



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:26 AM UTC

PDB ID : 8ICK / pdb_00008ick
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), MGCL2 (5 MILLIMOLAR), AND MNCL2 (5 MILLIMOLAR)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1996-04-19
Resolution : 2.70 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](#) ①) 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

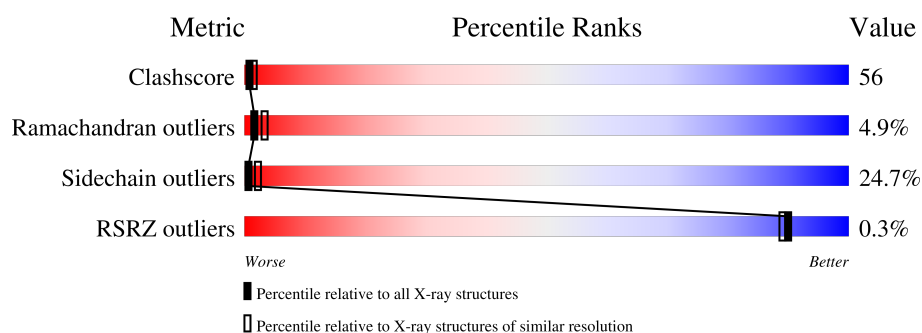
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

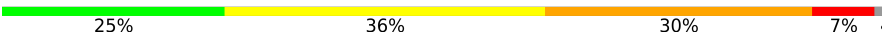
The reported resolution of this entry is 2.70 Å.

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	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	
2	P	8	
3	A	335	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3092 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*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	8	Total	C	N	O	P	0	0	0
			165	79	29	49	8			

- 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	27	0	0
			2623	1657	458	499	9			

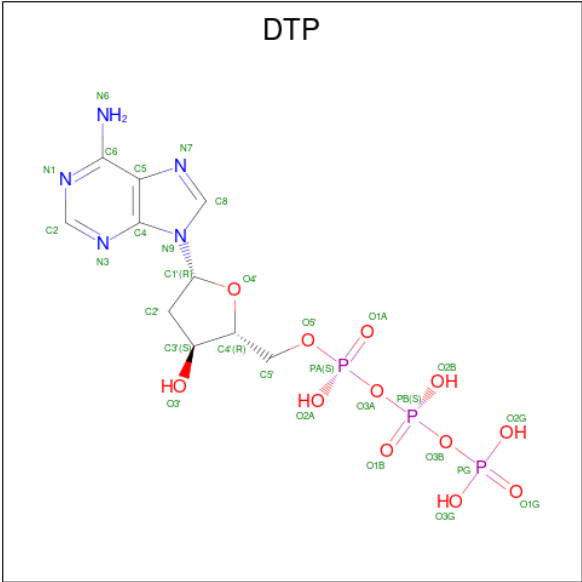
- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- 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)

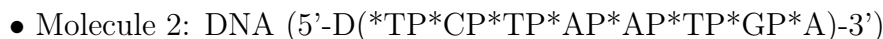


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	T	14	Total	O	0	0
			14	14		
7	P	21	Total	O	0	0
			21	21		
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	179.49Å 57.64Å 48.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 20.00 – 2.71	Depositor EDS
% Data completeness (in resolution range)	82.0 (20.00-2.70) 82.2 (20.00-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.70Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.174 , (Not available) 0.166 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 172.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3092	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.61% 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: MN, NA, DTP

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	0.94	0/162	4.28	17/249 (6.8%)
2	P	1.03	1/184 (0.5%)	4.06	16/280 (5.7%)
3	A	1.49	18/2672 (0.7%)	2.18	128/3590 (3.6%)
All	All	1.44	19/3018 (0.6%)	2.52	161/4119 (3.9%)

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	1	0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	94	SER	N-CA	-6.74	1.38	1.46
3	A	30	SER	C-N	-6.52	1.24	1.33
3	A	116	ASP	CA-C	-6.49	1.44	1.52
3	A	67	THR	N-CA	-6.24	1.38	1.46
3	A	66	GLY	N-CA	-6.21	1.39	1.44
2	P	1	DT	OP3-P	5.86	1.60	1.48
3	A	329	GLU	CA-C	-5.81	1.45	1.53
3	A	330	PRO	N-CA	-5.70	1.40	1.47
3	A	138	ILE	CA-CB	-5.66	1.47	1.54
3	A	119	ILE	CA-CB	-5.63	1.47	1.53
3	A	26	GLU	C-N	-5.60	1.26	1.33
3	A	94	SER	CA-CB	-5.42	1.44	1.53
3	A	27	LYS	N-CA	-5.38	1.39	1.46
3	A	197	HIS	N-CA	-5.28	1.40	1.45
3	A	65	VAL	C-N	-5.27	1.27	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	36	TYR	N-CA	-5.14	1.40	1.46
3	A	137	ARG	C-N	-5.10	1.27	1.33
3	A	66	GLY	C-N	-5.06	1.27	1.33
3	A	266	TYR	CA-C	-5.02	1.46	1.52

