



Full wwPDB NMR Structure Validation Report ⓘ

Nov 1, 2021 – 12:59 pm GMT

PDB ID : 7BLM
Title : AG repetition attached to a compact i-motif clip at 3'-end
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Deposited on : 2021-01-18

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.23.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

2 Ensemble composition and analysis

This entry contains 4 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 882 atoms, of which 322 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called AGAG(CH⁺)C(CH⁺).

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
1	A	7	221	67	81	29	38	6	0
1	B	7	221	67	81	29	38	6	0

- Molecule 2 is a DNA chain called AGAGC(CH⁺)C.


Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
2	C	7	220	67	80	29	38	6	0
2	D	7	220	67	80	29	38	6	0

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: AGAG(CH+)C(CH+)

Chain A: 

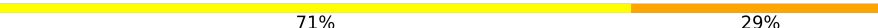


- Molecule 1: AGAG(CH+)C(CH+)

Chain B: 




- Molecule 2: AGAGC(CH+)C

Chain C: 



- Molecule 2: AGAGC(CH+)C

Chain D: 

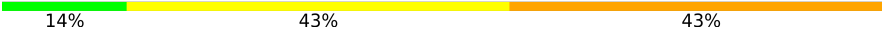


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

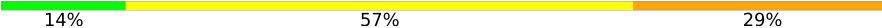
4.2.1 Score per residue for model 1

- Molecule 1: AGAG(CH+)C(CH+)

Chain A:  14% 43% 43%

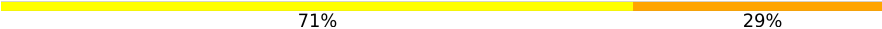
A1 G2 A3 G4 C5 C6 C7

- Molecule 1: AGAG(CH+)C(CH+)

Chain B:  14% 57% 29%

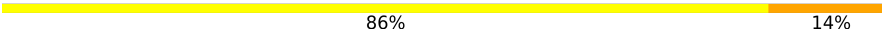
A8 G9 A10 G11 C12 C13 C14

- Molecule 2: AGAGC(CH+)C

Chain C:  71% 29%

A15 G16 A17 G18 C19 C20 C21

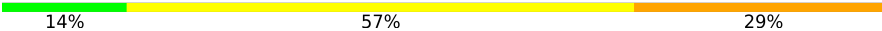
- Molecule 2: AGAGC(CH+)C

Chain D:  86% 14%

A22 G23 A24 G25 C26 C27 C28

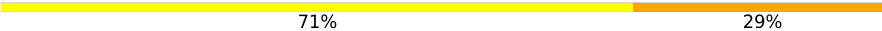
4.2.2 Score per residue for model 2

- Molecule 1: AGAG(CH+)C(CH+)

Chain A:  14% 57% 29%

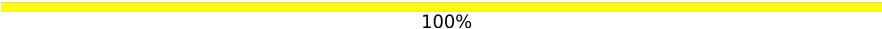
A1 G2 A3 G4 C5 C6 C7

- Molecule 1: AGAG(CH+)C(CH+)

Chain B:  71% 29%

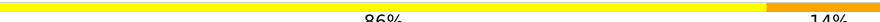
A8 G9 A10 G11 C12 C13 C14

- Molecule 2: AGAGC(CH+)C

Chain C:  100%

A15 G16 A17 G18 C19 C20 C21

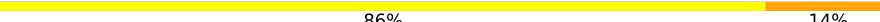
- Molecule 2: AGAGC(CH+)C

Chain D:  86% 14%

A22
G23
A24
G25
C26
C27
C28

4.2.3 Score per residue for model 3

- Molecule 1: AGAG(CH+)C(CH+)

Chain A:  86% 14%

A1
G2
A3
G4
C5
C6
C7

- Molecule 1: AGAG(CH+)C(CH+)

