



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:04 AM UTC

PDB ID : 8ICA / pdb_00008ica
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7) COMPLEXED WITH SEVEN BASE PAIRS OF DNA; SOAKED IN THE PRESENCE OF DATP (1 MILLIMOLAR) AND CACL2 (5 MILLIMOLAR)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1995-12-15
Resolution : 3.00 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 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

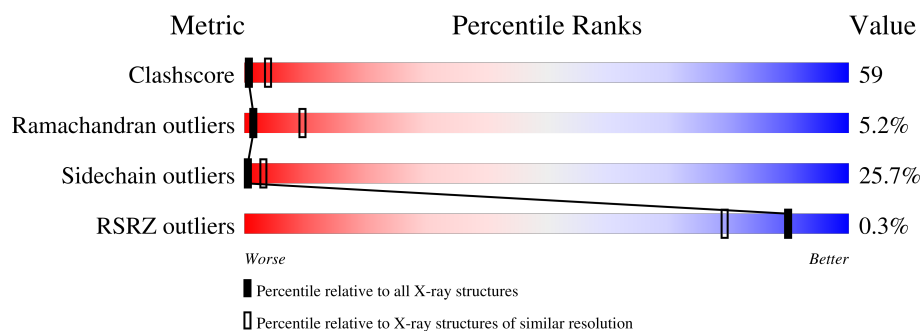
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	T	8	12% 88%
2	P	7	29% 71%
3	A	335	20% 38% 33% 7%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3067 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
1	T	8	Total	C	N	O	P	0	0	0
			145	69	27	42	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	P	0	0	0
			144	69	24	44	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	327	Total	C	N	O	S	19	0	0
			2623	1657	458	499	9			

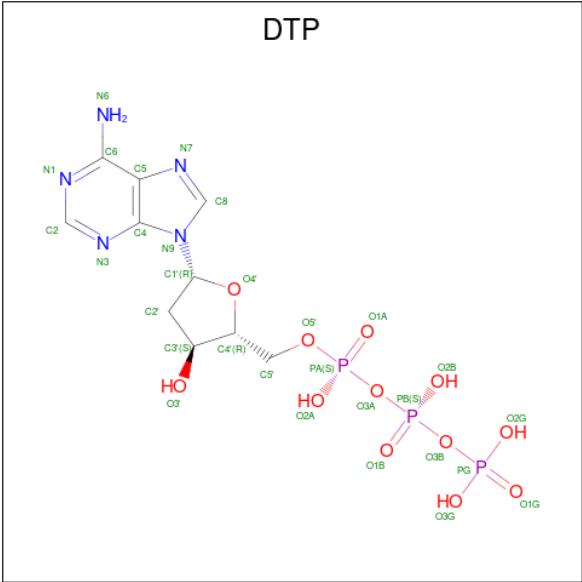
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 6 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	T	14	Total	O	0	0
			14	14		
7	P	18	Total	O	0	0
			18	18		
7	A	111	Total	O	0	0
			111	111		

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	179.84Å 57.72Å 48.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-3.00) 89.5 (20.00-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.70Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.159 , (Not available) 0.153 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 246.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3067	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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, DTP, 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	T	0.78	0/162	3.34	15/249 (6.0%)
2	P	1.13	1/160 (0.6%)	4.33	19/243 (7.8%)
3	A	1.54	21/2672 (0.8%)	2.24	143/3590 (4.0%)
All	All	1.49	22/2994 (0.7%)	2.49	177/4082 (4.3%)

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
3	A	2	0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DT	OP3-P	7.37	1.63	1.48
3	A	224	ILE	CA-CB	-6.89	1.45	1.54
3	A	241	LEU	CA-C	-6.64	1.45	1.53
3	A	242	PRO	N-CA	-6.01	1.39	1.47
3	A	224	ILE	CA-C	-5.99	1.45	1.52
3	A	15	ILE	CA-C	-5.88	1.46	1.52
3	A	63	PRO	N-CA	-5.80	1.40	1.47
3	A	116	ASP	CA-C	-5.72	1.45	1.52
3	A	170	ASP	CA-C	-5.67	1.45	1.52
3	A	30	SER	C-N	-5.65	1.26	1.33
3	A	106	ILE	CA-C	-5.64	1.45	1.52
3	A	149	ARG	C-N	5.57	1.38	1.33
3	A	65	VAL	CA-C	-5.46	1.47	1.52
3	A	165	GLU	N-CA	-5.28	1.40	1.46
3	A	147	GLU	CD-OE2	5.23	1.35	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	261	PRO	CA-C	-5.23	1.47	1.52
3	A	24	ASN	CA-C	-5.21	1.46	1.52
3	A	99	PHE	CA-C	5.21	1.59	1.52
3	A	217	GLN	N-CA	-5.12	1.40	1.46
3	A	251	PRO	N-CA	-5.06	1.41	1.47
3	A	291	PHE	CA-C	-5.04	1.48	1.53
3	A	326	LYS	CE-NZ	-5.00	1.34	1.49

