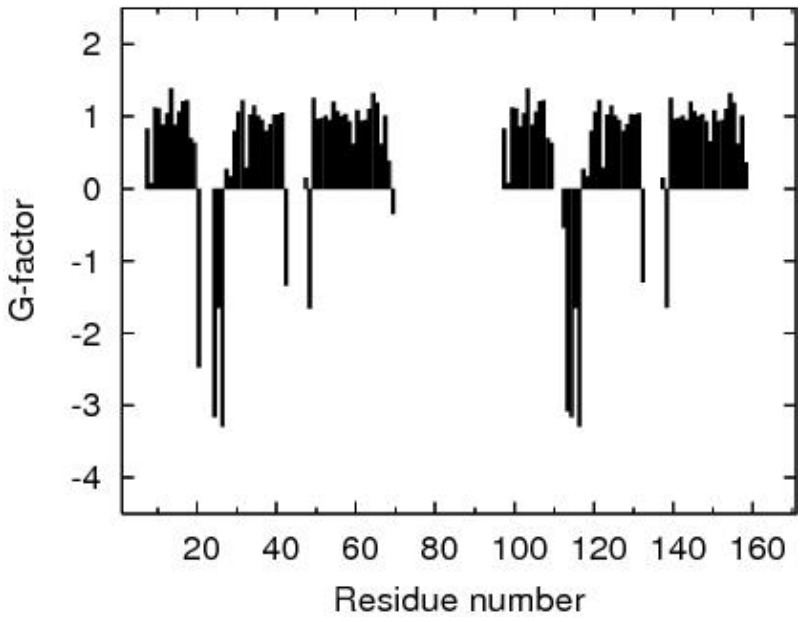

S(phi) v/s Residue number
S(phi)
1
0.8
0.6
0.4
0.2
0
20
40
60
80
100
120
140
160
Residue number