Chain B:  14% 71% 14%

A8
G9
A10
G11
C12
C13
C14

- Molecule 2: AGAGC(CH+)C

Chain C:  71% 29%

A15
G16
A17
G18
C19
C20
C21

- Molecule 2: AGAGC(CH+)C

Chain D:  71% 29%

A22
G23
A24
G25
C26
C27
C28

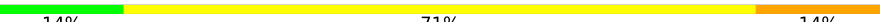
4.2.4 Score per residue for model 4

- Molecule 1: AGAG(CH+)C(CH+)

Chain A:  71% 29%


A1
G2
A3
G4
C5
C6
C7

- Molecule 1: AGAG(CH+)C(CH+)

Chain B:  14% 71% 14%

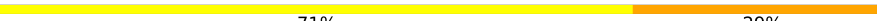
A8
G9
A10
G11
C12
C13
C14

- Molecule 2: AGAGC(CH⁺)C

Chain C:  86% 14%

A15	G16	A17	G18	C19	C20	C21
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- Molecule 2: AGAGC(CH⁺)C

Chain D:  71% 29%

A22	G23	A24	C25	C26	C27	C28
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5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 3000 calculated structures, 4 were deposited, based on the following criterion: *Snapshot every 100 nanoseconds taken from initial 300 ns of 1 microsecond unrestrained MD.*

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

Software name	Classification	Version
Amber	refinement	16
Amber	structure calculation	16

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	50
Number of shifts mapped to atoms	49
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	1
Assignment completeness (well-defined parts)	7%

6 Model quality i

6.1 Standard geometry i

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

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	2.23±0.02	3±0/114 (2.6± 0.0%)	2.45±0.06	12±2/172 (7.1± 1.3%)
1	B	2.24±0.02	3±0/114 (2.6± 0.0%)	2.48±0.02	11±2/172 (6.5± 1.0%)
2	C	2.53±0.02	6±0/135 (4.4± 0.0%)	2.51±0.04	16±1/204 (7.6± 0.4%)
2	D	2.53±0.02	6±0/135 (4.4± 0.0%)	2.53±0.06	16±2/204 (8.1± 0.8%)
All	All	2.40	72/1992 (3.6%)	2.50	222/3008 (7.4%)

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	A	0.0±0.0	2.0±0.7
1	B	0.0±0.0	1.5±0.5
2	C	0.0±0.0	1.5±0.5
2	D	0.0±0.0	1.5±0.5
All	All	0	26

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
1	A	6	DC	C5-C6	12.75	1.44	1.34	3	4
1	B	13	DC	C5-C6	12.71	1.44	1.34	4	4
2	C	19	DC	C5-C6	12.30	1.44	1.34	2	4
2	D	26	DC	C5-C6	12.29	1.44	1.34	3	4
2	C	21	DC	C5-C6	12.14	1.44	1.34	2	4
2	D	28	DC	C5-C6	12.09	1.44	1.34	4	4
1	A	6	DC	C2-N3	8.29	1.42	1.35	2	4
2	C	19	DC	C2-N3	8.27	1.42	1.35	4	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	C	21	DC	C2-N3	8.27	1.42	1.35	2	4
2	D	28	DC	C2-N3	8.01	1.42	1.35	1	4
2	D	26	DC	C2-N3	8.01	1.42	1.35	2	4
1	B	13	DC	C2-N3	7.97	1.42	1.35	1	4
1	A	6	DC	N1-C6	7.71	1.41	1.37	4	4
1	B	13	DC	N1-C6	7.46	1.41	1.37	1	4
2	D	28	DC	N1-C6	7.41	1.41	1.37	1	4
2	C	19	DC	N1-C6	7.36	1.41	1.37	3	4
2	C	21	DC	N1-C6	7.24	1.41	1.37	4	4
2	D	26	DC	N1-C6	7.11	1.41	1.37	3	4

