

wwPDB NMR Structure Validation Summary Report (i)

Apr 21, 2024 – 03:33 AM EDT

:	2MF0
:	19534
:	Structural basis of the non-coding RNA RsmZ acting as protein sponge: Con-
	former L of $RsmZ(1-72)/RsmE(dimer)$ 1to3 complex
:	Duss, O.; Michel, E.; Yulikov, M.; Schubert, M.; Jeschke, G.; Allain, F.HT.
:	2013-10-02
	:

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/NMRValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

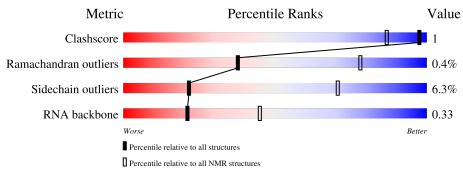
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 5%.

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f NMR} \ { m archive} \ (\#{ m Entries})$
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428
RNA backbone	4643	676

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 <=5%

Mol	Chain	Length	Quality of chain					
1	А	70	66%	•	16%	16%		
1	В	70	74%		10%	16%		
1	С	70	70%	•	11%	16%		
1	D	70	71%	•	11%	16%		
1	Е	70	64%	•	17%	16%		
1	F	70	66%	•	16%	16%		
2	G	72	36% 49%			15%		



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 4 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:1-A:48, B:1-B:59, C:1-	0.43	4					
	C:51, D:1-D:51 (209)							
2	E:2-E:48, F:1-F:48 (95)	0.24	20					

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 4 clusters and 1 single-model cluster was found.

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7852 atoms, of which 3615 are hydrogens and 0 are deuteriums.

Mol	Chain	Residues		I	Atom	S			Trace							
1	٨	59	Total	С	Η	Ν	0	S	0							
	А	- 59	920	280	472	81	86	1	0							
1	В	59	Total	С	Н	Ν	0	S	0							
	D	59	920	280	472	81	86	1	0							
1	С	59	Total	С	Н	Ν	0	\mathbf{S}	0							
1	U	U	U	U	U	U	U	U	00	920	280	472	81	86	1	0
1	D	59	Total	С	Η	Ν	Ο	\mathbf{S}	0							
	D		920	280	472	81	86	1	0							
1	Е	59	Total	С	Η	Ν	Ο	\mathbf{S}	0							
1	Ľ		920	280	472	81	86	1	0							
1	F	59	Total	С	Η	N	Ο	\mathbf{S}	0							
	T,		920	280	472	81	86	1	0							

• Molecule 1 is a protein called Carbon storage regulator homolog.

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	60	LYS	-	expression tag	UNP Q4KEY0
А	61	ARG	-	expression tag	UNP Q4KEY0
A	62	GLU	-	expression tag	UNP Q4KEY0
А	63	THR	-	expression tag	UNP Q4KEY0
А	64	PRO	-	expression tag	UNP Q4KEY0
A	65	HIS	-	expression tag	UNP Q4KEY0
А	66	HIS	-	expression tag	UNP Q4KEY0
A	67	HIS	-	expression tag	UNP Q4KEY0
A	68	HIS	-	expression tag	UNP Q4KEY0
A	69	HIS	-	expression tag	UNP Q4KEY0
А	70	HIS	-	expression tag	UNP Q4KEY0
В	60	LYS	-	expression tag	UNP Q4KEY0
В	61	ARG	-	expression tag	UNP Q4KEY0
В	62	GLU	-	expression tag	UNP Q4KEY0
В	63	THR	-	expression tag	UNP Q4KEY0
В	64	PRO	-	expression tag	UNP Q4KEY0
В	65	HIS	-	expression tag	UNP Q4KEY0
В	66	HIS	-	expression tag	UNP Q4KEY0
В	67	HIS	-	expression tag	UNP Q4KEY0
В	68	HIS	-	expression tag	UNP Q4KEY0
В	69	HIS	-	expression tag	UNP Q4KEY0



