Full wwPDB NMR Structure Validation Report (i)

Jun 5, 2023 – 01:08 PM JST

PDB ID	:	6KFJ
BMRB ID	:	36268
Title	:	NMR solution structure of the 1:1 complex of wtTel26 G-quadruplex and a tripodal cationic fluorescent probe NBTE
Authors	:	Liu, W.; Liu, L.Y.; Mao, Z.W.
Deposited on	:	2019-07-07

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:

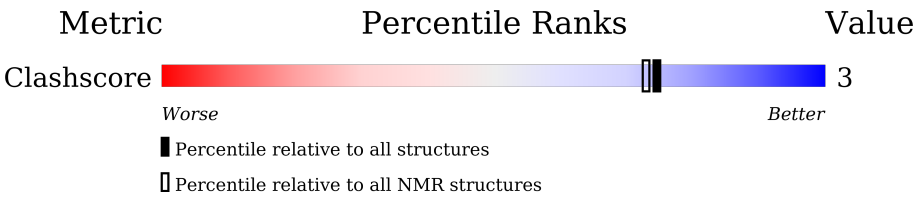
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

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 44%.

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	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	A	26	88% 12%

2 Ensemble composition and analysis (i)

This entry contains 15 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.

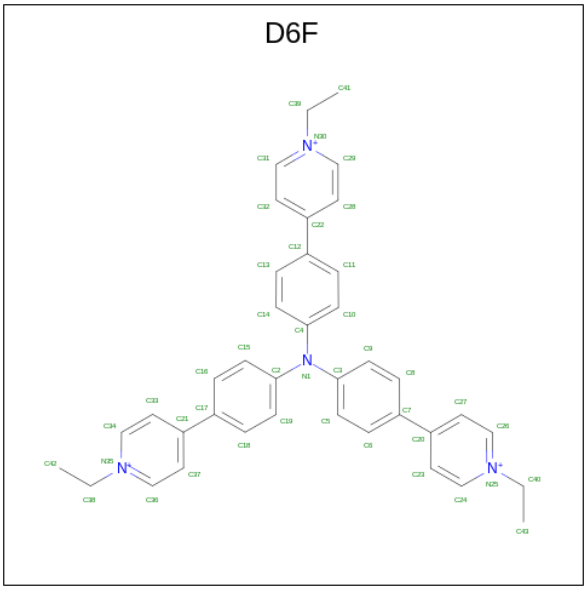
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 925 atoms, of which 337 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called G-quadruplex DNA wtTel26.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	26	843	260	298	100	160	25	0

- Molecule 2 is 4,4',4''-(nitrilotris(benzene-4,1-diyl))tris(1-ethylpyridin-1-ium) iodide (three-letter code: D6F) (formula: $C_{39}H_{39}N_4$).



Mol	Chain	Residues	Atoms			
			Total	C	H	N
2	A	1	82	39	39	4

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: G-quadruplex DNA wtTel26

Chain A: 88% 12%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

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: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.2 Score per residue for model 2

• Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.3 Score per residue for model 3

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 88% 12%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.4 Score per residue for model 4

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 88% 12%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.5 Score per residue for model 5

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.6 Score per residue for model 6

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.7 Score per residue for model 7

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.8 Score per residue for model 8

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.9 Score per residue for model 9

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.10 Score per residue for model 10

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.11 Score per residue for model 11

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.12 Score per residue for model 12

- Molecule 1: G-quadruplex DNA wtTel26

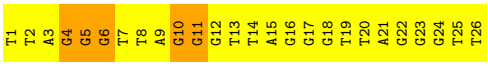
Chain A: 85% 15%

T1 T2 A3 G4 G5 G6 T7 T8 A9 G10 G11 G12 T13 T14 A15 G16 G17 G18 T19 T20 A21 G22 G23 G24 T25 T26

4.2.13 Score per residue for model 13

- Molecule 1: G-quadruplex DNA wtTel26

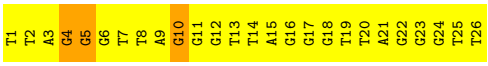
Chain A: 81% 19%



4.2.14 Score per residue for model 14

- Molecule 1: G-quadruplex DNA wtTel26

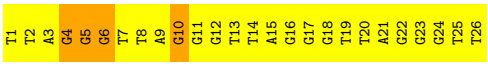
Chain A: 88% 12%



4.2.15 Score per residue for model 15

- Molecule 1: G-quadruplex DNA wtTel26

Chain A: 85% 15%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 15 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	refinement	
X-PLOR NIH	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	293
Number of shifts mapped to atoms	293
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	44%