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
1	A	1	DA	N1-C6-N6	-8.92	113.25	118.60	4	4
2	D	26	DC	N3-C4-C5	8.40	125.26	121.90	4	4
2	C	21	DC	N3-C4-C5	8.30	125.22	121.90	4	4
2	C	19	DC	N3-C4-C5	8.11	125.14	121.90	2	4
2	D	26	DC	N3-C2-O2	-8.08	116.24	121.90	4	4
1	B	8	DA	N1-C6-N6	-8.06	113.76	118.60	1	4
2	D	22	DA	N1-C6-N6	-8.04	113.78	118.60	3	3
2	D	28	DC	N3-C4-C5	8.01	125.10	121.90	2	4
2	D	28	DC	N1-C2-O2	7.96	123.67	118.90	3	4
1	B	13	DC	N1-C2-O2	7.78	123.57	118.90	3	4
2	C	19	DC	N3-C2-O2	-7.78	116.45	121.90	2	4
2	C	15	DA	N1-C6-N6	-7.75	113.95	118.60	1	4
2	C	21	DC	N1-C2-O2	7.75	123.55	118.90	2	4
2	D	28	DC	N3-C2-O2	-7.70	116.51	121.90	2	4
2	C	21	DC	N3-C2-O2	-7.68	116.52	121.90	2	4
1	A	6	DC	N1-C2-O2	7.63	123.48	118.90	2	4
2	C	19	DC	N1-C2-O2	7.63	123.48	118.90	2	4
2	D	26	DC	N1-C2-O2	7.60	123.46	118.90	4	4
1	B	13	DC	N3-C2-O2	-7.60	116.58	121.90	4	4
1	A	6	DC	N3-C2-O2	-7.42	116.71	121.90	4	4
1	A	1	DA	C5-C6-N1	7.29	121.35	117.70	2	4
1	B	13	DC	N3-C4-C5	7.18	124.77	121.90	2	4
1	A	6	DC	N3-C4-C5	7.02	124.71	121.90	4	4
2	D	25	DG	O4'-C1'-N9	6.87	112.81	108.00	3	4
1	B	8	DA	C5-C6-N1	6.68	121.04	117.70	4	4
1	A	4	DG	O4'-C1'-N9	6.65	112.65	108.00	4	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	C	15	DA	C5-C6-N1	6.63	121.02	117.70	4	4
2	D	23	DG	N1-C6-O6	-6.45	116.03	119.90	3	4
1	A	4	DG	N1-C6-O6	-6.44	116.04	119.90	2	1
1	A	6	DC	O4'-C1'-N1	6.40	112.48	108.00	4	1
1	B	9	DG	N1-C6-O6	-6.32	116.11	119.90	3	4
2	D	22	DA	C5-C6-N1	6.31	120.86	117.70	3	4
1	B	11	DG	O4'-C1'-N9	6.30	112.41	108.00	1	3
1	B	13	DC	O4'-C4'-C3'	-6.27	101.99	104.50	3	2
2	D	24	DA	N1-C6-N6	-6.26	114.84	118.60	3	3
2	D	26	DC	N3-C4-N4	-6.25	113.63	118.00	4	2
1	A	6	DC	C4-C5-C6	-6.21	114.30	117.40	4	4
