



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 02:13 AM BST

PDB ID : 6CTJ
Title : Ternary complex crystal structure of DNA polymerase Beta with a dideoxy terminated primer with CHCH3, beta, gamma dTTP analogue
Authors : Batra, V.K.; Wilson, S.H.
Deposited on : 2018-03-23
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	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)	:	2.13.1

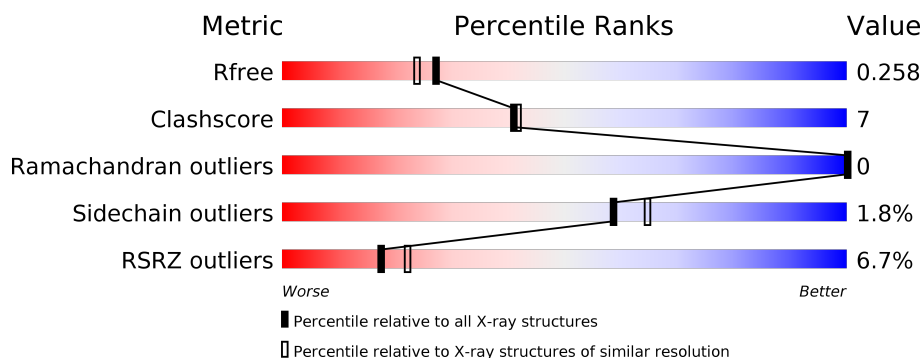
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 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	T	16	<div> <div style="width: 81%; background-color: green;"></div> <div style="width: 19%; background-color: yellow;"></div> </div> <div>81% 19%</div>
2	P	10	<div> <div style="width: 50%; background-color: green;"></div> <div style="width: 40%; background-color: yellow;"></div> <div style="width: 10%; background-color: orange;"></div> </div> <div>50% 40% 10%</div>
3	D	5	<div> <div style="width: 80%; background-color: green;"></div> <div style="width: 20%; background-color: orange;"></div> </div> <div>80% 20%</div>
4	A	335	<div> <div style="width: 7%; background-color: red;"></div> <div style="width: 81%; background-color: green;"></div> <div style="width: 15%; background-color: yellow;"></div> <div style="width: 3%; background-color: grey;"></div> </div> <div>7% 81% 15% ..</div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 3486 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(*CP*CP*GP*AP*CP*AP*GP*CP*GP*CP*AP*TP*CP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	16	Total	C	N	O	P	0	0	0
			322	153	63	91	15			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	10	Total	C	N	O	P	0	0	0
			202	97	38	58	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	5	Total	C	N	O	P	0	0	0
			106	49	20	32	5			

- Molecule 4 is a protein called DNA polymerase beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	326	Total	C	N	O	S	0	1	0
			2611	1649	456	497	9			

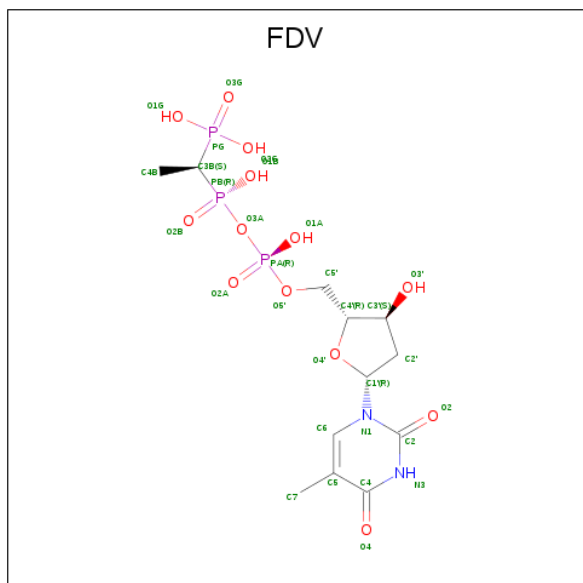
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	LEU	ALA	conflict	UNP P06746

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	P	1	Total Na 1 1	0	0
5	A	1	Total Na 1 1	0	0

- Molecule 6 is 5'-O-[(R)-hydroxy({(R)-hydroxy[(1S)-1-phosphonoethyl]phosphoryl}oxy)phosphoryl]thymidine (three-letter code: FDV) (formula: C₁₂H₂₁N₂O₁₃P₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	T	33	Total 33	O 33	0	0
9	P	13	Total 13	O 13	0	0
9	D	9	Total 9	O 9	0	0
9	A	154	Total 154	O 154	0	0

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

Diagram illustrating a sequence of nodes: C1, C2, G3, G7, and C16. The nodes are arranged in a sequence, with C1, C2, and G3 grouped together in a blue box, G7 in a yellow box, and C16 in a blue box. Arrows indicate a flow from C1 to C2 to G3 to G7 to C16.

