



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 02:28 am BST

PDB ID : 9ICV
Title : DNA POLYMERASE BETA (E.C.2.7.7.7)/DNA COMPLEX + 2'-DEOXY ADENOSINE-5'-TRIPHOSPHATE, SOAKED IN THE PRESENCE OF DATP AND ZNCL2
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1995-12-16
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

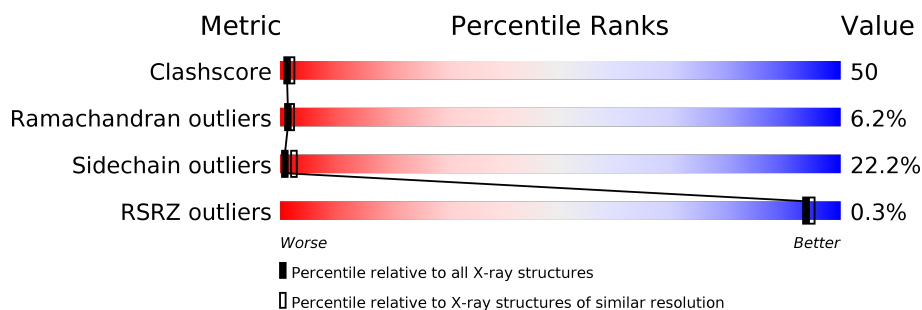
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



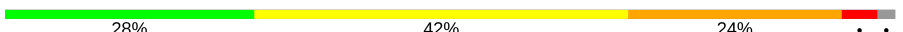
The reported resolution of this entry is 2.70 Å.

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	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 on 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	 13% 13% 75%
2	P	8	 13% 25% 63%
3	A	335	 28% 42% 24% . .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3072 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
			148	69	24	47	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	26	0	0
			2623	1657	458	499	9			

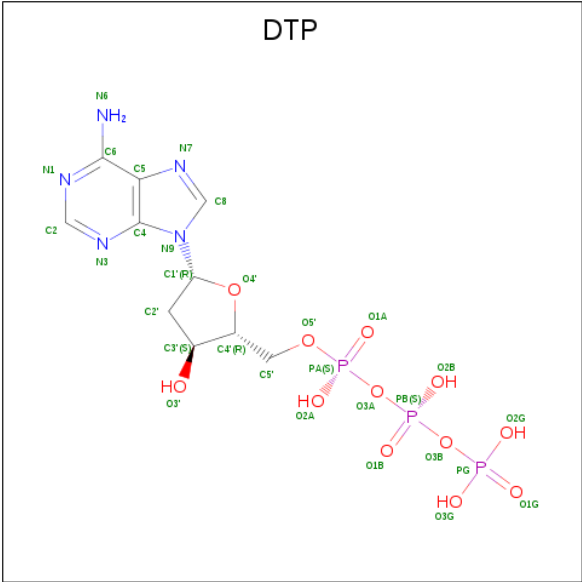
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Zn	0	0
			3	3		

- Molecule 5 is SODIUM ION (three-letter code: 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 (three-letter code: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	179.97Å 57.63Å 48.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 11.90 – 2.71	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-2.70) 92.1 (11.90-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	3.70	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.70Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	0.178 , (Not available) 0.171 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	43.7	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.17 , 111.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3072	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 6.35% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ZN, 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	1.92	6/162 (3.7%)	3.39	21/249 (8.4%)
2	P	2.27	7/164 (4.3%)	4.15	23/250 (9.2%)
3	A	1.30	26/2672 (1.0%)	1.76	67/3590 (1.9%)
All	All	1.41	39/2998 (1.3%)	2.12	111/4089 (2.7%)

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	3	0

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	58	GLU	CD-OE1	9.05	1.35	1.25
2	P	3	DT	N1-C2	8.44	1.44	1.38
3	A	147	GLU	CD-OE2	7.33	1.33	1.25
3	A	309	GLU	CD-OE2	7.14	1.33	1.25
3	A	329	GLU	CD-OE2	7.11	1.33	1.25
2	P	3	DT	C1'-N1	7.06	1.58	1.49
3	A	249	GLU	CD-OE2	7.04	1.33	1.25
2	P	2	DC	C1'-N1	6.98	1.58	1.49
1	T	6	DG	C3'-O3'	-6.95	1.34	1.44
3	A	117	GLU	CD-OE2	6.90	1.33	1.25
3	A	75	GLU	CD-OE1	6.86	1.33	1.25
3	A	154	GLU	CD-OE2	6.85	1.33	1.25
3	A	295	GLU	CD-OE2	6.83	1.33	1.25
3	A	86	GLU	CD-OE1	6.80	1.33	1.25
3	A	71	GLU	CD-OE1	6.78	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	186	GLU	CD-OE1	6.68	1.32	1.25
3	A	172	GLU	CD-OE2	6.58	1.32	1.25
3	A	129	GLU	CD-OE1	6.58	1.32	1.25
3	A	288	GLU	CD-OE2	6.52	1.32	1.25
3	A	335	GLU	CD-OE2	6.34	1.32	1.25
3	A	153	GLU	CD-OE2	6.26	1.32	1.25
3	A	216	GLU	CD-OE2	6.16	1.32	1.25
2	P	5	DA	N9-C4	6.09	1.41	1.37
2	P	6	DT	P-O5'	-6.09	1.53	1.59
3	A	203	GLU	CD-OE1	5.95	1.32	1.25
1	T	5	DA	C4'-O4'	-5.92	1.39	1.45
3	A	123	GLU	CD-OE1	5.91	1.32	1.25
3	A	36	TYR	CB-CG	-5.90	1.42	1.51
1	T	1	DC	C3'-O3'	5.61	1.51	1.44
1	T	5	DA	N7-C5	-5.59	1.35	1.39
1	T	5	DA	C5-C6	-5.52	1.36	1.41
3	A	26	GLU	CD-OE1	5.42	1.31	1.25
3	A	9	GLU	CD-OE2	5.29	1.31	1.25
3	A	39	TYR	CB-CG	-5.29	1.43	1.51
3	A	247	GLU	CD-OE1	5.21	1.31	1.25
2	P	3	DT	N1-C6	-5.10	1.34	1.38
1	T	5	DA	C3'-O3'	-5.08	1.37	1.44
2	P	3	DT	C5-C7	5.07	1.53	1.50
3	A	326	LYS	CE-NZ	-5.07	1.36	1.49

