



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:55 PM GMT

PDB ID : 1HUZ
Title : CRYSTAL STRUCTURE OF DNA POLYMERASE COMPLEXED WITH
DNA AND CR-PCP
Authors : Arndt, J.W.; Gong, W.; Zhong, X.; Showalter, A.K.; Liu, J.; Lin, Z.; Paxson,
C.; Tsai, M.-D.; Chan, M.K.
Deposited on : 2001-01-04
Resolution : 2.60 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

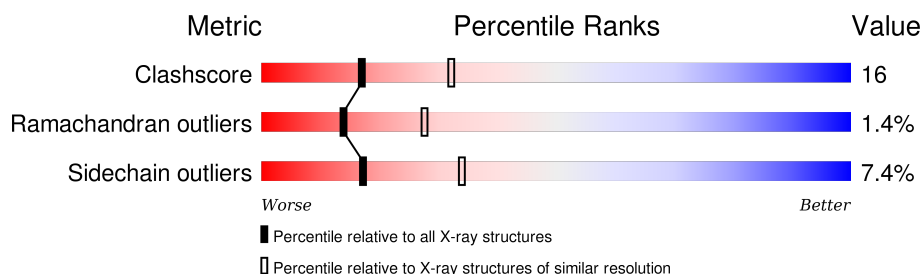
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	11	
1	T	11	
2	D	8	
2	P	8	
3	A	335	
3	B	335	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MDN	B	338	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5994 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 5'-D(*AP*AP*TP*AP*GP*GP*CP*GP*TP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	8	Total	C	N	O	P	0	0	0
			167	78	33	48	8			
1	C	8	Total	C	N	O	P	0	0	0
			167	78	33	48	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	8	Total	C	N	O	P	0	0	0
			161	76	29	48	8			
2	D	8	Total	C	N	O	P	0	0	0
			161	76	29	48	8			

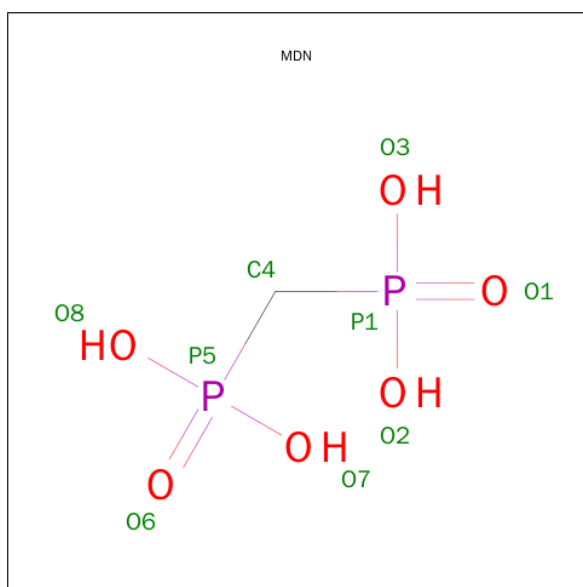
- Molecule 3 is a protein called DNA POLYMERASE BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	325	Total	C	N	O	S	0	0	0
			2598	1639	457	493	9			
3	B	325	Total	C	N	O	S	0	0	0
			2598	1639	457	493	9			

- Molecule 4 is CHROMIUM ION (three-letter code: CR) (formula: Cr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cr	0	0
			1	1		
4	A	1	Total	Cr	0	0
			1	1		

- Molecule 5 is METHYLENEDIPHOSPHONIC ACID (three-letter code: MDN) (formula: CH₆O₆P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			9	1	6	2		
5	B	1	Total	C	O	P	0	0
			9	1	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	41	Total	O	0	0
			41	41		
6	B	61	Total	O	0	0
			61	61		
6	C	5	Total	O	0	0
			5	5		
6	D	6	Total	O	0	0
			6	6		
6	P	3	Total	O	0	0
			3	3		
6	T	6	Total	O	0	0
			6	6		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

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

Chain T: 



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

Chain C: 



- Molecule 2: 5'-D(P*CP*GP*AP*CP*GP*CP*CP*T)-3'

Chain P: 



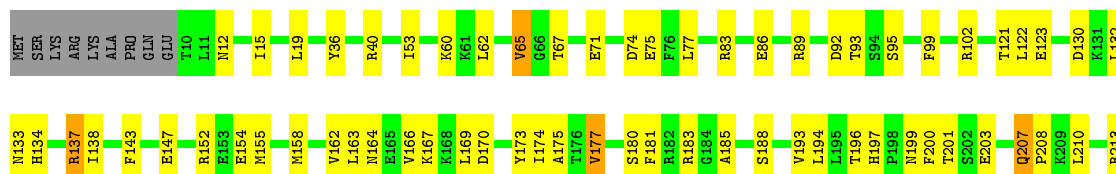
- Molecule 2: 5'-D(P*CP*GP*AP*CP*GP*CP*CP*T)-3'

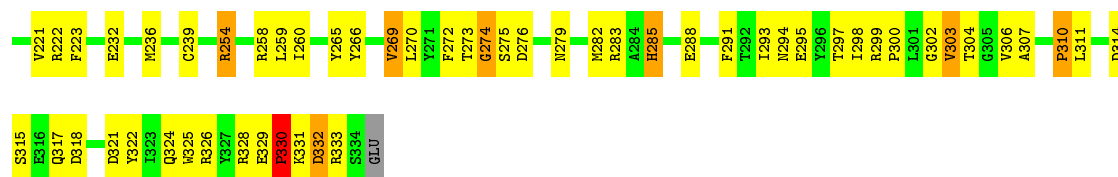
Chain D: 



- Molecule 3: DNA POLYMERASE BETA

Chain A: 





• Molecule 3: DNA POLYMERASE BETA

Chain B: 60% 33%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.78Å 56.13Å 85.41Å 90.00° 106.94° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.60)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.224 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5994	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CR, MDN

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	C	3.77	27/187 (14.4%)	3.66	51/287 (17.8%)
1	T	3.72	29/187 (15.5%)	3.66	47/287 (16.4%)
2	D	5.04	35/179 (19.6%)	4.58	70/273 (25.6%)
2	P	5.20	46/179 (25.7%)	4.23	57/273 (20.9%)
3	A	0.70	1/2645 (0.0%)	0.80	0/3562
3	B	0.64	0/2645	0.83	7/3562 (0.2%)
All	All	1.68	138/6022 (2.3%)	1.67	232/8244 (2.8%)

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
1	C	0	5
1	T	0	4
2	D	0	8
2	P	0	6
All	All	0	23