All (161) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	7	DA	C4-N9-C1'	-33.24	77.20	127.05
1	T	7	DA	C8-N9-C1'	31.30	174.00	127.05
2	P	7	DG	C4-N9-C1'	-25.56	88.67	127.00
2	P	7	DG	C8-N9-C1'	25.00	164.51	127.00
2	P	8	DA	C8-N9-C1'	19.92	156.93	127.05
2	P	8	DA	C4-N9-C1'	-19.54	97.75	127.05
2	P	2	DC	C2-N1-C1'	17.07	145.31	119.70
1	T	6	DG	C4-N9-C1'	-16.70	101.96	127.00
2	P	6	DT	C2-N1-C1'	16.42	143.98	119.35
1	T	6	DG	C8-N9-C1'	16.41	151.62	127.00
2	P	1	DT	C2-N1-C1'	16.38	143.92	119.35
2	P	1	DT	C6-N1-C1'	-16.13	95.15	119.35
2	P	6	DT	C6-N1-C1'	-16.00	95.34	119.35
2	P	2	DC	C6-N1-C1'	-15.57	96.35	119.70
1	T	4	DT	C6-N1-C1'	-13.65	98.87	119.35
1	T	4	DT	C2-N1-C1'	13.52	139.62	119.35
1	T	1	DC	C6-N1-C1'	-13.02	100.18	119.70
1	T	1	DC	C2-N1-C1'	12.72	138.78	119.70
3	A	49	TYR	CA-C-N	10.70	131.74	120.83
3	A	49	TYR	C-N-CA	10.70	131.74	120.83
1	T	2	DA	C4-N9-C1'	-10.42	111.42	127.05
1	T	2	DA	C8-N9-C1'	9.93	141.94	127.05
2	P	3	DT	C2-N1-C1'	9.81	134.07	119.35
1	T	5	DA	C8-N9-C1'	9.71	141.62	127.05
1	T	1	DC	P-O3'-C3'	9.35	134.22	120.20
1	T	3	DT	C2-N1-C1'	9.31	133.32	119.35
3	A	83	ARG	N-CA-CB	9.29	123.48	110.01
3	A	266	TYR	CA-CB-CG	-9.16	97.42	113.90
1	T	5	DA	C4-N9-C1'	-9.13	113.35	127.05
2	P	3	DT	C6-N1-C1'	-9.02	105.82	119.35
3	A	116	ASP	CA-CB-CG	-8.96	103.64	112.60
2	P	7	DG	P-O3'-C3'	8.92	133.58	120.20
3	A	30	SER	CA-C-N	-8.87	107.38	123.34
3	A	30	SER	C-N-CA	-8.87	107.38	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	116	ASP	N-CA-CB	8.81	123.22	109.82
3	A	49	TYR	O-C-N	8.74	129.08	121.30
3	A	20	THR	CB-CA-C	8.59	125.46	110.85
3	A	168	LYS	N-CA-CB	8.55	123.39	110.22
1	T	3	DT	C6-N1-C1'	-8.30	106.89	119.35
3	A	224	ILE	CB-CA-C	-8.27	100.66	110.91
3	A	45	VAL	N-CA-CB	8.21	121.08	110.57
3	A	192	ASP	CB-CA-C	-8.13	97.59	111.41
3	A	27	LYS	N-CA-CB	-8.09	98.23	110.12
3	A	286	ALA	CA-C-N	8.04	130.89	120.44
3	A	286	ALA	C-N-CA	8.04	130.89	120.44
3	A	195	LEU	N-CA-CB	-8.03	97.71	111.69
3	A	309	GLU	CA-C-N	7.88	129.69	119.84
3	A	309	GLU	C-N-CA	7.88	129.69	119.84
3	A	45	VAL	N-CA-C	7.86	117.92	110.53
3	A	292	THR	CB-CA-C	7.84	123.37	109.65
3	A	119	ILE	N-CA-CB	-7.80	102.24	111.60
3	A	99	PHE	N-CA-C	7.50	119.09	111.07
3	A	169	VAL	CA-C-N	-7.39	111.21	122.81
3	A	169	VAL	C-N-CA	-7.39	111.21	122.81
3	A	130	ASP	CA-CB-CG	7.37	119.97	112.60
2	P	5	DA	C8-N9-C1'	-7.36	116.01	127.05
3	A	40	ARG	N-CA-C	7.25	120.60	111.69
3	A	115	VAL	O-C-N	7.16	128.81	121.87
3	A	116	ASP	CB-CA-C	7.15	122.28	110.92
3	A	41	LYS	N-CA-CB	7.12	120.58	110.12
3	A	30	SER	O-C-N	-7.10	113.48	122.43
3	A	134	HIS	CA-CB-CG	7.09	120.89	113.80
3	A	17	ASP	CB-CA-C	7.03	122.00	110.90
3	A	17	ASP	N-CA-CB	6.86	120.02	110.07
2	P	5	DA	C4-N9-C1'	6.86	137.34	127.05
3	A	320	PHE	CA-CB-CG	-6.84	106.96	113.80
2	P	3	DT	N1-C1'-C2'	6.73	123.59	113.50
3	A	173	TYR	CB-CA-C	-6.72	98.17	109.53
3	A	124	ASP	N-CA-C	-6.70	103.67	110.97
3	A	230	LYS	CA-C-N	-6.60	114.86	122.85
3	A	230	LYS	C-N-CA	-6.60	114.86	122.85
3	A	306	VAL	CB-CA-C	-6.58	100.19	110.52
3	A	94	SER	CA-CB-OG	-6.57	97.97	111.10
3	A	273	THR	N-CA-CB	6.55	120.38	110.30
3	A	253	ARG	N-CA-C	6.54	120.06	109.40
3	A	288	GLU	N-CA-C	-6.53	104.09	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	214	VAL	N-CA-C	6.48	116.64	110.42
3	A	92	ASP	N-CA-CB	6.47	119.62	110.12
3	A	157	GLN	N-CA-CB	6.46	119.72	110.16
3	A	59	ALA	O-C-N	6.42	128.68	122.07
