



Full wwPDB NMR Structure Validation Report ⓘ

Apr 28, 2026 – 12:54 PM EDT

PDB ID : 9DLN / pdb_00009dlh
BMRB ID : 31204
Title : NMR structures of small molecules bound to a model of an RNA CAG repeat expansion
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Deposited on : 2024-09-11

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

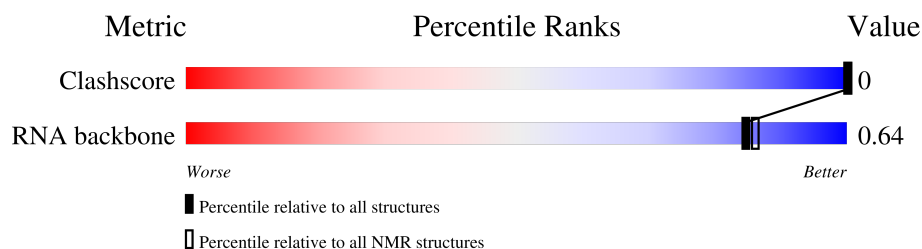
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR



The overall completeness of chemical shifts assignment is 16%.

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	229148	14424
RNA backbone	8273	777

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	13	 85% 15%
1	B	13	 85% 15%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

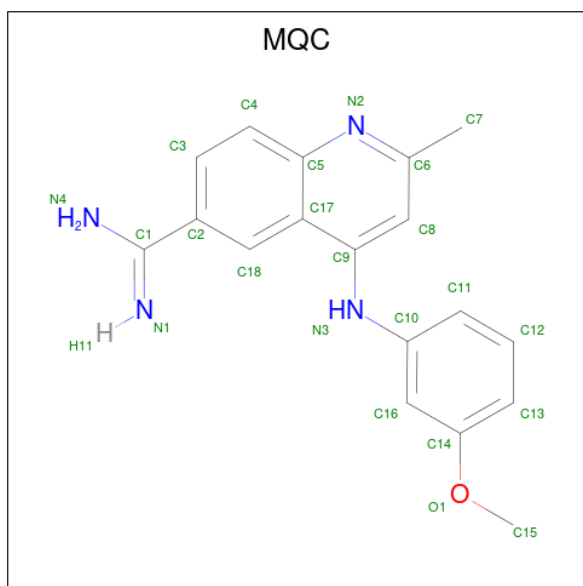
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 879 atoms, of which 306 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3').

Mol	Chain	Residues	Atoms						Trace
1	A	13	Total	C	H	N	O	P	0
			418	124	143	51	88	12	
1	B	13	Total	C	H	N	O	P	0
			418	124	143	51	88	12	

- Molecule 2 is 4-[(3-methoxyphenyl)amino]-2-methylquinoline-6-carboximidamide (CCD ID: MQC) (formula: C₁₈H₁₈N₄O) (labeled as "Ligand of Interest" by depositor).



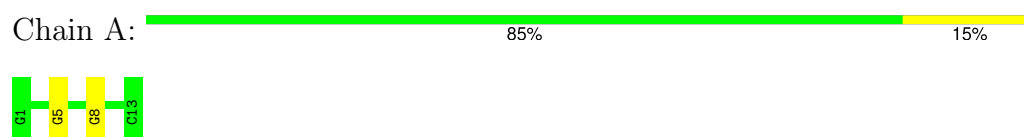
Mol	Chain	Residues	Atoms				
2	A	1	Total	C	H	N	O
			43	18	20	4	1

4 Residue-property plots

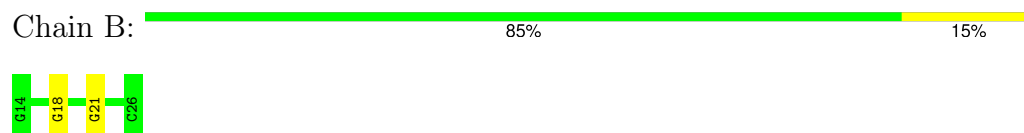
4.1 Average score per residue in the NMR ensemble

