



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:40 PM BST

PDB ID : 2JS3
Title : NMR Structure of protein Q6N9A4_RHOPA. Northeast Structural Genomics Consortium target RpT8
Authors : Singarapu, K.K.; Wu, Y.; Yee, A.; Eletsky, A.; Sukumaran, D.; Garcia, M.; Xiao, R.; Bansal, S.; Baran, M.C.; Montelione, G.T.; James, P.H.; Arrowsmith, C.H.; Szyperski, T.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2007-06-29

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

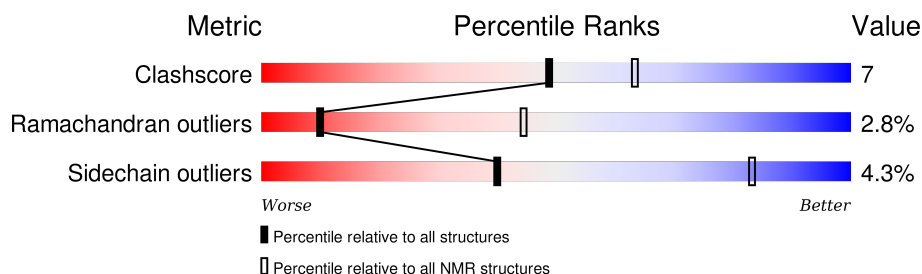
Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	96	
1	B	96	

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:17-A:45, A:53-A:69, A:74-A:90, B:18-B:69, B:74-B:89 (131)	1.56	2

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 4 single-model clusters were found.

Cluster number	Models
1	4, 6, 8, 9, 12, 14, 16, 17, 18, 20
2	3, 7, 15
3	2, 11, 13
Single-model clusters	1; 5; 10; 19

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2902 atoms, of which 1440 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms						Trace
1	A	96	Total	C	H	N	O	S	0
			1451	449	720	136	141	5	
1	B	96	Total	C	H	N	O	S	0
			1451	449	720	136	141	5	

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP Q6N9A4
A	2	GLY	-	CLONING ARTIFACT	UNP Q6N9A4
A	3	SER	-	CLONING ARTIFACT	UNP Q6N9A4
A	4	SER	-	CLONING ARTIFACT	UNP Q6N9A4
A	5	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	6	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	7	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	8	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	9	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	10	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
A	11	SER	-	CLONING ARTIFACT	UNP Q6N9A4
A	12	SER	-	CLONING ARTIFACT	UNP Q6N9A4
A	13	GLY	-	CLONING ARTIFACT	UNP Q6N9A4
A	14	ARG	-	CLONING ARTIFACT	UNP Q6N9A4
A	15	GLU	-	CLONING ARTIFACT	UNP Q6N9A4
A	16	ASN	-	CLONING ARTIFACT	UNP Q6N9A4
A	17	LEU	-	CLONING ARTIFACT	UNP Q6N9A4
A	18	TYR	-	CLONING ARTIFACT	UNP Q6N9A4
A	19	PHE	-	CLONING ARTIFACT	UNP Q6N9A4
A	20	GLN	-	CLONING ARTIFACT	UNP Q6N9A4
A	21	GLY	-	CLONING ARTIFACT	UNP Q6N9A4
B	1	MET	-	CLONING ARTIFACT	UNP Q6N9A4
B	2	GLY	-	CLONING ARTIFACT	UNP Q6N9A4
B	3	SER	-	CLONING ARTIFACT	UNP Q6N9A4
B	4	SER	-	CLONING ARTIFACT	UNP Q6N9A4
B	5	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
B	6	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
B	7	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
B	8	HIS	-	CLONING ARTIFACT	UNP Q6N9A4

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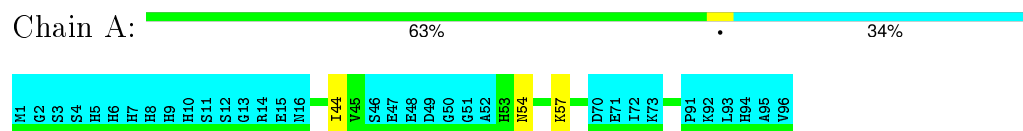
Chain	Residue	Modelled	Actual	Comment	Reference
B	9	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
B	10	HIS	-	CLONING ARTIFACT	UNP Q6N9A4
B	11	SER	-	CLONING ARTIFACT	UNP Q6N9A4
B	12	SER	-	CLONING ARTIFACT	UNP Q6N9A4
B	13	GLY	-	CLONING ARTIFACT	UNP Q6N9A4
B	14	ARG	-	CLONING ARTIFACT	UNP Q6N9A4
B	15	GLU	-	CLONING ARTIFACT	UNP Q6N9A4
B	16	ASN	-	CLONING ARTIFACT	UNP Q6N9A4
B	17	LEU	-	CLONING ARTIFACT	UNP Q6N9A4
B	18	TYR	-	CLONING ARTIFACT	UNP Q6N9A4
B	19	PHE	-	CLONING ARTIFACT	UNP Q6N9A4
B	20	GLN	-	CLONING ARTIFACT	UNP Q6N9A4
B	21	GLY	-	CLONING ARTIFACT	UNP Q6N9A4

4 Residue-property plots [i](#)

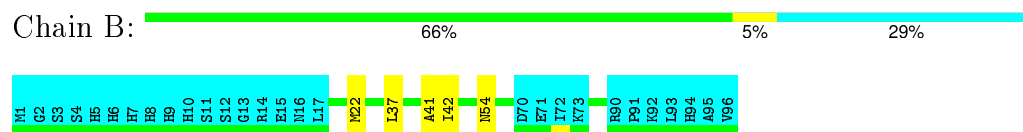
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein

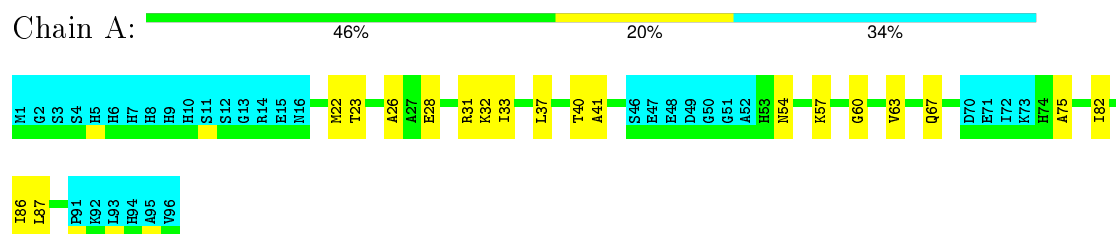


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Uncharacterized protein



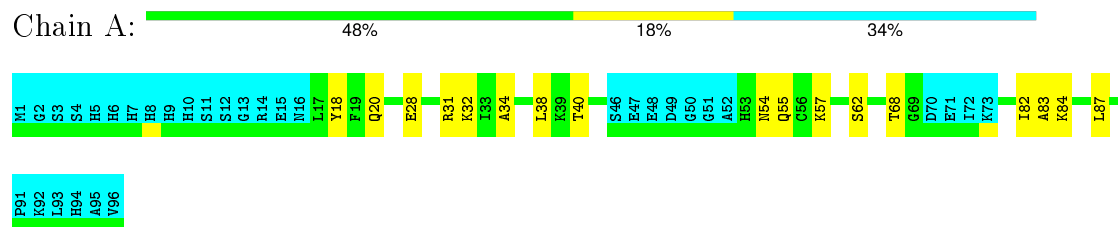
- Molecule 1: Uncharacterized protein



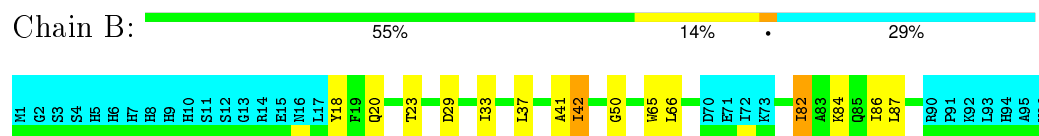


4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Uncharacterized protein

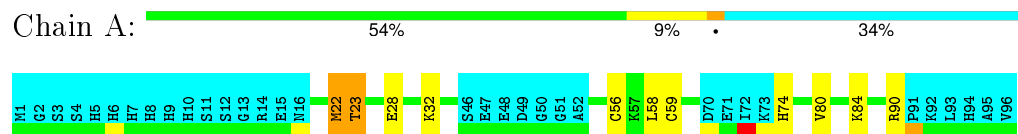


- Molecule 1: Uncharacterized protein

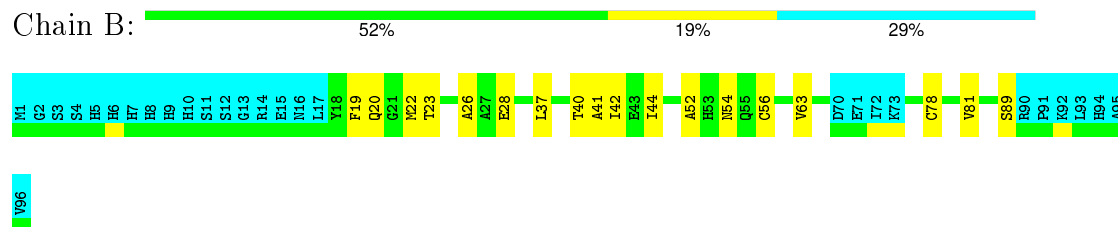


4.2.3 Score per residue for model 3

- Molecule 1: Uncharacterized protein

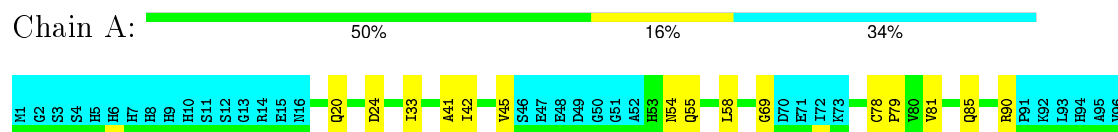


- Molecule 1: Uncharacterized protein

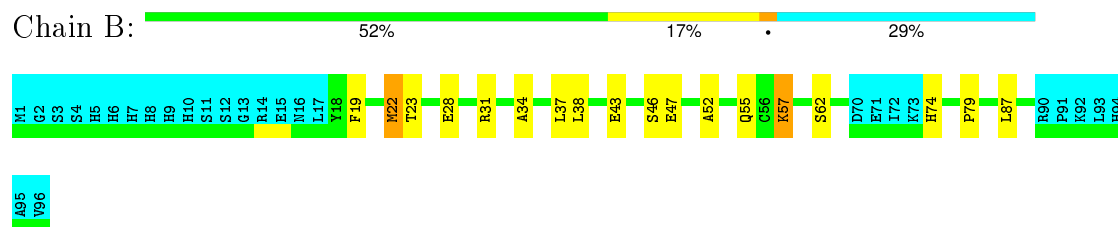


4.2.4 Score per residue for model 4

- Molecule 1: Uncharacterized protein

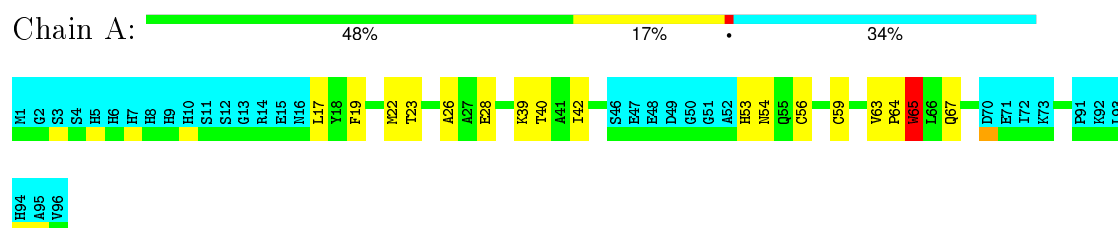


- Molecule 1: Uncharacterized protein

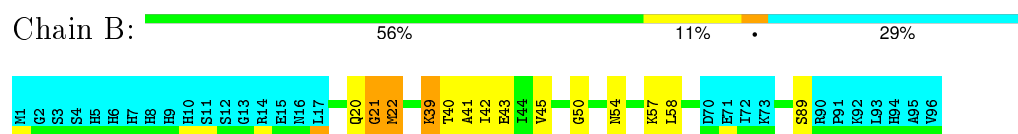


4.2.5 Score per residue for model 5

- Molecule 1: Uncharacterized protein

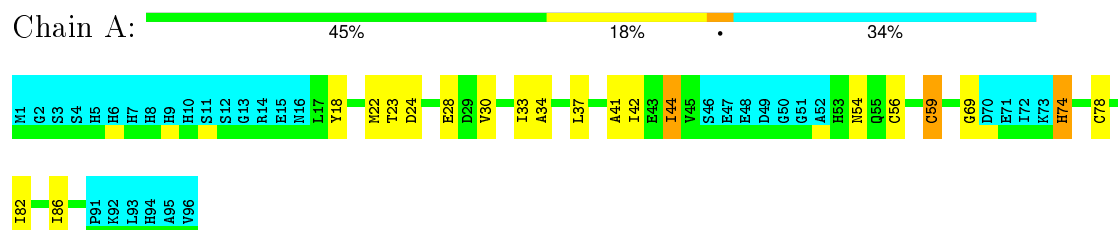


- Molecule 1: Uncharacterized protein



4.2.6 Score per residue for model 6

- Molecule 1: Uncharacterized protein



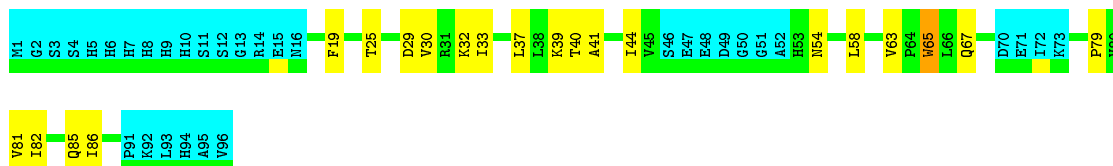
- Molecule 1: Uncharacterized protein



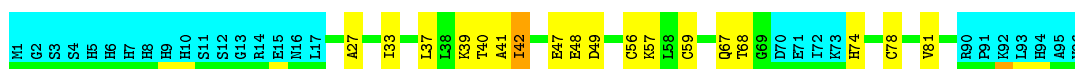


4.2.7 Score per residue for model 7

- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4.2.8 Score per residue for model 8

- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4.2.9 Score per residue for model 9

- Molecule 1: Uncharacterized protein



P91
K92
L93
H94
A95
V96

- Molecule 1: Uncharacterized protein

Chain B: 

M1 G2 G3 S3 S4 H5 H6 H7 H8 H9 H10 H11 S12 G13 G14 R14 E15 N16 L17 Y18 F19 Q20 G21 M22 T23 D23 V36 R31 K32 L37 A41 N54 L58 S62 W65 L66 Q67 D70 E71 I72 K73 D77 C78 P79 I82 L87 R90 P91 K92 L93

H94
A95
V96

4.2.10 Score per residue for model 10

- Molecule 1: Uncharacterized protein

Chain A: 

M1 G2 S3 S4 H5 H6 H7 H8 H9 H10 H11 S12 G13 G14 R14 E15 M16 T23 E28 K32 I33 L38 K39 T40 A41 I42 E43 I44 V45 S46 E47 E48 D49 G50 G51 A52 H53 N54 P64 D70 E71 I72 K73 H74 A75 E76 D77 C78 I82 P91 K92 L93 H94

A95
V96

- Molecule 1: Uncharacterized protein

Chain B: 

M1 G2 S3 S4 H5 H6 H7 H8 H9 H10 H11 S12 G13 G14 R14 E15 M16 L17 A36 L37 T40 A41 N54 Q55 L58 S62 V63 D70 E71 I72 K73 P79 V80 R90 P91 K92 L93 H94 A95 V96

4.2.11 Score per residue for model 11

- Molecule 1: Uncharacterized protein

Chain A: 

M1 G2 S3 S4 H5 H6 H7 H8 H9 H10 H11 S12 G13 G14 R14 E15 M16 L17 E28 K32 K39 S46 E47 E48 D49 G50 G51 A52 H53 N54 V63 P64 V65 D70 E71 I72 K73 P91 K92 L93 H94 A95 V96

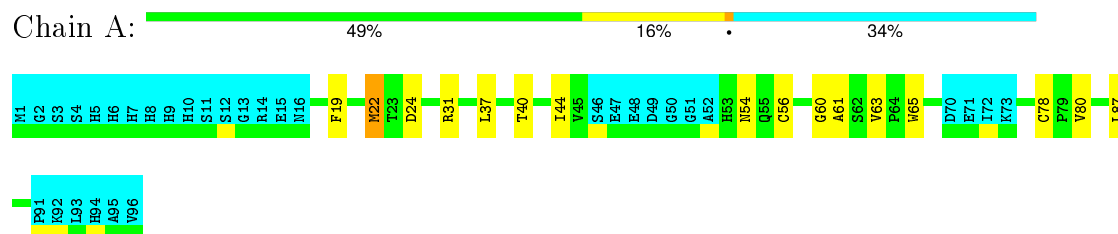
- Molecule 1: Uncharacterized protein

Chain B: 

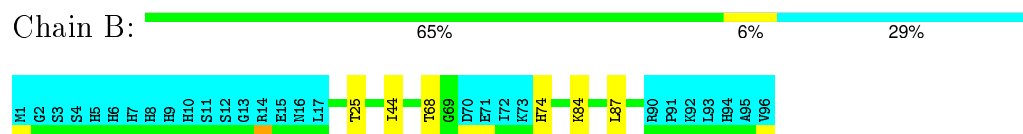
M1 G2 S3 S4 H5 H6 H7 H8 H9 H10 H11 S12 G13 G14 R14 E15 M16 L17 G21 M22 A26 A27 E28 R31 L37 T40 A41 G50 K57 W65 T68 G69 D70 E71 I72 K73 R90 P91 K92 L93 H94 A95 V96