Continu Chain	Residue	vious page Modelled	Actual	Commont	Reference
		HIS	Actual	Comment	
B	70		-	expression tag	UNP Q4KEY0
C	60	LYS	-	expression tag	UNP Q4KEY0
C	61	ARG	-	expression tag	UNP Q4KEY0
C	62	GLU	-	expression tag	UNP Q4KEY0
C	63	THR	-	expression tag	UNP Q4KEY0
C	64	PRO	-	expression tag	UNP Q4KEY0
C	65	HIS	-	expression tag	UNP Q4KEY0
C	66	HIS	-	expression tag	UNP Q4KEY0
C	67	HIS	-	expression tag	UNP Q4KEY0
С	68	HIS	-	expression tag	UNP Q4KEY0
C	69	HIS	-	expression tag	UNP Q4KEY0
С	70	HIS	-	expression tag	UNP Q4KEY0
D	60	LYS	-	expression tag	UNP Q4KEY0
D	61	ARG	-	expression tag	UNP Q4KEY0
D	62	GLU	-	expression tag	UNP Q4KEY0
D	63	THR	-	expression tag	UNP Q4KEY0
D	64	PRO	-	expression tag	UNP Q4KEY0
D	65	HIS	-	expression tag	UNP Q4KEY0
D	66	HIS	-	expression tag	UNP Q4KEY0
D	67	HIS	-	expression tag	UNP Q4KEY0
D	68	HIS	-	expression tag	UNP Q4KEY0
D	69	HIS	-	expression tag	UNP Q4KEY0
D	70	HIS	-	expression tag	UNP Q4KEY0
Е	60	LYS	-	expression tag	UNP Q4KEY0
Е	61	ARG	-	expression tag	UNP Q4KEY0
Е	62	GLU	-	expression tag	UNP Q4KEY0
Е	63	THR	-	expression tag	UNP Q4KEY0
Е	64	PRO	-	expression tag	UNP Q4KEY0
Е	65	HIS	-	expression tag	UNP Q4KEY0
Е	66	HIS	-	expression tag	UNP Q4KEY0
Е	67	HIS	-	expression tag	UNP Q4KEY0
Е	68	HIS	-	expression tag	UNP Q4KEY0
Е	69	HIS	-	expression tag	UNP Q4KEY0
Е	70	HIS	-	expression tag	UNP Q4KEY0
F	60	LYS	-	expression tag	UNP Q4KEY0
F	61	ARG	-	expression tag	UNP Q4KEY0
F	62	GLU	-	expression tag	UNP Q4KEY0
F	63	THR	-	expression tag	UNP Q4KEY0
F	64	PRO	-	expression tag	UNP Q4KEY0
F	65	HIS	-	expression tag	UNP Q4KEY0
F	66	HIS	-	expression tag	UNP Q4KEY0
F	67	HIS	-	expression tag	UNP Q4KEY0
L	1	1	1	· · 0	· · ·

Continued from previous page...



Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	68	HIS	-	expression tag	UNP Q4KEY0
F	69	HIS	-	expression tag	UNP Q4KEY0
F	70	HIS	-	expression tag	UNP Q4KEY0

• Molecule 2 is a RNA chain called RNA_(72-MER).

Mol	Chain	Residues	Atoms				Trace		
2	G	72	Total	С	Н	Ν	0	Р	0
_	2 G	л (2	2332	693	783	295	490	71	Ŭ

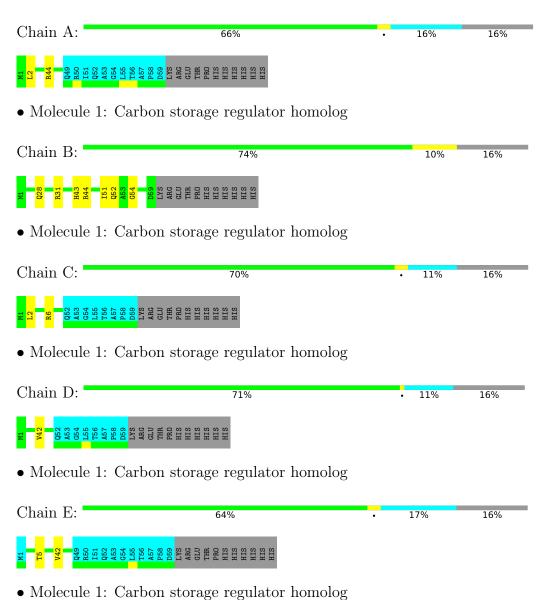


4 Residue-property plots (i)

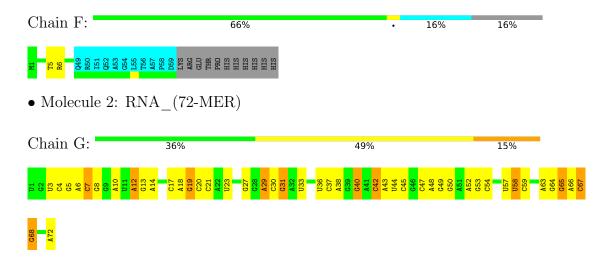
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: Carbon storage regulator homolog