All (111) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	4	DT	C6-N1-C1'	-24.21	84.08	120.40
2	P	2	DC	C2-N1-C1'	23.66	144.83	118.80
1	T	4	DT	C2-N1-C1'	22.19	153.71	118.20
2	P	2	DC	C6-N1-C1'	-20.75	95.90	120.80
2	P	1	DT	C6-N1-C1'	-16.85	95.12	120.40
2	P	7	DG	C8-N9-C1'	16.79	148.83	127.00
2	P	7	DG	C4-N9-C1'	-15.99	105.71	126.50
2	P	1	DT	C2-N1-C1'	15.41	142.86	118.20
2	P	6	DT	C6-N1-C1'	-13.78	99.74	120.40
2	P	6	DT	C2-N1-C1'	12.66	138.45	118.20
2	P	3	DT	C2-N1-C1'	12.45	138.12	118.20
2	P	3	DT	O4'-C1'-N1	12.29	116.60	108.00
2	P	3	DT	C6-N1-C1'	-11.87	102.60	120.40
1	T	7	DA	C4-N9-C1'	-11.69	105.27	126.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	7	DA	C8-N9-C1'	11.30	148.04	127.70
1	T	6	DG	O4'-C1'-N9	11.27	115.89	108.00
2	P	5	DA	C4-N9-C1'	11.14	146.36	126.30
2	P	5	DA	C8-N9-C1'	-11.03	107.85	127.70
2	P	3	DT	N3-C2-O2	-10.19	116.19	122.30
1	T	1	DC	P-O3'-C3'	9.63	131.25	119.70
1	T	5	DA	N1-C6-N6	9.24	124.14	118.60
3	A	92	ASP	CB-CG-OD2	-9.00	110.20	118.30
3	A	39	TYR	CB-CG-CD1	-8.90	115.66	121.00
3	A	314	ASP	CB-CG-OD2	-8.74	110.44	118.30
3	A	130	ASP	CB-CG-OD2	-8.47	110.68	118.30
3	A	130	ASP	CB-CG-OD1	8.07	125.57	118.30
2	P	7	DG	O4'-C1'-N9	8.01	113.61	108.00
3	A	192	ASP	CB-CG-OD2	-7.80	111.28	118.30
3	A	116	ASP	CB-CA-C	7.79	125.98	110.40
1	T	4	DT	O4'-C1'-N1	7.70	113.39	108.00
3	A	266	TYR	CA-CB-CG	-7.44	99.27	113.40
2	P	1	DT	O4'-C1'-N1	7.41	113.18	108.00
3	A	91	ASP	CB-CG-OD1	-7.35	111.68	118.30
3	A	101	THR	CA-CB-CG2	7.26	122.56	112.40
3	A	79	THR	CA-CB-CG2	-7.12	102.42	112.40
1	T	4	DT	O4'-C1'-C2'	-7.07	100.25	105.90
3	A	332	ASP	CB-CG-OD1	-7.06	111.95	118.30
3	A	92	ASP	CB-CG-OD1	7.04	124.64	118.30
3	A	263	ASP	CB-CG-OD2	-6.93	112.07	118.30
3	A	74	ASP	CB-CG-OD1	6.88	124.49	118.30
2	P	3	DT	N1-C1'-C2'	6.84	125.59	112.60
2	P	2	DC	O4'-C1'-N1	6.82	112.78	108.00
3	A	299	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	T	6	DG	C4-N9-C1'	-6.70	117.79	126.50
1	T	5	DA	C6-C5-N7	-6.66	127.64	132.30
1	T	3	DT	C6-C5-C7	-6.66	118.91	122.90
3	A	256	ASP	CB-CG-OD1	6.62	124.25	118.30
3	A	326	LYS	CD-CE-NZ	6.60	126.89	111.70
3	A	226	ASP	CB-CG-OD1	6.59	124.23	118.30
3	A	246	ASP	CB-CG-OD1	-6.56	112.40	118.30
2	P	1	DT	P-O5'-C5'	-6.54	110.44	120.90
3	A	36	TYR	CA-CB-CG	-6.50	101.06	113.40
3	A	116	ASP	N-CA-CB	6.48	122.26	110.60
1	T	5	DA	C5-C6-N6	-6.37	118.61	123.70
1	T	2	DA	O4'-C1'-N9	6.34	112.44	108.00
2	P	2	DC	C4'-C3'-C2'	-6.33	97.40	103.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	6	DG	C8-N9-C1'	6.33	135.22	127.00
3	A	126	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	T	4	DT	C1'-O4'-C4'	-6.23	103.87	110.10
3	A	89	ARG	NE-CZ-NH1	6.19	123.39	120.30
3	A	91	ASP	CB-CG-OD2	6.15	123.83	118.30
3	A	157	GLN	N-CA-CB	6.13	121.64	110.60
3	A	124	ASP	CB-CG-OD2	-6.13	112.78	118.30
3	A	314	ASP	CB-CG-OD1	6.08	123.77	118.30
3	A	333	ARG	NE-CZ-NH1	5.99	123.30	120.30
3	A	116	ASP	CB-CG-OD1	5.95	123.65	118.30
2	P	2	DC	P-O5'-C5'	-5.93	111.42	120.90
3	A	83	ARG	N-CA-CB	5.88	121.19	110.60
3	A	291	PHE	CB-CA-C	-5.85	98.70	110.40
3	A	246	ASP	CB-CG-OD2	5.78	123.50	118.30
3	A	222	HIS	CA-CB-CG	-5.78	103.78	113.60
3	A	219	GLN	CB-CA-C	-5.73	98.94	110.40
1	T	1	DC	O4'-C1'-C2'	5.73	110.48	105.90
3	A	332	ASP	CB-CG-OD2	5.71	123.44	118.30
3	A	39	TYR	CB-CG-CD2	5.69	124.41	121.00
3	A	116	ASP	CB-CG-OD2	-5.67	113.20	118.30
3	A	45	VAL	CA-CB-CG1	-5.63	102.45	110.90
3	A	126	ARG	NE-CZ-NH2	-5.61	117.49	120.30
3	A	195	LEU	CB-CA-C	-5.61	99.55	110.20
1	T	3	DT	C4-C5-C7	5.52	122.31	119.00
1	T	1	DC	C6-N1-C2	5.52	122.51	120.30
3	A	74	ASP	CB-CG-OD2	-5.49	113.36	118.30
3	A	224	ILE	CA-CB-CG1	-5.49	100.57	111.00
3	A	253	ARG	NE-CZ-NH1	5.46	123.03	120.30
3	A	40	ARG	N-CA-CB	5.45	120.40	110.60
2	P	6	DT	C4'-C3'-C2'	-5.38	98.25	103.10
3	A	33	ILE	N-CA-CB	-5.38	98.44	110.80
1	T	4	DT	O5'-P-OP2	-5.38	100.86	105.70
3	A	17	ASP	CB-CA-C	5.37	121.13	110.40
3	A	49	TYR	C-N-CD	-5.32	108.90	120.60
3	A	243	SER	CB-CA-C	5.30	120.16	110.10
3	A	27	LYS	CB-CA-C	5.29	120.98	110.40
3	A	178	CYS	CA-CB-SG	-5.26	104.54	114.00
3	A	157	GLN	CB-CA-C	5.23	120.87	110.40
3	A	122	LEU	CB-CG-CD2	-5.22	102.13	111.00
3	A	39	TYR	CA-CB-CG	-5.21	103.51	113.40
3	A	12	ASN	CB-CA-C	5.19	120.77	110.40
3	A	195	LEU	N-CA-CB	-5.16	100.08	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	83	ARG	NE-CZ-NH1	5.16	122.88	120.30
3	A	49	TYR	CA-CB-CG	5.15	123.19	113.40
3	A	168	LYS	N-CA-CB	5.14	119.85	110.60
3	A	192	ASP	CB-CG-OD1	5.13	122.92	118.30
2	P	3	DT	N1-C2-O2	5.12	127.19	123.10
3	A	315	SER	N-CA-CB	5.10	118.15	110.50
1	T	5	DA	C4-C5-C6	5.09	119.55	117.00
3	A	276	ASP	CB-CG-OD2	-5.08	113.72	118.30
3	A	78	ALA	CB-CA-C	5.08	117.72	110.10
3	A	256	ASP	CB-CG-OD2	-5.07	113.74	118.30
3	A	35	LYS	CA-C-N	-5.05	106.08	117.20
3	A	266	TYR	CB-CG-CD1	-5.05	117.97	121.00
3	A	68	LYS	N-CA-CB	5.02	119.64	110.60

