



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 11:20 AM UTC

PDB ID : 8ICF / pdb\_00008icf  
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 (10 MILLIMOLAR) AND MGCL2 (50 MILLIMOLAR)  
Authors : Pelletier, H.; Sawaya, M.R.  
Deposited on : 1996-04-19  
Resolution : 2.90 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

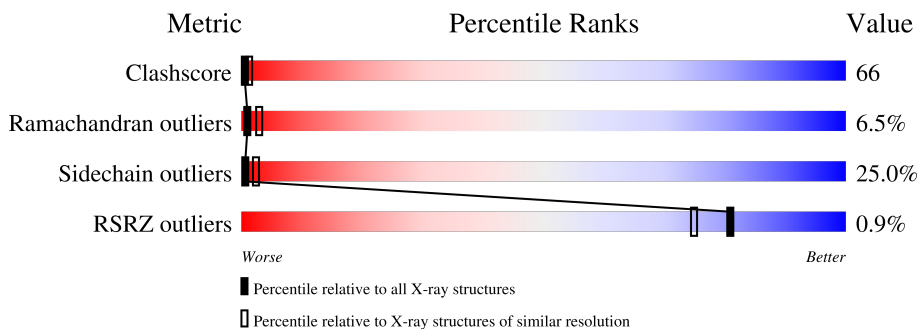
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	 12% 12% 25% 62%
2	P	7	 14% 14% 86%
3	A	335	 21% 38% 33% 6% •

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3062 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\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	P	7	144	69	24	44	7	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	18	0	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

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

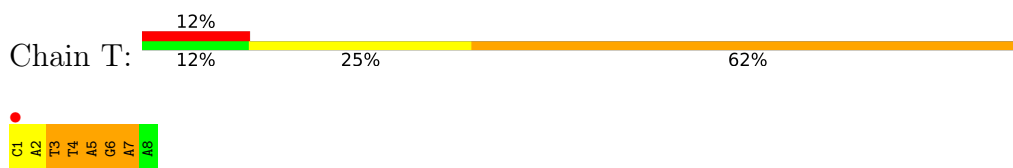
- Molecule 5 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>)



### 3 Residue-property plots

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.

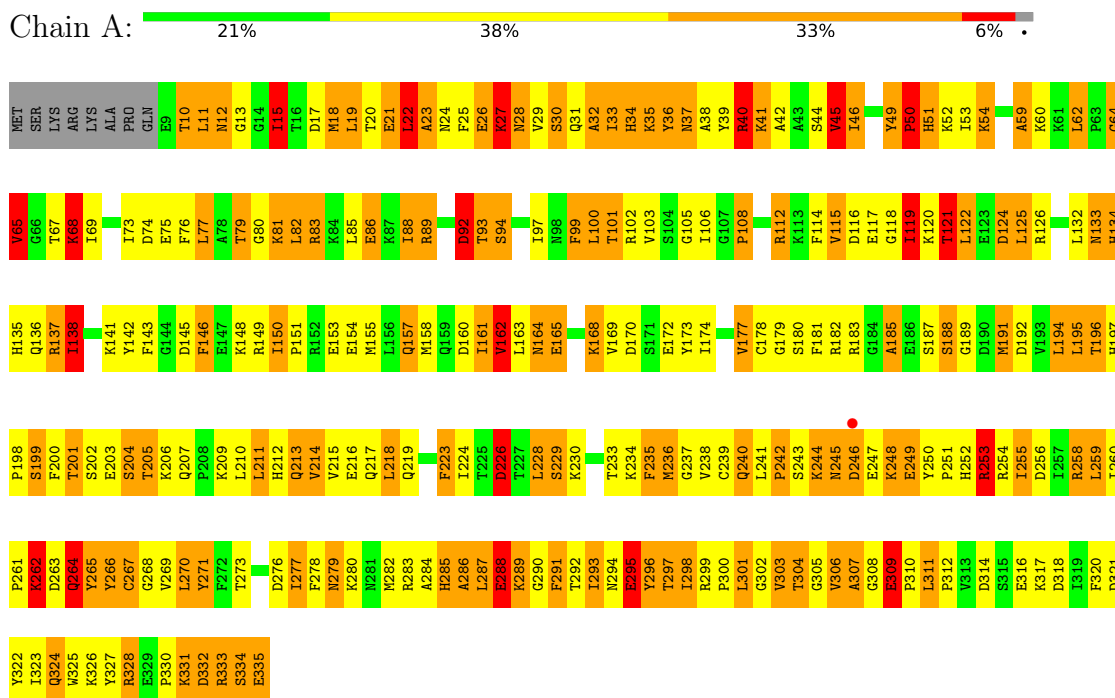
- Molecule 1: DNA (5'-D(\*CP\*AP\*TP\*TP\*AP\*GP\*AP\*A)-3')



- Molecule 2: DNA (5'-D(\*TP\*CP\*TP\*AP\*AP\*TP\*G)-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, $\alpha$ , $\beta$ , $\gamma$	178.88Å 57.71Å 48.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	94.0 (20.00-2.90) 93.5 (20.00-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 2.70Å)	Xtrriage
Refinement program	TNT 5-D	Depositor
R, $R_{free}$	0.185 , (Not available) 0.176 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtrriage
Anisotropy	0.301	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.19 , 167.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3062	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% 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: DTP, NA

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	0.97	0/162	3.27	16/249 (6.4%)
2	P	1.14	1/160 (0.6%)	3.88	16/243 (6.6%)
3	A	1.46	12/2672 (0.4%)	2.22	130/3590 (3.6%)
All	All	1.43	13/2994 (0.4%)	2.43	162/4082 (4.0%)

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 (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	242	PRO	N-CA	-6.49	1.39	1.47
2	P	1	DT	OP3-P	6.13	1.60	1.48
3	A	30	SER	C-N	-6.04	1.25	1.33
3	A	138	ILE	CA-CB	-5.97	1.46	1.54
3	A	224	ILE	CA-C	-5.73	1.45	1.52
3	A	258	ARG	CA-C	5.71	1.59	1.52
3	A	23	ALA	N-CA	-5.46	1.40	1.46
3	A	138	ILE	N-CA	-5.42	1.39	1.46
3	A	125	LEU	CA-C	-5.41	1.46	1.52
3	A	106	ILE	CA-C	-5.31	1.46	1.52
3	A	124	ASP	CA-C	-5.29	1.45	1.52
3	A	27	LYS	N-CA	-5.12	1.40	1.46
3	A	177	VAL	N-CA	-5.03	1.40	1.46