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: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

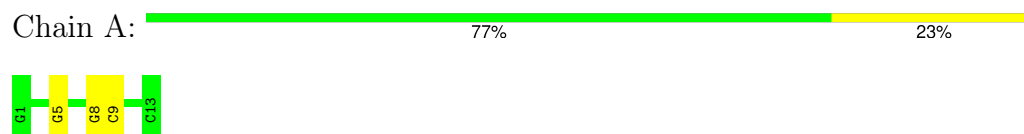


4.2 Scores per residue for each member of the ensemble

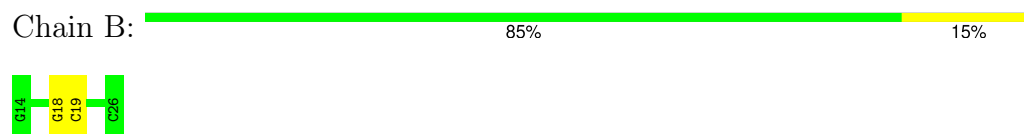
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

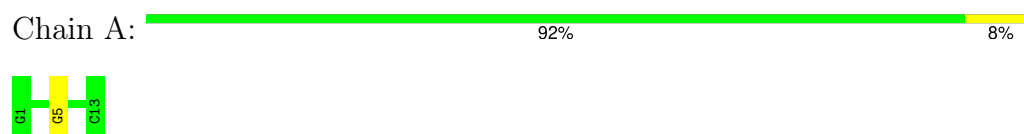


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

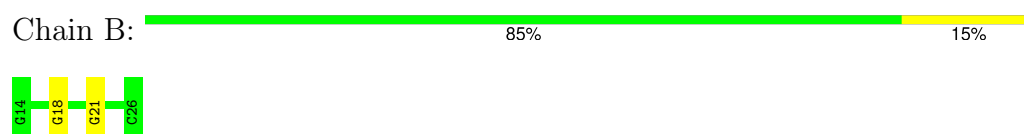


4.2.2 Score per residue for model 2

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

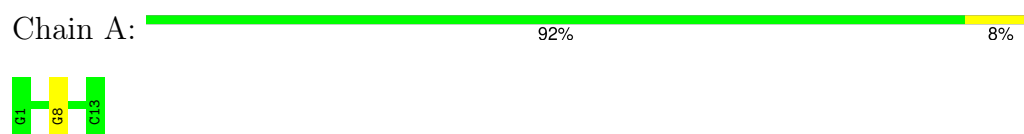


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

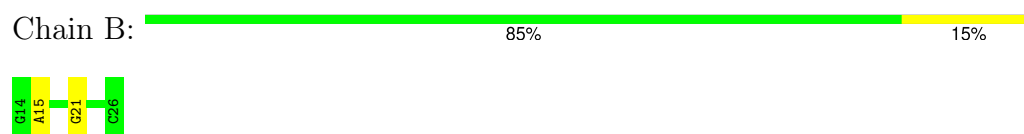


4.2.3 Score per residue for model 3

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')




4.2.4 Score per residue for model 4

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  92% 8%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  85% 15%



4.2.5 Score per residue for model 5

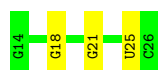
- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  92% 8%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  77% 23%



4.2.6 Score per residue for model 6

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  69% 31%




- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  92% 8%



4.2.7 Score per residue for model 7

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  77% 23%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  92% 8%



4.2.8 Score per residue for model 8

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  100%

There are no outlier residues in this chain.


