



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 1, 2025 – 04:07 PM EDT

PDB ID : 9DRC / pdb\_00009drc  
Title : Ternary substrate complex of DNA polymerase iota R71A mutant with DNA (template A) and dTTP  
Authors : Frevert, Z.; Reusch, D.; Freudenthal, B.; Washington, M.T.  
Deposited on : 2024-09-25  
Resolution : 2.45 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

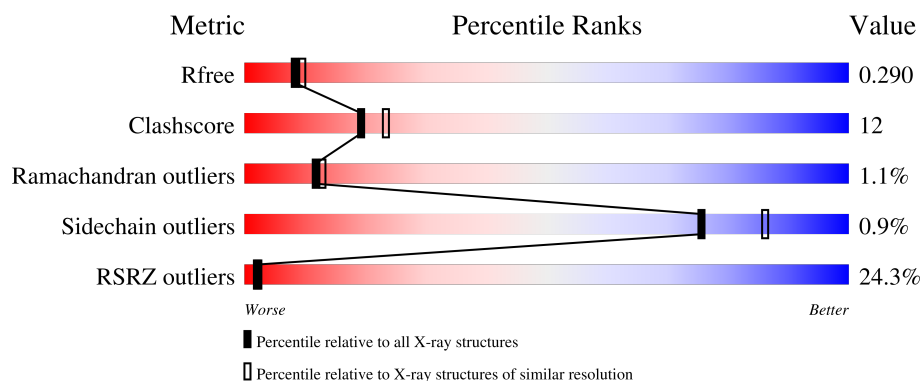
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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))
$R_{free}$	164625	1096 (2.46-2.46)
Clashscore	180529	1178 (2.46-2.46)
Ramachandran outliers	177936	1170 (2.46-2.46)
Sidechain outliers	177891	1170 (2.46-2.46)
RSRZ outliers	164620	1096 (2.46-2.46)

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  $\geq 3$ , 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	420	
2	B	18	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6210 atoms, of which 2929 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 iota.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	362	Total	C	H	N	O	S	2	0	0
			5755	1793	2916	490	535	21			

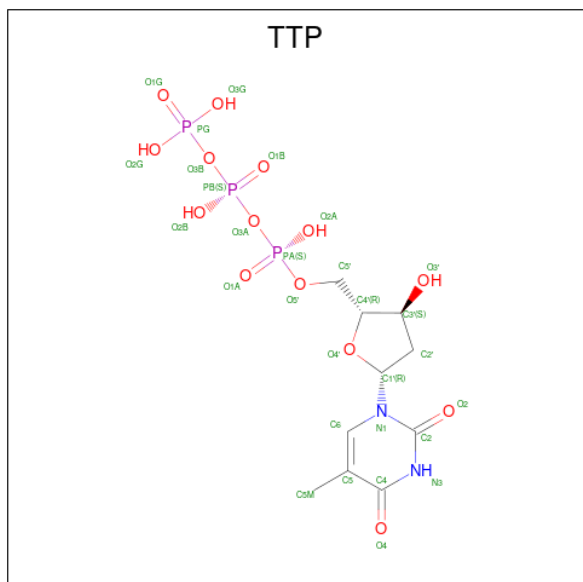
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	ALA	ARG	conflict	UNP Q9UNA4

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	16	Total	C	N	O	P	0	1	0
			350	165	69	99	17			

- Molecule 3 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>2</sub>O<sub>14</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			42	10	13	2	14	3		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Ca	0	0
			2	2		