All (177) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	1	DT	C6-N1-C1'	-27.15	78.62	119.35
2	P	1	DT	C2-N1-C1'	27.13	160.04	119.35
1	T	7	DA	C4-N9-C1'	-22.79	92.87	127.05
1	T	7	DA	C8-N9-C1'	20.81	158.26	127.05
1	T	4	DT	C6-N1-C1'	-20.70	88.29	119.35
1	T	4	DT	C2-N1-C1'	20.66	150.34	119.35
2	P	6	DT	C6-N1-C1'	-19.31	90.38	119.35
2	P	6	DT	C2-N1-C1'	19.04	147.91	119.35
2	P	7	DG	C8-N9-C1'	18.24	154.36	127.00
2	P	7	DG	C4-N9-C1'	-18.19	99.72	127.00
2	P	3	DT	C2-N1-C1'	14.93	141.75	119.35
2	P	3	DT	C6-N1-C1'	-14.78	97.18	119.35
3	A	150	ILE	N-CA-C	12.61	119.03	107.56
2	P	2	DC	C2-N1-C1'	12.47	138.41	119.70
3	A	28	ASN	CA-CB-CG	-11.81	100.79	112.60
2	P	2	DC	C6-N1-C1'	-11.46	102.51	119.70
3	A	168	LYS	N-CA-CB	10.49	125.22	110.01
3	A	116	ASP	N-CA-CB	9.92	124.40	109.91
3	A	88	ILE	CB-CA-C	-9.89	99.08	112.04
3	A	303	VAL	N-CA-C	9.86	120.67	110.62
2	P	5	DA	C4-N9-C1'	9.85	141.82	127.05
3	A	266	TYR	CA-CB-CG	-9.44	96.91	113.90
2	P	5	DA	C8-N9-C1'	-9.32	113.07	127.05
3	A	157	GLN	N-CA-CB	8.84	123.24	110.16
3	A	83	ARG	N-CA-CB	8.58	122.44	109.91
3	A	49	TYR	CA-C-N	8.49	130.46	119.84
3	A	49	TYR	C-N-CA	8.49	130.46	119.84
3	A	309	GLU	CA-C-N	8.42	130.36	119.84
3	A	309	GLU	C-N-CA	8.42	130.36	119.84
3	A	243	SER	N-CA-C	-8.12	97.45	109.15
3	A	15	ILE	N-CA-CB	7.96	119.30	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	20	THR	CB-CA-C	7.91	123.40	110.90
3	A	49	TYR	O-C-N	7.82	127.57	121.47
3	A	68	LYS	N-CA-CB	7.72	121.18	109.91
1	T	2	DA	C4-N9-C1'	-7.58	115.68	127.05
3	A	92	ASP	CB-CA-C	7.52	122.88	110.92
3	A	92	ASP	N-CA-CB	7.46	121.16	109.82
3	A	222	HIS	CA-CB-CG	-7.42	106.38	113.80
3	A	40	ARG	N-CA-C	7.41	120.80	111.69
1	T	6	DG	C8-N9-C1'	7.34	138.00	127.00
1	T	6	DG	C4-N9-C1'	-7.30	116.05	127.00
3	A	311	LEU	CA-C-N	7.23	129.13	120.23
3	A	311	LEU	C-N-CA	7.23	129.13	120.23
3	A	99	PHE	CA-CB-CG	-7.22	106.58	113.80
1	T	2	DA	C8-N9-C1'	7.21	137.86	127.05
3	A	116	ASP	CB-CA-C	7.14	121.95	110.96
3	A	30	SER	CA-C-N	-7.10	111.90	122.83
3	A	30	SER	C-N-CA	-7.10	111.90	122.83
3	A	292	THR	CB-CA-C	7.02	119.92	110.94
3	A	170	ASP	N-CA-C	-7.02	96.75	108.75
3	A	159	GLN	CB-CA-C	-7.01	98.77	110.68
2	P	1	DT	C1'-O4'-C4'	-6.95	99.27	109.70
3	A	291	PHE	CA-CB-CG	-6.92	106.88	113.80
3	A	17	ASP	CB-CA-C	6.89	121.69	110.88
3	A	54	LYS	N-CA-C	6.87	121.83	113.38
3	A	115	VAL	O-C-N	6.81	128.48	121.87
3	A	223	PHE	CA-CB-CG	-6.77	107.03	113.80
3	A	97	ILE	CB-CA-C	-6.73	103.36	111.97
3	A	77	LEU	N-CA-CB	6.66	119.73	110.07
3	A	137	ARG	N-CA-C	-6.60	103.35	111.40
3	A	211	LEU	CA-C-N	6.57	129.92	120.79
3	A	211	LEU	C-N-CA	6.57	129.92	120.79
3	A	256	ASP	CA-CB-CG	6.55	119.15	112.60
3	A	241	LEU	CB-CA-C	-6.53	99.66	109.26
1	T	5	DA	P-O5'-C5'	-6.53	110.20	120.00
3	A	40	ARG	N-CA-CB	6.52	119.92	110.20
2	P	3	DT	N1-C1'-C2'	6.51	123.27	113.50
3	A	334	SER	N-CA-C	6.33	119.86	111.75
3	A	86	GLU	N-CA-CB	6.29	119.19	110.07
3	A	309	GLU	N-CA-C	6.28	123.69	109.81
3	A	161	ILE	N-CA-C	6.26	116.43	110.42
3	A	176	THR	CA-C-N	-6.26	114.55	122.43
3	A	176	THR	C-N-CA	-6.26	114.55	122.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	256	ASP	N-CA-CB	6.26	122.33	111.13
3	A	228	LEU	N-CA-C	-6.25	103.78	111.40
3	A	12	ASN	CB-CA-C	6.24	121.24	110.01
3	A	278	PHE	CA-CB-CG	-6.20	107.60	113.80
3	A	53	ILE	N-CA-CB	6.20	117.28	110.53
3	A	62	LEU	N-CA-C	6.20	119.68	110.39
1	T	6	DG	O4'-C1'-N9	6.17	117.66	108.40
3	A	178	CYS	N-CA-C	6.16	118.06	109.31
3	A	212	HIS	CA-CB-CG	-6.12	107.68	113.80
3	A	214	VAL	N-CA-C	6.12	116.28	110.53
1	T	3	DT	C2-N1-C1'	6.09	128.48	119.35
3	A	277	ILE	N-CA-CB	6.08	120.03	110.31
3	A	116	ASP	CA-CB-CG	-6.05	106.55	112.60
3	A	157	GLN	CB-CA-C	6.05	121.14	110.85