4.2.12 Score per residue for model 12

- Molecule 1: Uncharacterized protein

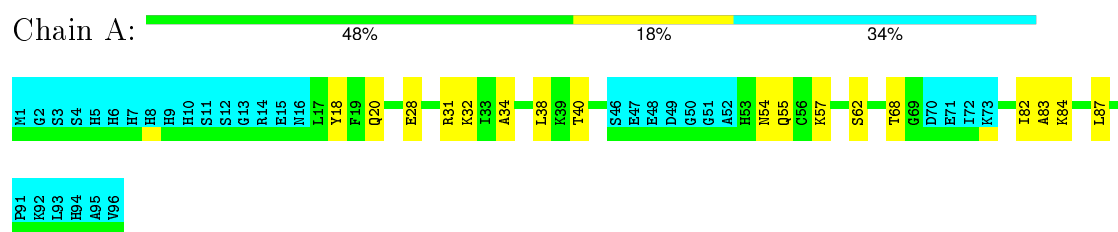


- Molecule 1: Uncharacterized protein

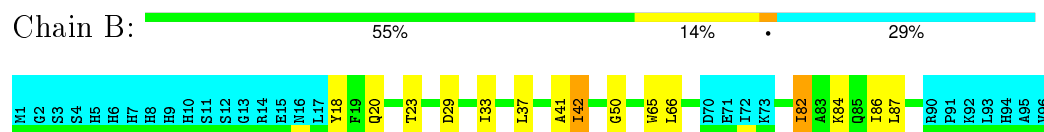


4.2.13 Score per residue for model 13

- Molecule 1: Uncharacterized protein

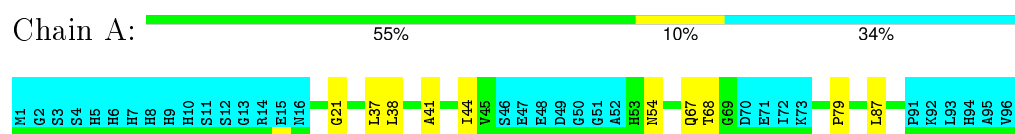


- Molecule 1: Uncharacterized protein

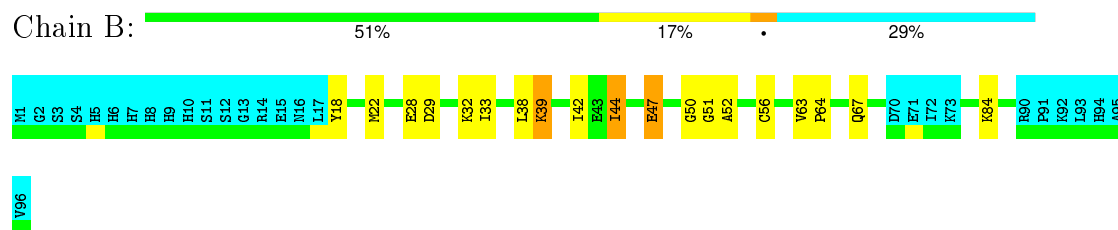


4.2.14 Score per residue for model 14

- Molecule 1: Uncharacterized protein

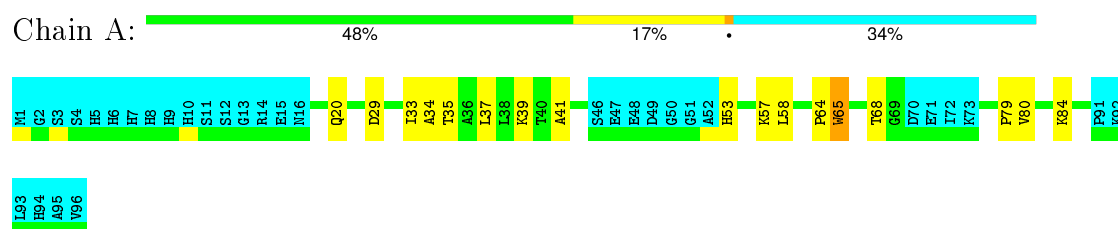


- Molecule 1: Uncharacterized protein

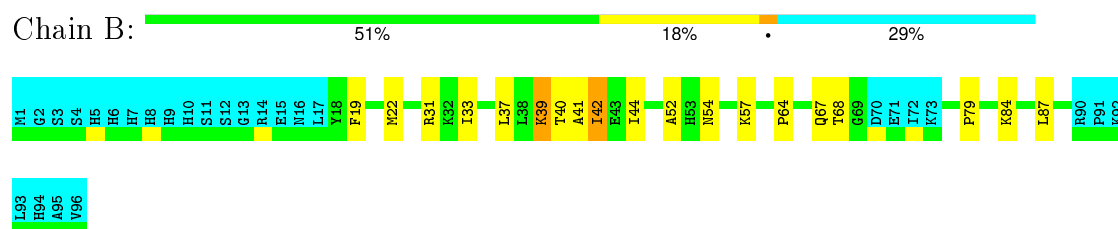


4.2.15 Score per residue for model 15

- Molecule 1: Uncharacterized protein

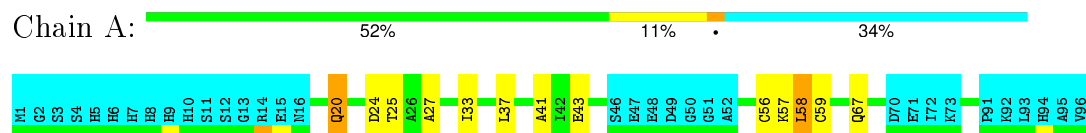


- Molecule 1: Uncharacterized protein

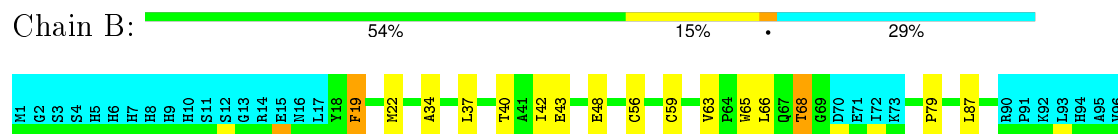


4.2.16 Score per residue for model 16

- Molecule 1: Uncharacterized protein

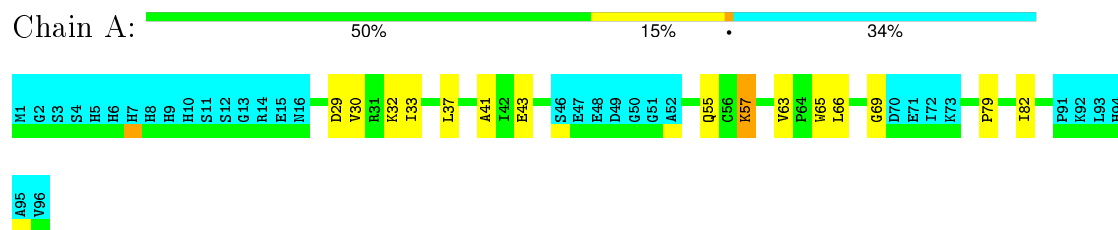


- Molecule 1: Uncharacterized protein

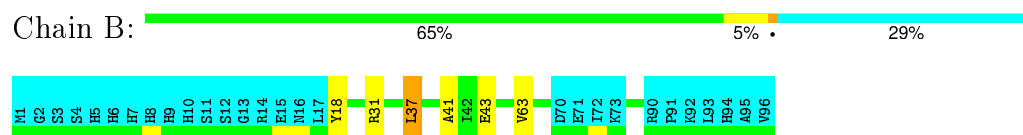


4.2.17 Score per residue for model 17

- Molecule 1: Uncharacterized protein

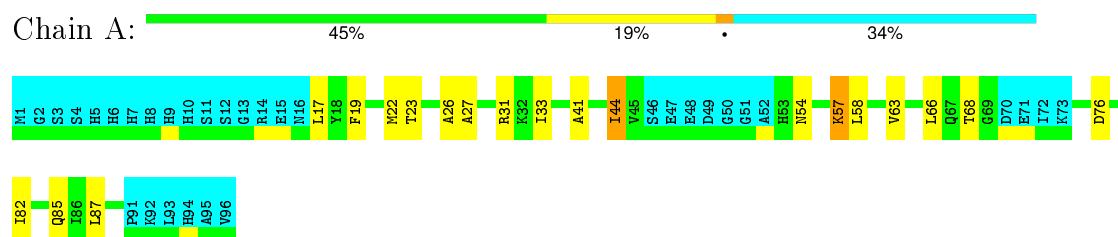


- Molecule 1: Uncharacterized protein

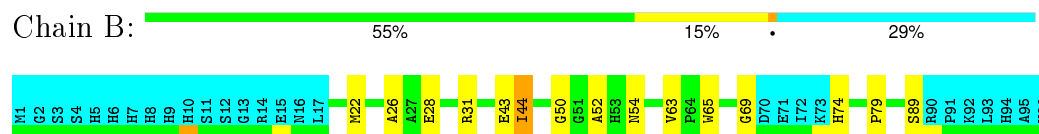


4.2.18 Score per residue for model 18

- Molecule 1: Uncharacterized protein

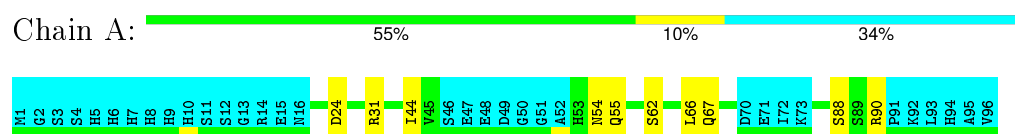


- Molecule 1: Uncharacterized protein

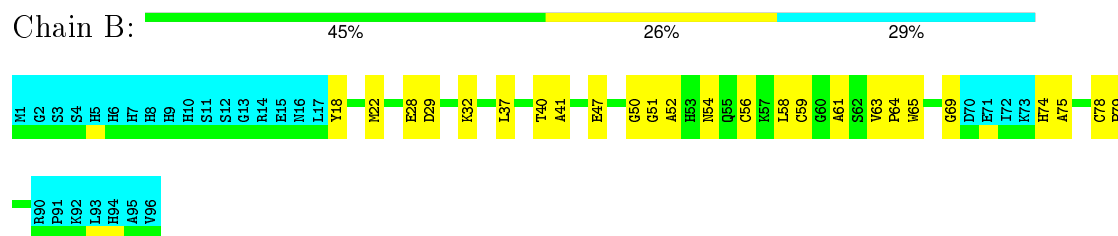


4.2.19 Score per residue for model 19

- Molecule 1: Uncharacterized protein

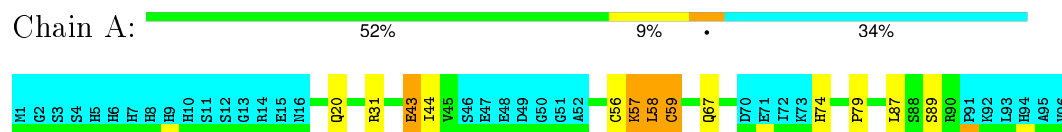


- Molecule 1: Uncharacterized protein



4.2.20 Score per residue for model 20

- Molecule 1: Uncharacterized protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	refinement	
CNS	refinement	
Molmol	structure solution	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 15352
Number of chemical shift lists	1
Total number of shifts	2060
Number of shifts mapped to atoms	2060
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	477	491	489	8±3
1	B	503	499	497	8±3
All	All	19600	19800	19720	293

