



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:23 AM GMT

PDB ID : 244D
Title : THE HIGH-RESOLUTION CRYSTAL STRUCTURE OF A PARALLEL-STRANDED GUANINE TETRAPLEX
Authors : Laughlan, G.; Murchie, A.I.H.; Norman, D.G.; Moore, M.H.; Moody, P.C.E.; Lilley, D.M.J.; Luisi, B.
Deposited on : 1995-10-19
Resolution : 1.20 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

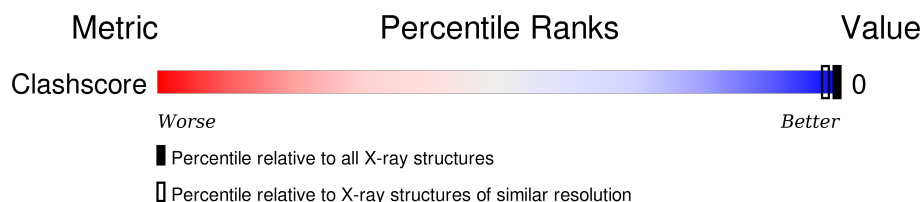
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.20 Å.

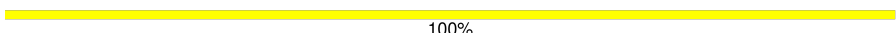
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1607 (1.26-1.14)

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	A	6	 100%
1	B	6	 17% 83%
1	C	6	 17% 83%
1	D	6	 100%
1	E	6	 100%
1	F	6	 100%
1	G	6	 100%
1	H	6	 100%
1	I	6	 33% 67%

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Mol	Chain	Length	Quality of chain
1	J	6	 83%17%
1	K	6	 17%83%
1	L	6	 100%
1	M	6	 100%
1	N	6	 17%83%
1	O	6	 100%
1	P	6	 17%67%17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2453 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(*TP*GP*GP*GP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	B	6	Total	C	N	O	P	0	0	0
			108	50	22	31	5			
1	C	6	Total	C	N	O	P	0	0	1
			109	50	22	32	5			
1	D	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	E	6	Total	C	N	O	P	0	0	0
			108	50	22	31	5			
1	F	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	G	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	H	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	I	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	J	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	K	6	Total	C	N	O	P	0	0	0
			108	50	22	31	5			
1	L	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	M	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	N	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			
1	O	6	Total	C	N	O	P	0	0	0
			108	50	22	31	5			
1	P	6	Total	C	N	O	P	0	0	0
			125	60	24	36	5			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	3	Total 3	Na 3	0	0
2	B	1	Total 1	Na 1	0	0
2	I	3	Total 3	Na 3	0	0
2	A	3	Total 3	Na 3	0	0
2	L	1	Total 1	Na 1	0	0
2	M	3	Total 3	Na 3	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total 1	Ca 1	0	0
3	D	1	Total 1	Ca 1	0	0
3	B	1	Total 1	Ca 1	0	0
3	C	1	Total 1	Ca 1	0	0
3	A	2	Total 2	Ca 2	0	0
3	N	1	Total 1	Ca 1	0	0
3	L	1	Total 1	Ca 1	0	0
3	M	1	Total 1	Ca 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total 37	O 37	0	0
4	B	32	Total 32	O 32	0	0
4	C	26	Total 26	O 26	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	49	Total 49	O 49	0	0
4	E	28	Total 28	O 28	0	0
4	F	28	Total 28	O 28	0	0
4	G	31	Total 31	O 31	0	0
4	H	28	Total 28	O 28	0	0
4	I	36	Total 36	O 36	0	0
4	J	24	Total 24	O 24	0	0
4	K	19	Total 19	O 19	0	0
4	L	37	Total 37	O 37	0	0
4	M	41	Total 41	O 41	0	0
4	N	35	Total 35	O 35	0	0
4	O	28	Total 28	O 28	0	0
4	P	35	Total 35	O 35	0	0

3 Residue-property plots

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: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain A:  100%