3	A	143	PHE	CA-CB-CG	-6.03	107.77	113.80
3	A	267	CYS	N-CA-CB	5.99	118.69	110.01
3	A	192	ASP	CB-CA-C	-5.96	100.98	111.22
3	A	214	VAL	N-CA-CB	5.95	118.19	110.57
1	T	3	DT	C6-N1-C1'	-5.93	110.46	119.35
3	A	241	LEU	N-CA-CB	5.88	118.43	110.14
2	P	3	DT	C4'-C3'-O3'	-5.85	101.23	110.00
3	A	246	ASP	N-CA-C	5.78	123.11	110.80
2	P	6	DT	P-O5'-C5'	-5.77	111.34	120.00
3	A	24	ASN	CA-CB-CG	-5.74	106.86	112.60
3	A	102	ARG	CD-NE-CZ	-5.73	116.38	124.40
3	A	215	VAL	N-CA-CB	5.72	117.63	110.47
3	A	31	GLN	N-CA-C	-5.72	106.11	112.57
3	A	169	VAL	N-CA-CB	5.70	116.83	110.62
3	A	12	ASN	N-CA-CB	5.69	119.15	110.44
3	A	333	ARG	N-CA-C	-5.66	106.42	113.15
3	A	68	LYS	O-C-N	5.62	127.87	122.03
3	A	310	PRO	N-CA-C	5.62	124.04	112.47
1	T	1	DC	P-O3'-C3'	5.61	128.62	120.20
3	A	52	LYS	CA-C-N	-5.61	113.92	121.66
3	A	52	LYS	C-N-CA	-5.61	113.92	121.66
3	A	41	LYS	N-CA-CB	5.60	118.45	110.16
3	A	128	ASN	CA-CB-CG	-5.60	107.00	112.60
3	A	246	ASP	CA-C-N	5.59	132.22	121.54
3	A	246	ASP	C-N-CA	5.59	132.22	121.54
3	A	267	CYS	CB-CA-C	-5.58	102.12	110.88
3	A	316	GLU	CA-C-N	5.58	132.20	121.54
3	A	316	GLU	C-N-CA	5.58	132.20	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	63	PRO	N-CA-CB	5.57	108.27	103.36
3	A	320	PHE	CA-CB-CG	-5.57	108.23	113.80
3	A	21	GLU	CA-C-N	5.54	127.97	120.65
3	A	21	GLU	C-N-CA	5.54	127.97	120.65
3	A	64	GLY	N-CA-C	-5.53	108.00	115.36
3	A	129	GLU	CA-C-N	5.51	128.68	120.31
3	A	129	GLU	C-N-CA	5.51	128.68	120.31
3	A	98	ASN	O-C-N	5.50	127.95	122.12
3	A	146	PHE	N-CA-CB	5.47	118.72	110.30
3	A	121	THR	N-CA-C	5.45	118.53	110.46
3	A	197	HIS	CA-C-N	5.45	125.10	119.05
3	A	197	HIS	C-N-CA	5.45	125.10	119.05
3	A	182	ARG	O-C-N	5.45	127.75	122.09
3	A	99	PHE	N-CA-C	5.44	118.25	111.24
3	A	261	PRO	N-CA-C	-5.43	101.97	110.50
2	P	1	DT	O4'-C1'-N1	5.42	116.53	108.40
3	A	273	THR	N-CA-CB	5.42	119.23	110.40
1	T	3	DT	P-O5'-C5'	5.41	128.11	120.00
3	A	34	HIS	CA-CB-CG	-5.32	108.48	113.80
3	A	15	ILE	O-C-N	5.32	127.42	121.94
3	A	242	PRO	O-C-N	5.32	129.82	122.64
3	A	126	ARG	N-CA-C	5.30	116.75	111.07
3	A	321	ASP	CB-CA-C	-5.28	102.36	110.81
3	A	250	TYR	N-CA-C	5.28	117.57	110.29
3	A	197	HIS	O-C-N	5.26	125.94	121.83
3	A	155	MET	CA-C-N	5.25	127.75	120.29
3	A	155	MET	C-N-CA	5.25	127.75	120.29
3	A	179	GLY	CA-C-N	5.24	127.56	120.38
3	A	179	GLY	C-N-CA	5.24	127.56	120.38
2	P	1	DT	O4'-C4'-C3'	-5.23	97.55	105.40
3	A	291	PHE	N-CA-C	5.23	118.33	108.65
3	A	312	PRO	N-CA-C	5.23	118.71	110.50
3	A	292	THR	N-CA-CB	5.22	118.00	110.37
3	A	32	ALA	N-CA-C	5.21	117.58	108.52
3	A	114	PHE	CA-C-N	5.21	127.59	120.46
3	A	114	PHE	C-N-CA	5.21	127.59	120.46
3	A	235	PHE	CA-CB-CG	-5.21	108.59	113.80
3	A	266	TYR	CA-C-O	-5.21	115.09	120.92
3	A	253	ARG	N-CA-C	5.18	117.94	109.59
3	A	66	GLY	O-C-N	5.16	128.07	122.96
3	A	129	GLU	N-CA-C	5.16	118.35	111.75
3	A	261	PRO	CB-CA-C	-5.15	105.94	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	45	VAL	N-CA-CB	5.15	117.94	110.52
3	A	12	ASN	N-CA-C	5.15	119.54	113.16
3	A	52	LYS	N-CA-CB	5.14	117.71	109.28
3	A	241	LEU	O-C-N	5.13	128.62	121.64
3	A	252	HIS	O-C-N	5.12	129.03	123.04
2	P	1	DT	C5'-C4'-O4'	5.11	117.07	109.40
1	T	4	DT	N1-C1'-C2'	5.11	121.16	113.50
3	A	91	ASP	N-CA-CB	5.11	119.12	110.49
3	A	161	ILE	CB-CA-C	-5.11	105.43	111.97
3	A	332	ASP	N-CA-CB	5.09	117.84	110.47
3	A	191	MET	N-CA-C	5.07	117.88	109.46
3	A	30	SER	O-C-N	-5.07	117.39	123.06
3	A	98	ASN	CA-C-N	5.06	129.07	120.88
3	A	98	ASN	C-N-CA	5.06	129.07	120.88
3	A	94	SER	CA-CB-OG	-5.05	101.00	111.10
3	A	296	TYR	CB-CA-C	-5.05	100.99	109.27
3	A	91	ASP	N-CA-C	5.04	121.53	110.80
3	A	108	PRO	CB-CA-C	-5.04	104.31	112.62
3	A	271	TYR	CA-CB-CG	-5.01	104.88	113.90
3	A	87	LYS	CB-CA-C	5.00	118.88	110.92