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:ARG:HG3	1:A:87:LEU:HA	0.92	1.41	13	6
1:B:44:ILE:HD11	1:B:52:ALA:HB1	0.91	1.41	20	4
1:B:39:LYS:HE3	1:B:39:LYS:HA	0.82	1.51	14	1
1:B:39:LYS:HA	1:B:39:LYS:HE3	0.81	1.50	15	2
1:B:22:MET:HA	1:B:26:ALA:HB2	0.79	1.52	3	3
1:A:33:ILE:HA	1:B:79:PRO:HB3	0.79	1.53	16	4
1:A:20:GLN:HA	1:B:23:THR:HA	0.77	1.56	13	2
1:B:42:ILE:HD13	1:B:56:CYS:HA	0.75	1.59	3	2
1:B:54:ASN:HB3	1:B:63:VAL:HB	0.75	1.56	18	2
1:B:42:ILE:HD12	1:B:56:CYS:HA	0.74	1.58	14	1
1:B:59:CYS:HB2	1:B:78:CYS:HB2	0.74	1.58	1	1
1:B:57:LYS:HA	1:B:57:LYS:HE3	0.71	1.62	11	1
1:B:37:LEU:HA	1:B:41:ALA:HB2	0.71	1.61	15	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:MET:HA	1:A:26:ALA:HB2	0.70	1.62	1	2
1:A:56:CYS:HB3	1:A:61:ALA:HB3	0.69	1.63	12	1
1:A:56:CYS:SG	1:A:59:CYS:HB3	0.67	2.30	20	3
1:A:37:LEU:HA	1:A:41:ALA:HB3	0.66	1.66	17	1
1:A:85:GLN:HB3	1:A:90:ARG:HD3	0.66	1.66	4	1
1:B:47:GLU:HG2	1:B:51:GLY:H	0.66	1.49	14	1
1:A:55:GLN:HB2	1:A:62:SER:HB3	0.65	1.67	8	1
1:A:37:LEU:HA	1:A:41:ALA:HB2	0.63	1.71	15	4
1:A:59:CYS:SG	1:A:74:HIS:HA	0.63	2.33	20	1
1:A:43:GLU:HG2	1:B:43:GLU:HB3	0.63	1.69	17	1
1:A:38:LEU:HD11	1:A:87:LEU:HD22	0.62	1.71	13	3
1:B:42:ILE:HD13	1:B:54:ASN:HD21	0.62	1.53	20	1
1:B:28:GLU:HA	1:B:31:ARG:HG2	0.62	1.72	4	1
1:B:29:ASP:HA	1:B:32:LYS:HD3	0.60	1.73	20	1
1:B:37:LEU:HA	1:B:41:ALA:CB	0.60	2.26	7	3
1:B:42:ILE:HD12	1:B:57:LYS:HG2	0.60	1.73	15	1
1:A:42:ILE:HD11	1:A:56:CYS:HA	0.60	1.72	5	1
1:B:42:ILE:HG21	1:B:56:CYS:HA	0.60	1.72	20	1
1:B:63:VAL:HG22	1:B:64:PRO:HD2	0.60	1.71	14	1
1:B:42:ILE:HG13	1:B:56:CYS:HA	0.59	1.75	16	1
1:A:60:GLY:HA2	1:A:75:ALA:HB3	0.59	1.74	1	1
1:A:55:GLN:HG3	1:A:62:SER:HB3	0.58	1.75	19	1
1:A:57:LYS:H	1:A:57:LYS:HD3	0.58	1.59	17	1
1:A:27:ALA:HA	1:B:19:PHE:CE1	0.57	2.34	16	1
1:B:54:ASN:HD21	1:B:65:TRP:HA	0.57	1.59	9	1
1:A:79:PRO:HB2	1:B:33:ILE:HG23	0.57	1.77	7	1
1:A:20:GLN:HE21	1:A:20:GLN:HA	0.57	1.59	16	1
1:A:40:THR:HB	1:B:57:LYS:CB	0.57	2.30	1	2
1:A:63:VAL:HG22	1:A:64:PRO:HD2	0.57	1.75	9	2
1:B:38:LEU:HA	1:B:84:LYS:HE2	0.56	1.78	14	1
1:B:22:MET:SD	1:B:26:ALA:HB2	0.56	2.41	11	1
1:A:28:GLU:O	1:A:32:LYS:HG3	0.56	1.99	1	4
1:A:40:THR:HB	1:B:41:ALA:HB1	0.56	1.77	10	1
1:B:31:ARG:HG2	1:B:87:LEU:HB2	0.56	1.78	15	1
1:B:58:LEU:HD23	1:B:79:PRO:HD2	0.56	1.77	9	2
1:A:59:CYS:HA	1:A:78:CYS:SG	0.55	2.41	6	1
1:B:46:SER:HA	1:B:52:ALA:H	0.55	1.60	8	1
1:B:34:ALA:O	1:B:37:LEU:HG	0.55	2.01	4	3
1:A:37:LEU:HA	1:A:41:ALA:CB	0.55	2.31	17	1
1:A:84:LYS:HD2	1:A:87:LEU:HD11	0.55	1.78	13	2
1:A:40:THR:HG23	1:B:42:ILE:HG23	0.55	1.78	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:63:VAL:O	1:B:69:GLY:HA3	0.54	2.02	19	1
1:B:38:LEU:HD11	1:B:87:LEU:HD22	0.54	1.79	4	1
1:A:54:ASN:HB3	1:A:63:VAL:HB	0.54	1.78	18	2
1:A:58:LEU:HD11	1:B:41:ALA:HA	0.54	1.79	3	1
1:B:63:VAL:HG12	1:B:65:TRP:H	0.54	1.63	18	2
1:A:55:GLN:HG2	1:A:62:SER:HB3	0.54	1.80	13	2
1:A:54:ASN:HB2	1:A:65:TRP:HA	0.54	1.79	5	2
1:A:34:ALA:O	1:A:37:LEU:HG	0.54	2.03	6	2
1:B:65:TRP:O	1:B:66:LEU:HB2	0.54	2.03	13	4
1:B:34:ALA:HB1	1:B:87:LEU:HD23	0.54	1.79	16	2
1:B:42:ILE:CD1	1:B:56:CYS:HA	0.53	2.33	7	1
1:A:17:LEU:HB3	1:A:22:MET:HA	0.53	1.81	5	1
1:B:37:LEU:HA	1:B:41:ALA:HB3	0.52	1.81	1	2
1:A:44:ILE:HG22	1:A:54:ASN:HB2	0.52	1.81	19	1
1:B:56:CYS:HB2	1:B:61:ALA:HB3	0.52	1.79	19	1
1:A:31:ARG:HG2	1:A:87:LEU:HA	0.52	1.82	18	1
1:B:19:PHE:HA	1:B:22:MET:SD	0.52	2.44	16	1
1:A:17:LEU:HB2	1:A:22:MET:H	0.52	1.64	8	1
