



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:53 AM GMT

PDB ID : 3NGD
Title : Structural Basis for Proficient Incorporation of dTTP Opposite O6-methylguanine by Human DNA Polymerase Iota
Authors : Pence, M.G.
Deposited on : 2010-06-11
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

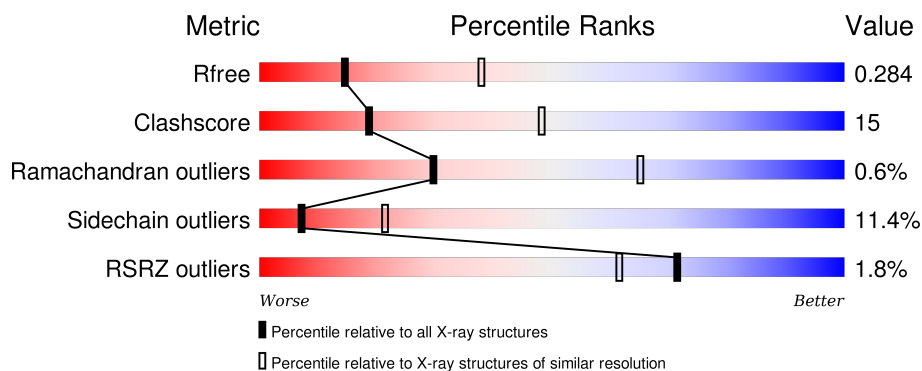
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	C	18	
1	D	18	
2	A	420	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DCP	A	875	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3299 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.

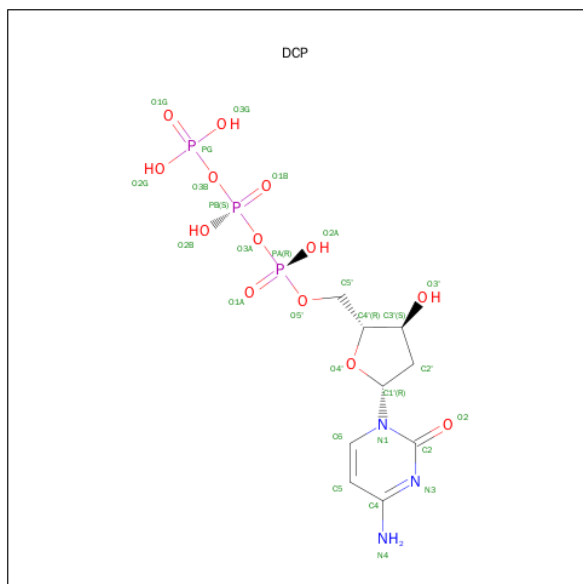
- Molecule 1 is a DNA chain called 5'-D(*TP*CP*TP*(6OG)P*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*(DOC))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	7	Total	C	N	O	P	0	0	0
			142	67	29	39	7			
1	D	8	Total	C	N	O	P	0	0	0
			167	79	30	50	8			

- Molecule 2 is a protein called DNA polymerase iota.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	370	Total	C	N	O	S	0	0	0
			2898	1826	504	547	21			

- Molecule 3 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C₉H₁₆N₃O₁₃P₃).

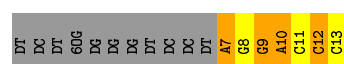


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	4	Total	O	0	0
			4	4		
4	D	8	Total	O	0	0
			8	8		
4	A	52	Total	O	0	0
			52	52		

- Molecule 1: 5'-D(*TP*CP*TP*(6OG)P*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*(DOC))-3'



DT
DC
DT
G840
G841
G842
G843
T844
C845
C846
T847
DA
DG
DG
DA
DC
DC
DOC

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	98.00 Å 98.00 Å 202.55 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	80.00 – 2.80 39.14 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.9 (80.00-2.80) 96.9 (39.14-2.80)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.215 , 0.284 0.222 , 0.284	Depositor DCC
R_{free} test set	704 reflections (5.14%)	DCC
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 14407 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3299	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DOC, 6OG, DCP

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	C	0.97	0/139	2.25	10/212 (4.7%)
1	D	1.21	0/160	2.15	9/245 (3.7%)
2	A	0.71	1/2936 (0.0%)	0.84	4/3957 (0.1%)
All	All	0.76	1/3235 (0.0%)	1.06	23/4414 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	311	CYS	CB-SG	-5.71	1.72	1.81

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	11	DC	O4'-C4'-C3'	-11.78	98.93	106.00
1	D	844	DT	O4'-C4'-C3'	-9.44	100.34	106.00
1	C	8	DG	O4'-C1'-N9	8.94	114.25	108.00
1	D	844	DT	C6-C5-C7	-8.05	118.07	122.90
2	A	379	VAL	CB-CA-C	-7.96	96.27	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	C	142	0	78	4	1
1	D	167	0	93	4	1
2	A	2898	0	2963	91	0
3	A	28	0	12	6	0
4	A	52	0	0	1	0
4	C	4	0	0	0	0
4	D	8	0	0	0	0
All	All	3299	0	3146	98	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 15.

