Full wwPDB NMR Structure Validation Report (i)

Mar 7, 2026 – 02:59 AM UTC

PDB ID	:	1S88 / pdb_00001s88
Title	:	NMR structure of a DNA duplex with two INA nucleotides inserted opposite each other, dCTCAACXCAAGCT:dAGCTTGXGTTGAG
Authors	:	Nielsen, C.B.; Petersen, M.; Pedersen, E.B.; Hansen, P.E.; Christensen, U.B.
Deposited on	:	2004-01-31

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 (i)) were used in the production of this report:

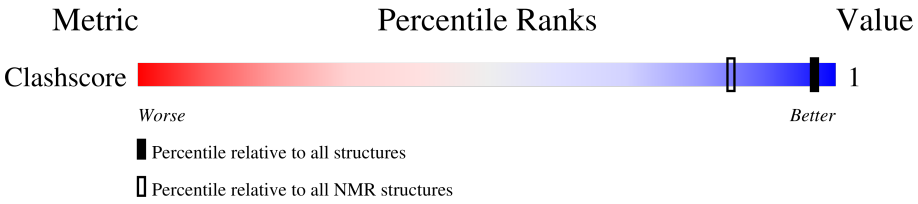
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (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 was not calculated.

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

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	A	13	85% 15%
2	B	13	54% 46%

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 844 atoms, of which 306 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	13	416	135	152	44	73	12	0

- Molecule 2 is a DNA chain called 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	13	428	139	154	46	77	12	0

4 Residue-property plots

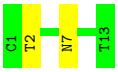
4.1 Average score per residue in the NMR ensemble

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: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:





• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:





4.2 Scores per residue for each member of the ensemble

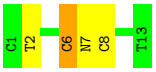
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

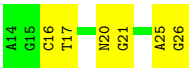




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:

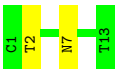




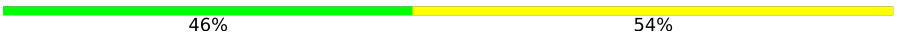
4.2.2 Score per residue for model 2

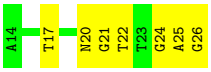
• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

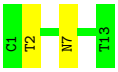
Chain B: 



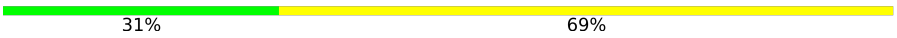
4.2.3 Score per residue for model 3

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

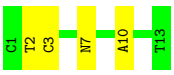
Chain B: 



4.2.4 Score per residue for model 4

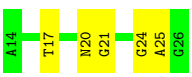
• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B: 

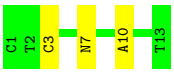


4.2.5 Score per residue for model 5

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:





• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:





4.2.6 Score per residue for model 6

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

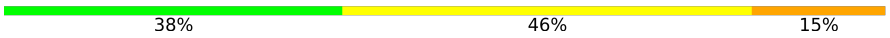
Chain A:

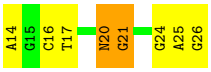




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



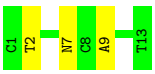


4.2.7 Score per residue for model 7

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

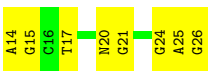




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



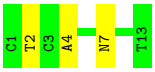


4.2.8 Score per residue for model 8

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

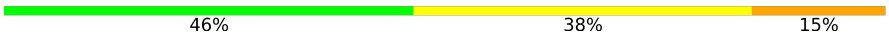
Chain A:

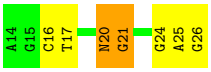




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



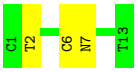


4.2.9 Score per residue for model 9

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

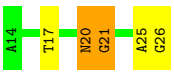




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



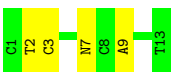


4.2.10 Score per residue for model 10

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

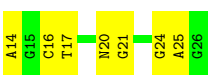




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



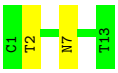


4.2.11 Score per residue for model 11

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

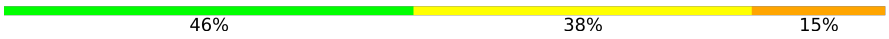
Chain A:

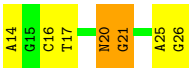




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



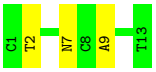


4.2.12 Score per residue for model 12

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:





• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



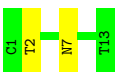


4.2.13 Score per residue for model 13

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:





• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:

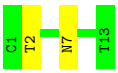




4.2.14 Score per residue for model 14

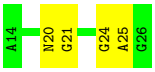
• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

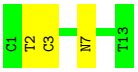
Chain B: 



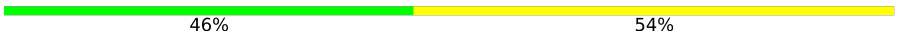
4.2.15 Score per residue for model 15

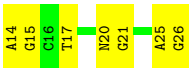
• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

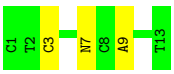
Chain B: 



4.2.16 Score per residue for model 16

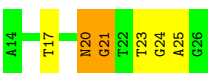
• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A: 



• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B: 

