



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:27 PM GMT

PDB ID : 1P47  
Title : Crystal Structure of tandem Zif268 molecules complexed to DNA  
Authors : Peisach, E.; Pabo, C.O.  
Deposited on : 2003-04-21  
Resolution : 2.20 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](mailto: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.

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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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

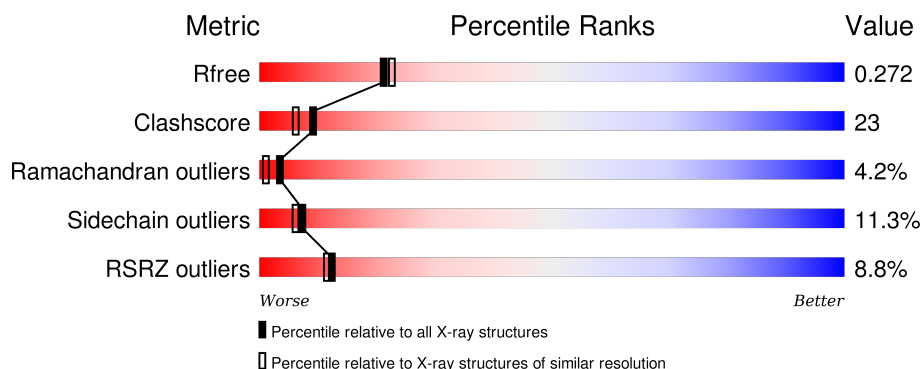
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	C	22	<div> <div>45%</div> <div>55%</div> </div>
2	D	22	<div> <div>45%</div> <div>55%</div> </div>
3	A	87	<div> <div>5%</div> <div>48%</div> <div>33%</div> <div>17%</div> <div>•</div> </div>
3	B	87	<div> <div>17%</div> <div>32%</div> <div>40%</div> <div>18%</div> <div>6%</div> <div>•</div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2433 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(\*GP\*TP\*GP\*GP\*CP\*GP\*TP\*GP\*GP\*GP\*CP\*GP\*GP\*CP\*GP\*TP\*GP\*GP\*GP\*CP\*GP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	22	Total	C	N	O	P	0	0	0
			461	216	90	134	21			

- Molecule 2 is a DNA chain called 5'-D(\*CP\*AP\*CP\*GP\*CP\*CP\*CP\*AP\*CP\*GP\*CP\*CP\*GP\*CP\*CP\*CP\*AP\*CP\*GP\*CP\*CP\*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	22	Total	C	N	O	P	0	0	0
			435	206	82	126	21			

- Molecule 3 is a protein called Early growth response protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	87	Total	C	N	O	S	0	0	0
			730	443	155	125	7			
3	B	84	Total	C	N	O	S	0	0	0
			701	427	148	119	7			

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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	21	Total 21	O 21	0	0
5	C	24	Total 24	O 24	0	0
5	D	19	Total 19	O 19	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.

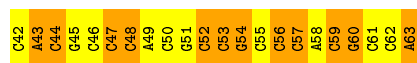
- Molecule 1: 5'-D(\*GP\*TP\*GP\*GP\*CP\*GP\*TP\*GP\*GP\*GP\*CP\*GP\*GP\*CP\*GP\*TP\*GP\*GP\*GP\*CP\*GP\*T)-3'

Chain C: 



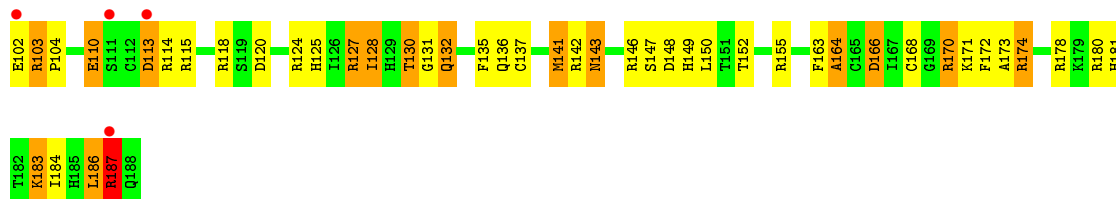
- Molecule 2: 5'-D(\*CP\*AP\*CP\*GP\*CP\*CP\*CP\*AP\*CP\*GP\*CP\*CP\*GP\*CP\*CP\*CP\*AP\*CP\*GP\*CP\*CP\*A)-3'

Chain D: 



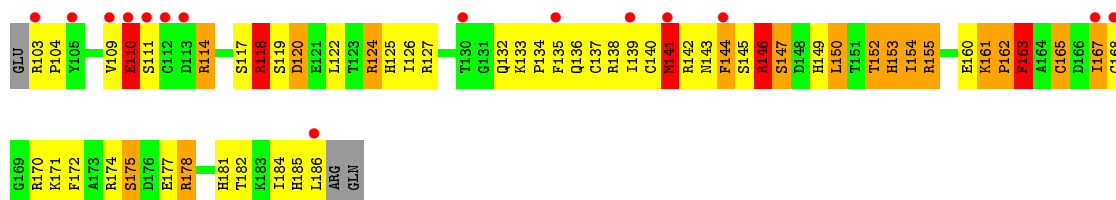
- Molecule 3: Early growth response protein 1

Chain A: 



- Molecule 3: Early growth response protein 1

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.63 Å 70.63 Å 99.61 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.86 – 2.20 38.62 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.4 (60.86-2.20) 87.5 (38.62-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.20 Å)	Xtriage
Refinement program	REFMAC 5.1.22	Depositor
R, $R_{free}$	0.214 , 0.267 0.226 , 0.272	Depositor DCC
$R_{free}$ test set	2428 reflections (10.85%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.4	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 56.4	EDS
Estimated twinning fraction	0.018 for -h,-k,l 0.057 for h,-h-k,-l 0.034 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 24823 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2433	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	4.97	141/518 (27.2%)	5.53	264/802 (32.9%)
2	D	4.35	111/486 (22.8%)	5.85	247/744 (33.2%)
3	A	2.00	16/746 (2.1%)	1.80	18/996 (1.8%)
3	B	2.07	22/717 (3.1%)	1.69	16/958 (1.7%)
All	All	3.37	290/2467 (11.8%)	4.00	545/3500 (15.6%)