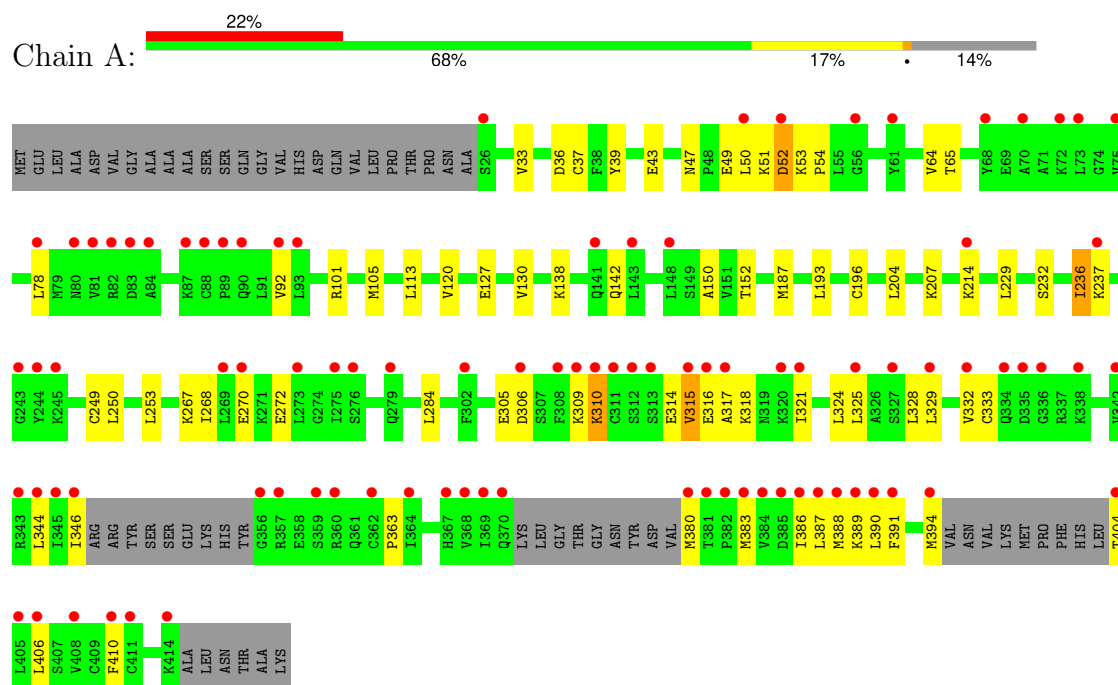
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	53	Total	O	0	0
			53	53		
5	B	8	Total	O	0	0
			8	8		

### 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 iota



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.28Å 97.28Å 202.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.89 – 2.45 24.89 – 2.45	Depositor EDS
% Data completeness (in resolution range)	85.0 (24.89-2.45) 74.6 (24.89-2.45)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.85 (at 2.44Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.248 , 0.294 0.249 , 0.290	Depositor DCC
$R_{free}$ test set	20083 reflections (9.46%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.0	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	6210	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: TTP, CA

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	0.16	0/2877	0.30	0/3877
2	B	0.20	0/393	0.32	0/604
All	All	0.17	0/3270	0.30	0/4481

There are no bond length outliers.

There are no bond angle outliers.

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	A	2839	2916	2922	52	2
2	B	350	0	190	20	1
3	A	29	13	13	2	0
4	A	2	0	0	0	0
5	A	53	0	0	2	0
5	B	8	0	0	0	0
All	All	3281	2929	3125	73	2

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 12.

