



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 06:18 PM UTC

PDB ID : 6K3X / pdb_00006k3x
BMRB ID : 36252
Title : G-quadruplex complex with linear dinucleotide d(AG)
Authors : Winnerdy, F.R.; Heddi, B.; Phan, A.T.
Deposited on : 2019-05-22

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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
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

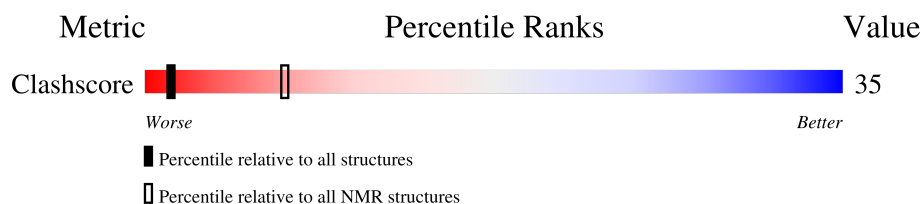
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

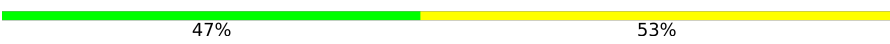
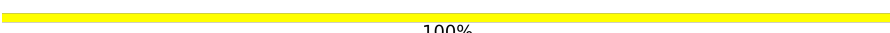
The overall completeness of chemical shifts assignment is 43%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	17	 47% 53%
2	B	2	 100%

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

There are 2 unique types of molecules in this entry. The entry contains 618 atoms, of which 219 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3').

Mol	Chain	Residues	Atoms						Trace
1	A	17	Total	C	H	N	O	P	0
			554	170	195	67	106	16	

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

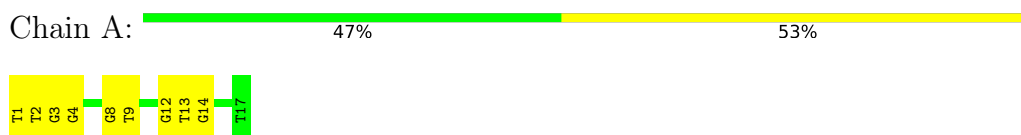
Mol	Chain	Residues	Atoms						Trace
2	B	2	Total	C	H	N	O	P	0
			64	20	24	10	9	1	

4 Residue-property plots [i](#)

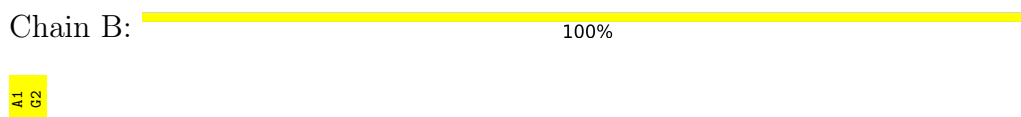
4.1 Average score per residue in the NMR ensemble

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(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')



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

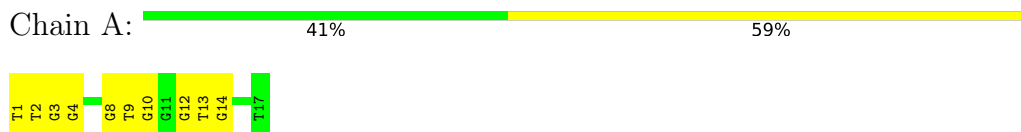


4.2 Scores per residue for each member of the ensemble

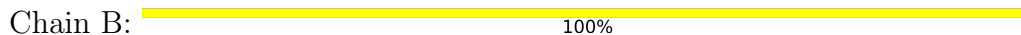
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')



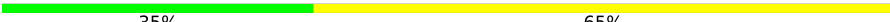
- Molecule 2: DNA (5'-D(*AP*G)-3')



A1
G2

4.2.2 Score per residue for model 2

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  35% 65%

T1	T2	G3	G4	G8	T9	G10	G11	G12	T13	G14	G15	G16	T17
----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----

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

Chain B:  100%

A1
G2

4.2.3 Score per residue for model 3

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  35% 65%

T1	T2	G3	G4	T5	G8	T9	G12	T13	G14	G15	G16	T17
----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----