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	1
3	A	0	3
All	All	0	4

All (290) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	54	DG	C8-N7	22.30	1.44	1.30
1	C	8	DG	N7-C5	19.76	1.51	1.39
1	C	1	DG	N7-C5	18.82	1.50	1.39
1	C	17	DG	C8-N7	18.07	1.41	1.30
2	D	51	DG	C8-N7	17.90	1.41	1.30
1	C	18	DG	C8-N7	16.67	1.41	1.30
2	D	53	DC	N1-C6	-16.19	1.27	1.37
1	C	14	DC	C4'-C3'	16.17	1.69	1.53
1	C	13	DG	P-O5'	14.81	1.74	1.59
1	C	21	DG	C6-N1	14.07	1.49	1.39
2	D	57	DC	N1-C6	-13.92	1.28	1.37
1	C	21	DG	C5-C4	13.87	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	DG	C6-O6	13.55	1.36	1.24
1	C	10	DG	C8-N7	13.23	1.38	1.30
1	C	2	DT	C2-O2	13.18	1.32	1.22
1	C	15	DG	C5-C6	-12.97	1.29	1.42
1	C	21	DG	C8-N7	12.19	1.38	1.30
1	C	12	DG	C6-N1	-12.11	1.31	1.39
2	D	53	DC	C2-N3	-11.77	1.26	1.35
1	C	19	DG	C3'-O3'	-11.55	1.28	1.44
1	C	16	DT	C5-C7	11.53	1.56	1.50
2	D	51	DG	N7-C5	11.53	1.46	1.39
1	C	4	DG	C6-N1	11.46	1.47	1.39
2	D	45	DG	N1-C2	11.36	1.46	1.37
1	C	4	DG	N3-C4	11.36	1.43	1.35
1	C	19	DG	C6-O6	11.34	1.34	1.24
2	D	50	DC	C5-C6	11.32	1.43	1.34
1	C	10	DG	N1-C2	11.31	1.46	1.37
2	D	55	DC	C2-O2	-11.20	1.14	1.24
1	C	5	DC	C4'-C3'	11.19	1.64	1.53
2	D	49	DA	N3-C4	-10.95	1.28	1.34
1	C	1	DG	C3'-O3'	10.78	1.57	1.44
1	C	3	DG	C8-N7	10.70	1.37	1.30
1	C	5	DC	C4-C5	-10.50	1.34	1.43
1	C	12	DG	C8-N7	10.44	1.37	1.30
2	D	43	DA	N3-C4	-10.33	1.28	1.34
2	D	51	DG	C2-N2	-10.31	1.24	1.34
1	C	3	DG	C5-C4	-10.28	1.31	1.38
1	C	14	DC	N1-C6	-10.25	1.31	1.37
1	C	6	DG	C2'-C1'	10.23	1.62	1.52
1	C	19	DG	N7-C5	10.22	1.45	1.39
2	D	53	DC	P-OP2	10.11	1.66	1.49
2	D	46	DC	N3-C4	-9.99	1.26	1.33
1	C	12	DG	N1-C2	-9.84	1.29	1.37
2	D	62	DC	N3-C4	-9.77	1.27	1.33
1	C	10	DG	C6-N1	9.75	1.46	1.39
1	C	14	DC	C3'-O3'	-9.73	1.31	1.44
1	C	6	DG	N1-C2	9.63	1.45	1.37
2	D	43	DA	C8-N7	9.62	1.38	1.31
1	C	15	DG	C2-N3	-9.61	1.25	1.32
1	C	6	DG	C6-N1	-9.61	1.32	1.39
2	D	60	DG	N1-C2	9.57	1.45	1.37
2	D	52	DC	N1-C6	-9.33	1.31	1.37
1	C	16	DT	C4-C5	-9.23	1.36	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	55	DC	O3'-P	9.13	1.72	1.61
2	D	56	DC	N1-C2	-9.09	1.31	1.40
1	C	1	DG	N1-C2	9.08	1.45	1.37
2	D	48	DC	N3-C4	-9.08	1.27	1.33
1	C	1	DG	N9-C8	9.06	1.44	1.37
2	D	53	DC	C3'-O3'	-9.00	1.32	1.44
1	C	22	DT	C1'-N1	8.97	1.60	1.49
2	D	54	DG	C4'-O4'	8.96	1.54	1.45
1	C	14	DC	C5-C6	8.93	1.41	1.34
2	D	54	DG	C5-C6	-8.84	1.33	1.42
2	D	49	DA	C6-N6	8.81	1.41	1.33
2	D	59	DC	N1-C6	-8.80	1.31	1.37
2	D	54	DG	N7-C5	-8.75	1.33	1.39
1	C	3	DG	C3'-O3'	-8.70	1.32	1.44
2	D	56	DC	C2-N3	8.64	1.42	1.35
1	C	16	DT	N3-C4	-8.56	1.31	1.38
1	C	11	DC	C1'-N1	8.56	1.60	1.49
2	D	49	DA	C6-N1	-8.50	1.29	1.35
2	D	51	DG	C6-O6	8.49	1.31	1.24
1	C	12	DG	C5-C4	-8.48	1.32	1.38
1	C	13	DG	N9-C8	-8.46	1.31	1.37
1	C	1	DG	O3'-P	8.37	1.71	1.61
1	C	18	DG	N7-C5	8.25	1.44	1.39
2	D	54	DG	C2-N2	8.19	1.42	1.34
1	C	4	DG	N7-C5	-8.19	1.34	1.39
2	D	63	DA	N9-C4	8.18	1.42	1.37
1	C	7	DT	N3-C4	-8.18	1.32	1.38
1	C	2	DT	C5-C6	-8.15	1.28	1.34
1	C	3	DG	N9-C4	8.06	1.44	1.38
1	C	22	DT	C2'-C1'	8.03	1.60	1.52
2	D	52	DC	C4'-O4'	8.02	1.53	1.45
2	D	62	DC	C1'-N1	8.00	1.59	1.49
3	B	174	ARG	NE-CZ	7.95	1.43	1.33
2	D	52	DC	P-OP2	7.90	1.62	1.49
1	C	14	DC	C4-N4	7.89	1.41	1.33
3	A	124	ARG	CG-CD	7.89	1.71	1.51
2	D	45	DG	C3'-O3'	7.88	1.54	1.44
1	C	9	DG	C8-N7	7.82	1.35	1.30
2	D	42	DC	O3'-P	7.81	1.70	1.61
2	D	57	DC	C2-N3	7.79	1.42	1.35
1	C	13	DG	C3'-O3'	-7.77	1.33	1.44
3	A	113	ASP	CB-CG	7.77	1.68	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	5	DC	N1-C6	-7.75	1.32	1.37
1	C	18	DG	C2-N3	7.73	1.39	1.32
1	C	6	DG	C8-N7	-7.73	1.26	1.30
1	C	2	DT	C2'-C1'	7.72	1.60	1.52
2	D	43	DA	C5-C4	7.71	1.44	1.38
2	D	52	DC	O3'-P	7.70	1.70	1.61
1	C	7	DT	C5-C6	-7.69	1.28	1.34
2	D	56	DC	C4-C5	-7.68	1.36	1.43
1	C	11	DC	C4'-O4'	7.67	1.52	1.45
1	C	6	DG	C5-C4	-7.56	1.33	1.38
2	D	57	DC	P-O5'	-7.51	1.52	1.59
1	C	14	DC	C2'-C1'	7.48	1.59	1.52
2	D	57	DC	N3-C4	-7.47	1.28	1.33
3	A	171	LYS	CD-CE	7.46	1.70	1.51
2	D	45	DG	N9-C4	7.43	1.43	1.38
2	D	50	DC	O5'-C5'	7.40	1.60	1.42
2	D	51	DG	C3'-O3'	7.38	1.53	1.44
1	C	7	DT	C4-O4	7.37	1.29	1.23
2	D	50	DC	C2'-C1'	7.36	1.59	1.52
1	C	16	DT	C2-N3	-7.36	1.31	1.37
3	A	132	GLN	CG-CD	7.36	1.68	1.51
2	D	57	DC	C4-C5	7.32	1.48	1.43
2	D	54	DG	C4'-C3'	7.30	1.60	1.53
1	C	17	DG	N1-C2	7.27	1.43	1.37
1	C	8	DG	C8-N7	7.25	1.35	1.30
1	C	2	DT	O4'-C1'	-7.22	1.33	1.42
1	C	3	DG	P-O5'	7.19	1.67	1.59
1	C	10	DG	N9-C8	7.18	1.42	1.37
1	C	15	DG	C5-C4	-7.16	1.33	1.38
3	B	165	CYS	CA-C	7.16	1.71	1.52
2	D	56	DC	C4-N4	7.08	1.40	1.33
3	A	174	ARG	CZ-NH1	7.04	1.42	1.33
2	D	53	DC	C4'-O4'	7.00	1.52	1.45
1	C	13	DG	C2'-C1'	6.98	1.59	1.52
1	C	6	DG	C3'-O3'	6.93	1.52	1.44
1	C	11	DC	C2-N3	6.93	1.41	1.35
2	D	46	DC	C2-N3	6.92	1.41	1.35
1	C	15	DG	C8-N7	6.92	1.35	1.30
2	D	52	DC	N3-C4	-6.91	1.29	1.33
1	C	1	DG	C6-N1	-6.85	1.34	1.39
1	C	16	DT	C1'-N1	-6.85	1.37	1.47
2	D	47	DC	C4-C5	-6.83	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	61	DC	C4-N4	6.80	1.40	1.33
2	D	43	DA	C6-N6	6.76	1.39	1.33
2	D	55	DC	P-OP1	-6.76	1.37	1.49
2	D	55	DC	N1-C6	-6.75	1.33	1.37