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	40	ARG	CA
3	A	101	THR	CB
3	A	116	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	7	0
2	P	148	0	80	13	0
3	A	2623	0	2641	265	0
4	A	3	0	0	0	0
5	A	2	0	0	0	0
6	A	9	0	0	0	0
7	A	108	0	0	17	0
7	P	21	0	0	1	0
7	T	13	0	0	2	0
All	All	3072	0	2801	283	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 50.

All (283) 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:1:DT:H2''	2:P:2:DC:H5'	1.36	1.07
3:A:243:SER:HB3	3:A:249:GLU:HA	1.45	0.97
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.46	0.95
3:A:245:ASN:N	3:A:245:ASN:HD22	1.68	0.92
3:A:41:LYS:HD3	3:A:42:ALA:N	1.85	0.92
3:A:15:ILE:HD13	3:A:73:ILE:HG23	1.50	0.91
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.52	0.89
3:A:245:ASN:H	3:A:245:ASN:HD22	1.24	0.83
1:T:6:DG:H2''	1:T:7:DA:C8	2.14	0.83
3:A:41:LYS:HD3	3:A:42:ALA:H	1.45	0.81
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.62	0.81
3:A:243:SER:CB	3:A:249:GLU:HA	2.11	0.81
3:A:172:GLU:HB3	3:A:197:HIS:NE2	1.96	0.81
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.11	0.81
3:A:31:GLN:HB2	3:A:112:ARG:HH12	1.45	0.81
3:A:172:GLU:HG3	3:A:198:PRO:HG2	1.61	0.81
3:A:12:ASN:HB3	3:A:46:ILE:HD12	1.64	0.80
3:A:73:ILE:HG22	3:A:77:LEU:CD2	2.11	0.80
3:A:11:LEU:HD23	3:A:11:LEU:H	1.46	0.79
3:A:212:HIS:HB3	7:A:541:HOH:O	1.81	0.79
3:A:108:PRO:O	3:A:112:ARG:HG3	1.83	0.78
3:A:31:GLN:HB2	3:A:112:ARG:NH1	1.98	0.78
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.66	0.77
3:A:244:LYS:HB3	3:A:245:ASN:HD22	1.49	0.76
3:A:172:GLU:CG	3:A:198:PRO:HG2	2.15	0.76
3:A:271:TYR:HB2	7:A:592:HOH:O	1.84	0.75
3:A:244:LYS:HB3	3:A:245:ASN:ND2	2.02	0.75
3:A:73:ILE:HG22	3:A:77:LEU:HD22	1.67	0.75
3:A:18:MET:HE2	3:A:82:LEU:HD13	1.68	0.75
3:A:294:ASN:ND2	3:A:297:THR:H	1.85	0.74
3:A:12:ASN:HB3	3:A:46:ILE:CD1	2.17	0.74
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.17	0.74
3:A:121:THR:HG23	3:A:124:ASP:CG	2.08	0.74
2:P:1:DT:C2'	2:P:2:DC:H5'	2.17	0.73
3:A:245:ASN:H	3:A:245:ASN:ND2	1.87	0.72
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.24	0.72
3:A:172:GLU:HB3	3:A:197:HIS:CD2	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:15:ILE:HD13	3:A:73:ILE:CG2	2.19	0.72
3:A:277:ILE:HG13	3:A:335:GLU:HB3	1.72	0.72
3:A:323:ILE:O	3:A:324:GLN:HG2	1.90	0.71
3:A:18:MET:CE	3:A:76:PHE:HB2	2.21	0.70
3:A:16:THR:HG21	3:A:47:ALA:HB2	1.72	0.70
3:A:58:GLU:O	3:A:61:LYS:HG3	1.92	0.69
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.74	0.69
3:A:60:LYS:HA	3:A:65:VAL:CG2	2.23	0.69
3:A:172:GLU:HB3	3:A:197:HIS:HE2	1.58	0.69
3:A:18:MET:CE	3:A:82:LEU:HD13	2.23	0.69
3:A:73:ILE:O	3:A:77:LEU:HD22	1.93	0.68
3:A:259:LEU:O	3:A:260:ILE:HD13	1.94	0.68
3:A:277:ILE:HG12	3:A:335:GLU:HA	1.76	0.68
3:A:59:ALA:O	3:A:62:LEU:HB2	1.94	0.67
2:P:1:DT:H73	7:P:571:HOH:O	1.95	0.67
3:A:228:LEU:HB2	3:A:236:MET:O	1.96	0.66
3:A:155:MET:HA	3:A:158:MET:HE3	1.77	0.66
3:A:245:ASN:N	3:A:245:ASN:ND2	2.38	0.66
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.28	0.66
3:A:277:ILE:HG13	3:A:335:GLU:CB	2.27	0.65
3:A:294:ASN:HB2	3:A:295:GLU:OE1	1.95	0.65
3:A:119:ILE:HG23	3:A:124:ASP:CB	2.26	0.65
1:T:5:DA:H1'	7:T:564:HOH:O	1.97	0.65
3:A:285:HIS:NE2	7:A:583:HOH:O	2.29	0.65
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.62	0.65