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	12	ASN	CA
3	A	92	ASP	CA

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	145	0	80	9	0
2	P	144	0	81	15	0
3	A	2623	0	2641	313	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
6	A	9	0	0	0	0
7	A	111	0	0	18	0
7	P	18	0	0	0	0
7	T	14	0	0	4	0
All	All	3067	0	2802	333	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 59.

All (333) 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:18:MET:HE2	3:A:82:LEU:HD22	1.27	1.13
2:P:6:DT:H2''	2:P:7:DG:H5''	1.29	1.08
3:A:243:SER:HB3	3:A:249:GLU:HA	1.38	1.05
2:P:5:DA:H2''	2:P:6:DT:H5''	1.40	1.03
3:A:245:ASN:N	3:A:245:ASN:HD22	1.53	1.02
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.29	0.98
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.48	0.94
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.50	0.94
3:A:155:MET:HE2	3:A:188:SER:HB2	1.53	0.89
3:A:245:ASN:HD22	3:A:245:ASN:H	1.15	0.88
2:P:6:DT:C2'	2:P:7:DG:H5''	2.04	0.87
3:A:155:MET:HE2	3:A:188:SER:CB	2.03	0.87
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.58	0.85
2:P:5:DA:H2''	2:P:6:DT:C5'	2.05	0.85
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.60	0.82
3:A:165:GLU:OE1	3:A:168:LYS:HD3	1.81	0.81
3:A:286:ALA:HB1	3:A:291:PHE:HB2	1.63	0.81
3:A:18:MET:HE2	3:A:82:LEU:CD2	2.09	0.81
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.20	0.81
2:P:1:DT:H2''	2:P:2:DC:H5'	1.63	0.79
3:A:270:LEU:CD2	3:A:282:MET:HE1	2.13	0.79
3:A:291:PHE:HD2	3:A:323:ILE:HG22	1.46	0.78
3:A:128:ASN:N	3:A:128:ASN:HD22	1.82	0.78
3:A:150:ILE:HD13	3:A:253:ARG:HG2	1.65	0.78
3:A:81:LYS:HZ3	3:A:86:GLU:HB3	1.48	0.77
3:A:121:THR:HG23	3:A:124:ASP:CG	2.10	0.77
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.15	0.76
3:A:81:LYS:NZ	3:A:86:GLU:HB3	2.01	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.51	0.76
3:A:306:VAL:HG22	7:A:650:HOH:O	1.85	0.75
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.67	0.75
3:A:182:ARG:HG2	3:A:182:ARG:NH1	1.97	0.75
3:A:243:SER:CB	3:A:249:GLU:HA	2.17	0.75
3:A:255:ILE:HG12	3:A:256:ASP:N	2.00	0.74
3:A:37:ASN:HB3	7:A:556:HOH:O	1.86	0.74
3:A:323:ILE:O	3:A:324:GLN:HG2	1.87	0.74
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.70	0.74
2:P:1:DT:C2'	2:P:2:DC:H5'	2.18	0.73
3:A:100:LEU:HD21	3:A:119:ILE:O	1.89	0.73
3:A:123:GLU:O	3:A:127:LYS:HG2	1.89	0.73
3:A:155:MET:HA	3:A:158:MET:HE3	1.70	0.72
3:A:114:PHE:O	3:A:119:ILE:HG12	1.89	0.72
3:A:291:PHE:O	3:A:301:LEU:HD22	1.90	0.72
3:A:128:ASN:N	3:A:128:ASN:ND2	2.37	0.71
3:A:330:PRO:HA	3:A:333:ARG:HG2	1.73	0.71
3:A:291:PHE:CD2	3:A:323:ILE:HG22	2.25	0.71
2:P:6:DT:H2''	2:P:7:DG:C5'	2.16	0.70
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.91	0.70
3:A:41:LYS:HD3	3:A:42:ALA:H	1.55	0.70
3:A:129:GLU:HG2	3:A:137:ARG:HD3	1.72	0.70
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.21	0.70
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.72	0.70
3:A:327:TYR:HD1	3:A:328:ARG:N	1.90	0.70
3:A:121:THR:O	3:A:124:ASP:HB2	1.91	0.70
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.74	0.69
3:A:31:GLN:HB2	3:A:112:ARG:NH1	2.07	0.69
3:A:31:GLN:HB2	3:A:112:ARG:HH12	1.56	0.69
3:A:245:ASN:H	3:A:245:ASN:ND2	1.87	0.69
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.28	0.68
3:A:245:ASN:N	3:A:245:ASN:ND2	2.28	0.68
3:A:12:ASN:HD21	3:A:53:ILE:H	1.40	0.68
3:A:277:ILE:HG12	3:A:335:GLU:HA	1.75	0.68
3:A:11:LEU:HD23	3:A:11:LEU:H	1.57	0.67
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.24	0.67
1:T:5:DA:N3	7:T:659:HOH:O	2.28	0.67
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.43	0.67
3:A:244:LYS:HB3	3:A:245:ASN:ND2	2.10	0.67
3:A:294:ASN:HB2	3:A:295:GLU:OE1	1.95	0.67
3:A:127:LYS:HB2	3:A:128:ASN:ND2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:18:MET:HE1	3:A:76:PHE:CB	2.25	0.66
3:A:210:LEU:HB3	3:A:259:LEU:HD21	1.77	0.66
3:A:330:PRO:HA	3:A:333:ARG:CG	2.26	0.66
3:A:244:LYS:HB3	3:A:245:ASN:HD22	1.60	0.66
1:T:6:DG:N7	7:T:652:HOH:O	2.29	0.66
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.11	0.66
3:A:60:LYS:HG3	3:A:60:LYS:O	1.96	0.66
1:T:5:DA:H2''	1:T:6:DG:O5'	1.97	0.65
3:A:172:GLU:HB3	3:A:197:HIS:NE2	2.10	0.65
3:A:276:ASP:O	3:A:280:LYS:HG3	1.96	0.65
3:A:79:THR:O	3:A:81:LYS:N	2.29	0.65
3:A:292:THR:O	3:A:298:ILE:HA	1.97	0.65
3:A:294:ASN:O	3:A:296:TYR:N	2.30	0.65
3:A:210:LEU:CB	3:A:259:LEU:HD21	2.28	0.64
3:A:286:ALA:O	3:A:291:PHE:N	2.31	0.63
3:A:212:HIS:HB3	7:A:541:HOH:O	1.96	0.63
3:A:270:LEU:HD23	3:A:319:ILE:HD13	1.78	0.63
3:A:243:SER:HB3	3:A:249:GLU:CA	2.23	0.63
3:A:279:ASN:O	3:A:283:ARG:HG3	1.99	0.63
3:A:18:MET:CE	3:A:82:LEU:HD22	2.17	0.63
3:A:209:LYS:HA	3:A:212:HIS:HB2	1.80	0.63
3:A:42:ALA:O	3:A:46:ILE:HG23	1.99	0.63
3:A:41:LYS:HD3	3:A:42:ALA:N	2.14	0.63
3:A:277:ILE:HG13	3:A:335:GLU:HB2	1.80	0.63
3:A:326:LYS:O	3:A:328:ARG:HG2	1.98	0.63
2:P:5:DA:H2'	2:P:6:DT:H72	1.81	0.62
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.81	0.62
3:A:92:ASP:HB3	7:A:647:HOH:O	1.99	0.62
3:A:183:ARG:HD3	3:A:273:THR:O	1.99	0.62
3:A:53:ILE:O	3:A:54:LYS:HD2	2.00	0.61
3:A:154:GLU:O	3:A:158:MET:HG3	1.99	0.61
3:A:267:CYS:SG	3:A:297:THR:HA	2.40	0.61