The worst 5 of 98 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:309:LYS:HD2	2:A:309:LYS:O	1.41	1.21
2:A:310:LYS:HG3	2:A:349:TYR:CE1	1.80	1.17
2:A:310:LYS:CG	2:A:349:TYR:CE1	2.41	1.03
2:A:349:TYR:HD2	2:A:349:TYR:N	1.56	0.98
2:A:349:TYR:N	2:A:349:TYR:CD2	2.29	0.95

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)
1:C:7:DA:P	1:D:847:DT:O3'[10_445]	1.91	0.29

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
2	A	362/420 (86%)	331 (91%)	29 (8%)	2 (1%)	30 65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	379	VAL
2	A	52	ASP

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	Rotameric	Outliers	Percentiles
2	A	332/376 (88%)	294 (89%)	38 (11%)	7 21

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	229	LEU
2	A	272	GLU
2	A	385	ASP
2	A	248	LYS
2	A	276	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	202	ASN
2	A	393	ASN
2	A	262	GLN
2	A	178	GLN
2	A	279	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 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	DOC	C	13	1	11,19,20	1.59	2 (18%)	14,26,29	1.41	2 (14%)
1	6OG	D	840	1	16,25,26	1.01	0	21,36,39	1.85	6 (28%)

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	DOC	C	13	1	-	0/3/18/19	0/2/2/2
1	6OG	D	840	1	-	0/5/23/24	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	13	DOC	C4-N3	2.26	1.39	1.35
1	C	13	DOC	C6-N1	4.09	1.41	1.35

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	840	6OG	N3-C2-N1	-3.47	122.15	127.44
1	D	840	6OG	C-O6-C6	-3.28	113.86	117.26
1	D	840	6OG	C5-C6-N1	-2.71	119.02	123.81
1	C	13	DOC	O4'-C4'-C5'	-2.30	106.15	109.54
1	D	840	6OG	O4'-C1'-C2'	-2.10	102.09	106.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	13	DOC	3	0
1	D	840	6OG	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	DCP	A	875	-	21,29,29	1.93	5 (23%)	33,45,45	1.76	8 (24%)

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	DCP	A	875	-	-	0/18/34/34	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	875	DCP	PG-O2G	2.28	1.62	1.54
3	A	875	DCP	O4'-C1'	2.33	1.47	1.42
3	A	875	DCP	PA-O5'	3.32	1.74	1.59
3	A	875	DCP	C6-N1	3.76	1.41	1.35
3	A	875	DCP	C4-N3	5.13	1.45	1.35

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	875	DCP	PB-O3B-PG	-2.96	122.74	132.67
3	A	875	DCP	C5-C4-N3	-2.72	118.36	121.80
3	A	875	DCP	C5-C4-N4	-2.70	117.17	121.31
3	A	875	DCP	C6-N1-C2	-2.26	117.62	121.28
3	A	875	DCP	PB-O3A-PA	-2.11	126.81	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	875	DCP	6	0

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, 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	C	6/18 (33%)	-0.47	0	100	100	28, 43, 47, 52	0
1	D	7/18 (38%)	-0.44	0	100	100	26, 31, 38, 40	0
2	A	370/420 (88%)	-0.15	7 (1%)	70	59	17, 43, 89, 136	0
All	All	383/456 (83%)	-0.16	7 (1%)	71	61	17, 43, 88, 136	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	351	SER	4.9
2	A	348	ARG	3.2
2	A	350	SER	3.0
2	A	333	CYS	2.9
2	A	349	TYR	2.7

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, 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	LLDF	B-factors(Å ²)	Q<0.9
1	6OG	D	840	23/24	0.94	0.15	-	25,39,48,50	0
1	DOC	C	13	18/19	0.97	0.11	-	8,12,14,15	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	DCP	A	875	28/28	0.84	0.28	5.31	42,50,56,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.