2	D	61	DC	C2-N3	-6.75	1.30	1.35
2	D	63	DA	C2-N3	6.74	1.39	1.33
2	D	49	DA	C8-N7	6.72	1.36	1.31
2	D	42	DC	N1-C6	-6.69	1.33	1.37
1	C	18	DG	N1-C2	6.67	1.43	1.37
1	C	3	DG	N9-C8	-6.62	1.33	1.37
2	D	52	DC	C4-C5	6.61	1.48	1.43
1	C	10	DG	C2-N3	-6.59	1.27	1.32
3	B	147	SER	CA-CB	6.59	1.62	1.52
3	B	175	SER	CB-OG	6.59	1.50	1.42
2	D	46	DC	C4'-O4'	6.58	1.51	1.45
2	D	56	DC	N1-C6	6.58	1.41	1.37
2	D	60	DG	C5-C6	-6.56	1.35	1.42
3	B	178	ARG	CB-CG	6.55	1.70	1.52
3	B	177	GLU	C-O	6.52	1.35	1.23
3	A	183	LYS	CE-NZ	6.50	1.65	1.49
3	A	132	GLN	CB-CG	6.49	1.70	1.52
1	C	14	DC	N3-C4	6.48	1.38	1.33
1	C	19	DG	C2-N3	6.48	1.38	1.32
3	B	119	SER	CB-OG	6.48	1.50	1.42
2	D	63	DA	N3-C4	-6.47	1.30	1.34
1	C	22	DT	C3'-O3'	6.42	1.52	1.44
2	D	49	DA	O3'-P	6.41	1.68	1.61
3	B	168	CYS	CB-SG	6.40	1.93	1.82
1	C	22	DT	C2-O2	6.35	1.27	1.22
1	C	3	DG	C2-N3	6.33	1.37	1.32
1	C	4	DG	C5-C4	6.25	1.42	1.38
1	C	13	DG	N7-C5	6.24	1.43	1.39
3	B	177	GLU	CG-CD	6.24	1.61	1.51
1	C	8	DG	C5-C4	-6.23	1.33	1.38
2	D	60	DG	C8-N7	6.23	1.34	1.30
1	C	9	DG	N9-C8	6.21	1.42	1.37
2	D	52	DC	C3'-C2'	6.18	1.59	1.52
1	C	10	DG	N3-C4	-6.18	1.31	1.35
1	C	12	DG	N3-C4	6.17	1.39	1.35
1	C	21	DG	C5-C6	-6.16	1.36	1.42
2	D	56	DC	N3-C4	-6.14	1.29	1.33
1	C	7	DT	C1'-N1	6.14	1.57	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	8	DG	C5'-C4'	6.13	1.58	1.51
3	B	153	HIS	C-O	6.13	1.34	1.23
1	C	14	DC	C4-C5	-6.12	1.38	1.43
2	D	57	DC	C2'-C1'	6.11	1.58	1.52
2	D	52	DC	C2-N3	6.11	1.40	1.35
1	C	15	DG	C3'-O3'	-6.10	1.36	1.44
1	C	5	DC	P-OP1	-6.09	1.38	1.49
2	D	58	DA	N3-C4	6.06	1.38	1.34
2	D	54	DG	C3'-O3'	6.05	1.51	1.44
1	C	7	DT	N1-C2	-6.05	1.33	1.38
1	C	20	DC	C4-C5	-6.05	1.38	1.43
1	C	4	DG	C5-C6	-6.05	1.36	1.42
1	C	7	DT	C4'-O4'	6.03	1.51	1.45
2	D	62	DC	C2-O2	6.02	1.29	1.24
1	C	10	DG	C5-C4	6.00	1.42	1.38
1	C	18	DG	C6-O6	5.99	1.29	1.24
1	C	22	DT	C5-C7	-5.98	1.46	1.50
2	D	59	DC	C4-C5	-5.98	1.38	1.43
3	B	147	SER	CB-OG	5.96	1.50	1.42
1	C	9	DG	C2-N3	-5.93	1.28	1.32
1	C	17	DG	C5'-C4'	5.90	1.57	1.51
1	C	21	DG	N9-C8	5.90	1.42	1.37
2	D	63	DA	C3'-C2'	5.90	1.59	1.52
1	C	4	DG	C4'-C3'	5.88	1.59	1.53
3	A	163	PHE	CE1-CZ	5.87	1.48	1.37
2	D	63	DA	P-O5'	5.86	1.65	1.59
1	C	9	DG	C6-N1	5.85	1.43	1.39
2	D	62	DC	C2-N3	5.85	1.40	1.35
3	A	172	PHE	CE1-CZ	5.83	1.48	1.37
2	D	50	DC	P-OP1	5.79	1.58	1.49
2	D	63	DA	C5-C6	-5.74	1.35	1.41
1	C	21	DG	C2'-C1'	5.74	1.58	1.52
1	C	9	DG	C5-C6	-5.73	1.36	1.42
3	B	154	ILE	CB-CG2	5.73	1.70	1.52
2	D	44	DC	O3'-P	5.71	1.68	1.61
1	C	11	DC	N3-C4	-5.66	1.29	1.33
2	D	49	DA	C5-C6	-5.62	1.35	1.41
1	C	5	DC	O4'-C1'	5.60	1.49	1.42
3	B	177	GLU	CD-OE2	5.60	1.31	1.25
1	C	13	DG	C5-C4	-5.59	1.34	1.38
2	D	51	DG	O4'-C1'	-5.59	1.35	1.42
2	D	51	DG	C2'-C1'	5.59	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	174	ARG	CG-CD	5.59	1.66	1.51
2	D	48	DC	C2'-C1'	5.58	1.57	1.52
2	D	58	DA	N9-C4	5.54	1.41	1.37
3	B	172	PHE	CE1-CZ	5.54	1.47	1.37
1	C	12	DG	C3'-O3'	-5.54	1.36	1.44
3	A	168	CYS	CB-SG	5.54	1.91	1.82
2	D	54	DG	O5'-C5'	5.51	1.56	1.42
3	A	147	SER	CA-CB	5.50	1.61	1.52
1	C	20	DC	C4-N4	5.50	1.38	1.33
3	B	141	MET	SD-CE	5.50	2.08	1.77
1	C	17	DG	N3-C4	-5.49	1.31	1.35
2	D	59	DC	C5-C6	5.49	1.38	1.34
1	C	5	DC	C5-C6	-5.49	1.29	1.34
2	D	56	DC	C1'-N1	5.48	1.56	1.49
2	D	49	DA	N7-C5	5.48	1.42	1.39
1	C	12	DG	C4'-O4'	5.48	1.50	1.45
2	D	45	DG	N3-C4	5.48	1.39	1.35
1	C	15	DG	N9-C8	5.47	1.41	1.37
1	C	10	DG	C3'-O3'	-5.45	1.36	1.44
1	C	12	DG	C2-N3	5.45	1.37	1.32
2	D	45	DG	C6-N1	5.43	1.43	1.39
2	D	44	DC	C2'-C1'	5.43	1.57	1.52
3	A	110	GLU	CG-CD	5.40	1.60	1.51
2	D	42	DC	C5-C6	5.39	1.38	1.34
2	D	45	DG	C6-O6	5.39	1.28	1.24
3	B	150	LEU	CA-CB	-5.38	1.41	1.53
1	C	1	DG	C4'-O4'	5.38	1.50	1.45
2	D	55	DC	C3'-C2'	-5.38	1.45	1.52
1	C	18	DG	C2-N2	5.36	1.40	1.34
3	A	183	LYS	CB-CG	5.33	1.67	1.52
3	B	163	PHE	CB-CG	5.33	1.60	1.51
2	D	54	DG	P-O5'	5.32	1.65	1.59
2	D	62	DC	C5-C6	5.32	1.38	1.34
1	C	4	DG	C6-O6	5.31	1.28	1.24
2	D	45	DG	C5-C6	5.29	1.47	1.42
1	C	1	DG	C4'-C3'	5.29	1.58	1.53
1	C	7	DT	O3'-P	5.29	1.67	1.61
1	C	14	DC	C1'-N1	-5.29	1.39	1.47
1	C	19	DG	N3-C4	5.28	1.39	1.35
1	C	5	DC	N3-C4	-5.27	1.30	1.33
1	C	6	DG	P-O5'	-5.25	1.54	1.59
1	C	21	DG	P-O5'	5.25	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	21	DG	C4'-O4'	5.24	1.50	1.45
1	C	14	DC	O4'-C1'	5.24	1.48	1.42
3	A	135	PHE	CE2-CZ	-5.23	1.27	1.37
1	C	7	DT	C5-C7	-5.23	1.47	1.50
2	D	57	DC	C4'-O4'	5.23	1.50	1.45
3	B	167	ILE	CB-CG2	5.22	1.69	1.52
2	D	55	DC	P-O5'	5.21	1.65	1.59
1	C	20	DC	C2-N3	-5.20	1.31	1.35
3	B	111	SER	CB-OG	5.20	1.49	1.42
3	B	175	SER	CA-CB	5.19	1.60	1.52
3	A	143	ASN	C-O	5.18	1.33	1.23
2	D	52	DC	C1'-N1	5.18	1.55	1.49
1	C	9	DG	C5-C4	5.16	1.42	1.38
1	C	12	DG	C4'-C3'	5.14	1.58	1.53
2	D	45	DG	C2-N3	5.11	1.36	1.32
3	B	124	ARG	CG-CD	5.11	1.64	1.51
2	D	61	DC	C4'-O4'	5.10	1.50	1.45
2	D	52	DC	P-O5'	5.08	1.64	1.59
2	D	49	DA	C5-C4	5.07	1.42	1.38
2	D	63	DA	C8-N7	5.05	1.35	1.31
1	C	4	DG	C2-N2	5.03	1.39	1.34
2	D	43	DA	N7-C5	5.02	1.42	1.39
2	D	47	DC	C4'-O4'	5.02	1.50	1.45
1	C	1	DG	C8-N7	5.02	1.33	1.30
1	C	7	DT	C2-N3	5.01	1.41	1.37
3	A	173	ALA	CA-CB	5.00	1.62	1.52