T1 G2 G3 G4 G5 T6

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain B:  17% 83%

T11 G12 G13 G14 G15 T16

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain C:  17% 83%

T21 G22 G23 G24 G25 T26

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain D:  100%

T31 G32 G33 G34 G35 T36

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain E:  100%


T41 G42 G43 G44 G45 T46

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain F:  100%


T51
G52
G53
G54
G55
T56

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain G:  100%

T61
G62
G63
G64
G65
T66

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain H:  100%


T71
G72
G73
G74
G75
T76

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain I:  33% 67%

T81
G84
G85
T86

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain J:  83% 17%

T91
G92
G93
G94
G95
T96

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain K:  17% 83%


T101
G102
G103
G104
G105
T106

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain L:  100%

T111
G112
G113
G114
G115
T116

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain M:  100%

T121
G122
G123
G124
G125
T126

- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain N:  17% 83%

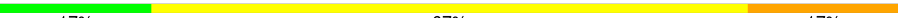
T131	G132	G133	G134	G135	T136
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- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain O:  100%

T141	G142	G143	G144	G145	T146
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- Molecule 1: DNA (5'-D(*TP*GP*GP*GP*GP*T)-3')

Chain P:  17% 67% 17%

T151	G152	G153	G154	G155	T156
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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	Depositor
Cell constants a, b, c, α , β , γ	28.76 Å 35.47 Å 56.77 Å 74.39° 77.64° 89.73°	Depositor
Resolution (Å)	8.00 – 1.20	Depositor
% Data completeness (in resolution range)	97.7 (8.00-1.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELX-93	Depositor
R, R_{free}	0.124 , 0.176	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2453	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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: NA, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	2.06	4/140 (2.9%)	2.69	14/216 (6.5%)
1	B	1.82	0/121	2.92	9/186 (4.8%)
1	C	2.06	3/122 (2.5%)	2.61	11/189 (5.8%)
1	D	2.03	6/140 (4.3%)	2.51	16/216 (7.4%)
1	E	1.91	2/121 (1.7%)	2.57	6/186 (3.2%)
1	F	2.21	7/140 (5.0%)	2.83	21/216 (9.7%)
1	G	2.15	4/140 (2.9%)	2.92	19/216 (8.8%)
1	H	1.95	2/140 (1.4%)	2.67	18/216 (8.3%)
1	I	2.19	4/140 (2.9%)	2.48	11/216 (5.1%)
1	J	1.84	2/140 (1.4%)	2.86	21/216 (9.7%)
1	K	2.02	3/121 (2.5%)	3.22	16/186 (8.6%)
1	L	2.26	5/140 (3.6%)	2.88	15/216 (6.9%)
1	M	2.02	6/140 (4.3%)	2.42	15/216 (6.9%)
1	N	2.19	3/140 (2.1%)	3.26	18/216 (8.3%)
1	O	2.19	5/121 (4.1%)	2.69	12/186 (6.5%)
1	P	1.93	2/140 (1.4%)	3.09	20/216 (9.3%)
All	All	2.06	58/2146 (2.7%)	2.80	242/3309 (7.3%)