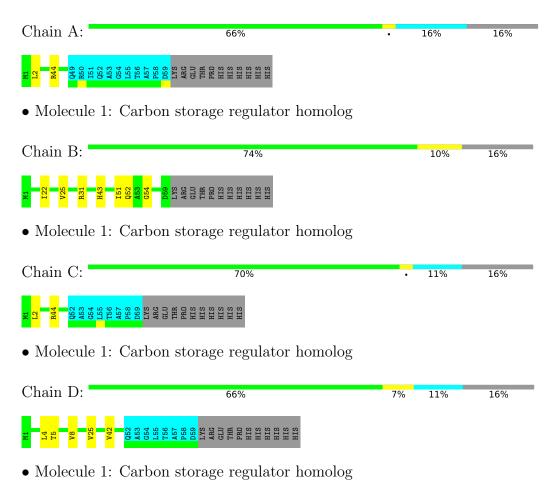




4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 4. Colouring as in section 4.1 above.

• Molecule 1: Carbon storage regulator homolog





Chain E:	63%	·	17%	16%	-
M1 L2 T5 V42 R50 R50 R50 Q52 Q52	A53 156 155 156 156 156 156 156 156 158 118 118 118 118 118 118 118 118 118	HIS			
• Molecule 1: 0	Carbon storage regulato	r homolog			
Chain F:	66%	•	16%	16%	
M1 15 R5 R50 151 151 A52 A53 C54	L55 T56 P58 P58 P58 P58 P10 P10 P11 P115 H115 H115 H115 H115 H115 H115				
• Molecule 2: 1	RNA_(72-MER)				
Chain G:	42%	40%		14%	·
U1 02 03 03 03 03 04 05 05 03 013 013	A14 C17 C17 C17 C17 C17 C17 C20 C21 C21 C24 C24 C24 C24 C24 C24 C26 C26 C26 C27 C28 C27 C28 C27 C27 C27 C27 C27 C27 C27 C27 C27 C27	A32 U33 U36 U36 A38 A38 C37 C37 C37 C42 C41 C42 C42 C42 C42 C42	C45 C47 C47 C47 C47 C47 C47 C48 C49 G50 G50	452 653 054 058 058 059 059	A63 G64 G65 A66 C67 C67
A72					



5 Refinement protocol and experimental data overview (i)

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

Of the 2500 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure solution	
Amber	refinement	

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)	working_cs.cif
Number of chemical shift lists	2
Total number of shifts	292
Number of shifts mapped to atoms	292
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	5%