All (545) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	60	DG	O4'-C1'-N9	26.72	126.71	108.00
1	C	4	DG	C5-N7-C8	25.58	117.09	104.30
2	D	56	DC	N3-C4-C5	-21.41	113.34	121.90
1	C	8	DG	C5-N7-C8	-20.22	94.19	104.30
1	C	16	DT	N3-C2-O2	-19.44	110.64	122.30
2	D	54	DG	O5'-P-OP2	-19.43	87.38	110.70
1	C	4	DG	N7-C8-N9	-19.14	103.53	113.10
1	C	2	DT	O5'-P-OP1	-17.39	89.84	110.70
2	D	51	DG	N1-C2-N3	17.03	134.12	123.90
1	C	17	DG	N9-C4-C5	16.86	112.14	105.40
1	C	4	DG	C4-C5-N7	-16.66	104.14	110.80
1	C	6	DG	C2-N3-C4	-16.61	103.60	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	55	DC	N1-C2-N3	16.15	130.50	119.20
2	D	55	DC	C2-N3-C4	-16.04	111.88	119.90
2	D	56	DC	O5'-P-OP1	16.04	129.95	110.70
2	D	43	DA	N1-C2-N3	16.02	137.31	129.30
1	C	2	DT	O4'-C4'-C3'	15.71	115.43	106.00
2	D	51	DG	C6-N1-C2	-15.63	115.72	125.10
2	D	55	DC	C6-N1-C2	-15.50	114.10	120.30
1	C	21	DG	O4'-C1'-C2'	-15.29	93.67	105.90
2	D	61	DC	O4'-C1'-N1	15.17	118.62	108.00
1	C	6	DG	C6-C5-N7	-15.08	121.35	130.40
2	D	47	DC	C5-C6-N1	15.08	128.54	121.00
2	D	56	DC	C6-N1-C2	-15.02	114.29	120.30
1	C	14	DC	O4'-C1'-N1	14.94	118.46	108.00
1	C	11	DC	O4'-C1'-N1	14.91	118.44	108.00
1	C	15	DG	N3-C2-N2	-14.87	109.49	119.90
3	A	118	ARG	NE-CZ-NH2	14.80	127.70	120.30
2	D	47	DC	C2-N3-C4	14.68	127.24	119.90
2	D	45	DG	O4'-C1'-C2'	-14.67	94.16	105.90
2	D	57	DC	O4'-C1'-N1	14.59	118.21	108.00
2	D	53	DC	C2-N3-C4	14.50	127.15	119.90
1	C	8	DG	N7-C8-N9	14.49	120.34	113.10
2	D	46	DC	P-O3'-C3'	-14.43	102.38	119.70
2	D	45	DG	C6-N1-C2	-14.40	116.46	125.10
1	C	6	DG	N1-C2-N3	14.35	132.51	123.90
1	C	19	DG	C5-N7-C8	-14.26	97.17	104.30
2	D	57	DC	N3-C4-C5	-14.23	116.21	121.90
1	C	16	DT	O4'-C1'-C2'	-14.17	94.56	105.90
2	D	51	DG	N3-C2-N2	-14.09	110.04	119.90
1	C	14	DC	N3-C4-C5	-14.04	116.28	121.90
1	C	14	DC	C6-N1-C2	-13.98	114.71	120.30
2	D	53	DC	N3-C4-C5	-13.93	116.33	121.90
2	D	50	DC	P-O5'-C5'	-13.92	98.63	120.90
3	A	118	ARG	NE-CZ-NH1	-13.87	113.36	120.30
2	D	49	DA	C2-N3-C4	-13.77	103.72	110.60
2	D	43	DA	N9-C4-C5	13.72	111.29	105.80
2	D	42	DC	N1-C2-O2	-13.43	110.84	118.90
2	D	48	DC	O5'-P-OP1	-13.39	93.65	105.70
2	D	56	DC	O4'-C1'-C2'	-13.33	95.23	105.90
1	C	8	DG	C4-C5-N7	13.31	116.12	110.80
2	D	49	DA	C4-C5-C6	13.21	123.61	117.00
1	C	18	DG	N9-C4-C5	13.18	110.67	105.40
1	C	21	DG	C2-N3-C4	-13.14	105.33	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	56	DC	C4-C5-C6	13.01	123.90	117.40
1	C	3	DG	C5-C6-N1	12.91	117.95	111.50
2	D	50	DC	OP1-P-OP2	12.75	138.72	119.60
1	C	21	DG	N1-C2-N3	12.70	131.52	123.90
2	D	52	DC	O5'-P-OP2	-12.69	94.28	105.70
1	C	5	DC	N3-C4-N4	-12.66	109.14	118.00
2	D	52	DC	OP2-P-O3'	12.64	133.02	105.20
2	D	49	DA	C5-C6-N1	-12.61	111.39	117.70
1	C	7	DT	OP1-P-OP2	12.55	138.43	119.60
1	C	13	DG	O5'-P-OP1	-12.47	94.48	105.70
2	D	49	DA	O4'-C4'-C3'	-12.40	98.56	106.00
1	C	10	DG	N9-C4-C5	12.36	110.34	105.40
1	C	20	DC	O4'-C4'-C3'	-12.31	98.61	106.00
1	C	19	DG	N7-C8-N9	12.28	119.24	113.10
2	D	45	DG	C5-C6-O6	-12.28	121.23	128.60
2	D	43	DA	O4'-C1'-C2'	-12.26	96.09	105.90
1	C	7	DT	O5'-P-OP1	-12.25	94.67	105.70
1	C	17	DG	C8-N9-C4	-12.25	101.50	106.40
2	D	48	DC	N3-C4-N4	-12.20	109.46	118.00
1	C	18	DG	C8-N9-C4	-12.18	101.53	106.40
2	D	54	DG	C6-C5-N7	-12.12	123.13	130.40
2	D	62	DC	O5'-P-OP1	-12.11	94.80	105.70
2	D	44	DC	N3-C4-N4	-12.08	109.55	118.00
2	D	55	DC	N1-C2-O2	-12.07	111.66	118.90
2	D	49	DA	OP1-P-O3'	-12.06	78.67	105.20
2	D	52	DC	N3-C4-C5	-12.05	117.08	121.90
2	D	63	DA	C2-N3-C4	-12.03	104.58	110.60
1	C	16	DT	N1-C2-O2	12.01	132.71	123.10
1	C	21	DG	OP1-P-OP2	12.01	137.61	119.60
1	C	16	DT	O4'-C4'-C3'	-11.94	98.83	106.00
1	C	21	DG	C4-C5-N7	-11.92	106.03	110.80
1	C	18	DG	C5-N7-C8	-11.92	98.34	104.30
2	D	52	DC	P-O3'-C3'	-11.88	105.44	119.70
2	D	46	DC	N3-C4-C5	-11.87	117.15	121.90
2	D	47	DC	C6-N1-C2	-11.86	115.56	120.30
1	C	5	DC	C5-C4-N4	11.84	128.49	120.20
1	C	3	DG	C5-C6-O6	-11.82	121.51	128.60
1	C	21	DG	O4'-C1'-N9	11.81	116.27	108.00
2	D	55	DC	O5'-P-OP1	11.78	124.83	110.70
1	C	4	DG	C5-C6-O6	11.70	135.62	128.60
2	D	49	DA	O4'-C1'-C2'	-11.66	96.58	105.90
1	C	8	DG	O4'-C4'-C3'	-11.51	99.09	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	60	DG	C6-N1-C2	-11.50	118.20	125.10
1	C	11	DC	C2-N3-C4	-11.33	114.23	119.90
2	D	46	DC	OP1-P-O3'	11.31	130.07	105.20
1	C	22	DT	C4-C5-C7	-11.29	112.22	119.00
2	D	56	DC	O4'-C4'-C3'	-11.25	99.25	106.00
2	D	53	DC	O5'-P-OP1	11.19	124.13	110.70
2	D	42	DC	O4'-C1'-N1	11.13	115.79	108.00
2	D	43	DA	N1-C6-N6	-11.06	111.96	118.60
2	D	57	DC	C4-C5-C6	11.05	122.93	117.40
2	D	48	DC	N1-C2-O2	10.95	125.47	118.90
1	C	5	DC	O4'-C1'-N1	10.93	115.65	108.00
1	C	18	DG	N7-C8-N9	10.88	118.54	113.10
2	D	51	DG	C6-C5-N7	-10.87	123.88	130.40
1	C	15	DG	N1-C2-N3	10.84	130.41	123.90
2	D	45	DG	N3-C2-N2	-10.71	112.40	119.90
1	C	19	DG	C6-C5-N7	-10.70	123.98	130.40
1	C	15	DG	C2-N3-C4	-10.66	106.57	111.90
2	D	49	DA	OP1-P-OP2	10.64	135.56	119.60
1	C	4	DG	C6-C5-N7	10.63	136.78	130.40
2	D	44	DC	C5-C4-N4	10.62	127.64	120.20
2	D	49	DA	O5'-P-OP1	-10.62	96.14	105.70
2	D	59	DC	O5'-P-OP2	-10.57	96.19	105.70
2	D	45	DG	C6-C5-N7	-10.55	124.07	130.40
2	D	48	DC	C5-C6-N1	-10.54	115.73	121.00
2	D	54	DG	C2-N3-C4	-10.49	106.66	111.90
1	C	2	DT	P-O3'-C3'	-10.48	107.13	119.70
2	D	46	DC	N3-C4-N4	10.46	125.32	118.00
2	D	56	DC	C2-N3-C4	10.43	125.12	119.90
2	D	56	DC	N3-C4-N4	10.42	125.30	118.00
1	C	17	DG	N3-C4-N9	-10.40	119.76	126.00
1	C	14	DC	C5-C6-N1	10.30	126.15	121.00
1	C	15	DG	N7-C8-N9	-10.29	107.96	113.10
1	C	19	DG	C4-C5-N7	10.28	114.91	110.80
3	B	165	CYS	CA-CB-SG	-10.22	95.61	114.00
1	C	6	DG	O4'-C1'-C2'	-10.21	97.73	105.90
1	C	10	DG	C4-C5-N7	-10.19	106.72	110.80
2	D	63	DA	C8-N9-C4	-10.19	101.72	105.80
3	A	155	ARG	NE-CZ-NH1	10.16	125.38	120.30
2	D	50	DC	O5'-P-OP2	-10.15	96.57	105.70
1	C	5	DC	C2-N3-C4	-10.13	114.83	119.90
1	C	8	DG	N3-C4-C5	10.13	133.67	128.60