All (138) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DC	P-O5'	25.10	1.84	1.59
2	D	1	DC	P-O5'	25.03	1.84	1.59
2	P	3	DA	N9-C4	21.61	1.50	1.37
1	C	9	DT	C5-C7	19.53	1.61	1.50
2	P	8	DT	C4'-O4'	18.46	1.63	1.45
2	D	3	DA	C6-N6	17.24	1.47	1.33
2	D	3	DA	N9-C4	17.07	1.48	1.37
2	D	1	DC	C4'-C3'	16.44	1.69	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	9	DT	C5-C7	15.57	1.59	1.50
3	A	310	PRO	N-CD	-14.86	1.27	1.47
2	D	1	DC	O4'-C1'	14.19	1.59	1.42
2	P	2	DG	C2-N3	13.70	1.43	1.32
2	D	2	DG	C2'-C1'	13.63	1.66	1.52
2	P	5	DG	C8-N7	13.23	1.38	1.30
2	P	1	DC	C4'-C3'	13.10	1.66	1.53
2	P	1	DC	C4'-O4'	12.80	1.57	1.45
2	D	7	DC	O4'-C1'	12.26	1.56	1.42
2	D	2	DG	N3-C4	12.25	1.44	1.35
2	P	1	DC	C5'-C4'	12.01	1.64	1.51
1	T	9	DT	N1-C2	11.97	1.47	1.38
2	D	8	DT	C4-C5	-11.39	1.34	1.45
2	P	2	DG	N7-C5	11.31	1.46	1.39
2	D	8	DT	C2-N3	11.25	1.46	1.37
1	C	9	DT	N3-C4	10.70	1.47	1.38
1	T	7	DC	N3-C4	10.69	1.41	1.33
1	C	10	DC	N1-C6	10.64	1.43	1.37
2	D	4	DC	N1-C6	10.07	1.43	1.37
2	D	6	DC	C4'-C3'	-9.84	1.42	1.52
2	D	2	DG	N9-C4	9.82	1.45	1.38
1	C	5	DG	N1-C2	9.74	1.45	1.37
1	T	6	DG	C6-N1	9.53	1.46	1.39
2	P	3	DA	N9-C8	-9.40	1.30	1.37
2	P	2	DG	N9-C8	9.37	1.44	1.37
2	D	6	DC	P-O5'	-9.36	1.50	1.59
1	T	11	DG	N9-C4	9.23	1.45	1.38
2	P	2	DG	P-O5'	9.21	1.69	1.59
2	D	1	DC	O5'-C5'	8.86	1.64	1.42
1	T	5	DG	C5-C4	8.74	1.44	1.38
1	C	7	DC	C4-N4	8.66	1.41	1.33
1	C	5	DG	O3'-P	-8.65	1.50	1.61
1	T	6	DG	N9-C4	8.56	1.44	1.38
1	C	8	DG	N7-C5	8.51	1.44	1.39
1	T	8	DG	C5'-C4'	8.36	1.60	1.51
2	D	1	DC	O3'-P	8.34	1.71	1.61
1	C	11	DG	C4'-O4'	8.34	1.53	1.45
2	P	1	DC	O4'-C1'	8.17	1.52	1.42
1	C	8	DG	C2-N3	8.12	1.39	1.32
2	D	1	DC	C5'-C4'	7.99	1.60	1.51
1	T	10	DC	C4-N4	7.96	1.41	1.33
2	D	2	DG	N9-C8	-7.95	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DC	C3'-C2'	7.93	1.61	1.52
2	D	8	DT	C4'-O4'	7.87	1.52	1.45
2	D	5	DG	N7-C5	7.87	1.44	1.39
1	T	11	DG	C4'-O4'	7.75	1.52	1.45
1	C	8	DG	N9-C4	7.75	1.44	1.38
2	P	3	DA	O3'-P	-7.71	1.51	1.61
2	D	7	DC	O3'-P	-7.48	1.52	1.61
2	P	8	DT	P-OP1	7.48	1.61	1.49
1	C	11	DG	P-O5'	-7.45	1.52	1.59
2	D	1	DC	C4'-O4'	7.44	1.52	1.45
1	T	7	DC	C2-N3	7.39	1.41	1.35
1	C	10	DC	C2-N3	7.38	1.41	1.35
2	P	4	DC	N1-C2	7.38	1.47	1.40
2	P	3	DA	N7-C5	7.31	1.43	1.39
2	P	6	DC	C4'-C3'	-7.29	1.45	1.52
1	C	4	DA	N3-C4	-7.28	1.30	1.34
1	T	11	DG	N7-C5	7.23	1.43	1.39
2	P	8	DT	P-OP2	7.20	1.61	1.49
1	C	6	DG	C6-N1	7.13	1.44	1.39
2	P	3	DA	C5-C6	7.08	1.47	1.41
2	D	4	DC	C4'-O4'	7.07	1.52	1.45
2	P	3	DA	C6-N6	7.06	1.39	1.33
2	D	3	DA	C4'-O4'	6.90	1.51	1.45
1	T	6	DG	C8-N7	6.89	1.35	1.30
1	T	5	DG	C6-N1	6.84	1.44	1.39
2	P	6	DC	N1-C6	-6.82	1.33	1.37
2	D	4	DC	O3'-P	-6.80	1.52	1.61
1	C	5	DG	C8-N7	-6.75	1.26	1.30
2	P	8	DT	C4-C5	6.74	1.51	1.45
2	P	2	DG	C5-C4	6.72	1.43	1.38
2	P	4	DC	N3-C4	6.67	1.38	1.33
1	C	11	DG	N9-C8	-6.63	1.33	1.37
2	P	2	DG	C6-N1	6.62	1.44	1.39
2	P	2	DG	C4'-O4'	-6.60	1.38	1.45
2	D	1	DC	C4-N4	6.59	1.39	1.33
1	C	11	DG	C2-N3	6.55	1.38	1.32
1	T	8	DG	N9-C4	6.50	1.43	1.38
2	P	2	DG	C5-C6	6.49	1.48	1.42
1	T	11	DG	N9-C8	6.45	1.42	1.37
1	C	6	DG	O3'-P	-6.35	1.53	1.61
1	T	7	DC	C4'-C3'	6.29	1.59	1.53
2	P	6	DC	P-O5'	-6.27	1.53	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	DG	P-O5'	6.20	1.66	1.59
1	T	10	DC	C3'-C2'	6.16	1.59	1.52
1	T	7	DC	C2-O2	6.09	1.29	1.24
1	T	5	DG	O3'-P	-6.08	1.53	1.61
2	P	6	DC	C5'-C4'	6.06	1.58	1.51
2	P	4	DC	C2-N3	6.05	1.40	1.35
2	P	6	DC	N3-C4	6.02	1.38	1.33
1	C	8	DG	C5-C4	5.95	1.42	1.38
2	P	5	DG	C3'-O3'	-5.91	1.36	1.44
1	C	4	DA	P-O5'	5.88	1.65	1.59
2	P	5	DG	N3-C4	-5.82	1.31	1.35
1	T	10	DC	N1-C6	5.82	1.40	1.37
2	P	1	DC	C4-N4	5.81	1.39	1.33
2	D	5	DG	C4'-O4'	5.69	1.50	1.45
1	C	10	DC	P-O5'	-5.67	1.54	1.59
2	D	1	DC	C3'-C2'	5.66	1.59	1.52
2	D	3	DA	C5-C6	5.64	1.46	1.41
2	P	8	DT	C2-N3	-5.63	1.33	1.37
2	D	6	DC	C3'-O3'	-5.56	1.36	1.44
2	P	3	DA	O4'-C1'	-5.55	1.35	1.42
1	T	5	DG	C8-N7	5.53	1.34	1.30
2	P	8	DT	C1'-N1	-5.45	1.39	1.47
1	T	6	DG	C4'-C3'	5.44	1.58	1.53
1	C	6	DG	C5'-C4'	-5.44	1.45	1.51
2	P	3	DA	C8-N7	5.43	1.35	1.31
1	T	4	DA	N3-C4	-5.41	1.31	1.34
1	T	8	DG	N3-C4	-5.40	1.31	1.35
2	D	2	DG	O4'-C1'	-5.39	1.35	1.42
1	C	5	DG	C6-N1	5.37	1.43	1.39
2	P	4	DC	P-O5'	-5.37	1.54	1.59
2	D	6	DC	N1-C2	-5.36	1.34	1.40
1	T	8	DG	C6-N1	-5.36	1.35	1.39
2	P	5	DG	C2-N3	5.32	1.37	1.32
2	P	7	DC	C4'-O4'	-5.28	1.39	1.45
2	P	1	DC	N1-C6	5.25	1.40	1.37
1	C	6	DG	C2'-C1'	5.24	1.57	1.52
1	C	10	DC	C4'-C3'	-5.24	1.47	1.52
1	C	9	DT	C2-N3	5.21	1.42	1.37
2	P	1	DC	N3-C4	5.20	1.37	1.33
1	C	6	DG	N9-C4	5.19	1.42	1.38
1	T	10	DC	P-O5'	-5.16	1.54	1.59
1	T	5	DG	C2'-C1'	-5.15	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	DC	C3'-O3'	5.14	1.50	1.44
2	D	6	DC	N3-C4	5.04	1.37	1.33
1	T	5	DG	C4'-O4'	5.02	1.50	1.45
2	P	2	DG	C2-N2	-5.00	1.29	1.34