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: D6F

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	1.86±0.00	10±0/612 (1.6± 0.0%)	2.40±0.00	43±1/948 (4.5± 0.1%)
All	All	1.86	150/9180 (1.6%)	2.40	639/14220 (4.5%)

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	8	DT	C5-C7	8.92	1.55	1.50	1	15
1	A	13	DT	C5-C7	8.89	1.55	1.50	1	15
1	A	1	DT	C5-C7	8.84	1.55	1.50	5	15
1	A	26	DT	C5-C7	8.83	1.55	1.50	12	15
1	A	2	DT	C5-C7	8.82	1.55	1.50	11	15
1	A	7	DT	C5-C7	8.82	1.55	1.50	11	15
1	A	20	DT	C5-C7	8.81	1.55	1.50	14	15
1	A	19	DT	C5-C7	8.78	1.55	1.50	5	15
1	A	14	DT	C5-C7	8.75	1.55	1.50	15	15
1	A	25	DT	C5-C7	8.74	1.55	1.50	4	15

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
1	A	10	DG	N7-C8-N9	9.71	117.96	113.10	1	15
1	A	11	DG	N7-C8-N9	9.66	117.93	113.10	4	15
1	A	5	DG	N7-C8-N9	9.52	117.86	113.10	12	15
1	A	17	DG	N7-C8-N9	9.48	117.84	113.10	13	15
1	A	12	DG	N7-C8-N9	9.46	117.83	113.10	10	15
1	A	18	DG	N7-C8-N9	9.45	117.82	113.10	8	15
1	A	23	DG	N7-C8-N9	9.45	117.82	113.10	12	15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	22	DG	N7-C8-N9	9.39	117.80	113.10	4	15
1	A	6	DG	N7-C8-N9	9.38	117.79	113.10	4	15
1	A	4	DG	N7-C8-N9	9.34	117.77	113.10	15	15
1	A	16	DG	N7-C8-N9	9.34	117.77	113.10	10	15
1	A	24	DG	N7-C8-N9	9.33	117.77	113.10	14	15
1	A	10	DG	C8-N9-C4	-8.85	102.86	106.40	10	15
1	A	5	DG	C8-N9-C4	-8.57	102.97	106.40	12	15
1	A	17	DG	C8-N9-C4	-8.04	103.19	106.40	8	15
1	A	4	DG	C8-N9-C4	-8.02	103.19	106.40	15	15
1	A	11	DG	C8-N9-C4	-8.00	103.20	106.40	9	15
1	A	6	DG	C8-N9-C4	-7.97	103.21	106.40	12	15
1	A	23	DG	C8-N9-C4	-7.93	103.23	106.40	1	15
1	A	22	DG	C8-N9-C4	-7.93	103.23	106.40	9	15
1	A	12	DG	C8-N9-C4	-7.85	103.26	106.40	10	15
1	A	16	DG	C8-N9-C4	-7.84	103.26	106.40	12	15
1	A	24	DG	C8-N9-C4	-7.84	103.26	106.40	7	15
1	A	18	DG	C8-N9-C4	-7.84	103.27	106.40	9	15
1	A	3	DA	N7-C8-N9	7.75	117.68	113.80	13	15
1	A	15	DA	N7-C8-N9	7.70	117.65	113.80	6	15
1	A	21	DA	N7-C8-N9	7.69	117.65	113.80	11	15
1	A	9	DA	N7-C8-N9	7.60	117.60	113.80	4	15
1	A	3	DA	C8-N9-C4	-7.02	102.99	105.80	14	15
1	A	15	DA	C8-N9-C4	-6.69	103.12	105.80	10	15
1	A	9	DA	C8-N9-C4	-6.69	103.12	105.80	10	15
1	A	21	DA	C8-N9-C4	-6.68	103.13	105.80	9	15
1	A	16	DG	O4'-C1'-N9	6.55	112.59	108.00	13	15
1	A	22	DG	O4'-C1'-N9	6.40	112.48	108.00	3	15
1	A	11	DG	O4'-C1'-N9	6.14	112.30	108.00	14	15
1	A	2	DT	O4'-C1'-N1	5.65	111.95	108.00	11	15
1	A	17	DG	O4'-C1'-N9	5.50	111.85	108.00	5	6
1	A	25	DT	C6-C5-C7	-5.22	119.77	122.90	14	15
1	A	13	DT	O4'-C1'-N1	5.16	111.61	108.00	3	4
1	A	11	DG	C5-N7-C8	-5.13	101.74	104.30	12	5
1	A	20	DT	C6-C5-C7	-5.10	119.84	122.90	15	12
1	A	7	DT	C6-C5-C7	-5.09	119.85	122.90	6	8
1	A	19	DT	C6-C5-C7	-5.08	119.85	122.90	14	11
1	A	13	DT	C6-C5-C7	-5.08	119.85	122.90	14	15
1	A	8	DT	C6-C5-C7	-5.08	119.86	122.90	1	8
1	A	1	DT	C6-C5-C7	-5.06	119.87	122.90	2	9
1	A	14	DT	C6-C5-C7	-5.04	119.87	122.90	12	4
1	A	26	DT	C6-C5-C7	-5.03	119.88	122.90	8	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	2	DT	C6-C5-C7	-5.02	119.89	122.90	15	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
1	A	545	298	298	3±0
All	All	8820	5055	4470	43

