



Full wwPDB NMR Structure Validation Report ⓘ

Mar 10, 2026 – 09:16 AM UTC

PDB ID : 6FY6 / pdb_00006fy6
BMRB ID : 34244
Title : Concerted dynamics of metallo-base pairs in an A/B-form helical transition (major species)
Authors : Schmidt, O.P.; Jurt, S.; Johannsen, S.; Karimi, A.; Sigel, R.K.O.; Luedtke, N.W.
Deposited on : 2018-03-11

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

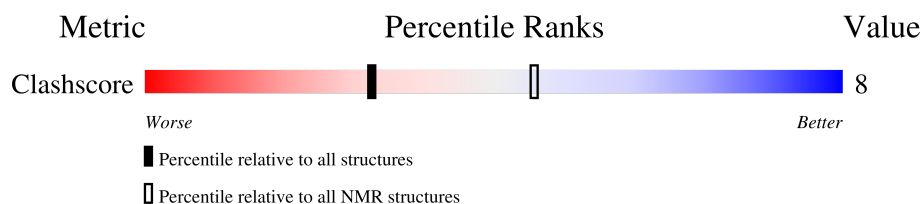
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 49%.

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	14	 86% 14%
1	B	14	 86% 14%

2 Ensemble composition and analysis ⓘ

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 884 atoms, of which 318 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
1	A	14	Total	C	H	N	O	P	0
			441	136	159	50	83	13	
1	B	14	Total	C	H	N	O	P	0
			441	136	159	50	83	13	

- Molecule 2 is MERCURY (II) ION (CCD ID: HG) (formula: Hg).

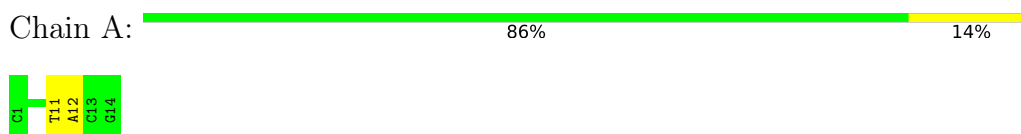
Mol	Chain	Residues	Atoms	
2	A	2	Total	Hg
			2	2

4 Residue-property plots

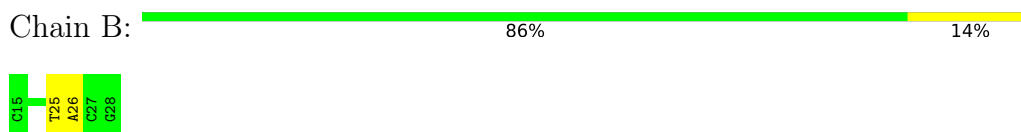
4.1 Average score per residue in the NMR ensemble

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



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



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



There are no outlier residues in this chain.

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

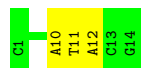


There are no outlier residues in this chain.

4.2.2 Score per residue for model 2

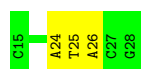
- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

Chain A:  79% 21%



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

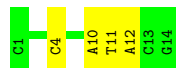
Chain B:  79% 21%



4.2.3 Score per residue for model 3

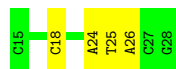
- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

