



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2021 – 05:43 PM EDT

PDB ID : 3HWT
Title : Ternary complex of DNA polymerase lambda bound to a two nucleotide gapped DNA substrate with a scrunched dA
Authors : Garcia-Diaz, M.; Bebenek, K.; Larrea, A.A.; Pedersen, L.C.; Kunkel, T.A.
Deposited on : 2009-06-18
Resolution : 1.95 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 : 2.23.2
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) : 2.23.2

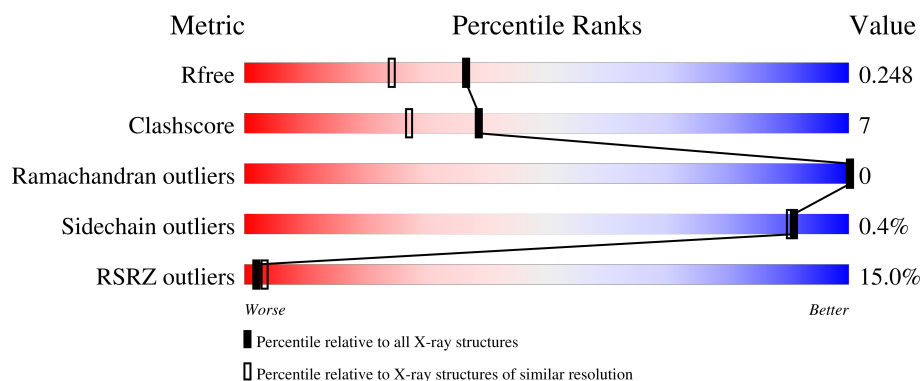
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	335	<div> <div>15%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>5%</div> </div> </div>
2	T	12	<div> <div>83%</div> <div>8%</div> <div>8%</div> </div>
3	P	6	<div> <div>67%</div> <div>17%</div> <div>17%</div> </div>
4	D	4	<div> <div>75%</div> <div>25%</div> </div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 3241 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 lambda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	3	0
			2410	1515	439	445	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	expression tag	UNP Q9UGP5
A	543	ALA	CYS	engineered mutation	UNP Q9UGP5

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	12	Total	C	N	O	P	0	0	0
			244	117	48	68	11			

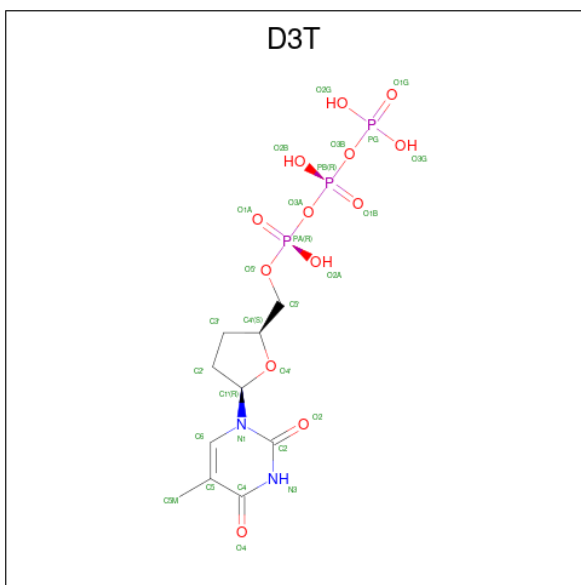
- Molecule 3 is a DNA chain called 5'-D(*CP*AP*GP*TP*AP*(2DT))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	6	Total	C	N	O	P	0	0	0
			119	59	22	33	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			

- Molecule 5 is 2',3'-DIDEOXY-THYMIDINE-5'-TRIPHOSPHATE (three-letter code: D3T) (formula: C₁₀H₁₇N₂O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			28	10	2	13	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Mg 1 1	0	0