6 Model quality (i)

6.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles		
	RMSZ	$\#Z{>}5$	RMSZ	$\#Z{>}5$		
1	А	$0.38 {\pm} 0.00$	$0{\pm}0/370~(~0.0{\pm}~0.0\%)$	$0.80{\pm}0.02$	$0{\pm}0/501~(~0.0{\pm}~0.0\%)$	
1	В	$0.38 {\pm} 0.00$	$0{\pm}0/451~(~0.0{\pm}~0.0\%)$	$0.87 {\pm} 0.02$	$0{\pm}0/6{10}~(~0.1{\pm}~0.1\%)$	
1	С	$0.38 {\pm} 0.00$	$0{\pm}0/398~(~0.0{\pm}~0.0\%)$	$0.80{\pm}0.02$	$0{\pm}0/538~(~0.0{\pm}~0.0\%)$	
1	D	$0.38 {\pm} 0.00$	$0{\pm}0/398~(~0.0{\pm}~0.0\%)$	$0.84{\pm}0.02$	$0{\pm}0/538~(~0.0{\pm}~0.1\%)$	
1	Е	$0.38 {\pm} 0.00$	$0{\pm}0/362~(~0.0{\pm}~0.0\%)$	$0.80{\pm}0.02$	$0{\pm}0/491~(~0.0{\pm}~0.0\%)$	
1	F	$0.38 {\pm} 0.00$	$0{\pm}0/370~(~0.0{\pm}~0.0\%)$	$0.78 {\pm} 0.03$	$0{\pm}0/501~(~0.0{\pm}~0.0\%)$	
2	G	1.01 ± 0.00	$0{\pm}0/1737~(~0.0{\pm}~0.0\%)$	1.67 ± 0.02	$22{\pm}3/2709$ ($0.8{\pm}$ $0.1\%)$	
All	All	0.72	0/81720~(~0.0%)	1.28	450/117760~(~0.4%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	С	$0.0{\pm}0.0$	$0.6{\pm}0.6$
1	А	$0.0{\pm}0.0$	0.3 ± 0.5
1	F	$0.0{\pm}0.0$	0.5 ± 0.5
1	Е	$0.0{\pm}0.0$	0.1 ± 0.4
1	В	$0.0{\pm}0.0$	0.1 ± 0.3
2	G	$0.0{\pm}0.0$	16.2 ± 2.7
All	All	0	356

There are no bond-length outliers.

5 of 70 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Dec	Type	Atoma	7	Observed(°)	$Ideal(^{o})$	Moo	dels
	Unain	nes	туре	Atoms		Z Observed()		Worst	Total
2	G	17	С	O4'-C1'-N1	10.15	116.32	108.20	12	8
2	G	58	U	O4'-C1'-N1	9.68	115.94	108.20	16	13
2	G	7	С	N3-C2-O2	-9.54	115.22	121.90	8	6
2	G	7	С	N1-C2-O2	9.49	124.59	118.90	16	6



Continued from previous page	Continued	from	previous	page
------------------------------	-----------	------	----------	------

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\operatorname{Ideal}(^{o})$	Moo Worst	lels Total
2	G	37	С	O4'-C1'-N1	9.37	115.70	108.20	13	10

There are no chirality outliers.

5 of 58 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	G	12	А	Sidechain	20
2	G	29	А	Sidechain	20
2	G	31	G	Sidechain	20
2	G	66	А	Sidechain	20
2	G	14	А	Sidechain	18

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	В	448	472	472	1±1
1	D	395	422	422	1±1
1	А	367	390	390	0±0
1	С	395	422	422	0±1
1	F	367	390	390	0 ± 0
1	Е	359	379	379	0±0
2	G	1549	783	783	1±1
All	All	77600	65160	65160	74

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 1.

5 of 33 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:D:47:ILE:HD12	2:G:7:C:C2	0.65	2.27	15	1	
1:D:8:VAL:HG11	1:D:25:VAL:HG12	0.63	1.68	11	5	
1:D:51:ILE:HD11	2:G:7:C:C2	0.62	2.29	11	2	
2:G:29:A:H2'	2:G:30:C:H5"	0.59	1.75	19	1	



Continued from previous page...

Atom 1	Atom-2	Clash(Å)	Distance(Å)	Moo	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:D:51:ILE:HD12	1:D:51:ILE:N	0.57	2.15	10	5

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

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	Perce	ntiles
1	А	47/70~(67%)	$43 \pm 1 \ (92 \pm 1\%)$	4 ± 1 ($8\pm1\%$)	0±0 (0±0%)	54	85
1	В	57/70~(81%)	52 ± 1 (90 $\pm2\%$)	$4\pm1~(8\pm2\%)$	$1\pm1~(2\pm1\%)$	12	54
1	С	50/70~(71%)	50 ± 1 (100 $\pm1\%$)	0±0 (0±1%)	0±0 (0±1%)	50	82
1	D	50/70~(71%)	49 ± 1 (97 $\pm2\%$)	$1\pm1 (3\pm2\%)$	0±0 (0±0%)	100	100
1	Е	47/70~(67%)	$45 \pm 1 \ (96 \pm 2\%)$	$2\pm1 (4\pm2\%)$	0±0 (0±0%)	100	100
1	F	47/70~(67%)	44 ± 1 (94 $\pm2\%$)	$3\pm1~(6\pm2\%)$	0±0 (0±0%)	100	100
All	All	5960/8400~(71%)	5645~(95%)	291~(5%)	24 (0%)	38	78

5 of 7 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	В	54	GLY	16
1	В	15	GLY	2
1	В	16	ASP	2
1	С	15	GLY	1
1	С	16	ASP	1

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed and the total number of residues.



