

Full wwPDB X-ray Structure Validation Report (i)

Feb 25, 2024 – 05:43 AM EST

PDB ID : 5DB6

Title: Structure of human DNA polymerase beta Host-Guest complex with the

N7MG base paired with a dC

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Deposited on : 2015-08-20

Resolution : 2.83 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.orgA 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:

Mol Probity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

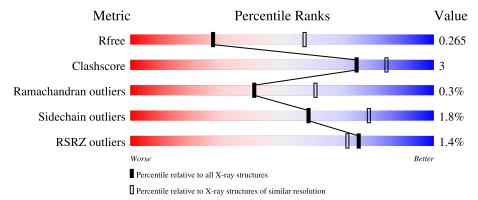
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.83 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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 <=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	335	89%	7% ••
2	Т	16	100%	
3	Р	10	90%	10%
4	D	5	80%	20%



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3290 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 polymerase beta.

\mathbf{Mol}	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
1	A	327	Total 2593	C 1642	N 454	O 488	S 9	0	0	0

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

Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
2	Т	16	Total	С	N	О	Р	0	0	0
	1	10	321	153	60	93	15		0	

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

Mol	Chain	Residues		A	tor	ns			ZeroOcc	AltConf	Trace
3	Р	10	Total		F			Р	0	0	0
	-	10	207	99	1	40	58	9			

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

Mol	Chain	Residues		\mathbf{At}	oms			ZeroOcc	AltConf	Trace
1	D	5	Total	С	N	О	Р	0	0	0
T	D	0	106	49	20	32	5			U

• Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Na 2 2	0	0

• Molecule 6 is water.



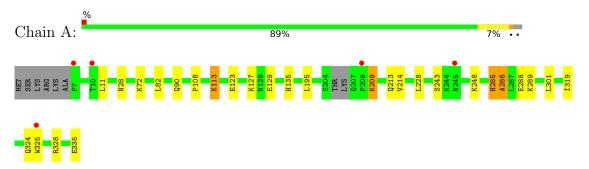
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	50	Total O 50 50	0	0
6	Т	4	Total O 4 4	0	0
6	Р	5	Total O 5 5	0	0
6	D	2	Total O 2 2	0	0



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 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 2: DNA (5'-D(*CP*CP*GP*AP*CP*GP*TP*CP*GP*CP*AP*TP*CP*AP*GP*C)-3')

Chain T:

There are no outlier residues recorded for this chain.

• Molecule 3: DNA (5'-D(*GP*CP*TP*(FMG)P*AP*TP*GP*CP*GP*A)-3')

Chain P: 90% 10%



• Molecule 4: DNA (5'-D(P*GP*TP*CP*GP*G)-3')

Chain D: 80% 20%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	54.14Å 78.83Å 54.76Å	Donositon
a, b, c, α , β , γ	90.00° 105.92° 90.00°	Depositor
Resolution (Å)	19.71 - 2.83	Depositor
Resolution (A)	19.71 - 2.83	EDS
% Data completeness	94.3 (19.71-2.83)	Depositor
(in resolution range)	93.8 (19.71-2.83)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.10 (at 2.83Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.185 , 0.266	Depositor
10, 10 free	0.188 , 0.265	DCC
R_{free} test set	507 reflections $(4.81%)$	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31 , 29.2	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.041 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3290	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.06% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ 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.

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: NA, FMG

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).

Mal	Chain	Bo	nd lengths	Bond angles		
Mol	Chain	RMSZ		RMSZ	# Z > 5	
1	A	0.27	0/2642	0.47	$1/3552 \ (0.0\%)$	
2	Т	0.47	0/359	0.80	0/551	
3	Р	0.52	0/204	0.88	0/311	
4	D	1.08	1/118 (0.8%)	0.88	0/179	
All	All	0.37	1/3323 (0.0%)	0.57	1/4593 (0.0%)	

All (1) bond length outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
4	D	1	DG	OP3-P	-10.55	1.48	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	285	HIS	C-N-CA	6.42	137.75	121.70

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	2593	0	2595	18	0
2	Т	321	0	180	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Р	207	0	116	0	0
4	D	106	0	57	0	0
5	A	2	0	0	0	0
6	A	50	0	0	0	0
6	D	2	0	0	0	0
6	Р	5	0	0	0	0
6	Т	4	0	0	0	0
All	All	3290	0	2948	18	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 3.