A diagram showing a horizontal connection between two nodes, G1 and G5. G1 is represented by an orange rectangle on the left, and G5 is represented by a green rectangle on the right. A red T-bar symbol connects the two nodes, indicating an inhibitory relationship.

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.47Å 76.95Å 55.01Å 90.00° 103.88° 90.00°	Depositor
Resolution (Å)	23.12 – 2.10 23.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.5 (23.12-2.10) 90.1 (23.12-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.09Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.191 , 0.257 0.192 , 0.258	Depositor DCC
R_{free} test set	2000 reflections (8.82%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3486	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% 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: NA, MG, FDV, DOC, CL

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	T	0.89	0/361	0.98	1/554 (0.2%)
2	P	0.83	0/206	0.95	0/317
3	D	1.28	1/118 (0.8%)	0.85	0/179
4	A	0.41	0/2663	0.55	0/3579
All	All	0.57	1/3348 (0.0%)	0.66	1/4629 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	DG	OP3-P	-10.51	1.48	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	7	DG	C1'-O4'-C4'	-5.20	104.90	110.10

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	T	322	0	179	2	0
2	P	202	0	114	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	106	0	57	1	0
4	A	2611	0	2619	38	0
5	A	1	0	0	0	0
5	P	1	0	0	0	0
6	A	30	0	0	0	0
7	A	1	0	0	0	0
8	A	3	0	0	1	0
9	A	154	0	0	9	0
9	D	9	0	0	1	0
9	P	13	0	0	2	0
9	T	33	0	0	0	0
All	All	3486	0	2969	44	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 7.

All (44) 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)
4:A:157:GLN:NE2	9:A:501:HOH:O	1.94	0.99
4:A:275:SER:OG	4:A:335:GLU:OXT	2.02	0.78
4:A:147:GLU:OE2	9:A:502:HOH:O	2.03	0.76
9:D:105:HOH:O	8:A:405:CL:CL	2.44	0.72
4:A:208:PRO:O	4:A:209:LYS:HB3	1.92	0.68
2:P:7:DG:OP2	9:P:201:HOH:O	2.11	0.68
4:A:212:HIS:NE2	4:A:216:GLU:OE2	2.28	0.67
4:A:329:GLU:OE1	9:A:503:HOH:O	2.13	0.66
4:A:197:HIS:CD2	4:A:198:PRO:HD2	2.32	0.65
1:T:2:DC:H2"	1:T:3:DG:C8	2.33	0.64
4:A:148:LYS:O	9:A:504:HOH:O	2.15	0.63
4:A:40:ARG:HG2	4:A:277:ILE:HD11	1.81	0.62
4:A:127:LYS:NZ	9:A:508:HOH:O	2.28	0.61
4:A:16:THR:HG21	9:A:540:HOH:O	2.02	0.60
4:A:328:ARG:NH2	9:A:513:HOH:O	2.35	0.59
4:A:277:ILE:HB	4:A:335:GLU:OXT	2.04	0.58
4:A:244:LYS:HE3	4:A:247:GLU:OE1	2.05	0.57
4:A:159:GLN:HG3	4:A:177:VAL:HG21	1.86	0.56
4:A:13:GLY:HA2	4:A:16:THR:HG22	1.88	0.55
4:A:199:SER:HA	4:A:206:LYS:HD2	1.88	0.54
4:A:49:TYR:CE2	4:A:51:HIS:HB3	2.44	0.53
4:A:328:ARG:NH1	4:A:335:GLU:OE2	2.34	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:2:DC:H2''	1:T:3:DG:N7	2.22	0.53
3:D:1:DG:OP1	4:A:68:LYS:HD3	2.11	0.51
4:A:226:ASP:HB2	4:A:238:VAL:HB	1.95	0.49
4:A:202:SER:N	4:A:263:ASP:OD2	2.34	0.49
4:A:207:GLN:O	4:A:210:LEU:HG	2.13	0.48
2:P:9:DG:H2''	2:P:10:DOC:O5'	2.13	0.48
4:A:200:PHE:CD1	4:A:205:THR:HB	2.49	0.47
4:A:31:GLN:OE1	4:A:112:ARG:NH2	2.42	0.46
4:A:254:ARG:NH2	9:A:520:HOH:O	2.47	0.46
4:A:200:PHE:HD1	4:A:205:THR:HB	1.80	0.46
4:A:103:VAL:HB	4:A:106:ILE:HD12	1.98	0.45
4:A:266:TYR:HA	4:A:269:VAL:HG12	1.97	0.45
4:A:301:LEU:HD12	4:A:301:LEU:HA	1.71	0.44
4:A:49:TYR:HA	4:A:50:PRO:HD3	1.80	0.44
4:A:192:ASP:HB3	4:A:272:PHE:CZ	2.53	0.43
4:A:195:LEU:HD21	4:A:214:VAL:HG21	2.01	0.42
2:P:2:DC:H2'	2:P:3:DT:H71	2.02	0.42
4:A:230:LYS:HD3	4:A:235:PHE:HD1	1.85	0.42
4:A:311:LEU:HD13	4:A:322:TYR:CE1	2.55	0.41
4:A:148:LYS:NZ	9:A:516:HOH:O	2.38	0.41
4:A:274:GLY:HA3	4:A:275:SER:HA	1.87	0.40
9:P:210:HOH:O	4:A:110:ALA:HB2	2.20	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	
4	A	325/335 (97%)	317 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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
4	A	286 / 296 (97%)	281 (98%)	5 (2%)	60 67