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  92% 8%



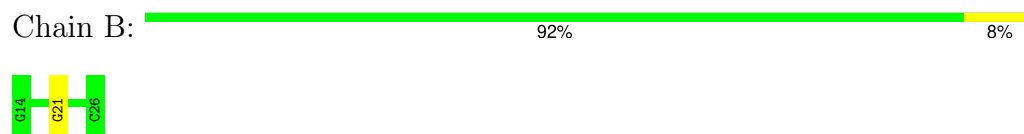
4.2.9 Score per residue for model 9

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  85% 15%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

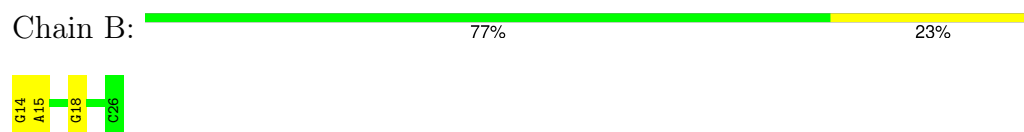


4.2.10 Score per residue for model 10

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

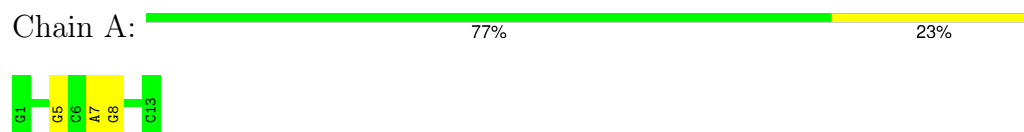


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

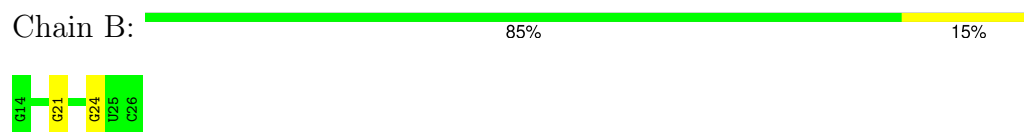


4.2.11 Score per residue for model 11

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')




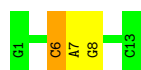
- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')



4.2.12 Score per residue for model 12

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  77% 15% 8%




- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  100%

There are no outlier residues in this chain.


4.2.13 Score per residue for model 13

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  85% 15%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  85% 15%



4.2.14 Score per residue for model 14

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  92% 8%




- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  92% 8%



4.2.15 Score per residue for model 15

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  85% 15%




- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

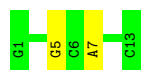
Chain B:  92% 8%




4.2.16 Score per residue for model 16

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  85% 15%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  85% 15%