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	81	DT	C5-C7	10.38	1.56	1.50
1	F	51	DT	C5-C7	8.78	1.55	1.50
1	M	122	DG	C2'-C1'	8.08	1.60	1.52
1	L	111	DT	C5-C7	7.81	1.54	1.50
1	G	66	DT	O4'-C1'	7.27	1.50	1.42
1	E	41	DT	C5-C7	7.08	1.54	1.50
1	F	56	DT	C5-C7	7.07	1.54	1.50
1	J	91	DT	C5-C7	6.94	1.54	1.50
1	N	136	DT	O4'-C1'	6.87	1.50	1.42
1	I	86	DT	C5-C7	6.77	1.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	45	DG	N1-C2	6.77	1.43	1.37
1	K	105	DG	C8-N7	6.68	1.34	1.30
1	L	116	DT	C5-C7	6.66	1.54	1.50
1	A	2	DG	N1-C2	6.61	1.43	1.37
1	K	101	DT	C5-C7	6.58	1.53	1.50
1	M	121	DT	C5-C7	6.54	1.53	1.50
1	A	6	DT	O4'-C1'	6.53	1.50	1.42
1	H	71	DT	C5-C7	6.46	1.53	1.50
1	F	52	DG	C2-N3	6.43	1.37	1.32
1	O	143	DG	C6-N1	6.40	1.44	1.39
1	L	114	DG	O4'-C1'	6.29	1.49	1.42
1	C	23	DG	C2-N3	6.22	1.37	1.32
1	O	142	DG	C2'-C1'	6.19	1.58	1.52
1	O	141	DT	C5-C7	6.16	1.53	1.50
1	F	54	DG	O4'-C1'	6.06	1.49	1.42
1	I	86	DT	O4'-C1'	6.05	1.49	1.42
1	G	66	DT	C5-C7	5.96	1.53	1.50
1	I	84	DG	C2-N3	5.87	1.37	1.32
1	A	6	DT	C2'-C1'	-5.86	1.46	1.52
1	D	32	DG	C2'-C1'	5.86	1.58	1.52
1	H	71	DT	C2-O2	5.85	1.27	1.22
1	D	34	DG	O4'-C1'	5.84	1.49	1.42
1	D	32	DG	N3-C4	5.74	1.39	1.35
1	K	102	DG	P-O5'	5.65	1.65	1.59
1	L	112	DG	C6-O6	5.64	1.29	1.24
1	M	124	DG	O4'-C1'	5.61	1.49	1.42
1	G	61	DT	C5-C6	5.49	1.38	1.34
1	C	23	DG	O4'-C1'	5.48	1.48	1.42
1	D	36	DT	C5-C7	5.45	1.53	1.50
1	J	93	DG	C2-N3	5.45	1.37	1.32
1	L	115	DG	O4'-C1'	5.40	1.48	1.42
1	N	135	DG	O4'-C1'	5.39	1.48	1.42
1	F	55	DG	O4'-C1'	5.35	1.48	1.42
1	O	142	DG	C8-N7	5.31	1.34	1.30
1	M	125	DG	O4'-C1'	5.28	1.48	1.42
1	F	53	DG	C6-O6	5.25	1.28	1.24
1	P	154	DG	O4'-C1'	5.23	1.48	1.42
1	D	35	DG	O4'-C1'	5.20	1.48	1.42
1	O	144	DG	N1-C2	5.18	1.41	1.37
1	M	121	DT	N1-C6	5.10	1.41	1.38
1	C	23	DG	C6-O6	5.10	1.28	1.24
1	D	31	DT	C5-C7	5.08	1.53	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	62	DG	C8-N7	5.06	1.33	1.30
1	F	56	DT	C4'-O4'	5.05	1.50	1.45
1	M	126	DT	C5-C6	5.02	1.37	1.34
1	P	154	DG	C6-N1	5.02	1.43	1.39
1	N	135	DG	C6-O6	5.02	1.28	1.24
1	A	2	DG	C5-C4	5.01	1.41	1.38

