

wwPDB X-ray Structure Validation Summary Report (i)

Oct 5, 2023 – 12:28 AM EDT

PDB ID	:	6VF7
Title	:	DNA Polymerase Mu, 8-oxodGTP:At Ground State Ternary Complex, 50 mM
		Mn2+~(15~min)
Authors	:	Jamsen, J.A.; Wilson, S.H.
Deposited on	:	2020-01-03
Resolution	:	1.87 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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\hbox{-}RAY\,DIFFRACTION$

The reported resolution of this entry is 1.87 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 3408 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 protein called DNA-directed DNA/RNA polymerase mu.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	326	Total 2642	C 1687	N 473	0 473	S 9	0	17	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	127	GLY	-	expression tag	UNP Q9NP87
А	128	SER	-	expression tag	UNP Q9NP87
А	129	ALA	-	expression tag	UNP Q9NP87
А	130	ALA	-	expression tag	UNP Q9NP87
А	131	ALA	-	expression tag	UNP Q9NP87
A	?	-	PRO	deletion	UNP Q9NP87
А	?	-	GLY	deletion	UNP Q9NP87
А	?	-	ALA	deletion	UNP Q9NP87
A	?	-	ALA	deletion	UNP Q9NP87
А	?	-	VAL	deletion	UNP Q9NP87
А	?	-	GLY	deletion	UNP Q9NP87
А	?	-	GLY	deletion	UNP Q9NP87
А	?	-	SER	deletion	UNP Q9NP87
А	?	-	THR	deletion	UNP Q9NP87
А	?	-	ARG	deletion	UNP Q9NP87
А	?	-	PRO	deletion	UNP Q9NP87
А	?	-	CYS	deletion	UNP Q9NP87
А	410	GLY	PRO	conflict	UNP Q9NP87

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is a DNA chain called DNA (5'-D(*CP*GP*GP*CP*AP*TP*AP*CP*G)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Т	9	Total 182	C 87	N 36	O 51	Р 8	0	0	0

• Molecule 3 is a DNA chain called DNA (5'-D(*CP*GP*TP*A)-3').



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	D	4	Total	С	Ν	0	Р	0	0	0
3	Г	4	79	39	15	22	3	0	0	0

• Molecule 4 is a DNA chain called DNA (5'-D(P*GP*CP*CP*G)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	D	4	Total 124	C 57	N 24	O 37	Р 6	0	2	0

• Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

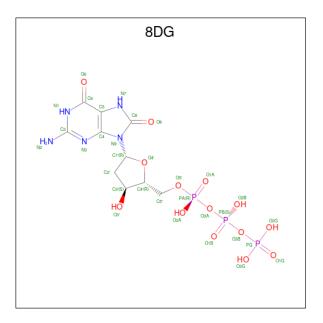
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	6	Total Mn 6 6	0	0
5	Т	1	Total Mn 1 1	0	0
5	D	1	Total Mn 1 1	0	0

• Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	А	1	Total 1	Na 1	0	0

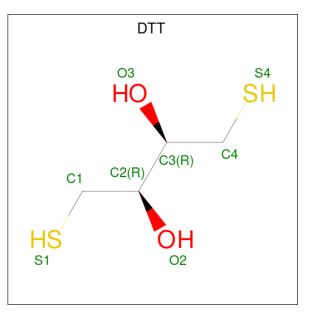
• Molecule 7 is 8-OXO-2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: 8DG) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	۸	1	Total	С	Ν	Ο	Р	0	0
1	A	1	32	10	5	14	3	0	0

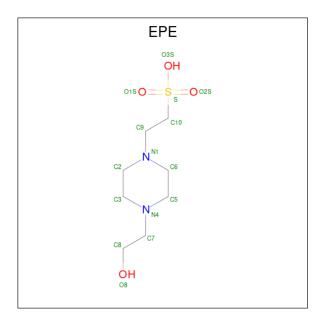
- Molecule 8 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $\rm C_4H_{10}O_2S_2).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	1	Total S 1 1	0	0

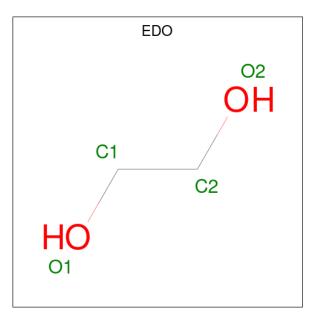
• Molecule 9 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).