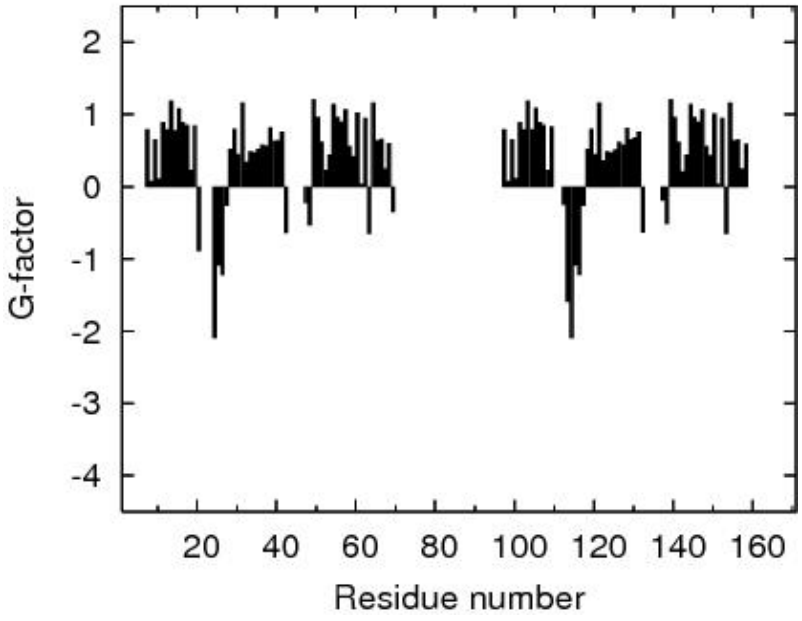
RPF Precision Map

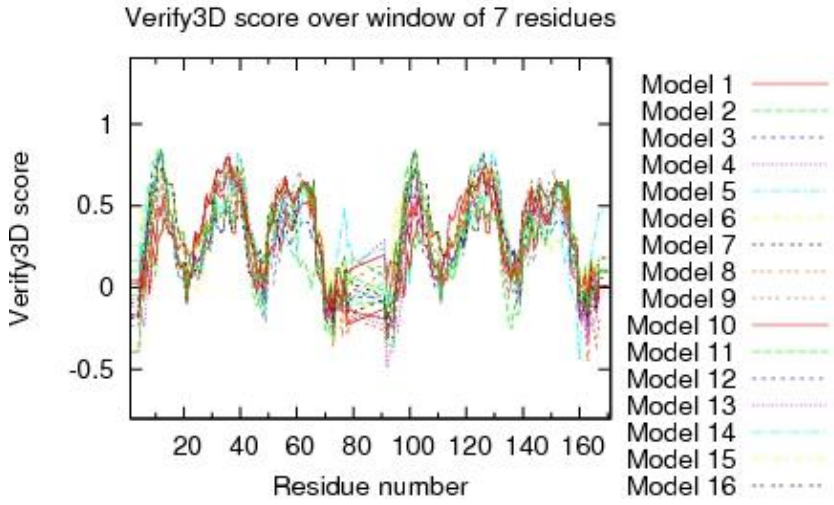


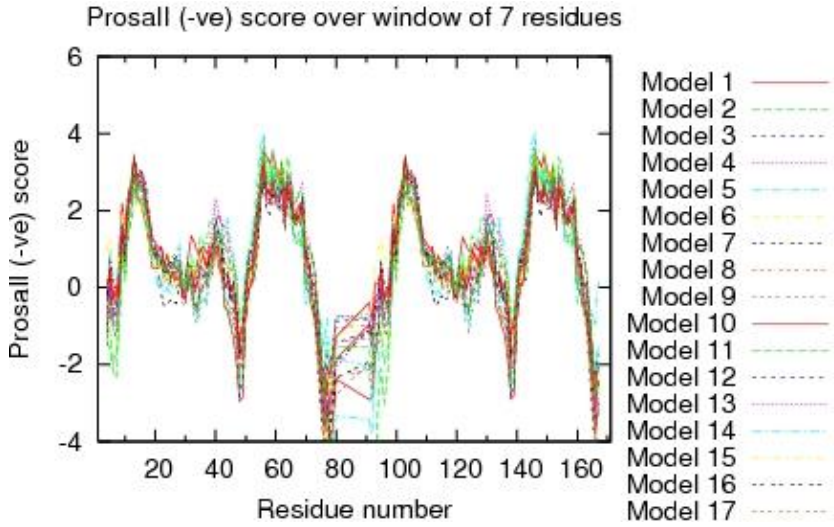
Procheck G-factor for phi-psi

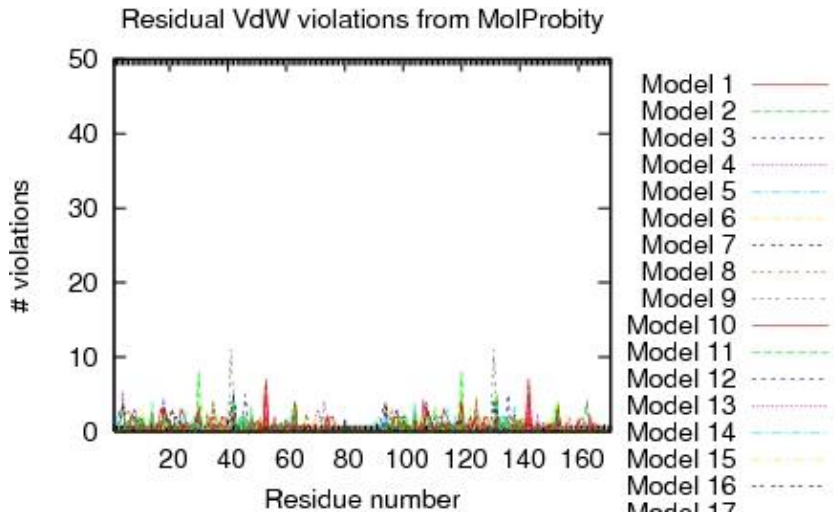


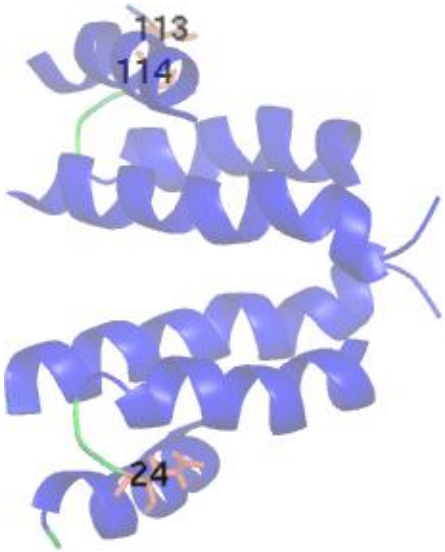
Procheck G-factor for all dihedral angles




Verify3D score over window of 7 residues
Verify3D score
1
0.5
0
-0.5
20 40 60 80 100 120 140 160
Residue number
Model 1
Model 2
Model 3
Model 4
Model 5
Model 6
Model 7
Model 8
Model 9
Model 10
Model 11
Model 12
Model 13
Model 14
Model 15
Model 16


Prosall (-ve) score over window of 7 residues
Prosall (-ve) score
6
4
2
0
-2
-4
20 40 60 80 100 120 140 160
Residue number
Model 1
Model 2
Model 3
Model 4
Model 5
Model 6
Model 7
Model 8
Model 9
Model 10
Model 11
Model 12
Model 13
Model 14
Model 15
Model 16
Model 17


Residual VdW violations from MolProbity
violations
50
40
30
20
10
0
20 40 60 80 100 120 140 160
Residue number
Model 1
Model 2
Model 3
Model 4
Model 5
Model 6
Model 7
Model 8
Model 9
Model 10
Model 11
Model 12
Model 13
Model 14
Model 15
Model 16



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

References:

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3. Sippl M J, "Recognition of Errors in Three-Dimensional Structures of Proteins", Proteins 17 (1993): 355-362
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5. Laskowski R Ai et al, "AQUA and PROCHECK_NMR: Programs for checking the quality of proteins structures solved by NMR", J Biomolec NMR 8 (1996): 477-486
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12. Richardson D C, Richardson J S, "The kinemage: a tool for scientific communication", Prot Sci 1(1) (1992): 3-9
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Software Environment

Software for structure quality evaluation:

DSSP	DsspCMBI-April-2000
pdbstat	PdbStat-5.4 Version
AutoAssign	Version 2.4.0 (uses only AVS scripts)
RPF analysis	ASDP-1.0
PDB validation	Version 8.061
Verify3D	Version 1.0 corrected by Aneerban
ProsaII	Prosa2003
PROCHECK	Version 3.5.4
MolMol	Version 2K.2

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 5.8.0
convert	ImageMagick 5.5.6
ps2pdf	Ghostscript 7.05
htmldoc	v1.9
gnuplot	Version 3.7 patchlevel 3
jpegtopnm	year 2000
pnmcrop	year 2000
pnmtojpeg	year 2000