3:A:327:TYR:HD1	3:A:328:ARG:N	1.95	0.65
3:A:26:GLU:HB2	3:A:36:TYR:HB2	1.78	0.64
1:T:5:DA:H2''	1:T:6:DG:O5'	1.97	0.64
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.45	0.64
3:A:286:ALA:HA	3:A:323:ILE:CG2	2.27	0.64
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.28	0.63
3:A:293:ILE:HD13	3:A:298:ILE:CG1	2.23	0.63
3:A:330:PRO:HA	3:A:333:ARG:CG	2.28	0.63
3:A:154:GLU:O	3:A:158:MET:HG3	1.98	0.63
3:A:270:LEU:HD23	3:A:319:ILE:HD13	1.81	0.63
3:A:295:GLU:HA	7:A:592:HOH:O	1.98	0.62
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.99	0.62
1:T:6:DG:N7	7:T:652:HOH:O	2.30	0.62
3:A:88:ILE:HG22	3:A:89:ARG:N	2.12	0.62
3:A:270:LEU:HD13	3:A:316:GLU:OE2	1.98	0.62
3:A:29:VAL:HG21	3:A:94:SER:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.82	0.62
3:A:233:THR:HB	7:A:538:HOH:O	1.99	0.62
3:A:295:GLU:H	3:A:295:GLU:CD	2.04	0.61
3:A:292:THR:O	3:A:298:ILE:HA	2.00	0.61
3:A:278:PHE:HB2	3:A:333:ARG:O	2.01	0.61
3:A:79:THR:O	3:A:81:LYS:N	2.33	0.61
3:A:31:GLN:HE21	3:A:112:ARG:NH1	1.99	0.60
3:A:166:VAL:O	3:A:169:VAL:HG13	2.01	0.60
3:A:60:LYS:HA	3:A:65:VAL:HG22	1.84	0.60
3:A:81:LYS:NZ	3:A:86:GLU:HB3	2.16	0.60
3:A:122:LEU:C	3:A:122:LEU:HD23	2.22	0.60
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.99	0.60
3:A:27:LYS:HB3	3:A:36:TYR:CD1	2.37	0.60
3:A:196:THR:OG1	3:A:197:HIS:N	2.33	0.59
3:A:326:LYS:O	3:A:326:LYS:HG3	2.01	0.59
3:A:183:ARG:HH11	3:A:275:SER:HA	1.67	0.59
3:A:200:PHE:HB2	7:A:625:HOH:O	2.03	0.59
3:A:60:LYS:HG3	3:A:60:LYS:O	2.02	0.58
3:A:122:LEU:HD21	3:A:126:ARG:CZ	2.33	0.58
3:A:125:LEU:HD22	3:A:132:LEU:HD21	1.84	0.58
3:A:150:ILE:HD13	3:A:253:ARG:HG2	1.82	0.58
1:T:1:DC:H2"	1:T:2:DA:OP2	2.04	0.58
3:A:303:VAL:C	3:A:305:GLY:H	2.06	0.58
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.43	0.58
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.85	0.58
3:A:248:LYS:HG2	3:A:248:LYS:O	2.04	0.57
3:A:123:GLU:O	3:A:127:LYS:HG2	2.05	0.57
3:A:306:VAL:HG23	3:A:307:ALA:N	2.20	0.57
3:A:133:ASN:HD22	3:A:134:HIS:N	2.03	0.56
3:A:315:SER:OG	3:A:316:GLU:N	2.38	0.56
3:A:289:LYS:N	3:A:289:LYS:HD3	2.18	0.56
3:A:11:LEU:CD2	3:A:11:LEU:H	2.19	0.56
3:A:15:ILE:HD11	3:A:77:LEU:HD11	1.86	0.56
3:A:12:ASN:HD21	3:A:53:ILE:H	1.54	0.56
3:A:299:ARG:HG2	3:A:310:PRO:HA	1.88	0.56
3:A:308:GLY:O	3:A:309:GLU:HB2	2.06	0.55
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.41	0.55
3:A:26:GLU:HG3	3:A:35:LYS:HB2	1.89	0.55
3:A:291:PHE:CD1	3:A:300:PRO:HA	2.41	0.55
3:A:286:ALA:HA	3:A:323:ILE:HG21	1.88	0.55
3:A:41:LYS:NZ	3:A:64:GLY:O	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:15:ILE:HB	3:A:46:ILE:CD1	2.37	0.55
3:A:190:ASP:OD1	3:A:190:ASP:N	2.34	0.55
2:P:6:DT:H2''	2:P:7:DG:H5''	1.88	0.55
3:A:292:THR:O	3:A:298:ILE:HG13	2.07	0.54
3:A:211:LEU:O	3:A:211:LEU:HD12	2.07	0.54
3:A:49:TYR:CE2	3:A:51:HIS:HB2	2.41	0.54
3:A:81:LYS:HZ3	3:A:86:GLU:HB3	1.70	0.54
3:A:18:MET:HE1	3:A:76:PHE:CB	2.38	0.54
3:A:15:ILE:CG2	3:A:46:ILE:HD13	2.37	0.54
3:A:317:LYS:O	3:A:320:PHE:N	2.41	0.54
3:A:82:LEU:HB3	3:A:85:LEU:HB2	1.89	0.54
3:A:172:GLU:HG2	3:A:198:PRO:HG2	1.90	0.54
3:A:331:LYS:HG2	3:A:332:ASP:N	2.05	0.54
3:A:150:ILE:HG21	3:A:158:MET:CE	2.38	0.54
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.90	0.54
2:P:5:DA:H2''	2:P:6:DT:H5'	1.89	0.54