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	4	DT	C6-N1-C1'	-24.11	83.18	119.35
2	P	1	DT	C6-N1-C1'	-23.93	83.45	119.35
2	P	1	DT	C2-N1-C1'	23.18	154.12	119.35
1	T	4	DT	C2-N1-C1'	22.89	153.69	119.35
2	P	3	DT	C2-N1-C1'	20.97	150.80	119.35
2	P	3	DT	C6-N1-C1'	-20.77	88.20	119.35
3	A	28	ASN	CA-CB-CG	-15.86	96.74	112.60
2	P	6	DT	C2-N1-C1'	14.05	140.42	119.35
2	P	6	DT	C6-N1-C1'	-13.81	98.64	119.35
1	T	5	DA	C4-N9-C1'	-12.77	107.90	127.05
2	P	2	DC	C2-N1-C1'	12.62	138.63	119.70
1	T	5	DA	C8-N9-C1'	12.33	145.55	127.05
1	T	7	DA	C4-N9-C1'	-11.34	110.05	127.05
2	P	7	DG	C8-N9-C1'	11.17	143.75	127.00
3	A	49	TYR	CA-C-N	11.07	133.67	119.84
3	A	49	TYR	C-N-CA	11.07	133.67	119.84
2	P	2	DC	C6-N1-C1'	-10.70	103.66	119.70
2	P	7	DG	C4-N9-C1'	-10.55	111.17	127.00
1	T	6	DG	C4-N9-C1'	-10.17	111.75	127.00
3	A	157	GLN	N-CA-CB	9.97	124.78	110.12
1	T	7	DA	C8-N9-C1'	9.92	141.94	127.05
2	P	3	DT	P-O3'-C3'	9.73	134.79	120.20
1	T	6	DG	C8-N9-C1'	9.71	141.56	127.00
3	A	34	HIS	CA-CB-CG	-9.55	104.25	113.80
3	A	32	ALA	N-CA-C	8.90	121.73	109.54
3	A	223	PHE	N-CA-C	-8.76	100.28	112.45
3	A	318	ASP	CA-CB-CG	-8.70	103.90	112.60
3	A	177	VAL	CB-CA-C	8.46	120.98	111.08
3	A	99	PHE	CA-CB-CG	-8.29	105.51	113.80
3	A	134	HIS	CA-CB-CG	8.15	121.95	113.80
3	A	288	GLU	N-CA-C	-8.14	100.74	111.24
3	A	65	VAL	N-CA-C	7.95	119.31	107.15
3	A	271	TYR	N-CA-C	7.85	119.75	111.03
3	A	51	HIS	CA-CB-CG	7.71	121.51	113.80
3	A	33	ILE	N-CA-CB	-7.64	98.62	111.23
3	A	50	PRO	CB-CA-C	-7.58	99.06	111.56
3	A	309	GLU	CA-C-N	7.46	129.17	119.84
3	A	309	GLU	C-N-CA	7.46	129.17	119.84
3	A	309	GLU	N-CA-C	7.39	126.14	109.81
3	A	146	PHE	N-CA-CB	7.37	122.85	110.32
3	A	181	PHE	O-C-N	7.34	129.72	122.09
3	A	12	ASN	N-CA-CB	7.30	121.47	110.95
3	A	267	CYS	N-CA-C	-7.22	102.81	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	214	VAL	N-CA-CB	7.21	119.80	110.57
3	A	88	ILE	CB-CA-C	-7.19	102.30	112.22
1	T	1	DC	P-O3'-C3'	7.16	130.94	120.20
3	A	271	TYR	N-CA-CB	-7.15	99.62	109.98
3	A	36	TYR	CA-CB-CG	-7.10	101.12	113.90
3	A	92	ASP	N-CA-C	6.99	118.55	111.07
1	T	3	DT	C2-N1-C1'	6.92	129.73	119.35
3	A	150	ILE	N-CA-CB	6.84	120.50	111.40
3	A	181	PHE	CA-C-N	6.82	129.98	120.29
3	A	181	PHE	C-N-CA	6.82	129.98	120.29
3	A	291	PHE	N-CA-C	6.80	117.25	108.34
3	A	240	GLN	N-CA-C	6.76	119.40	108.32
1	T	3	DT	C6-N1-C1'	-6.72	109.26	119.35
3	A	86	GLU	N-CA-CB	6.70	119.73	110.01
3	A	137	ARG	CD-NE-CZ	-6.70	115.02	124.40
3	A	35	LYS	N-CA-C	-6.69	103.99	111.28
3	A	162	VAL	N-CA-C	6.69	116.84	110.42
3	A	181	PHE	CA-CB-CG	-6.67	107.13	113.80
3	A	108	PRO	N-CA-CB	6.67	110.25	103.25
3	A	116	ASP	N-CA-CB	6.57	121.59	110.49
2	P	3	DT	P-O5'-C5'	6.56	129.84	120.00
3	A	15	ILE	N-CA-CB	6.52	120.77	110.54
3	A	297	THR	N-CA-C	6.46	116.81	108.34
3	A	83	ARG	N-CA-CB	6.44	119.31	109.91
3	A	124	ASP	CB-CA-C	-6.41	99.79	110.68
3	A	195	LEU	N-CA-C	6.38	120.10	109.95
3	A	105	GLY	CA-C-N	-6.35	114.29	123.06
3	A	105	GLY	C-N-CA	-6.35	114.29	123.06
3	A	24	ASN	CA-CB-CG	-6.33	106.27	112.60
1	T	4	DT	N1-C1'-C2'	6.33	122.99	113.50
3	A	59	ALA	O-C-N	6.33	128.59	122.07
3	A	332	ASP	N-CA-CB	6.26	119.19	110.56
3	A	64	GLY	N-CA-C	-6.21	107.30	114.69
3	A	40	ARG	N-CA-C	6.20	118.03	111.28
3	A	37	ASN	N-CA-C	-6.17	104.66	111.82
2	P	3	DT	O4'-C1'-N1	6.15	117.62	108.40
3	A	164	ASN	CA-C-N	-6.10	112.14	120.44
3	A	164	ASN	C-N-CA	-6.10	112.14	120.44
1	T	7	DA	N9-C1'-C2'	-6.08	104.39	113.50
3	A	181	PHE	CB-CA-C	-6.07	101.10	110.81
1	T	4	DT	P-O5'-C5'	6.04	129.06	120.00
3	A	192	ASP	CA-C-N	-6.00	115.22	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	192	ASP	C-N-CA	-6.00	115.22	122.90
3	A	215	VAL	CB-CA-C	5.94	119.82	112.04
3	A	196	THR	N-CA-C	5.94	117.87	108.79
3	A	246	ASP	N-CA-C	5.91	123.40	110.80
3	A	114	PHE	CA-C-O	5.90	126.78	120.70
3	A	226	ASP	N-CA-C	5.89	118.24	108.99
3	A	296	TYR	CB-CA-C	-5.87	98.70	109.15
3	A	86	GLU	CB-CA-C	5.85	120.06	110.88
3	A	235	PHE	CA-CB-CG	-5.84	107.96	113.80
3	A	169	VAL	N-CA-CB	5.78	117.18	110.65
3	A	49	TYR	O-C-N	5.77	127.96	121.32
3	A	312	PRO	CA-C-N	5.77	130.54	123.10
3	A	312	PRO	C-N-CA	5.77	130.54	123.10
3	A	334	SER	CB-CA-C	5.76	120.03	110.81
2	P	3	DT	N3-C4-O4	-5.76	113.96	122.60
3	A	303	VAL	N-CA-C	5.76	120.18	111.89
3	A	30	SER	CA-C-N	-5.70	114.03	123.37
3	A	30	SER	C-N-CA	-5.70	114.03	123.37
3	A	258	ARG	N-CA-C	5.69	118.37	108.76
3	A	25	PHE	N-CA-C	5.68	117.27	111.14
3	A	165	GLU	N-CA-CB	5.68	118.30	110.07
1	T	3	DT	P-O5'-C5'	5.65	128.48	120.00
3	A	296	TYR	N-CA-C	5.64	121.04	114.04
3	A	92	ASP	N-CA-CB	5.62	118.16	110.01
3	A	214	VAL	O-C-N	5.61	127.73	121.90
3	A	229	SER	N-CA-CB	5.54	119.53	110.90
3	A	17	ASP	CB-CA-C	5.50	120.20	110.85
3	A	270	LEU	CB-CA-C	-5.49	101.51	110.85
2	P	3	DT	N1-C1'-C2'	5.49	121.73	113.50
3	A	223	PHE	CA-C-N	-5.48	115.08	122.91
3	A	223	PHE	C-N-CA	-5.48	115.08	122.91
3	A	219	GLN	CB-CA-C	-5.47	102.26	110.90
1	T	4	DT	C1'-O4'-C4'	-5.46	101.51	109.70
3	A	26	GLU	CA-C-O	5.42	126.23	120.10
3	A	267	CYS	O-C-N	5.42	129.27	122.23
3	A	246	ASP	CA-C-N	5.42	131.88	121.54
3	A	246	ASP	C-N-CA	5.42	131.88	121.54
3	A	279	ASN	CA-CB-CG	-5.39	107.21	112.60
3	A	264	GLN	CB-CG-CD	-5.37	103.47	112.60
3	A	333	ARG	N-CA-C	-5.37	107.03	113.21
3	A	115	VAL	N-CA-CB	-5.36	104.28	110.55
3	A	216	GLU	CB-CG-CD	-5.33	103.55	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	304	THR	CA-C-O	5.28	125.75	119.10
3	A	229	SER	N-CA-C	5.26	116.90	107.80
3	A	12	ASN	CB-CA-C	5.24	118.77	109.75
3	A	196	THR	N-CA-CB	5.24	119.69	111.56
3	A	286	ALA	CA-C-N	5.24	127.73	120.29
3	A	286	ALA	C-N-CA	5.24	127.73	120.29
3	A	160	ASP	N-CA-C	-5.24	105.69	111.71
3	A	253	ARG	N-CA-C	5.24	118.10	109.72
3	A	215	VAL	N-CA-CB	5.22	116.99	110.47
3	A	334	SER	N-CA-C	5.21	117.36	111.11
3	A	119	ILE	N-CA-CB	-5.21	105.35	111.39
3	A	285	HIS	N-CA-C	5.20	116.76	111.14
3	A	168	LYS	N-CA-CB	5.20	118.35	110.14
3	A	118	GLY	CA-C-N	-5.19	114.64	122.01
3	A	118	GLY	C-N-CA	-5.19	114.64	122.01
3	A	11	LEU	N-CA-CB	5.19	119.13	110.41
3	A	266	TYR	N-CA-C	5.19	119.09	112.34
3	A	45	VAL	N-CA-C	5.17	115.39	110.53
3	A	22	LEU	N-CA-CB	-5.17	102.24	109.94
3	A	276	ASP	CA-CB-CG	-5.16	107.44	112.60
3	A	92	ASP	CB-CA-C	5.15	118.97	110.88
3	A	54	LYS	N-CA-CB	5.12	118.07	110.49
3	A	270	LEU	CA-C-N	5.12	127.59	120.63
3	A	270	LEU	C-N-CA	5.12	127.59	120.63
3	A	211	LEU	CA-C-N	5.10	127.83	120.38
3	A	211	LEU	C-N-CA	5.10	127.83	120.38
3	A	121	THR	N-CA-C	5.10	116.73	109.14
3	A	40	ARG	N-CA-CB	5.09	117.60	110.12
3	A	68	LYS	CB-CA-C	5.08	119.32	110.68
3	A	82	LEU	N-CA-CB	-5.06	102.07	111.13
3	A	62	LEU	CA-C-N	5.05	126.16	119.84
3	A	62	LEU	C-N-CA	5.05	126.16	119.84
2	P	4	DA	C8-N9-C1'	-5.04	119.49	127.05
3	A	246	ASP	O-C-N	5.04	129.29	122.59
3	A	213	GLN	CB-CA-C	-5.03	102.30	110.85