2	C	16	DG	N1-C6-O6	-6.16	116.20	119.90	3	3
1	B	13	DC	C4-C5-C6	-6.08	114.36	117.40	4	4
1	A	3	DA	N1-C6-N6	-6.07	114.96	118.60	3	1
2	C	16	DG	O4'-C1'-N9	6.02	112.22	108.00	3	2
1	B	10	DA	N1-C6-N6	-6.00	115.00	118.60	2	1
2	C	18	DG	O4'-C1'-N9	5.89	112.12	108.00	1	4
1	A	2	DG	N1-C6-O6	-5.88	116.38	119.90	4	4
1	B	13	DC	N3-C4-N4	-5.87	113.89	118.00	4	1
2	D	24	DA	C4-C5-C6	-5.86	114.07	117.00	3	1
1	B	11	DG	N3-C4-C5	-5.86	125.67	128.60	3	4
1	A	4	DG	N3-C4-C5	-5.84	125.68	128.60	3	2
2	D	28	DC	C4-C5-C6	-5.83	114.49	117.40	3	4
1	A	6	DC	N3-C4-N4	-5.82	113.93	118.00	4	2
2	C	18	DG	N1-C6-O6	-5.71	116.47	119.90	3	1
2	D	26	DC	C4-C5-C6	-5.67	114.57	117.40	4	4
1	A	3	DA	C4-C5-C6	-5.66	114.17	117.00	3	1
2	D	25	DG	N1-C6-O6	-5.62	116.53	119.90	2	2
1	A	2	DG	O4'-C1'-N9	5.60	111.92	108.00	3	2
2	C	15	DA	C4-C5-C6	-5.60	114.20	117.00	4	3
2	C	17	DA	C5-C6-N1	5.59	120.49	117.70	2	3
2	C	18	DG	N3-C4-C5	-5.57	125.81	128.60	2	4
1	A	4	DG	O4'-C1'-C2'	-5.57	101.44	105.90	2	1
2	D	24	DA	C5-C6-N1	5.57	120.48	117.70	3	4
2	C	19	DC	C4-C5-C6	-5.56	114.62	117.40	2	4
2	C	17	DA	N1-C6-N6	-5.54	115.27	118.60	3	2
2	C	19	DC	N3-C4-N4	-5.53	114.13	118.00	2	1
2	D	25	DG	N3-C4-C5	-5.52	125.84	128.60	4	2
2	D	25	DG	OP1-P-OP2	-5.49	111.37	119.60	2	2
1	A	3	DA	C5-C6-N1	5.47	120.44	117.70	3	2
2	D	22	DA	C4-C5-C6	-5.43	114.28	117.00	3	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	4	DG	C2-N3-C4	5.38	114.59	111.90	3	1
1	A	4	DG	C5-C6-N1	5.38	114.19	111.50	3	1
1	B	8	DA	C4-C5-C6	-5.36	114.32	117.00	1	4
2	C	17	DA	C4-C5-C6	-5.14	114.43	117.00	4	2
1	A	4	DG	OP1-P-OP2	-5.14	111.89	119.60	2	1
1	B	11	DG	OP1-P-OP2	-5.13	111.90	119.60	2	1
2	C	21	DC	C4-C5-C6	-5.11	114.84	117.40	4	1
1	B	11	DG	N3-C4-N9	5.05	129.03	126.00	2	1
1	A	1	DA	C4-C5-C6	-5.01	114.50	117.00	4	1