3	A	291	PHE	N-CA-C	6.41	117.89	108.86
3	A	213	GLN	CB-CA-C	-6.34	100.92	110.88
3	A	161	ILE	N-CA-C	6.28	116.45	110.42
3	A	219	GLN	N-CA-CB	-6.26	100.87	110.20
3	A	235	PHE	CA-CB-CG	-6.21	107.59	113.80
1	T	6	DG	N9-C1'-C2'	-6.17	104.24	113.50
3	A	211	LEU	CA-C-N	6.15	128.44	120.44
3	A	211	LEU	C-N-CA	6.15	128.44	120.44
3	A	207	GLN	CA-C-N	6.15	126.61	119.47
3	A	207	GLN	C-N-CA	6.15	126.61	119.47
3	A	253	ARG	CD-NE-CZ	6.13	132.99	124.40
3	A	29	VAL	N-CA-CB	6.10	118.84	110.54
3	A	12	ASN	N-CA-CB	6.09	119.76	110.44
3	A	241	LEU	CA-C-N	6.09	127.45	119.84
3	A	241	LEU	C-N-CA	6.09	127.45	119.84
3	A	170	ASP	N-CA-C	-6.01	100.10	109.72
3	A	303	VAL	N-CA-C	6.00	121.83	109.34
3	A	11	LEU	CA-C-N	-5.99	111.53	122.38
3	A	11	LEU	C-N-CA	-5.99	111.53	122.38
3	A	64	GLY	CA-C-N	-5.99	115.23	122.90
3	A	64	GLY	C-N-CA	-5.99	115.23	122.90
3	A	72	LYS	CB-CA-C	5.98	121.02	110.85
3	A	329	GLU	O-C-N	5.96	127.91	121.60
3	A	246	ASP	N-CA-C	5.91	123.39	110.80
3	A	86	GLU	N-CA-CB	5.90	118.89	110.16
3	A	74	ASP	N-CA-C	5.87	118.15	111.11
3	A	24	ASN	CA-C-N	-5.85	110.73	120.68
3	A	24	ASN	C-N-CA	-5.85	110.73	120.68
3	A	249	GLU	CB-CA-C	5.85	119.45	109.80
3	A	292	THR	N-CA-CB	5.81	120.57	110.81
3	A	271	TYR	N-CA-CB	-5.78	100.72	110.49
3	A	85	LEU	N-CA-C	-5.75	105.15	111.82
3	A	93	THR	CA-C-O	5.71	126.82	120.82
3	A	243	SER	CA-C-N	5.70	132.44	121.54
3	A	243	SER	C-N-CA	5.70	132.44	121.54
3	A	335	GLU	N-CA-CB	5.64	120.08	110.50
1	T	7	DA	N9-C1'-C2'	-5.59	105.11	113.50
3	A	50	PRO	CB-CA-C	-5.57	102.94	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	92	ASP	CB-CA-C	5.57	120.03	110.79
3	A	137	ARG	CA-C-O	5.55	126.31	120.42
3	A	235	PHE	CA-C-O	-5.51	114.68	120.80
3	A	98	ASN	CA-CB-CG	-5.51	107.09	112.60
3	A	74	ASP	N-CA-CB	5.49	118.12	109.94
3	A	334	SER	N-CA-CB	5.46	118.25	110.06
3	A	321	ASP	CA-CB-CG	-5.46	107.14	112.60
3	A	12	ASN	CB-CA-C	5.41	119.75	110.01
3	A	181	PHE	CB-CA-C	-5.41	101.81	110.79
3	A	59	ALA	CB-CA-C	-5.40	102.41	110.88
3	A	314	ASP	CA-CB-CG	-5.37	107.23	112.60
3	A	312	PRO	N-CA-CB	5.36	107.59	103.30
3	A	97	ILE	CB-CA-C	-5.34	104.94	112.14
3	A	68	LYS	N-CA-CB	5.33	117.80	110.07
3	A	261	PRO	N-CA-C	-5.30	101.55	112.47
3	A	163	LEU	N-CA-C	5.29	117.05	111.28
3	A	299	ARG	CB-CA-C	5.29	115.89	109.85
3	A	253	ARG	CA-C-O	5.27	126.39	120.70
3	A	214	VAL	CB-CA-C	5.26	118.71	111.97
3	A	112	ARG	CA-C-N	5.25	127.26	120.44
3	A	112	ARG	C-N-CA	5.25	127.26	120.44
3	A	87	LYS	CB-CA-C	5.24	119.18	110.90
3	A	88	ILE	CB-CA-C	-5.22	105.20	112.04
3	A	214	VAL	N-CA-CB	5.21	116.65	110.55
3	A	20	THR	N-CA-CB	5.20	117.85	110.16
3	A	15	ILE	N-CA-CB	5.16	116.24	110.62
3	A	16	THR	CA-C-N	-5.13	113.47	120.44
3	A	16	THR	C-N-CA	-5.13	113.47	120.44
3	A	177	VAL	CA-CB-CG2	-5.12	101.69	110.40
3	A	34	HIS	CA-CB-CG	-5.11	108.69	113.80
3	A	40	ARG	N-CA-CB	5.11	117.81	110.20
3	A	23	ALA	O-C-N	5.10	127.33	122.03
3	A	49	TYR	CA-CB-CG	5.10	123.08	113.90
3	A	176	THR	CA-C-N	-5.06	116.15	122.48
3	A	176	THR	C-N-CA	-5.06	116.15	122.48
3	A	192	ASP	CA-C-N	-5.05	115.85	122.37
3	A	192	ASP	C-N-CA	-5.05	115.85	122.37
3	A	32	ALA	N-CA-C	5.05	116.83	109.71
3	A	206	LYS	N-CA-C	5.03	121.51	110.80
3	A	332	ASP	N-CA-C	5.02	119.09	112.92
3	A	285	HIS	N-CA-C	5.01	116.82	111.36
3	A	31	GLN	N-CA-C	-5.01	104.43	110.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	315	SER	N-CA-CB	5.00	118.95	110.49