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	309	GLU	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	10	0
3	A	2623	0	2641	356	0
4	A	2	0	0	0	0
5	A	13	0	0	1	0
6	A	103	0	0	21	0
6	P	18	0	0	1	0
6	T	14	0	0	1	0
All	All	3062	0	2802	373	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 66.

All (373) 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:191:MET:HG2	3:A:255:ILE:HG13	1.35	1.06
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.37	1.03
3:A:245:ASN:H	3:A:245:ASN:ND2	1.56	1.00
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.59	1.00
3:A:155:MET:HA	3:A:158:MET:HE3	1.41	0.99
3:A:245:ASN:HD22	3:A:245:ASN:N	1.59	0.94
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.49	0.94
3:A:155:MET:HE2	3:A:188:SER:HB2	1.48	0.93
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.49	0.93
3:A:12:ASN:HD21	3:A:53:ILE:H	1.14	0.92
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.06	0.90
3:A:172:GLU:HB3	3:A:197:HIS:NE2	1.87	0.89
3:A:259:LEU:HD12	3:A:260:ILE:H	1.37	0.87
3:A:31:GLN:HE21	3:A:112:ARG:HH12	0.87	0.87
3:A:264:GLN:NE2	3:A:296:TYR:HB3	1.89	0.87
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.04	0.87
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.10	0.86
3:A:60:LYS:HA	3:A:65:VAL:HG23	1.55	0.86
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.72	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:286:ALA:HB1	3:A:291:PHE:HB2	1.58	0.85
3:A:73:ILE:HG22	3:A:77:LEU:HD22	1.60	0.83
3:A:330:PRO:HA	3:A:333:ARG:CG	2.08	0.83
3:A:277:ILE:HD13	3:A:277:ILE:H	1.45	0.82
3:A:178:CYS:SG	3:A:194:LEU:HD23	2.19	0.82
3:A:217:GLN:HE21	3:A:217:GLN:HA	1.46	0.81
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.44	0.81
3:A:259:LEU:HD12	3:A:260:ILE:N	1.95	0.81
2:P:5:DA:H2''	2:P:6:DT:H5'	1.62	0.80
3:A:212:HIS:HB3	6:A:541:HOH:O	1.82	0.80
2:P:5:DA:H2''	2:P:6:DT:C5'	2.12	0.79
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.13	0.79
3:A:41:LYS:HE2	3:A:64:GLY:HA2	1.63	0.79
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.18	0.79
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.64	0.78
3:A:18:MET:HG2	3:A:22:LEU:HD23	1.66	0.78
3:A:277:ILE:HG12	3:A:335:GLU:HA	1.64	0.77
3:A:330:PRO:HA	3:A:333:ARG:HG2	1.66	0.77
3:A:323:ILE:O	3:A:324:GLN:HG2	1.84	0.76
1:T:6:DG:H2''	1:T:7:DA:C8	2.20	0.76
3:A:191:MET:CG	3:A:255:ILE:HG13	2.15	0.76
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.50	0.76
3:A:73:ILE:HG22	3:A:77:LEU:CD2	2.16	0.75
3:A:207:GLN:O	3:A:210:LEU:HB2	1.86	0.75
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.16	0.75
3:A:229:SER:OG	3:A:236:MET:HE2	1.86	0.75
3:A:270:LEU:CD2	3:A:282:MET:HE1	2.15	0.74
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.67	0.74
3:A:233:THR:HB	6:A:538:HOH:O	1.86	0.74
3:A:180:SER:HA	3:A:183:ARG:HE	1.52	0.74
3:A:15:ILE:HB	3:A:46:ILE:CD1	2.18	0.74
3:A:33:ILE:HG23	3:A:34:HIS:H	1.53	0.73
3:A:15:ILE:O	3:A:19:LEU:HB2	1.87	0.73
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.02	0.73
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.19	0.72
3:A:151:PRO:HG2	3:A:154:GLU:CG	2.20	0.72
3:A:108:PRO:O	3:A:112:ARG:HG3	1.89	0.72
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.18	0.71
3:A:41:LYS:HD3	3:A:42:ALA:N	2.05	0.71
3:A:18:MET:HE2	3:A:82:LEU:HD22	1.72	0.71
3:A:245:ASN:H	3:A:245:ASN:HD22	0.80	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:172:GLU:HB3	3:A:197:HIS:CD2	2.26	0.71
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.25	0.71
3:A:155:MET:HA	3:A:158:MET:CE	2.18	0.70
3:A:121:THR:O	3:A:124:ASP:HB2	1.91	0.70
3:A:120:LYS:N	3:A:124:ASP:OD2	2.24	0.70
3:A:165:GLU:HB3	3:A:217:GLN:CG	2.21	0.70
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.23	0.69
3:A:331:LYS:HG2	3:A:332:ASP:N	2.03	0.69
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.73	0.69
3:A:12:ASN:HA	6:A:553:HOH:O	1.92	0.69
1:T:5:DA:H2''	1:T:6:DG:O5'	1.93	0.68
3:A:82:LEU:HD23	3:A:85:LEU:HB2	1.75	0.68
3:A:180:SER:CB	3:A:183:ARG:HH21	2.05	0.68
3:A:79:THR:O	3:A:81:LYS:N	2.27	0.68
3:A:151:PRO:HG2	3:A:154:GLU:HG3	1.75	0.68
3:A:41:LYS:HD3	3:A:42:ALA:H	1.59	0.68
3:A:165:GLU:HB3	3:A:217:GLN:HG2	1.75	0.68
3:A:200:PHE:HE2	3:A:261:PRO:HD3	1.60	0.67
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.75	0.67
