



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 25, 2023 – 02:28 AM EDT

PDB ID : 8ICY  
Title : DNA POLYMERASE BETA (E.C.2.7.7.7)/DNA COMPLEX + THYMIDIN E-5'-TRIPHOSPHATE, SOAKED IN THE PRESENCE OF DTTP AND MNCL2  
Authors : Pelletier, H.; Sawaya, M.R.  
Deposited on : 1995-12-15  
Resolution : 3.10 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](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>.

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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 : 2.34  
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) : 2.34

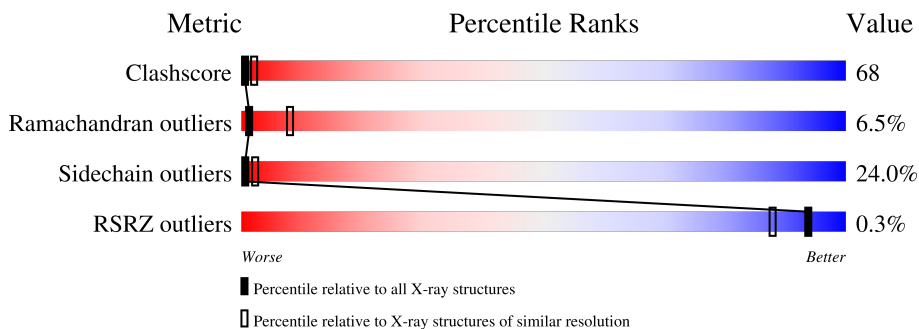
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 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	T	8	
2	P	8	
3	A	335	

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
6	TTP	A	338	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3088 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\*AP\*TP\*TP\*AP\*GP\*AP\*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	T	8	145	69	27	42	7	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(\*TP\*CP\*TP\*AP\*AP\*TP\*GP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	P	8	164	79	26	51	8	0	0	0

- Molecule 3 is a protein called PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	327	2623	1657	458	499	9	9	0	0

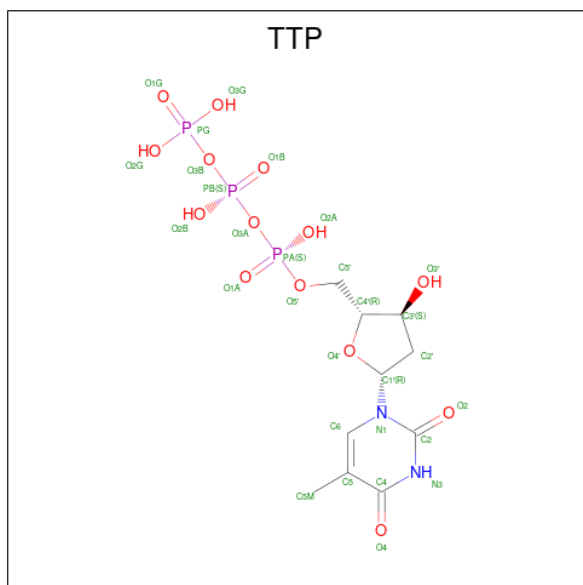
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
4	A	1	1	1	0	0

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

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

- Molecule 6 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>2</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	P	0	0
			20	5	12	3		

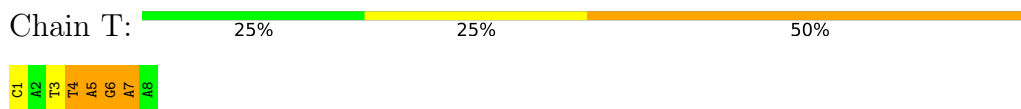
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	T	15	Total	O	0	0
			15	15		
7	P	19	Total	O	0	0
			19	19		
7	A	99	Total	O	0	0
			99	99		

### 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.

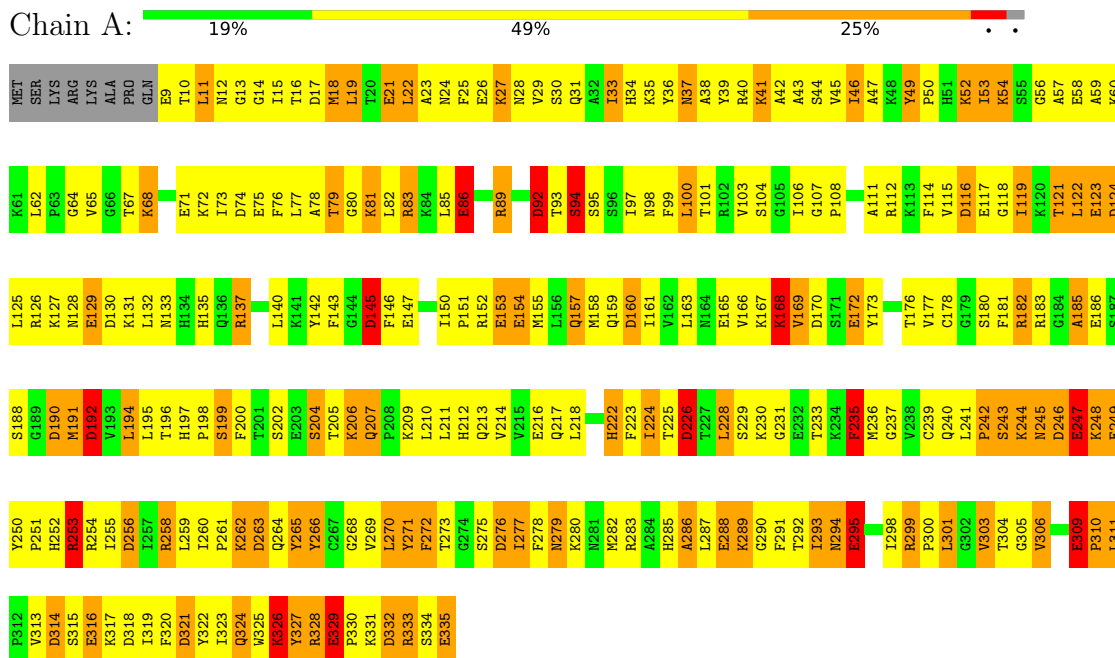
- Molecule 1: DNA (5'-D(\*CP\*AP\*TP\*TP\*AP\*GP\*AP\*A)-3')



- Molecule 2: DNA (5'-D(\*TP\*CP\*TP\*AP\*AP\*TP\*GP\*T)-3')



- Molecule 3: PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7))



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	179.79Å 57.62Å 48.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 11.92 – 2.86	Depositor EDS
% Data completeness (in resolution range)	94.0 (20.00-3.10) 90.7 (11.92-2.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	5.90	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 2.87Å)	Xtrriage
Refinement program	TNT 5-D	Depositor
R, $R_{free}$	0.168 , (Not available) 0.161 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.2	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.13 , 129.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3088	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.14% 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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NA, TTP, MN

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	2.21	8/162 (4.9%)	3.64	22/249 (8.8%)
2	P	2.30	6/182 (3.3%)	4.17	31/277 (11.2%)
3	A	1.31	24/2672 (0.9%)	1.76	54/3590 (1.5%)
All	All	1.45	38/3016 (1.3%)	2.16	107/4116 (2.6%)