All (232) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	7	DC	O4'-C1'-N1	17.57	120.30	108.00
2	D	1	DC	O4'-C1'-N1	16.33	119.43	108.00
2	D	7	DC	P-O3'-C3'	15.26	138.01	119.70
2	P	7	DC	O4'-C4'-C3'	-14.81	97.11	106.00
2	P	1	DC	O4'-C4'-C3'	-14.01	97.59	106.00
1	C	6	DG	C2-N3-C4	13.86	118.83	111.90
2	D	1	DC	O4'-C4'-C3'	-12.78	98.33	106.00
2	D	1	DC	C6-N1-C2	-12.73	115.21	120.30
2	P	6	DC	O4'-C4'-C3'	-12.61	98.43	106.00
1	T	8	DG	O4'-C4'-C3'	-12.25	98.65	106.00
2	P	8	DT	N1-C2-N3	11.99	121.79	114.60
2	P	6	DC	O4'-C1'-N1	11.76	116.23	108.00
2	P	8	DT	O4'-C4'-C3'	-11.74	98.95	106.00
2	D	2	DG	N3-C2-N2	11.67	128.07	119.90
1	T	8	DG	N3-C2-N2	11.66	128.06	119.90
2	P	7	DC	OP2-P-O3'	11.38	130.24	105.20
2	D	5	DG	C2-N3-C4	11.28	117.54	111.90
1	C	8	DG	N3-C2-N2	11.27	127.79	119.90
1	T	10	DC	O4'-C4'-C3'	-11.17	99.30	106.00
2	D	3	DA	C5-N7-C8	10.96	109.38	103.90
2	P	7	DC	C3'-C2'-C1'	-10.77	89.57	102.50
2	P	2	DG	N3-C2-N2	10.63	127.34	119.90
2	D	8	DT	O4'-C1'-N1	10.48	115.34	108.00
2	D	8	DT	O5'-P-OP2	-10.29	96.44	105.70
1	C	10	DC	N3-C4-N4	10.00	125.00	118.00
2	P	5	DG	C4-C5-N7	-9.99	106.81	110.80
1	C	11	DG	N3-C2-N2	9.88	126.81	119.90
2	P	1	DC	C6-N1-C2	-9.86	116.36	120.30
1	T	10	DC	N3-C4-C5	-9.79	117.98	121.90
2	D	6	DC	N1-C2-O2	-9.79	113.03	118.90
1	T	8	DG	N1-C2-N2	-9.78	107.40	116.20
2	P	1	DC	O4'-C1'-N1	9.56	114.69	108.00
2	D	3	DA	C5-C6-N1	-9.47	112.96	117.70
2	D	2	DG	N1-C2-N2	-9.44	107.71	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	6	DC	N3-C4-C5	-9.41	118.14	121.90
1	C	4	DA	C5-N7-C8	9.39	108.60	103.90
1	C	10	DC	O4'-C1'-C2'	-9.39	98.39	105.90
2	P	7	DC	OP1-P-O3'	-9.33	84.68	105.20
2	P	2	DG	P-O3'-C3'	9.28	130.84	119.70
1	C	6	DG	N1-C2-N3	-9.18	118.39	123.90
2	D	2	DG	N7-C8-N9	9.18	117.69	113.10
1	C	7	DC	N1-C2-O2	9.09	124.35	118.90
2	P	6	DC	N3-C4-C5	-9.01	118.30	121.90
2	D	1	DC	O5'-P-OP1	8.93	121.41	110.70
1	T	7	DC	C5-C4-N4	-8.90	113.97	120.20
1	T	7	DC	N3-C4-N4	8.88	124.22	118.00
1	T	10	DC	N3-C4-N4	8.84	124.19	118.00
2	D	3	DA	O4'-C1'-C2'	-8.81	98.85	105.90
1	C	11	DG	C5-C6-O6	-8.81	123.32	128.60
2	P	5	DG	N7-C8-N9	-8.77	108.72	113.10
1	T	6	DG	N3-C2-N2	8.72	126.00	119.90
1	T	4	DA	O4'-C1'-N9	-8.64	101.95	108.00
1	T	11	DG	O5'-P-OP2	-8.57	97.99	105.70
2	P	5	DG	O4'-C4'-C3'	-8.57	100.86	106.00
2	P	1	DC	C4'-C3'-C2'	8.55	110.80	103.10
1	C	10	DC	C2-N3-C4	8.55	124.17	119.90
1	T	8	DG	O4'-C1'-C2'	-8.48	99.11	105.90
1	C	4	DA	C4-C5-N7	-8.45	106.47	110.70
2	D	7	DC	C6-N1-C2	-8.41	116.94	120.30
2	P	5	DG	C2-N3-C4	8.40	116.10	111.90
2	P	8	DT	O4'-C1'-N1	8.31	113.82	108.00
2	D	5	DG	C1'-O4'-C4'	-8.31	101.78	110.10
1	T	7	DC	N1-C2-N3	-8.10	113.53	119.20
2	D	6	DC	O5'-P-OP1	-8.10	98.41	105.70
1	T	5	DG	N3-C2-N2	8.04	125.53	119.90
2	P	2	DG	C5-N7-C8	-8.03	100.28	104.30
2	D	6	DC	O4'-C1'-N1	8.02	113.61	108.00
1	T	11	DG	N1-C2-N3	-7.96	119.12	123.90
2	P	8	DT	C4'-C3'-C2'	7.93	110.24	103.10
1	C	9	DT	O5'-P-OP2	-7.88	98.60	105.70
2	D	8	DT	O4'-C4'-C3'	-7.88	101.27	106.00
1	T	6	DG	N1-C6-O6	7.83	124.59	119.90
1	C	9	DT	OP1-P-OP2	7.78	131.26	119.60
2	P	2	DG	N1-C2-N2	-7.78	109.20	116.20
2	D	4	DC	P-O3'-C3'	7.77	129.03	119.70
1	T	11	DG	N3-C2-N2	7.74	125.32	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	10	DC	N3-C4-C5	-7.72	118.81	121.90
2	D	4	DC	N1-C2-O2	7.71	123.53	118.90
2	D	4	DC	C6-N1-C2	-7.71	117.22	120.30
1	C	4	DA	O4'-C1'-N9	-7.71	102.61	108.00
1	T	10	DC	P-O5'-C5'	7.67	133.17	120.90
1	C	4	DA	C5-C6-N1	-7.66	113.87	117.70
2	D	7	DC	O4'-C4'-C3'	-7.65	101.41	106.00
2	P	5	DG	C4'-C3'-C2'	7.63	109.97	103.10
1	C	4	DA	N7-C8-N9	-7.58	110.01	113.80
2	D	3	DA	C4-C5-C6	7.56	120.78	117.00
2	D	3	DA	O4'-C4'-C3'	-7.45	101.52	104.50
2	D	6	DC	C2-N1-C1'	-7.41	110.64	118.80
2	D	4	DC	N3-C2-O2	-7.38	116.73	121.90
1	T	7	DC	C5-C6-N1	7.36	124.68	121.00
1	T	9	DT	O4'-C1'-C2'	-7.30	100.06	105.90
2	D	5	DG	N1-C6-O6	-7.27	115.54	119.90
1	C	10	DC	O4'-C4'-C3'	-7.23	101.61	104.50
1	C	8	DG	P-O5'-C5'	-7.20	109.38	120.90
1	T	11	DG	C2-N3-C4	7.19	115.49	111.90
2	D	1	DC	O5'-P-OP2	7.18	119.32	110.70
2	P	1	DC	P-O5'-C5'	7.16	132.36	120.90
1	T	11	DG	O4'-C4'-C3'	-7.16	101.64	104.50
2	D	3	DA	C8-N9-C4	-7.12	102.95	105.80
2	P	7	DC	C6-N1-C1'	7.04	129.25	120.80
2	D	1	DC	N1-C1'-C2'	-7.03	99.25	112.60
1	C	5	DG	N1-C2-N3	-7.00	119.70	123.90
1	C	6	DG	N1-C6-O6	6.98	124.09	119.90
1	T	6	DG	N1-C2-N3	-6.92	119.75	123.90
1	C	11	DG	O4'-C4'-C3'	-6.91	101.73	104.50
2	P	7	DC	N3-C4-C5	-6.91	119.14	121.90
1	C	5	DG	C5-C6-O6	-6.91	124.45	128.60
2	P	4	DC	N3-C4-N4	6.90	122.83	118.00
2	D	8	DT	N3-C4-C5	6.89	119.33	115.20
1	C	7	DC	N3-C4-C5	-6.88	119.15	121.90
1	C	5	DG	N1-C6-O6	6.85	124.01	119.90
2	D	8	DT	C5-C4-O4	-6.82	120.12	124.90
2	P	3	DA	C4-C5-N7	-6.82	107.29	110.70
1	C	9	DT	C2-N3-C4	-6.82	123.11	127.20
2	D	7	DC	OP1-P-O3'	6.81	120.19	105.20
2	D	6	DC	C6-N1-C1'	6.80	128.96	120.80