3:A:291:PHE:HD2	3:A:323:ILE:HG22	1.60	0.67
3:A:268:GLY:O	3:A:271:TYR:HB3	1.94	0.67
3:A:18:MET:CE	3:A:82:LEU:HD13	2.25	0.67
3:A:103:VAL:HA	6:A:600:HOH:O	1.92	0.67
3:A:200:PHE:HB2	6:A:625:HOH:O	1.93	0.67
3:A:149:ARG:NH2	3:A:188:SER:HA	2.10	0.67
3:A:189:GLY:N	5:A:338:DTP:O2G	2.28	0.67
3:A:264:GLN:HE22	3:A:296:TYR:HB3	1.57	0.66
3:A:200:PHE:CD2	3:A:261:PRO:HA	2.30	0.66
3:A:155:MET:HE2	3:A:188:SER:CB	2.25	0.66
3:A:182:ARG:NH1	3:A:273:THR:HG21	2.11	0.66
3:A:11:LEU:HD23	3:A:11:LEU:H	1.60	0.65
3:A:286:ALA:O	3:A:291:PHE:N	2.28	0.65
3:A:15:ILE:HG21	3:A:73:ILE:HD13	1.79	0.65
3:A:194:LEU:HD11	3:A:258:ARG:HD3	1.78	0.65
3:A:217:GLN:HA	3:A:217:GLN:NE2	2.10	0.65
3:A:302:GLY:H	3:A:307:ALA:HB3	1.60	0.65
3:A:286:ALA:HB2	3:A:293:ILE:HD11	1.78	0.65
3:A:228:LEU:HB2	3:A:236:MET:O	1.96	0.65
3:A:41:LYS:NZ	3:A:64:GLY:O	2.29	0.65
1:T:6:DG:N7	6:T:652:HOH:O	2.29	0.64
3:A:302:GLY:HA3	3:A:307:ALA:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:18:MET:O	3:A:21:GLU:HB2	1.98	0.63
3:A:18:MET:HE2	3:A:82:LEU:HD13	1.80	0.63
3:A:172:GLU:HG2	3:A:198:PRO:HG2	1.80	0.62
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.32	0.62
3:A:35:LYS:O	3:A:38:ALA:HB3	1.99	0.62
3:A:155:MET:CE	3:A:188:SER:HB2	2.26	0.62
3:A:267:CYS:N	6:A:508:HOH:O	2.28	0.62
3:A:60:LYS:HA	3:A:65:VAL:CG2	2.27	0.62
3:A:122:LEU:HB3	6:A:623:HOH:O	1.99	0.62
3:A:26:GLU:HA	3:A:30:SER:OG	2.00	0.61
3:A:33:ILE:HG23	3:A:34:HIS:N	2.15	0.61
3:A:133:ASN:H	3:A:136:GLN:HE21	1.48	0.61
3:A:300:PRO:HD2	3:A:308:GLY:O	2.01	0.61
3:A:122:LEU:O	3:A:126:ARG:HG3	2.01	0.61
3:A:291:PHE:CD2	3:A:323:ILE:HG22	2.35	0.61
3:A:133:ASN:ND2	3:A:135:HIS:H	1.99	0.60
3:A:253:ARG:NH1	6:A:503:HOH:O	2.33	0.60
3:A:59:ALA:O	3:A:65:VAL:HG21	2.01	0.60
3:A:150:ILE:HD13	3:A:253:ARG:HG2	1.83	0.60
3:A:280:LYS:O	3:A:284:ALA:N	2.33	0.60
3:A:18:MET:HE3	3:A:76:PHE:HB2	1.84	0.60
3:A:162:VAL:CG1	3:A:218:LEU:HD21	2.31	0.60
3:A:285:HIS:HD2	3:A:323:ILE:HD12	1.66	0.60
3:A:306:VAL:HG22	6:A:650:HOH:O	2.00	0.59
3:A:311:LEU:HB3	3:A:322:TYR:CE2	2.37	0.59
3:A:200:PHE:HE2	3:A:261:PRO:CD	2.14	0.59
3:A:203:GLU:O	3:A:205:THR:N	2.36	0.59
3:A:277:ILE:HD11	3:A:334:SER:O	2.02	0.59
3:A:302:GLY:H	3:A:307:ALA:CB	2.15	0.59
3:A:68:LYS:HB2	3:A:68:LYS:NZ	2.17	0.59
3:A:177:VAL:HG11	3:A:191:MET:HE2	1.85	0.59
3:A:180:SER:HA	3:A:183:ARG:NE	2.18	0.59
3:A:41:LYS:O	3:A:45:VAL:HG13	2.02	0.58
3:A:133:ASN:HD22	3:A:135:HIS:H	1.50	0.58
3:A:288:GLU:C	3:A:290:GLY:H	2.11	0.58
3:A:18:MET:HG2	3:A:22:LEU:CD2	2.33	0.58
3:A:237:GLY:O	3:A:254:ARG:NH1	2.36	0.58
3:A:248:LYS:O	3:A:248:LYS:HG2	2.03	0.58
3:A:180:SER:CA	3:A:183:ARG:HH21	2.15	0.57
3:A:142:TYR:CE1	3:A:252:HIS:CG	2.93	0.57
3:A:330:PRO:CA	3:A:333:ARG:HG2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:245:ASN:ND2	3:A:245:ASN:N	2.30	0.57
3:A:240:GLN:NE2	3:A:250:TYR:O	2.32	0.57
3:A:326:LYS:HE3	3:A:328:ARG:HH21	1.69	0.57
3:A:172:GLU:CG	3:A:198:PRO:HG2	2.34	0.56
3:A:306:VAL:HG23	3:A:307:ALA:N	2.20	0.56
2:P:6:DT:H2''	2:P:7:DG:H5''	1.88	0.56
3:A:33:ILE:O	3:A:37:ASN:N	2.36	0.56
3:A:236:MET:HG3	3:A:256:ASP:OD1	2.05	0.56
3:A:23:ALA:HA	3:A:39:TYR:HD2	1.71	0.56
3:A:265:TYR:CE2	3:A:269:VAL:HG21	2.41	0.56
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.88	0.56
3:A:157:GLN:HE22	3:A:244:LYS:NZ	2.04	0.56
3:A:20:THR:O	3:A:23:ALA:HB3	2.07	0.55
3:A:163:LEU:HD23	3:A:163:LEU:N	2.19	0.55
3:A:195:LEU:O	3:A:260:ILE:N	2.39	0.55
3:A:282:MET:HB3	6:A:555:HOH:O	2.06	0.55
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.88	0.55
3:A:88:ILE:HG22	3:A:89:ARG:N	2.18	0.55
3:A:278:PHE:HB2	3:A:333:ARG:O	2.05	0.55
3:A:288:GLU:O	3:A:290:GLY:N	2.39	0.55
3:A:75:GLU:OE2	3:A:83:ARG:N	2.35	0.55
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.37	0.54
3:A:270:LEU:HA	3:A:316:GLU:OE2	2.07	0.54
3:A:277:ILE:H	3:A:277:ILE:CD1	2.17	0.54
3:A:177:VAL:O	3:A:182:ARG:HD2	2.08	0.54
3:A:93:THR:HG22	3:A:94:SER:N	2.22	0.54
3:A:266:TYR:CD1	3:A:266:TYR:N	2.76	0.54
3:A:277:ILE:HD13	3:A:277:ILE:N	2.18	0.54
3:A:122:LEU:O	3:A:122:LEU:HD23	2.08	0.54
3:A:150:ILE:N	3:A:188:SER:O	2.41	0.54
3:A:326:LYS:O	3:A:328:ARG:HG2	2.06	0.54
3:A:15:ILE:HB	3:A:46:ILE:HD11	1.88	0.54
3:A:327:TYR:HE1	3:A:333:ARG:HH21	1.55	0.54
3:A:79:THR:C	3:A:81:LYS:H	2.17	0.53
3:A:309:GLU:N	3:A:309:GLU:OE1	2.40	0.53