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	P	1	0
3	A	1	0
All	All	2	0

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	1	DC	C3'-O3'	9.13	1.55	1.44
2	P	3	DT	N1-C2	8.18	1.44	1.38
3	A	147	GLU	CD-OE2	7.71	1.34	1.25
3	A	295	GLU	CD-OE2	7.58	1.33	1.25
3	A	75	GLU	CD-OE1	7.57	1.33	1.25
2	P	1	DT	C5-C7	7.55	1.54	1.50
3	A	154	GLU	CD-OE2	7.51	1.33	1.25
3	A	216	GLU	CD-OE2	7.37	1.33	1.25
2	P	5	DA	N9-C4	7.11	1.42	1.37
3	A	335	GLU	CD-OE2	7.05	1.33	1.25
3	A	329	GLU	CD-OE2	6.99	1.33	1.25
3	A	172	GLU	CD-OE2	6.95	1.33	1.25
3	A	247	GLU	CD-OE1	6.92	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	5	DA	C3'-O3'	-6.90	1.34	1.44
3	A	71	GLU	CD-OE1	6.85	1.33	1.25
3	A	129	GLU	CD-OE1	6.80	1.33	1.25
3	A	249	GLU	CD-OE2	6.79	1.33	1.25
3	A	86	GLU	CD-OE1	6.74	1.33	1.25
3	A	117	GLU	CD-OE2	6.60	1.32	1.25
2	P	2	DC	C1'-N1	6.55	1.57	1.49
1	T	5	DA	N7-C5	-6.26	1.35	1.39
3	A	153	GLU	CD-OE2	6.00	1.32	1.25
2	P	7	DG	C3'-O3'	5.98	1.51	1.44
1	T	5	DA	C6-N1	5.62	1.39	1.35
3	A	288	GLU	CD-OE2	5.60	1.31	1.25
3	A	186	GLU	CD-OE1	5.51	1.31	1.25
2	P	3	DT	C1'-N1	5.49	1.56	1.49
3	A	58	GLU	CD-OE1	5.44	1.31	1.25
3	A	316	GLU	CD-OE2	5.33	1.31	1.25
1	T	6	DG	C3'-O3'	-5.31	1.37	1.44
3	A	21	GLU	CD-OE1	5.30	1.31	1.25
1	T	5	DA	C5-C6	-5.28	1.36	1.41
3	A	326	LYS	CE-NZ	-5.27	1.35	1.49
3	A	123	GLU	CD-OE2	5.23	1.31	1.25
3	A	9	GLU	CD-OE2	5.16	1.31	1.25
1	T	1	DC	O3'-P	5.10	1.67	1.61
3	A	94	SER	CA-CB	-5.06	1.45	1.52
1	T	1	DC	C4'-C3'	5.04	1.58	1.53

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	2	DC	C2-N1-C1'	26.81	148.29	118.80
2	P	2	DC	C6-N1-C1'	-23.73	92.33	120.80
2	P	8	DT	C6-N1-C1'	-19.61	90.98	120.40
2	P	8	DT	C2-N1-C1'	17.35	145.95	118.20
1	T	6	DG	C8-N9-C1'	17.12	149.26	127.00
1	T	6	DG	C4-N9-C1'	-17.02	104.37	126.50
1	T	4	DT	C6-N1-C1'	-16.46	95.71	120.40
1	T	4	DT	C2-N1-C1'	15.00	142.20	118.20
2	P	3	DT	C6-N1-C1'	-14.41	98.79	120.40
2	P	3	DT	C2-N1-C1'	14.03	140.64	118.20
2	P	3	DT	O4'-C1'-N1	13.96	117.77	108.00
1	T	1	DC	C6-N1-C1'	-13.32	104.81	120.80
1	T	1	DC	C2-N1-C1'	12.40	132.44	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	1	DC	P-O3'-C3'	12.37	134.55	119.70
1	T	7	DA	C4-N9-C1'	-11.67	105.30	126.30
2	P	3	DT	P-O3'-C3'	11.21	133.16	119.70
1	T	6	DG	O4'-C1'-N9	11.04	115.73	108.00
1	T	7	DA	C8-N9-C1'	10.61	146.79	127.70
2	P	7	DG	C4-N9-C1'	-10.24	113.19	126.50
1	T	5	DA	N1-C6-N6	9.93	124.56	118.60
2	P	5	DA	C4-N9-C1'	9.82	143.98	126.30
2	P	3	DT	N3-C2-O2	-9.44	116.64	122.30
3	A	253	ARG	NE-CZ-NH1	9.41	125.01	120.30
2	P	5	DA	C8-N9-C1'	-9.38	110.82	127.70
1	T	5	DA	P-O5'-C5'	-9.37	105.92	120.90
2	P	7	DG	C8-N9-C1'	9.21	138.97	127.00
2	P	6	DT	C6-N1-C1'	-9.12	106.73	120.40
1	T	4	DT	O4'-C1'-N1	8.72	114.10	108.00
2	P	7	DG	P-O3'-C3'	8.61	130.03	119.70
2	P	7	DG	P-O5'-C5'	-8.41	107.44	120.90
3	A	328	ARG	NE-CZ-NH2	-8.30	116.15	120.30
3	A	256	ASP	CB-CG-OD2	-8.19	110.93	118.30
3	A	17	ASP	CB-CG-OD1	-8.10	111.01	118.30
2	P	6	DT	C2-N1-C1'	8.05	131.08	118.20
3	A	130	ASP	CB-CG-OD2	-8.02	111.08	118.30
3	A	190	ASP	CB-CG-OD1	7.99	125.49	118.30
3	A	256	ASP	CB-CG-OD1	7.87	125.38	118.30
1	T	4	DT	C1'-O4'-C4'	-7.75	102.35	110.10
3	A	49	TYR	CB-CA-C	7.71	125.82	110.40
3	A	157	GLN	N-CA-CB	7.48	124.07	110.60
3	A	276	ASP	CB-CG-OD2	-7.41	111.63	118.30
3	A	83	ARG	N-CA-CB	7.18	123.52	110.60
3	A	130	ASP	CB-CG-OD1	7.17	124.76	118.30
3	A	192	ASP	CB-CG-OD2	-7.09	111.92	118.30
3	A	263	ASP	CB-CG-OD2	-6.95	112.04	118.30
2	P	8	DT	C3'-C2'-C1'	-6.94	94.17	102.50
3	A	173	TYR	CB-CA-C	-6.91	96.58	110.40
2	P	2	DC	O4'-C1'-N1	6.80	112.76	108.00
1	T	3	DT	P-O3'-C3'	-6.77	111.58	119.70
3	A	321	ASP	CB-CG-OD2	-6.71	112.26	118.30
3	A	182	ARG	NE-CZ-NH2	-6.63	116.98	120.30
2	P	8	DT	O4'-C1'-N1	6.55	112.59	108.00
3	A	226	ASP	CB-CG-OD2	-6.53	112.43	118.30
2	P	7	DG	C4'-C3'-C2'	6.51	108.96	103.10
3	A	160	ASP	CB-CG-OD1	6.50	124.15	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	116	ASP	CA-CB-CG	-6.47	99.16	113.40
3	A	266	TYR	CA-CB-CG	-6.42	101.21	113.40
3	A	124	ASP	CB-CG-OD2	-6.40	112.54	118.30
2	P	4	DA	C4-N9-C1'	6.37	137.76	126.30
3	A	116	ASP	CB-CG-OD2	-6.36	112.58	118.30
3	A	224	ILE	CA-CB-CG1	-6.35	98.93	111.00
3	A	276	ASP	CB-CG-OD1	6.23	123.91	118.30
3	A	168	LYS	N-CA-CB	6.15	121.67	110.60
3	A	98	ASN	CB-CA-C	6.13	122.66	110.40
1	T	1	DC	C6-N1-C2	6.02	122.71	120.30
2	P	1	DT	C2-N1-C1'	5.85	127.56	118.20
3	A	299	ARG	NE-CZ-NH1	5.85	123.22	120.30
2	P	7	DG	C4'-C3'-O3'	5.84	124.30	109.70
3	A	137	ARG	NE-CZ-NH2	-5.83	117.38	120.30
2	P	1	DT	C6-N1-C1'	-5.82	111.67	120.40
3	A	53	ILE	CB-CA-C	5.78	123.16	111.60
3	A	92	ASP	CB-CG-OD2	-5.77	113.10	118.30
3	A	235	PHE	N-CA-C	-5.77	95.43	111.00
1	T	5	DA	C6-C5-N7	-5.71	128.30	132.30
1	T	4	DT	P-O5'-C5'	5.70	130.02	120.90
3	A	318	ASP	CB-CG-OD2	-5.65	113.21	118.30
3	A	243	SER	CB-CA-C	5.64	120.82	110.10
3	A	160	ASP	CB-CG-OD2	-5.61	113.25	118.30
3	A	263	ASP	CB-CG-OD1	5.61	123.35	118.30
3	A	318	ASP	CB-CG-OD1	5.58	123.32	118.30
3	A	326	LYS	CD-CE-NZ	5.58	124.54	111.70
3	A	40	ARG	N-CA-CB	5.55	120.59	110.60
3	A	272	PHE	N-CA-CB	5.53	120.56	110.60
3	A	286	ALA	C-N-CA	5.53	135.53	121.70
2	P	4	DA	C8-N9-C1'	-5.52	117.77	127.70
2	P	6	DT	P-O3'-C3'	-5.51	113.08	119.70
3	A	182	ARG	NE-CZ-NH1	5.47	123.03	120.30
2	P	3	DT	N1-C2-O2	5.44	127.45	123.10
3	A	314	ASP	CB-CG-OD1	-5.42	113.42	118.30
3	A	333	ARG	NE-CZ-NH1	-5.40	117.60	120.30
2	P	7	DG	O4'-C1'-C2'	5.38	110.21	105.90
3	A	17	ASP	CB-CG-OD2	5.33	123.09	118.30
3	A	222	HIS	N-CA-CB	5.26	120.08	110.60
1	T	4	DT	C6-C5-C7	-5.26	119.74	122.90
3	A	145	ASP	CB-CG-OD2	-5.26	113.56	118.30
3	A	190	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	T	3	DT	C6-C5-C7	-5.17	119.80	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	177	VAL	CA-CB-CG2	-5.15	103.17	110.90
3	A	170	ASP	N-CA-C	-5.15	97.11	111.00
2	P	1	DT	C4-C5-C7	5.13	122.08	119.00
3	A	258	ARG	NE-CZ-NH1	5.12	122.86	120.30
3	A	314	ASP	CB-CG-OD2	5.09	122.88	118.30
3	A	306	VAL	CB-CA-C	-5.05	101.80	111.40
1	T	7	DA	C8-N9-C4	5.04	107.82	105.80
1	T	3	DT	O4'-C1'-N1	5.03	111.52	108.00
3	A	137	ARG	NE-CZ-NH1	5.03	122.81	120.30
2	P	2	DC	P-O3'-C3'	5.03	125.73	119.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	P	7	DG	C3'
3	A	49	TYR	CA