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Na 1 1	0	0

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		

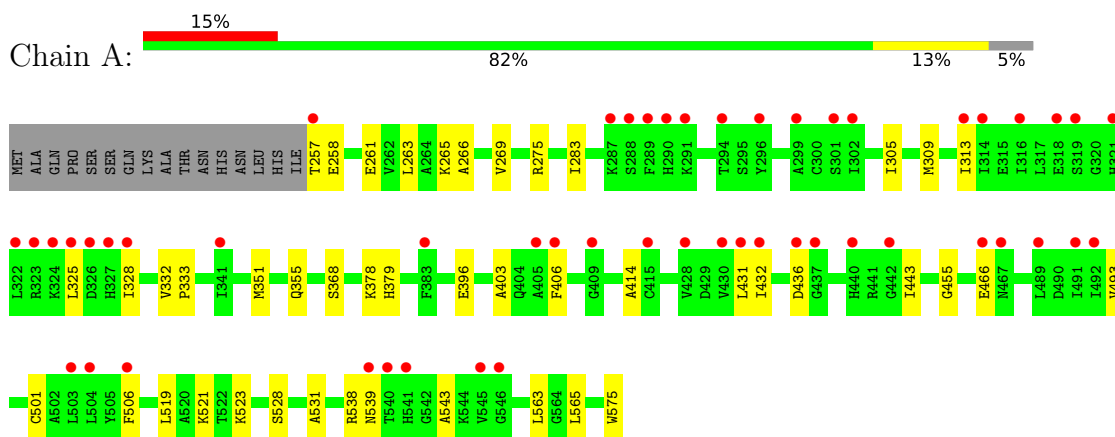
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	242	Total	O	0	0
			242	242		
9	T	59	Total	O	0	0
			59	59		
9	P	37	Total	O	0	0
			37	37		
9	D	13	Total	O	0	0
			13	13		

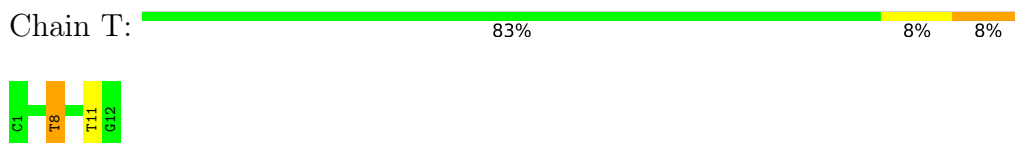
3 Residue-property plots [i](#)

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.

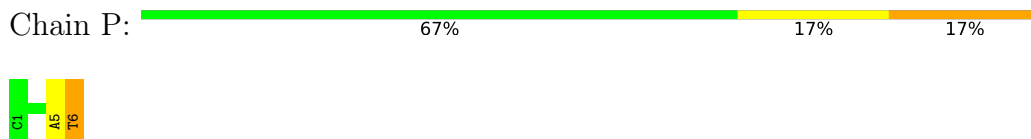
- Molecule 1: DNA polymerase lambda



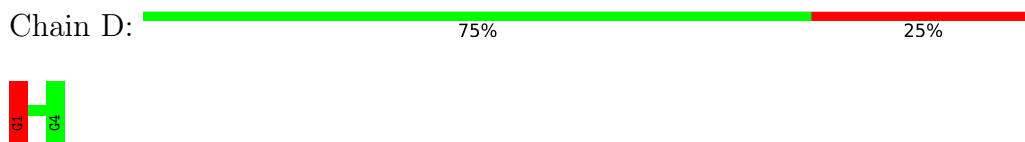
- Molecule 2: 5'-D(*CP*GP*GP*CP*AP*AP*AP*TP*AP*CP*TP*G)-3'



- Molecule 3: 5'-D(*CP*AP*GP*TP*AP*(2DT))-3'



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.02Å 68.33Å 137.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.95 25.47 – 1.95	Depositor EDS
% Data completeness (in resolution range)	93.1 (50.00-1.95) 93.0 (25.47-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 1.95Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.228 , 0.261 0.219 , 0.248	Depositor DCC
R_{free} test set	1891 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.4	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	3241	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2DT, D3T, EDO, NA, MG

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	A	0.30	0/2456	0.52	0/3323
2	T	0.35	0/274	0.78	0/421
3	P	0.35	0/112	0.78	0/171
4	D	0.98	1/92 (1.1%)	0.83	0/138
All	All	0.35	1/2934 (0.0%)	0.58	0/4053

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	T	0	1
4	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	DG	OP3-P	-7.37	1.52	1.61

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	1	DG	Sidechain
2	T	8	DT	Sidechain