2	P	2	DG	O4'-C1'-N9	-6.74	103.28	108.00
1	C	7	DC	C2-N3-C4	6.73	123.27	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	1	DC	N3-C2-O2	-6.73	117.19	121.90
2	P	1	DC	O5'-C5'-C4'	6.73	127.81	111.00
2	P	4	DC	C5-C4-N4	-6.72	115.50	120.20
2	D	4	DC	C3'-C2'-C1'	6.70	110.54	102.50
2	D	3	DA	C4-C5-N7	-6.68	107.36	110.70
2	D	1	DC	C4'-C3'-C2'	6.66	109.09	103.10
2	P	5	DG	C5-N7-C8	6.64	107.62	104.30
2	P	4	DC	O4'-C1'-C2'	-6.60	100.62	105.90
1	C	6	DG	C5-C6-O6	-6.54	124.68	128.60
1	T	6	DG	C2-N3-C4	6.51	115.16	111.90
2	P	4	DC	C2-N3-C4	-6.51	116.64	119.90
2	P	2	DG	C5-C6-O6	-6.48	124.71	128.60
2	P	4	DC	C4-C5-C6	6.48	120.64	117.40
2	D	5	DG	OP1-P-O3'	6.47	119.44	105.20
1	C	4	DA	C5-C6-N6	6.44	128.85	123.70
1	C	6	DG	P-O5'-C5'	-6.41	110.64	120.90
2	P	6	DC	O5'-P-OP1	-6.41	99.93	105.70
2	P	8	DT	N3-C2-O2	-6.40	118.46	122.30
1	C	10	DC	O3'-P-O5'	6.37	116.11	104.00
2	P	5	DG	N9-C4-C5	6.33	107.93	105.40
2	D	2	DG	N3-C4-N9	6.31	129.79	126.00
1	C	4	DA	N9-C4-C5	6.26	108.31	105.80
2	D	5	DG	N1-C2-N3	-6.26	120.14	123.90
2	D	5	DG	O5'-P-OP2	-6.24	100.08	105.70
1	C	8	DG	N1-C2-N2	-6.20	110.62	116.20
2	D	2	DG	C8-N9-C4	-6.19	103.92	106.40
1	T	4	DA	P-O5'-C5'	-6.18	111.01	120.90
1	T	5	DG	C1'-O4'-C4'	-6.16	103.94	110.10
2	P	2	DG	C1'-O4'-C4'	6.14	116.24	110.10
3	B	253	ARG	NE-CZ-NH2	6.13	123.37	120.30
1	T	4	DA	C5-C6-N1	-6.13	114.64	117.70
2	P	5	DG	C1'-O4'-C4'	-6.13	103.97	110.10
2	D	4	DC	O3'-P-O5'	6.13	115.64	104.00
2	D	5	DG	N3-C4-C5	-6.09	125.56	128.60
1	C	8	DG	P-O3'-C3'	6.08	126.99	119.70
1	T	9	DT	N3-C2-O2	-6.05	118.67	122.30
3	B	137	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	T	8	DG	C4'-C3'-C2'	6.03	108.53	103.10
3	B	326	ARG	NE-CZ-NH2	6.01	123.31	120.30
2	P	3	DA	C5-N7-C8	5.96	106.88	103.90
2	D	8	DT	C2-N3-C4	-5.96	123.63	127.20
2	D	1	DC	P-O3'-C3'	-5.95	112.56	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	299	ARG	NE-CZ-NH2	5.92	123.26	120.30
2	P	8	DT	C2-N3-C4	-5.87	123.68	127.20
2	P	6	DC	C6-N1-C1'	5.84	127.81	120.80
2	P	2	DG	N7-C8-N9	5.83	116.02	113.10
1	C	6	DG	C3'-C2'-C1'	-5.83	95.50	102.50
1	C	10	DC	C5-C4-N4	-5.79	116.15	120.20
1	T	10	DC	O4'-C1'-N1	-5.78	103.96	108.00
1	C	11	DG	N1-C6-O6	5.77	123.36	119.90
1	T	7	DC	P-O3'-C3'	5.76	126.62	119.70
2	D	3	DA	P-O3'-C3'	5.76	126.61	119.70
3	B	328	ARG	NE-CZ-NH2	5.76	123.18	120.30
1	T	4	DA	N9-C4-C5	5.75	108.10	105.80
1	T	10	DC	O4'-C1'-C2'	-5.74	101.31	105.90
1	T	6	DG	C5-C6-O6	-5.73	125.16	128.60
1	C	5	DG	C2-N3-C4	5.70	114.75	111.90
2	D	8	DT	N3-C2-O2	5.69	125.72	122.30
1	T	10	DC	C2-N3-C4	5.68	122.74	119.90
2	P	7	DC	C2-N1-C1'	-5.67	112.56	118.80
2	D	2	DG	N9-C1'-C2'	5.67	123.37	112.60
2	P	4	DC	P-O3'-C3'	5.61	126.43	119.70
1	T	9	DT	N3-C4-C5	5.59	118.56	115.20
1	C	8	DG	C4'-C3'-C2'	5.59	108.13	103.10
2	D	5	DG	P-O3'-C3'	5.58	126.40	119.70
1	C	4	DA	O5'-P-OP1	5.57	117.38	110.70
2	D	4	DC	C1'-O4'-C4'	-5.52	104.58	110.10
3	B	254	ARG	NE-CZ-NH2	5.51	123.06	120.30
2	D	1	DC	N3-C2-O2	-5.51	118.04	121.90
1	T	9	DT	C5-C4-O4	-5.50	121.05	124.90
1	T	8	DG	C3'-C2'-C1'	-5.49	95.91	102.50
1	T	5	DG	P-O3'-C3'	-5.49	113.12	119.70
2	P	7	DC	C6-N1-C2	-5.47	118.11	120.30
2	D	1	DC	C2'-C3'-O3'	-5.45	94.62	112.60
2	D	5	DG	C6-C5-N7	5.45	133.67	130.40
1	C	10	DC	C1'-O4'-C4'	-5.36	104.74	110.10
1	C	7	DC	P-O5'-C5'	-5.36	112.32	120.90
1	C	4	DA	O4'-C4'-C3'	-5.32	102.37	104.50
2	P	3	DA	C5-C6-N1	-5.32	115.04	117.70
1	T	5	DG	C8-N9-C4	-5.30	104.28	106.40
2	D	2	DG	N3-C4-C5	-5.30	125.95	128.60
2	D	6	DC	O4'-C4'-C3'	-5.28	102.39	104.50
2	D	1	DC	C5-C6-N1	5.27	123.64	121.00
2	D	4	DC	OP1-P-OP2	5.26	127.48	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	7	DC	N1-C2-O2	5.25	122.05	118.90
2	D	1	DC	O5'-C5'-C4'	5.25	124.11	111.00
1	C	6	DG	N3-C2-N2	5.22	123.56	119.90
1	C	11	DG	N1-C2-N2	-5.22	111.50	116.20
2	D	5	DG	N9-C4-C5	5.22	107.49	105.40
1	C	11	DG	C2-N3-C4	5.21	114.51	111.90
2	P	6	DC	C2-N1-C1'	-5.20	113.08	118.80
2	D	4	DC	P-O5'-C5'	-5.19	112.60	120.90
2	D	5	DG	N7-C8-N9	-5.18	110.51	113.10
2	P	3	DA	C6-N1-C2	5.18	121.71	118.60
2	P	8	DT	N3-C4-O4	5.16	123.00	119.90
1	C	5	DG	O4'-C1'-N9	-5.16	104.39	108.00
2	P	5	DG	C5'-C4'-O4'	-5.15	99.52	109.30
1	T	8	DG	C4-C5-C6	5.13	121.88	118.80
2	D	4	DC	N3-C4-N4	-5.13	114.41	118.00
1	C	8	DG	C4-C5-N7	-5.12	108.75	110.80
1	T	6	DG	C5-N7-C8	5.10	106.85	104.30
1	C	7	DC	O4'-C4'-C3'	-5.10	102.46	104.50
1	C	11	DG	O4'-C1'-N9	5.09	111.56	108.00
2	P	5	DG	N3-C4-C5	-5.08	126.06	128.60
2	D	8	DT	C4'-C3'-C2'	5.08	107.67	103.10
1	T	9	DT	C2-N3-C4	-5.07	124.16	127.20
2	D	5	DG	C4-C5-N7	-5.06	108.78	110.80
1	T	11	DG	O4'-C1'-N9	-5.05	104.46	108.00
1	T	8	DG	C1'-O4'-C4'	5.03	115.13	110.10
2	D	1	DC	N1-C2-O2	5.03	121.92	118.90
1	C	4	DA	P-O5'-C5'	-5.02	112.87	120.90
1	T	7	DC	P-O5'-C5'	-5.02	112.87	120.90
3	B	137	ARG	NE-CZ-NH2	-5.01	117.79	120.30
2	P	3	DA	O4'-C1'-C2'	-5.01	101.89	105.90