Chain A:  71% 29%



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

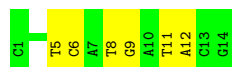
Chain B:  71% 29%



4.2.4 Score per residue for model 4

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

Chain A:  57% 43%

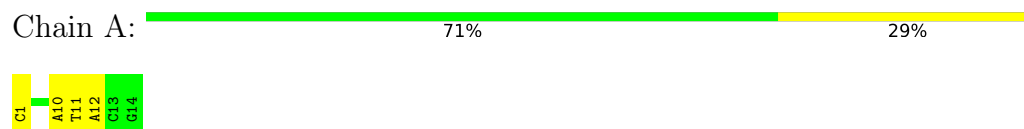


- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

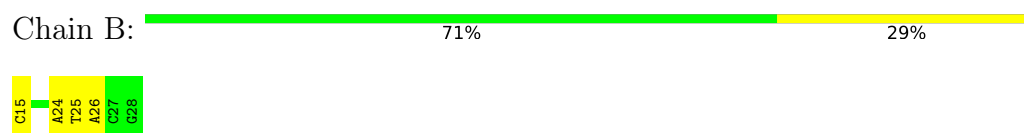


4.2.5 Score per residue for model 5

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

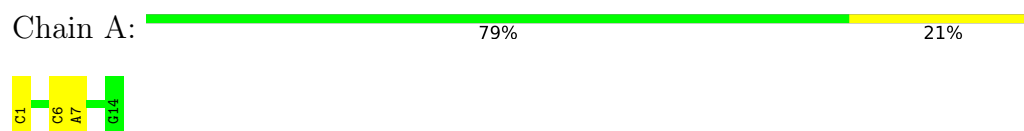


- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

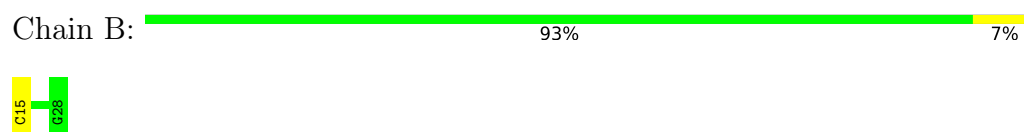


4.2.6 Score per residue for model 6

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

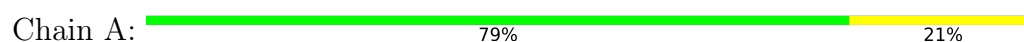


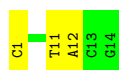
- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major



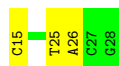
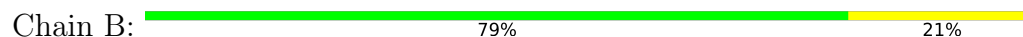
4.2.7 Score per residue for model 7

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



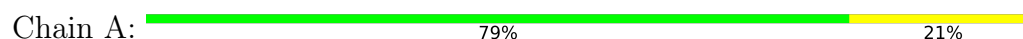


- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

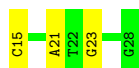
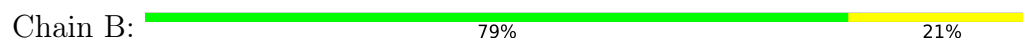


4.2.8 Score per residue for model 8

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



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

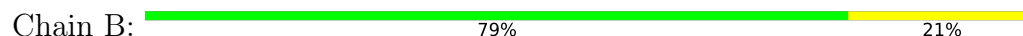


4.2.9 Score per residue for model 9

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



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



4.2.10 Score per residue for model 10

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

Chain A:  86% 14%



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

Chain B:  86% 14%



4.2.11 Score per residue for model 11

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

Chain A:  86% 14%



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

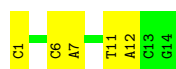
Chain B:  86% 14%



4.2.12 Score per residue for model 12

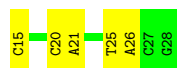
- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

Chain A:  64% 36%



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

Chain B:  64% 36%



4.2.13 Score per residue for model 13

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

Chain A:  64% 36%



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

Chain B:  64% 36%



4.2.14 Score per residue for model 14

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

Chain A:  86% 14%



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

Chain B:  86% 14%



4.2.15 Score per residue for model 15

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

Chain A:  86% 14%



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

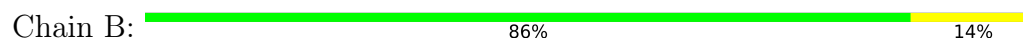


4.2.16 Score per residue for model 16

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



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



4.2.17 Score per residue for model 17

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



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



4.2.18 Score per residue for model 18

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

Chain A:  64% 36%



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

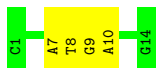
Chain B:  64% 36%



4.2.19 Score per residue for model 19

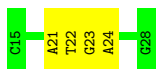
- Molecule 1: DNA (5'-D(*CP*GP*TP*CP*TP*CP*AP*TP*GP*AP*TP*AP*CP*G)-3')_major

Chain A:  71% 29%



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

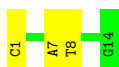
Chain B:  71% 29%



4.2.20 Score per residue for model 20

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

Chain A:  79% 21%



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

Chain B:

79%

21%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 20 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
Xplor-NIH	structure calculation	2.46
Xplor-NIH	refinement	2.46

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	292
Number of shifts mapped to atoms	292
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	49%

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: HG

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	282	159	159	4±2
1	B	282	159	159	4±2
All	All	11320	6360	6360	150