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.42	0.53
3:A:32:ALA:O	3:A:36:TYR:HB3	2.08	0.53
3:A:311:LEU:HB3	3:A:322:TYR:HE2	1.73	0.53
3:A:103:VAL:HG22	3:A:143:PHE:CD2	2.43	0.53
1:T:4:DT:H2''	1:T:5:DA:C8	2.44	0.53
3:A:253:ARG:HH11	3:A:253:ARG:CG	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:18:MET:HE2	3:A:82:LEU:CD2	2.38	0.53
3:A:253:ARG:NH1	6:A:620:HOH:O	2.37	0.53
3:A:300:PRO:HD3	3:A:309:GLU:O	2.07	0.53
3:A:213:GLN:HG2	6:A:644:HOH:O	2.08	0.53
3:A:205:THR:HA	6:A:624:HOH:O	2.08	0.52
3:A:226:ASP:OD1	3:A:238:VAL:HB	2.09	0.52
3:A:21:GLU:OE1	3:A:85:LEU:HD11	2.09	0.52
3:A:173:TYR:OH	3:A:213:GLN:NE2	2.42	0.52
3:A:150:ILE:O	3:A:187:SER:HA	2.09	0.52
3:A:158:MET:HG3	3:A:241:LEU:HD21	1.91	0.52
3:A:33:ILE:HA	3:A:36:TYR:HD2	1.75	0.52
3:A:150:ILE:HD11	3:A:253:ARG:HG2	1.91	0.52
3:A:146:PHE:HB2	6:A:514:HOH:O	2.10	0.52
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.40	0.52
1:T:4:DT:H2''	1:T:5:DA:O5'	2.10	0.51
3:A:45:VAL:HG23	3:A:62:LEU:HD23	1.92	0.51
3:A:292:THR:O	3:A:298:ILE:HA	2.11	0.51
3:A:23:ALA:HA	3:A:39:TYR:CD2	2.44	0.51
3:A:251:PRO:O	3:A:253:ARG:HD2	2.11	0.51
3:A:198:PRO:O	3:A:200:PHE:N	2.44	0.51
3:A:162:VAL:HG13	3:A:218:LEU:HD21	1.92	0.51
3:A:260:ILE:HG22	3:A:261:PRO:N	2.27	0.50
3:A:253:ARG:NH2	6:A:620:HOH:O	2.42	0.49
3:A:277:ILE:HG13	3:A:335:GLU:HB2	1.94	0.49
3:A:317:LYS:O	3:A:320:PHE:N	2.45	0.49
2:P:5:DA:H2''	2:P:6:DT:H5''	1.93	0.49
3:A:145:ASP:HB3	3:A:252:HIS:O	2.12	0.49
3:A:212:HIS:N	3:A:212:HIS:CD2	2.79	0.49
1:T:2:DA:H2''	1:T:3:DT:OP2	2.11	0.49
2:P:1:DT:H2''	2:P:2:DC:H5'	1.94	0.49
3:A:74:ASP:O	3:A:77:LEU:N	2.46	0.49
1:T:4:DT:H2''	1:T:5:DA:H8	1.78	0.48
3:A:179:GLY:O	3:A:182:ARG:HB3	2.13	0.48
3:A:198:PRO:C	3:A:200:PHE:H	2.22	0.48
3:A:243:SER:OG	3:A:249:GLU:HA	2.13	0.48
3:A:18:MET:HE3	3:A:76:PHE:CB	2.43	0.48
3:A:277:ILE:CG1	3:A:335:GLU:HB2	2.43	0.48
3:A:158:MET:CG	3:A:241:LEU:HD21	2.44	0.48
3:A:243:SER:CB	3:A:249:GLU:HA	2.43	0.48
3:A:291:PHE:CD1	3:A:300:PRO:HA	2.48	0.48
3:A:33:ILE:CG2	3:A:34:HIS:H	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:49:TYR:CE2	3:A:51:HIS:HB2	2.49	0.48
3:A:83:ARG:O	3:A:86:GLU:N	2.46	0.48
3:A:200:PHE:CE2	3:A:261:PRO:HA	2.48	0.48
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.39	0.48
3:A:332:ASP:C	3:A:334:SER:H	2.21	0.48
3:A:99:PHE:O	3:A:102:ARG:HG3	2.14	0.48
3:A:195:LEU:HG	3:A:196:THR:N	2.29	0.48
3:A:12:ASN:ND2	3:A:53:ILE:H	1.96	0.47
3:A:200:PHE:CE2	3:A:261:PRO:HD3	2.45	0.47
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.94	0.47
3:A:182:ARG:HH11	3:A:273:THR:CG2	2.27	0.47
3:A:303:VAL:C	3:A:305:GLY:H	2.22	0.47
1:T:4:DT:O2	2:P:4:DA:H2	1.97	0.47
3:A:210:LEU:HB3	3:A:259:LEU:HD21	1.95	0.47
3:A:59:ALA:C	3:A:65:VAL:HG21	2.38	0.47
3:A:306:VAL:O	3:A:307:ALA:HB2	2.14	0.47
3:A:40:ARG:O	3:A:44:SER:HB2	2.15	0.47
3:A:165:GLU:OE1	3:A:217:GLN:OE1	2.33	0.47
3:A:196:THR:OG1	3:A:197:HIS:N	2.44	0.47
3:A:234:LYS:HD2	6:A:617:HOH:O	2.14	0.47
3:A:285:HIS:CD2	3:A:323:ILE:HD12	2.48	0.47
3:A:327:TYR:HD1	3:A:328:ARG:N	2.13	0.47
3:A:265:TYR:O	3:A:268:GLY:N	2.48	0.47
3:A:289:LYS:N	3:A:289:LYS:HD3	2.30	0.46
3:A:196:THR:HB	3:A:265:TYR:CD1	2.49	0.46
3:A:223:PHE:CE2	3:A:239:CYS:CB	2.98	0.46
3:A:75:GLU:O	3:A:79:THR:HG23	2.15	0.46
3:A:65:VAL:HG23	3:A:65:VAL:O	2.16	0.46
3:A:115:VAL:C	3:A:117:GLU:H	2.24	0.46
3:A:264:GLN:HE21	3:A:264:GLN:HB3	1.42	0.46
3:A:302:GLY:N	3:A:307:ALA:CB	2.78	0.46
3:A:301:LEU:HD12	3:A:302:GLY:H	1.80	0.46
3:A:22:LEU:HD13	3:A:22:LEU:HA	1.35	0.46
3:A:15:ILE:HG21	3:A:73:ILE:CD1	2.45	0.46
3:A:89:ARG:HD3	3:A:89:ARG:C	2.40	0.46
3:A:165:GLU:OE2	3:A:168:LYS:HD3	2.16	0.46
3:A:182:ARG:HH11	3:A:273:THR:HG21	1.80	0.46
3:A:28:ASN:N	3:A:28:ASN:ND2	2.51	0.46
3:A:317:LYS:HG3	3:A:321:ASP:OD2	2.15	0.46
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.94	0.45
3:A:223:PHE:O	3:A:239:CYS:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:279:ASN:O	3:A:283:ARG:HG3	2.16	0.45
3:A:302:GLY:CA	3:A:307:ALA:HB2	2.46	0.45
3:A:15:ILE:H	3:A:15:ILE:HG12	1.64	0.45
3:A:201:THR:HG23	3:A:204:SER:OG	2.16	0.45
3:A:158:MET:O	3:A:161:ILE:N	2.50	0.45
3:A:73:ILE:O	3:A:77:LEU:HD22	2.17	0.45
3:A:125:LEU:HD22	3:A:132:LEU:HD21	1.99	0.45
3:A:200:PHE:HE2	3:A:261:PRO:N	2.15	0.45
3:A:311:LEU:HD13	3:A:311:LEU:N	2.32	0.45
3:A:195:LEU:HA	3:A:195:LEU:HD12	1.54	0.45