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	4	DA	Sidechain
1	C	6	DG	Sidechain
1	C	7	DC	Sidechain
1	C	8	DG	Sidechain
1	C	9	DT	Sidechain
2	D	1	DC	Sidechain
2	D	2	DG	Sidechain

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Mol	Chain	Res	Type	Group
2	D	3	DA	Sidechain
2	D	4	DC	Sidechain
2	D	5	DG	Sidechain
2	D	6	DC	Sidechain
2	D	7	DC	Sidechain
2	D	8	DT	Sidechain
2	P	1	DC	Sidechain
2	P	2	DG	Sidechain
2	P	3	DA	Sidechain
2	P	5	DG	Sidechain
2	P	6	DC	Sidechain
2	P	7	DC	Sidechain
1	T	11	DG	Sidechain
1	T	5	DG	Sidechain
1	T	6	DG	Sidechain
1	T	8	DG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	167	0	90	3	0
1	T	167	0	90	0	0
2	D	161	0	90	4	0
2	P	161	0	90	4	0
3	A	2598	0	2604	87	0
3	B	2598	0	2604	95	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	9	0	2	0	0
5	B	9	0	2	0	0
6	A	41	0	0	2	0
6	B	61	0	0	7	0
6	C	5	0	0	1	0
6	D	6	0	0	0	0
6	P	3	0	0	0	0
6	T	6	0	0	0	0
All	All	5994	0	5572	187	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 16.