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	292	THR	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	7	0
2	P	165	0	92	21	0
3	A	2623	0	2641	296	0
4	A	2	0	0	0	0
5	A	2	0	0	0	0
6	A	9	0	0	0	0
7	A	111	0	0	22	0
7	P	21	0	0	1	0
7	T	14	0	0	3	0
All	All	3092	0	2813	318	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 56.

All (318) 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)
2:P:5:DA:H2''	2:P:6:DT:H5''	1.26	1.17
3:A:18:MET:HE2	3:A:82:LEU:HD22	1.16	1.08
3:A:243:SER:HB3	3:A:249:GLU:HA	1.43	1.01
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.61	0.99
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.43	0.98
3:A:245:ASN:H	3:A:245:ASN:HD22	1.11	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:245:ASN:HD22	3:A:245:ASN:N	1.60	0.95
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.50	0.94
1:T:6:DG:H2''	1:T:7:DA:C8	2.04	0.91
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.50	0.91
2:P:6:DT:H2''	2:P:7:DG:H5''	1.53	0.91
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.19	0.90
3:A:11:LEU:HD23	3:A:11:LEU:H	1.37	0.89
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.14	0.86
2:P:8:DA:H4'	3:A:272:PHE:CE1	2.11	0.86
2:P:5:DA:H2''	2:P:6:DT:C5'	2.05	0.85
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.61	0.83
3:A:121:THR:HG23	3:A:124:ASP:CG	2.06	0.81
3:A:60:LYS:HA	3:A:65:VAL:HG23	1.61	0.81
3:A:294:ASN:HD22	3:A:294:ASN:H	1.31	0.78
3:A:18:MET:HG2	3:A:19:LEU:N	1.99	0.76
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.14	0.76
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.83	0.76
2:P:6:DT:H2''	2:P:7:DG:C5'	2.15	0.76
3:A:125:LEU:HD22	3:A:132:LEU:HD21	1.68	0.76
3:A:31:GLN:HB2	3:A:112:ARG:NH1	2.02	0.75
3:A:60:LYS:HA	3:A:65:VAL:CG2	2.16	0.75
3:A:245:ASN:N	3:A:245:ASN:ND2	2.35	0.73
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.71	0.72
2:P:6:DT:C2'	2:P:7:DG:H5''	2.19	0.72
3:A:150:ILE:HD13	3:A:253:ARG:HG2	1.72	0.72
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.21	0.71
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.71	0.71
3:A:12:ASN:HD21	3:A:53:ILE:H	1.36	0.70
3:A:59:ALA:O	3:A:62:LEU:HB2	1.90	0.70
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.22	0.70
2:P:7:DG:H2''	2:P:8:DA:H5'	1.73	0.69
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.93	0.69
3:A:218:LEU:HB3	3:A:224:ILE:HD12	1.75	0.69
3:A:277:ILE:HD13	3:A:277:ILE:H	1.57	0.69
3:A:157:GLN:O	3:A:161:ILE:HG13	1.92	0.69
2:P:7:DG:C8	2:P:7:DG:H5'	2.29	0.68
3:A:210:LEU:HB2	3:A:259:LEU:HD21	1.76	0.67
3:A:155:MET:HA	3:A:158:MET:HE3	1.75	0.67
3:A:218:LEU:CB	3:A:224:ILE:HD12	2.25	0.67
3:A:89:ARG:HD3	3:A:89:ARG:C	2.20	0.67
3:A:285:HIS:NE2	7:A:583:HOH:O	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.78	0.66
3:A:210:LEU:CB	3:A:259:LEU:HD21	2.26	0.66
3:A:292:THR:O	3:A:298:ILE:HA	1.95	0.66
3:A:243:SER:CB	3:A:249:GLU:HA	2.23	0.66
3:A:279:ASN:O	3:A:283:ARG:HG3	1.96	0.65
3:A:294:ASN:HD22	3:A:294:ASN:N	1.92	0.65
3:A:295:GLU:CD	3:A:295:GLU:H	2.04	0.65
3:A:323:ILE:C	3:A:324:GLN:HG2	2.22	0.65
3:A:12:ASN:ND2	3:A:53:ILE:H	1.94	0.65
3:A:18:MET:HE1	3:A:76:PHE:CB	2.27	0.64
3:A:323:ILE:O	3:A:324:GLN:HG2	1.98	0.64
2:P:1:DT:H2''	2:P:2:DC:H5'	1.81	0.63
3:A:258:ARG:NH1	7:A:662:HOH:O	2.26	0.63
3:A:264:GLN:HA	7:A:536:HOH:O	1.99	0.63
3:A:11:LEU:H	3:A:11:LEU:CD2	2.10	0.63
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.38	0.63
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.81	0.62
3:A:233:THR:HB	7:A:538:HOH:O	1.99	0.62
3:A:298:ILE:HA	7:A:593:HOH:O	2.00	0.62
3:A:266:TYR:HB2	3:A:313:VAL:CG1	2.29	0.62
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.15	0.62
3:A:268:GLY:O	3:A:271:TYR:HB3	1.99	0.62
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.30	0.61
3:A:294:ASN:HB2	3:A:295:GLU:OE1	1.99	0.61
3:A:25:PHE:CD2	3:A:88:ILE:HD13	2.35	0.61
3:A:154:GLU:O	3:A:158:MET:HG3	2.01	0.61
2:P:5:DA:C2'	2:P:6:DT:H5''	2.15	0.61
3:A:276:ASP:O	3:A:280:LYS:HG3	2.00	0.61
3:A:151:PRO:HG2	3:A:154:GLU:HG3	1.82	0.61
3:A:291:PHE:CD1	3:A:300:PRO:HA	2.36	0.61
3:A:60:LYS:HG3	3:A:60:LYS:O	1.98	0.61
3:A:150:ILE:CG2	3:A:158:MET:HE1	2.25	0.61
3:A:292:THR:O	3:A:298:ILE:HG13	2.00	0.61
3:A:41:LYS:HD3	3:A:42:ALA:H	1.65	0.60
3:A:133:ASN:O	3:A:137:ARG:HG3	2.01	0.60
3:A:30:SER:HB3	7:A:561:HOH:O	2.00	0.60
3:A:270:LEU:HD21	3:A:282:MET:CE	2.31	0.60
3:A:309:GLU:N	3:A:309:GLU:OE1	2.34	0.60
3:A:277:ILE:HG12	3:A:335:GLU:HB2	1.83	0.60
3:A:245:ASN:H	3:A:245:ASN:ND2	1.90	0.60
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:150:ILE:N	3:A:188:SER:O	2.27	0.59
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.85	0.59
3:A:326:LYS:HG3	3:A:326:LYS:O	2.02	0.58
3:A:330:PRO:O	3:A:333:ARG:HG2	2.03	0.58
3:A:125:LEU:CD2	3:A:132:LEU:HD21	2.34	0.58
3:A:212:HIS:HB3	7:A:541:HOH:O	2.03	0.58
3:A:275:SER:OG	3:A:277:ILE:HD13	2.04	0.58
3:A:169:VAL:HG22	3:A:170:ASP:N	2.18	0.58