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

Chain B:  100%

A1
G2

4.2.4 Score per residue for model 4

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  41% 59%

T1	T2	G3	G4	T5	G12	T13	G14	G15	G16	T17
----	----	----	----	----	-----	-----	-----	-----	-----	-----

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

Chain B:  100%

A1
G2

4.2.5 Score per residue for model 5

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  41%  59%

T1
T2
G3
T5
G8
T9
G12
T13
G14
T17

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

Chain B:  100%

A1
G2

4.2.6 Score per residue for model 6

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  65%  35%

T1
T2
G3
G8
T9
G14
T17

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

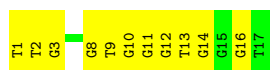
Chain B:  100%

A1
G2

4.2.7 Score per residue for model 7

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  35%  65%



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

Chain B: 100%



4.2.8 Score per residue for model 8

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A: 47% 53%



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

Chain B: 100%



4.2.9 Score per residue for model 9

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A: 53% 47%



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

Chain B: 100%



4.2.10 Score per residue for model 10

- Molecule 1: DNA (5'-D(*TP*TP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*TP*GP*GP*GP*T)-3')

Chain A:  41% 59%



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

Chain B:  100%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing, molecular dynamics*.

Of the 100 calculated structures, 10 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
X-PLOR NIH	structure calculation	
X-PLOR NIH	refinement	

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	2
Total number of shifts	182
Number of shifts mapped to atoms	182
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

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
1	A	359	195	195	16±3
2	B	40	24	24	6±0
All	All	3990	2190	2190	214

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 35.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:DG:H4'	1:A:13:DT:O5'	0.89	1.67	10	5
2:B:1:DA:H4'	2:B:2:DG:O5'	0.79	1.76	5	10
1:A:12:DG:H1'	1:A:13:DT:OP2	0.78	1.79	1	4
1:A:13:DT:H1'	1:A:14:DG:OP2	0.78	1.79	3	2
1:A:8:DG:H1'	1:A:9:DT:OP2	0.76	1.80	1	2
1:A:1:DT:H1'	1:A:2:DT:OP1	0.76	1.80	9	10
1:A:2:DT:H1'	1:A:3:DG:OP2	0.76	1.81	8	10
1:A:2:DT:C4	1:A:14:DG:N3	0.72	2.58	3	10
1:A:4:DG:H4'	1:A:5:DT:OP2	0.72	1.84	3	2
1:A:9:DT:H1'	1:A:11:DG:OP2	0.70	1.87	7	1
1:A:2:DT:H4'	1:A:3:DG:O5'	0.69	1.88	8	10
1:A:5:DT:H1'	1:A:6:DG:OP1	0.69	1.88	9	1
1:A:8:DG:H4'	1:A:9:DT:O5'	0.69	1.86	5	5