2	D	46	DC	C6-N1-C2	-10.12	116.25	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	19	DG	C2-N3-C4	-10.09	106.86	111.90
1	C	14	DC	N3-C4-N4	10.06	125.04	118.00
1	C	3	DG	O4'-C1'-C2'	10.06	113.95	105.90
2	D	59	DC	C5-C4-N4	10.04	127.23	120.20
1	C	7	DT	O4'-C1'-C2'	-10.04	97.87	105.90
1	C	17	DG	O4'-C1'-N9	10.01	115.01	108.00
2	D	45	DG	O4'-C4'-C3'	-9.99	100.00	106.00
2	D	61	DC	P-O5'-C5'	-9.98	104.93	120.90
2	D	45	DG	N1-C2-N3	9.95	129.87	123.90
1	C	9	DG	C2-N3-C4	-9.94	106.93	111.90
2	D	60	DG	OP1-P-OP2	9.90	134.45	119.60
2	D	45	DG	O4'-C1'-N9	9.87	114.91	108.00
2	D	47	DC	O5'-P-OP2	9.82	122.48	110.70
2	D	52	DC	C1'-O4'-C4'	-9.81	100.29	110.10
2	D	43	DA	C4-C5-N7	-9.77	105.81	110.70
2	D	43	DA	C6-N1-C2	-9.73	112.76	118.60
2	D	51	DG	OP1-P-O3'	-9.72	83.82	105.20
2	D	52	DC	OP1-P-OP2	9.71	134.16	119.60
2	D	44	DC	N1-C2-O2	9.71	124.72	118.90
2	D	45	DG	N1-C6-O6	9.70	125.72	119.90
1	C	13	DG	N1-C2-N3	9.68	129.71	123.90
1	C	13	DG	OP1-P-OP2	9.67	134.11	119.60
2	D	57	DC	O5'-P-OP2	9.67	122.30	110.70
2	D	42	DC	C6-N1-C1'	9.64	132.37	120.80
1	C	1	DG	C4'-C3'-C2'	-9.62	94.44	103.10
1	C	20	DC	O4'-C1'-N1	9.53	114.67	108.00
2	D	51	DG	C5-C6-O6	-9.53	122.88	128.60
2	D	59	DC	O5'-P-OP1	9.52	122.12	110.70
2	D	56	DC	C2-N1-C1'	9.48	129.23	118.80
2	D	58	DA	OP1-P-OP2	9.44	133.76	119.60
1	C	6	DG	C4-C5-C6	9.40	124.44	118.80
1	C	7	DT	C4-C5-C7	-9.37	113.38	119.00
1	C	20	DC	P-O3'-C3'	9.32	130.88	119.70
1	C	14	DC	N3-C2-O2	-9.31	115.38	121.90
2	D	61	DC	N1-C2-O2	9.28	124.47	118.90
1	C	21	DG	C4-N9-C1'	9.24	138.51	126.50
1	C	10	DG	O4'-C1'-C2'	-9.24	98.51	105.90
1	C	18	DG	O4'-C1'-C2'	-9.23	98.52	105.90
2	D	49	DA	N1-C2-N3	9.22	133.91	129.30
1	C	17	DG	C6-N1-C2	-9.22	119.57	125.10
2	D	43	DA	C5-C6-N6	9.21	131.07	123.70
1	C	2	DT	C5'-C4'-O4'	-9.21	91.80	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	12	DG	OP1-P-O3'	9.19	125.41	105.20
2	D	62	DC	OP1-P-OP2	9.13	133.30	119.60
1	C	18	DG	C6-N1-C2	-9.13	119.62	125.10
3	B	146	ARG	NE-CZ-NH2	9.13	124.86	120.30
1	C	11	DC	C6-N1-C2	-9.12	116.65	120.30
1	C	15	DG	N9-C4-C5	9.12	109.05	105.40
2	D	48	DC	C5-C4-N4	9.10	126.57	120.20
1	C	12	DG	P-O5'-C5'	-9.09	106.36	120.90
2	D	56	DC	C1'-O4'-C4'	9.09	119.19	110.10
2	D	42	DC	C2-N1-C1'	-9.03	108.87	118.80
1	C	10	DG	N3-C2-N2	-9.01	113.59	119.90
2	D	54	DG	P-O3'-C3'	-8.99	108.91	119.70
1	C	4	DG	C8-N9-C4	8.99	110.00	106.40
2	D	44	DC	C4'-C3'-C2'	-8.97	95.03	103.10
2	D	54	DG	C4-C5-N7	8.96	114.38	110.80
2	D	59	DC	N3-C4-N4	-8.95	111.74	118.00
1	C	21	DG	N9-C4-C5	8.93	108.97	105.40
1	C	6	DG	O5'-P-OP1	8.92	121.41	110.70
1	C	8	DG	C1'-O4'-C4'	8.91	119.01	110.10
1	C	15	DG	C5-N7-C8	8.90	108.75	104.30
3	B	178	ARG	NE-CZ-NH2	-8.88	115.86	120.30
2	D	63	DA	O4'-C1'-N9	8.86	114.20	108.00
2	D	46	DC	O5'-P-OP2	8.80	121.26	110.70
1	C	10	DG	N7-C8-N9	-8.80	108.70	113.10
1	C	21	DG	C5-N7-C8	8.78	108.69	104.30
1	C	6	DG	N3-C2-N2	-8.78	113.75	119.90
2	D	60	DG	O4'-C1'-C2'	-8.76	98.89	105.90
2	D	46	DC	C4-C5-C6	8.72	121.76	117.40
2	D	62	DC	O5'-P-OP2	8.72	121.16	110.70
2	D	51	DG	C2-N3-C4	-8.67	107.56	111.90
1	C	1	DG	C6-N1-C2	-8.65	119.91	125.10
1	C	15	DG	O4'-C1'-N9	8.65	114.05	108.00
2	D	45	DG	O5'-P-OP2	8.63	121.06	110.70
2	D	43	DA	C4-C5-C6	8.61	121.30	117.00
2	D	51	DG	C4-C5-C6	8.61	123.96	118.80
1	C	21	DG	C4-C5-C6	8.57	123.94	118.80
2	D	46	DC	O3'-P-O5'	-8.56	87.73	104.00
1	C	19	DG	O4'-C1'-N9	8.55	113.99	108.00
1	C	10	DG	C6-N1-C2	-8.49	120.01	125.10
2	D	57	DC	C5'-C4'-C3'	-8.48	98.83	114.10
1	C	22	DT	N3-C2-O2	-8.48	117.21	122.30
2	D	57	DC	C6-N1-C2	-8.45	116.92	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	48	DC	C6-N1-C2	8.45	123.68	120.30
1	C	13	DG	C2-N3-C4	-8.42	107.69	111.90
2	D	52	DC	O5'-P-OP1	8.37	120.74	110.70
2	D	43	DA	OP1-P-OP2	8.37	132.15	119.60
1	C	9	DG	O4'-C1'-C2'	-8.36	99.21	105.90
1	C	11	DC	N1-C2-N3	8.34	125.04	119.20
1	C	15	DG	C4-C5-C6	8.29	123.77	118.80
1	C	5	DC	C4-C5-C6	8.27	121.53	117.40
1	C	5	DC	N3-C2-O2	-8.27	116.11	121.90
2	D	52	DC	N3-C4-N4	8.25	123.78	118.00
1	C	12	DG	C6-C5-N7	-8.23	125.46	130.40
2	D	43	DA	C1'-O4'-C4'	8.23	118.33	110.10
3	A	127	ARG	NE-CZ-NH1	-8.23	116.19	120.30
1	C	19	DG	O5'-P-OP1	-8.20	98.32	105.70
1	C	18	DG	O4'-C1'-N9	8.19	113.73	108.00
1	C	18	DG	C1'-O4'-C4'	8.18	118.28	110.10
2	D	47	DC	C4-C5-C6	-8.17	113.31	117.40
1	C	2	DT	C4'-C3'-C2'	-8.16	95.75	103.10
1	C	8	DG	O4'-C1'-N9	8.16	113.71	108.00
1	C	21	DG	P-O3'-C3'	8.16	129.49	119.70
2	D	43	DA	O4'-C1'-N9	8.13	113.69	108.00
2	D	47	DC	N3-C4-C5	-8.09	118.66	121.90
1	C	3	DG	C2-N3-C4	8.09	115.94	111.90
1	C	3	DG	O4'-C4'-C3'	8.02	110.81	106.00
1	C	8	DG	N3-C4-N9	-8.01	121.19	126.00
2	D	60	DG	C5-C6-N1	8.01	115.50	111.50
1	C	7	DT	N3-C4-C5	-8.00	110.40	115.20
1	C	3	DG	C1'-O4'-C4'	-7.95	102.15	110.10
1	C	6	DG	O5'-P-OP2	-7.93	98.57	105.70
1	C	18	DG	C5'-C4'-O4'	-7.91	94.26	109.30
2	D	45	DG	C4-C5-C6	7.91	123.54	118.80
1	C	13	DG	N1-C2-N2	-7.88	109.10	116.20
2	D	56	DC	P-O5'-C5'	-7.88	108.30	120.90
2	D	53	DC	C5-C6-N1	7.84	124.92	121.00
2	D	58	DA	P-O5'-C5'	-7.84	108.36	120.90
2	D	53	DC	O3'-P-O5'	-7.73	89.31	104.00
2	D	62	DC	C5-C6-N1	7.71	124.86	121.00
2	D	54	DG	OP1-P-OP2	7.69	131.14	119.60
1	C	6	DG	C6-N1-C2	-7.68	120.49	125.10
2	D	51	DG	C5-N7-C8	-7.65	100.47	104.30
2	D	51	DG	N3-C4-C5	-7.61	124.80	128.60
1	C	16	DT	C4-C5-C7	-7.58	114.45	119.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	DT	C5-C4-O4	-7.57	119.60	124.90
2	D	49	DA	C5-C6-N6	7.55	129.74	123.70
2	D	46	DC	C2-N1-C1'	7.54	127.09	118.80
2	D	46	DC	N1-C2-O2	-7.53	114.38	118.90
1	C	21	DG	C8-N9-C1'	-7.50	117.25	127.00
2	D	59	DC	C6-N1-C2	-7.47	117.31	120.30
2	D	56	DC	N1-C2-O2	-7.46	114.42	118.90
2	D	52	DC	P-O5'-C5'	-7.45	108.98	120.90
1	C	1	DG	N3-C2-N2	-7.44	114.69	119.90
2	D	50	DC	O5'-P-OP1	7.41	119.59	110.70
3	B	155	ARG	NE-CZ-NH1	7.39	124.00	120.30
1	C	10	DG	C5-N7-C8	7.37	107.98	104.30
2	D	61	DC	N3-C2-O2	-7.36	116.75	121.90