3:A:25:PHE:CG	3:A:88:ILE:HD13	2.39	0.57
3:A:291:PHE:HD1	3:A:300:PRO:HA	1.70	0.57
1:T:3:DT:H73	7:T:661:HOH:O	2.05	0.57
1:T:5:DA:H2''	1:T:6:DG:O5'	2.03	0.57
3:A:244:LYS:HB3	3:A:245:ASN:HD22	1.70	0.57
3:A:294:ASN:N	3:A:294:ASN:ND2	2.53	0.56
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.39	0.56
3:A:232:GLU:O	3:A:233:THR:HG23	2.05	0.56
3:A:248:LYS:O	3:A:248:LYS:HG2	2.05	0.56
3:A:299:ARG:HG2	3:A:310:PRO:N	2.20	0.56
2:P:5:DA:H2'	2:P:6:DT:H71	1.88	0.56
3:A:182:ARG:NH2	3:A:316:GLU:OE2	2.32	0.55
3:A:259:LEU:O	3:A:260:ILE:HD13	2.05	0.55
1:T:1:DC:O2	2:P:7:DG:N2	2.38	0.55
3:A:89:ARG:HD3	3:A:89:ARG:O	2.06	0.55
2:P:1:DT:H2''	2:P:2:DC:C5'	2.36	0.55
3:A:41:LYS:NZ	3:A:64:GLY:O	2.31	0.55
3:A:306:VAL:HG22	7:A:650:HOH:O	2.05	0.55
3:A:60:LYS:NZ	3:A:67:THR:HG22	2.22	0.55
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.37	0.55
3:A:180:SER:HB2	3:A:185:ALA:HB2	1.90	0.54
3:A:150:ILE:HG21	3:A:158:MET:CE	2.30	0.54
3:A:196:THR:OG1	3:A:197:HIS:N	2.40	0.54
3:A:317:LYS:O	3:A:320:PHE:N	2.41	0.54
3:A:83:ARG:O	3:A:86:GLU:N	2.40	0.54
3:A:18:MET:CE	3:A:76:PHE:HB2	2.32	0.54
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.38	0.54
1:T:6:DG:N7	7:T:652:HOH:O	2.32	0.53
3:A:114:PHE:HB3	3:A:119:ILE:HB	1.91	0.53
3:A:327:TYR:HD1	3:A:328:ARG:N	2.06	0.53
2:P:6:DT:H2''	2:P:7:DG:C8	2.42	0.53
3:A:210:LEU:HB2	3:A:259:LEU:CD2	2.39	0.53
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:170:ASP:OD1	3:A:171:SER:N	2.42	0.53
3:A:41:LYS:HD3	3:A:42:ALA:N	2.23	0.53
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.44	0.53
3:A:277:ILE:HG12	3:A:335:GLU:CB	2.39	0.53
3:A:56:GLY:O	3:A:59:ALA:HB3	2.08	0.53
3:A:182:ARG:NH1	3:A:182:ARG:HG2	2.23	0.52
3:A:226:ASP:HB2	3:A:238:VAL:HB	1.92	0.52
3:A:264:GLN:HB3	3:A:296:TYR:O	2.09	0.52
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.91	0.52
3:A:16:THR:HG21	3:A:47:ALA:HB2	1.92	0.52
3:A:152:ARG:NH2	3:A:181:PHE:O	2.43	0.52
3:A:303:VAL:C	3:A:305:GLY:H	2.17	0.52
3:A:41:LYS:O	3:A:44:SER:HB3	2.10	0.52
3:A:277:ILE:CG1	3:A:335:GLU:HB2	2.40	0.52
3:A:288:GLU:C	3:A:290:GLY:H	2.19	0.51
3:A:234:LYS:HD3	7:A:617:HOH:O	2.10	0.51
3:A:294:ASN:ND2	3:A:297:THR:H	2.09	0.51
3:A:298:ILE:HG23	3:A:298:ILE:O	2.11	0.50
3:A:332:ASP:C	3:A:334:SER:H	2.20	0.50
3:A:244:LYS:HB3	3:A:245:ASN:ND2	2.27	0.50
1:T:7:DA:H61	2:P:1:DT:H3	1.58	0.50
3:A:41:LYS:HE2	3:A:64:GLY:HA2	1.94	0.50
3:A:291:PHE:O	3:A:301:LEU:HD22	2.11	0.50
3:A:31:GLN:HE21	3:A:112:ARG:HH22	1.60	0.50
3:A:259:LEU:HD12	3:A:260:ILE:H	1.75	0.50
3:A:270:LEU:HD13	3:A:316:GLU:OE1	2.12	0.50
3:A:31:GLN:O	3:A:31:GLN:HG2	2.12	0.49
3:A:205:THR:HA	7:A:624:HOH:O	2.11	0.49
3:A:299:ARG:HG2	3:A:310:PRO:CD	2.42	0.49
3:A:294:ASN:H	3:A:294:ASN:ND2	2.04	0.49
3:A:322:TYR:C	3:A:324:GLN:H	2.20	0.49
3:A:57:ALA:HA	3:A:60:LYS:HB3	1.93	0.49
3:A:124:ASP:O	3:A:128:ASN:ND2	2.36	0.49
3:A:183:ARG:NH1	3:A:275:SER:HA	2.28	0.49
3:A:271:TYR:CD2	3:A:272:PHE:N	2.81	0.49
3:A:286:ALA:HB1	3:A:291:PHE:HB2	1.93	0.49
3:A:27:LYS:HG3	3:A:28:ASN:ND2	2.28	0.49
3:A:60:LYS:HE3	3:A:66:GLY:HA2	1.95	0.49
3:A:200:PHE:C	3:A:201:THR:HG22	2.37	0.49
3:A:243:SER:HB3	3:A:249:GLU:HB2	1.95	0.49
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:286:ALA:O	3:A:291:PHE:HB2	2.12	0.49
3:A:286:ALA:HA	3:A:323:ILE:HG22	1.95	0.48
3:A:12:ASN:HB2	3:A:46:ILE:HD12	1.94	0.48
3:A:241:LEU:HB2	3:A:250:TYR:CD2	2.48	0.48
3:A:27:LYS:HG3	3:A:28:ASN:HD22	1.78	0.48
3:A:72:LYS:HG2	3:A:82:LEU:HD11	1.94	0.48
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.78	0.48
3:A:228:LEU:HB2	3:A:236:MET:O	2.13	0.48
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.28	0.48
3:A:230:LYS:HG3	3:A:235:PHE:HD1	1.77	0.48
3:A:327:TYR:CD1	3:A:328:ARG:N	2.82	0.48
3:A:207:GLN:HB2	7:A:625:HOH:O	2.13	0.48
3:A:142:TYR:CE2	3:A:238:VAL:HG11	2.49	0.47
3:A:49:TYR:CE2	3:A:53:ILE:HG13	2.50	0.47
3:A:254:ARG:CZ	3:A:254:ARG:HB3	2.44	0.47
3:A:316:GLU:O	3:A:320:PHE:HD2	1.97	0.47
3:A:31:GLN:HE21	3:A:112:ARG:NH2	2.12	0.47
3:A:213:GLN:HG3	7:A:644:HOH:O	2.15	0.47
3:A:133:ASN:ND2	3:A:135:HIS:H	2.13	0.47
3:A:242:PRO:HG2	7:A:589:HOH:O	2.14	0.47
3:A:249:GLU:HG3	3:A:250:TYR:N	2.29	0.47
2:P:3:DT:H5''	7:P:615:HOH:O	2.14	0.47
3:A:282:MET:HB3	7:A:555:HOH:O	2.15	0.47
3:A:289:LYS:N	3:A:289:LYS:HD3	2.26	0.47
3:A:299:ARG:HG2	3:A:310:PRO:HD3	1.95	0.47
3:A:31:GLN:HE21	3:A:112:ARG:CZ	2.28	0.47
3:A:170:ASP:HB3	3:A:173:TYR:CD2	2.50	0.47
3:A:200:PHE:CD2	3:A:261:PRO:HA	2.50	0.47
2:P:7:DG:H5'	2:P:7:DG:H8	1.79	0.46
3:A:123:GLU:HG3	7:A:623:HOH:O	2.14	0.46
3:A:60:LYS:HZ2	3:A:67:THR:HG22	1.79	0.46
3:A:292:THR:C	3:A:293:ILE:HG12	2.36	0.46
3:A:29:VAL:HG21	3:A:94:SER:OG	2.15	0.46
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.74	0.46
3:A:191:MET:HB2	3:A:191:MET:HE3	1.77	0.46
3:A:218:LEU:HB2	3:A:224:ILE:HD12	1.97	0.46
3:A:81:LYS:NZ	3:A:86:GLU:HB2	2.31	0.46
3:A:122:LEU:CD2	3:A:126:ARG:NH2	2.79	0.46
3:A:200:PHE:CE2	3:A:261:PRO:N	2.84	0.45