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1:DA:H1'	2:B:2:DG:OP2	0.66	1.91	6	4
1:A:9:DT:H1'	1:A:10:DG:OP2	0.62	1.94	2	1
1:A:2:DT:C1'	1:A:3:DG:OP2	0.60	2.49	1	10
2:B:2:DG:OP2	2:B:2:DG:N2	0.60	2.34	1	10
1:A:2:DT:O4	1:A:14:DG:H1'	0.60	1.95	9	10
1:A:4:DG:C4'	1:A:5:DT:OP2	0.57	2.53	3	2
2:B:1:DA:C4'	2:B:2:DG:O5'	0.57	2.52	1	10
1:A:13:DT:C1'	1:A:14:DG:OP2	0.57	2.52	3	2
1:A:12:DG:C1'	1:A:13:DT:OP2	0.57	2.52	5	3
1:A:9:DT:C1'	1:A:11:DG:OP2	0.57	2.53	7	1
1:A:1:DT:C1'	1:A:2:DT:OP1	0.56	2.54	9	10
1:A:2:DT:O4	1:A:14:DG:C1'	0.55	2.53	10	6
1:A:13:DT:H4'	1:A:14:DG:O5'	0.54	2.02	3	1
1:A:9:DT:H4'	1:A:10:DG:O5'	0.54	2.02	2	1
1:A:13:DT:H2''	1:A:14:DG:OP2	0.53	2.02	4	1
1:A:9:DT:O3'	1:A:10:DG:H3'	0.51	2.05	1	2
1:A:12:DG:O6	1:A:16:DG:O6	0.51	2.28	4	2
1:A:5:DT:O4'	1:A:5:DT:OP2	0.51	2.29	5	1
1:A:5:DT:O2	2:B:2:DG:O3'	0.51	2.28	10	1
1:A:3:DG:H2''	1:A:4:DG:OP2	0.51	2.05	1	6
1:A:8:DG:C1'	1:A:9:DT:OP2	0.51	2.54	1	1
1:A:9:DT:O4'	1:A:9:DT:OP2	0.51	2.28	6	2
1:A:9:DT:O4'	1:A:9:DT:OP1	0.51	2.29	7	2
1:A:16:DG:O6	2:B:2:DG:O6	0.51	2.29	2	2
1:A:13:DT:O4'	1:A:13:DT:OP2	0.51	2.29	10	1
1:A:5:DT:C1'	1:A:6:DG:OP1	0.50	2.60	9	1
2:B:1:DA:C2'	2:B:1:DA:N3	0.50	2.75	5	4
1:A:5:DT:C2'	1:A:6:DG:OP1	0.49	2.60	9	1
1:A:4:DG:H1'	1:A:5:DT:OP1	0.48	2.08	3	1
1:A:5:DT:OP1	1:A:5:DT:H4'	0.48	2.08	3	1
1:A:1:DT:C2'	1:A:2:DT:OP1	0.48	2.61	9	10
1:A:9:DT:C2'	1:A:10:DG:OP2	0.48	2.61	2	1
1:A:8:DG:C2'	1:A:9:DT:OP2	0.47	2.62	1	1
1:A:4:DG:H2''	1:A:5:DT:OP2	0.46	2.10	4	1
2:B:1:DA:N3	2:B:1:DA:C2'	0.45	2.79	2	2
1:A:8:DG:O6	1:A:12:DG:O6	0.45	2.35	2	1
1:A:9:DT:C1'	1:A:10:DG:OP2	0.44	2.64	2	1
2:B:1:DA:N3	2:B:1:DA:H2'	0.43	2.28	10	2
1:A:5:DT:H2''	1:A:6:DG:OP1	0.43	2.13	9	1
1:A:12:DG:C2'	1:A:13:DT:OP2	0.43	2.67	1	1
1:A:2:DT:C6	1:A:14:DG:N2	0.43	2.87	8	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1:DA:H1'	2:B:2:DG:C2	0.43	2.49	8	8
1:A:13:DT:O2	1:A:15:DG:OP1	0.42	2.38	4	1
1:A:8:DG:H2''	1:A:9:DT:OP2	0.42	2.14	7	1
1:A:8:DG:H4'	1:A:9:DT:OP1	0.42	2.14	2	1
1:A:9:DT:H2''	1:A:10:DG:OP2	0.42	2.13	2	1
1:A:12:DG:C4'	1:A:13:DT:O5'	0.41	2.55	10	1
1:A:10:DG:C2	1:A:11:DG:C5	0.41	3.09	8	1
1:A:13:DT:C2'	1:A:14:DG:OP2	0.41	2.69	3	1
1:A:2:DT:C5	1:A:14:DG:C2	0.41	3.09	8	1
1:A:5:DT:H4'	1:A:5:DT:OP1	0.41	2.15	10	1
2:B:1:DA:C1'	2:B:2:DG:OP2	0.41	2.68	6	1
2:B:1:DA:H1'	2:B:2:DG:N2	0.40	2.31	6	1
1:A:7:DG:H2''	1:A:8:DG:O5'	0.40	2.15	8	1

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 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

The completeness of assignment taking into account all chemical shift lists is 43% for the well-defined parts and 43% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_1*

7.1.1 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	166
Number of shifts mapped to atoms	166
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

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

7.1.3 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 39%, i.e. 148 atoms were assigned a chemical shift out of a possible 380. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Sugar	119/228 (52%)	119/133 (89%)	0/95 (0%)	0/0 (—%)
Base	29/152 (19%)	29/95 (31%)	0/26 (0%)	0/31 (0%)
Overall	148/380 (39%)	148/228 (65%)	0/121 (0%)	0/31 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 39%, i.e. 148 atoms were assigned a chemical shift out of a possible 380. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Sugar	119/228 (52%)	119/133 (89%)	0/95 (0%)	0/0 (—%)
Base	29/152 (19%)	29/95 (31%)	0/26 (0%)	0/31 (0%)
Overall	148/380 (39%)	148/228 (65%)	0/121 (0%)	0/31 (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

7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_2*

7.2.1 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	16
Number of shifts mapped to atoms	16
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

7.2.2 Chemical shift referencing [i](#)

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

7.2.3 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 4%, i.e. 16 atoms were assigned a chemical shift out of a possible 380. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Sugar	12/228 (5%)	12/133 (9%)	0/95 (0%)	0/0 (—%)
Base	4/152 (3%)	4/95 (4%)	0/26 (0%)	0/31 (0%)
Overall	16/380 (4%)	16/228 (7%)	0/121 (0%)	0/31 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 4%, i.e. 16 atoms were assigned a chemical shift out of a possible 380. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Sugar	12/228 (5%)	12/133 (9%)	0/95 (0%)	0/0 (—%)
Base	4/152 (3%)	4/95 (4%)	0/26 (0%)	0/31 (0%)
Overall	16/380 (4%)	16/228 (7%)	0/121 (0%)	0/31 (0%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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