3:A:27:LYS:HB3	3:A:36:TYR:CG	2.36	0.61
3:A:270:LEU:HD23	3:A:319:ILE:HG21	1.81	0.61
3:A:108:PRO:O	3:A:112:ARG:HG3	2.00	0.61
2:P:5:DA:C2'	2:P:6:DT:H5''	2.24	0.61
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.82	0.60
3:A:11:LEU:H	3:A:11:LEU:CD2	2.14	0.60
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.37	0.60
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.84	0.60
3:A:142:TYR:CE2	3:A:238:VAL:HG11	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:270:LEU:HD13	3:A:316:GLU:OE2	2.02	0.60
3:A:289:LYS:HD3	3:A:289:LYS:N	2.15	0.60
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.99	0.59
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.33	0.59
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.32	0.59
3:A:309:GLU:N	3:A:309:GLU:OE1	2.36	0.59
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.32	0.58
3:A:302:GLY:N	3:A:307:ALA:HB3	2.18	0.58
3:A:188:SER:HB3	7:A:656:HOH:O	2.04	0.58
3:A:15:ILE:CG2	3:A:46:ILE:HD13	2.34	0.58
3:A:326:LYS:O	3:A:326:LYS:HG3	2.02	0.58
3:A:141:LYS:HE2	3:A:142:TYR:CZ	2.38	0.58
3:A:180:SER:HB2	3:A:185:ALA:HB2	1.86	0.57
3:A:270:LEU:C	3:A:270:LEU:HD12	2.29	0.57
3:A:31:GLN:HE21	3:A:112:ARG:NH1	2.02	0.57
3:A:303:VAL:C	3:A:305:GLY:H	2.13	0.57
3:A:271:TYR:HB2	7:A:592:HOH:O	2.05	0.56
3:A:29:VAL:HA	3:A:97:ILE:HD12	1.87	0.56
3:A:264:GLN:NE2	3:A:296:TYR:HB3	2.20	0.56
3:A:302:GLY:H	3:A:307:ALA:HB3	1.71	0.56
3:A:332:ASP:C	3:A:334:SER:H	2.13	0.56
3:A:43:ALA:O	3:A:47:ALA:HB2	2.05	0.56
1:T:6:DG:H2''	1:T:7:DA:C8	2.41	0.56
3:A:159:GLN:O	3:A:163:LEU:HG	2.06	0.55
3:A:83:ARG:HA	3:A:86:GLU:HG2	1.88	0.55
3:A:179:GLY:O	3:A:182:ARG:HB3	2.07	0.55
3:A:150:ILE:HG21	3:A:158:MET:CE	2.33	0.55
3:A:327:TYR:HE1	3:A:333:ARG:HH21	1.52	0.55
3:A:18:MET:HG2	3:A:19:LEU:N	2.11	0.55
3:A:129:GLU:O	3:A:132:LEU:HB2	2.07	0.55
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.40	0.55
3:A:248:LYS:O	3:A:248:LYS:HG2	2.06	0.55
3:A:277:ILE:HG13	3:A:335:GLU:CB	2.37	0.55
3:A:300:PRO:HD3	3:A:311:LEU:HD22	1.88	0.55
3:A:303:VAL:O	3:A:305:GLY:N	2.40	0.55
3:A:120:LYS:N	3:A:124:ASP:OD2	2.38	0.54
3:A:285:HIS:CD2	3:A:323:ILE:HD12	2.42	0.54
3:A:15:ILE:HG21	3:A:46:ILE:HD13	1.88	0.54
1:T:7:DA:H1'	7:T:634:HOH:O	2.05	0.54
3:A:319:ILE:O	3:A:322:TYR:HB2	2.07	0.54
3:A:282:MET:HA	3:A:325:TRP:CH2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:323:ILE:C	3:A:324:GLN:HG2	2.32	0.54
3:A:97:ILE:HD13	3:A:112:ARG:HG2	1.88	0.54
3:A:207:GLN:O	3:A:210:LEU:HB2	2.08	0.53
3:A:62:LEU:HD13	3:A:62:LEU:N	2.23	0.53
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.38	0.53
3:A:33:ILE:O	3:A:36:TYR:HB3	2.08	0.53
3:A:66:GLY:O	3:A:70:ALA:HB2	2.09	0.53
3:A:250:TYR:HB3	7:A:577:HOH:O	2.09	0.53
3:A:328:ARG:O	3:A:333:ARG:NE	2.30	0.52
3:A:270:LEU:CD2	3:A:319:ILE:HG21	2.39	0.52
2:P:5:DA:H5"	3:A:107:GLY:N	2.24	0.52
3:A:114:PHE:HB3	3:A:119:ILE:HB	1.91	0.52
3:A:141:LYS:HE2	3:A:142:TYR:OH	2.10	0.52
3:A:11:LEU:HD23	3:A:11:LEU:N	2.20	0.52
3:A:77:LEU:HD13	3:A:77:LEU:N	2.25	0.52
3:A:58:GLU:O	3:A:61:LYS:HG3	2.09	0.51
3:A:254:ARG:NH1	3:A:255:ILE:N	2.59	0.51
3:A:26:GLU:O	3:A:30:SER:O	2.28	0.51
3:A:121:THR:OG1	3:A:122:LEU:N	2.40	0.51
3:A:172:GLU:HB3	3:A:197:HIS:CD2	2.46	0.51
3:A:251:PRO:O	3:A:253:ARG:HD2	2.11	0.51
3:A:18:MET:CE	3:A:76:PHE:HB2	2.41	0.51
3:A:288:GLU:C	3:A:290:GLY:H	2.19	0.51
3:A:79:THR:O	3:A:79:THR:OG1	2.29	0.51
3:A:240:GLN:NE2	3:A:250:TYR:O	2.39	0.50
3:A:151:PRO:HB2	3:A:154:GLU:HG3	1.93	0.50
3:A:241:LEU:HB2	3:A:250:TYR:CD2	2.47	0.50
3:A:270:LEU:HD12	3:A:270:LEU:O	2.12	0.50
3:A:69:ILE:O	3:A:72:LYS:N	2.45	0.50
3:A:101:THR:HA	3:A:106:ILE:HG22	1.93	0.50
3:A:282:MET:HE2	7:A:555:HOH:O	2.11	0.50
2:P:5:DA:P	3:A:107:GLY:HA3	2.51	0.49
3:A:152:ARG:HA	3:A:155:MET:HB2	1.93	0.49
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.94	0.49
3:A:203:GLU:O	3:A:205:THR:N	2.45	0.49
3:A:177:VAL:HG11	3:A:191:MET:HE2	1.94	0.49
3:A:194:LEU:HD11	3:A:258:ARG:HD3	1.94	0.49
3:A:183:ARG:HH11	3:A:275:SER:HA	1.77	0.49
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.94	0.49
3:A:286:ALA:O	3:A:291:PHE:HB2	2.13	0.49
3:A:207:GLN:HB2	7:A:625:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:236:MET:HG2	3:A:256:ASP:OD1	2.12	0.49
3:A:295:GLU:HA	7:A:592:HOH:O	2.12	0.49
3:A:180:SER:HB2	3:A:185:ALA:CB	2.43	0.49
3:A:145:ASP:HB3	3:A:252:HIS:O	2.12	0.49
3:A:234:LYS:HD3	7:A:617:HOH:O	2.12	0.48
3:A:321:ASP:C	3:A:324:GLN:H	2.22	0.48
3:A:330:PRO:CA	3:A:333:ARG:HG2	2.41	0.48
3:A:157:GLN:O	3:A:160:ASP:HB3	2.14	0.48
3:A:155:MET:HE3	3:A:181:PHE:HB2	1.96	0.48
3:A:89:ARG:HD3	3:A:89:ARG:C	2.38	0.48
3:A:123:GLU:HG3	7:A:623:HOH:O	2.13	0.48
3:A:245:ASN:O	3:A:246:ASP:O	2.31	0.48
3:A:12:ASN:HB3	3:A:46:ILE:HD12	1.95	0.47
3:A:254:ARG:HH11	3:A:255:ILE:N	2.11	0.47
3:A:228:LEU:HD12	3:A:228:LEU:HA	1.73	0.47
3:A:68:LYS:HB2	3:A:68:LYS:NZ	2.28	0.47
3:A:133:ASN:ND2	7:A:512:HOH:O	2.38	0.47
3:A:331:LYS:HG2	3:A:332:ASP:N	2.12	0.47
3:A:41:LYS:NZ	3:A:64:GLY:O	2.37	0.47
3:A:119:ILE:HG22	3:A:124:ASP:HB3	1.96	0.47
3:A:133:ASN:H	3:A:136:GLN:HE21	1.62	0.47
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.30	0.47
3:A:15:ILE:HD11	3:A:77:LEU:HD11	1.97	0.47