3:A:250:TYR:HB3	7:A:577:HOH:O	2.15	0.45
3:A:128:ASN:ND2	3:A:128:ASN:N	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:159:GLN:O	3:A:163:LEU:HG	2.15	0.45
3:A:210:LEU:HB3	3:A:259:LEU:HD21	1.97	0.45
3:A:251:PRO:HG2	3:A:253:ARG:NH2	2.32	0.45
3:A:328:ARG:O	3:A:333:ARG:NE	2.40	0.45
3:A:84:LYS:O	3:A:88:ILE:HG13	2.16	0.45
3:A:282:MET:HE3	7:A:555:HOH:O	2.15	0.45
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.45	0.45
3:A:31:GLN:HB2	3:A:112:ARG:HH12	1.79	0.45
3:A:195:LEU:HD23	3:A:259:LEU:HD13	1.97	0.45
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.34	0.45
3:A:295:GLU:OE1	3:A:295:GLU:N	2.42	0.45
3:A:298:ILE:N	7:A:578:HOH:O	2.28	0.45
3:A:299:ARG:CD	3:A:310:PRO:HD3	2.47	0.45
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.62	0.45
3:A:111:ALA:O	3:A:115:VAL:HG23	2.17	0.45
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.98	0.45
3:A:183:ARG:HH11	3:A:275:SER:HA	1.82	0.45
2:P:8:DA:H4'	3:A:272:PHE:CD1	2.50	0.44
3:A:185:ALA:HB3	7:A:530:HOH:O	2.17	0.44
3:A:260:ILE:HA	3:A:261:PRO:HD3	1.75	0.44
3:A:29:VAL:HA	3:A:97:ILE:HD12	1.98	0.44
3:A:54:LYS:HD2	3:A:54:LYS:HA	1.32	0.44
3:A:81:LYS:NZ	3:A:86:GLU:CB	2.80	0.44
3:A:243:SER:CB	3:A:249:GLU:HB2	2.47	0.44
3:A:243:SER:HB3	3:A:249:GLU:CA	2.31	0.44
3:A:59:ALA:C	3:A:65:VAL:HG21	2.43	0.44
3:A:243:SER:HB3	3:A:249:GLU:CB	2.47	0.44
3:A:98:ASN:O	3:A:101:THR:HB	2.18	0.43
3:A:182:ARG:HH12	3:A:273:THR:HG21	1.82	0.43
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.34	0.43
3:A:120:LYS:N	3:A:124:ASP:OD2	2.44	0.43
3:A:271:TYR:HB2	7:A:592:HOH:O	2.17	0.43
3:A:163:LEU:HD23	3:A:163:LEU:HA	1.50	0.43
3:A:83:ARG:HA	3:A:86:GLU:HG2	1.99	0.43
3:A:150:ILE:HD11	3:A:253:ARG:HG2	1.98	0.43
3:A:262:LYS:O	3:A:262:LYS:HG3	2.03	0.43
3:A:26:GLU:HB2	3:A:36:TYR:HB2	1.99	0.43
3:A:62:LEU:HD12	3:A:62:LEU:HA	1.58	0.43
3:A:260:ILE:HG23	3:A:260:ILE:HD12	1.70	0.43
3:A:22:LEU:HA	3:A:22:LEU:HD13	1.38	0.43
3:A:99:PHE:CD1	3:A:99:PHE:C	2.96	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.83	0.43
3:A:223:PHE:O	3:A:239:CYS:HA	2.19	0.43
3:A:294:ASN:O	3:A:296:TYR:N	2.52	0.43
3:A:241:LEU:HA	3:A:242:PRO:HD2	1.59	0.42
3:A:285:HIS:CD2	3:A:289:LYS:HG2	2.54	0.42
3:A:27:LYS:HG3	3:A:28:ASN:N	2.35	0.42
3:A:320:PHE:CE1	3:A:328:ARG:HG3	2.55	0.42
3:A:22:LEU:HD22	3:A:85:LEU:CD1	2.49	0.42
3:A:29:VAL:O	3:A:29:VAL:HG12	2.19	0.42
3:A:68:LYS:O	3:A:72:LYS:HE3	2.19	0.42
3:A:322:TYR:HD1	3:A:322:TYR:HA	1.54	0.42
3:A:23:ALA:HB2	3:A:39:TYR:HB3	2.00	0.42
3:A:327:TYR:CD1	3:A:327:TYR:C	2.97	0.42
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.54	0.42
3:A:156:LEU:HD23	3:A:156:LEU:HA	1.91	0.42
3:A:266:TYR:HB2	3:A:313:VAL:HG12	2.00	0.42
3:A:22:LEU:HD22	3:A:85:LEU:HD11	2.01	0.42
3:A:215:VAL:O	3:A:219:GLN:HB2	2.19	0.42
3:A:260:ILE:HD13	3:A:260:ILE:HA	1.68	0.42
3:A:11:LEU:HD23	3:A:11:LEU:N	2.14	0.42
3:A:27:LYS:CB	3:A:36:TYR:CD1	3.03	0.42
3:A:79:THR:O	3:A:81:LYS:N	2.48	0.42
3:A:85:LEU:O	3:A:89:ARG:HB2	2.19	0.42
3:A:315:SER:O	3:A:317:LYS:N	2.53	0.42
3:A:12:ASN:HD21	3:A:53:ILE:N	2.10	0.42
3:A:49:TYR:CD2	3:A:53:ILE:HG13	2.55	0.42
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.72	0.42
3:A:229:SER:OG	3:A:236:MET:HE2	2.19	0.42
3:A:41:LYS:HZ3	3:A:64:GLY:C	2.23	0.41
3:A:73:ILE:HG22	3:A:77:LEU:HD22	2.02	0.41
3:A:235:PHE:CD2	3:A:235:PHE:C	2.98	0.41
1:T:7:DA:H4'	7:T:634:HOH:O	2.20	0.41
3:A:182:ARG:NH1	3:A:273:THR:CG2	2.82	0.41
3:A:303:VAL:C	3:A:305:GLY:N	2.78	0.41
2:P:5:DA:P	3:A:107:GLY:HA3	2.60	0.41
3:A:293:ILE:CD1	3:A:298:ILE:HD12	2.50	0.41
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.98	0.41
3:A:278:PHE:CD2	3:A:333:ARG:HB3	2.55	0.41
3:A:293:ILE:CD1	3:A:298:ILE:CD1	2.99	0.41
3:A:322:TYR:C	3:A:324:GLN:N	2.79	0.41
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:287:LEU:HA	3:A:287:LEU:HD13	1.31	0.41
3:A:301:LEU:HD12	3:A:301:LEU:HA	1.61	0.41
2:P:2:DC:H6	2:P:2:DC:H2'	1.47	0.41
3:A:115:VAL:O	3:A:118:GLY:N	2.54	0.41
3:A:215:VAL:HG12	3:A:219:GLN:OE1	2.21	0.41
3:A:45:VAL:C	3:A:47:ALA:N	2.77	0.41
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.86	0.41
3:A:282:MET:HG2	7:A:555:HOH:O	2.20	0.41
3:A:25:PHE:CD1	3:A:25:PHE:C	2.99	0.41
3:A:116:ASP:C	3:A:118:GLY:N	2.79	0.41
3:A:210:LEU:HD23	3:A:210:LEU:HA	1.85	0.41
3:A:211:LEU:HD21	3:A:235:PHE:HB2	2.03	0.41
3:A:196:THR:OG1	3:A:260:ILE:O	2.33	0.40
3:A:228:LEU:HA	3:A:228:LEU:HD12	1.44	0.40
3:A:327:TYR:HD1	3:A:328:ARG:C	2.29	0.40
3:A:184:GLY:O	3:A:185:ALA:O	2.39	0.40
3:A:293:ILE:HA	7:A:593:HOH:O	2.21	0.40
3:A:210:LEU:CB	3:A:259:LEU:CD2	2.98	0.40
3:A:255:ILE:HG12	3:A:256:ASP:N	2.36	0.40
3:A:267:CYS:SG	3:A:297:THR:HA	2.61	0.40
3:A:326:LYS:O	3:A:328:ARG:HG2	2.22	0.40
2:P:8:DA:H4'	3:A:272:PHE:HE1	1.78	0.40
3:A:73:ILE:HG21	3:A:73:ILE:HD13	1.77	0.40
3:A:172:GLU:HB3	3:A:197:HIS:NE2	2.37	0.40
3:A:299:ARG:HA	3:A:300:PRO:HD3	1.88	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%)	39 (12%)	16 (5%)	1 3