1:A:20:GLN:HG3	1:B:23:THR:HA	0.52	1.80	8	1
1:B:23:THR:HG23	1:B:25:THR:H	0.52	1.65	8	1
1:A:63:VAL:HG12	1:A:65:TRP:H	0.51	1.65	7	1
1:A:57:LYS:HD3	1:A:57:LYS:H	0.51	1.64	18	1
1:A:36:ALA:HB1	1:B:58:LEU:HD21	0.51	1.82	9	1
1:A:63:VAL:CG2	1:A:64:PRO:HD2	0.50	2.36	11	2
1:B:84:LYS:HA	1:B:87:LEU:HG	0.50	1.83	12	1
1:A:38:LEU:HA	1:A:42:ILE:HG12	0.50	1.82	10	1
1:B:40:THR:HG23	1:B:41:ALA:H	0.49	1.65	5	1
1:B:43:GLU:HB2	1:B:57:LYS:HE3	0.49	1.83	4	1
1:B:59:CYS:HB3	1:B:75:ALA:HB3	0.49	1.83	1	1
1:A:56:CYS:HB2	1:A:59:CYS:SG	0.49	2.47	5	1
1:A:33:ILE:HA	1:B:79:PRO:HB2	0.49	1.84	18	1
1:A:37:LEU:HA	1:A:40:THR:HG22	0.49	1.85	12	2
1:A:79:PRO:HB2	1:B:33:ILE:HG22	0.49	1.84	14	1
1:B:79:PRO:O	1:B:82:ILE:HG22	0.49	2.07	1	1
1:B:47:GLU:CG	1:B:51:GLY:H	0.49	2.21	14	1
1:A:39:LYS:HG3	1:A:40:THR:HG23	0.49	1.85	5	1
1:B:29:ASP:HA	1:B:32:LYS:NZ	0.49	2.22	14	1
1:A:39:LYS:HG3	1:A:40:THR:HG22	0.48	1.84	7	1
1:B:47:GLU:HG2	1:B:51:GLY:N	0.48	2.22	14	1
1:B:42:ILE:HG22	1:B:54:ASN:ND2	0.48	2.23	5	1
1:B:28:GLU:O	1:B:32:LYS:HG3	0.48	2.08	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:75:ALA:HB3	1:B:78:CYS:SG	0.48	2.47	19	1
1:B:42:ILE:HG22	1:B:43:GLU:H	0.48	1.69	16	1
1:B:25:THR:HA	1:B:28:GLU:OE2	0.48	2.09	20	1
1:A:17:LEU:HG	1:A:22:MET:H	0.48	1.67	18	1
1:B:39:LYS:CE	1:B:39:LYS:HA	0.48	2.32	15	1
1:A:81:VAL:O	1:A:85:GLN:HG2	0.48	2.08	7	1
1:A:19:PHE:HD2	1:B:22:MET:HB3	0.48	1.69	5	1
1:B:37:LEU:HD13	1:B:80:VAL:HG13	0.48	1.86	20	3
1:B:84:LYS:O	1:B:87:LEU:HG	0.48	2.09	13	2
1:B:55:GLN:HG2	1:B:62:SER:HB3	0.48	1.84	10	1
1:A:57:LYS:HA	1:A:57:LYS:HE3	0.47	1.85	13	2
1:B:37:LEU:HD21	1:B:80:VAL:HG13	0.47	1.86	10	1
1:A:39:LYS:HA	1:A:39:LYS:HE2	0.47	1.87	10	1
1:A:82:ILE:O	1:A:86:ILE:HG13	0.47	2.09	7	3
1:A:31:ARG:HG3	1:A:87:LEU:HB2	0.47	1.85	9	1
1:A:58:LEU:HD23	1:A:79:PRO:HD2	0.47	1.86	4	1
1:A:78:CYS:SG	1:A:80:VAL:HG22	0.47	2.50	12	1
1:A:79:PRO:HA	1:B:33:ILE:HG22	0.47	1.87	15	1
1:A:30:VAL:O	1:A:33:ILE:HG12	0.47	2.09	17	2
1:A:37:LEU:CA	1:A:41:ALA:HB2	0.47	2.40	15	2
1:A:54:ASN:H	1:A:63:VAL:CG2	0.46	2.23	12	1
1:A:41:ALA:O	1:A:57:LYS:HE2	0.46	2.10	18	1
1:A:54:ASN:O	1:A:62:SER:HA	0.46	2.10	13	3
1:B:39:LYS:HG3	1:B:40:THR:HG22	0.46	1.87	7	1
1:B:21:GLY:O	1:B:22:MET:HB2	0.46	2.09	5	1
1:B:63:VAL:CG2	1:B:64:PRO:HD2	0.46	2.40	14	1
1:B:54:ASN:ND2	1:B:65:TRP:HA	0.46	2.23	9	1
1:B:29:ASP:O	1:B:32:LYS:HB3	0.46	2.11	9	1
1:A:78:CYS:O	1:A:81:VAL:HG22	0.46	2.11	4	1
1:B:59:CYS:SG	1:B:74:HIS:HA	0.46	2.50	19	1
1:A:32:LYS:HZ2	1:A:32:LYS:HB2	0.45	1.71	11	1
1:A:44:ILE:HA	1:A:54:ASN:HA	0.45	1.89	10	1
1:A:42:ILE:HD12	1:A:54:ASN:HD21	0.45	1.71	4	1
1:B:82:ILE:O	1:B:86:ILE:HG13	0.45	2.12	1	3
1:A:41:ALA:HB1	1:A:57:LYS:HD3	0.45	1.87	1	1
1:A:45:VAL:HG22	1:A:55:GLN:NE2	0.45	2.27	4	1
1:B:29:ASP:HA	1:B:32:LYS:HZ3	0.45	1.71	14	1
1:B:68:THR:HG23	1:B:69:GLY:H	0.45	1.71	1	1
1:A:22:MET:O	1:A:23:THR:HB	0.45	2.12	6	1
1:B:28:GLU:HG3	1:B:31:ARG:NH2	0.45	2.27	18	1
1:A:57:LYS:HB2	1:A:57:LYS:HZ2	0.45	1.72	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:ALA:HB3	1:A:78:CYS:SG	0.45	2.52	10	1
1:B:54:ASN:O	1:B:62:SER:HA	0.44	2.11	10	2
1:B:78:CYS:SG	1:B:80:VAL:HG22	0.44	2.52	8	1
1:B:78:CYS:O	1:B:81:VAL:HG22	0.44	2.12	3	2
1:A:54:ASN:HB3	1:A:63:VAL:O	0.44	2.12	1	1
1:B:54:ASN:HB3	1:B:63:VAL:O	0.44	2.12	1	1
1:A:33:ILE:O	1:A:37:LEU:HG	0.44	2.11	9	1
1:B:18:TYR:O	1:B:22:MET:HG2	0.44	2.12	9	2
1:B:31:ARG:HG3	1:B:87:LEU:HB2	0.44	1.89	9	1