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	A	2410	0	2326	36	0
2	T	244	0	136	3	0
3	P	119	0	70	3	0
4	D	83	0	45	2	0
5	A	28	0	13	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	4	0	6	0	0
9	A	242	0	0	4	0
9	D	13	0	0	0	0
9	P	37	0	0	0	0
9	T	59	0	0	1	0
All	All	3241	0	2596	41	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 (41) 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)
1:A:539:ASN:HD21	1:A:543:ALA:HB3	1.55	0.71
1:A:443:ILE:HD11	1:A:493:VAL:HG21	1.79	0.64
1:A:275:ARG:HH12	4:D:1:DG:P	2.22	0.63
9:A:616:HOH:O	2:T:11:DT:H5''	1.99	0.62
1:A:396:GLU:HG3	1:A:414:ALA:HB2	1.85	0.57
1:A:261:GLU:HG3	1:A:283:ILE:HD13	1.87	0.57
3:P:5:DA:H2'	3:P:6:2DT:H73	1.86	0.56
1:A:519:LEU:CD2	1:A:565:LEU:HD11	2.37	0.55
1:A:528:SER:HB2	2:T:8:DT:H5'	1.90	0.53
1:A:431:LEU:C	1:A:431:LEU:HD23	2.30	0.52
1:A:309:MET:O	1:A:313:ILE:HG13	2.10	0.52
1:A:443:ILE:HD11	1:A:493:VAL:CG2	2.39	0.52
1:A:523:LYS:HE3	1:A:563:LEU:O	2.11	0.50
3:P:5:DA:C2'	3:P:6:2DT:H73	2.42	0.49
1:A:403:ALA:HA	1:A:406:PHE:CE1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:MET:O	1:A:355:GLN:HG3	2.13	0.48
1:A:455:GLY:HA2	9:A:614:HOH:O	2.14	0.48
1:A:539:ASN:ND2	1:A:543:ALA:HB3	2.25	0.48
1:A:257:THR:HG22	1:A:258:GLU:N	2.28	0.48
1:A:332:VAL:HB	1:A:333:PRO:HD3	1.95	0.48
1:A:368:SER:HB3	9:A:177:HOH:O	2.14	0.47
1:A:265:LYS:O	1:A:269:VAL:HG13	2.13	0.47
1:A:305:ILE:HG23	1:A:309:MET:HB3	1.98	0.46
1:A:263:LEU:HD23	1:A:328:ILE:HD11	1.97	0.46
1:A:431:LEU:HD23	1:A:432:ILE:N	2.31	0.46
1:A:269:VAL:HG21	1:A:332:VAL:HG13	1.98	0.45
1:A:519:LEU:HD22	1:A:565:LEU:HD11	1.99	0.45
1:A:436:ASP:OD2	1:A:436:ASP:C	2.56	0.45
1:A:466:GLU:H	1:A:466:GLU:CD	2.20	0.44
1:A:266:ALA:O	1:A:269:VAL:HG22	2.18	0.43
1:A:275:ARG:NH1	4:D:1:DG:O5'	2.52	0.43
9:A:644:HOH:O	3:P:6:2DT:H3'1	2.17	0.43
1:A:575:TRP:CD1	1:A:575:TRP:N	2.86	0.42
1:A:378:LYS:HE3	1:A:379:HIS:NE2	2.34	0.42
1:A:501:CYS:SG	1:A:531:ALA:HA	2.60	0.42
1:A:466:GLU:CD	1:A:466:GLU:N	2.73	0.41
1:A:263:LEU:HG	1:A:325:LEU:CD2	2.50	0.41
1:A:521:LYS:HG3	1:A:538:ARG:CZ	2.50	0.41
2:T:8:DT:H2'	9:T:127:HOH:O	2.20	0.41
1:A:261:GLU:CG	1:A:283:ILE:HD13	2.49	0.41
1:A:263:LEU:HG	1:A:325:LEU:HD23	2.02	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	320/335 (96%)	310 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	236/280 (84%)	235 (100%)	1 (0%)	91	90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	506	PHE

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	400	GLN
1	A	511	HIS

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	2DT	P	6	2,3	14,20,21	1.18	2 (14%)	12,28,31	4.25	2 (16%)

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	2DT	P	6	2,3	-	1/4/18/19	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	6	2DT	C4-N3	3.25	1.38	1.33
3	P	6	2DT	C6-C5	-2.01	1.34	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	6	2DT	C4-N3-C2	14.36	127.27	115.14
3	P	6	2DT	C5M-C5-C6	2.00	122.91	118.68

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	6	2DT	O4'-C1'-N1-C6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	6	2DT	3	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
5	D3T	A	576	6	22,29,29	1.15	1 (4%)	25,45,45	3.04	3 (12%)
8	EDO	A	2801	-	3,3,3	0.54	0	2,2,2	0.58	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
5	D3T	A	576	6	-	4/19/31/31	0/2/2/2
8	EDO	A	2801	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	576	D3T	C4-N3	3.13	1.38	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	576	D3T	C4-N3-C2	14.40	127.30	115.14
5	A	576	D3T	C5M-C5-C6	2.10	123.12	118.68
5	A	576	D3T	O2G-PG-O1G	2.02	118.58	110.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	576	D3T	PB-O3B-PG-O2G
5	A	576	D3T	PB-O3B-PG-O3G