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	185	ALA
3	A	204	SER
3	A	206	LYS
3	A	244	LYS
3	A	246	ASP
3	A	13	GLY
3	A	205	THR
3	A	289	LYS
3	A	295	GLU
3	A	316	GLU
3	A	207	GLN
3	A	262	LYS
3	A	202	SER
3	A	309	GLU
3	A	310	PRO
3	A	298	ILE

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%)	217 (75%)	71 (25%)	1 2

All (71) 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	27	LYS
3	A	30	SER
3	A	33	ILE
3	A	37	ASN

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Mol	Chain	Res	Type
3	A	41	LYS
3	A	44	SER
3	A	46	ILE
3	A	52	LYS
3	A	54	LYS
3	A	60	LYS
3	A	62	LEU
3	A	65	VAL
3	A	67	THR
3	A	68	LYS
3	A	77	LEU
3	A	79	THR
3	A	81	LYS
3	A	85	LEU
3	A	89	ARG
3	A	90	GLN
3	A	92	ASP
3	A	100	LEU
3	A	101	THR
3	A	121	THR
3	A	122	LEU
3	A	138	ILE
3	A	153	GLU
3	A	157	GLN
3	A	161	ILE
3	A	168	LYS
3	A	169	VAL
3	A	172	GLU
3	A	174	ILE
3	A	182	ARG
3	A	188	SER
3	A	191	MET
3	A	194	LEU
3	A	195	LEU
3	A	201	THR
3	A	213	GLN
3	A	214	VAL
3	A	218	LEU
3	A	228	LEU
3	A	230	LYS
3	A	233	THR
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	262	LYS
3	A	264	GLN
3	A	273	THR
3	A	277	ILE
3	A	279	ASN
3	A	287	LEU
3	A	289	LYS
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	301	LEU
3	A	303	VAL
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	325	TRP
3	A	331	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	51	HIS
3	A	98	ASN
3	A	128	ASN
3	A	133	ASN
3	A	136	GLN
3	A	159	GLN
3	A	212	HIS
3	A	213	GLN
3	A	245	ASN
3	A	252	HIS
3	A	279	ASN
3	A	294	ASN
3	A	324	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 5 ligands modelled in this entry, 4 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	1.41	1 (16%)	12,13,50	1.23	1 (8%)

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	-	2/6/6/34	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	338	DTP	PB-O3A	2.44	1.63	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	338	DTP	O2G-PG-O1G	2.27	119.69	110.83

There are no chirality outliers.

