

Full wwPDB NMR Structure Validation Report (i)

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BMRB ID	:	36315
Title	:	Solution NMR Structures of DNA minidumbbell formed by 5'-CTTG CATG-
		3'.
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Deposited on	:	2020-02-21

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 (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 40%.

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	Percei	ntile Ranks	Value
Clashscore			0
	Worse		Better
	Percentile relative to all structu	ires	
	Percentile relative to all NMR s	tructures	
	TT71 1 1 1		1
Motrio	Whole archive	NMR archive	

Metric	$egin{array}{llllllllllllllllllllllllllllllllllll$	${f NMR} { m archive} \ (\#{ m Entries})$
Clashscore	158937	12864

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	8	38%	62%



2 Ensemble composition and analysis (i)

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 260 atoms, of which 93 are hydrogens and 0 are deuteriums.

• Molecule 1 is a DNA chain called DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3').

Mol	Chain	Residues		I	Aton	ns			Trace
1	٨	0	Total	С	Η	Ν	0	Р	0
	A	0	253	78	93	27	48	7	0

• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mo	l Cł	nain	Residues	Ator	ns
2	-	A	7	Total 7	Na 7



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: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')

Chain A:	38%	62%
8 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		

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: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')

Chain A: 12% 75% 12%

4.2.2 Score per residue for model 2

• Molecule 1: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')

Chain A: 38% 62%

4.2.3 Score per residue for model 3

• Molecule 1: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')



Chain A:	38%		62%	
C1 12 13 13 14 04 17 17 08				
4.2.4 Score	per residue fo	or model 4		
• Molecule 1: I	DNA (5'-D(*CP	P*TP*TP*GP*CP*A	AP*TP*G)-3')	
Chain A: 12%	_	62%	25	%
C1 72 76 76 76 76 78 78 78				
4.2.5 Score	per residue fo	or model 5		
• Molecule 1: D	DNA (5'-D(*CP	P*TP*TP*GP*CP*A	.P*TP*G)-3')	
Chain A:	25%	62%		12%
22 132 148 148 148 132 148 132 148 148 148 148 148 148 148 148 148 148				
4.2.6 Score	per residue fo	or model 6		
• Molecule 1: I	DNA (5'-D(*CP	P*TP*TP*GP*CP*A	AP*TP*G)-3')	
Chain A: 12%		88%		
00000000000000000000000000000000000000				
4.2.7 Score	per residue fo	or model 7		
• Molecule 1: I	DNA (5'-D(*CP	P*TP*TP*GP*CP*A	•P*TP*G)-3')	
Chain A: 12%		88%		
68 148 148 148 148 17 148 17 17 17 17 17 17 17 17 17 17 17 17 17				
4.2.8 Score	per residue fo	or model 8		

• Molecule 1: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')



Chain A:	25%	75%	
C1 T2 C5 C5 T7 T7	œ		
4.2.9 S	core per residu	ue for model 9	
• Molecul	e 1: DNA (5'-D	(*CP*TP*TP*GP*CP*AP*TP*G)-3')	
Chain A:	25%	62%	12%
C1 T2 G4 C5 C5 T7	89		
4.2.10	Score per resid	due for model 10	
• Molecul	e 1: DNA (5'-D	(*CP*TP*TP*GP*CP*AP*TP*G)-3')	
Chain A:	38%	50%	12%
C1 T2 C5 C5 T7	89 9		
4.2.11	Score per resid	due for model 11	
• Molecul	e 1: DNA (5'-D	(*CP*TP*TP*GP*CP*AP*TP*G)-3')	
Chain A:	25%	50%	25%
C1 T2 E4 E5 A6 T7	⁸		
4.2.12	Score per resid	due for model 12	
• Molecul	e 1: DNA (5'-D	(*CP*TP*TP*GP*CP*AP*TP*G)-3')	
Chain A:	38%	62%	
C1 T2 C5 C5 T7	8		
4.2.13	Score per resid	due for model 13	

• Molecule 1: DNA (5'-D(*CP*TP*TP*GP*CP*AP*TP*G)-3')



Chain A:	50%	38%	12%
C 1 1 2 2 6 4 7 6 8 7 7 6 8			
4.2.14 Score p	per residue for model	14	
• Molecule 1: DN	IA (5'-D(*CP*TP*TP*	GP*CP*AP*TP*G)-3')	
Chain A:	50%	38%	12%
66 132 132 132 132 132 132 132 133 133 133			
4.2.15 Score p	per residue for model	15	
• Molecule 1: DN	JA (5'-D(*CP*TP*TP*0	GP*CP*AP*TP*G)-3')	
Chain A: 2	5%	75%	
66 11 12 13 13 14 14 15 13 14 14 15 13 14 14 15 13 14 14 15 15 14 14 14 14 14 14 14 14 14 14 14 14 14			
4.2.16 Score p	per residue for model	16	
• Molecule 1: DN	IA (5'-D(*CP*TP*TP*0	GP*CP*AP*TP*G)-3')	
Chain A:	38%	50%	12%
11 12 12 12 12 12 12 12 12 12 12 12 12 1			
4.2.17 Score p	per residue for model	17	
• Molecule 1: DN	IA (5'-D(*CP*TP*TP*0	GP*CP*AP*TP*G)-3')	
Chain A: 2	5%	75%	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
1919 Game -	on nosiduo for model	10	
-	per residue for model		
• Molecule 1: DN	IA (5'-D(*CP*TP*TP*0	GP*CP*AP*TP*G)-3'	