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	T	145	0	80	5	0
2	P	164	0	93	31	0
3	A	2623	0	2641	359	0
4	A	1	0	0	0	0
5	A	2	0	0	0	0
6	A	20	0	6	10	0
7	A	99	0	0	21	0
7	P	19	0	0	5	0
7	T	15	0	0	3	0
All	All	3088	0	2820	388	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 68.

All (388) 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)
3:A:218:LEU:HB3	3:A:224:ILE:HD12	1.22	1.12
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.48	1.11
2:P:5:DA:H2''	2:P:6:DT:H5'	1.33	1.09
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.36	1.06
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.38	1.05
2:P:7:DG:H2''	2:P:8:DT:H5'	1.39	1.04
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.58	1.01
3:A:277:ILE:HD13	3:A:277:ILE:H	1.25	1.01
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.41	1.00
3:A:129:GLU:HG2	3:A:137:ARG:HD3	1.45	0.99
2:P:1:DT:H2''	2:P:2:DC:H5'	1.44	0.96
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.29	0.95
2:P:8:DT:H4'	3:A:272:PHE:HE2	1.30	0.95
3:A:29:VAL:HG21	3:A:94:SER:HB2	1.47	0.95
3:A:23:ALA:HB2	3:A:39:TYR:HB2	1.53	0.90
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.02	0.89
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.02	0.89
3:A:22:LEU:HD22	3:A:85:LEU:HD11	1.54	0.89
3:A:245:ASN:N	3:A:245:ASN:HD22	1.68	0.89
2:P:7:DG:C2'	2:P:8:DT:H5'	2.03	0.88
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.55	0.88
2:P:6:DT:H2''	2:P:7:DG:H5''	1.54	0.87
3:A:31:GLN:HB2	3:A:112:ARG:NH1	1.89	0.87
3:A:27:LYS:HE2	3:A:28:ASN:HD21	1.39	0.87
3:A:180:SER:HA	3:A:183:ARG:HE	1.39	0.85
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.59	0.85
3:A:285:HIS:NE2	3:A:289:LYS:HG2	1.93	0.84
2:P:8:DT:H4'	3:A:272:PHE:CE2	2.12	0.84
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.12	0.84
3:A:81:LYS:NZ	3:A:86:GLU:HB2	1.93	0.84
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.13	0.83
3:A:255:ILE:HG12	3:A:256:ASP:N	1.95	0.81
3:A:123:GLU:HG3	7:A:623:HOH:O	1.82	0.80
3:A:85:LEU:O	3:A:89:ARG:HB2	1.81	0.80
3:A:245:ASN:H	3:A:245:ASN:ND2	1.80	0.80
3:A:81:LYS:HZ2	3:A:86:GLU:HB2	1.46	0.80
3:A:286:ALA:HB1	3:A:323:ILE:HG21	1.63	0.79
3:A:286:ALA:HB2	3:A:323:ILE:HD13	1.65	0.79
3:A:155:MET:HE2	3:A:181:PHE:HB2	1.65	0.79
3:A:68:LYS:HB2	3:A:68:LYS:NZ	1.97	0.79
3:A:306:VAL:HG22	7:A:650:HOH:O	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:15:ILE:CG2	3:A:46:ILE:HD13	2.12	0.79
3:A:18:MET:HE3	3:A:76:PHE:CD2	2.19	0.78
3:A:245:ASN:N	3:A:245:ASN:ND2	2.29	0.78
1:T:6:DG:H2''	1:T:7:DA:C8	2.18	0.78
3:A:11:LEU:HD23	3:A:11:LEU:H	1.48	0.77
3:A:42:ALA:O	3:A:46:ILE:HG23	1.84	0.77
7:P:510:HOH:O	3:A:108:PRO:HD2	1.84	0.77
3:A:19:LEU:HD23	3:A:43:ALA:HA	1.67	0.77
3:A:111:ALA:O	3:A:115:VAL:HG23	1.85	0.76
3:A:180:SER:CB	3:A:183:ARG:HH21	1.99	0.76
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.67	0.75
3:A:182:ARG:HH11	3:A:273:THR:CG2	1.98	0.75
3:A:311:LEU:HB3	3:A:322:TYR:HE2	1.52	0.75
3:A:29:VAL:HG21	3:A:94:SER:CB	2.17	0.74
3:A:165:GLU:OE1	3:A:168:LYS:HD3	1.87	0.74
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.01	0.74
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.52	0.74
3:A:259:LEU:O	3:A:260:ILE:HD13	1.86	0.74
3:A:21:GLU:OE1	3:A:85:LEU:HG	1.87	0.74
3:A:255:ILE:HG12	3:A:256:ASP:H	1.52	0.73
3:A:270:LEU:CD1	3:A:333:ARG:HH12	2.01	0.73
3:A:166:VAL:O	3:A:169:VAL:HG13	1.88	0.73
3:A:59:ALA:O	3:A:65:VAL:HG21	1.89	0.73
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.70	0.72
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.19	0.72
2:P:6:DT:C2'	2:P:7:DG:H5''	2.20	0.71
3:A:12:ASN:HA	7:A:553:HOH:O	1.89	0.71
3:A:181:PHE:HA	7:A:530:HOH:O	1.90	0.71
3:A:268:GLY:O	3:A:271:TYR:HB3	1.89	0.71
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.72	0.71
2:P:1:DT:H2''	2:P:2:DC:C5'	2.19	0.71
3:A:204:SER:O	3:A:206:LYS:N	2.23	0.71
3:A:31:GLN:HE21	3:A:112:ARG:HH12	0.76	0.71
3:A:12:ASN:HD21	3:A:53:ILE:H	1.36	0.71
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.20	0.71
2:P:5:DA:H2''	2:P:6:DT:C5'	2.15	0.70
3:A:18:MET:HE2	3:A:82:LEU:HD22	1.74	0.70
3:A:294:ASN:HB2	3:A:295:GLU:OE1	1.91	0.70
3:A:291:PHE:HD2	3:A:323:ILE:HG22	1.55	0.69
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.22	0.69
2:P:6:DT:H2'	7:P:567:HOH:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:7:DG:H2'	2:P:8:DT:H71	1.73	0.69
3:A:183:ARG:HD3	3:A:273:THR:O	1.93	0.69
3:A:218:LEU:CB	3:A:224:ILE:HD12	2.13	0.68