All (242) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	131	DT	P-O3'-C3'	24.31	148.87	119.70
1	B	16	DT	OP1-P-OP2	21.63	152.05	119.60
1	K	106	DT	OP1-P-OP2	-19.06	91.01	119.60
1	E	46	DT	OP1-P-OP2	17.50	145.85	119.60
1	K	102	DG	OP1-P-OP2	15.91	143.46	119.60
1	I	86	DT	O4'-C1'-N1	-15.13	97.41	108.00
1	M	124	DG	O4'-C1'-N9	-12.69	99.12	108.00
1	G	66	DT	O4'-C1'-N1	-12.34	99.36	108.00
1	O	146	DT	OP1-P-OP2	11.84	137.37	119.60
1	G	61	DT	N3-C2-O2	11.77	129.36	122.30
1	N	131	DT	C4-C5-C7	11.74	126.05	119.00
1	O	141	DT	N3-C4-O4	-11.72	112.87	119.90
1	N	136	DT	O4'-C1'-N1	-11.28	100.10	108.00
1	P	156	DT	OP1-P-OP2	11.19	136.39	119.60
1	L	114	DG	O4'-C1'-N9	-11.08	100.24	108.00
1	A	6	DT	O4'-C1'-N1	-10.98	100.31	108.00
1	P	154	DG	O4'-C1'-N9	-10.94	100.34	108.00
1	L	116	DT	O4'-C4'-C3'	-10.46	99.72	106.00
1	P	151	DT	C5-C4-O4	-10.29	117.69	124.90
1	K	101	DT	N3-C2-O2	10.28	128.47	122.30
1	D	36	DT	O4'-C4'-C3'	-10.28	99.83	106.00
1	J	96	DT	OP1-P-OP2	10.25	134.97	119.60
1	E	44	DG	O4'-C1'-N9	-10.11	100.92	108.00
1	C	24	DG	O4'-C1'-N9	-9.89	101.08	108.00
1	F	56	DT	O4'-C4'-C3'	-9.78	100.13	106.00
1	D	34	DG	O4'-C1'-N9	-9.69	101.21	108.00
1	G	61	DT	O4'-C1'-N1	-9.63	101.26	108.00
1	H	74	DG	O4'-C1'-N9	-9.60	101.28	108.00
1	D	31	DT	N3-C2-O2	-9.59	116.55	122.30
1	F	54	DG	O4'-C1'-N9	-9.42	101.40	108.00
1	I	86	DT	C2-N3-C4	-9.42	121.55	127.20
1	N	131	DT	O4'-C1'-N1	-9.40	101.42	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	151	DT	N3-C4-O4	9.29	125.47	119.90
1	M	122	DG	O4'-C1'-N9	9.26	114.48	108.00
1	B	11	DT	C6-C5-C7	-9.18	117.39	122.90
1	B	11	DT	C5-C6-N1	-9.18	118.19	123.70
1	M	126	DT	O4'-C4'-C3'	-9.14	100.52	106.00
1	N	131	DT	C6-C5-C7	-9.12	117.42	122.90
1	F	56	DT	C5-C6-N1	-8.99	118.30	123.70
1	P	151	DT	P-O3'-C3'	8.96	130.46	119.70
1	J	91	DT	N3-C2-O2	8.94	127.66	122.30
1	O	141	DT	C5-C4-O4	8.88	131.12	124.90
1	N	135	DG	C5-C6-N1	8.85	115.92	111.50
1	D	33	DG	C5-C6-N1	8.79	115.89	111.50
1	G	63	DG	N9-C4-C5	8.74	108.90	105.40
1	A	5	DG	C2-N3-C4	8.73	116.27	111.90
1	F	51	DT	C2-N3-C4	-8.51	122.09	127.20
1	P	153	DG	P-O3'-C3'	8.40	129.78	119.70
1	N	135	DG	C2-N3-C4	8.37	116.09	111.90
1	E	42	DG	O4'-C4'-C3'	-8.37	100.98	106.00
1	A	4	DG	O4'-C1'-N9	-8.35	102.16	108.00
1	J	96	DT	C6-N1-C2	8.26	125.43	121.30
1	F	56	DT	C2-N3-C4	-8.15	122.31	127.20
1	F	53	DG	C2-N3-C4	8.12	115.96	111.90
1	G	63	DG	C4-C5-N7	-8.11	107.56	110.80
1	J	94	DG	O4'-C1'-N9	-8.09	102.34	108.00
1	J	96	DT	C4-C5-C7	8.07	123.84	119.00
1	K	101	DT	N1-C1'-C2'	8.05	127.89	112.60
1	C	25	DG	C5-C6-O6	-8.04	123.77	128.60