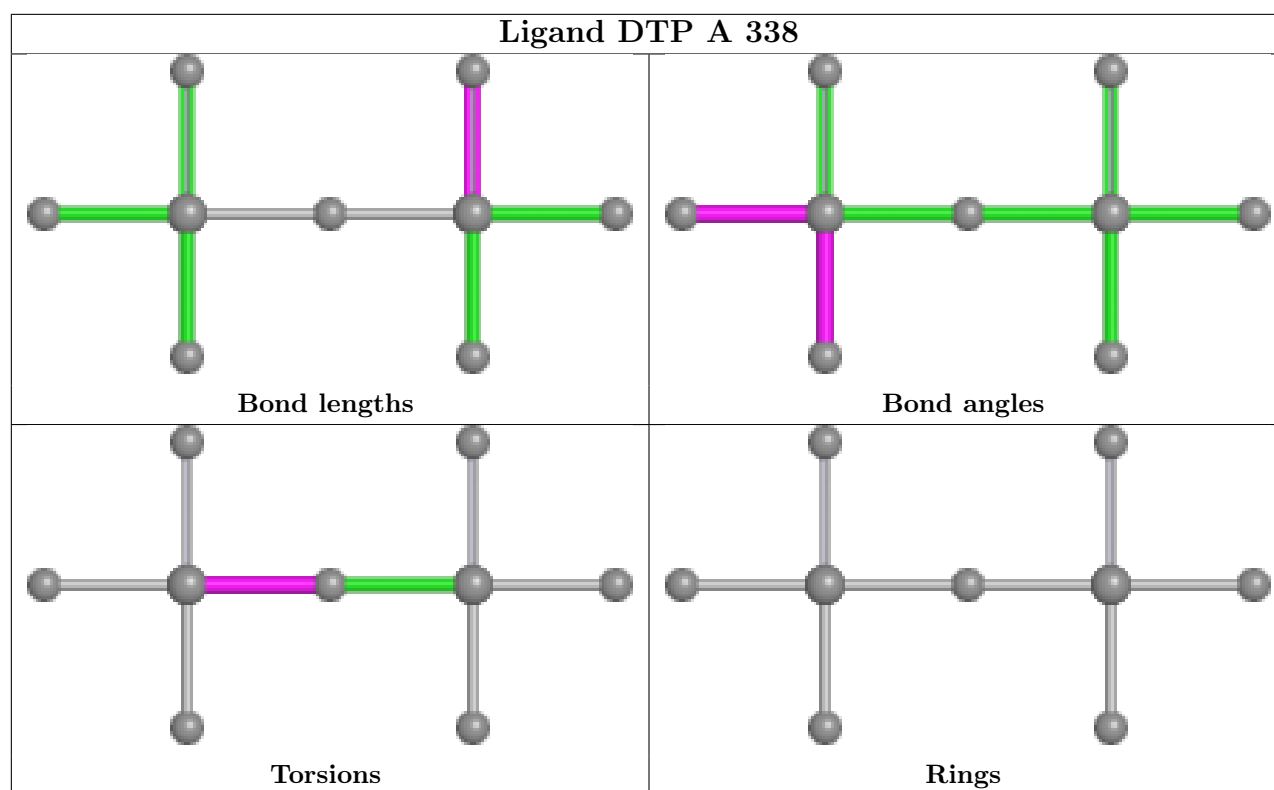
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	338	DTP	PB-O3B-PG-O2G
6	A	338	DTP	PB-O3B-PG-O1G

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(Å ²)	Q<0.9
1	T	8/8 (100%)	-0.65	0 100 100	20, 47, 99, 99	0
2	P	8/8 (100%)	-0.81	1 (12%) 8 7	20, 39, 63, 100	0
3	A	324/335 (96%)	-0.91	0 100 100	10, 38, 84, 100	1 (0%)
All	All	340/351 (96%)	-0.90	1 (0%) 90 89	10, 39, 88, 100	1 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	8	DA	2.1

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.

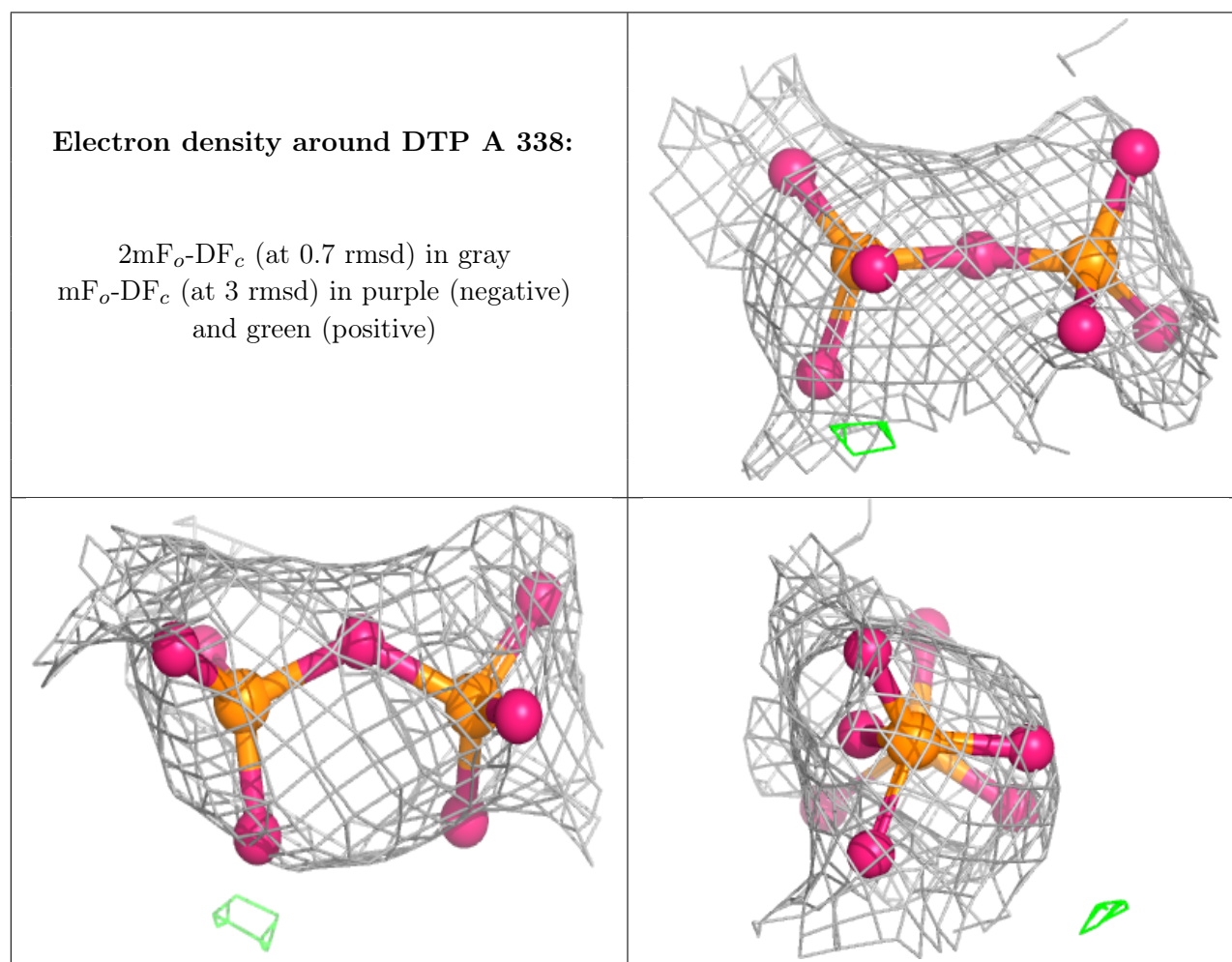
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MN	A	339	1/1	0.75	0.08	30,30,30,30	1
4	MN	A	340	1/1	0.87	0.07	30,30,30,30	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	DTP	A	338	9/30	0.87	0.10	52,54,83,85	9
5	NA	A	342	1/1	0.94	0.10	50,50,50,50	0
5	NA	A	341	1/1	0.99	0.02	23,23,23,23	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.