3:A:236:MET:HG3	3:A:256:ASP:OD1	2.07	0.53
3:A:244:LYS:CB	3:A:245:ASN:HD22	2.19	0.53
3:A:217:GLN:O	3:A:220:LYS:HB3	2.08	0.53
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.39	0.53
3:A:262:LYS:HG3	3:A:262:LYS:O	2.03	0.53
3:A:191:MET:HG2	3:A:255:ILE:HG13	1.89	0.53
3:A:18:MET:HE3	3:A:76:PHE:HB2	1.88	0.53
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.24	0.53
3:A:35:LYS:O	3:A:38:ALA:HB3	2.09	0.53
1:T:4:DT:O2	2:P:4:DA:H2	1.91	0.52
3:A:200:PHE:CE2	3:A:261:PRO:HD3	2.44	0.52
3:A:278:PHE:CE1	3:A:325:TRP:HZ3	2.27	0.52
2:P:5:DA:H2''	2:P:6:DT:C5'	2.40	0.52
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.44	0.52
3:A:15:ILE:HB	3:A:46:ILE:HD11	1.90	0.52
3:A:243:SER:HB3	3:A:249:GLU:CA	2.31	0.52
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.90	0.52
3:A:306:VAL:HG22	7:A:650:HOH:O	2.10	0.51
3:A:73:ILE:HG22	3:A:77:LEU:HD21	1.90	0.51
3:A:234:LYS:HD3	7:A:617:HOH:O	2.10	0.51
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.41	0.51
3:A:309:GLU:H	3:A:310:PRO:HD3	1.75	0.51
3:A:165:GLU:O	3:A:169:VAL:HG12	2.11	0.51
3:A:146:PHE:HB2	7:A:514:HOH:O	2.11	0.51
2:P:1:DT:H2''	2:P:2:DC:C5'	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:148:LYS:HB3	7:A:620:HOH:O	2.10	0.50
3:A:16:THR:HG23	3:A:46:ILE:CG1	2.41	0.50
3:A:291:PHE:HD1	3:A:300:PRO:HA	1.76	0.50
3:A:329:GLU:O	3:A:333:ARG:HG2	2.11	0.50
3:A:182:ARG:NH2	3:A:316:GLU:OE1	2.32	0.50
3:A:151:PRO:HG2	3:A:154:GLU:HG3	1.92	0.50
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.91	0.50
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.75	0.50
3:A:30:SER:HB3	7:A:561:HOH:O	2.11	0.50
3:A:316:GLU:O	3:A:320:PHE:HD2	1.95	0.50
3:A:294:ASN:HD21	3:A:297:THR:H	1.57	0.49
3:A:12:ASN:HA	7:A:553:HOH:O	2.12	0.49
3:A:270:LEU:HD12	3:A:270:LEU:O	2.12	0.49
3:A:295:GLU:OE1	3:A:295:GLU:N	2.27	0.49
3:A:165:GLU:OE1	3:A:168:LYS:NZ	2.28	0.49
3:A:82:LEU:HD23	3:A:85:LEU:HB2	1.95	0.49
3:A:326:LYS:O	3:A:328:ARG:HG2	2.12	0.49
3:A:19:LEU:HD23	3:A:43:ALA:HA	1.94	0.49
3:A:309:GLU:H	3:A:310:PRO:CD	2.27	0.48
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.95	0.48
3:A:270:LEU:HD23	3:A:319:ILE:HG21	1.94	0.48
3:A:172:GLU:HG3	3:A:198:PRO:CG	2.38	0.48
3:A:243:SER:HB3	3:A:249:GLU:HB2	1.95	0.48
3:A:103:VAL:HG22	3:A:143:PHE:CD2	2.48	0.48
3:A:11:LEU:N	3:A:11:LEU:HD23	2.15	0.48
3:A:209:LYS:HA	3:A:209:LYS:HD3	1.69	0.48
1:T:4:DT:N3	2:P:4:DA:C2	2.78	0.47
2:P:6:DT:H5'	2:P:6:DT:H6	1.79	0.47
3:A:62:LEU:HA	3:A:62:LEU:HD12	1.49	0.47
3:A:144:GLY:N	7:A:590:HOH:O	2.45	0.47
3:A:303:VAL:O	3:A:305:GLY:N	2.48	0.47
3:A:253:ARG:CG	3:A:253:ARG:HH11	2.26	0.47
3:A:270:LEU:C	3:A:270:LEU:HD12	2.32	0.47
3:A:286:ALA:CA	3:A:323:ILE:HG21	2.45	0.46
3:A:286:ALA:HA	3:A:323:ILE:HG22	1.97	0.46
3:A:79:THR:O	3:A:79:THR:OG1	2.33	0.46
3:A:171:SER:O	3:A:171:SER:OG	2.33	0.46
3:A:282:MET:HB3	3:A:282:MET:HE2	1.88	0.46
3:A:12:ASN:HB3	3:A:46:ILE:HD11	1.96	0.46
3:A:275:SER:HB2	7:A:663:HOH:O	2.15	0.46
3:A:289:LYS:HA	3:A:289:LYS:HD3	1.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.31	0.46
3:A:183:ARG:NH1	3:A:275:SER:HA	2.31	0.46
3:A:127:LYS:HE3	3:A:127:LYS:HB3	1.62	0.46
3:A:62:LEU:HD12	3:A:63:PRO:HD2	1.98	0.46
2:P:2:DC:H2'	2:P:2:DC:H6	1.28	0.45
3:A:195:LEU:HA	3:A:195:LEU:HD12	1.70	0.45
3:A:30:SER:HA	7:A:558:HOH:O	2.17	0.45