2	D	51	DG	P-O5'-C5'	-7.35	109.14	120.90
2	D	62	DC	C6-N1-C2	-7.34	117.36	120.30
1	C	21	DG	N1-C2-N2	-7.33	109.60	116.20
2	D	62	DC	C2-N3-C4	7.32	123.56	119.90
1	C	4	DG	N1-C6-O6	-7.32	115.51	119.90
2	D	48	DC	C5'-C4'-O4'	-7.31	95.41	109.30
1	C	18	DG	OP1-P-O3'	7.30	121.25	105.20
2	D	51	DG	P-O3'-C3'	-7.30	110.94	119.70
2	D	53	DC	C5'-C4'-O4'	-7.27	95.49	109.30
1	C	3	DG	N1-C2-N3	-7.26	119.54	123.90
1	C	12	DG	C5-N7-C8	-7.26	100.67	104.30
2	D	48	DC	N3-C2-O2	-7.26	116.82	121.90
1	C	2	DT	OP1-P-OP2	7.24	130.45	119.60
1	C	19	DG	N3-C2-N2	7.23	124.96	119.90
2	D	61	DC	C5-C4-N4	7.23	125.26	120.20
2	D	52	DC	O4'-C4'-C3'	7.22	110.33	106.00
2	D	55	DC	O4'-C4'-C3'	-7.21	101.61	104.50
2	D	47	DC	O5'-P-OP1	-7.21	99.21	105.70
3	A	113	ASP	CB-CG-OD2	7.21	124.78	118.30
2	D	51	DG	N1-C6-O6	7.19	124.22	119.90
1	C	9	DG	N3-C4-C5	7.19	132.20	128.60
1	C	22	DT	O4'-C4'-C3'	-7.18	101.63	104.50
2	D	43	DA	OP2-P-O3'	7.17	120.97	105.20
1	C	18	DG	O4'-C4'-C3'	-7.13	101.65	104.50
1	C	12	DG	C4-C5-N7	7.10	113.64	110.80
1	C	18	DG	C5-C6-O6	-7.05	124.37	128.60
1	C	22	DT	C5-C6-N1	-7.02	119.49	123.70
1	C	15	DG	C6-N1-C2	-7.01	120.89	125.10
1	C	15	DG	O5'-P-OP1	-7.00	99.40	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	8	DG	C2-N3-C4	-6.99	108.41	111.90
1	C	10	DG	C5-C6-O6	6.98	132.79	128.60
1	C	6	DG	C4-N9-C1'	6.97	135.57	126.50
1	C	12	DG	C8-N9-C4	-6.97	103.61	106.40
1	C	15	DG	N3-C4-N9	-6.97	121.82	126.00
2	D	59	DC	P-O3'-C3'	6.96	128.05	119.70
1	C	3	DG	N3-C2-N2	6.94	124.76	119.90
2	D	44	DC	N3-C2-O2	-6.93	117.05	121.90
2	D	43	DA	O4'-C4'-C3'	-6.91	101.74	104.50
2	D	54	DG	C8-N9-C4	-6.85	103.66	106.40
1	C	9	DG	N3-C4-N9	-6.84	121.89	126.00
1	C	10	DG	C1'-O4'-C4'	6.83	116.93	110.10
1	C	9	DG	N1-C2-N3	6.82	127.99	123.90
2	D	61	DC	OP1-P-OP2	6.82	129.83	119.60
2	D	43	DA	C5'-C4'-O4'	6.80	122.23	109.30
1	C	19	DG	N1-C6-O6	6.78	123.97	119.90
1	C	21	DG	N3-C4-N9	-6.78	121.93	126.00
3	A	132	GLN	CA-CB-CG	6.76	128.28	113.40
1	C	4	DG	O3'-P-O5'	-6.74	91.19	104.00
2	D	52	DC	O3'-P-O5'	-6.72	91.22	104.00
1	C	10	DG	O5'-P-OP2	6.71	118.75	110.70
1	C	21	DG	C1'-O4'-C4'	6.71	116.81	110.10
1	C	12	DG	N3-C4-C5	-6.70	125.25	128.60
1	C	10	DG	N3-C4-N9	-6.69	121.98	126.00
1	C	5	DC	O4'-C4'-C3'	-6.69	101.82	104.50
1	C	16	DT	N3-C4-O4	-6.69	115.89	119.90
2	D	45	DG	N3-C4-N9	6.68	130.01	126.00
2	D	62	DC	N3-C4-N4	-6.68	113.32	118.00
1	C	8	DG	C4-C5-C6	-6.67	114.80	118.80
1	C	13	DG	O3'-P-O5'	-6.65	91.36	104.00
1	C	10	DG	C4-C5-C6	6.64	122.78	118.80
2	D	55	DC	C4-C5-C6	6.63	120.72	117.40
1	C	1	DG	O4'-C1'-N9	6.62	112.63	108.00
2	D	63	DA	N3-C4-N9	-6.61	122.11	127.40
1	C	8	DG	O4'-C1'-C2'	-6.59	100.63	105.90
2	D	47	DC	O4'-C1'-C2'	-6.59	100.63	105.90
2	D	56	DC	O3'-P-O5'	-6.58	91.50	104.00
1	C	8	DG	N1-C6-O6	-6.56	115.96	119.90
2	D	57	DC	N1-C2-N3	6.55	123.78	119.20
3	A	150	LEU	CB-CG-CD1	-6.55	99.87	111.00
2	D	55	DC	OP2-P-O3'	6.54	119.58	105.20
1	C	15	DG	C4-C5-N7	-6.52	108.19	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	17	DG	C8-N9-C1'	6.52	135.47	127.00
1	C	18	DG	N1-C2-N3	6.50	127.80	123.90
1	C	19	DG	N1-C2-N2	-6.49	110.36	116.20
2	D	53	DC	O4'-C1'-N1	-6.48	103.47	108.00
1	C	1	DG	P-O3'-C3'	6.47	127.47	119.70
2	D	58	DA	C6-N1-C2	6.46	122.48	118.60
3	B	124	ARG	NE-CZ-NH2	-6.46	117.07	120.30
2	D	54	DG	O4'-C1'-C2'	-6.45	100.74	105.90
1	C	13	DG	C4-C5-C6	6.42	122.66	118.80
2	D	63	DA	N9-C4-C5	6.42	108.37	105.80
2	D	60	DG	O4'-C4'-C3'	-6.40	101.94	104.50
1	C	6	DG	C8-N9-C1'	-6.40	118.68	127.00
2	D	45	DG	O5'-P-OP1	-6.40	99.94	105.70
1	C	21	DG	C5-C6-N1	-6.38	108.31	111.50
1	C	13	DG	C6-N1-C2	-6.38	121.27	125.10
1	C	8	DG	C8-N9-C4	-6.38	103.85	106.40
1	C	19	DG	O3'-P-O5'	-6.37	91.89	104.00
1	C	4	DG	O4'-C4'-C3'	-6.37	101.95	104.50
2	D	42	DC	O4'-C1'-C2'	6.36	110.98	105.90
2	D	63	DA	N7-C8-N9	6.33	116.97	113.80
2	D	57	DC	OP1-P-O3'	-6.31	91.32	105.20
3	B	178	ARG	NE-CZ-NH1	6.30	123.45	120.30
2	D	52	DC	C4-C5-C6	6.29	120.55	117.40
3	B	167	ILE	CG1-CB-CG2	6.28	125.22	111.40
2	D	43	DA	C2-N3-C4	-6.27	107.47	110.60
2	D	60	DG	N1-C6-O6	-6.27	116.14	119.90
2	D	63	DA	C4-C5-C6	6.27	120.13	117.00
2	D	49	DA	N9-C4-C5	6.26	108.31	105.80
1	C	16	DT	O5'-P-OP1	-6.26	100.06	105.70
2	D	58	DA	C5'-C4'-C3'	-6.26	102.84	114.10
2	D	45	DG	C3'-C2'-C1'	-6.26	94.99	102.50
1	C	18	DG	C5'-C4'-C3'	6.24	125.33	114.10
2	D	42	DC	N3-C2-O2	6.24	126.27	121.90
3	B	152	THR	CA-CB-CG2	-6.23	103.67	112.40
1	C	18	DG	N3-C4-N9	-6.22	122.27	126.00
2	D	58	DA	OP1-P-O3'	-6.20	91.56	105.20
1	C	18	DG	C6-C5-N7	-6.19	126.69	130.40
1	C	16	DT	C6-N1-C2	-6.18	118.21	121.30
2	D	60	DG	C6-C5-N7	-6.17	126.69	130.40
2	D	62	DC	O4'-C1'-N1	6.17	112.32	108.00
2	D	53	DC	OP1-P-O3'	6.14	118.71	105.20
2	D	54	DG	C4-C5-C6	6.14	122.49	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	53	DC	C6-N1-C1'	6.13	128.15	120.80
2	D	58	DA	O4'-C1'-C2'	-6.12	101.00	105.90
2	D	46	DC	C3'-C2'-C1'	6.11	109.83	102.50
1	C	22	DT	C2-N3-C4	-6.10	123.54	127.20
1	C	17	DG	C3'-C2'-C1'	6.09	109.81	102.50
2	D	61	DC	C6-N1-C2	6.09	122.74	120.30
3	B	110	GLU	N-CA-C	6.07	127.39	111.00
2	D	51	DG	O4'-C1'-C2'	-6.06	101.05	105.90
2	D	43	DA	C8-N9-C4	-6.05	103.38	105.80
1	C	20	DC	N3-C2-O2	-6.04	117.67	121.90
2	D	63	DA	N1-C2-N3	6.01	132.31	129.30
1	C	5	DC	O4'-C1'-C2'	-6.01	101.09	105.90
2	D	49	DA	C4-C5-N7	-6.00	107.70	110.70
2	D	43	DA	C5'-C4'-C3'	-5.98	103.33	114.10
1	C	11	DC	OP1-P-OP2	5.98	128.57	119.60
2	D	52	DC	C5'-C4'-C3'	-5.98	103.34	114.10
2	D	62	DC	C5-C4-N4	5.97	124.38	120.20
2	D	54	DG	C5-C6-N1	-5.97	108.52	111.50
2	D	60	DG	C4-C5-C6	5.96	122.38	118.80
2	D	55	DC	N3-C2-O2	-5.96	117.73	121.90
1	C	4	DG	C2-N3-C4	-5.95	108.93	111.90
1	C	11	DC	O5'-P-OP1	-5.94	100.36	105.70
3	A	164	ALA	CB-CA-C	5.93	119.00	110.10
3	A	124	ARG	CG-CD-NE	-5.93	99.35	111.80
1	C	15	DG	O5'-P-OP2	5.92	117.80	110.70
2	D	52	DC	OP1-P-O3'	-5.92	92.18	105.20
2	D	47	DC	OP1-P-O3'	5.91	118.19	105.20