All (73) 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:43:GLU:OE2	1:A:101:ARG:NH2	2.07	0.88
2:B:13:DG:H1'	2:B:14:DG:H5'	1.58	0.86
1:A:388:MET:HE3	1:A:388:MET:HA	1.63	0.81
2:B:11:DT:H2''	2:B:12:DA:H5'	1.66	0.78
1:A:272:GLU:N	1:A:272:GLU:OE2	2.21	0.74
2:B:8:DT:H5''	2:B:8:DT:H6	1.53	0.73
3:A:501:TTP:O4'	5:A:602:HOH:O	2.07	0.73
1:A:380:MET:SD	1:A:380:MET:N	2.63	0.72
1:A:321:ILE:HD11	1:A:406:LEU:HD22	1.76	0.68
2:B:3:DA:H5''	2:B:4[A]:DA:H2	1.61	0.66
1:A:113:LEU:HD21	1:A:187:MET:HE2	1.79	0.64
2:B:11:DT:H5'	2:B:11:DT:H6	1.63	0.64
1:A:332:VAL:HG11	1:A:410:PHE:CD2	2.33	0.63
1:A:33:VAL:HG11	1:A:187:MET:HE1	1.81	0.62
1:A:325:LEU:HD13	1:A:329:LEU:CD2	2.30	0.62
1:A:64:VAL:HA	1:A:78:LEU:HD23	1.83	0.60
1:A:344:LEU:HD13	1:A:387:LEU:HD22	1.83	0.60
2:B:3:DA:H5''	2:B:4[A]:DA:C2	2.38	0.59
1:A:332:VAL:HG11	1:A:410:PHE:HD2	1.66	0.58
1:A:325:LEU:HD13	1:A:329:LEU:HD23	1.83	0.58
1:A:50:LEU:CD2	1:A:92:VAL:HG11	2.34	0.57
5:A:620:HOH:O	2:B:12:DA:H2'	2.03	0.57
1:A:50:LEU:HA	1:A:53:LYS:HE3	1.86	0.57
1:A:388:MET:HE1	1:A:391:PHE:CD2	2.39	0.57
2:B:11:DT:H5'	2:B:11:DT:C6	2.39	0.56
1:A:383:MET:HA	1:A:386:ILE:HD12	1.88	0.56
1:A:49:GLU:O	1:A:53:LYS:HE2	2.06	0.56
2:B:6:DG:H2''	2:B:7:DG:O5'	2.07	0.54
1:A:204:LEU:HD22	1:A:284:LEU:HD22	1.90	0.54
1:A:321:ILE:HD12	1:A:406:LEU:HD13	1.91	0.53
2:B:3:DA:H2'	2:B:4[A]:DA:C2	2.45	0.52
1:A:314:GLU:HG2	1:A:316:GLU:H	1.73	0.52
1:A:309:LYS:O	1:A:310:LYS:HG3	2.10	0.52
1:A:250:LEU:HA	1:A:253:LEU:HD13	1.92	0.51
1:A:310:LYS:O	1:A:310:LYS:HD2	2.10	0.51
1:A:321:ILE:CD1	1:A:406:LEU:HD13	2.41	0.50
1:A:138:LYS:O	1:A:142:GLN:OE1	2.29	0.50
1:A:344:LEU:CD1	1:A:387:LEU:HD22	2.42	0.50
1:A:267:LYS:N	1:A:267:LYS:HD3	2.27	0.49
1:A:324:LEU:O	1:A:328:LEU:HD12	2.13	0.49
1:A:249:CYS:O	1:A:253:LEU:HD12	2.13	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:DT:H6	2:B:8:DT:C5'	2.23	0.49
1:A:36:ASP:O	1:A:37:CYS:C	2.56	0.48
1:A:120:VAL:HG22	1:A:130:VAL:HG22	1.98	0.46
1:A:388:MET:HE1	1:A:391:PHE:HD2	1.79	0.46
1:A:47:ASN:OD1	1:A:50:LEU:HG	2.16	0.46
3:A:501:TTP:H1'	2:B:18:DC:H2'	1.97	0.46
1:A:315:VAL:O	1:A:318:LYS:N	2.46	0.46
1:A:310:LYS:H	1:A:404:THR:HG22	1.81	0.45
2:B:5:DG:H2''	2:B:6:DG:O5'	2.17	0.45
1:A:317:ALA:HB1	1:A:391:PHE:HE2	1.83	0.44
2:B:11:DT:H2''	2:B:12:DA:C5'	2.41	0.43
1:A:127:GLU:OE1	1:A:207:LYS:NZ	2.51	0.43
1:A:229:LEU:O	1:A:232:SER:OG	2.32	0.43
1:A:236:ILE:HD12	1:A:237:LYS:N	2.33	0.43
1:A:344:LEU:HD13	1:A:387:LEU:CD2	2.48	0.43
1:A:196:CYS:SG	1:A:214:LYS:O	2.77	0.43
1:A:390:LEU:O	1:A:394:MET:HG3	2.19	0.43
2:B:13:DG:H2''	2:B:14:DG:O5'	2.18	0.43
2:B:17:DC:H2'	2:B:18:DC:C6	2.54	0.42
2:B:10:DC:H2''	2:B:11:DT:H5'	2.02	0.42
1:A:268:ILE:O	1:A:272:GLU:OE2	2.37	0.42
1:A:324:LEU:HD22	1:A:324:LEU:H	1.84	0.42
1:A:53:LYS:HB2	1:A:54:PRO:HD2	2.01	0.41
1:A:105:MET:CG	1:A:193:LEU:HD11	2.50	0.41
2:B:8:DT:C5'	2:B:8:DT:C6	3.03	0.41
1:A:47:ASN:OD1	1:A:47:ASN:C	2.63	0.41
2:B:16:DC:H2''	2:B:17:DC:H5'	2.02	0.41
2:B:16:DC:H2'	2:B:17:DC:C6	2.56	0.41
1:A:346:ILE:HG22	1:A:406:LEU:HD23	2.03	0.41
1:A:39:TYR:HB2	1:A:65:THR:HG21	2.03	0.40
1:A:51:LYS:O	1:A:52:ASP:CB	2.69	0.40
1:A:150:ALA:O	1:A:152:THR:HG23	2.21	0.40