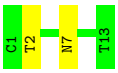


4.2.17 Score per residue for model 17

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

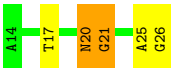




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



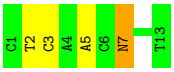


4.2.18 Score per residue for model 18

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

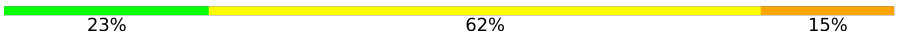
Chain A:

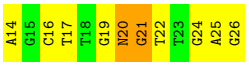




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:



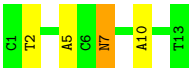


4.2.19 Score per residue for model 19

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

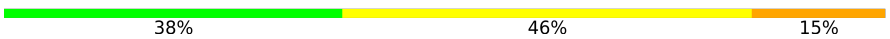
Chain A:





• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:





4.2.20 Score per residue for model 20

• Molecule 1: 5'-D(*CP*TP*CP*AP*AP*CP*(2DM)P*CP*AP*AP*GP*CP*T)-3'

Chain A:

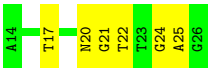




• Molecule 2: 5'-D(*AP*GP*CP*TP*TP*GP*(2DM)P*GP*TP*TP*GP*AP*G)-3'

Chain B:





5 Refinement protocol and experimental data overview

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

Of the 40 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2DM

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	0.61±0.01	0±0/265 (0.0± 0.0%)	1.13±0.03	1±0/403 (0.2± 0.1%)
2	B	0.68±0.01	0±0/277 (0.0± 0.0%)	1.29±0.03	0±0/425 (0.0± 0.1%)
All	All	0.65	0/10840 (0.0%)	1.22	20/16560 (0.1%)

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	1.0±0.8
2	B	0.0±0.0	5.3±1.3
All	All	0	127

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.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	6	DC	C2'-C3'-O3'	6.06	120.60	111.50	1	1
2	B	24	DG	C5'-C4'-C3'	5.17	122.66	114.90	5	1
1	A	2	DT	C6-C5-C7	-5.15	116.28	124.00	10	16
2	B	15	DG	O3'-P-O5'	-5.12	96.33	104.00	7	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)
2	B	21	DG	Sidechain	20
2	B	25	DA	Sidechain	20
2	B	17	DT	Sidechain	19
2	B	24	DG	Sidechain	14
2	B	26	DG	Sidechain	13
2	B	16	DC	Sidechain	8
2	B	14	DA	Sidechain	7
1	A	3	DC	Sidechain	6
2	B	22	DT	Sidechain	5
1	A	10	DA	Sidechain	4
1	A	9	DA	Sidechain	4
1	A	6	DC	Sidechain	2
1	A	5	DA	Sidechain	2
1	A	8	DC	Sidechain	1
1	A	4	DA	Sidechain	1
2	B	23	DT	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
1	A	264	152	152	0±0
2	B	274	154	154	1±1
All	All	10760	6120	6120	11

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.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:20:2DM:C4'	2:B:21:DG:C8	0.44	3.01	6	9
1:A:7:2DM:C6	2:B:19:DG:H2"	0.41	2.46	18	2

6.3 Torsion angles

6.3.1 Protein backbone

There are no protein molecules in this entry.

6.3.2 Protein sidechains

There are no protein molecules in this entry.

6.3.3 RNA

There are no RNA molecules in this entry.

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

2 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	2DM	A	7	1	26,29,30	1.12±0.01	3±0 (10±1%)
2	2DM	B	20	2	26,29,30	1.07±0.01	3±1 (12±3%)

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
1	2DM	A	7	1	36,41,44	0.94±0.03	2±1 (4±1%)
2	2DM	B	20	2	36,41,44	0.82±0.07	0±1 (0±1%)

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	2DM	A	7	1	-	0±0,9,11,12	0±0,4,4,4
2	2DM	B	20	2	-	0±0,9,11,12	0±0,4,4,4

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	2DM	C4-C5	3.00	1.43	1.35	17	20
2	B	20	2DM	C2-C1	2.59	1.42	1.37	5	20
1	A	7	2DM	C9-C10	2.33	1.41	1.35	5	20
2	B	20	2DM	C9-C10	2.18	1.41	1.35	1	20
1	A	7	2DM	C2-C1	2.14	1.41	1.37	19	16
2	B	20	2DM	C7-C6	2.11	1.41	1.36	9	13
2	B	20	2DM	C4-C5	2.06	1.40	1.35	6	9
2	B	20	2DM	C7-C8	2.04	1.41	1.36	8	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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	7	2DM	C4'-O4'-C3'	2.82	118.98	112.66	2	16
2	B	20	2DM	C4'-O4'-C3'	2.76	118.85	112.66	5	4
1	A	7	2DM	C4-C5-C13	2.39	117.81	121.34	16	17
2	B	20	2DM	O4'-C4'-C1	2.34	106.30	112.24	4	2
2	B	20	2DM	O4'-C3'-C2'	2.04	115.84	109.56	10	1
1	A	7	2DM	O4'-C3'-C2'	2.01	115.73	109.56	14	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no oligosaccharides 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

No chemical shift data were provided