1	C	6	DG	OP1-P-OP2	-5.89	110.76	119.60
1	C	9	DG	OP1-P-OP2	5.89	128.44	119.60
1	C	2	DT	N1-C1'-C2'	5.89	123.79	112.60
1	C	21	DG	C3'-C2'-C1'	5.88	109.55	102.50
1	C	5	DC	OP1-P-O3'	5.88	118.13	105.20
1	C	20	DC	C4-C5-C6	5.87	120.33	117.40
2	D	60	DG	C3'-C2'-C1'	-5.87	95.46	102.50
1	C	21	DG	C6-N1-C2	-5.84	121.59	125.10
3	A	120	ASP	OD1-CG-OD2	-5.84	112.20	123.30
1	C	3	DG	C4-N9-C1'	-5.84	118.91	126.50
2	D	54	DG	N3-C4-N9	-5.83	122.50	126.00
1	C	18	DG	N3-C2-N2	-5.82	115.82	119.90
2	D	50	DC	N1-C2-N3	5.82	123.27	119.20
1	C	18	DG	C4-C5-C6	5.82	122.29	118.80
1	C	16	DT	P-O5'-C5'	5.81	130.20	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	22	DT	C6-C5-C7	5.80	126.38	122.90
2	D	50	DC	O4'-C1'-N1	-5.80	103.94	108.00
2	D	62	DC	C4-C5-C6	-5.80	114.50	117.40
1	C	13	DG	O5'-P-OP2	-5.80	100.48	105.70
2	D	42	DC	P-O3'-C3'	-5.79	112.75	119.70
1	C	14	DC	C2-N3-C4	5.79	122.79	119.90
2	D	57	DC	O5'-P-OP1	-5.78	100.50	105.70
2	D	52	DC	C4'-C3'-C2'	-5.78	97.90	103.10
2	D	60	DG	P-O5'-C5'	-5.78	111.66	120.90
2	D	59	DC	OP1-P-OP2	5.77	128.26	119.60
2	D	46	DC	O5'-C5'-C4'	-5.77	96.58	111.00
2	D	46	DC	C4'-C3'-O3'	5.75	124.07	109.70
1	C	16	DT	C6-C5-C7	5.74	126.35	122.90
3	B	120	ASP	CB-CG-OD1	5.74	123.46	118.30
1	C	8	DG	C5-C6-N1	5.74	114.37	111.50
1	C	18	DG	P-O5'-C5'	-5.72	111.75	120.90
1	C	4	DG	OP2-P-O3'	5.70	117.73	105.20
2	D	50	DC	C6-N1-C2	-5.69	118.03	120.30
1	C	15	DG	O4'-C1'-C2'	-5.68	101.36	105.90
2	D	43	DA	C4-N9-C1'	5.67	136.51	126.30
3	B	155	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	C	15	DG	C6-C5-N7	-5.66	127.00	130.40
1	C	22	DT	C4-C5-C6	5.66	121.39	118.00
1	C	1	DG	N9-C4-C5	5.65	107.66	105.40
2	D	54	DG	O5'-P-OP1	-5.65	100.61	105.70
1	C	19	DG	O5'-P-OP2	5.64	117.47	110.70
1	C	20	DC	O4'-C1'-C2'	-5.63	101.39	105.90
2	D	51	DG	OP2-P-O3'	5.63	117.58	105.20
1	C	10	DG	OP2-P-O3'	5.62	117.55	105.20
1	C	7	DT	C6-N1-C2	-5.61	118.49	121.30
1	C	1	DG	C3'-C2'-C1'	5.61	109.23	102.50
1	C	20	DC	C4'-C3'-C2'	5.61	108.14	103.10
2	D	42	DC	C5'-C4'-C3'	-5.60	104.02	114.10
1	C	18	DG	N1-C6-O6	5.59	123.25	119.90
2	D	56	DC	OP1-P-OP2	-5.58	111.22	119.60
1	C	3	DG	O5'-P-OP2	-5.58	100.68	105.70
1	C	6	DG	C4-C5-N7	5.57	113.03	110.80
3	A	124	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	C	19	DG	C5-C6-N1	-5.54	108.73	111.50
1	C	3	DG	N3-C4-C5	-5.51	125.84	128.60
1	C	2	DT	N3-C4-O4	5.49	123.19	119.90
1	C	4	DG	O5'-P-OP1	-5.49	100.76	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	55	DC	OP1-P-O3'	-5.48	93.15	105.20
1	C	17	DG	C4-C5-N7	-5.47	108.61	110.80
1	C	14	DC	C1'-O4'-C4'	-5.46	104.64	110.10
1	C	11	DC	C4-C5-C6	5.46	120.13	117.40
2	D	59	DC	O4'-C4'-C3'	-5.45	102.32	104.50
1	C	21	DG	C8-N9-C4	-5.45	104.22	106.40
1	C	6	DG	C5-C6-N1	-5.44	108.78	111.50
3	A	152	THR	OG1-CB-CG2	-5.42	97.53	110.00
2	D	45	DG	N9-C4-C5	-5.41	103.24	105.40
1	C	14	DC	N1-C2-O2	5.40	122.14	118.90
1	C	3	DG	O3'-P-O5'	-5.40	93.75	104.00
1	C	13	DG	N9-C1'-C2'	5.40	122.86	112.60
1	C	10	DG	OP1-P-O3'	-5.39	93.34	105.20
1	C	17	DG	N1-C2-N3	5.39	127.13	123.90
3	B	104	PRO	N-CA-C	5.38	126.08	112.10
2	D	58	DA	N7-C8-N9	5.36	116.48	113.80
2	D	56	DC	OP1-P-O3'	-5.35	93.42	105.20
2	D	61	DC	C5'-C4'-O4'	5.35	119.46	109.30
3	A	166	ASP	N-CA-CB	5.33	120.20	110.60
1	C	4	DG	C5-C6-N1	-5.33	108.84	111.50
2	D	55	DC	O4'-C1'-N1	5.32	111.73	108.00
2	D	43	DA	C3'-C2'-C1'	5.32	108.88	102.50
1	C	15	DG	N1-C6-O6	5.32	123.09	119.90
1	C	1	DG	OP1-P-O3'	5.30	116.86	105.20
3	A	146	ARG	NE-CZ-NH1	-5.29	117.65	120.30
3	B	177	GLU	OE1-CD-OE2	-5.29	116.96	123.30
1	C	14	DC	OP1-P-OP2	5.27	127.50	119.60
1	C	7	DT	P-O3'-C3'	-5.26	113.39	119.70
1	C	3	DG	C5'-C4'-C3'	-5.26	104.63	114.10
2	D	43	DA	P-O5'-C5'	5.26	129.31	120.90
1	C	10	DG	OP1-P-OP2	5.24	127.47	119.60
1	C	19	DG	N3-C4-C5	5.24	131.22	128.60
2	D	47	DC	C5'-C4'-C3'	-5.24	104.67	114.10
1	C	12	DG	P-O3'-C3'	5.23	125.98	119.70
3	A	142	ARG	NE-CZ-NH1	-5.23	117.68	120.30
2	D	63	DA	C6-C5-N7	-5.23	128.64	132.30
1	C	18	DG	C8-N9-C1'	5.23	133.80	127.00
1	C	21	DG	O3'-P-O5'	5.22	113.92	104.00
2	D	61	DC	N3-C4-C5	-5.21	119.81	121.90
2	D	61	DC	N3-C4-N4	-5.21	114.36	118.00
1	C	11	DC	N1-C2-O2	-5.20	115.78	118.90
3	A	166	ASP	CB-CG-OD2	5.19	122.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	49	DA	C6-C5-N7	-5.19	128.67	132.30
1	C	5	DC	O3'-P-O5'	-5.18	94.15	104.00
1	C	7	DT	C4-C5-C6	5.18	121.11	118.00
1	C	17	DG	N3-C2-N2	-5.18	116.27	119.90
2	D	51	DG	N9-C4-C5	5.18	107.47	105.40
2	D	46	DC	N1-C2-N3	5.17	122.82	119.20
3	A	135	PHE	O-C-N	-5.17	114.42	122.70
1	C	10	DG	O4'-C1'-N9	-5.15	104.39	108.00
3	B	118	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	C	9	DG	O5'-P-OP2	-5.15	101.07	105.70
1	C	22	DT	C3'-C2'-C1'	-5.15	96.32	102.50
3	B	144	PHE	CB-CA-C	-5.15	100.10	110.40
3	A	120	ASP	CB-CG-OD1	5.15	122.93	118.30
1	C	4	DG	C6-N1-C2	5.14	128.19	125.10
1	C	13	DG	P-O3'-C3'	-5.14	113.53	119.70
2	D	47	DC	O3'-P-O5'	-5.14	94.24	104.00
1	C	3	DG	C4'-C3'-O3'	-5.13	96.88	109.70
1	C	1	DG	N3-C4-C5	-5.13	126.04	128.60
1	C	4	DG	O4'-C1'-N9	-5.12	104.42	108.00
1	C	2	DT	O3'-P-O5'	-5.09	94.33	104.00
1	C	11	DC	OP2-P-O3'	5.07	116.36	105.20
2	D	58	DA	C5-C6-N1	-5.07	115.16	117.70
2	D	42	DC	N1-C2-N3	5.05	122.73	119.20
1	C	17	DG	N1-C6-O6	-5.03	116.88	119.90
1	C	16	DT	C3'-C2'-C1'	-5.03	96.47	102.50
2	D	58	DA	C5-N7-C8	-5.02	101.39	103.90
1	C	19	DG	P-O3'-C3'	5.00	125.70	119.70
2	D	47	DC	N3-C4-N4	5.00	121.50	118.00
3	B	163	PHE	N-CA-C	5.00	124.50	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	164	ALA	Mainchain
3	A	174	ARG	Mainchain
3	A	187	ARG	Peptide
1	C	14	DC	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	461	0	245	14	0
2	D	435	0	242	14	0
3	A	730	0	714	20	0
3	B	701	0	687	49	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
5	A	36	0	0	7	0
5	B	21	0	0	13	0
5	C	24	0	0	3	0
5	D	19	0	0	1	0
All	All	2433	0	1888	93	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 23.