3:A:49:TYR:CZ	3:A:51:HIS:HB2	2.51	0.45
3:A:155:MET:HE2	3:A:188:SER:HB2	1.97	0.45
3:A:309:GLU:N	3:A:310:PRO:CD	2.79	0.45
3:A:311:LEU:HA	3:A:311:LEU:HD12	1.59	0.45
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.94	0.45
3:A:127:LYS:HG2	3:A:127:LYS:H	1.17	0.45
3:A:294:ASN:HD22	3:A:294:ASN:C	2.19	0.45
3:A:195:LEU:O	3:A:260:ILE:N	2.47	0.45
3:A:267:CYS:SG	3:A:297:THR:HA	2.57	0.45
3:A:178:CYS:SG	3:A:194:LEU:CD2	3.04	0.45
3:A:206:LYS:O	3:A:207:GLN:HB2	2.17	0.45
3:A:26:GLU:O	3:A:30:SER:O	2.34	0.45
3:A:11:LEU:CD2	3:A:11:LEU:N	2.79	0.44
3:A:259:LEU:C	3:A:260:ILE:HD13	2.38	0.44
3:A:310:PRO:HB3	7:A:626:HOH:O	2.17	0.44
3:A:298:ILE:HG23	3:A:298:ILE:O	2.18	0.44
3:A:183:ARG:HD3	3:A:273:THR:O	2.17	0.44
3:A:230:LYS:HB3	3:A:230:LYS:HE2	1.82	0.44
3:A:327:TYR:HE1	3:A:333:ARG:HH21	1.65	0.44
3:A:278:PHE:CE2	3:A:333:ARG:CD	3.00	0.44
3:A:183:ARG:HH11	3:A:275:SER:CA	2.30	0.43
3:A:31:GLN:NE2	3:A:112:ARG:NH1	2.62	0.43
3:A:56:GLY:H	3:A:74:ASP:CG	2.22	0.43
2:P:6:DT:H2'	2:P:6:DT:H5'	1.82	0.43
3:A:278:PHE:HE1	3:A:325:TRP:HZ3	1.65	0.43
3:A:299:ARG:HG2	3:A:310:PRO:CA	2.48	0.43
3:A:223:PHE:CZ	3:A:239:CYS:SG	3.12	0.43
3:A:150:ILE:N	3:A:188:SER:O	2.31	0.43
3:A:279:ASN:O	3:A:283:ARG:HG3	2.18	0.43
3:A:31:GLN:N	7:A:641:HOH:O	2.29	0.43
3:A:200:PHE:CE2	3:A:261:PRO:N	2.87	0.43
3:A:150:ILE:CG1	3:A:253:ARG:HG2	2.49	0.42
3:A:121:THR:HG23	3:A:124:ASP:OD2	2.19	0.42
3:A:42:ALA:O	3:A:46:ILE:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:194:LEU:HA	3:A:194:LEU:HD12	1.52	0.42
3:A:266:TYR:O	3:A:270:LEU:HB2	2.19	0.42
3:A:286:ALA:O	3:A:291:PHE:HB2	2.19	0.42
3:A:323:ILE:C	3:A:324:GLN:HG2	2.38	0.42
3:A:278:PHE:HE1	3:A:325:TRP:CZ3	2.37	0.42
3:A:157:GLN:O	3:A:161:ILE:HG13	2.19	0.42
3:A:288:GLU:C	3:A:290:GLY:H	2.23	0.42
2:P:6:DT:C2'	2:P:7:DG:H5''	2.48	0.42
3:A:81:LYS:NZ	3:A:86:GLU:CB	2.82	0.42
3:A:228:LEU:HD12	3:A:228:LEU:HA	1.83	0.42
3:A:287:LEU:HA	3:A:287:LEU:HD13	1.50	0.42
3:A:264:GLN:NE2	3:A:296:TYR:HB3	2.35	0.42
3:A:294:ASN:HD22	3:A:297:THR:H	1.66	0.42
3:A:322:TYR:C	3:A:324:GLN:H	2.22	0.42
3:A:118:GLY:HA2	3:A:120:LYS:HE3	2.02	0.42
3:A:16:THR:HG23	3:A:46:ILE:HG12	2.02	0.41
3:A:33:ILE:H	3:A:33:ILE:HG22	1.40	0.41
3:A:250:TYR:HA	3:A:251:PRO:HD3	1.83	0.41
3:A:274:GLY:HA2	3:A:279:ASN:OD1	2.20	0.41
3:A:49:TYR:CE2	3:A:53:ILE:HG13	2.55	0.41
3:A:197:HIS:CG	3:A:198:PRO:CD	3.03	0.41
3:A:133:ASN:HD21	3:A:135:HIS:HB3	1.85	0.41
3:A:125:LEU:HD23	3:A:125:LEU:HA	1.81	0.41
3:A:159:GLN:O	3:A:163:LEU:HG	2.19	0.41
3:A:223:PHE:O	3:A:239:CYS:HB2	2.21	0.41
3:A:200:PHE:O	3:A:261:PRO:HA	2.21	0.41
3:A:241:LEU:HA	3:A:242:PRO:HD2	1.82	0.41
3:A:54:LYS:HD2	3:A:54:LYS:HA	1.85	0.41
3:A:15:ILE:CD1	3:A:73:ILE:HG23	2.37	0.41
3:A:152:ARG:HH11	3:A:152:ARG:HD3	1.69	0.41
3:A:18:MET:HE2	3:A:82:LEU:CD1	2.43	0.41
3:A:306:VAL:O	3:A:307:ALA:HB2	2.21	0.41
3:A:194:LEU:N	3:A:194:LEU:HD13	2.36	0.41
3:A:133:ASN:O	3:A:137:ARG:HG3	2.21	0.40
3:A:151:PRO:HB2	3:A:153:GLU:HG2	2.02	0.40
3:A:150:ILE:HG12	3:A:253:ARG:HG2	2.03	0.40
3:A:264:GLN:HE21	3:A:264:GLN:HB3	1.33	0.40
3:A:194:LEU:HD12	3:A:258:ARG:CG	2.50	0.40
3:A:294:ASN:HD21	3:A:297:THR:N	2.19	0.40
3:A:243:SER:CB	3:A:249:GLU:HB2	2.52	0.40
3:A:293:ILE:CD1	3:A:298:ILE:CD1	3.00	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%)	272 (84%)	33 (10%)	20 (6%)	1 2

