



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:50 PM GMT

PDB ID : 5E36  
Title : Crystal structure of 2'-propargyl-modified DNA 8mer-duplex  
Authors : Sheng, J.; Gan, J.  
Deposited on : 2015-10-02  
Resolution : 1.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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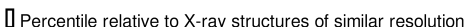
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

**i**

## X-RAY DIFFRACTION

A.

2479 (1 60-1 60)100%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 704 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 DNA chain called DNA (5'-D(\*GP\*(OMU)P\*GP\*TP\*(5JO)P\*CP\*AP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	8	Total 166	C 81	N 30	O 48	P 7	0	0	0
1	B	8	Total 166	C 81	N 30	O 48	P 7	0	0	0
1	C	8	Total 166	C 81	N 30	O 48	P 7	0	0	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	65	Total	O	0	0
			65	65		
3	B	68	Total	O	0	0
			68	68		
3	C	71	Total	O	0	0
			71	71		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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: DNA (5'-D(\*GP\*(OMU)P\*GP\*TP\*(5JO)P\*CP\*AP\*C)-3')

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: DNA (5'-D(\*GP\*(OMU)P\*GP\*TP\*(5JO)P\*CP\*AP\*C)-3')

Chain B:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: DNA (5'-D(\*GP\*(OMU)P\*GP\*TP\*(5JO)P\*CP\*AP\*C)-3')

Chain C:  100%

There are no outlier residues recorded for this chain.

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	32.03Å 55.53Å 75.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.76 – 1.60 27.75 – 1.59	Depositor EDS
% Data completeness (in resolution range)	98.6 (27.76-1.60) 98.6 (27.75-1.59)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.137 , 0.161 0.146 , 0.154	Depositor DCC
$R_{free}$ test set	486 reflections (5.62%)	DCC
Wilson B-factor (Å <sup>2</sup> )	8.2	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 42.8	EDS
Estimated twinning fraction	0.323 for H, K, L 0.383 for 1/2H+1/2K, 3/2H-1/2K, -L 0.293 for -1/2H+1/2K, 3/2H+1/2K, -L 0.480 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.487 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
Reported twinning fraction	0.323 for H, K, L 0.383 for 1/2H+1/2K, 3/2H-1/2K, -L 0.293 for -1/2H+1/2K, 3/2H+1/2K, -L	Depositor
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	1 of 9210 reflections (0.011%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	704	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.30% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, 5JO, OMU

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	0.30	0/133	0.74	0/201
1	B	0.29	0/133	0.59	0/201
1	C	0.30	0/133	0.64	0/201
All	All	0.30	0/399	0.66	0/603

There are no bond length outliers.

There are no bond angle outliers.

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	166	0	94	0	0
1	B	166	0	94	0	0
1	C	166	0	94	0	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	65	0	0	0	0
3	B	68	0	0	0	0
3	C	71	0	0	0	1
All	All	704	0	282	0	1

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.

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:161:HOH:O	3:C:161:HOH:O[3_554]	2.13	0.07

## 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](#)

There are no RNA molecules in this entry.

## 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	OMU	A	2	1	14,22,23	0.80	0	19,31,34	1.60	1 (5%)
1	5JO	A	5	1	20,27,28	0.98	1 (5%)	19,38,41	0.59	0
1	OMU	B	2	1	14,22,23	0.87	1 (7%)	19,31,34	1.80	1 (5%)
1	5JO	B	5	1	20,27,28	0.96	1 (5%)	19,38,41	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	OMU	C	2	1	14,22,23	0.80	0	19,31,34	1.63	1 (5%)
1	5JO	C	5	1	20,27,28	0.96	1 (5%)	19,38,41	0.69	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
1	OMU	A	2	1	-	0/5/27/28	0/2/2/2
1	5JO	A	5	1	-	0/6/29/30	0/3/3/3
1	OMU	B	2	1	-	0/5/27/28	0/2/2/2
1	5JO	B	5	1	-	0/6/29/30	0/3/3/3
1	OMU	C	2	1	-	0/5/27/28	0/2/2/2
1	5JO	C	5	1	-	0/6/29/30	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2	OMU	O4'-C1'	2.10	1.44	1.41
1	C	5	5JO	C7'-C8'	3.25	1.25	1.18
1	B	5	5JO	C7'-C8'	3.33	1.25	1.18
1	A	5	5JO	C7'-C8'	3.34	1.25	1.18

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2	OMU	C4-N3-C2	5.72	120.24	114.21
1	C	2	OMU	C4-N3-C2	6.13	120.67	114.21
1	B	2	OMU	C4-N3-C2	6.78	121.36	114.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.



## 5.6 Ligand geometry

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	6/8 (75%)	-0.56	0 100 100	9, 9, 10, 11	0
1	B	6/8 (75%)	-0.55	0 100 100	8, 9, 9, 11	0
1	C	6/8 (75%)	-0.50	0 100 100	9, 9, 9, 11	0
All	All	18/24 (75%)	-0.54	0 100 100	8, 9, 11, 11	0

There are no RSRZ outliers to report.

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	5JO	B	5	25/26	0.97	0.07	-	7,8,9,10	0
1	OMU	A	2	21/22	0.96	0.08	-	8,8,8,9	0
1	OMU	C	2	21/22	0.97	0.07	-	8,8,9,9	0
1	OMU	B	2	21/22	0.97	0.08	-	8,8,8,9	0
1	5JO	C	5	25/26	0.96	0.08	-	8,9,10,10	0
1	5JO	A	5	25/26	0.96	0.08	-	9,9,11,12	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	B	101	1/1	0.99	0.03	-	9,9,9,9	1
2	MG	A	101	1/1	0.99	0.12	-	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.