



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2022 – 12:21 PM EDT

PDB ID : 5V1K  
Title : Structure of R-GNA dodecamer  
Authors : Pallan, P.S.; Egli, M.  
Deposited on : 2017-03-02  
Resolution : 1.18 Å(reported)

This is a Full wwPDB X-ray 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.28.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

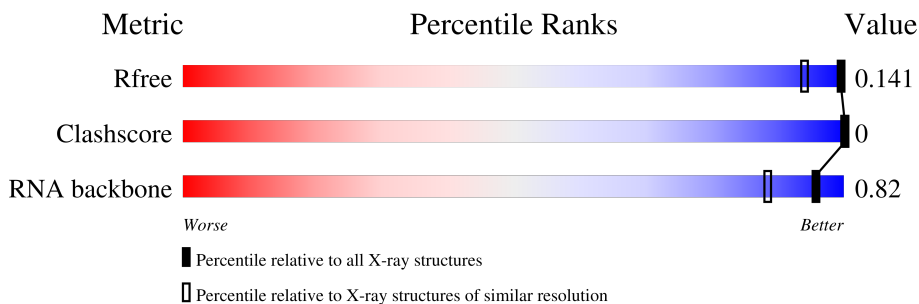
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.18 Å.

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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1123 (1.20-1.16)
Clashscore	141614	1182 (1.20-1.16)
RNA backbone	3102	1000 (2.34-0.62)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	12	 33% 67%
1	B	12	 42% 58%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 701 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called RNA (5'-R(\*CP\*GP\*CP\*GP\*AP\*AP\*(5BU)P\*(8RJ)P\*AP\*GP\*CP\*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	Br	C	N	O	P			
1	A	12	278	2	123	50	90	13	0	2	0
1	B	12	253	1	114	48	79	11	0	0	0

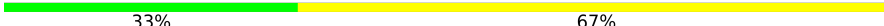
- Molecule 2 is water.

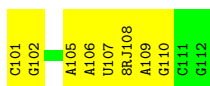
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	70	70	70	0	0
2	B	100	100	100	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

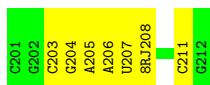
- Molecule 1: RNA (5'-R(\*CP\*GP\*CP\*GP\*AP\*AP\*(5BU)P\*(8RJ)P\*AP\*GP\*CP\*G)-3')

Chain A:  33% 67%



- Molecule 1: RNA (5'-R(\*CP\*GP\*CP\*GP\*AP\*AP\*(5BU)P\*(8RJ)P\*AP\*GP\*CP\*G)-3')

Chain B:  42% 58%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	23.68Å 27.68Å 29.05Å 73.00° 87.17° 66.58°	Depositor
Resolution (Å)	50.00 – 1.18 21.67 – 1.18	Depositor EDS
% Data completeness (in resolution range)	94.8 (50.00-1.18) 94.7 (21.67-1.18)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.33 (at 1.18Å)	Xtrriage
Refinement program	SHELXL	Depositor
R, $R_{free}$	(Not available) , (Not available) 0.148 , 0.141	Depositor DCC
$R_{free}$ test set	1576 reflections (7.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.1	Xtrriage
Anisotropy	0.027	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 73.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	701	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 8RJ, 5BU

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 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	1.68	4/240 (1.7%)	1.88	6/371 (1.6%)
1	B	1.48	4/240 (1.7%)	1.62	4/371 (1.1%)
All	All	1.58	8/480 (1.7%)	1.76	10/742 (1.3%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	105	A	C2'-O2'	9.34	1.53	1.41
1	A	109	A	P-OP1	-7.78	1.35	1.49
1	A	106	A	P-OP1	7.67	1.61	1.49
1	B	205	A	C2'-O2'	7.33	1.51	1.41
1	B	211	C	C2'-O2'	6.72	1.50	1.41
1	B	203	C	P-OP2	-5.75	1.39	1.49
1	B	206	A	C2'-O2'	5.16	1.48	1.41
1	A	102	G	P-OP2	5.09	1.57	1.49

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	G	C5-C6-O6	-7.29	124.23	128.60
1	A	106	A	N7-C8-N9	-6.39	110.60	113.80
1	B	204	G	N3-C2-N2	5.91	124.03	119.90
1	B	211	C	C4-C5-C6	5.74	120.27	117.40
1	A	110	G	N1-C6-O6	5.60	123.26	119.90
1	B	211	C	C5-C6-N1	-5.32	118.34	121.00
1	B	205	A	N7-C8-N9	-5.29	111.16	113.80
1	A	101	C	N3-C4-N4	5.23	121.66	118.00
1	A	106	A	N1-C2-N3	-5.20	126.70	129.30
1	A	106	A	C4-C5-C6	-5.12	114.44	117.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	278	0	130	0	0
1	B	253	0	121	0	0
2	A	70	0	0	0	0
2	B	100	0	0	0	0
All	All	701	0	251	0	0