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	185	ALA
3	A	202	SER
3	A	204	SER
3	A	205	THR
3	A	206	LYS
3	A	244	LYS
3	A	246	ASP
3	A	304	THR
3	A	309	GLU
3	A	13	GLY
3	A	80	GLY
3	A	265	TYR
3	A	316	GLU
3	A	78	ALA
3	A	207	GLN
3	A	266	TYR
3	A	10	THR
3	A	310	PRO
3	A	247	GLU
3	A	33	ILE

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%)	224 (78%)	64 (22%)	1 2

All (64) 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
3	A	40	ARG
3	A	41	LYS
3	A	46	ILE
3	A	54	LYS
3	A	61	LYS
3	A	62	LEU
3	A	67	THR
3	A	77	LEU
3	A	79	THR
3	A	81	LYS
3	A	89	ARG
3	A	92	ASP
3	A	94	SER
3	A	100	LEU
3	A	121	THR
3	A	127	LYS
3	A	133	ASN
3	A	138	ILE
3	A	153	GLU
3	A	157	GLN
3	A	168	LYS
3	A	169	VAL
3	A	188	SER
3	A	190	ASP
3	A	194	LEU

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Mol	Chain	Res	Type
3	A	201	THR
3	A	205	THR
3	A	214	VAL
3	A	226	ASP
3	A	228	LEU
3	A	230	LYS
3	A	233	THR
3	A	245	ASN
3	A	248	LYS
3	A	249	GLU
3	A	253	ARG
3	A	258	ARG
3	A	264	GLN
3	A	270	LEU
3	A	277	ILE
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	304	THR
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	325	TRP
3	A	327	TYR
3	A	331	LYS
3	A	335	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) 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	133	ASN
3	A	136	GLN
3	A	213	GLN

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Mol	Chain	Res	Type
3	A	245	ASN
3	A	264	GLN
3	A	294	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 5 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	1.50	1 (16%)	13,13,50	1.25	2 (15%)

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	2.39	1.64	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	338	DTP	O2G-PG-O3B	2.29	112.32	104.64
6	A	338	DTP	O3G-PG-O3B	-2.07	97.70	104.64

There are no chirality outliers.

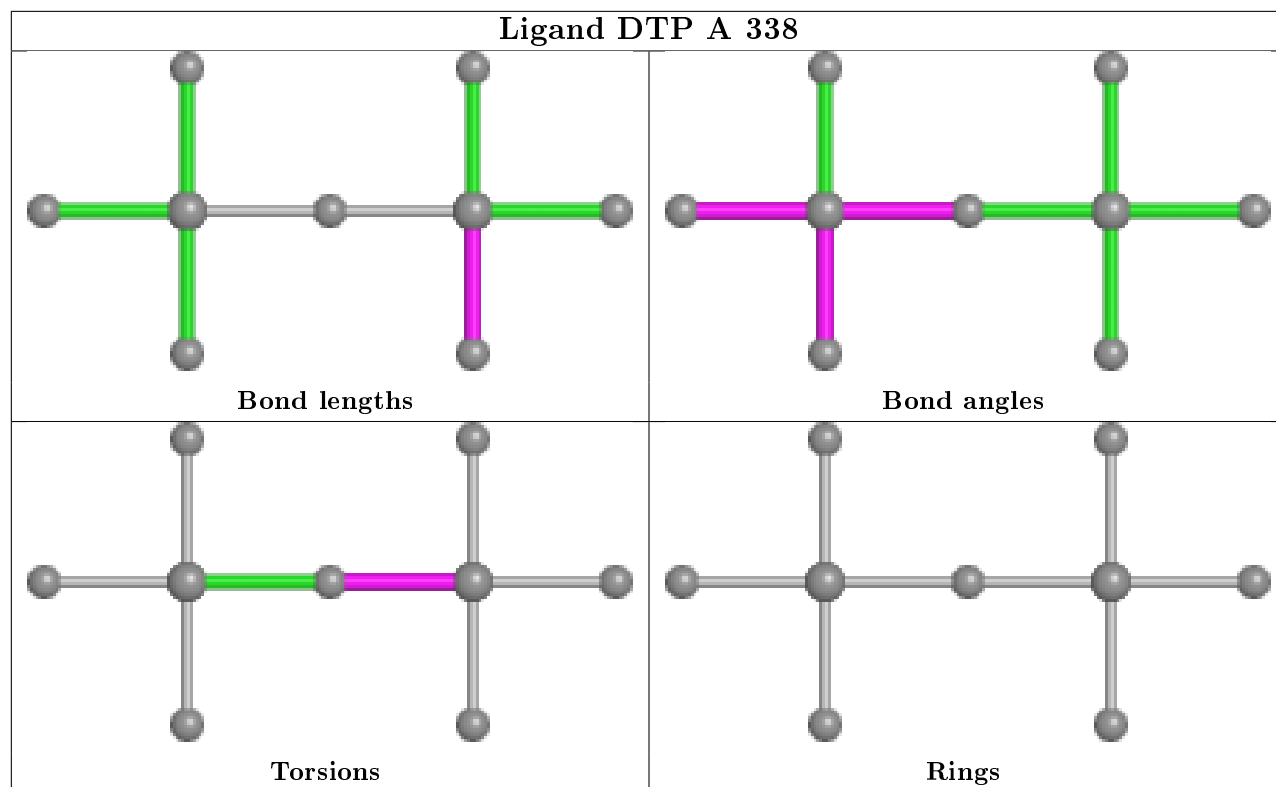
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	338	DTP	PG-O3B-PB-O2B
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(Å ²)	Q<0.9
1	T	8/8 (100%)	-0.69	0 100 100	20, 43, 100, 100	0
2	P	8/8 (100%)	-0.67	1 (12%) 3 3	22, 30, 83, 100	0
3	A	324/335 (96%)	-1.13	0 100 100	7, 35, 82, 100	0
All	All	340/351 (96%)	-1.10	1 (0%) 94 95	7, 35, 84, 100	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	8	DA	2.7