All (2) 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:A:305:GLU:H	2:B:6:DG:OP2[10_665]	1.36	0.24
1:A:270:GLU:OE1	1:A:389:LYS:NZ[10_665]	2.07	0.13

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	354/420 (84%)	336 (95%)	14 (4%)	4 (1%)	12 13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	ASP
1	A	310	LYS
1	A	306	ASP
1	A	363	PRO

### 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
1	A	328/375 (88%)	325 (99%)	3 (1%)	75 86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	236	ILE
1	A	315	VAL
1	A	333	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	ASN
1	A	141	GLN
1	A	142	GLN
1	A	178	GLN
1	A	334	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](#)

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 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$
3	TTP	A	501	4	29,30,30	1.37	6 (20%)	43,47,47	1.76	7 (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	TTP	A	501	4	-	9/22/34/34	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	TTP	C6-C5	3.04	1.39	1.34
3	A	501	TTP	C4-C5	2.57	1.49	1.44
3	A	501	TTP	C4-N3	-2.50	1.34	1.38
3	A	501	TTP	C6-N1	-2.37	1.34	1.38
3	A	501	TTP	C2-N3	-2.14	1.34	1.38
3	A	501	TTP	C2-N1	2.05	1.41	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	TTP	N3-C2-N1	5.14	121.58	114.89
3	A	501	TTP	C4-N3-C2	-5.09	120.67	127.34
3	A	501	TTP	C5-C4-N3	4.25	119.02	115.32
3	A	501	TTP	O4-C4-C5	-3.68	120.71	124.92
3	A	501	TTP	C5-C6-N1	-3.46	119.55	123.31
3	A	501	TTP	O2-C2-N1	-2.30	119.80	122.80
3	A	501	TTP	C3'-C2'-C1'	2.04	107.59	102.60

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	TTP	C5'-O5'-PA-O2A
3	A	501	TTP	C5'-O5'-PA-O3A
3	A	501	TTP	O4'-C4'-C5'-O5'
3	A	501	TTP	C2'-C1'-N1-C2
3	A	501	TTP	C3'-C4'-C5'-O5'
3	A	501	TTP	C2'-C1'-N1-C6
3	A	501	TTP	C5'-O5'-PA-O1A
3	A	501	TTP	C4'-C5'-O5'-PA
3	A	501	TTP	PB-O3A-PA-O2A

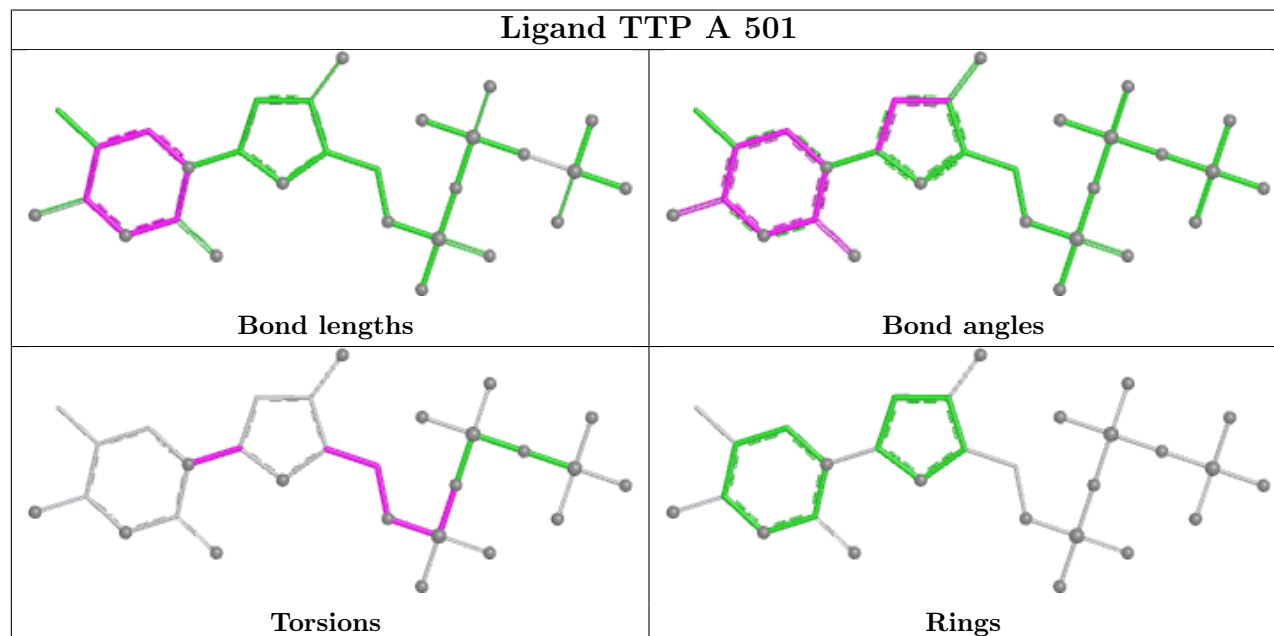
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	TTP	2	0