3:A:200:PHE:CE2	3:A:261:PRO:CA	3.00	0.45
3:A:205:THR:HG23	3:A:205:THR:O	2.17	0.45
3:A:328:ARG:HB2	3:A:333:ARG:HD3	1.98	0.45
3:A:287:LEU:HA	3:A:287:LEU:HD13	1.22	0.45
3:A:333:ARG:NH1	6:A:584:HOH:O	2.38	0.45
3:A:321:ASP:O	3:A:324:GLN:N	2.48	0.45
3:A:28:ASN:ND2	3:A:108:PRO:HG3	2.32	0.45
3:A:69:ILE:O	3:A:73:ILE:HG13	2.16	0.45
3:A:28:ASN:HD22	3:A:28:ASN:HA	0.90	0.44
3:A:41:LYS:CD	3:A:42:ALA:N	2.79	0.44
3:A:262:LYS:O	3:A:262:LYS:HG3	2.12	0.44
3:A:267:CYS:SG	3:A:297:THR:HA	2.57	0.44
3:A:320:PHE:O	3:A:324:GLN:N	2.51	0.44
3:A:60:LYS:CA	3:A:65:VAL:HG23	2.38	0.44
3:A:99:PHE:CD1	3:A:99:PHE:C	2.95	0.44
3:A:254:ARG:CZ	3:A:254:ARG:HB3	2.46	0.44
3:A:42:ALA:O	3:A:46:ILE:HG23	2.16	0.44
3:A:253:ARG:NH1	3:A:253:ARG:CG	2.79	0.44
3:A:29:VAL:HG21	3:A:94:SER:HB2	1.98	0.44
3:A:270:LEU:HD12	3:A:270:LEU:O	2.17	0.44
3:A:301:LEU:HD12	3:A:302:GLY:N	2.32	0.44
3:A:260:ILE:CG2	3:A:261:PRO:N	2.79	0.44
3:A:194:LEU:HD13	3:A:194:LEU:HA	1.55	0.44
3:A:18:MET:HE2	3:A:82:LEU:CD1	2.46	0.44
3:A:40:ARG:HE	3:A:40:ARG:HB2	1.18	0.44
3:A:209:LYS:HD3	3:A:209:LYS:HA	1.43	0.44
3:A:223:PHE:CE2	3:A:239:CYS:HB2	2.53	0.44
3:A:182:ARG:NH1	3:A:273:THR:CG2	2.77	0.44
3:A:282:MET:HE3	6:A:555:HOH:O	2.17	0.43
3:A:54:LYS:HD2	3:A:54:LYS:HA	1.62	0.43
3:A:197:HIS:CD2	3:A:198:PRO:CD	2.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:6:DT:H5'	2:P:6:DT:C6	2.53	0.43
3:A:103:VAL:HG22	3:A:143:PHE:HD2	1.83	0.43
3:A:248:LYS:HD2	3:A:248:LYS:N	2.32	0.43
3:A:122:LEU:HD23	3:A:122:LEU:C	2.44	0.43
3:A:277:ILE:HG12	3:A:335:GLU:CA	2.41	0.43
3:A:18:MET:CE	3:A:82:LEU:HD22	2.46	0.43
3:A:180:SER:HB2	3:A:185:ALA:CB	2.48	0.43
3:A:261:PRO:HB2	3:A:264:GLN:HG3	2.00	0.43
3:A:132:LEU:O	3:A:137:ARG:NE	2.51	0.43
3:A:85:LEU:HD12	3:A:85:LEU:HA	1.47	0.43
3:A:165:GLU:HB2	3:A:218:LEU:CD1	2.49	0.43
3:A:280:LYS:HA	3:A:283:ARG:HB2	1.99	0.43
3:A:27:LYS:HG3	3:A:28:ASN:N	2.34	0.43
3:A:316:GLU:O	3:A:320:PHE:HD2	2.02	0.43
3:A:201:THR:O	3:A:203:GLU:N	2.52	0.43
3:A:211:LEU:HB3	3:A:212:HIS:HD2	1.84	0.42
3:A:270:LEU:HA	3:A:270:LEU:HD12	1.65	0.42
3:A:115:VAL:C	3:A:117:GLU:N	2.77	0.42
3:A:196:THR:OG1	3:A:260:ILE:O	2.27	0.42
3:A:259:LEU:HD13	3:A:259:LEU:HA	1.78	0.42
3:A:97:ILE:O	3:A:101:THR:HB	2.19	0.42
3:A:138:ILE:O	3:A:138:ILE:HG22	2.19	0.42
3:A:200:PHE:C	3:A:201:THR:HG22	2.43	0.42
3:A:287:LEU:CD1	3:A:301:LEU:HD23	2.50	0.42
3:A:77:LEU:HA	3:A:77:LEU:HD12	1.39	0.42
3:A:92:ASP:HB3	6:A:647:HOH:O	2.19	0.42
3:A:182:ARG:HH11	3:A:182:ARG:HG2	1.84	0.42
3:A:243:SER:HB3	3:A:249:GLU:HA	2.00	0.42
3:A:33:ILE:HA	3:A:36:TYR:CD2	2.54	0.42
3:A:125:LEU:HA	3:A:125:LEU:HD23	1.64	0.42
3:A:141:LYS:HB2	6:A:622:HOH:O	2.20	0.42
3:A:76:PHE:CD1	3:A:76:PHE:C	2.96	0.42
3:A:323:ILE:C	3:A:324:GLN:HG2	2.43	0.42
3:A:150:ILE:HG23	3:A:151:PRO:HD2	2.02	0.42
3:A:151:PRO:HG2	3:A:154:GLU:HB2	2.02	0.42
2:P:6:DT:H5'	2:P:6:DT:H6	1.85	0.42
3:A:295:GLU:CD	3:A:295:GLU:H	2.14	0.42
3:A:322:TYR:C	3:A:324:GLN:H	2.27	0.42
3:A:11:LEU:HD23	3:A:11:LEU:N	2.25	0.41
3:A:200:PHE:CE2	3:A:261:PRO:N	2.88	0.41
3:A:261:PRO:C	3:A:263:ASP:N	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:261:PRO:O	3:A:263:ASP:N	2.53	0.41
2:P:4:DA:H5'	6:P:569:HOH:O	2.21	0.41
3:A:137:ARG:HH11	3:A:137:ARG:HD2	1.52	0.41
3:A:194:LEU:CD1	3:A:258:ARG:CG	2.98	0.41
3:A:172:GLU:HG3	3:A:198:PRO:CG	2.51	0.41
3:A:299:ARG:HA	3:A:300:PRO:HD3	1.97	0.41
3:A:45:VAL:CG2	3:A:46:ILE:N	2.84	0.41
3:A:164:ASN:O	3:A:168:LYS:HG2	2.20	0.41
3:A:73:ILE:CG2	3:A:77:LEU:HD22	2.40	0.41
3:A:100:LEU:HD12	3:A:100:LEU:HA	1.46	0.41
3:A:133:ASN:H	3:A:136:GLN:NE2	2.17	0.41
3:A:143:PHE:CD1	3:A:143:PHE:C	2.98	0.41
3:A:183:ARG:NH2	6:A:631:HOH:O	2.54	0.41
3:A:191:MET:HE2	3:A:191:MET:HB2	1.77	0.41
3:A:291:PHE:HB3	3:A:292:THR:H	1.67	0.41
3:A:170:ASP:HB3	3:A:173:TYR:CE2	2.56	0.41
1:T:5:DA:H2	2:P:3:DT:O2	2.04	0.40
3:A:235:PHE:CD2	3:A:235:PHE:C	2.97	0.40
3:A:287:LEU:HD11	3:A:301:LEU:HD23	2.02	0.40
3:A:321:ASP:C	3:A:324:GLN:H	2.30	0.40
3:A:62:LEU:HA	3:A:62:LEU:HD12	1.79	0.40
3:A:151:PRO:HG2	3:A:154:GLU:CB	2.51	0.40
3:A:277:ILE:CG1	3:A:335:GLU:CB	3.00	0.40
3:A:15:ILE:HG21	3:A:73:ILE:HG23	2.04	0.40
3:A:49:TYR:HA	3:A:50:PRO:HD3	1.37	0.40
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.57	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%)	267 (82%)	37 (11%)	21 (6%)	<b>1</b> <b>3</b>