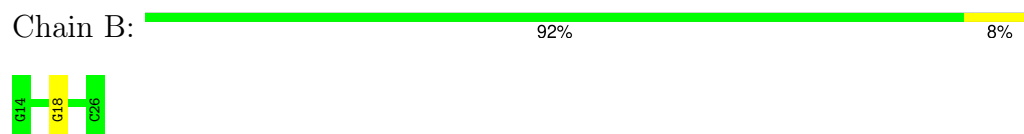
4.2.17 Score per residue for model 17

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  92% 8%

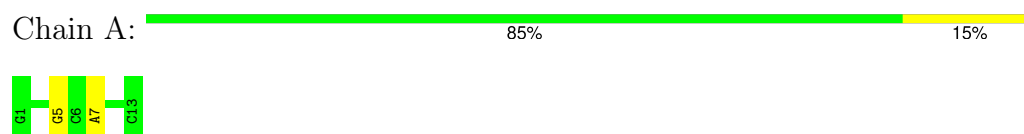


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

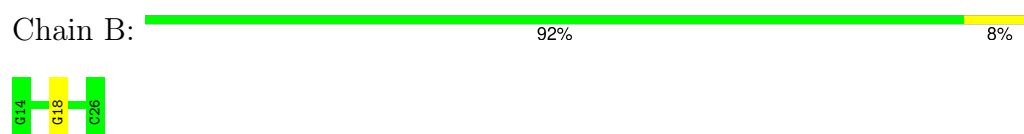


4.2.18 Score per residue for model 18

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

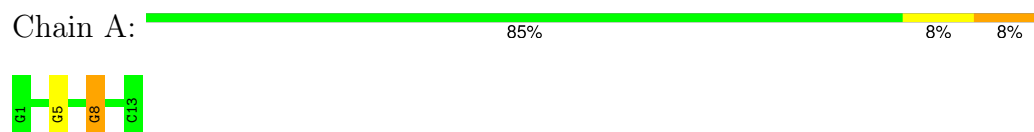


- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

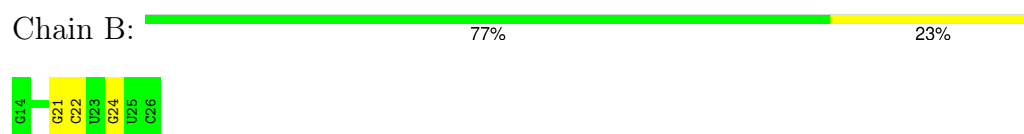


4.2.19 Score per residue for model 19

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')



4.2.20 Score per residue for model 20

- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain A:  92% 8%



- Molecule 1: CAG_13mer RNA (5'-R(*GP*AP*CP*AP*GP*CP*AP*GP*CP*UP*GP*UP*C)-3')

Chain B:  92% 8%



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
Amber	structure calculation	20

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	1
Total number of shifts	94
Number of shifts mapped to atoms	94
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	16%

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MQC

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	A	0.85±0.02	0±0/307 (0.0± 0.0%)	1.06±0.03	0±0/477 (0.0± 0.1%)
1	B	0.85±0.02	0±0/307 (0.0± 0.0%)	1.05±0.03	0±0/477 (0.0± 0.0%)
All	All	0.85	0/12280 (0.0%)	1.05	2/19080 (0.0%)

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	A	0.0±0.0	1.8±1.0
1	B	0.0±0.0	1.5±0.7
All	All	0	66

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	8	G	O4'-C4'-C3'	5.14	109.14	104.00	19	2

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	5	G	Sidechain	15
1	B	18	G	Sidechain	13
1	A	8	G	Sidechain	10
1	B	21	G	Sidechain	10

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	7	A	Sidechain	4
1	A	9	C	Sidechain	3
1	B	15	A	Sidechain	2
1	A	6	C	Sidechain	2
1	B	24	G	Sidechain	2
1	B	19	C	Sidechain	1
1	B	25	U	Sidechain	1
1	A	11	G	Sidechain	1
1	A	12	U	Sidechain	1
1	B	22	C	Sidechain	1

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
All	All	11460	6120	5720	-

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 -.

There are no clashes.

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

6.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

6.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	A	12/13 (92%)	0±0 (0±0%)	0±1 (2±4%)	0.72±0.00

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	12/13 (92%)	0±0 (0±0%)	0±0 (1±3%)	0.69±0.00
All	All	481/520 (92%)	0 (0%)	6 (1%)	0.70

The overall RNA backbone suiteness is 0.64.

There are no RNA backbone outliers to report.

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	6	C	2
1	A	11	G	1
1	B	14	G	1
1	A	7	A	1
1	B	21	G	1

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	MQC	A	101	-	25,25,25	1.47±0.03	4±1 (16±2%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles

that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	MQC	A	101	-	31,35,35	1.37±0.08	4±1 (14±2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MQC	A	101	-	-	0±0,10,10,10	0±0,3,3,3

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	101	MQC	C6-N2	3.76	1.40	1.33	7	20
2	A	101	MQC	C1-N1	3.07	1.40	1.27	4	20
2	A	101	MQC	C18-C2	2.64	1.42	1.37	18	18
2	A	101	MQC	C1-N4	2.53	1.40	1.33	17	19
2	A	101	MQC	C8-C9	2.31	1.42	1.38	10	7