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	362/420 (86%)	1.10	92 (25%) 2 2	24, 55, 104, 122	0
2	B	16/18 (88%)	0.77	0 100 100	29, 44, 63, 78	1 (6%)
All	All	378/438 (86%)	1.08	92 (24%) 2 2	24, 54, 104, 122	1 (0%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	391	PHE	5.3
1	A	346	ILE	4.7
1	A	343	ARG	4.6
1	A	356	GLY	4.4
1	A	344	LEU	4.4
1	A	308	PHE	4.3
1	A	61	TYR	4.2
1	A	386	ILE	4.1
1	A	273	LEU	4.0
1	A	315	VAL	4.0
1	A	408	VAL	4.0
1	A	78	LEU	3.7
1	A	380	MET	3.7
1	A	390	LEU	3.7
1	A	394	MET	3.7
1	A	357	ARG	3.7
1	A	388	MET	3.6
1	A	325	LEU	3.6
1	A	404	THR	3.4
1	A	245	LYS	3.4
1	A	52	ASP	3.3
1	A	406	LEU	3.3
1	A	389	LYS	3.3
1	A	302	PHE	3.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	364	ILE	3.3
1	A	269	LEU	3.3
1	A	306	ASP	3.3
1	A	68	TYR	3.2
1	A	329	LEU	3.2
1	A	336	GLY	3.2
1	A	148	LEU	3.1
1	A	360	ARG	3.1
1	A	369	ILE	3.1
1	A	359	SER	3.1
1	A	405	LEU	3.1
1	A	311	CYS	3.1
1	A	73	LEU	3.0
1	A	243	GLY	3.0
1	A	312	SER	3.0
1	A	244	TYR	3.0
1	A	75	VAL	3.0
1	A	309	LYS	2.9
1	A	317	ALA	2.9
1	A	327	SER	2.9
1	A	385	ASP	2.9
1	A	320	LYS	2.8
1	A	214	LYS	2.8
1	A	143	LEU	2.7
1	A	381	THR	2.7
1	A	384	VAL	2.7
1	A	383	MET	2.7
1	A	316	GLU	2.7
1	A	83	ASP	2.7
1	A	276	SER	2.7
1	A	313	SER	2.7
1	A	72	LYS	2.6
1	A	387	LEU	2.5
1	A	321	ILE	2.5
1	A	279	GLN	2.5
1	A	367	HIS	2.5
1	A	410	PHE	2.5
1	A	50	LEU	2.5
1	A	414	LYS	2.5
1	A	88	CYS	2.5
1	A	93	LEU	2.5
1	A	370	GLN	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	368	VAL	2.4
1	A	82	ARG	2.4
1	A	26	SER	2.4
1	A	411	CYS	2.4
1	A	92	VAL	2.4
1	A	84	ALA	2.4
1	A	335	ASP	2.3
1	A	310	LYS	2.3
1	A	332	VAL	2.3
1	A	80	ASN	2.3
1	A	275	ILE	2.3
1	A	87	LYS	2.3
1	A	89	PRO	2.3
1	A	141	GLN	2.3
1	A	334	GLN	2.3
1	A	345	ILE	2.2
1	A	70	ALA	2.2
1	A	338	LYS	2.2
1	A	270	GLU	2.1
1	A	81	VAL	2.1
1	A	342	VAL	2.0
1	A	56	GLY	2.0
1	A	90	GLN	2.0
1	A	362	CYS	2.0
1	A	237	LYS	2.0
1	A	382	PRO	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