All (187) 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:D:1:DC:C5'	2:D:1:DC:O5'	1.64	1.44
2:P:8:DT:O4'	2:P:8:DT:C4'	1.63	1.38
3:B:248:ASN:O	3:B:249:GLU:HG2	1.41	1.18
3:A:183:ARG:HD3	3:A:274:GLY:O	1.64	0.98
3:B:180:SER:HA	3:B:183:ARG:HG2	1.54	0.90
3:B:207:GLN:HG2	3:B:210:LEU:HG	1.52	0.89
3:B:248:ASN:O	3:B:249:GLU:CG	2.25	0.85
3:A:154:GLU:O	3:A:158:MET:HG3	1.82	0.78
3:B:169:LEU:HD23	3:B:173:TYR:HE1	1.48	0.78
3:B:166:VAL:CG1	3:B:173:TYR:HB3	2.15	0.77
3:B:166:VAL:HG13	3:B:173:TYR:HB3	1.65	0.76
3:A:155:MET:HA	3:A:158:MET:CE	2.16	0.75
3:A:155:MET:HA	3:A:158:MET:HE3	1.68	0.75
3:B:293:ILE:HG12	3:B:298:ILE:HD13	1.69	0.73
3:B:183:ARG:HH12	3:B:275:SER:HA	1.54	0.72
3:A:60:LYS:HA	3:A:65:VAL:HG22	1.72	0.70
3:B:121:THR:HG22	3:B:123:GLU:H	1.57	0.70
3:B:169:LEU:HD23	3:B:173:TYR:CE1	2.27	0.69
3:A:303:VAL:HG12	3:A:304:THR:H	1.57	0.69
3:A:133:ASN:O	3:A:137:ARG:HG2	1.93	0.68
3:A:169:LEU:HD21	3:A:213:ARG:HB3	1.76	0.67
3:B:285:HIS:CE1	3:B:325:TRP:HE1	2.13	0.67
3:A:12:ASN:HD21	3:A:53:ILE:H	1.43	0.67
3:B:299:ARG:HH11	3:B:299:ARG:HG2	1.60	0.66
3:B:298:ILE:HG13	3:B:298:ILE:O	1.94	0.66
3:B:91:ASP:HB3	3:B:94:SER:HB2	1.76	0.66
3:B:12:ASN:HD21	3:B:53:ILE:H	1.44	0.66
3:B:266:TYR:O	3:B:269:VAL:HG23	1.95	0.65
3:A:207:GLN:HG2	3:A:210:LEU:HG	1.78	0.65
3:A:299:ARG:HG2	3:A:299:ARG:HH11	1.64	0.63
3:B:201:THR:HG22	3:B:203:GLU:H	1.66	0.61
3:A:155:MET:SD	3:A:158:MET:HE1	2.41	0.61
3:B:200:PHE:HB3	6:B:1007:HOH:O	2.01	0.60
3:A:174:ILE:HB	3:A:196:THR:CG2	2.32	0.60
2:P:8:DT:C5	3:A:276:ASP:HB3	2.36	0.59
3:A:121:THR:HG22	3:A:123:GLU:H	1.67	0.59
3:A:328:ARG:HE	3:A:332:ASP:HB3	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:163:LEU:HD23	3:A:175:ALA:HB3	1.84	0.59
3:B:208:PRO:HB3	3:B:232:GLU:HG2	1.85	0.58
3:A:303:VAL:HG12	3:A:304:THR:N	2.18	0.58
3:A:200:PHE:HB2	3:A:210:LEU:HD12	1.85	0.57
3:B:164:ASN:HA	3:B:167:LYS:HE2	1.87	0.57
3:A:258:ARG:NH2	3:A:295:GLU:OE2	2.37	0.57
3:B:36:TYR:O	3:B:40:ARG:HG2	2.05	0.57
3:B:174:ILE:HB	3:B:196:THR:CG2	2.34	0.57
3:A:293:ILE:HG12	3:A:298:ILE:HD13	1.87	0.57
3:A:164:ASN:HA	3:A:167:LYS:HE2	1.87	0.56
3:A:180:SER:OG	3:A:188:SER:HB3	2.05	0.56
3:B:92:ASP:HB3	6:B:1016:HOH:O	2.05	0.56
3:A:201:THR:HG22	3:A:203:GLU:H	1.70	0.56
3:A:158:MET:O	3:A:162:VAL:HG23	2.05	0.56
3:A:99:PHE:O	3:A:102:ARG:HB2	2.05	0.56
3:A:266:TYR:CE2	3:A:315:SER:HA	2.41	0.56
3:B:183:ARG:NH1	3:B:275:SER:HA	2.20	0.56
3:A:208:PRO:HB3	3:A:232:GLU:HG2	1.87	0.56
3:B:28:ASN:HD22	3:B:98:ASN:HD21	1.54	0.56
3:B:28:ASN:HD22	3:B:98:ASN:ND2	2.04	0.56
3:A:197:HIS:CD2	3:A:199:ASN:H	2.25	0.55
3:B:279:ASN:O	3:B:283:ARG:HG3	2.07	0.55
3:B:265:TYR:O	3:B:269:VAL:HG22	2.06	0.54
3:A:163:LEU:HD21	3:A:175:ALA:O	2.07	0.54
3:A:166:VAL:CG1	3:A:173:TYR:HB3	2.38	0.54
3:B:330:PRO:HA	3:B:333:ARG:HD2	1.90	0.53
3:A:162:VAL:O	3:A:166:VAL:HG23	2.08	0.53
3:B:134:HIS:HD2	6:B:1004:HOH:O	1.91	0.53
3:A:155:MET:SD	3:A:158:MET:CE	2.97	0.53
3:B:266:TYR:HA	3:B:269:VAL:CG2	2.38	0.53
3:B:174:ILE:HB	3:B:196:THR:HG22	1.90	0.53
3:A:315:SER:HB2	3:A:317:GLN:OE1	2.08	0.53
3:A:222:ARG:HG3	3:A:222:ARG:HH11	1.73	0.53
3:B:299:ARG:HG2	3:B:299:ARG:NH1	2.22	0.52
3:A:183:ARG:O	3:A:331:LYS:HA	2.09	0.52
3:A:299:ARG:HG2	3:A:299:ARG:NH1	2.25	0.52
3:A:223:PHE:O	3:A:239:CYS:HA	2.10	0.51
3:A:197:HIS:HD2	3:A:199:ASN:HB2	1.74	0.51
3:A:285:HIS:CD2	3:A:325:TRP:HE1	2.28	0.51
3:A:15:ILE:O	3:A:19:LEU:HG	2.10	0.51
3:B:243:SER:HB2	3:B:249:GLU:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:300:PRO:HD3	3:A:311:LEU:CD2	2.41	0.51
3:A:297:THR:HB	3:A:310:PRO:HB3	1.92	0.50
3:A:155:MET:HA	3:A:158:MET:HE2	1.90	0.50
3:A:174:ILE:HB	3:A:196:THR:HG22	1.93	0.50
3:B:28:ASN:HA	3:B:108:PRO:HG3	1.94	0.50
3:B:240:GLN:HB3	6:B:1059:HOH:O	2.10	0.50
3:B:317:GLN:HG3	3:B:327:TYR:CD2	2.47	0.50
3:A:134:HIS:CE1	3:A:138:ILE:HD11	2.47	0.50
3:B:42:ALA:HB1	3:B:65:VAL:HG22	1.94	0.49
3:A:86:GLU:HG3	6:A:1006:HOH:O	2.11	0.49
3:B:275:SER:HB3	3:B:278:PHE:H	1.77	0.49
3:B:59:ALA:O	3:B:62:LEU:HB2	2.12	0.49
6:C:57:HOH:O	3:B:133:ASN:HB3	2.12	0.49
3:B:270:LEU:HD21	3:B:282:MET:CE	2.43	0.49
3:B:154:GLU:HA	3:B:157:GLN:HE21	1.78	0.49
3:B:285:HIS:O	3:B:288:GLU:HB3	2.13	0.48
3:A:36:TYR:O	3:A:40:ARG:HG2	2.13	0.48