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

Mol	Chain	Res	Type
4	A	204	SER
4	A	206	LYS
4	A	209	LYS
4	A	263	ASP
4	A	272	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	197	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DOC	P	10	1,2	14,19,20	0.80	0	13,26,29	1.11	1 (7%)

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
2	DOC	P	10	1,2	-	1/4/18/19	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	10	DOC	C2-N3-C4	3.44	119.83	116.34

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	10	DOC	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	10	DOC	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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 lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	FDV	A	401	7	25,31,31	3.31	10 (40%)	30,49,49	1.54	2 (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
6	FDV	A	401	7	-	10/22/40/40	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	401	FDV	C2'-C3'	-9.13	1.28	1.52
6	A	401	FDV	O4'-C4'	-7.70	1.27	1.45
6	A	401	FDV	O4'-C1'	6.04	1.55	1.42
6	A	401	FDV	C1'-N1	-4.97	1.34	1.49
6	A	401	FDV	C3'-C4'	4.10	1.64	1.53
6	A	401	FDV	PB-O3A	4.08	1.62	1.58
6	A	401	FDV	C2-N3	-2.39	1.33	1.38
6	A	401	FDV	O3'-C3'	2.39	1.48	1.43
6	A	401	FDV	C7-C5	2.36	1.55	1.51
6	A	401	FDV	PG-O1G	-2.26	1.51	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	401	FDV	C4-N3-C2	5.94	120.16	115.14
6	A	401	FDV	O3A-PB-C3B	2.95	112.76	103.85

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	FDV	PA-O3A-PB-O1B
6	A	401	FDV	C4B-C3B-PG-O1G

Continued on next page...