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	6	DC	Sidechain	4
2	D	25	DG	Sidechain	4
1	A	4	DG	Sidechain	3
1	B	13	DC	Sidechain	3
2	C	16	DG	Sidechain	3
2	C	18	DG	Sidechain	2
1	A	1	DA	Sidechain	1
1	B	11	DG	Sidechain	1
1	B	8	DA	Sidechain	1
1	B	9	DG	Sidechain	1
2	D	28	DC	Sidechain	1
2	C	19	DC	Sidechain	1
2	D	26	DC	Sidechain	1

6.2 Too-close contacts

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	2240	1288	1288	-

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](#)

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are 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
1	DNR	B	12	2,1	15,20,21	1.73±0.01	2±0 (16±3%)
2	DNR	C	20	2,1	15,20,21	1.69±0.02	2±0 (15±2%)
1	DNR	A	5	2,1	15,20,21	1.72±0.01	2±0 (13±0%)
2	DNR	D	27	2,1	15,20,21	1.68±0.02	2±0 (13±0%)
1	DNR	A	7	2,1	15,20,21	1.71±0.02	3±0 (18±2%)
1	DNR	B	14	2,1	15,20,21	1.73±0.01	2±0 (15±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	Counts	Bond angles	
						RMSZ	#Z>2
1	DNR	B	12	2,1	17,28,31	1.90±0.02	1±0 (5±0%)
2	DNR	C	20	2,1	17,28,31	1.88±0.02	1±0 (5±0%)
1	DNR	A	5	2,1	17,28,31	1.82±0.02	1±0 (5±0%)
2	DNR	D	27	2,1	17,28,31	1.87±0.01	1±0 (5±0%)
1	DNR	A	7	2,1	17,28,31	1.67±0.09	1±0 (7±2%)
1	DNR	B	14	2,1	17,28,31	1.70±0.04	1±0 (7±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
1	DNR	B	12	2,1	-	0±0,4,21,22	0±0,2,2,2
2	DNR	C	20	2,1	-	0±0,4,21,22	0±0,2,2,2
1	DNR	A	5	2,1	-	0±0,4,21,22	0±0,2,2,2
2	DNR	D	27	2,1	-	0±0,4,21,22	0±0,2,2,2
1	DNR	A	7	2,1	-	0±0,4,21,22	0±0,2,2,2
1	DNR	B	14	2,1	-	0±0,4,21,22	0±0,2,2,2

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
1	A	7	DNR	C6-N1	5.31	1.42	1.35	4	4
1	B	14	DNR	C6-N1	5.25	1.42	1.35	2	4
1	B	12	DNR	C6-N1	5.13	1.42	1.35	4	4
1	A	5	DNR	C6-N1	5.06	1.42	1.35	2	4
2	C	20	DNR	C6-N1	5.05	1.42	1.35	2	4
2	D	27	DNR	C6-N1	4.96	1.42	1.35	3	4
1	B	14	DNR	C6-C5	3.08	1.44	1.38	3	4
1	A	5	DNR	C6-C5	3.00	1.44	1.38	4	4
1	B	12	DNR	C6-C5	2.97	1.44	1.38	2	4
1	A	7	DNR	C6-C5	2.95	1.44	1.38	2	4
2	C	20	DNR	C6-C5	2.91	1.44	1.38	2	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	D	27	DNR	C6-C5	2.85	1.44	1.38	1	4
1	A	7	DNR	C2-N3	2.17	1.42	1.38	3	3
1	B	12	DNR	C2-N3	2.08	1.42	1.38	1	2
1	B	14	DNR	C2-N3	2.03	1.42	1.38	2	1
2	C	20	DNR	C2-N3	2.01	1.42	1.38	4	1

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
1	A	5	DNR	C2-N3-C4	7.13	123.56	116.34	4	4
2	C	20	DNR	C2-N3-C4	7.07	123.50	116.34	3	4
1	B	12	DNR	C2-N3-C4	7.02	123.45	116.34	4	4
2	D	27	DNR	C2-N3-C4	6.95	123.39	116.34	4	4
1	B	14	DNR	C2-N3-C4	6.45	122.88	116.34	3	4
1	A	7	DNR	C2-N3-C4	6.25	122.67	116.34	1	4
1	A	7	DNR	O4'-C1'-C2'	2.45	101.62	106.25	1	1
1	B	14	DNR	O4'-C1'-C2'	2.18	102.14	106.25	1	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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

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 7% for the well-defined parts and 7% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *starch_output*

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	50
Number of shifts mapped to atoms	49
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	1
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atoms found in structure. The only occurrence is reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	6	DC	H3	15.575	0.001	1

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 7%, i.e. 33 atoms were assigned a chemical shift out of a possible 448. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	33/448 (7%)	33/272 (12%)	0/146 (0%)	0/30 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 7%, i.e. 33 atoms were assigned a chemical shift out of a possible 448. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	33/448 (7%)	33/272 (12%)	0/146 (0%)	0/30 (0%)

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* (RCI) plot could be generated from the current chemical shift list (starch_output). RCI is only applicable to proteins.