3:A:174:ILE:O	3:A:195:LEU:HD12	2.15	0.47
3:A:83:ARG:O	3:A:86:GLU:N	2.48	0.46
3:A:172:GLU:CG	3:A:198:PRO:HG2	2.46	0.46
3:A:79:THR:C	3:A:81:LYS:H	2.21	0.46
3:A:214:VAL:CG2	3:A:215:VAL:N	2.78	0.46
3:A:260:ILE:HG22	3:A:261:PRO:O	2.15	0.46
3:A:148:LYS:HB3	7:A:620:HOH:O	2.16	0.46
3:A:25:PHE:CG	3:A:88:ILE:HD13	2.51	0.46
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.81	0.46
3:A:211:LEU:HD21	3:A:235:PHE:HB2	1.97	0.46
3:A:44:SER:O	3:A:47:ALA:HB3	2.16	0.46
3:A:296:TYR:O	3:A:297:THR:HG23	2.16	0.46
3:A:203:GLU:CD	3:A:203:GLU:H	2.24	0.45
3:A:212:HIS:N	3:A:212:HIS:CD2	2.83	0.45
3:A:268:GLY:O	3:A:271:TYR:HB3	2.16	0.45
3:A:172:GLU:HG2	3:A:198:PRO:HG2	1.98	0.45
3:A:182:ARG:NH1	3:A:273:THR:CG2	2.79	0.45
3:A:270:LEU:HA	3:A:316:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:299:ARG:HG2	3:A:310:PRO:CD	2.46	0.45
3:A:21:GLU:OE1	3:A:85:LEU:HG	2.17	0.45
3:A:152:ARG:HD2	3:A:185:ALA:O	2.16	0.45
3:A:285:HIS:NE2	3:A:289:LYS:CG	2.80	0.45
3:A:41:LYS:HZ2	3:A:42:ALA:HB2	1.82	0.45
1:T:3:DT:H73	7:T:660:HOH:O	2.17	0.45
3:A:249:GLU:HG3	3:A:250:TYR:N	2.31	0.45
3:A:299:ARG:HG2	3:A:310:PRO:N	2.31	0.45
3:A:195:LEU:O	3:A:260:ILE:N	2.50	0.45
3:A:183:ARG:NH1	3:A:275:SER:HA	2.31	0.44
3:A:330:PRO:O	3:A:333:ARG:HG2	2.17	0.44
3:A:287:LEU:HD13	3:A:287:LEU:HA	1.34	0.44
3:A:23:ALA:HB2	3:A:39:TYR:HB2	2.00	0.44
3:A:169:VAL:HG22	3:A:170:ASP:N	2.33	0.44
3:A:321:ASP:O	3:A:324:GLN:N	2.49	0.44
1:T:4:DT:O2	2:P:4:DA:H2	2.00	0.44
3:A:182:ARG:HH11	3:A:273:THR:CG2	2.30	0.44
3:A:230:LYS:HG3	3:A:235:PHE:HD1	1.83	0.44
3:A:12:ASN:ND2	7:A:642:HOH:O	2.48	0.44
3:A:266:TYR:O	3:A:270:LEU:N	2.39	0.44
3:A:274:GLY:HA3	3:A:275:SER:HA	1.72	0.44
3:A:60:LYS:NZ	3:A:67:THR:HG22	2.32	0.43
3:A:62:LEU:HA	3:A:62:LEU:HD12	1.63	0.43
3:A:204:SER:O	3:A:204:SER:OG	2.29	0.43
3:A:212:HIS:CD2	3:A:212:HIS:H	2.35	0.43
3:A:81:LYS:NZ	3:A:86:GLU:CB	2.78	0.43
3:A:119:ILE:HG22	3:A:124:ASP:CB	2.48	0.43
3:A:25:PHE:CD1	3:A:25:PHE:C	2.96	0.43
3:A:34:HIS:O	3:A:38:ALA:N	2.48	0.43
3:A:41:LYS:O	3:A:44:SER:HB3	2.19	0.43
3:A:200:PHE:CE2	3:A:261:PRO:HD3	2.53	0.43
3:A:295:GLU:OE1	3:A:295:GLU:N	2.51	0.43
3:A:317:LYS:O	3:A:320:PHE:N	2.51	0.43
3:A:15:ILE:HG22	3:A:19:LEU:HD22	1.99	0.43
3:A:11:LEU:CD2	3:A:11:LEU:N	2.79	0.43
3:A:279:ASN:HD22	3:A:279:ASN:HA	1.53	0.43
3:A:103:VAL:HB	3:A:106:ILE:HD12	2.01	0.43
3:A:209:LYS:HA	3:A:209:LYS:HD3	1.96	0.43
3:A:254:ARG:CZ	3:A:254:ARG:HB3	2.49	0.43
1:T:1:DC:H2"	1:T:2:DA:OP2	2.19	0.43
3:A:31:GLN:N	7:A:641:HOH:O	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:195:LEU:O	3:A:259:LEU:HD12	2.19	0.43
3:A:196:THR:OG1	3:A:197:HIS:N	2.51	0.43
3:A:264:GLN:HB3	3:A:296:TYR:O	2.19	0.43
3:A:211:LEU:HB3	3:A:212:HIS:HD2	1.83	0.43
3:A:295:GLU:CD	3:A:295:GLU:H	2.27	0.43
3:A:301:LEU:HA	3:A:301:LEU:HD12	1.39	0.43
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.53	0.43
3:A:293:ILE:HD12	3:A:293:ILE:HG23	1.70	0.43
3:A:304:THR:H	3:A:304:THR:HG23	1.20	0.43
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.58	0.42
3:A:77:LEU:N	3:A:77:LEU:CD1	2.79	0.42
3:A:133:ASN:ND2	3:A:135:HIS:H	2.17	0.42
3:A:165:GLU:HB3	3:A:217:GLN:CG	2.47	0.42
3:A:56:GLY:H	3:A:74:ASP:CG	2.27	0.42
3:A:260:ILE:HG22	3:A:261:PRO:N	2.34	0.42
3:A:327:TYR:C	3:A:327:TYR:CD1	2.98	0.42
3:A:194:LEU:HD12	3:A:194:LEU:HA	1.77	0.42
3:A:302:GLY:HA3	3:A:307:ALA:HB2	2.01	0.42
3:A:311:LEU:HA	3:A:312:PRO:HD2	1.75	0.42
2:P:2:DC:H2'	2:P:2:DC:O5'	2.20	0.42
3:A:181:PHE:HA	7:A:530:HOH:O	2.19	0.42
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.43	0.42
3:A:265:TYR:O	3:A:268:GLY:N	2.53	0.42
3:A:59:ALA:O	3:A:62:LEU:HB2	2.20	0.41
3:A:259:LEU:HD12	3:A:259:LEU:HA	1.70	0.41
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.50	0.41
3:A:18:MET:HE1	3:A:76:PHE:HB3	2.02	0.41
3:A:205:THR:HA	7:A:624:HOH:O	2.20	0.41
3:A:88:ILE:HD13	3:A:88:ILE:HG21	1.72	0.41
3:A:217:GLN:O	3:A:220:LYS:HB3	2.20	0.41
3:A:243:SER:HB3	3:A:249:GLU:CB	2.49	0.41
3:A:316:GLU:O	3:A:320:PHE:HD2	2.03	0.41
3:A:28:ASN:HD22	3:A:28:ASN:HA	0.93	0.41
3:A:38:ALA:O	3:A:41:LYS:HD3	2.21	0.41
3:A:149:ARG:NH2	3:A:187:SER:O	2.53	0.41
3:A:241:LEU:HD12	3:A:250:TYR:CD1	2.55	0.41
3:A:327:TYR:CD1	3:A:328:ARG:N	2.79	0.41
3:A:183:ARG:HE	3:A:183:ARG:HB2	1.67	0.41
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.55	0.41
3:A:169:VAL:HG22	3:A:173:TYR:HE2	1.84	0.41
1:T:2:DA:N6	2:P:5:DA:N6	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:68:LYS:O	3:A:72:LYS:HE3	2.20	0.41
3:A:145:ASP:OD2	3:A:252:HIS:HB2	2.20	0.41
3:A:250:TYR:HA	3:A:251:PRO:HD3	1.90	0.41
3:A:84:LYS:O	3:A:88:ILE:HG13	2.20	0.41
3:A:19:LEU:HD23	3:A:43:ALA:HA	2.03	0.41
3:A:205:THR:O	3:A:206:LYS:O	2.38	0.41
3:A:244:LYS:CB	3:A:245:ASN:HD22	2.31	0.40
2:P:6:DT:H2"	2:P:7:DG:C8	2.56	0.40
3:A:11:LEU:HD23	3:A:12:ASN:H	1.86	0.40
3:A:99:PHE:CD2	3:A:99:PHE:C	2.97	0.40
3:A:317:LYS:O	3:A:320:PHE:HB2	2.21	0.40
3:A:82:LEU:HB3	3:A:85:LEU:HB2	2.02	0.40
3:A:100:LEU:HD12	3:A:100:LEU:HA	1.70	0.40
3:A:270:LEU:HD13	3:A:270:LEU:HA	1.77	0.40
3:A:291:PHE:HB3	3:A:292:THR:H	1.53	0.40
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.66	0.40
3:A:62:LEU:N	3:A:62:LEU:CD1	2.78	0.40
3:A:322:TYR:C	3:A:324:GLN:H	2.28	0.40