1	K	105	DG	O4'-C1'-N9	-7.93	102.45	108.00
1	P	155	DG	C5-C6-N1	7.92	115.46	111.50
1	P	151	DT	O4'-C1'-N1	-7.89	102.48	108.00
1	O	142	DG	O4'-C1'-N9	7.88	113.52	108.00
1	K	101	DT	P-O3'-C3'	-7.87	110.25	119.70
1	L	115	DG	O5'-P-OP2	-7.83	98.66	105.70
1	A	4	DG	C8-N9-C4	-7.83	103.27	106.40
1	N	134	DG	O4'-C1'-N9	-7.79	102.55	108.00
1	N	131	DT	N3-C2-O2	7.79	126.97	122.30
1	H	71	DT	C4-C5-C7	7.67	123.60	119.00
1	C	23	DG	O4'-C1'-N9	-7.66	102.64	108.00
1	H	76	DT	P-O5'-C5'	7.63	133.12	120.90
1	K	101	DT	O4'-C4'-C3'	-7.58	101.45	106.00
1	P	155	DG	C5-C6-O6	-7.57	124.06	128.60
1	F	51	DT	N3-C2-O2	-7.53	117.78	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	32	DG	O4'-C1'-N9	7.52	113.27	108.00
1	L	116	DT	N3-C4-O4	-7.50	115.40	119.90
1	J	94	DG	C5-C6-O6	-7.39	124.16	128.60
1	N	131	DT	N1-C2-O2	-7.38	117.20	123.10
1	K	101	DT	N1-C2-O2	-7.34	117.23	123.10
1	L	116	DT	C2-N3-C4	-7.33	122.80	127.20
1	C	25	DG	C2-N3-C4	7.32	115.56	111.90
1	J	95	DG	O4'-C1'-N9	-7.31	102.88	108.00
1	H	72	DG	O4'-C4'-C3'	-7.30	101.58	104.50
1	G	66	DT	C2-N3-C4	-7.29	122.83	127.20
1	L	116	DT	N3-C2-O2	-7.27	117.94	122.30
1	K	101	DT	O4'-C1'-N1	-7.27	102.91	108.00
1	F	55	DG	O4'-C1'-N9	-7.26	102.92	108.00
1	B	11	DT	C4-C5-C6	7.21	122.33	118.00
1	C	25	DG	C5-C6-N1	7.17	115.09	111.50
1	H	71	DT	C6-C5-C7	-7.17	118.60	122.90
1	P	154	DG	C6-N1-C2	-7.16	120.81	125.10
1	C	24	DG	P-O3'-C3'	7.15	128.28	119.70
1	K	102	DG	O5'-P-OP1	-7.15	99.27	105.70
1	P	154	DG	N1-C2-N3	7.05	128.13	123.90
1	E	45	DG	O4'-C1'-N9	-7.00	103.10	108.00
1	M	121	DT	C2-N3-C4	-7.00	123.00	127.20
1	J	91	DT	P-O3'-C3'	6.98	128.08	119.70
1	G	61	DT	N1-C2-O2	-6.92	117.56	123.10
1	P	153	DG	O4'-C1'-N9	-6.91	103.16	108.00
1	L	114	DG	OP1-P-OP2	6.89	129.94	119.60
1	P	156	DT	C5-C6-N1	-6.89	119.57	123.70
1	B	14	DG	C5-C6-N1	6.85	114.92	111.50
1	D	32	DG	N9-C4-C5	6.83	108.13	105.40
1	B	15	DG	P-O3'-C3'	6.82	127.89	119.70
1	D	36	DT	C6-C5-C7	6.81	126.99	122.90
1	A	6	DT	C5-C6-N1	-6.81	119.62	123.70
1	P	153	DG	N9-C4-C5	6.80	108.12	105.40
1	L	114	DG	C5-C6-O6	-6.79	124.53	128.60
1	H	75	DG	O4'-C1'-N9	-6.78	103.26	108.00
1	J	96	DT	C6-C5-C7	-6.77	118.84	122.90
1	F	51	DT	O4'-C1'-N1	-6.71	103.30	108.00
1	L	114	DG	O5'-P-OP2	-6.68	99.69	105.70
1	A	1	DT	O4'-C1'-N1	-6.68	103.33	108.00
1	O	145	DG	C5-C6-N1	6.67	114.84	111.50
1	I	86	DT	O4'-C1'-C2'	-6.64	100.58	105.90
1	C	23	DG	P-O3'-C3'	6.64	127.67	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	76	DT	C2-N3-C4	-6.64	123.22	127.20
1	I	86	DT	C5-C6-N1	-6.63	119.72	123.70
1	L	113	DG	C5-C6-O6	-6.59	124.65	128.60