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:DG:H2'	1:A:10:DG:N3	0.57	2.14	1	15
1:A:10:DG:H2"	1:A:11:DG:O5'	0.48	2.09	7	7
1:A:4:DG:H2"	1:A:5:DG:O5'	0.45	2.12	2	15
1:A:5:DG:H4'	1:A:6:DG:OP1	0.45	2.12	5	6

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)

1 ligand is 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
2	D6F	A	101	-	48,48,48	1.75±0.00	12±0 (25±0%)

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
2	D6F	A	101	-	66,66,66	0.68±0.05	1±1 (0±0%)

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
2	D6F	A	101	-	-	0±0,30,30,30	0±0,6,6,6

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
2	A	101	D6F	C2-N1	4.48	1.33	1.42	10	15
2	A	101	D6F	C4-N1	4.48	1.33	1.42	11	15
2	A	101	D6F	C3-N1	4.44	1.33	1.42	1	15
2	A	101	D6F	C21-C17	3.84	1.39	1.49	2	15
2	A	101	D6F	C20-C7	3.79	1.39	1.49	11	15
2	A	101	D6F	C12-C22	3.77	1.39	1.49	13	15
2	A	101	D6F	C36-N35	2.55	1.40	1.34	7	15
2	A	101	D6F	C24-N25	2.53	1.40	1.34	14	15
2	A	101	D6F	C31-N30	2.53	1.40	1.34	4	15
2	A	101	D6F	C26-N25	2.53	1.40	1.34	12	15
2	A	101	D6F	C34-N35	2.52	1.40	1.34	13	15
2	A	101	D6F	C29-N30	2.52	1.40	1.34	13	15

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
2	A	101	D6F	C2-N1-C3	2.78	125.48	119.71	13	7
2	A	101	D6F	C3-N1-C4	2.65	114.23	119.71	14	1

There are no chirality outliers.