There are no symmetry-related clashes.

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
3	A	325/335 (97%)	270 (83%)	38 (12%)	17 (5%)	1 9

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	204	SER
3	A	205	THR
3	A	206	LYS

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Mol	Chain	Res	Type
3	A	244	LYS
3	A	246	ASP
3	A	295	GLU
3	A	304	THR
3	A	13	GLY
3	A	80	GLY
3	A	185	ALA
3	A	247	GLU
3	A	265	TYR
3	A	310	PRO
3	A	207	GLN
3	A	222	HIS
3	A	289	LYS
3	A	309	GLU

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
3	A	288/295 (98%)	214 (74%)	74 (26%)	0 3

All (74) 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	20	THR
3	A	21	GLU
3	A	22	LEU
3	A	27	LYS
3	A	30	SER
3	A	33	ILE
3	A	37	ASN
3	A	41	LYS

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Mol	Chain	Res	Type
3	A	44	SER
3	A	46	ILE
3	A	52	LYS
3	A	62	LEU
3	A	67	THR
3	A	68	LYS
3	A	72	LYS
3	A	73	ILE
3	A	77	LEU
3	A	79	THR
3	A	81	LYS
3	A	85	LEU
3	A	89	ARG
3	A	92	ASP
3	A	97	ILE
3	A	100	LEU
3	A	101	THR
3	A	113	LYS
3	A	115	VAL
3	A	121	THR
3	A	122	LEU
3	A	127	LYS
3	A	128	ASN
3	A	133	ASN
3	A	136	GLN
3	A	138	ILE
3	A	145	ASP
3	A	153	GLU
3	A	161	ILE
3	A	168	LYS
3	A	169	VAL
3	A	172	GLU
3	A	182	ARG
3	A	194	LEU
3	A	213	GLN
3	A	214	VAL
3	A	218	LEU
3	A	225	THR
3	A	226	ASP
3	A	228	LEU
3	A	230	LYS
3	A	245	ASN

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Mol	Chain	Res	Type
3	A	248	LYS
3	A	249	GLU
3	A	253	ARG
3	A	255	ILE
3	A	264	GLN
3	A	270	LEU
3	A	277	ILE
3	A	279	ASN
3	A	287	LEU
3	A	294	ASN
3	A	295	GLU
3	A	298	ILE
3	A	301	LEU
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	324	GLN
3	A	325	TRP
3	A	331	LYS
3	A	335	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) 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	51	HIS
3	A	90	GLN
3	A	98	ASN
3	A	128	ASN
3	A	136	GLN
3	A	157	GLN
3	A	197	HIS
3	A	212	HIS
3	A	217	GLN
3	A	245	ASN
3	A	279	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	DTP	A	338	4	6,8,32	1.40	1 (16%)	12,13,50	1.11	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
6	DTP	A	338	4	-	6/6/6/34	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	338	DTP	PB-O3A	2.31	1.63	1.54

There are no bond angle outliers.

There are no chirality outliers.