3:A:291:PHE:CD2	3:A:323:ILE:HG22	2.27	0.68
3:A:22:LEU:HD22	3:A:85:LEU:CD1	2.23	0.68
3:A:122:LEU:HD23	3:A:126:ARG:NH1	2.09	0.68
3:A:276:ASP:O	3:A:280:LYS:HG3	1.93	0.68
3:A:299:ARG:HG2	3:A:310:PRO:HD3	1.74	0.68
3:A:68:LYS:O	3:A:72:LYS:HE3	1.93	0.68
3:A:323:ILE:O	3:A:324:GLN:HG2	1.95	0.67
3:A:165:GLU:O	3:A:169:VAL:HG12	1.93	0.67
3:A:328:ARG:O	3:A:333:ARG:NE	2.27	0.67
3:A:79:THR:O	3:A:81:LYS:N	2.27	0.67
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.24	0.66
3:A:254:ARG:CZ	3:A:254:ARG:HB3	2.25	0.66
3:A:41:LYS:HE2	3:A:64:GLY:HA2	1.78	0.66
3:A:165:GLU:HB3	3:A:217:GLN:CG	2.24	0.66
3:A:243:SER:HB3	3:A:249:GLU:HA	1.77	0.66
1:T:6:DG:N7	7:T:652:HOH:O	2.29	0.65
3:A:31:GLN:HB2	3:A:112:ARG:HH12	1.57	0.65
3:A:249:GLU:HG3	3:A:250:TYR:H	1.60	0.65
3:A:11:LEU:H	3:A:11:LEU:CD2	2.10	0.65
2:P:7:DG:H2''	2:P:8:DT:C5'	2.23	0.65
2:P:7:DG:C3'	2:P:8:DT:H5'	2.26	0.65
3:A:285:HIS:NE2	7:A:583:HOH:O	2.29	0.65
3:A:309:GLU:N	3:A:309:GLU:OE1	2.29	0.65
3:A:254:ARG:HB3	3:A:254:ARG:NH1	2.11	0.65
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.23	0.65
3:A:317:LYS:O	3:A:320:PHE:N	2.29	0.65
3:A:18:MET:O	3:A:21:GLU:HB2	1.97	0.65
3:A:18:MET:CE	3:A:76:PHE:HB2	2.20	0.65
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.78	0.65
3:A:327:TYR:HD1	3:A:328:ARG:N	1.94	0.64
3:A:243:SER:OG	3:A:249:GLU:HG3	1.97	0.64
2:P:8:DT:H3'	6:A:338:TTP:C5'	2.27	0.64
3:A:270:LEU:HD11	3:A:333:ARG:HH12	1.62	0.64
3:A:275:SER:O	3:A:279:ASN:HB2	1.96	0.64
3:A:292:THR:O	3:A:298:ILE:HA	1.97	0.64
3:A:49:TYR:CD1	3:A:53:ILE:HD11	2.33	0.63
3:A:14:GLY:O	3:A:18:MET:N	2.26	0.63
3:A:99:PHE:HD1	3:A:100:LEU:HD13	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:250:TYR:HB3	7:A:577:HOH:O	1.99	0.63
3:A:68:LYS:HB2	3:A:68:LYS:HZ2	1.62	0.63
3:A:277:ILE:HG13	3:A:335:GLU:HB3	1.81	0.63
3:A:289:LYS:HD3	3:A:289:LYS:N	2.10	0.63
3:A:37:ASN:HB3	7:A:556:HOH:O	1.98	0.63
3:A:196:THR:OG1	3:A:197:HIS:N	2.31	0.63
3:A:15:ILE:HG22	3:A:46:ILE:HD13	1.81	0.63
3:A:233:THR:HB	7:A:538:HOH:O	1.98	0.62
3:A:150:ILE:N	3:A:188:SER:O	2.29	0.62
3:A:29:VAL:CG2	3:A:94:SER:HB2	2.27	0.62
3:A:152:ARG:HA	3:A:155:MET:HB2	1.81	0.62
3:A:18:MET:HE1	3:A:76:PHE:CB	2.23	0.62
3:A:277:ILE:H	3:A:277:ILE:CD1	2.06	0.62
3:A:15:ILE:HD11	3:A:77:LEU:HD11	1.81	0.62
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.34	0.62
3:A:44:SER:O	3:A:47:ALA:HB3	2.00	0.62
3:A:29:VAL:HA	3:A:97:ILE:HD12	1.80	0.62
3:A:114:PHE:HB3	3:A:119:ILE:HB	1.82	0.61
3:A:326:LYS:HE3	3:A:328:ARG:HH21	1.65	0.61
3:A:103:VAL:HB	3:A:106:ILE:HD12	1.83	0.61
3:A:124:ASP:O	3:A:128:ASN:ND2	2.32	0.61
3:A:150:ILE:HG21	3:A:158:MET:CE	2.30	0.61
3:A:206:LYS:HG2	7:A:624:HOH:O	2.01	0.61
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.81	0.60
3:A:16:THR:HG23	3:A:46:ILE:HD11	1.83	0.60
3:A:11:LEU:HD23	3:A:11:LEU:N	2.17	0.60
3:A:53:ILE:O	3:A:54:LYS:HD2	2.01	0.60
3:A:212:HIS:HB3	7:A:541:HOH:O	2.02	0.60
3:A:209:LYS:HA	3:A:212:HIS:HB2	1.84	0.59
3:A:299:ARG:HG2	3:A:310:PRO:CD	2.31	0.59
3:A:218:LEU:HB3	3:A:224:ILE:CD1	2.15	0.59
3:A:180:SER:HA	3:A:183:ARG:NE	2.12	0.59
3:A:25:PHE:CE1	3:A:29:VAL:HB	2.38	0.58
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.33	0.58
3:A:145:ASP:OD1	3:A:145:ASP:N	2.33	0.58
3:A:18:MET:CE	3:A:82:LEU:HD13	2.34	0.57
3:A:251:PRO:O	3:A:253:ARG:HD2	2.04	0.57
3:A:121:THR:HG23	3:A:124:ASP:OD1	2.04	0.57
3:A:31:GLN:N	7:A:641:HOH:O	2.28	0.57
3:A:150:ILE:HG12	3:A:253:ARG:HG2	1.87	0.57
3:A:73:ILE:HG22	3:A:77:LEU:HD13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:191:MET:CG	3:A:255:ILE:HG13	2.26	0.57
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.87	0.57
3:A:155:MET:CE	3:A:181:PHE:HB2	2.34	0.56
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.25	0.56
3:A:237:GLY:O	3:A:254:ARG:NH1	2.38	0.56
3:A:245:ASN:HD22	3:A:245:ASN:H	1.39	0.56
3:A:41:LYS:O	3:A:44:SER:HB3	2.04	0.56
3:A:92:ASP:HA	3:A:95:SER:HB2	1.87	0.56
3:A:271:TYR:HB2	7:A:592:HOH:O	2.06	0.56
3:A:27:LYS:CE	3:A:28:ASN:HD21	2.13	0.56
3:A:165:GLU:O	3:A:168:LYS:N	2.39	0.56
3:A:270:LEU:HD11	3:A:333:ARG:NH1	2.20	0.56
3:A:49:TYR:CD2	3:A:50:PRO:HD2	2.40	0.56
3:A:286:ALA:CB	3:A:323:ILE:HD13	2.35	0.55
3:A:121:THR:HG23	3:A:124:ASP:CG	2.26	0.55
3:A:108:PRO:O	3:A:111:ALA:HB3	2.05	0.55
3:A:123:GLU:O	3:A:127:LYS:HG2	2.06	0.55
3:A:129:GLU:CG	3:A:137:ARG:HD3	2.30	0.55
3:A:277:ILE:HG12	3:A:335:GLU:HA	1.89	0.55
3:A:60:LYS:HG3	3:A:60:LYS:O	2.06	0.55
3:A:311:LEU:HB3	3:A:322:TYR:CE2	2.38	0.55
3:A:151:PRO:HG2	3:A:154:GLU:CD	2.27	0.55