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

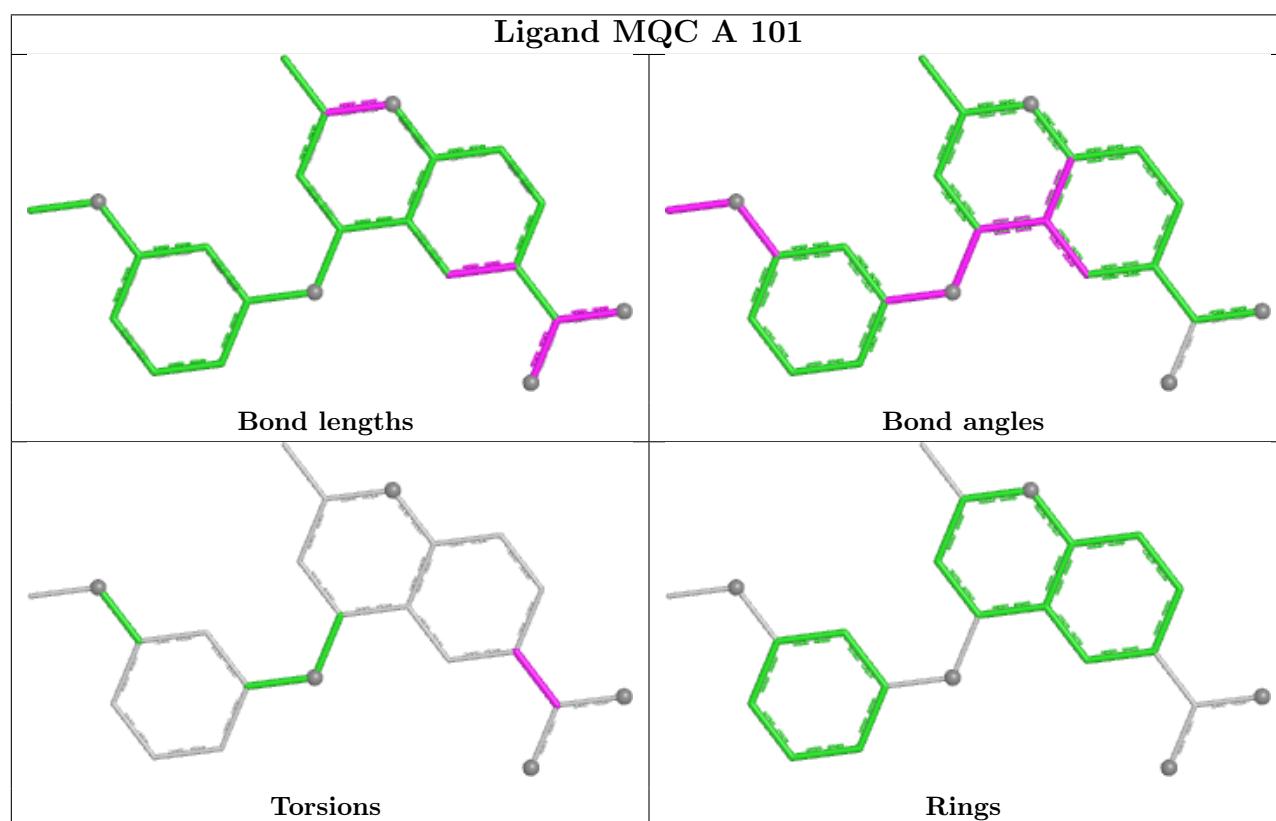
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	101	MQC	C10-N3-C9	4.57	136.34	126.36	3	19
2	A	101	MQC	C18-C17-C9	3.90	120.84	123.67	15	19
2	A	101	MQC	C9-C17-C5	3.69	120.38	118.01	7	19
2	A	101	MQC	C15-O1-C14	2.82	123.55	117.50	12	17
2	A	101	MQC	C8-C6-N2	2.67	119.56	122.60	14	10
2	A	101	MQC	C4-C5-C17	2.18	121.48	119.13	2	1
2	A	101	MQC	C17-C5-N2	2.09	120.59	122.80	11	3

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

The completeness of assignment taking into account all chemical shift lists is 16% for the well-defined parts and 16% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *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	94
Number of shifts mapped to atoms	94
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