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
1	А	41/60~(68%)	$38 \pm 1 (92 \pm 2\%)$	$3\pm1~(8\pm2\%)$	17	65
1	В	49/60~(82%)	$45 \pm 1 (92 \pm 3\%)$	4±1 (8±3%)	15	62
1	С	44/60~(73%)	42 ± 1 (96 $\pm2\%$)	$2\pm1 (4\pm2\%)$	33	81
1	D	44/60~(73%)	$41 \pm 1 (94 \pm 2\%)$	$3\pm1~(6\pm2\%)$	22	71
1	Ε	40/60~(67%)	38 ± 1 (94 $\pm3\%$)	$2\pm1~(6\pm3\%)$	22	71
1	F	41/60~(68%)	39 ± 1 (95 $\pm3\%$)	$2\pm1 (5\pm3\%)$	28	77
All	All	5180/7200~(72%)	4855 (94%)	325~(6%)	21	70

5 of 51 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	2	LEU	20
1	В	43	HIS	20
1	С	2	LEU	20
1	D	42	VAL	19
1	Е	42	VAL	19

6.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	G	71/72~(99%)	25 ± 3 ($35\pm4\%$)	$5\pm2~(7\pm2\%)$	$0.33 {\pm} 0.02$
All	All	1420/1440~(99%)	497~(35%)	101 (7%)	0.33

The overall RNA backbone suiteness is 0.33.

5 of 39 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	G	8	G	20
2	G	12	А	20
2	G	19	G	20
2	G	27	G	20
2	G	30	С	20

5 of 22 unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	G	29	A	20
2	G	67	С	15



Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
2	G	5	G	12
2	G	48	А	8
2	G	12	А	7

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 5% for the well-defined parts and 4% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: assigned_chem_shift_list_1

7.1.1 Bookkeeping (i)

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	280
Number of shifts mapped to atoms	280
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 5%, i.e. 274 atoms were assigned a chemical shift out of a possible 5624. 0 out of 49 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	15 N
Backbone	0/1537~(0%)	0/632~(0%)	0/608~(0%)	0/297~(0%)
Sidechain	0/2623~(0%)	0/1718~(0%)	0/802~(0%)	0/103~(0%)
Aromatic	0/96~(0%)	0/48~(0%)	0/42~(0%)	0/6~(0%)
Sugar	84/792~(11%)	42/432~(10%)	42/360~(12%)	0/0 (%)
Base	190/576~(33%)	95/360~(26%)	75/122~(61%)	20/94 (21%)
Overall	274/5624~(5%)	137/3190~(4%)	117/1934~(6%)	20/500~(4%)



7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

No $random \ coil \ index({\rm RCI})$ plot could be generated from the current chemical shift list. RCI is only applicable to proteins

7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: assigned_chem_shift_list_2

7.2.1 Bookkeeping (i)

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	12
Number of shifts mapped to atoms	12
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.2.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

7.2.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 0%, i.e. 12 atoms were assigned a chemical shift out of a possible 5624. 0 out of 49 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	0/1537~(0%)	0/632~(0%)	0/608~(0%)	0/297~(0%)
Sidechain	0/2623~(0%)	0/1718~(0%)	0/802~(0%)	0/103~(0%)
Aromatic	0/96~(0%)	0/48~(0%)	0/42~(0%)	0/6~(0%)

Continued on next page...



	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Sugar	4/792 (1%)	2/432~(0%)	2/360~(1%)	0/0 (%)
Base	8/576~(1%)	4/360~(1%)	3/122~(2%)	1/94~(1%)
Overall	12/5624~(0%)	6/3190~(0%)	5/1934~(0%)	1/500~(0%)

Continued from previous page...

7.2.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.2.5 Random Coil Index (RCI) plots (i)

No random coil index (RCI) plot could be generated from the current chemical shift list. RCI is only applicable to proteins

