



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 4KBD
Title : DNA STRUCTURE OF A MUTATED KB SITE
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Deposited on : 1998-11-30

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
<http://wwpdb.org/validation/2016/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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

2 Ensemble composition and analysis

This entry contains 3 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 1011 atoms, of which 363 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
1	A	16	501	154	183	53	96	15	0

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

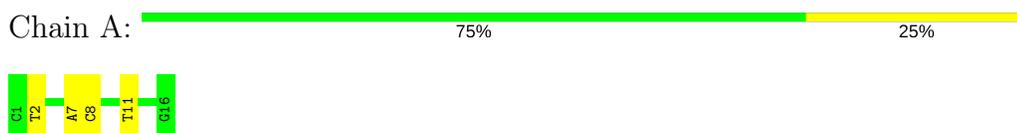
Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
2	B	16	510	157	180	68	90	15	0

4 Residue-property plots

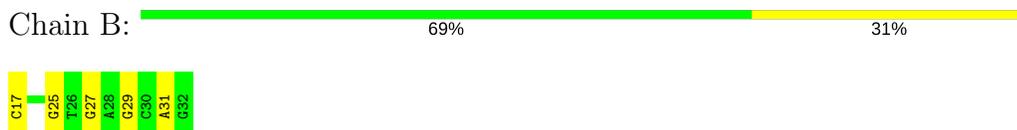
4.1 Average score per residue in the NMR ensemble

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(*CP*TP*GP*CP*TP*CP*AP*CP*TP*TP*TP*CP*CP*AP*GP*G)-3')



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



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

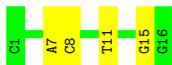
Chain B:  63% 38%



4.2.2 Score per residue for model 2

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

Chain A:  75% 25%



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

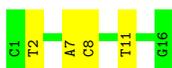
Chain B:  63% 38%



4.2.3 Score per residue for model 3

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

Chain A:  75% 25%



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

Chain B:  69% 31%



5 Refinement protocol and experimental data overview

Of the ? calculated structures, 3 were deposited, based on the following criterion: *ENERGY*.

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

Software name	Classification	Version
IRMA	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality i

6.1 Standard geometry i

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	0.93±0.01	0±0/354 (0.0±0.0%)	1.58±0.06	5±1/544 (1.0±0.2%)
2	B	1.01±0.03	0±0/372 (0.0±0.0%)	1.48±0.06	6±1/574 (1.0±0.1%)
All	All	0.97	0/2178 (0.0%)	1.53	34/3354 (1.0%)

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(°)	Ideal(°)	Models	
								Worst	Total
2	B	25	DG	O4'-C1'-C2'	-6.76	100.49	105.90	2	1
2	B	25	DG	O4'-C1'-N9	6.66	112.66	108.00	2	3
1	A	11	DT	O4'-C1'-N1	6.42	112.49	108.00	2	3
2	B	17	DC	O4'-C1'-N1	5.92	112.15	108.00	2	3
2	B	29	DG	O4'-C1'-N9	5.87	112.11	108.00	2	3
1	A	2	DT	O4'-C1'-N1	5.85	112.09	108.00	1	2
2	B	27	DG	O4'-C1'-N9	5.83	112.08	108.00	1	3
1	A	7	DA	O4'-C1'-N9	5.77	112.04	108.00	2	3
1	A	11	DT	O4'-C1'-C2'	-5.68	101.36	105.90	2	1
1	A	15	DG	P-O3'-C3'	5.58	126.40	119.70	2	1
2	B	31	DA	O4'-C1'-N9	5.46	111.82	108.00	1	3
1	A	8	DC	O4'-C1'-N1	5.40	111.78	108.00	2	3
1	A	15	DG	O4'-C1'-N9	5.36	111.75	108.00	2	1
2	B	32	DG	O4'-C1'-N9	5.22	111.66	108.00	2	1
1	A	14	DA	O4'-C1'-N9	5.13	111.59	108.00	1	1
1	A	12	DC	O4'-C1'-N1	5.11	111.58	108.00	1	1
2	B	20	DG	O4'-C1'-N9	5.09	111.56	108.00	1	1

There are no chirality outliers.

There are no planarity outliers.

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	1944	1089	1071	-

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](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates 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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided