



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2026 – 12:19 PM EDT

PDB ID : 8F5C / pdb_00008f5c
Title : Mirror-image DNA containing 2'-OMe-L-dC modification
Authors : Zhang, W.; Dantsu, Y.
Deposited on : 2022-11-13
Resolution : 1.15 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

A user guide is available at

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

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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

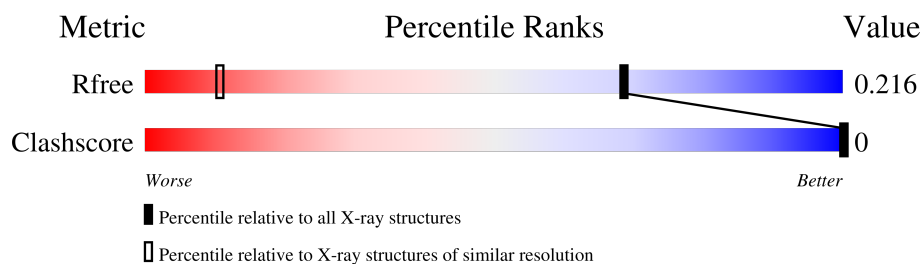
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

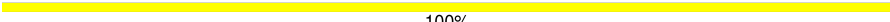
The reported resolution of this entry is 1.15 Å.

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}	180053	1380 (1.16-1.12)
Clashscore	190562	1393 (1.16-1.12)

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 ≥ 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	8	 100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 218 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(* (0DG))-R(P*(XE6))-D(P*(0DG)P*(0DT)P*(0DA)P*(0DC)P*(0DG)P*(0DC))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	8	Total	C	N	O	P	0	0	0
			163	78	31	47	7			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	53	Total	O	0	0
			53	53		

3 Residue-property plots

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 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 ($RSRZ > 2$). 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*(0DG))-R(P*(XE6))-D(P*(0DG)P*(0DT)P*(0DA)P*(0DC)P*(0DG)P*(0DC))-3')

Chain A:  100%

G1	XE62
G3	T4
A5	C6
G7	C8

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	41.90Å 41.90Å 23.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.71 – 1.15 20.71 – 1.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.71-1.15) 99.7 (20.71-1.15)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 1.15Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.193 , 0.204 0.197 , 0.216	Depositor DCC
R_{free} test set	367 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	18.1	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 81.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	218	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 0DA, 0DT, XE6, 0DG, MG, 0DC

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	163	0	79	0	0
2	A	2	0	0	0	0
3	A	53	0	0	0	0
All	All	218	0	79	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](#)

There are no RNA molecules in this entry.

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

8 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	0DA	A	5	1	20,23,24	1.96	5 (25%)	28,33,36	1.38	4 (14%)
1	0DC	A	6	1	17,20,21	1.12	0	23,28,31	0.97	1 (4%)
1	0DC	A	8	1	17,20,21	1.30	2 (11%)	23,28,31	1.01	1 (4%)
1	0DT	A	4	1	18,21,22	2.10	6 (33%)	25,30,33	2.38	7 (28%)
1	0DG	A	7	1	21,24,25	1.32	3 (14%)	30,35,38	0.88	1 (3%)
1	XE6	A	2	1	19,22,23	1.15	2 (10%)	25,31,34	1.14	2 (8%)
1	0DG	A	1	1	21,21,25	1.27	3 (14%)	31,31,38	0.80	1 (3%)
1	0DG	A	3	2,1	21,24,25	1.26	2 (9%)	30,35,38	1.17	3 (10%)