3:A:200:PHE:CD1	3:A:259:LEU:HG	2.49	0.48
3:B:247:GLU:O	3:B:248:ASN:C	2.51	0.48
3:B:162:VAL:O	3:B:166:VAL:HG23	2.12	0.48
3:A:200:PHE:HB2	3:A:210:LEU:CD1	2.42	0.48
3:B:195:LEU:HD23	3:B:259:LEU:HD13	1.94	0.48
3:A:197:HIS:HD2	3:A:199:ASN:H	1.60	0.48
3:A:294:ASN:HB3	3:A:297:THR:H	1.79	0.48
3:A:152:ARG:HD2	3:A:185:ALA:O	2.13	0.48
3:B:236:MET:HG3	3:B:254:ARG:NH2	2.28	0.48
3:B:206:LYS:O	3:B:207:GLN:HB2	2.13	0.48
3:A:321:ASP:HB2	6:A:1016:HOH:O	2.13	0.48
3:B:197:HIS:HD2	3:B:199:ASN:HB2	1.79	0.48
1:C:4:DA:H61	2:D:8:DT:H3	1.61	0.47
3:A:318:ASP:O	3:A:322:TYR:CD1	2.67	0.47
3:B:200:PHE:HB2	3:B:210:LEU:HD12	1.97	0.47
3:A:270:LEU:HD21	3:A:282:MET:HE2	1.96	0.46
3:A:328:ARG:NE	3:A:332:ASP:HB3	2.30	0.46
3:A:285:HIS:CE1	3:A:325:TRP:HE1	2.34	0.46
3:B:222:ARG:HH11	3:B:222:ARG:HG3	1.80	0.46
3:A:121:THR:HG22	3:A:122:LEU:N	2.31	0.46
3:A:285:HIS:O	3:A:288:GLU:HB3	2.15	0.46
2:D:6:DC:C4	2:D:7:DC:N4	2.83	0.46
3:A:279:ASN:O	3:A:283:ARG:HG3	2.15	0.46
3:A:75:GLU:OE2	3:A:83:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:194:LEU:HD11	3:A:260:ILE:HG13	1.97	0.46
3:B:318:ASP:O	3:B:322:TYR:CD1	2.69	0.46
3:B:12:ASN:ND2	3:B:53:ILE:H	2.11	0.46
3:B:143:PHE:O	3:B:147:GLU:HG2	2.16	0.46
3:A:302:GLY:N	3:A:306:VAL:O	2.46	0.46
3:B:275:SER:HB2	3:B:333:ARG:O	2.16	0.45
3:A:291:PHE:HA	3:A:300:PRO:HA	1.99	0.45
3:A:201:THR:HG21	3:A:203:GLU:OE2	2.16	0.45
3:B:258:ARG:NH2	3:B:295:GLU:OE1	2.49	0.45
3:B:129:GLU:O	3:B:137:ARG:HD3	2.16	0.45
3:A:169:LEU:HD23	3:A:173:TYR:HE1	1.81	0.45
3:B:201:THR:HG23	3:B:263:ASP:OD2	2.16	0.45
1:C:9:DT:H5'	3:B:229:SER:HB2	1.98	0.45
3:A:170:ASP:HB3	3:A:173:TYR:CD1	2.52	0.44
3:B:201:THR:HG22	3:B:202:SER:N	2.33	0.44
3:A:265:TYR:O	3:A:269:VAL:HG22	2.17	0.44
2:P:8:DT:C6	3:A:276:ASP:HB3	2.53	0.44
3:A:273:THR:HG22	3:A:274:GLY:N	2.32	0.44
3:B:180:SER:HA	3:B:183:ARG:CG	2.37	0.44
3:B:73:ILE:HG22	3:B:77:LEU:HD22	1.99	0.44
2:P:5:DG:H2''	2:P:6:DC:O5'	2.17	0.44
3:A:132:LEU:O	3:A:137:ARG:NH1	2.50	0.44
3:B:217:GLN:O	3:B:221:VAL:HG23	2.16	0.44
3:A:236:MET:HG3	3:A:254:ARG:NH2	2.33	0.44
3:B:326:ARG:HG2	6:B:1017:HOH:O	2.17	0.44
3:B:285:HIS:CG	3:B:325:TRP:HE1	2.36	0.43
3:B:160:ASP:O	3:B:164:ASN:HB2	2.17	0.43
3:B:164:ASN:O	3:B:168:LYS:HG3	2.18	0.43
3:A:298:ILE:O	3:A:298:ILE:HG13	2.18	0.43
3:A:177:VAL:HG22	3:A:181:PHE:CD2	2.53	0.43
3:A:222:ARG:NH1	3:A:222:ARG:HG3	2.34	0.43
3:B:260:ILE:HD13	6:B:1030:HOH:O	2.19	0.43
3:B:193:VAL:HG13	3:B:257:ILE:HG12	2.00	0.43
3:A:86:GLU:OE1	3:A:89:ARG:NH1	2.52	0.43
3:B:99:PHE:O	3:B:102:ARG:HB2	2.19	0.43
3:B:275:SER:O	3:B:276:ASP:C	2.57	0.42
3:B:169:LEU:HD21	3:B:213:ARG:HB3	2.01	0.42
3:B:180:SER:CA	3:B:183:ARG:HG2	2.39	0.42
3:A:330:PRO:HG3	3:A:333:ARG:NH1	2.35	0.42
3:B:191:MET:HG2	3:B:193:VAL:HG12	2.02	0.42
3:B:12:ASN:HD21	3:B:53:ILE:N	2.13	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:270:LEU:HD21	3:A:282:MET:CE	2.50	0.42
1:C:6:DG:H4'	3:B:295:GLU:OE1	2.20	0.42
3:B:300:PRO:HD3	3:B:311:LEU:CD2	2.50	0.42
3:A:143:PHE:O	3:A:147:GLU:HG2	2.19	0.42
3:A:299:ARG:HG3	3:A:307:ALA:HB1	2.01	0.42
3:B:199:ASN:HB2	3:B:210:LEU:HD11	2.02	0.41
3:B:170:ASP:HB3	3:B:173:TYR:CD1	2.55	0.41
3:B:248:ASN:O	3:B:249:GLU:CB	2.68	0.41
3:B:211:LEU:HD23	3:B:232:GLU:O	2.20	0.41
3:A:285:HIS:O	3:A:288:GLU:N	2.54	0.41
3:B:150:ILE:HA	3:B:151:PRO:HD3	1.93	0.41
3:B:177:VAL:HG22	3:B:181:PHE:CD2	2.56	0.41
3:B:326:ARG:HD3	6:B:1031:HOH:O	2.20	0.41
3:B:236:MET:HG3	3:B:254:ARG:HH22	1.85	0.41
3:B:190:ASP:HB2	3:B:254:ARG:O	2.20	0.41
3:B:121:THR:HG22	3:B:122:LEU:N	2.36	0.41
3:B:266:TYR:HA	3:B:269:VAL:HG23	2.03	0.41
3:A:197:HIS:CD2	3:A:199:ASN:HB2	2.54	0.40
3:B:297:THR:HB	3:B:310:PRO:HB3	2.02	0.40
3:B:114:LEU:HA	3:B:114:LEU:HD23	1.92	0.40
2:D:8:DT:C5	3:B:276:ASP:HB3	2.56	0.40
3:A:12:ASN:ND2	3:A:53:ILE:H	2.13	0.40
3:B:201:THR:CG2	3:B:202:SER:N	2.85	0.40
3:A:329:GLU:O	3:A:332:ASP:HB2	2.21	0.40
3:A:71:GLU:O	3:A:74:ASP:HB2	2.22	0.40
3:B:49:TYR:CE2	3:B:51:HIS:HB2	2.56	0.40
3:A:221:VAL:HG12	3:A:221:VAL:O	2.20	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	323/335 (96%)	298 (92%)	21 (6%)	4 (1%)	16	33
3	B	323/335 (96%)	289 (90%)	29 (9%)	5 (2%)	13	26
All	All	646/670 (96%)	587 (91%)	50 (8%)	9 (1%)	14	28