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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	8/12 (66%)	0	0
1	B	9/12 (75%)	0	0
All	All	17/24 (70%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	8RJ	A	108[A]	1	12,17,18	2.11	2 (16%)	8,23,26	3.60	1 (12%)
1	5BU	A	107[A]	1	15,22,23	2.89	4 (26%)	17,32,35	4.17	4 (23%)
1	8RJ	B	208	1	12,17,18	2.08	2 (16%)	8,23,26	2.36	2 (25%)
1	8RJ	A	108[B]	1	12,17,18	2.08	2 (16%)	8,23,26	3.60	1 (12%)
1	5BU	B	207	1	15,22,23	2.46	3 (20%)	17,32,35	3.52	4 (23%)
1	5BU	A	107[B]	1	15,22,23	2.95	4 (26%)	17,32,35	3.77	4 (23%)

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
1	8RJ	A	108[A]	1	-	0/7/9/10	0/1/1/1
1	5BU	A	107[A]	1	-	0/5/25/26	0/2/2/2
1	8RJ	B	208	1	-	0/7/9/10	0/1/1/1
1	8RJ	A	108[B]	1	-	2/7/9/10	0/1/1/1
1	5BU	B	207	1	-	0/5/25/26	0/2/2/2
1	5BU	A	107[B]	1	-	0/5/25/26	0/2/2/2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	107[A]	5BU	BR-C5	-9.17	1.64	1.90
1	A	107[B]	5BU	BR-C5	-8.77	1.65	1.90
1	B	207	5BU	BR-C5	-6.66	1.71	1.90
1	A	108[A]	8RJ	C5M-C5	-5.52	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	108[B]	8RJ	C5M-C5	-5.52	1.40	1.51
1	B	208	8RJ	C5M-C5	-5.27	1.41	1.51
1	B	207	5BU	C5-C4	5.25	1.45	1.38
1	A	107[B]	5BU	C5-C4	4.57	1.44	1.38
1	A	107[A]	5BU	C5-C4	4.42	1.44	1.38
1	A	107[B]	5BU	O2'-C2'	4.01	1.52	1.43
1	B	208	8RJ	C4-N3	3.82	1.39	1.33
1	A	108[A]	8RJ	C4-N3	3.49	1.39	1.33
1	A	108[B]	8RJ	C4-N3	3.49	1.39	1.33
1	B	207	5BU	C4-N3	3.42	1.39	1.33
1	A	107[B]	5BU	C4-N3	3.35	1.38	1.33
1	A	107[A]	5BU	C4-N3	3.22	1.38	1.33
1	A	107[A]	5BU	O2'-C2'	2.71	1.49	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107[A]	5BU	C2-N3-C4	14.47	127.36	115.14
1	A	107[B]	5BU	C2-N3-C4	13.65	126.67	115.14
1	B	207	5BU	C2-N3-C4	12.15	125.40	115.14
1	A	108[A]	8RJ	C2-N3-C4	10.00	123.58	115.14
1	A	108[B]	8RJ	C2-N3-C4	10.00	123.58	115.14
1	A	107[A]	5BU	C5-C4-N3	-7.32	114.87	123.64
1	B	208	8RJ	C2-N3-C4	6.22	120.39	115.14
1	B	207	5BU	C5-C6-N1	5.86	127.55	119.97
1	A	107[B]	5BU	C5-C4-N3	-4.99	117.66	123.64
1	A	107[B]	5BU	C5-C6-N1	3.82	124.91	119.97
1	B	207	5BU	BR-C5-C6	3.43	125.13	117.31
1	A	107[A]	5BU	C5-C6-N1	2.89	123.71	119.97
1	A	107[A]	5BU	C6-N1-C1'	2.81	125.54	119.24
1	B	207	5BU	C5-C4-N3	-2.75	120.35	123.64
1	A	107[B]	5BU	BR-C5-C6	2.48	122.95	117.31
1	B	208	8RJ	C1G-C2G-C3G	-2.08	107.01	111.62

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	108[B]	8RJ	O2G-C2G-C3G-O5'
1	A	108[B]	8RJ	C1G-C2G-C3G-O5'

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.