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 carbohydrates 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.

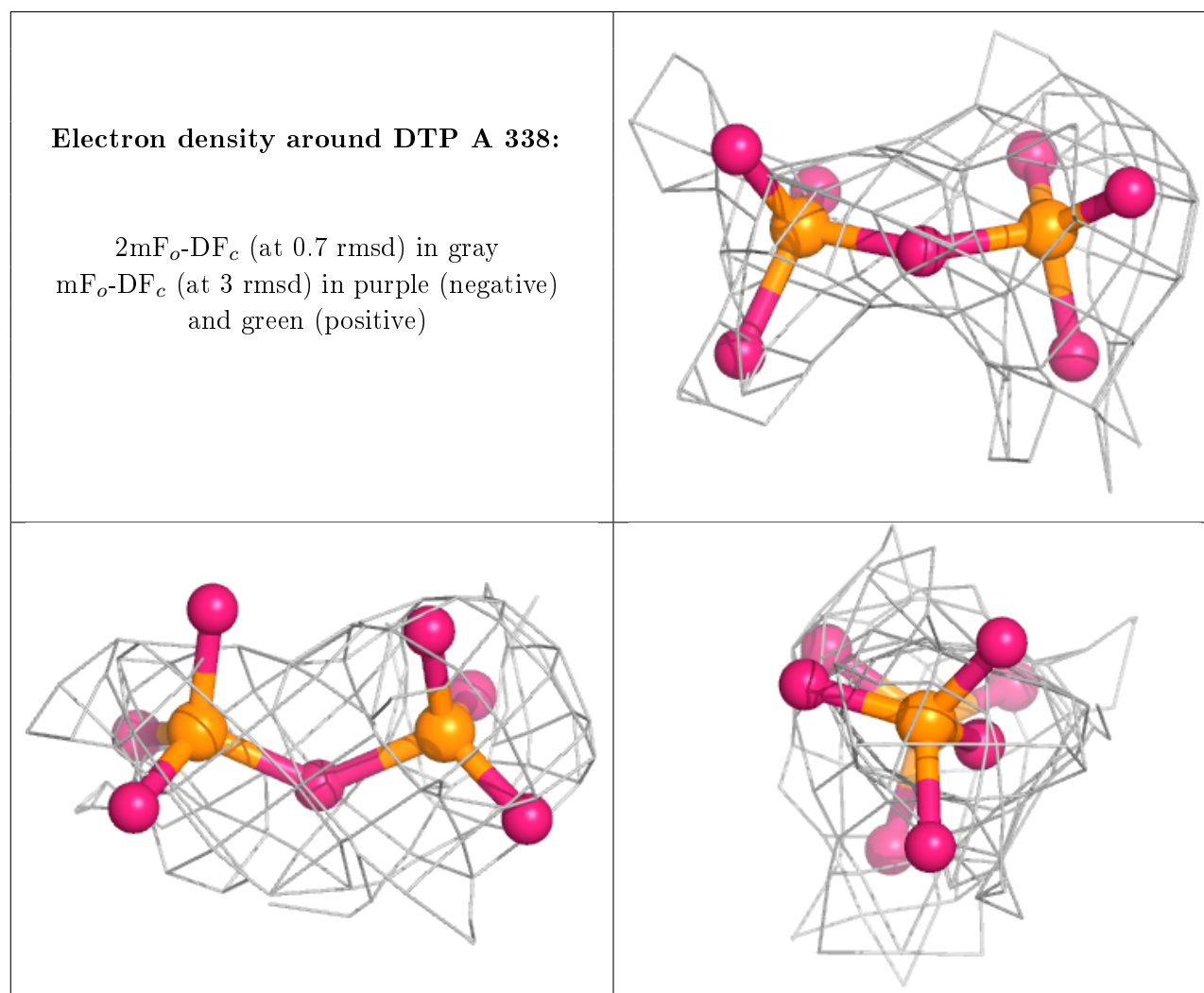
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NA	A	342	1/1	0.85	0.22	58,58,58,58	0
4	ZN	A	339	1/1	0.93	0.06	30,30,30,30	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	DTP	A	338	9/30	0.93	0.19	35,40,90,90	9
5	NA	A	341	1/1	0.99	0.05	15,15,15,15	0
4	ZN	A	343	1/1	0.99	0.02	30,30,30,30	1
4	ZN	A	340	1/1	0.99	0.05	30,30,30,30	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.