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

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 16%, i.e. 78 atoms were assigned a chemical shift out of a possible 494. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Sugar	44/286 (15%)	44/156 (28%)	0/130 (0%)	0/0 (—%)
Base	34/208 (16%)	34/130 (26%)	0/44 (0%)	0/34 (0%)
Overall	78/494 (16%)	78/286 (27%)	0/174 (0%)	0/34 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 16%, i.e. 78 atoms were assigned a chemical shift out of a possible 494. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Sugar	44/286 (15%)	44/156 (28%)	0/130 (0%)	0/0 (—%)
Base	34/208 (16%)	34/130 (26%)	0/44 (0%)	0/34 (0%)
Overall	78/494 (16%)	78/286 (27%)	0/174 (0%)	0/34 (0%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

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

8 NMR restraints analysis [i](#)

8.1 Conformationally restricting restraints [i](#)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	284
Intra-residue ($ i-j =0$)	152
Sequential ($ i-j =1$)	82
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	18
Hydrogen bond restraints	32
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	10.5
Number of long range restraints per residue ¹	0.0

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations [i](#)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model [i](#)

Distance violations less than 0.1 Å are not included in the calculation. There are no distance violations

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis ⓘ

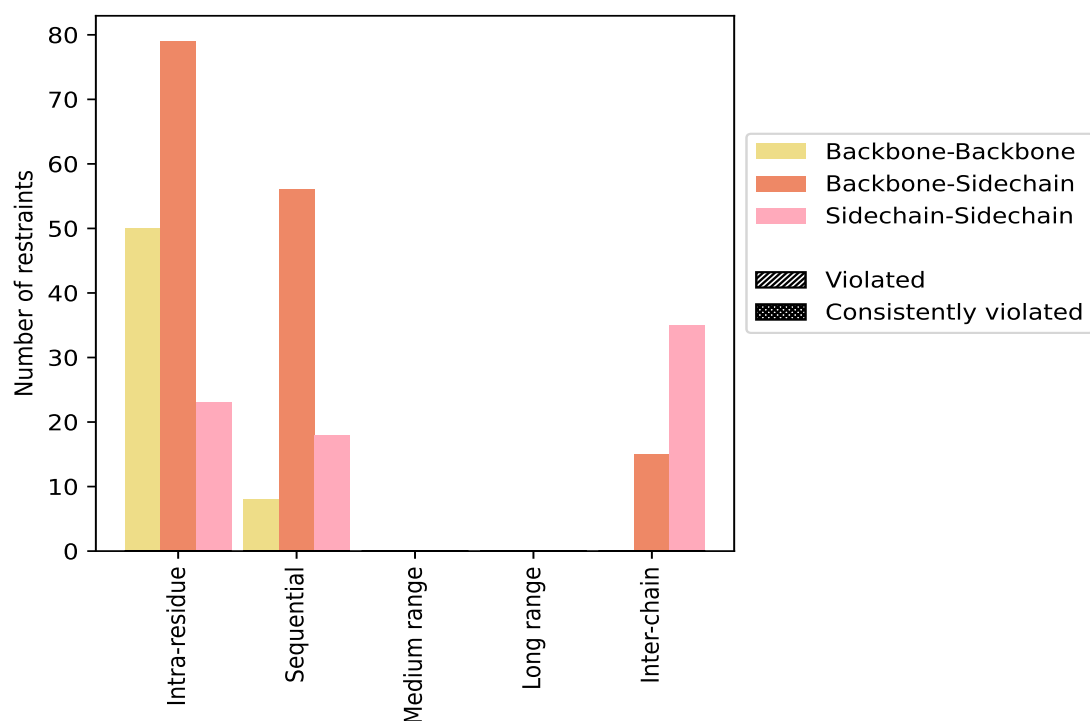
9.1 Summary of distance violations ⓘ

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	152	53.5	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	50	17.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	79	27.8	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	23	8.1	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	82	28.9	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	8	2.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	56	19.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	18	6.3	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	18	6.3	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	15	5.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	3	1.1	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	32	11.3	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	284	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	58	20.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	150	52.8	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	76	26.8	0	0.0	0.0	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfide bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model [i](#)

No violations found

9.3 Distance violation statistics for the ensemble [i](#)

No violations found

9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

9.5 All violated distance restraints [i](#)

No violations found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found