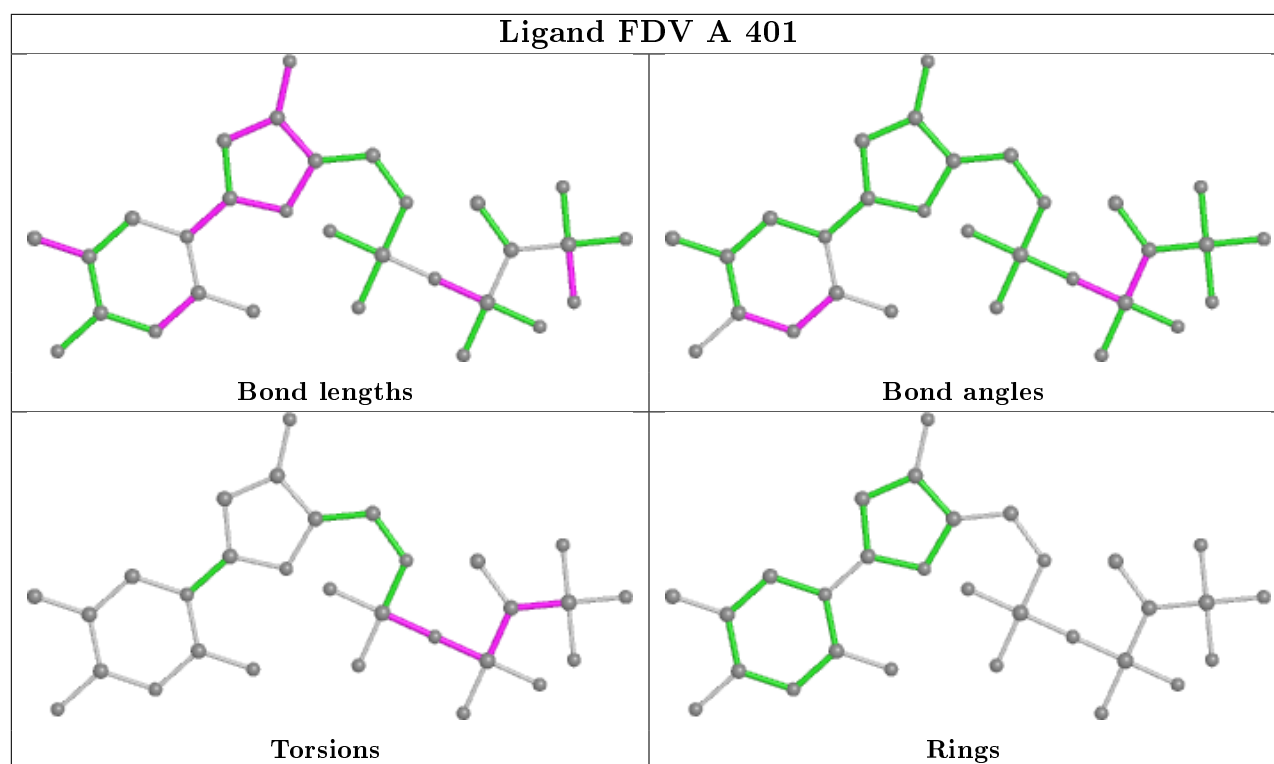
Continued from previous page...

Mol	Chain	Res	Type	Atoms
6	A	401	FDV	PB-C3B-PG-O3G
6	A	401	FDV	C4B-C3B-PG-O3G
6	A	401	FDV	PB-C3B-PG-O1G
6	A	401	FDV	PB-C3B-PG-O2G
6	A	401	FDV	PG-C3B-PB-O2B
6	A	401	FDV	C4B-C3B-PG-O2G
6	A	401	FDV	PB-O3A-PA-O1A
6	A	401	FDV	PG-C3B-PB-O1B

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 than 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.



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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	T	16/16 (100%)	-0.31	0 100 100	29, 37, 48, 51	0
2	P	9/10 (90%)	-0.26	0 100 100	24, 33, 43, 44	0
3	D	5/5 (100%)	-0.17	0 100 100	35, 35, 46, 47	0
4	A	326/335 (97%)	0.39	24 (7%) 14 18	22, 35, 61, 90	0
All	All	356/366 (97%)	0.34	24 (6%) 17 22	22, 35, 61, 90	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	206	LYS	10.7
4	A	207	GLN	10.7
4	A	303	VAL	6.0
4	A	208	PRO	5.0
4	A	200	PHE	4.8
4	A	199	SER	4.4
4	A	205	THR	3.9
4	A	305	GLY	3.9
4	A	203	GLU	3.6
4	A	304	THR	3.3
4	A	193	VAL	3.3
4	A	247	GLU	3.1
4	A	10	THR	2.8
4	A	197	HIS	2.6
4	A	302	GLY	2.6
4	A	306	VAL	2.6
4	A	220	LYS	2.6
4	A	257	ILE	2.4
4	A	244	LYS	2.3
4	A	301	LEU	2.3
4	A	246	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	A	204	SER	2.1
4	A	194	LEU	2.1
4	A	293	ILE	2.0