2:P:8:DT:H3'	6:A:338:TTP:C4'	2.36	0.55
3:A:253:ARG:HH11	3:A:253:ARG:CG	2.19	0.55
3:A:213:GLN:HG3	7:A:644:HOH:O	2.06	0.54
3:A:248:LYS:H	3:A:248:LYS:HD2	1.72	0.54
3:A:99:PHE:CD1	3:A:100:LEU:HD13	2.42	0.54
3:A:272:PHE:O	6:A:338:TTP:O3'	2.25	0.54
3:A:270:LEU:HD23	3:A:319:ILE:HG21	1.89	0.54
3:A:279:ASN:O	3:A:283:ARG:HD2	2.07	0.54
3:A:300:PRO:HD3	3:A:311:LEU:HD22	1.88	0.54
3:A:246:ASP:O	3:A:247:GLU:HB2	2.08	0.54
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.43	0.54
3:A:172:GLU:HG3	3:A:198:PRO:HG2	1.90	0.54
3:A:15:ILE:HB	3:A:46:ILE:CD1	2.38	0.53
3:A:15:ILE:HD13	3:A:73:ILE:HG23	1.90	0.53
3:A:295:GLU:H	3:A:295:GLU:CD	2.06	0.53
3:A:236:MET:HG3	3:A:256:ASP:OD1	2.08	0.53
3:A:157:GLN:O	3:A:160:ASP:HB3	2.09	0.53
3:A:230:LYS:HA	3:A:235:PHE:HA	1.90	0.53
3:A:18:MET:HE1	3:A:82:LEU:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:27:LYS:HB3	3:A:36:TYR:CG	2.44	0.53
2:P:8:DT:H3'	6:A:338:TTP:H5'2	1.91	0.52
3:A:122:LEU:HD23	3:A:126:ARG:CZ	2.38	0.52
3:A:180:SER:CA	3:A:183:ARG:HH21	2.22	0.52
3:A:211:LEU:HD21	3:A:235:PHE:HB2	1.90	0.52
3:A:41:LYS:HD3	3:A:42:ALA:H	1.75	0.52
3:A:303:VAL:C	3:A:305:GLY:H	2.13	0.52
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.45	0.52
3:A:285:HIS:HD2	3:A:323:ILE:HD12	1.75	0.52
3:A:240:GLN:O	3:A:242:PRO:HD3	2.08	0.52
3:A:128:ASN:ND2	3:A:128:ASN:N	2.58	0.51
3:A:295:GLU:HA	7:A:592:HOH:O	2.10	0.51
3:A:29:VAL:HA	3:A:97:ILE:CD1	2.40	0.51
3:A:41:LYS:NZ	3:A:64:GLY:O	2.41	0.51
3:A:92:ASP:O	3:A:95:SER:N	2.43	0.51
3:A:176:THR:HG22	3:A:178:CYS:SG	2.50	0.51
2:P:8:DT:OP2	6:A:338:TTP:O1A	2.28	0.51
3:A:278:PHE:CD2	3:A:333:ARG:HB3	2.45	0.51
3:A:188:SER:HB3	7:A:522:HOH:O	2.09	0.51
3:A:223:PHE:O	3:A:239:CYS:HA	2.11	0.51
3:A:277:ILE:CG1	3:A:335:GLU:HB3	2.41	0.51
3:A:15:ILE:O	3:A:19:LEU:HB2	2.10	0.51
3:A:200:PHE:O	3:A:262:LYS:N	2.40	0.51
3:A:249:GLU:HG3	3:A:250:TYR:N	2.26	0.51
3:A:46:ILE:HG13	3:A:47:ALA:N	2.24	0.51
3:A:254:ARG:CA	3:A:254:ARG:HH11	2.25	0.50
3:A:270:LEU:HD13	3:A:316:GLU:OE2	2.12	0.50
3:A:81:LYS:HZ3	3:A:86:GLU:HB2	1.73	0.50
3:A:114:PHE:HZ	3:A:132:LEU:HD23	1.76	0.50
3:A:270:LEU:HD12	3:A:270:LEU:O	2.12	0.50
3:A:327:TYR:CD1	3:A:328:ARG:N	2.78	0.50
3:A:167:LYS:O	3:A:167:LYS:HG3	2.06	0.50
3:A:270:LEU:HD12	3:A:270:LEU:C	2.31	0.50
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.73	0.49
3:A:207:GLN:HB3	7:A:625:HOH:O	2.12	0.49
3:A:241:LEU:HB2	3:A:250:TYR:CD2	2.47	0.49
3:A:317:LYS:O	3:A:320:PHE:HB2	2.12	0.49
3:A:26:GLU:O	3:A:30:SER:O	2.30	0.49
3:A:323:ILE:C	3:A:324:GLN:HG2	2.33	0.49
3:A:251:PRO:HG2	3:A:253:ARG:CZ	2.43	0.49
3:A:298:ILE:O	3:A:311:LEU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.34	0.49
3:A:52:LYS:HD3	3:A:54:LYS:HE3	1.95	0.49
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.41	0.49
3:A:288:GLU:OE1	3:A:288:GLU:HA	2.12	0.49
2:P:8:DT:C3'	6:A:338:TTP:C4'	2.91	0.48
3:A:19:LEU:HD23	3:A:43:ALA:CA	2.41	0.48
3:A:27:LYS:HE2	3:A:28:ASN:ND2	2.19	0.48
3:A:68:LYS:HB2	3:A:68:LYS:HZ3	1.77	0.48
3:A:321:ASP:OD1	3:A:321:ASP:N	2.41	0.48
2:P:8:DT:C2'	6:A:338:TTP:H5'2	2.43	0.48
3:A:271:TYR:CD1	3:A:283:ARG:NH2	2.79	0.48
3:A:152:ARG:O	3:A:155:MET:N	2.46	0.48
3:A:165:GLU:HA	3:A:168:LYS:HD3	1.96	0.48
3:A:180:SER:HB2	3:A:185:ALA:HB2	1.94	0.48
3:A:195:LEU:HD23	3:A:259:LEU:HD13	1.94	0.48
3:A:271:TYR:CE1	3:A:283:ARG:NH2	2.82	0.48
2:P:6:DT:H5'	7:P:567:HOH:O	2.14	0.48
2:P:8:DT:H3'	6:A:338:TTP:H4'	1.95	0.48
3:A:29:VAL:HG22	3:A:97:ILE:HD12	1.96	0.48
3:A:97:ILE:O	3:A:97:ILE:HG22	2.14	0.48
3:A:194:LEU:HD12	3:A:194:LEU:HA	1.63	0.48
3:A:286:ALA:O	3:A:291:PHE:HB2	2.14	0.48
3:A:285:HIS:CD2	3:A:289:LYS:HG2	2.49	0.48
3:A:249:GLU:CG	3:A:250:TYR:N	2.78	0.47
3:A:53:ILE:HG21	3:A:59:ALA:HB2	1.96	0.47
3:A:210:LEU:HB2	3:A:259:LEU:HD21	1.96	0.47
3:A:212:HIS:N	3:A:212:HIS:CD2	2.82	0.47
3:A:150:ILE:CG1	3:A:253:ARG:HG2	2.43	0.47
3:A:182:ARG:HH11	3:A:273:THR:CB	2.26	0.47
3:A:210:LEU:HB2	3:A:259:LEU:CD2	2.45	0.47
3:A:294:ASN:HB3	7:A:580:HOH:O	2.14	0.47
3:A:301:LEU:HD12	3:A:301:LEU:HA	1.55	0.47
3:A:210:LEU:CB	3:A:259:LEU:HD21	2.44	0.47
3:A:283:ARG:HG3	7:A:555:HOH:O	2.14	0.47
3:A:41:LYS:HD3	3:A:42:ALA:N	2.29	0.47
3:A:53:ILE:C	3:A:54:LYS:HD2	2.35	0.47
3:A:41:LYS:O	3:A:45:VAL:HG13	2.15	0.46
3:A:77:LEU:HD12	3:A:77:LEU:N	2.28	0.46
3:A:103:VAL:HG22	3:A:143:PHE:CD2	2.50	0.46
3:A:253:ARG:NH1	7:A:503:HOH:O	2.48	0.46
3:A:270:LEU:HA	3:A:316:GLU:OE2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:8:DT:OP2	3:A:192:ASP:OD2	2.34	0.46