1	P	154	DG	O5'-P-OP2	-6.57	99.79	105.70
1	N	135	DG	O4'-C1'-N9	-6.55	103.41	108.00
1	C	23	DG	N7-C8-N9	6.55	116.38	113.10
1	F	56	DT	O4'-C1'-N1	-6.54	103.42	108.00
1	O	145	DG	C4-C5-N7	6.51	113.41	110.80
1	J	96	DT	O4'-C1'-N1	-6.47	103.47	108.00
1	D	33	DG	C6-N1-C2	-6.46	121.22	125.10
1	A	5	DG	C5-C6-N1	6.44	114.72	111.50
1	L	115	DG	O4'-C1'-N9	-6.44	103.49	108.00
1	F	53	DG	N3-C4-C5	-6.43	125.38	128.60
1	I	84	DG	P-O3'-C3'	6.38	127.36	119.70
1	G	63	DG	C2-N3-C4	6.38	115.09	111.90
1	A	1	DT	C2-N3-C4	-6.37	123.38	127.20
1	H	72	DG	O5'-P-OP2	-6.34	99.99	105.70
1	A	2	DG	C5-C6-O6	-6.33	124.80	128.60
1	L	115	DG	OP1-P-OP2	6.32	129.07	119.60
1	O	144	DG	P-O3'-C3'	6.31	127.27	119.70
1	J	96	DT	C5-C6-N1	-6.28	119.93	123.70
1	M	123	DG	C2-N3-C4	6.28	115.04	111.90
1	F	51	DT	C5-C6-N1	-6.24	119.95	123.70
1	K	105	DG	C5-C6-N1	6.24	114.62	111.50
1	P	155	DG	C6-N1-C2	-6.21	121.37	125.10
1	G	66	DT	N3-C4-C5	6.17	118.90	115.20
1	O	144	DG	O4'-C1'-N9	-6.16	103.69	108.00
1	A	1	DT	C5-C6-N1	-6.10	120.04	123.70
1	K	105	DG	P-O3'-C3'	6.10	127.02	119.70
1	O	141	DT	C5-C6-N1	-6.08	120.05	123.70
1	D	31	DT	C2-N3-C4	-6.07	123.56	127.20
1	M	125	DG	C5-C6-O6	-6.06	124.96	128.60
1	D	36	DT	C4-C5-C7	-6.04	115.38	119.00
1	H	72	DG	P-O5'-C5'	6.03	130.55	120.90
1	M	125	DG	O4'-C1'-N9	-6.02	103.78	108.00
1	P	154	DG	P-O3'-C3'	6.02	126.92	119.70
1	L	113	DG	C6-N1-C2	-6.01	121.49	125.10
1	P	153	DG	C8-N9-C4	-5.99	104.01	106.40
1	G	62	DG	C2-N3-C4	5.98	114.89	111.90
1	K	104	DG	O4'-C1'-N9	-5.98	103.81	108.00
1	J	91	DT	C5-C6-N1	-5.97	120.12	123.70
1	P	156	DT	C4-C5-C6	5.95	121.57	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	56	DT	C4-C5-C6	5.94	121.57	118.00
1	K	102	DG	O4'-C1'-C2'	5.94	110.66	105.90
1	H	76	DT	N1-C2-N3	5.93	118.16	114.60
1	J	96	DT	O5'-P-OP2	-5.92	100.37	105.70
1	H	76	DT	O4'-C1'-C2'	-5.91	101.17	105.90
1	N	135	DG	C6-N1-C2	-5.91	121.55	125.10
1	K	105	DG	C6-N1-C2	-5.88	121.58	125.10
1	F	53	DG	N3-C4-N9	5.87	129.52	126.00
1	A	2	DG	N1-C6-O6	5.85	123.41	119.90
1	G	61	DT	C2-N3-C4	5.85	130.71	127.20
1	I	84	DG	C5-C6-N1	5.84	114.42	111.50
1	H	73	DG	N1-C2-N3	-5.84	120.40	123.90
1	G	61	DT	C4-C5-C7	5.83	122.50	119.00
1	H	72	DG	OP1-P-OP2	5.83	128.34	119.60
1	F	56	DT	C1'-O4'-C4'	-5.82	104.28	110.10
1	A	5	DG	N7-C8-N9	-5.78	110.21	113.10
1	F	56	DT	C6-C5-C7	-5.78	119.44	122.90
1	G	61	DT	C6-C5-C7	-5.78	119.43	122.90
1	G	63	DG	C5-N7-C8	5.75	107.18	104.30
1	P	154	DG	C2-N3-C4	-5.73	109.04	111.90
1	N	136	DT	C4'-C3'-C2'	5.73	108.25	103.10
1	J	91	DT	O3'-P-O5'	-5.72	93.12	104.00
1	A	6	DT	C6-N1-C2	5.72	124.16	121.30