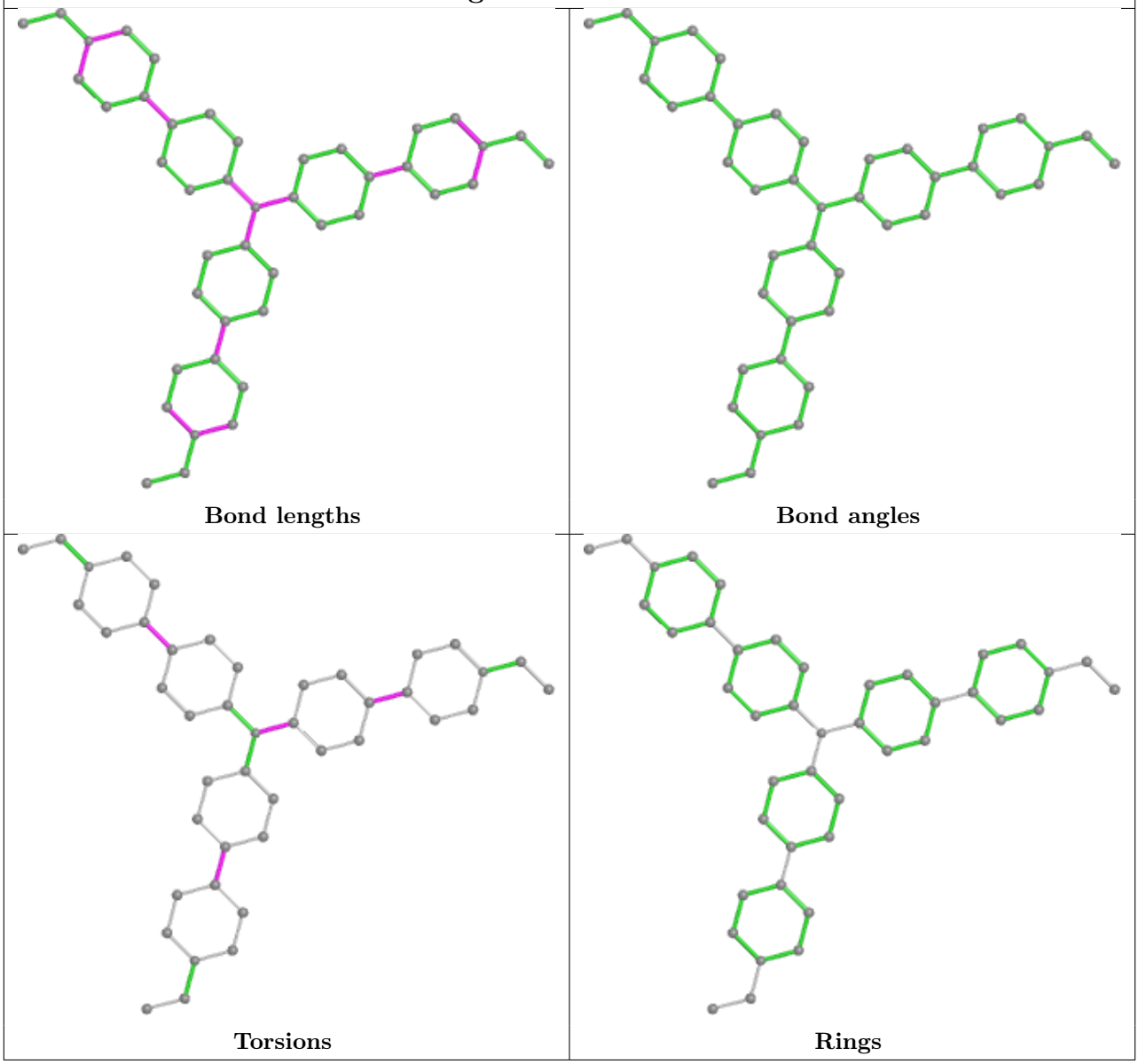
There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand D6F A 101



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 44% for the well-defined parts and 44% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *starch_output*

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	293
Number of shifts mapped to atoms	293
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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 44%, i.e. 224 atoms were assigned a chemical shift out of a possible 512. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Sugar	182/312 (58%)	182/182 (100%)	0/130 (0%)	0/0 (—%)
Base	42/200 (21%)	42/122 (34%)	0/40 (0%)	0/38 (0%)
Overall	224/512 (44%)	224/304 (74%)	0/170 (0%)	0/38 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 44%, i.e. 224 atoms were assigned a chemical shift out of a possible 512. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Sugar	182/312 (58%)	182/182 (100%)	0/130 (0%)	0/0 (—%)
Base	42/200 (21%)	42/122 (34%)	0/40 (0%)	0/38 (0%)
Overall	224/512 (44%)	224/304 (74%)	0/170 (0%)	0/38 (0%)