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	80	GLY
3	A	185	ALA
3	A	199	SER
3	A	202	SER
3	A	204	SER
3	A	205	THR
3	A	244	LYS
3	A	246	ASP
3	A	247	GLU
3	A	295	GLU
3	A	10	THR
3	A	134	HIS
3	A	206	LYS
3	A	262	LYS
3	A	289	LYS
3	A	307	ALA
3	A	310	PRO
3	A	265	TYR
3	A	13	GLY
3	A	50	PRO
3	A	306	VAL

### 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%)	216 (75%)	72 (25%)	<b>0</b> <b>2</b>

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	10	THR
3	A	15	ILE
3	A	18	MET
3	A	19	LEU
3	A	21	GLU
3	A	22	LEU
3	A	27	LYS
3	A	40	ARG
3	A	41	LYS
3	A	45	VAL
3	A	46	ILE
3	A	52	LYS
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	89	ARG
3	A	92	ASP
3	A	93	THR
3	A	94	SER
3	A	100	LEU
3	A	101	THR
3	A	112	ARG
3	A	119	ILE
3	A	121	THR
3	A	122	LEU
3	A	133	ASN
3	A	138	ILE
3	A	148	LYS
3	A	153	GLU
3	A	161	ILE
3	A	162	VAL
3	A	174	ILE
3	A	188	SER
3	A	191	MET
3	A	194	LEU
3	A	199	SER
3	A	201	THR
3	A	214	VAL
3	A	218	LEU
3	A	226	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	A	228	LEU
3	A	230	LYS
3	A	236	MET
3	A	242	PRO
3	A	245	ASN
3	A	248	LYS
3	A	249	GLU
3	A	253	ARG
3	A	255	ILE
3	A	259	LEU
3	A	262	LYS
3	A	264	GLN
3	A	277	ILE
3	A	287	LEU
3	A	288	GLU
3	A	293	ILE
3	A	294	ASN
3	A	295	GLU
3	A	298	ILE
3	A	301	LEU
3	A	304	THR
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	324	GLN
3	A	325	TRP
3	A	328	ARG
3	A	331	LYS
3	A	335	GLU

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

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	98	ASN
3	A	133	ASN
3	A	136	GLN
3	A	157	GLN
3	A	207	GLN
3	A	212	HIS

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Mol	Chain	Res	Type
3	A	213	GLN
3	A	217	GLN
3	A	245	ASN
3	A	252	HIS
3	A	264	GLN
3	A	279	ASN
3	A	294	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	DTP	A	338	-	10,12,32	1.76	2 (20%)	17,20,50	1.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	DTP	A	338	-	-	5/12/12/34	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	338	DTP	PB-O3A	3.26	1.63	1.59
5	A	338	DTP	PB-O3B	-2.98	1.56	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