1	F	56	DT	N3-C4-O4	-5.71	116.47	119.90
1	A	3	DG	C5-C6-N1	5.71	114.35	111.50
1	M	121	DT	N3-C4-C5	5.67	118.60	115.20
1	C	22	DG	C5-N7-C8	5.65	107.12	104.30
1	E	43	DG	N3-C4-C5	-5.65	125.78	128.60
1	G	63	DG	N3-C4-C5	-5.63	125.78	128.60
1	D	35	DG	O4'-C1'-N9	-5.62	104.06	108.00
1	G	66	DT	C5-C6-N1	-5.61	120.34	123.70
1	C	26	DT	C2-N3-C4	-5.59	123.84	127.20
1	B	11	DT	O4'-C1'-N1	-5.54	104.12	108.00
1	N	135	DG	N3-C4-N9	5.53	129.32	126.00
1	I	86	DT	N3-C2-O2	-5.52	118.99	122.30
1	H	71	DT	C6-N1-C2	5.51	124.06	121.30
1	O	145	DG	P-O3'-C3'	5.50	126.30	119.70
1	F	56	DT	N3-C2-O2	-5.47	119.02	122.30
1	G	64	DG	P-O3'-C3'	5.45	126.24	119.70
1	J	93	DG	O4'-C1'-N9	-5.43	104.20	108.00
1	O	145	DG	N3-C4-C5	5.43	131.32	128.60
1	M	123	DG	P-O3'-C3'	5.41	126.19	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	126	DT	O4'-C1'-N1	-5.40	104.22	108.00
1	J	91	DT	N1-C2-O2	-5.40	118.78	123.10
1	D	33	DG	N1-C6-O6	-5.38	116.67	119.90
1	J	92	DG	O4'-C4'-C3'	-5.36	102.36	104.50
1	L	112	DG	C5-C6-N1	5.34	114.17	111.50
1	N	132	DG	P-O3'-C3'	5.30	126.06	119.70
1	B	11	DT	N1-C2-N3	5.29	117.78	114.60
1	I	85	DG	P-O3'-C3'	5.29	126.04	119.70
1	H	75	DG	N3-C2-N2	-5.29	116.20	119.90
1	N	132	DG	C4'-C3'-C2'	5.27	107.85	103.10
1	C	26	DT	C6-C5-C7	-5.26	119.74	122.90
1	I	86	DT	C6-N1-C2	5.25	123.93	121.30
1	D	32	DG	N3-C4-C5	-5.24	125.98	128.60
1	J	93	DG	P-O3'-C3'	5.24	125.99	119.70
1	M	123	DG	C8-N9-C4	5.24	108.50	106.40
1	M	126	DT	C1'-O4'-C4'	-5.23	104.87	110.10
1	B	13	DG	O4'-C1'-N9	-5.21	104.36	108.00
1	I	81	DT	O4'-C1'-N1	-5.20	104.36	108.00
1	F	56	DT	C6-N1-C2	5.18	123.89	121.30
1	O	141	DT	O4'-C1'-N1	-5.17	104.38	108.00
1	G	65	DG	P-O3'-C3'	5.17	125.90	119.70
1	J	91	DT	C6-N1-C2	5.15	123.88	121.30
1	D	31	DT	N1-C2-N3	5.15	117.69	114.60
1	F	52	DG	O4'-C4'-C3'	-5.14	102.44	104.50
1	J	92	DG	C1'-O4'-C4'	-5.14	104.96	110.10
1	M	121	DT	C5-C4-O4	-5.14	121.30	124.90
1	J	94	DG	P-O3'-C3'	5.13	125.86	119.70
1	M	123	DG	N7-C8-N9	-5.13	110.54	113.10
1	G	63	DG	C4-C5-C6	5.12	121.87	118.80
1	H	76	DT	C3'-C2'-C1'	-5.12	96.36	102.50
1	I	84	DG	C5-C6-O6	-5.11	125.53	128.60
1	D	34	DG	C2-N3-C4	5.09	114.45	111.90
1	L	115	DG	O4'-C1'-C2'	-5.09	101.83	105.90
1	F	51	DT	N1-C2-N3	5.06	117.64	114.60
1	K	102	DG	O5'-P-OP2	-5.06	101.15	105.70
1	H	74	DG	C5-N7-C8	5.05	106.83	104.30
1	H	74	DG	C4-C5-N7	-5.05	108.78	110.80
1	N	136	DT	C6-C5-C7	-5.05	119.87	122.90
1	D	36	DT	O4'-C1'-N1	-5.03	104.48	108.00
1	M	124	DG	C4'-C3'-C2'	5.02	107.62	103.10
1	E	41	DT	C5-C6-N1	-5.02	120.69	123.70
1	N	135	DG	N3-C4-C5	-5.00	126.10	128.60