1:A:86:ILE:HG12	1:B:19:PHE:HE1	0.44	1.73	1	1
1:A:80:VAL:O	1:A:84:LYS:HG3	0.44	2.13	3	2
1:B:19:PHE:O	1:B:20:GLN:HB3	0.44	2.12	9	2
1:A:78:CYS:HB3	1:A:80:VAL:HG22	0.44	1.90	9	1
1:A:19:PHE:HA	1:A:22:MET:SD	0.44	2.53	12	1
1:A:20:GLN:HA	1:B:22:MET:O	0.44	2.13	20	1
1:A:56:CYS:CB	1:A:59:CYS:HB2	0.43	2.43	16	1
1:A:33:ILE:HG22	1:A:37:LEU:HD23	0.43	1.89	1	1
1:B:46:SER:HA	1:B:52:ALA:HA	0.43	1.91	6	2
1:A:29:ASP:O	1:A:32:LYS:HB3	0.43	2.13	8	1
1:A:35:THR:O	1:A:39:LYS:HG3	0.43	2.14	15	1
1:A:42:ILE:HG22	1:A:54:ASN:HD21	0.43	1.74	6	1
1:B:57:LYS:HD2	1:B:57:LYS:H	0.43	1.74	4	1
1:B:84:LYS:HA	1:B:87:LEU:CD2	0.43	2.43	8	1
1:B:47:GLU:HG3	1:B:51:GLY:HA3	0.43	1.89	19	1
1:B:44:ILE:HA	1:B:54:ASN:HA	0.43	1.91	15	1
1:B:64:PRO:HB2	1:B:67:GLN:CG	0.43	2.44	15	1
1:A:53:HIS:HA	1:A:64:PRO:O	0.43	2.13	15	1
1:B:19:PHE:HA	1:B:22:MET:HB2	0.43	1.90	15	1
1:B:19:PHE:O	1:B:22:MET:HB2	0.43	2.13	4	1
1:A:82:ILE:O	1:A:86:ILE:HG12	0.43	2.14	8	1
1:A:44:ILE:HD13	1:A:54:ASN:HA	0.43	1.90	14	1
1:A:33:ILE:HG22	1:B:79:PRO:HB2	0.43	1.91	10	1
1:A:58:LEU:HB2	1:B:41:ALA:HA	0.42	1.91	7	1
1:B:56:CYS:SG	1:B:59:CYS:HB3	0.42	2.53	16	1
1:A:27:ALA:O	1:A:31:ARG:HG3	0.42	2.13	18	1
1:B:44:ILE:HD12	1:B:44:ILE:O	0.42	2.14	12	1
1:A:83:ALA:HB2	1:B:33:ILE:HG21	0.42	1.91	13	2
1:A:58:LEU:HD21	1:A:79:PRO:HD2	0.42	1.89	15	1
1:A:40:THR:HB	1:B:57:LYS:HB2	0.42	1.92	5	1
1:A:42:ILE:HD13	1:A:69:GLY:HA3	0.42	1.90	6	1
1:A:88:SER:HB3	1:A:90:ARG:HG2	0.42	1.91	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:ASP:HA	1:A:32:LYS:HE2	0.42	1.91	17	1
1:A:85:GLN:HA	1:A:85:GLN:OE1	0.42	2.14	7	1
1:B:54:ASN:HB3	1:B:64:PRO:HD2	0.42	1.92	19	1
1:A:31:ARG:CG	1:A:87:LEU:HA	0.42	2.31	1	1
1:A:41:ALA:CB	1:A:57:LYS:HD3	0.42	2.44	1	1
1:A:56:CYS:SG	1:A:61:ALA:HB3	0.42	2.55	9	1
1:A:82:ILE:HG12	1:B:29:ASP:HB2	0.42	1.92	13	2
1:A:79:PRO:HA	1:A:82:ILE:HG22	0.41	1.90	17	1
1:A:29:ASP:HA	1:A:32:LYS:NZ	0.41	2.30	7	1
1:B:45:VAL:HG13	1:B:57:LYS:HE2	0.41	1.92	5	1
1:B:42:ILE:HG22	1:B:43:GLU:N	0.41	2.30	16	1
1:A:33:ILE:HA	1:B:79:PRO:CB	0.41	2.44	18	1
1:A:19:PHE:CE2	1:B:27:ALA:HA	0.41	2.50	7	1
1:B:44:ILE:CG2	1:B:52:ALA:HB1	0.41	2.45	3	1
1:B:42:ILE:HG23	1:B:57:LYS:CE	0.41	2.45	15	1
1:A:65:TRP:O	1:A:66:LEU:HB2	0.41	2.15	17	1
1:A:30:VAL:HG11	1:A:86:ILE:HG21	0.41	1.91	6	1
1:B:47:GLU:O	1:B:49:ASP:N	0.41	2.54	7	1
1:B:58:LEU:HB2	1:B:78:CYS:SG	0.41	2.56	1	1
1:B:29:ASP:O	1:B:32:LYS:HB2	0.41	2.15	20	1
1:A:82:ILE:O	1:A:85:GLN:HG2	0.41	2.15	18	1
1:B:43:GLU:HG2	1:B:57:LYS:HE3	0.41	1.91	1	1
1:B:36:ALA:O	1:B:40:THR:HG22	0.41	2.16	10	1
1:A:22:MET:HB2	1:A:26:ALA:CB	0.41	2.46	5	1
1:A:40:THR:CG2	1:B:42:ILE:HG23	0.41	2.45	13	2
1:A:60:GLY:HA2	1:A:75:ALA:CB	0.41	2.44	1	1
1:A:58:LEU:O	1:A:59:CYS:HB2	0.41	2.16	20	1
1:A:63:VAL:HG11	1:A:69:GLY:HA2	0.40	1.93	17	1
1:B:59:CYS:HA	1:B:78:CYS:SG	0.40	2.56	7	1
1:A:58:LEU:HD13	1:A:58:LEU:N	0.40	2.31	16	1
1:B:55:GLN:HA	1:B:62:SER:HB2	0.40	1.92	4	1
1:A:37:LEU:O	1:A:41:ALA:HB3	0.40	2.16	14	1
1:B:47:GLU:HB2	1:B:51:GLY:N	0.40	2.30	19	1
1:A:58:LEU:HD22	1:A:79:PRO:HG2	0.40	1.92	20	1
1:A:43:GLU:CD	1:A:57:LYS:HZ3	0.40	2.19	20	1
1:A:34:ALA:O	1:A:38:LEU:HG	0.40	2.16	13	2
1:A:44:ILE:HG23	1:A:54:ASN:HD22	0.40	1.75	7	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	63/96 (66%)	54±2 (86±4%)	7±2 (11±3%)	2±1 (2±2%)	11	48
1	B	68/96 (71%)	57±3 (84±4%)	9±2 (13±3%)	2±1 (3±2%)	8	40
All	All	2620/3840 (68%)	2231 (85%)	315 (12%)	74 (3%)	10	44