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	0DA	A	5	1	-	0/7/21/22	0/3/3/3
1	0DC	A	6	1	-	0/7/21/22	0/2/2/2
1	0DC	A	8	1	-	0/7/21/22	0/2/2/2
1	0DT	A	4	1	-	0/7/21/22	0/2/2/2
1	0DG	A	7	1	-	0/7/21/22	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	XE6	A	2	1	-	0/9/27/28	0/2/2/2
1	ODG	A	1	1	-	0/6/18/22	0/3/3/3
1	ODG	A	3	2,1	-	0/7/21/22	0/3/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	5	0DA	C1'-N9A	5.41	1.56	1.46
1	A	4	0DT	C5M-C5	-4.45	1.39	1.50
1	A	4	0DT	C2'-C1'	-3.63	1.42	1.52
1	A	4	0DT	C2-N1	-3.07	1.33	1.38
1	A	4	0DT	C2-N3	-3.07	1.32	1.38
1	A	5	0DA	C2'-C3'	-2.99	1.45	1.52
1	A	5	0DA	C2A-N1A	2.85	1.39	1.33
1	A	8	0DC	O3'-C3'	2.82	1.49	1.43
1	A	5	0DA	C5A-N7A	-2.78	1.34	1.39
1	A	7	ODG	C3'-C4'	-2.70	1.45	1.53
1	A	8	0DC	O4'-C4'	-2.64	1.39	1.45
1	A	3	ODG	C2-N2	-2.57	1.28	1.34
1	A	1	ODG	C3'-C4'	-2.46	1.46	1.53
1	A	7	ODG	C8-N9	-2.41	1.32	1.37
1	A	1	ODG	C2'-C1'	-2.41	1.45	1.52
1	A	4	0DT	C4-C5	-2.35	1.41	1.44
1	A	4	0DT	O2-C2	2.24	1.27	1.23
1	A	3	ODG	C8-N9	-2.23	1.32	1.37
1	A	5	0DA	C5A-C6A	-2.17	1.34	1.41
1	A	2	XE6	O4'-C1'	2.14	1.47	1.42
1	A	2	XE6	O3'-C3'	2.07	1.48	1.43
1	A	1	ODG	C5-N7	-2.06	1.34	1.39
1	A	7	ODG	O6-C6	2.02	1.27	1.23

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	0DT	C5M-C5-C4	6.85	126.10	118.78
1	A	4	0DT	C5-C4-N3	5.85	120.41	115.32
1	A	5	0DA	N1A-C2A-N3A	-3.80	122.83	128.58
1	A	4	0DT	C5M-C5-C6	-3.58	118.00	122.85
1	A	4	0DT	C4-N3-C2	-3.37	122.92	127.34
1	A	3	ODG	C2-N3-C4	2.86	117.22	112.30
1	A	2	XE6	C3'-C2'-C1'	-2.78	97.49	102.81
1	A	4	0DT	C6-C5-C4	-2.67	115.82	118.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	0DA	N3A-C4A-N9A	2.41	131.27	127.17
1	A	5	0DA	C5A-C4A-N3A	-2.38	123.44	126.72
1	A	4	0DT	N3-C2-N1	2.37	117.98	114.89
1	A	2	XE6	O4'-C4'-C3'	-2.35	100.49	105.15
1	A	3	0DG	N1-C2-N3	-2.27	119.17	123.32
1	A	1	0DG	C5'-C4'-C3'	2.26	120.46	114.82
1	A	3	0DG	C2'-C3'-C4'	-2.20	98.35	102.80
1	A	6	0DC	C3'-C2'-C1'	-2.18	97.26	102.60
1	A	7	0DG	C6-C5-N7	2.13	134.16	130.29
1	A	8	0DC	C2'-C1'-N1	-2.11	108.53	113.81
1	A	4	0DT	O4'-C1'-N1	2.04	111.48	107.86
1	A	5	0DA	C4A-N9A-C8A	2.02	107.86	105.74

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

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, 95th 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 ²)	Q<0.9
1	A	0/8	-	-	-	-

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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
1	ODC	A	8	19/20	0.94	0.08	14,19,24,32	0
1	ODT	A	4	20/21	0.95	0.08	14,20,24,25	0
1	ODA	A	5	21/22	0.95	0.07	13,15,25,31	0
1	ODG	A	3	22/23	0.95	0.07	14,16,21,24	0
1	ODC	A	6	19/20	0.96	0.07	13,15,19,20	0
1	ODG	A	7	22/23	0.96	0.07	13,14,20,26	0
1	ODG	A	1	19/23	0.96	0.06	14,15,18,19	0
1	XE6	A	2	21/22	0.97	0.06	14,17,20,20	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. The B-factors column lists the minimum,

median, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	102	1/1	0.87	0.11	22,22,22,22	1
2	MG	A	101	1/1	0.96	0.11	15,15,15,15	1

6.5 Other polymers [i](#)

There are no such residues in this entry.