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
2	DOC	P	10	18/19	0.96	0.14	25,28,32,32	0

6.3 Carbohydrates [i](#)

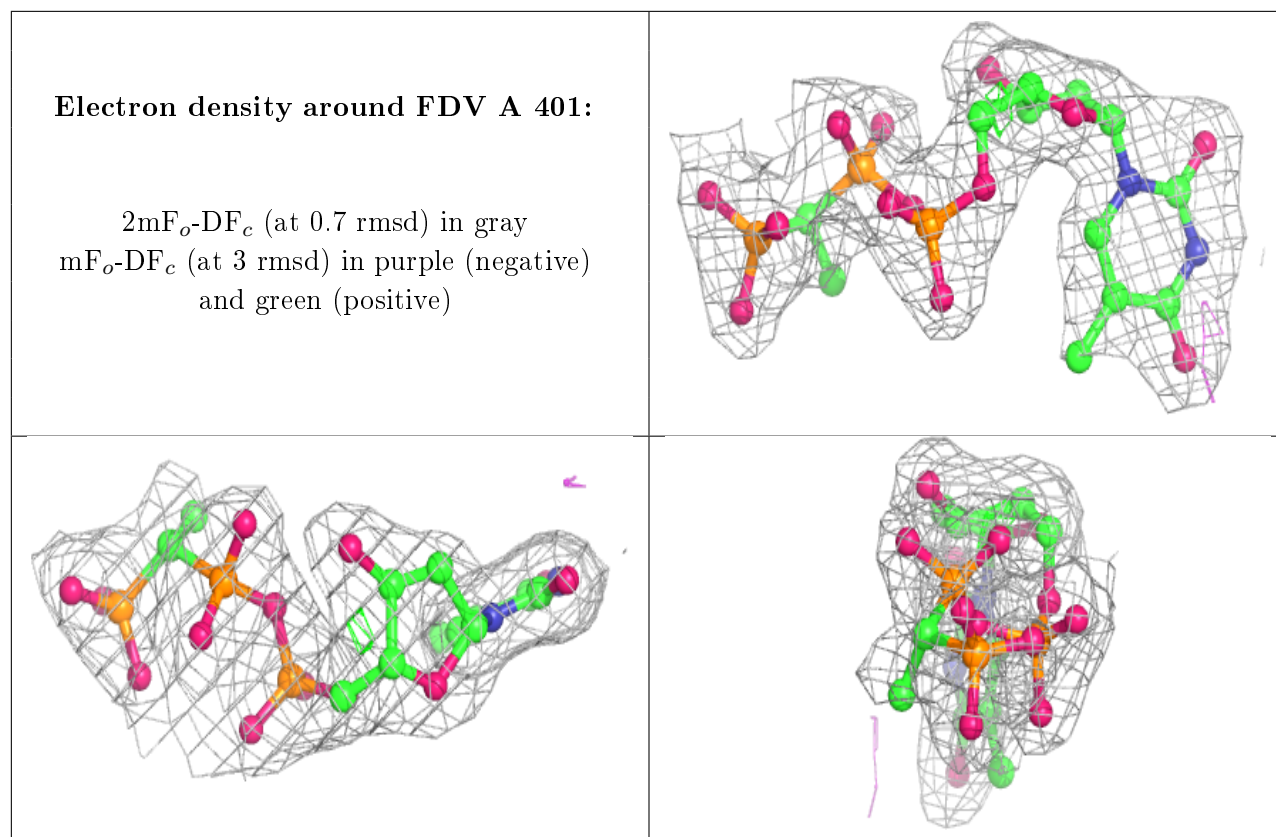
There are no monosaccharides in this entry.

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, 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
7	MG	A	402	1/1	0.82	0.07	28,28,28,28	0
5	NA	A	406	1/1	0.89	0.17	56,56,56,56	0
8	CL	A	404	1/1	0.92	0.09	50,50,50,50	0
5	NA	P	101	1/1	0.95	0.10	34,34,34,34	0
6	FDV	A	401	30/30	0.96	0.11	24,28,35,36	1
8	CL	A	405	1/1	0.96	0.14	42,42,42,42	0
8	CL	A	403	1/1	0.97	0.05	46,46,46,46	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.