All 33 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	50	GLY	9
1	B	40	THR	5
1	A	24	ASP	4
1	A	23	THR	4
1	B	58	LEU	3
1	A	65	TRP	3
1	A	68	THR	3
1	A	67	GLN	3
1	A	59	CYS	3
1	B	68	THR	3
1	B	23	THR	3
1	B	42	ILE	2
1	B	22	MET	2
1	B	74	HIS	2
1	A	22	MET	2
1	B	89	SER	2
1	B	21	GLY	2
1	B	48	GLU	2
1	B	18	TYR	2
1	A	20	GLN	2
1	A	21	GLY	1
1	B	65	TRP	1
1	A	19	PHE	1
1	A	60	GLY	1
1	B	20	GLN	1
1	A	64	PRO	1

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Mol	Chain	Res	Type	Models (Total)
1	B	67	GLN	1
1	A	17	LEU	1
1	A	89	SER	1
1	B	69	GLY	1
1	B	52	ALA	1
1	B	19	PHE	1
1	A	41	ALA	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	52/79 (66%)	50±1 (96±3%)	2±1 (4±3%)	42	84
1	B	54/79 (68%)	52±1 (95±2%)	2±1 (5±2%)	38	82
All	All	2120/3160 (67%)	2028 (96%)	92 (4%)	40	83

All 46 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	44	ILE	4
1	B	28	GLU	4
1	A	67	GLN	4
1	A	57	LYS	4
1	B	57	LYS	4
1	B	39	LYS	3
1	B	31	ARG	3
1	A	18	TYR	3
1	B	82	ILE	3
1	B	43	GLU	3
1	B	67	GLN	3
1	B	44	ILE	3
1	A	43	GLU	3
1	A	58	LEU	3
1	B	42	ILE	2
1	B	37	LEU	2
1	A	65	TRP	2

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Mol	Chain	Res	Type	Models (Total)
1	A	39	LYS	2
1	B	65	TRP	2
1	B	20	GLN	2
1	A	23	THR	2
1	A	28	GLU	2
1	A	32	LYS	2
1	B	68	THR	2
1	B	47	GLU	2
1	B	18	TYR	2
1	A	66	LEU	2
1	B	22	MET	1
1	A	53	HIS	1
1	A	55	GLN	1
1	A	22	MET	1
1	A	29	ASP	1
1	B	25	THR	1
1	B	89	SER	1
1	B	40	THR	1
1	B	54	ASN	1
1	B	84	LYS	1
1	A	68	THR	1
1	A	74	HIS	1
1	B	32	LYS	1
1	B	23	THR	1
1	B	29	ASP	1
1	A	25	THR	1
1	A	76	ASP	1
1	A	31	ARG	1
1	A	20	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 93% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15352

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	2060
Number of shifts mapped to atoms	2060
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	168	-0.33 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	156	0.04 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	162	-0.13 ± 0.17	None needed (< 0.5 ppm)
^{15}N	162	0.15 ± 0.45	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 93%, i.e. 1400 atoms were assigned a chemical shift out of a possible 1511. 21 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	642/647 (99%)	258/258 (100%)	257/262 (98%)	127/127 (100%)
Sidechain	692/774 (89%)	422/447 (94%)	262/300 (87%)	8/27 (30%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	66/90 (73%)	38/46 (83%)	26/34 (76%)	2/10 (20%)
Overall	1400/1511 (93%)	718/751 (96%)	545/596 (91%)	137/164 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1810 atoms were assigned a chemical shift out of a possible 2264. 26 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	822/948 (87%)	330/378 (87%)	330/384 (86%)	162/186 (87%)
Sidechain	914/1114 (82%)	562/652 (86%)	342/420 (81%)	10/42 (24%)
Aromatic	74/202 (37%)	42/102 (41%)	30/62 (48%)	2/38 (5%)
Overall	1810/2264 (80%)	934/1132 (83%)	702/866 (81%)	174/266 (65%)

7.1.4 Statistically unusual chemical shifts ⓘ

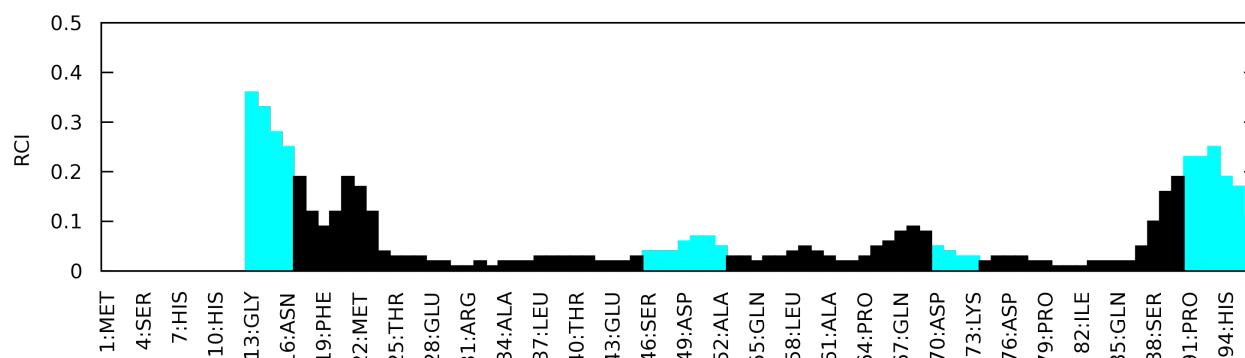
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	B	72	ILE	CG1	14.35	36.54 – 18.94	-7.6
1	A	72	ILE	CG1	14.35	36.54 – 18.94	-7.6

7.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