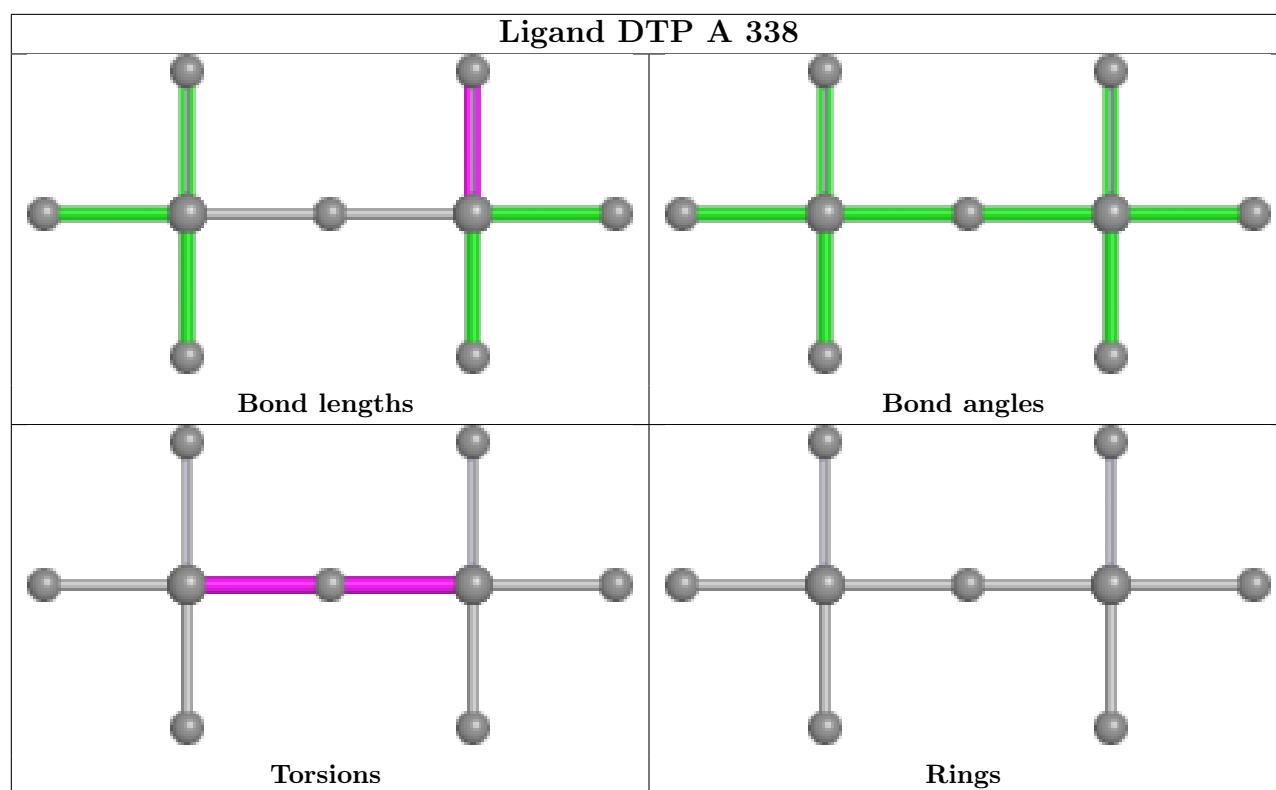
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	338	DTP	PG-O3B-PB-O2B
6	A	338	DTP	PB-O3B-PG-O1G
6	A	338	DTP	PG-O3B-PB-O1B
6	A	338	DTP	PB-O3B-PG-O2G
6	A	338	DTP	PB-O3B-PG-O3G
6	A	338	DTP	PG-O3B-PB-O3A

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9	
1	T	8/8 (100%)	-0.79	0	100	100	20, 42, 94, 99	0
2	P	7/7 (100%)	-1.12	0	100	100	13, 28, 43, 64	0
3	A	325/335 (97%)	-1.00	1 (0%)	90	79	4, 35, 86, 100	1 (0%)
All	All	340/350 (97%)	-1.00	1 (0%)	90	79	4, 36, 86, 100	1 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	246	ASP	3.2

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, 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.

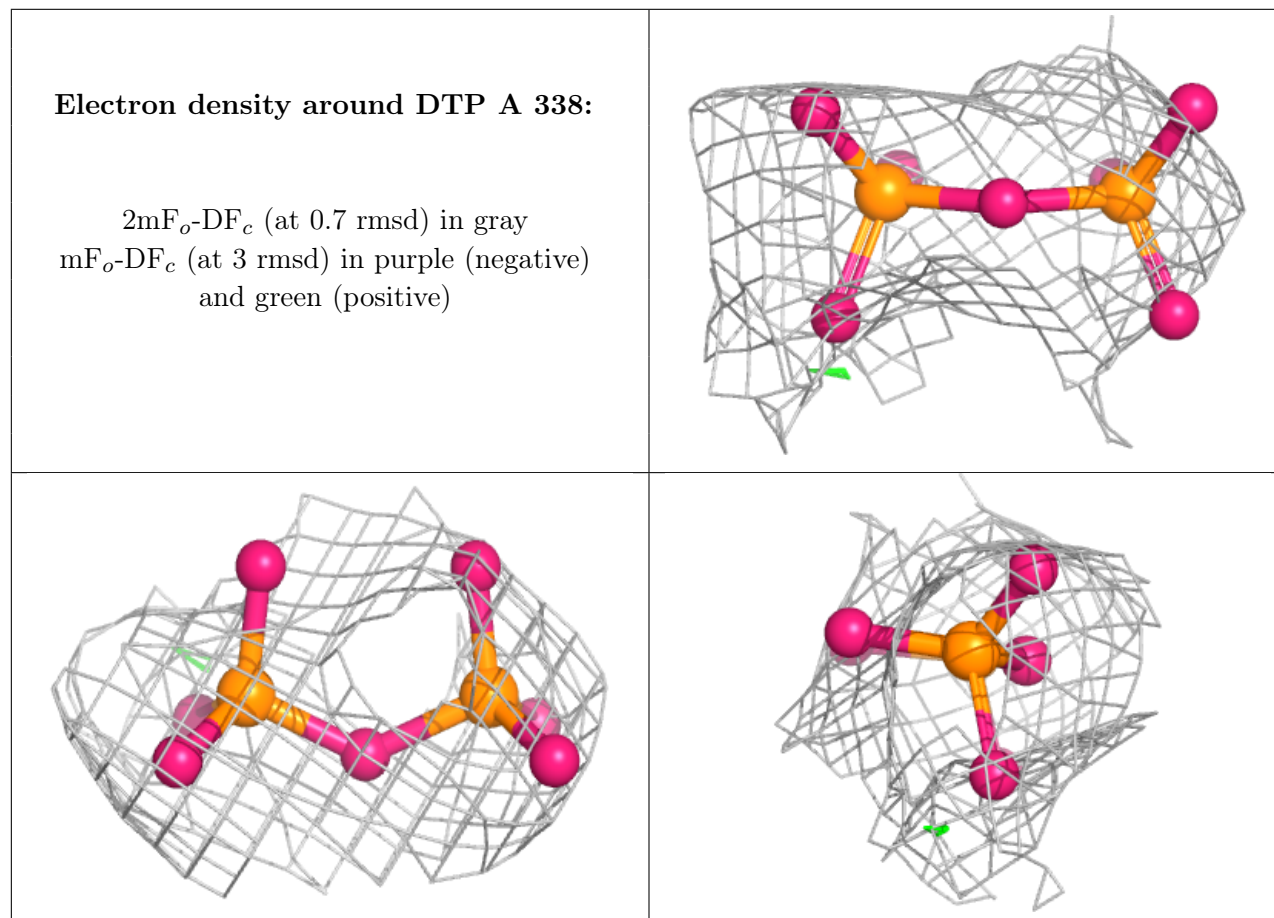
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	DTP	A	338	9/30	0.91	0.11	62,67,76,81	9
5	NA	A	342	1/1	0.93	0.08	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	A	339	1/1	0.93	0.07	30,30,30,30	1
5	NA	A	341	1/1	0.99	0.03	4,4,4,4	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.