



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:51 pm GMT

PDB ID : 2LB4  
Title : DNA / RNA Hybrid containing a central stereo specific Sp borano phosphate linkage  
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Deposited on : 2011-03-22

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

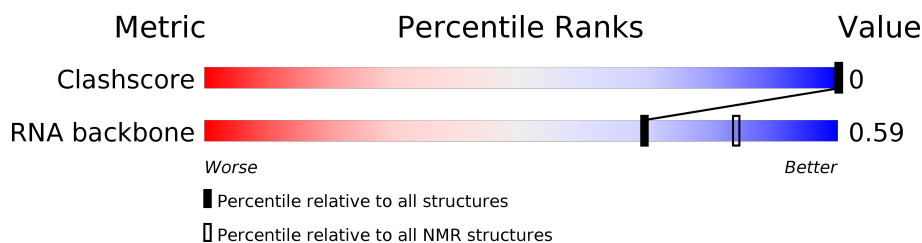
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*



The overall completeness of chemical shifts assignment is 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	125131	11601
RNA backbone	3398	623

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  $\geq 3$ , 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	9	
2	B	9	

## 2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 578 atoms, of which 207 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called DNA\_<sub>(5'-D(\*AP\*TP\*GP\*GP\*TP\*BGR\*CP\*TP\*C)-3')</sub><sub>-</sub>.

Mol	Chain	Residues	Atoms							Trace
1	A	9	Total	B	C	H	N	O	P	0
			289	1	88	107	32	53	8	

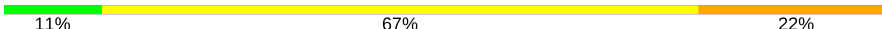
- Molecule 2 is a RNA chain called RNA\_<sub>(5'-R(\*GP\*AP\*GP\*CP\*AP\*CP\*CP\*AP\*U)-3')</sub><sub>-</sub>.

Mol	Chain	Residues	Atoms						Trace
2	B	9	Total	C	H	N	O	P	0
			289	86	100	36	59	8	

## 4 Residue-property plots


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(\*AP\*TP\*GP\*GP\*TP\*BGR\*CP\*TP\*C)-3')\_

Chain A: 

A1	T2	G3	G4	T5	<u>T6</u>	C7	T8	C9
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- Molecule 2: RNA\_(5'-R(\*GP\*AP\*GP\*CP\*AP\*CP\*CP\*AP\*U)-3')\_

Chain B: 

G10	A11	G12	C13	A14	C15	C16	A17	<u>U18</u>
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## 5 Refinement protocol and experimental data overview

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

Of the 10 calculated structures, 1 were deposited, based on the following criterion: *structure with lowest restraint violations*.

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

Software name	Classification	Version
AMBER	structure solution	9.0
AMBER	geometry optimization	9.0
AMBER	refinement	9.0
MARDIGRAS	refinement	5.21

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)	2lb4_cs.str
Number of chemical shift lists	1
Total number of shifts	172
Number of shifts mapped to atoms	172
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%

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

## 6 Model quality

### 6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BGR

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	1.70	0/177 (0.0%)	2.64	22/269 (8.2%)
2	B	1.57	0/211 (0.0%)	2.49	16/327 (4.9%)
All	All	1.63	0/388 (0.0%)	2.56	38/596 (6.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0	2
2	B	0	2
All	All	0	4

There are no bond-length outliers.

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	17	A	N1-C6-N6	-11.64	111.61	118.60
1	A	1	DA	N1-C6-N6	-10.89	112.06	118.60
2	B	17	A	C4-C5-C6	-9.06	112.47	117.00
2	B	11	A	C5-C6-N1	8.77	122.08	117.70
2	B	14	A	N1-C6-N6	-7.71	113.97	118.60
1	A	1	DA	C4-C5-C6	-7.59	113.20	117.00
2	B	18	U	O4'-C1'-N1	7.37	114.09	108.20
1	A	1	DA	O4'-C4'-C3'	7.05	110.23	106.00
1	A	8	DT	C6-C5-C7	-6.76	118.84	122.90
2	B	16	C	N3-C2-O2	-6.43	117.40	121.90
2	B	17	A	C6-C5-N7	6.42	136.79	132.30
1	A	1	DA	C5-C6-N1	6.30	120.85	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	DT	C4'-C3'-C2'	-6.28	97.45	103.10
1	A	7	DC	C3'-C2'-C1'	6.26	110.01	102.50
1	A	9	DC	N3-C2-O2	-6.12	117.61	121.90
1	A	5	DT	O4'-C1'-N1	6.11	112.28	108.00
2	B	10	G	C3'-C2'-C1'	6.06	106.35	101.50
2	B	14	A	C5-C6-N1	6.04	120.72	117.70
1	A	5	DT	C6-C5-C7	-6.02	119.29	122.90
1	A	2	DT	C6-C5-C7	-6.00	119.30	122.90
2	B	15	C	C5'-C4'-O4'	5.99	116.29	109.10
2	B	14	A	C4-C5-C6	-5.92	114.04	117.00
1	A	7	DC	N3-C2-O2	-5.84	117.81	121.90
1	A	1	DA	O4'-C1'-N9	5.77	112.04	108.00
1	A	7	DC	N1-C2-O2	5.75	122.35	118.90
1	A	4	DG	N1-C6-O6	-5.75	116.45	119.90
2	B	17	A	C5-C6-N1	5.62	120.51	117.70
1	A	7	DC	O4'-C1'-N1	5.42	111.80	108.00
1	A	1	DA	C6-C5-N7	5.38	136.07	132.30
1	A	7	DC	N3-C4-C5	5.33	124.03	121.90
2	B	13	C	N3-C2-O2	-5.32	118.17	121.90
1	A	5	DT	C3'-C2'-C1'	5.24	108.78	102.50
2	B	12	G	O4'-C1'-N9	5.18	112.35	108.20
1	A	2	DT	O4'-C4'-C3'	5.15	109.09	106.00
2	B	16	C	N1-C2-O2	5.13	121.98	118.90
2	B	17	A	C5-C6-N6	5.10	127.78	123.70
1	A	3	DG	N7-C8-N9	5.05	115.63	113.10
1	A	9	DC	N1-C2-O2	5.02	121.91	118.90

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	3	DG	Sidechain
2	B	18	U	Sidechain
2	B	17	A	Sidechain
1	A	4	DG	Sidechain

## 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	371	207	207	-

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](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	8/9 (89%)	0 (0%)	0 (0%)	0.60
All	All	8/9 (89%)	0 (0%)	0 (0%)	0.60

The overall RNA backbone suiteness is 0.59.

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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

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

### 7.1 Chemical shift list 1

File name: 2lb4\_cs.str

Chemical shift list name: *D2O*

#### 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	172
Number of shifts mapped to atoms	172
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 44%, i.e. 143 atoms were assigned a chemical shift out of a possible 327. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> 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	143/327 (44%)	109/191 (57%)	34/115 (30%)	0/21 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 44%, i.e. 143 atoms were assigned a chemical shift out of a possible 327. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
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	143/327 (44%)	109/191 (57%)	34/115 (30%)	0/21 (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 (D2O). RCI is only applicable to proteins.