There are no chirality outliers.

There are no planarity outliers.

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	A	125	0	70	0	0
1	B	108	0	57	0	0
1	C	109	0	57	0	0
1	D	125	0	70	0	0
1	E	108	0	57	0	0
1	F	125	0	70	0	0
1	G	125	0	69	0	0
1	H	125	0	70	0	0
1	I	125	0	70	0	0
1	J	125	0	70	1	0
1	K	108	0	57	0	0
1	L	125	0	70	0	0
1	M	125	0	70	0	0
1	N	125	0	70	0	0
1	O	108	0	57	0	0
1	P	125	0	70	1	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	E	3	0	0	0	0
2	I	3	0	0	0	0
2	L	1	0	0	0	0
2	M	3	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	P	1	0	0	0	0
4	A	37	0	0	0	0
4	B	32	0	0	0	0
4	C	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	49	0	0	0	0
4	E	28	0	0	0	0
4	F	28	0	0	0	0
4	G	31	0	0	0	0
4	H	28	0	0	0	0
4	I	36	0	0	0	0
4	J	24	0	0	0	0
4	K	19	0	0	0	0
4	L	37	0	0	0	0
4	M	41	0	0	0	0
4	N	35	0	0	0	0
4	O	28	0	0	0	0
4	P	35	0	0	0	0
All	All	2453	0	1054	1	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 0.

All (1) 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)
1:J:91:DT:O4'	1:P:151:DT:H2'	2.19	0.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

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 23 ligands modelled in this entry, 23 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 [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 ⓘ

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.