Mol	Chain	Residues	A	Atoms				AltConf
9	А	1	Total 5	C 1	O 3	S 1	0	0

• Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
10	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
10	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0



• Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	262	Total O 267 267	0	11
11	Т	28	TotalO2828	0	0
11	Р	14	Total O 14 14	0	0
11	D	12	Total O 13 13	0	1

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	60.16Å 68.93Å 110.45Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	35.03 - 1.87	Depositor	
% Data completeness	99.5 (35.03-1.87)	Depositor	
(in resolution range)		-	
R _{merge}	0.09	Depositor	
R _{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$2.46 (at 1.87 \text{\AA})$	Xtriage	
Refinement program	PHENIX 1.15.2_3472	Depositor	
R, R_{free}	0.166 , 0.197	Depositor	
Wilson B-factor $(Å^2)$	25.5	Xtriage	
Anisotropy	0.351	Xtriage	
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3408	wwPDB-VP	
Average B, all atoms $(Å^2)$	30.0	wwPDB-VP	

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 9 are monoatomic and 1 is modelled with single atom - leaving 5 for Mogul analysis.

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 length (or angles).

Mol	Type	Chain	hain Res Li		Bo	ond leng	ths	Bond angles		
	Type	Chain	nes	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
10	EDO	А	513	-	3,3,3	0.41	0	2,2,2	0.34	0
10	EDO	А	511	-	3,3,3	0.40	0	2,2,2	0.31	0
9	EPE	А	510	-	4,4,15	1.34	1 (25%)	5,6,20	1.55	1 (20%)
10	EDO	А	512	-	3,3,3	0.60	0	2,2,2	0.36	0
7	8DG	А	508	5	30,34,34	0.76	0	43,54,54	1.64	3 (6%)

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
10	EDO	А	513	-	-	0/1/1/1	-
7	8DG	А	508	5	-	10/22/34/34	0/3/3/3
10	EDO	А	511	-	-	0/1/1/1	-
10	EDO	A	512	-	_	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
9	А	510	EPE	C10-S	2.54	1.86	1.74

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
7	А	508	8DG	O4'-C1'-N9	6.75	115.08	108.29
7	А	508	8DG	C2'-C1'-N9	-5.79	109.16	116.01
9	А	510	EPE	O2S-S-O1S	-3.26	109.23	118.02
7	А	508	8DG	C4-C5-N7	2.44	110.77	106.08

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

N	Лоl	Chain	Res	Type	Atoms
	7	А	508	8DG	C2'-C1'-N9-C4
	7	А	508	8DG	O4'-C1'-N9-C4

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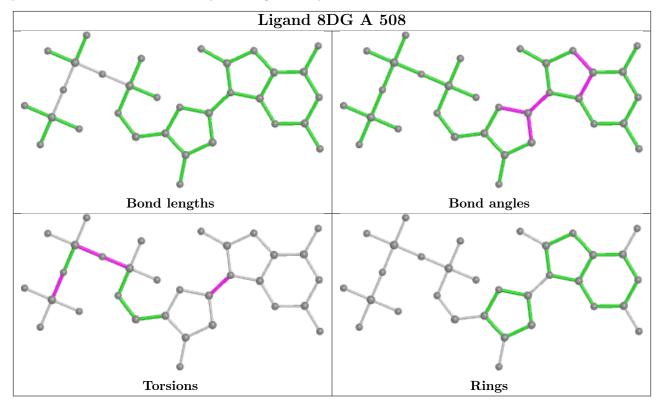
	Chain	-	10	Atoms
7	А	508	8DG	C2'-C1'-N9-C8
7	А	508	8DG	PA-O3A-PB-O1B
7	А	508	8DG	PA-O3A-PB-O2B

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There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