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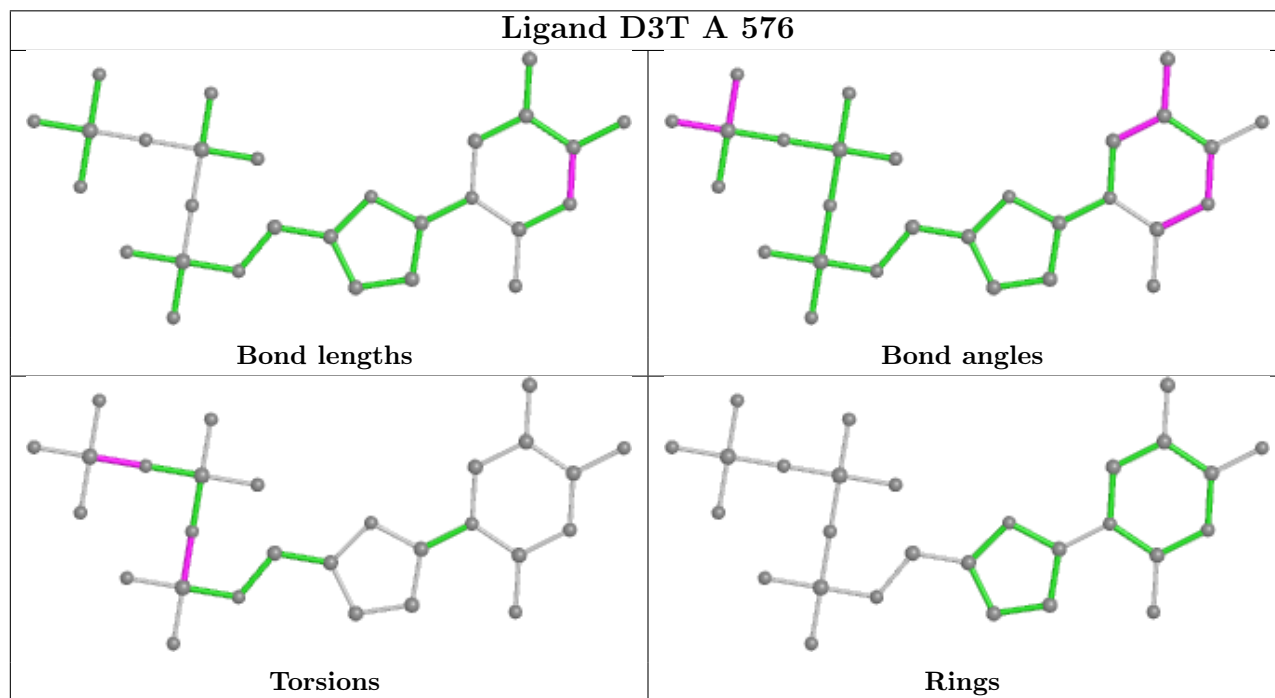
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Mol	Chain	Res	Type	Atoms
5	A	576	D3T	PB-O3A-PA-O1A
5	A	576	D3T	PB-O3A-PA-O2A

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 ⓘ

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

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	A	319/335 (95%)	0.78	51 (15%) 1 2	26, 41, 75, 85	1 (0%)
2	T	12/12 (100%)	-0.51	0 100 100	29, 34, 41, 48	0
3	P	5/6 (83%)	-0.58	0 100 100	26, 27, 30, 32	0
4	D	4/4 (100%)	0.00	0 100 100	41, 42, 44, 45	0
All	All	340/357 (95%)	0.71	51 (15%) 2 3	26, 40, 74, 85	1 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	491	ILE	5.7
1	A	291	LYS	5.0
1	A	406	PHE	4.6
1	A	328	ILE	4.6
1	A	322	LEU	4.4
1	A	327	HIS	4.3
1	A	540	THR	4.2
1	A	290	HIS	4.2
1	A	321	HIS	4.1
1	A	288	SER	4.1
1	A	492	ILE	4.0
1	A	294	THR	3.9
1	A	489	LEU	3.9
1	A	319	SER	3.9
1	A	323	ARG	3.9
1	A	405	ALA	3.8
1	A	437	GLY	3.8
1	A	430	VAL	3.7
1	A	545	VAL	3.7
1	A	299	ALA	3.5
1	A	546	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	314	ILE	3.2
1	A	326	ASP	3.2
1	A	316	ILE	3.2
1	A	467	ASN	3.1
1	A	541	HIS	3.0
1	A	325	LEU	2.9
1	A	506	PHE	2.8
1	A	428	VAL	2.8
1	A	313	ILE	2.7
1	A	289	PHE	2.6
1	A	302	ILE	2.6
1	A	504	LEU	2.6
1	A	440	HIS	2.6
1	A	257	THR	2.4
1	A	442	GLY	2.3
1	A	539	ASN	2.3
1	A	503	LEU	2.3
1	A	296	TYR	2.2
1	A	431	LEU	2.2
1	A	287	LYS	2.2
1	A	415	CYS	2.1
1	A	324	LYS	2.1
1	A	318	GLU	2.1
1	A	301	SER	2.1
1	A	436	ASP	2.1
1	A	341	ILE	2.1
1	A	466	GLU	2.1
1	A	383	PHE	2.1
1	A	432	ILE	2.0
1	A	409	GLY	2.0