3:A:19:LEU:HD12	3:A:19:LEU:HA	1.83	0.46
3:A:121:THR:O	3:A:124:ASP:HB2	2.15	0.46
3:A:128:ASN:HB3	3:A:131:LYS:HG3	1.97	0.46
2:P:6:DT:H6	7:P:567:HOH:O	1.98	0.46
3:A:79:THR:C	3:A:81:LYS:H	2.17	0.46
3:A:114:PHE:CZ	3:A:132:LEU:CD2	2.99	0.46
7:T:527:HOH:O	3:A:229:SER:HB3	2.16	0.46
3:A:279:ASN:HD22	3:A:279:ASN:HA	1.42	0.46
3:A:146:PHE:CD1	3:A:146:PHE:N	2.78	0.45
3:A:241:LEU:HB2	3:A:250:TYR:CG	2.51	0.45
1:T:5:DA:H5'	7:T:527:HOH:O	2.15	0.45
3:A:30:SER:HB3	7:A:561:HOH:O	2.16	0.45
3:A:321:ASP:O	3:A:324:GLN:N	2.48	0.45
2:P:8:DT:C3'	6:A:338:TTP:H5'2	2.47	0.45
3:A:57:ALA:HA	3:A:60:LYS:HB3	1.97	0.45
3:A:73:ILE:O	3:A:76:PHE:N	2.50	0.45
3:A:172:GLU:HB3	3:A:197:HIS:NE2	2.32	0.45
3:A:49:TYR:CE1	3:A:53:ILE:CG1	3.00	0.45
3:A:145:ASP:HB3	3:A:252:HIS:O	2.16	0.45
3:A:270:LEU:HD13	3:A:270:LEU:HA	1.62	0.45
3:A:83:ARG:O	3:A:83:ARG:HG3	2.15	0.45
3:A:263:ASP:O	3:A:264:GLN:HG2	2.17	0.45
3:A:332:ASP:OD1	3:A:332:ASP:O	2.35	0.45
1:T:4:DT:H5''	3:A:231:GLY:HA3	1.99	0.44
2:P:4:DA:H5''	7:P:614:HOH:O	2.17	0.44
3:A:18:MET:HG2	3:A:19:LEU:N	2.27	0.44
3:A:43:ALA:O	3:A:47:ALA:HB2	2.17	0.44
3:A:89:ARG:O	3:A:89:ARG:NE	2.47	0.44
3:A:254:ARG:NH1	3:A:254:ARG:CB	2.79	0.44
3:A:266:TYR:HB2	3:A:313:VAL:CG1	2.47	0.44
3:A:309:GLU:N	3:A:310:PRO:CD	2.79	0.44
3:A:163:LEU:HD23	3:A:163:LEU:HA	1.54	0.44
2:P:5:DA:P	3:A:107:GLY:HA3	2.57	0.44
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.61	0.44
3:A:248:LYS:O	3:A:248:LYS:HG2	2.16	0.44
3:A:298:ILE:O	3:A:298:ILE:HG23	2.17	0.44
3:A:266:TYR:O	3:A:270:LEU:N	2.44	0.44
3:A:282:MET:HE2	3:A:282:MET:HB3	1.66	0.44
3:A:15:ILE:HG21	3:A:46:ILE:HD13	1.97	0.44
3:A:285:HIS:CD2	3:A:323:ILE:HD12	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:315:SER:OG	3:A:316:GLU:N	2.51	0.43
2:P:6:DT:H2''	2:P:7:DG:C8	2.53	0.43
3:A:260:ILE:HG22	3:A:261:PRO:HD2	1.99	0.43
3:A:33:ILE:O	3:A:33:ILE:HG13	2.16	0.43
3:A:250:TYR:HD1	3:A:251:PRO:HD2	1.84	0.43
3:A:316:GLU:OE1	3:A:333:ARG:NH2	2.51	0.43
3:A:135:HIS:CD2	3:A:228:LEU:HG	2.52	0.43
3:A:12:ASN:HB3	3:A:46:ILE:HD12	2.01	0.43
3:A:31:GLN:CB	3:A:112:ARG:HH12	2.30	0.43
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.33	0.43
3:A:260:ILE:HG23	3:A:260:ILE:HD12	1.73	0.43
1:T:4:DT:O2	2:P:4:DA:H2	2.02	0.43
3:A:56:GLY:N	3:A:74:ASP:OD1	2.51	0.43
3:A:81:LYS:HZ3	3:A:86:GLU:HA	1.83	0.43
3:A:103:VAL:HG22	3:A:143:PHE:HD2	1.83	0.43
2:P:8:DT:OP2	3:A:190:ASP:OD2	2.37	0.43
3:A:100:LEU:HD21	3:A:119:ILE:O	2.19	0.43
3:A:122:LEU:CD2	3:A:126:ARG:NH1	2.80	0.42
3:A:235:PHE:CD2	3:A:235:PHE:C	2.91	0.42
3:A:288:GLU:C	3:A:290:GLY:H	2.21	0.42
3:A:106:ILE:O	3:A:106:ILE:HG22	2.09	0.42
3:A:18:MET:HE2	3:A:82:LEU:HD13	1.99	0.42
3:A:253:ARG:CG	3:A:253:ARG:NH1	2.80	0.42
3:A:244:LYS:C	3:A:246:ASP:H	2.23	0.42
3:A:18:MET:HE3	3:A:76:PHE:HD2	1.75	0.42
3:A:62:LEU:CD1	3:A:62:LEU:N	2.82	0.42
3:A:265:TYR:O	3:A:268:GLY:N	2.52	0.42
3:A:28:ASN:ND2	3:A:28:ASN:N	2.65	0.42
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.60	0.41
3:A:254:ARG:HH11	3:A:254:ARG:HA	1.84	0.41
2:P:8:DT:O3'	6:A:338:TTP:O4'	2.38	0.41
3:A:329:GLU:HA	3:A:330:PRO:HD2	1.78	0.41
3:A:34:HIS:O	3:A:37:ASN:N	2.54	0.41
3:A:180:SER:O	3:A:185:ALA:HB3	2.20	0.41
3:A:271:TYR:HD1	3:A:283:ARG:HH21	1.65	0.41
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.98	0.41
3:A:11:LEU:CD2	3:A:11:LEU:N	2.77	0.41
3:A:196:THR:O	3:A:197:HIS:HB2	2.21	0.41
3:A:293:ILE:CD1	3:A:298:ILE:CD1	2.99	0.41
3:A:115:VAL:O	3:A:118:GLY:N	2.52	0.41
3:A:142:TYR:CE1	3:A:252:HIS:ND1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:180:SER:HA	3:A:183:ARG:HH21	1.85	0.41
3:A:197:HIS:CE1	3:A:199:SER:HB2	2.56	0.41
3:A:210:LEU:HD11	7:A:625:HOH:O	2.21	0.41
3:A:271:TYR:HD2	3:A:272:PHE:CD1	2.38	0.41
3:A:49:TYR:CB	3:A:50:PRO:HD2	2.50	0.41
3:A:200:PHE:CE1	3:A:206:LYS:HA	2.56	0.41
3:A:83:ARG:O	3:A:86:GLU:N	2.53	0.40
3:A:270:LEU:HD23	3:A:319:ILE:HD13	2.03	0.40
3:A:288:GLU:C	3:A:289:LYS:HD3	2.41	0.40
3:A:265:TYR:O	3:A:269:VAL:HG23	2.21	0.40
3:A:327:TYR:HD1	3:A:328:ARG:H	1.63	0.40
3:A:35:LYS:O	3:A:38:ALA:HB3	2.20	0.40
3:A:73:ILE:HD13	3:A:73:ILE:HG21	1.75	0.40
3:A:191:MET:HE2	3:A:191:MET:HB2	1.82	0.40
3:A:226:ASP:OD1	3:A:226:ASP:N	2.54	0.40
3:A:291:PHE:CD1	3:A:300:PRO:HA	2.56	0.40
3:A:116:ASP:C	3:A:118:GLY:N	2.74	0.40
3:A:180:SER:HB2	3:A:185:ALA:CB	2.51	0.40
3:A:303:VAL:C	3:A:305:GLY:N	2.74	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
3	A	325/335 (97%)	253 (78%)	51 (16%)	21 (6%)	<b>1</b> <b>8</b>