All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	Clash overlap (Å)
1:A:325:TRP:HH2	1:A:328:ARG:HD3	1.22	1.04
1:A:325:TRP:CH2	1:A:328:ARG:HD3	2.09	0.87
1:A:328:ARG:NH2	1:A:335:GLU:OXT	2.20	0.72
1:A:285:HIS:HB3	1:A:286:ALA:HB2	1.72	0.71
1:A:285:HIS:O	1:A:288:GLU:HB3	2.05	0.57
1:A:72:LYS:HD3	1:A:82:LEU:HD21	1.87	0.55
1:A:28:ASN:HA	1:A:108:PRO:HB3	1.90	0.53
1:A:195:LEU:HD21	1:A:214:VAL:HG21	1.97	0.47
1:A:135:HIS:CD2	1:A:228:LEU:HD22	2.50	0.46
1:A:113:LYS:H	1:A:113:LYS:HD2	1.82	0.45
1:A:123:GLU:O	1:A:127:LYS:HG3	2.17	0.44
1:A:113:LYS:HD2	1:A:113:LYS:N	2.34	0.43
1:A:90:GLN:O	1:A:90:GLN:HG2	2.19	0.42
1:A:248:LYS:HE2	1:A:248:LYS:HB3	1.86	0.41
1:A:209:LYS:O	1:A:213:GLN:HG3	2.21	0.41
1:A:319:ILE:H	1:A:319:ILE:HG13	1.73	0.41
1:A:11:LEU:HD23	1:A:11:LEU:HA	1.92	0.40
1:A:289:LYS:HD2	1:A:324:GLN:NE2	2.37	0.40

There are no symmetry-related clashes.



5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	323/335~(96%)	310 (96%)	12 (4%)	1 (0%)	41 61	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	286	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Analysed Rotameric		Percentiles	
1	A	$280/295 \ (95\%)$	275 (98%)	5 (2%)	59 78	

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	LYS
1	A	129	GLU
1	A	209	LYS
1	A	243	SER
1	A	301	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	135	HIS
1	A	324	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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).

Mal	Tuno	Type Chain	Dec	Tiple	Bond length			Bond angles		
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	FMG	Р	4	3,2	20,26,27	1.30	2 (10%)	17,39,42	1.14	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
3	FMG	Р	4	3,2	-	0/3/25/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
3	P	4	FMG	C5-C4	3.57	1.46	1.39
3	Р	4	FMG	C6-N1	-2.12	1.34	1.37

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.

5.5 Carbohydrates (i)

There are no monosaccharides 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 (i)

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^{th} 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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	327/335~(97%)	-0.36	5 (1%) 73 70	8, 18, 54, 75	0
2	Т	16/16 (100%)	-0.46	0 100 100	13, 28, 36, 37	0
3	Р	9/10 (90%)	-0.46	0 100 100	12, 20, 31, 32	0
4	D	5/5 (100%)	-0.77	0 100 100	9, 10, 17, 22	0
All	All	357/366 (97%)	-0.37	5 (1%) 75 71	8, 18, 53, 75	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	325	TRP	4.9
1	A	7	PRO	4.4
1	A	245	ASN	3.8
1	A	10	THR	2.8
1	A	208	PRO	2.6

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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	FMG	Р	4	24/25	0.94	0.14	17,28,37,38	0

6.3 Carbohydrates (i)

There are no monosaccharides 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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	NA	A	402	1/1	0.79	0.18	19,19,19,19	0
5	NA	A	401	1/1	0.91	0.14	13,13,13,13	0

6.5 Other polymers (i)

There are no such residues in this entry.