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

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
3	2DT	P	6	19/20	0.96	0.11	29,31,38,42	0

6.3 Carbohydrates [i](#)

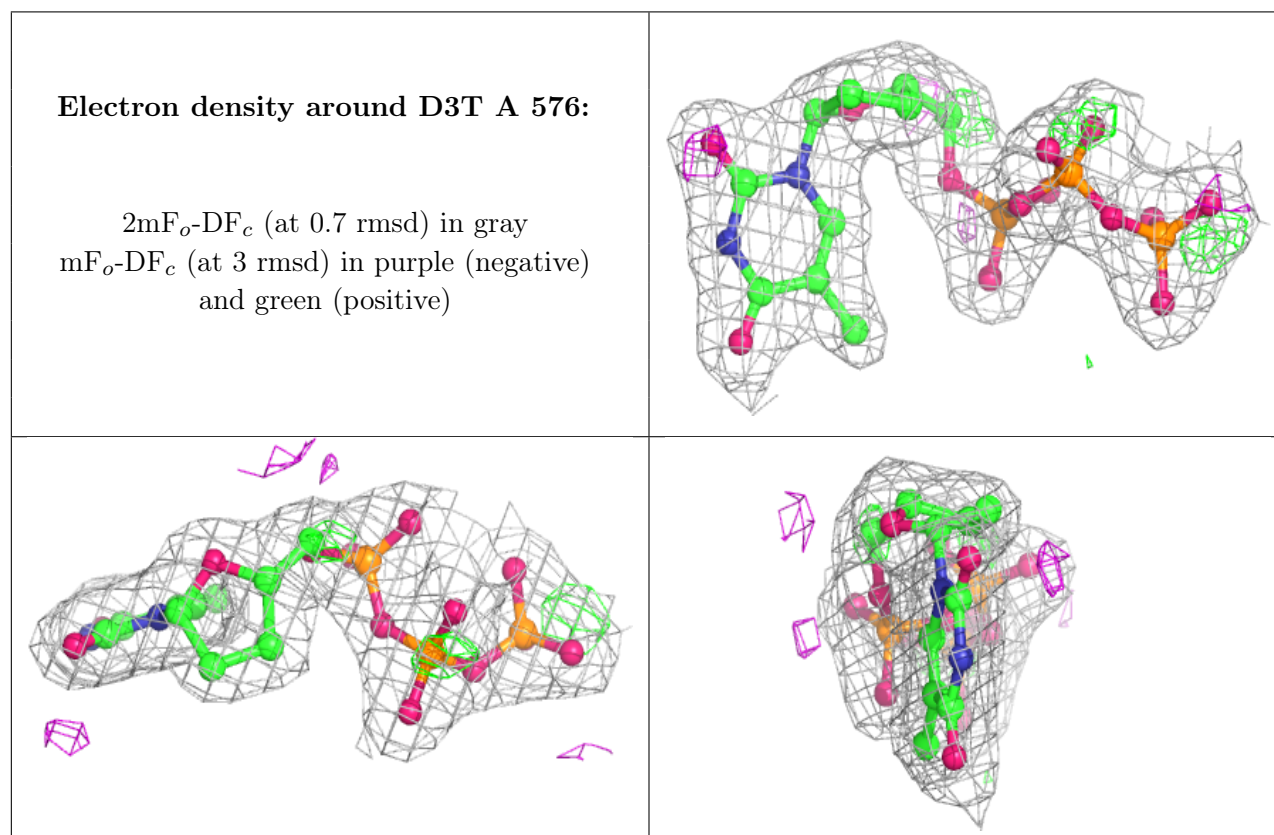
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
8	EDO	A	2801	4/4	0.90	0.34	52,52,53,55	0
6	MG	A	168	1/1	0.93	0.06	28,28,28,28	0
5	D3T	A	576	28/28	0.96	0.10	24,27,31,32	0
7	NA	A	169	1/1	0.99	0.08	27,27,27,27	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.