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	303	VAL
3	B	248	ASN
3	B	274	GLY
3	A	274	GLY
3	A	275	SER
3	B	249	GLU
3	B	275	SER
3	B	207	GLN
3	A	330	PRO

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	283/296 (96%)	262 (93%)	21 (7%)	17	34
3	B	283/296 (96%)	262 (93%)	21 (7%)	17	34
All	All	566/592 (96%)	524 (93%)	42 (7%)	17	34

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	62	LEU
3	A	65	VAL
3	A	67	THR
3	A	77	LEU
3	A	92	ASP
3	A	93	THR
3	A	95	SER

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Mol	Chain	Res	Type
3	A	130	ASP
3	A	137	ARG
3	A	177	VAL
3	A	193	VAL
3	A	207	GLN
3	A	254	ARG
3	A	269	VAL
3	A	272	PHE
3	A	285	HIS
3	A	314	ASP
3	A	324	GLN
3	A	326	ARG
3	A	330	PRO
3	A	332	ASP
3	B	44	SER
3	B	62	LEU
3	B	67	THR
3	B	77	LEU
3	B	93	THR
3	B	109	SER
3	B	125	LEU
3	B	130	ASP
3	B	137	ARG
3	B	176	THR
3	B	177	VAL
3	B	193	VAL
3	B	207	GLN
3	B	254	ARG
3	B	258	ARG
3	B	269	VAL
3	B	272	PHE
3	B	292	THR
3	B	314	ASP
3	B	324	GLN
3	B	330	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	128	ASN
3	A	157	GLN

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Mol	Chain	Res	Type
3	A	159	GLN
3	A	197	HIS
3	A	199	ASN
3	A	207	GLN
3	A	264	GLN
3	B	12	ASN
3	B	98	ASN
3	B	128	ASN
3	B	134	HIS
3	B	157	GLN
3	B	197	HIS
3	B	199	ASN
3	B	207	GLN
3	B	264	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	MDN	A	338	4	6,8,8	2.78	4 (66%)	12,13,13	2.80	5 (41%)
5	MDN	B	338	4	6,8,8	2.90	4 (66%)	12,13,13	2.73	7 (58%)

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	MDN	A	338	4	-	0/6/6/6	0/0/0/0
5	MDN	B	338	4	-	0/6/6/6	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	338	MDN	P5-O7	-4.00	1.45	1.54
5	A	338	MDN	P5-O7	-3.82	1.45	1.54
5	A	338	MDN	P5-O8	-2.83	1.48	1.54
5	B	338	MDN	P5-O8	-2.38	1.49	1.54
5	A	338	MDN	P1-O2	2.73	1.61	1.54
5	B	338	MDN	P1-O2	3.33	1.63	1.54
5	B	338	MDN	P5-O6	3.49	1.58	1.50
5	A	338	MDN	P5-O6	3.92	1.59	1.50

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	338	MDN	O3-P1-C4	-6.35	90.99	106.40
5	A	338	MDN	O3-P1-C4	-6.21	91.34	106.40
5	A	338	MDN	O2-P1-O3	-3.61	97.56	108.13
5	B	338	MDN	O8-P5-C4	-3.12	98.83	106.40
5	B	338	MDN	O2-P1-O3	-2.84	99.81	108.13
5	A	338	MDN	O8-P5-C4	-2.66	99.94	106.40
5	B	338	MDN	O8-P5-O7	2.04	114.11	108.13
5	B	338	MDN	O1-P1-C4	2.24	116.24	111.13
5	B	338	MDN	O2-P1-C4	2.36	112.13	106.40
5	A	338	MDN	O1-P1-C4	2.79	117.50	111.13
5	B	338	MDN	O2-P1-O1	3.58	121.57	112.40
5	A	338	MDN	O2-P1-O1	4.02	122.69	112.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.