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	204	SER
3	A	205	THR

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Mol	Chain	Res	Type
3	A	222	HIS
3	A	244	LYS
3	A	246	ASP
3	A	247	GLU
3	A	13	GLY
3	A	78	ALA
3	A	80	GLY
3	A	202	SER
3	A	310	PRO
3	A	185	ALA
3	A	262	LYS
3	A	265	TYR
3	A	289	LYS
3	A	324	GLN
3	A	242	PRO
3	A	271	TYR
3	A	334	SER
3	A	309	GLU
3	A	207	GLN

### 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
3	A	288/295 (98%)	219 (76%)	69 (24%)	<b>0</b>   <b>2</b>

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	10	THR
3	A	11	LEU
3	A	18	MET
3	A	19	LEU
3	A	22	LEU
3	A	24	ASN
3	A	27	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	A	33	ILE
3	A	37	ASN
3	A	41	LYS
3	A	46	ILE
3	A	52	LYS
3	A	54	LYS
3	A	67	THR
3	A	68	LYS
3	A	79	THR
3	A	81	LYS
3	A	86	GLU
3	A	89	ARG
3	A	92	ASP
3	A	93	THR
3	A	94	SER
3	A	100	LEU
3	A	101	THR
3	A	104	SER
3	A	119	ILE
3	A	121	THR
3	A	122	LEU
3	A	133	ASN
3	A	140	LEU
3	A	145	ASP
3	A	153	GLU
3	A	159	GLN
3	A	161	ILE
3	A	168	LYS
3	A	169	VAL
3	A	191	MET
3	A	192	ASP
3	A	194	LEU
3	A	199	SER
3	A	206	LYS
3	A	214	VAL
3	A	225	THR
3	A	226	ASP
3	A	228	LEU
3	A	235	PHE
3	A	245	ASN
3	A	248	LYS
3	A	253	ARG

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Mol	Chain	Res	Type
3	A	258	ARG
3	A	270	LEU
3	A	277	ILE
3	A	279	ASN
3	A	287	LEU
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	301	LEU
3	A	303	VAL
3	A	304	THR
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	325	TRP
3	A	326	LYS
3	A	327	TYR
3	A	329	GLU
3	A	331	LYS
3	A	332	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	37	ASN
3	A	98	ASN
3	A	133	ASN
3	A	136	GLN
3	A	213	GLN
3	A	217	GLN
3	A	245	ASN
3	A	279	ASN
3	A	285	HIS
3	A	294	ASN

### 5.3.3 RNA

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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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	TTP	A	338	4	16,20,30	1.21	1 (6%)	22,31,47	1.77	3 (13%)

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	TTP	A	338	4	-	8/18/28/34	0/1/1/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	338	TTP	O3'-C3'	-3.20	1.36	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	338	TTP	O3'-C3'-C4'	-5.31	89.80	110.10
6	A	338	TTP	PA-O5'-C5'	-3.18	103.01	121.68
6	A	338	TTP	O3'-C3'-C2'	-3.10	104.16	111.54

There are no chirality outliers.