Chain A:	12%	88%	
C1 C1 C2 C2 C2 C2 C2 C2 C2 C2 C2 C1 C2 C1 C2 C1 C2 C1 C2 C1 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2 C2			
4.2.19 Se	core per residue for model 19		
• Molecule	1: DNA (5'-D(*CP*TP*TP*GP*	*CP*AP*TP*G)-3')	
Chain A:	38%	62%	
Chain A:	38%	62%	
Chain A: 당업법 <mark>장왕왕동</mark> 왕	38%	62%	
11 122 132 13 13 13 13 13 13 13 14 14 14 14 14 14 14 14 14 14 14 14 14	38% core per residue for model 20		
⁵⁸²⁸⁸⁸ 888 4.2.20 Se			



5 Refinement protocol and experimental data overview (i)

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

Of the 500 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
Amber	refinement	
Amber	structure calculation	

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	72
Number of shifts mapped to atoms	72
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%



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: NA

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	E	Sond lengths	Bond angles		
IVIOI	Chain	RMSZ	$\#Z{>}5$	RMSZ	$\#Z{>}5$	
1	А	1.42 ± 0.02	$0{\pm}0/178$ ($0.0{\pm}$ $0.0\%)$	2.01 ± 0.06	$8{\pm}2/273~(~3.0{\pm}~0.6\%)$	
All	All	1.42	0/3560~(~0.0%)	2.01	162/5460 ($3.0%$)	

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	А	$0.0{\pm}0.0$	$0.7{\pm}0.8$
All	All	0	13

There are no bond-length outliers.

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

Mal	Mol Chain R		Turne	Atoms	Z	Observed(°)	Ideal(0)	Moo	dels
	Unam	Res	Type	Atoms		Observed(*)	$Ideal(^{o})$	Worst	Total
1	А	5	DC	O4'-C1'-N1	10.73	115.51	108.00	1	20
1	А	2	DT	P-O3'-C3'	9.13	130.65	119.70	2	20
1	А	2	DT	O4'-C1'-N1	8.16	113.71	108.00	17	19
1	А	1	DC	O4'-C1'-N1	7.94	113.56	108.00	5	17
1	А	6	DA	P-O3'-C3'	6.88	127.96	119.70	6	5
1	А	3	DT	O4'-C1'-N1	6.79	112.75	108.00	16	3
1	А	4	DG	O4'-C1'-N9	6.21	112.34	108.00	9	9
1	А	5	DC	C1'-O4'-C4'	-6.18	103.92	110.10	15	3
1	А	5	DC	P-O3'-C3'	6.03	126.94	119.70	16	6
1	А	2	DT	C6-C5-C7	-6.02	119.29	122.90	19	12
1	А	2	DT	O4'-C4'-C3'	6.00	109.60	106.00	11	4
1	А	7	DT	C6-C5-C7	-5.92	119.35	122.90	10	20

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Mol	Chain	Dec	Turne	Atoma	7	Observed(°)	Ideal(°)	Mod	dels
	Chain	nes	Type	Atoms		Observed(*)	Ideal(*)	Worst	Total
1	А	6	DA	O4'-C1'-N9	5.75	112.02	108.00	5	2
1	А	7	DT	O4'-C1'-N1	5.71	112.00	108.00	16	1
1	А	3	DT	C6-C5-C7	-5.69	119.48	122.90	16	20
1	А	3	DT	C4-C5-C6	5.01	121.01	118.00	9	1

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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	А	2	DT	Sidechain	8
1	А	6	DA	Sidechain	3
1	А	1	DC	Sidechain	2

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	3340	1860	1860	-

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score 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)

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)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

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 40% for the well-defined parts and 40% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: STAR.txt

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	72
Number of shifts mapped to atoms	72
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 40%, i.e. 63 atoms were assigned a chemical shift out of a possible 156. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Sugar	52/96~(54%)	52/56~(93%)	0/40~(0%)	$0/0 \ (\%)$
Base	11/60~(18%)	11/36~(31%)	0/14~(0%)	0/10~(0%)
Overall	63/156~(40%)	63/92~(68%)	0/54~(0%)	0/10~(0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 40%, i.e. 63 atoms were assigned a chemical shift out of a possible 156. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.



	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Sugar	52/96~(54%)	52/56~(93%)	0/40~(0%)	$0/0 \ (\%)$
Base	11/60~(18%)	11/36~(31%)	0/14~(0%)	0/10~(0%)
Overall	63/156~(40%)	63/92~(68%)	0/54~(0%)	0/10~(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. RCI is only applicable to proteins