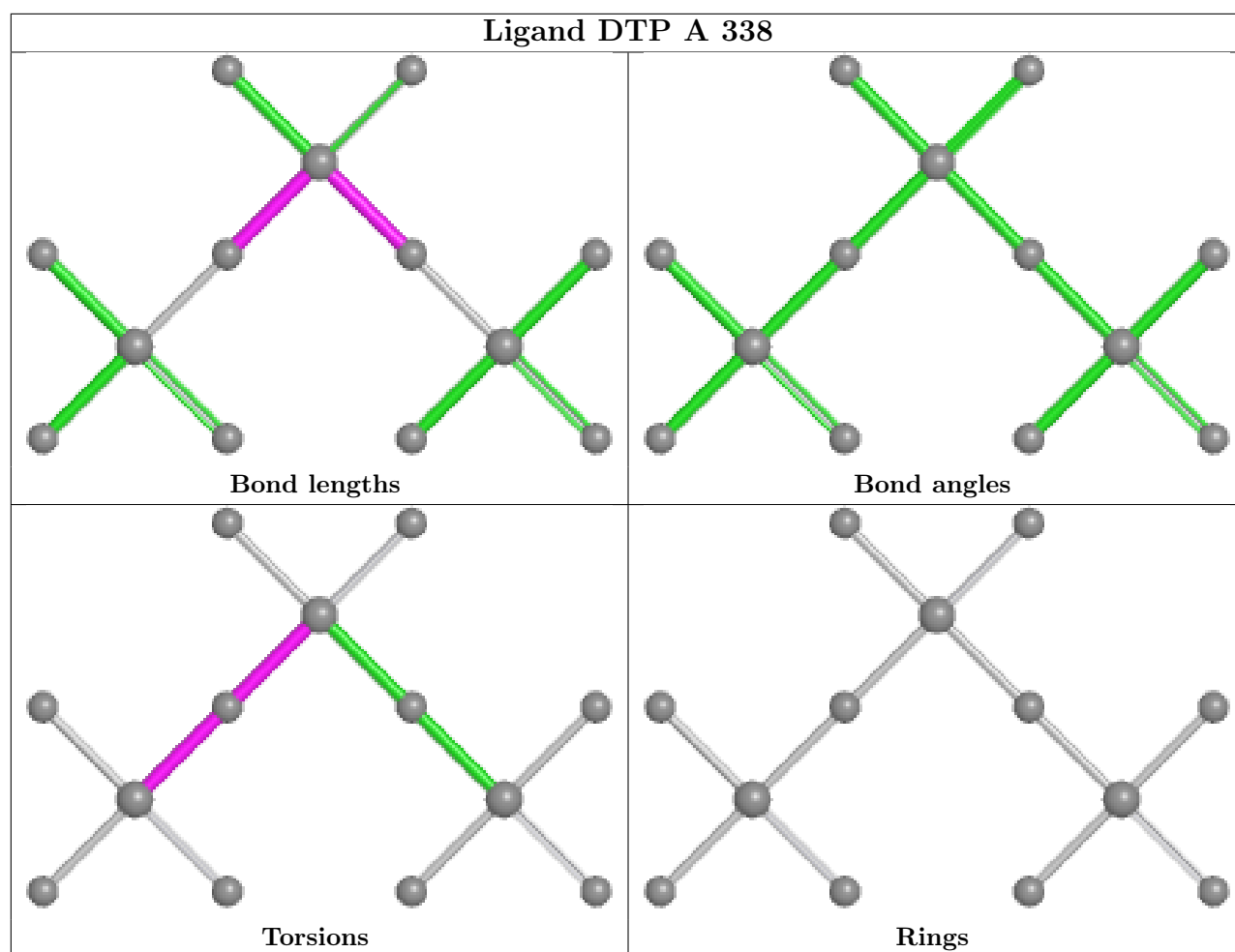
Mol	Chain	Res	Type	Atoms
5	A	338	DTP	PG-O3B-PB-O1B
5	A	338	DTP	PG-O3B-PB-O2B
5	A	338	DTP	PB-O3B-PG-O2G
5	A	338	DTP	PB-O3B-PG-O3G
5	A	338	DTP	PB-O3B-PG-O1G

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	338	DTP	1	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%)	0.29	1 (12%) 8 7	22, 45, 92, 100	0
2	P	7/7 (100%)	-0.30	1 (14%) 6 5	29, 30, 45, 96	0
3	A	325/335 (97%)	-0.49	1 (0%) 90 87	4, 34, 83, 100	0
All	All	340/350 (97%)	-0.47	3 (0%) 81 75	4, 34, 87, 100	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	1	DC	4.5
3	A	246	ASP	3.2
2	P	7	DG	2.2

### 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, 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.

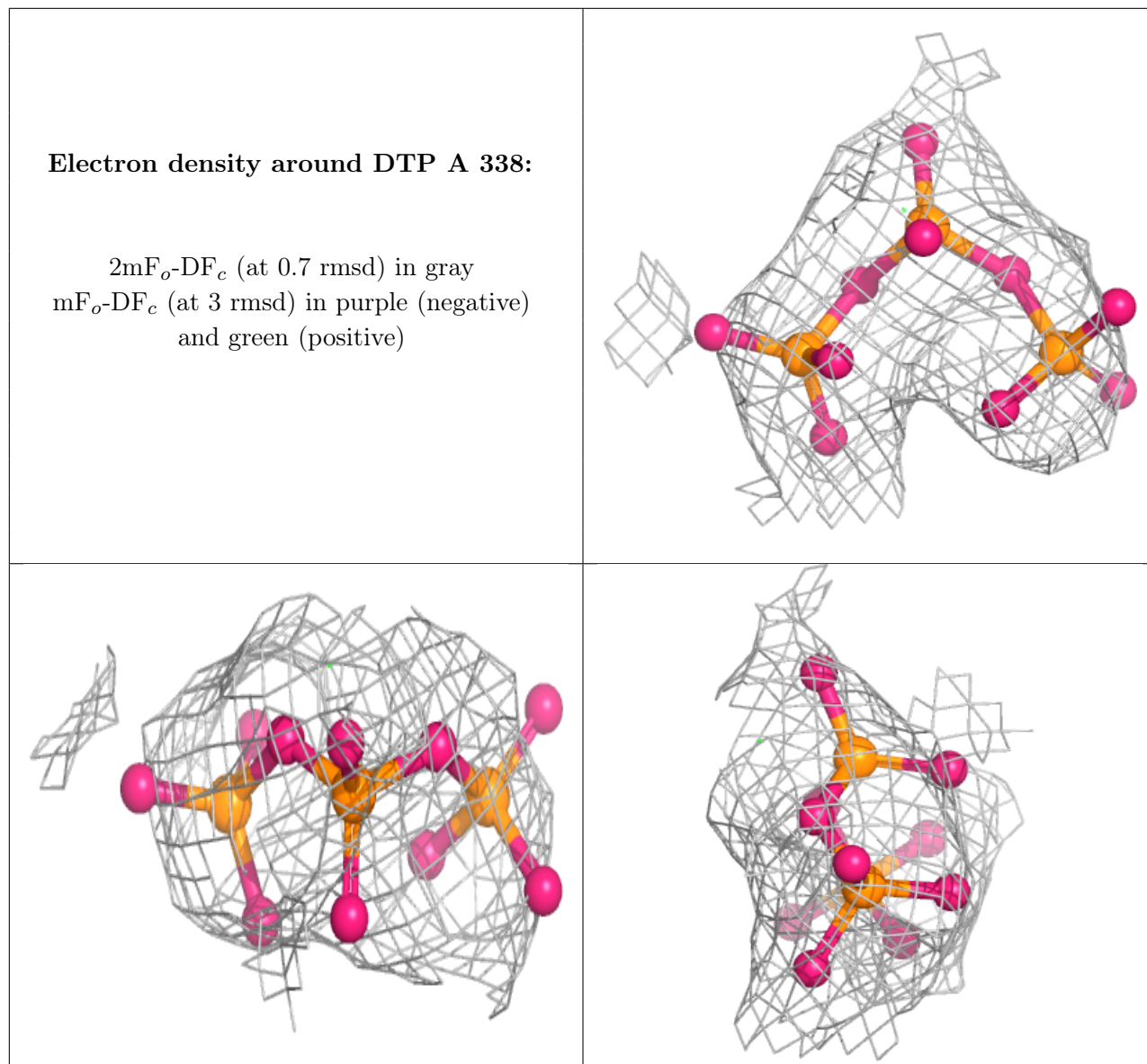
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	DTP	A	338	13/30	0.76	0.15	59,68,84,85	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NA	A	342	1/1	0.93	0.06	52,52,52,52	0
4	NA	A	341	1/1	0.98	0.05	17,17,17,17	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.