All (8) torsion outliers are listed below:

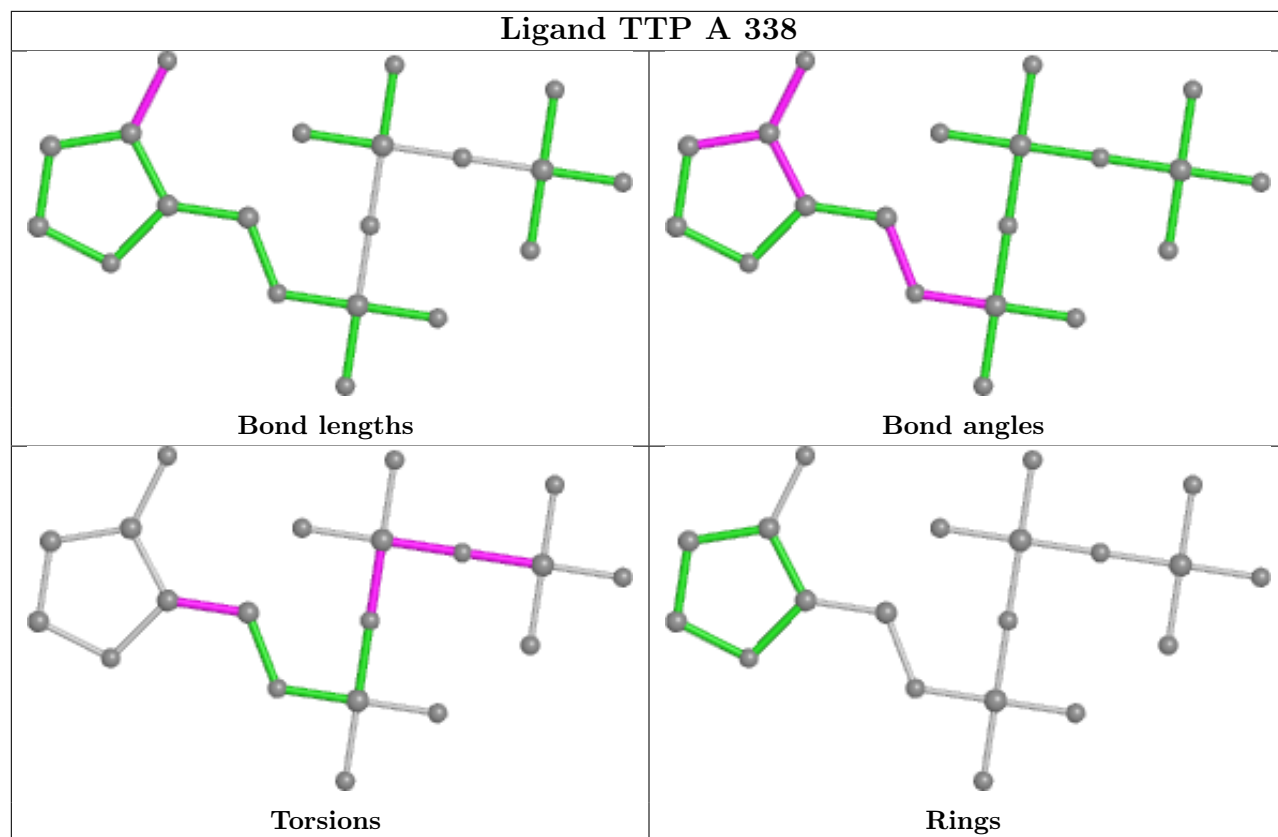
Mol	Chain	Res	Type	Atoms
6	A	338	TTP	PB-O3B-PG-O2G
6	A	338	TTP	O4'-C4'-C5'-O5'
6	A	338	TTP	PA-O3A-PB-O1B
6	A	338	TTP	PA-O3A-PB-O2B
6	A	338	TTP	PG-O3B-PB-O1B
6	A	338	TTP	PG-O3B-PB-O2B
6	A	338	TTP	C3'-C4'-C5'-O5'
6	A	338	TTP	PB-O3B-PG-O1G

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	338	TTP	10	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 [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<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	T	8/8 (100%)	-0.87	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	8, 34, 93, 97	0
2	P	8/8 (100%)	-0.63	1 (12%) <span style="border: 1px solid red; padding: 2px;">3</span> <span style="border: 1px solid red; padding: 2px;">1</span>	13, 29, 57, 99	0
3	A	326/335 (97%)	-0.93	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	1, 29, 84, 100	0
All	All	342/351 (97%)	-0.92	1 (0%) <span style="border: 1px solid blue; padding: 2px;">94</span> <span style="border: 1px solid blue; padding: 2px;">88</span>	1, 29, 87, 100	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	8	DT	2.4

### 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 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<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.

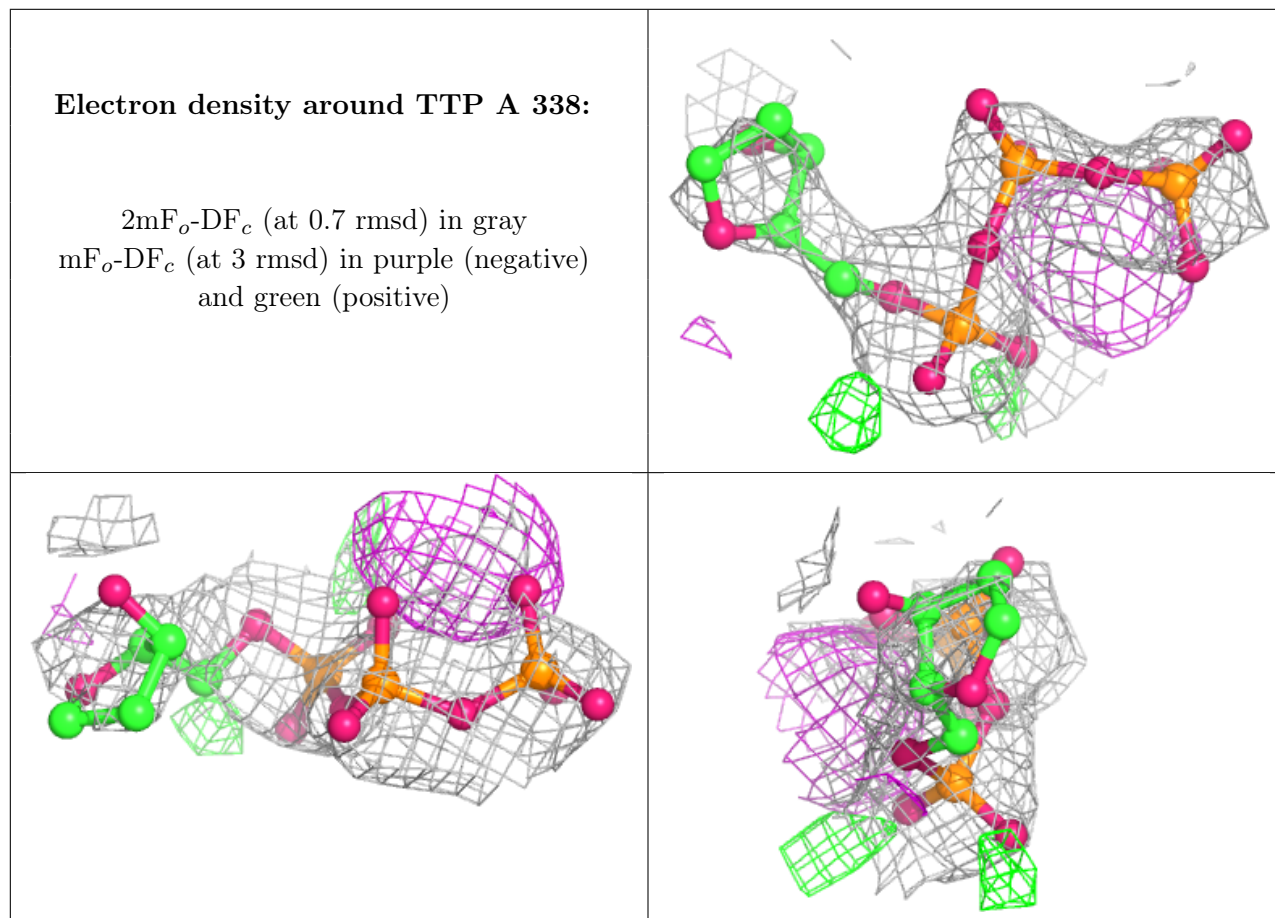
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	TTP	A	338	20/29	0.77	0.33	65,75,81,83	20
4	MN	A	339	1/1	0.84	0.49	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NA	A	342	1/1	0.91	0.21	50,50,50,50	0
5	NA	A	341	1/1	0.97	0.20	8,8,8,8	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.