7.1.4 Statistically unusual chemical shifts (i)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	14	DT	H2'	0.56	0.76 – 3.44	-5.7

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

8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	236
Intra-residue (|i-j|=0)	75
Sequential (|i-j|=1)	56
Medium range (|i-j|>1 and |i-j|<5)	7
Long range (|i-j|≥5)	98
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	75
Number of restraints per residue	9.1
Number of long range restraints per residue[1]	3.8

[1]Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations (i)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model (i)

Distance violations less than 0.1 Å are not included in the calculation.There are no distance violations

8.2.2 Average number of dihedral-angle violations per model (i)

Dihedral-angle violations less than 1° are not included in the calculation.There are no dihedral-angle violations

9 Distance violation analysis (i)

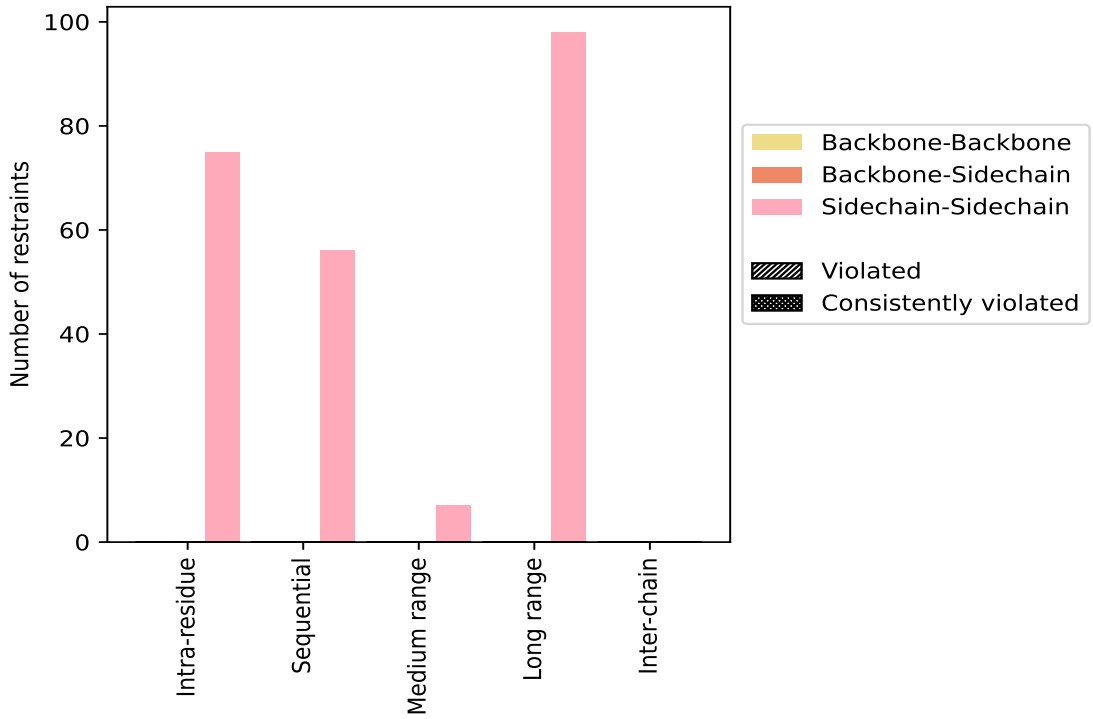
9.1 Summary of distance violations (i)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	75	31.8	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	75	31.8	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	56	23.7	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	56	23.7	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	7	3.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	7	3.0	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	98	41.5	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	98	41.5	0	0.0	0.0	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	236	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	236	100.0	0	0.0	0.0	0	0.0	0.0

[1] percentage calculated with respect to the total number of distance restraints, [2] percentage calculated with respect to the number of restraints in a particular restraint category, [3] violated in at least one model, [4] violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations (i)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model (i)

No violations found

9.3 Distance violation statistics for the ensemble (i)

No violations found

9.4 Most violated distance restraints in the ensemble (i)

No violations found

9.5 All violated distance restraints (i)

No violations found

10 Dihedral-angle violation analysis (i)

No dihedral-angle restraints found