



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 5KI5
Title : Structural impact of single ribonucleotides in DNA
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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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

2 Ensemble composition and analysis

This entry contains 10 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 569 atoms, of which 206 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	9	286	88	104	32	54	8	0

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

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	9	283	87	102	36	50	8	0

4 Residue-property plots

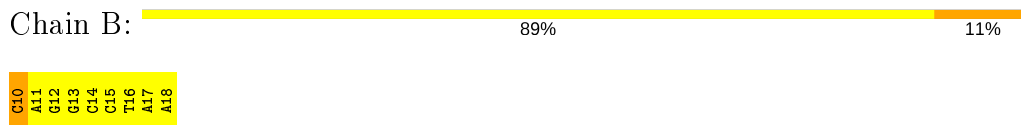
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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(*TP*TP*AP*GP*GP*CP*CP*TP*G)-3')



- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')



4.2 Scores per residue for each member of the ensemble

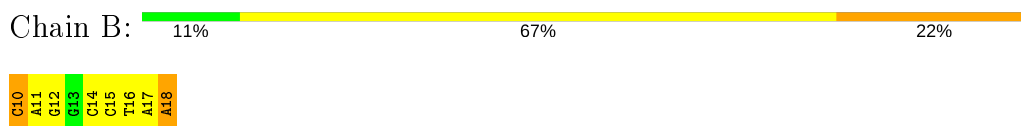
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

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



- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')




4.2.2 Score per residue for model 2

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

Chain A:  67% 33%

T1 T2 A3 G4 G5 C6 C7 T8 G9

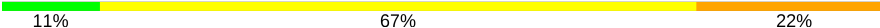
- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  89% 11%

G10 A11 G12 G13 C14 C15 T16 A17 A18


4.2.3 Score per residue for model 3

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

Chain A:  11% 67% 22%

T1 T2 A3 G4 G5 C6 C7 T8 G9

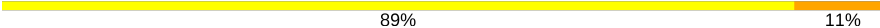
- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  11% 56% 33%

G10 A11 G12 G13 C14 C15 T16 A17 A18


4.2.4 Score per residue for model 4

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

Chain A:  89% 11%

T1 T2 A3 G4 G5 C6 C7 T8 G9

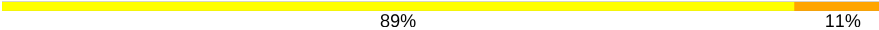
- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  78% 22%

G10 A11 G12 G13 C14 C15 T16 A17 A18

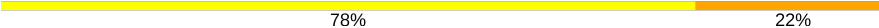
4.2.5 Score per residue for model 5

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

Chain A:  89% 11%

T1 T2 A3 G4 G5 C6 C7 T8 G9

- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  78% 22%

G10 A11 G12 G13 C14 C15 T16 A17 A18

4.2.6 Score per residue for model 6

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

Chain A:  11% 78% 11%

T1 T2 A3 G4 G5 C6 C7 T8 G9

- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  11% 78% 11%

G10 A11 G12 G13 C14 C15 T16 A17 A18

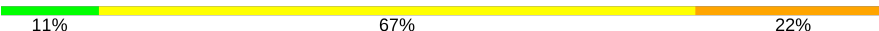
4.2.7 Score per residue for model 7

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

Chain A:  11% 89%

T1 T2 A3 G4 G5 C6 C7 T8 G9

- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

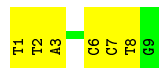
Chain B:  11% 67% 22%

G10 A11 G12 G13 C14 C15 T16 A17 A18


4.2.8 Score per residue for model 8

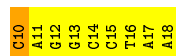
- Molecule 1: DNA (5'-D(*TP*TP*AP*GP*GP*CP*CP*TP*G)-3')

Chain A:  33% 67%



- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  89% 11%



4.2.9 Score per residue for model 9

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

Chain A:  22% 56% 22%



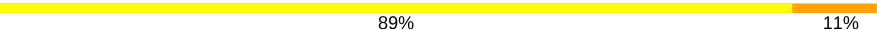
- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

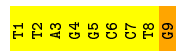
Chain B:  11% 78% 11%




4.2.10 Score per residue for model 10

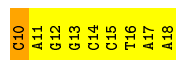
- Molecule 1: DNA (5'-D(*TP*TP*AP*GP*GP*CP*CP*TP*G)-3')

Chain A:  89% 11%



- Molecule 2: DNA (5'-D(*CP*AP*GP*GP*CP*CP*TP*AP*A)-3')

Chain B:  89% 11%



5 Refinement protocol and experimental data overview (i)

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

Of the 10 calculated structures, 10 were deposited, based on the following criterion: *back calculated data agree with experimental NOESY spectrum*.

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

Software name	Classification	Version
AMBER	structure calculation	9
CORMA	refinement	
MARDIGRAS	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	137
Number of shifts mapped to atoms	137
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	33%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	3630	2060	2060	-

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.

5.2 Torsion angles [i](#)

5.2.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.2.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.2.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.5 Ligand geometry [i](#)

There are no ligands in this entry.

5.6 Other polymers [i](#)

There are no such molecules in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 33% for the well-defined parts and 33% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *dGGxCshiftsout.str*

6.1.1 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	137
Number of shifts mapped to atoms	137
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

6.1.2 Chemical shift referencing

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

6.1.3 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 33%, i.e. 117 atoms were assigned a chemical shift out of a possible 357. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
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	117/357 (33%)	117/213 (55%)	0/121 (0%)	0/23 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 33%, i.e. 117 atoms were assigned a chemical shift out of a possible 357. 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	117/357 (33%)	117/213 (55%)	0/121 (0%)	0/23 (0%)

6.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

6.1.5 Random Coil Index (RCI) plots [i](#)

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