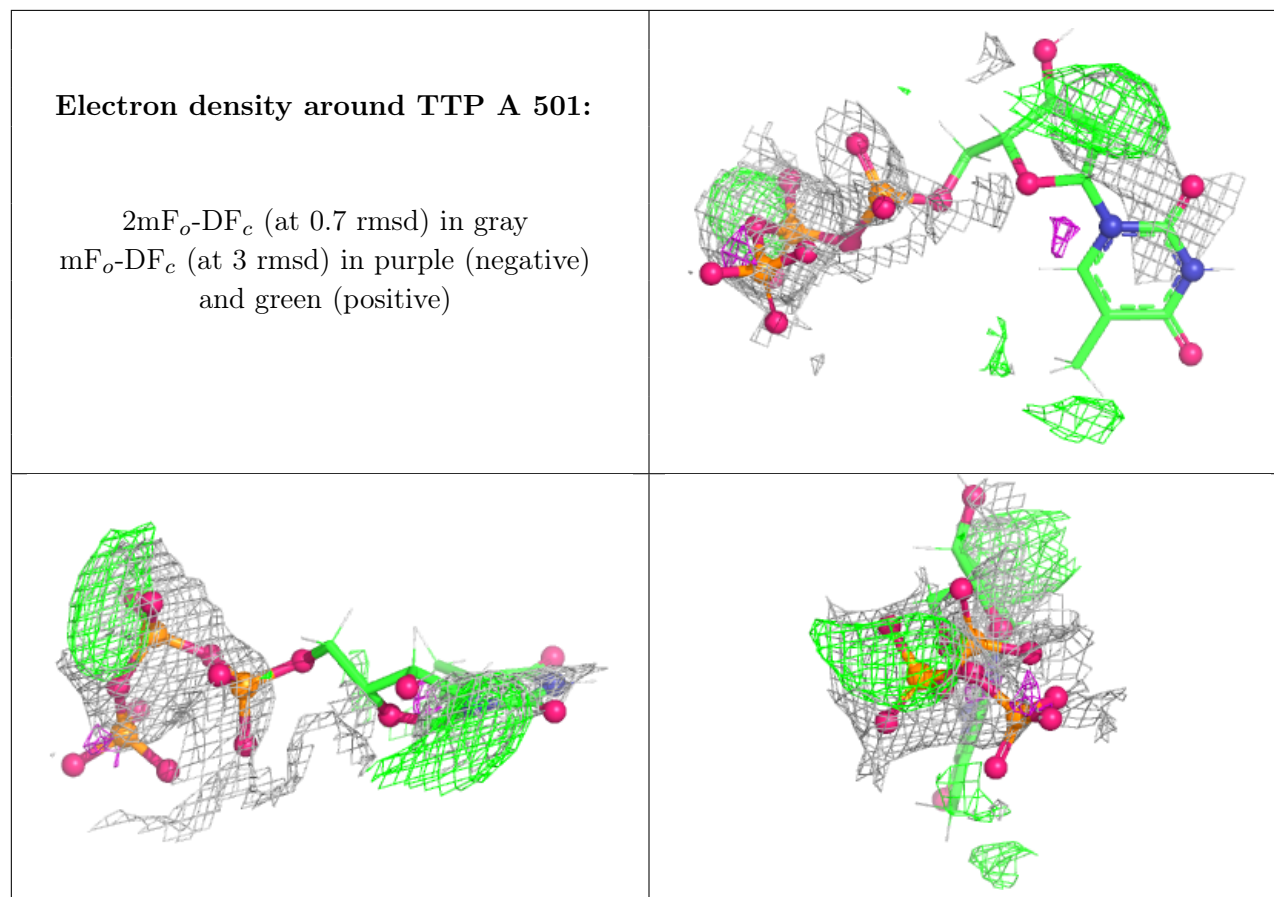
## 6.4 Ligands [i](#)

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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	CA	A	503	1/1	0.58	0.35	65,65,65,65	1
3	TTP	A	501	29/29	0.63	0.36	41,50,62,66	42
4	CA	A	502	1/1	0.84	0.10	32,32,32,32	1

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 ⓘ

There are no such residues in this entry.