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:15:DC:H6	1:B:15:DC:HO5'	0.92	0.94	20	9
1:A:1:DC:H6	1:A:1:DC:HO5'	0.91	0.92	8	8
1:B:25:DT:C4	1:B:26:DA:N6	0.75	2.55	3	9
1:A:11:DT:C4	1:A:12:DA:N6	0.74	2.55	3	9
1:A:9:DG:N2	1:B:21:DA:C2	0.72	2.58	18	3
1:A:7:DA:C2	1:B:23:DG:N2	0.72	2.58	18	3
1:A:11:DT:C4	1:A:12:DA:C6	0.66	2.84	3	5
1:B:15:DC:H6	1:B:15:DC:O5'	0.66	1.71	20	7
1:B:25:DT:C4	1:B:26:DA:C6	0.65	2.84	3	5
1:A:1:DC:H6	1:A:1:DC:O5'	0.65	1.72	8	6
1:A:11:DT:N3	1:A:12:DA:C5	0.64	2.66	16	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:25:DT:N3	1:B:26:DA:C5	0.64	2.65	16	3
1:B:25:DT:O4	1:B:26:DA:N6	0.63	2.32	10	12
1:A:7:DA:N6	1:B:21:DA:N6	0.63	2.47	19	1
1:A:11:DT:O4	1:A:12:DA:N6	0.62	2.32	10	12
1:B:25:DT:N3	1:B:26:DA:C6	0.61	2.68	17	4
1:A:11:DT:N3	1:A:12:DA:C6	0.60	2.69	17	4
1:A:5:DT:C4	1:A:6:DC:N4	0.55	2.75	4	1
1:B:19:DT:C4	1:B:20:DC:N4	0.55	2.75	4	1
1:B:25:DT:C2	1:B:26:DA:C5	0.55	2.94	17	2
1:A:11:DT:C2	1:A:12:DA:C5	0.55	2.94	17	2
1:B:25:DT:C2'	1:B:26:DA:C8	0.54	2.91	11	2
1:A:7:DA:C2	1:A:8:DT:C2	0.54	2.95	20	1
1:B:21:DA:C2	1:B:22:DT:C2	0.54	2.95	20	1
1:A:11:DT:C2'	1:A:12:DA:C8	0.53	2.91	11	2
1:A:9:DG:C2	1:B:21:DA:C2	0.53	2.96	18	2
1:A:7:DA:C2	1:B:23:DG:C2	0.52	2.97	18	3
1:A:10:DA:C2	1:A:11:DT:C2	0.49	3.01	2	1
1:B:24:DA:C2	1:B:25:DT:C2	0.48	3.02	2	1
1:A:1:DC:O5'	1:A:1:DC:C6	0.47	2.58	13	2
1:A:4:DC:N4	1:B:24:DA:N6	0.47	2.62	3	1
1:B:25:DT:H2''	1:B:26:DA:C8	0.44	2.46	11	1
1:A:9:DG:C6	1:A:10:DA:C6	0.44	3.04	19	1
1:A:11:DT:H2''	1:A:12:DA:C8	0.44	2.47	11	1
1:A:10:DA:N6	1:B:18:DC:N4	0.44	2.66	3	1
1:B:22:DT:C2'	1:B:23:DG:C8	0.44	3.01	19	2
1:B:23:DG:C6	1:B:24:DA:C6	0.43	3.05	19	1
1:A:9:DG:C2	1:A:10:DA:C2	0.43	3.07	19	1
1:A:8:DT:C2'	1:A:9:DG:C8	0.43	3.02	19	2
1:A:1:DC:H2''	1:A:2:DG:C8	0.43	2.48	14	1
1:B:15:DC:H2''	1:B:16:DG:C8	0.43	2.49	14	1
1:A:6:DC:C4	1:A:7:DA:N6	0.42	2.88	12	1
1:B:24:DA:H2''	1:B:25:DT:O5'	0.42	2.15	5	1
1:B:20:DC:C4	1:B:21:DA:N6	0.42	2.87	12	1
1:B:22:DT:H2''	1:B:23:DG:C8	0.42	2.50	18	1
1:A:1:DC:C2'	1:A:2:DG:C8	0.41	3.03	14	1
1:A:10:DA:H2''	1:A:11:DT:O5'	0.41	2.15	5	1
1:A:11:DT:H2'	1:A:12:DA:C8	0.41	2.50	11	1
1:A:8:DT:H2''	1:A:9:DG:C8	0.41	2.51	18	1
1:B:23:DG:C2	1:B:24:DA:C2	0.41	3.08	19	1
1:B:15:DC:C2'	1:B:16:DG:C8	0.41	3.04	14	1
1:A:6:DC:H2''	1:A:7:DA:C8	0.40	2.52	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:25:DT:H2'	1:B:26:DA:C8	0.40	2.51	11	1
1:B:15:DC:O5'	1:B:15:DC:C6	0.40	2.57	13	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 [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 49% for the well-defined parts and 49% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *chemical_shifts_major_4_converted_sr_adjusted_with_exchangeable_2*

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	292
Number of shifts mapped to atoms	292
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 [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 49%, i.e. 268 atoms were assigned a chemical shift out of a possible 550. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Sugar	186/336 (55%)	186/196 (95%)	0/140 (0%)	0/0 (—%)
Base	82/214 (38%)	82/130 (63%)	0/50 (0%)	0/34 (0%)
Overall	268/550 (49%)	268/326 (82%)	0/190 (0%)	0/34 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 49%, i.e. 268 atoms were assigned a chemical shift out of a possible 550. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Sugar	186/336 (55%)	186/196 (95%)	0/140 (0%)	0/0 (—%)
Base	82/214 (38%)	82/130 (63%)	0/50 (0%)	0/34 (0%)
Overall	268/550 (49%)	268/326 (82%)	0/190 (0%)	0/34 (0%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

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