All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:141:MET:SD	3:B:141:MET:CE	2.08	1.40
3:B:182:THR:HB	5:B:82:HOH:O	1.57	1.02
3:A:183:LYS:HB2	5:A:87:HOH:O	1.61	0.99
3:B:114:ARG:HH11	3:B:114:ARG:HG2	1.40	0.86
3:B:178:ARG:HD2	5:B:64:HOH:O	1.76	0.85
3:B:118:ARG:NH2	3:B:120:ASP:OD2	2.10	0.85
2:D:43:DA:H2''	2:D:44:DC:C5'	2.11	0.81
2:D:43:DA:H2''	2:D:44:DC:H5''	1.64	0.78
3:B:122:LEU:HD11	3:B:126:ILE:HD11	1.64	0.78
1:C:1:DG:H1'	5:C:41:HOH:O	1.83	0.77
3:B:122:LEU:CD1	3:B:126:ILE:HD11	2.15	0.77
2:D:47:DC:H2''	2:D:48:DC:H5'	1.67	0.77
1:C:8:DG:N7	3:A:149:HIS:NE2	2.31	0.75
3:A:102:GLU:HB2	5:A:94:HOH:O	1.86	0.74
2:D:52:DC:H2''	2:D:53:DC:H5'	1.71	0.73
2:D:60:DG:H2'	2:D:60:DG:O5'	1.90	0.72
1:C:1:DG:H2''	1:C:2:DT:H5''	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:DG:O6	2:D:48:DC:N4	2.17	0.70
3:B:114:ARG:HH11	3:B:114:ARG:CG	2.04	0.69
3:B:109:VAL:HG13	3:B:110:GLU:OE1	1.94	0.68
3:B:161:LYS:HB3	5:B:71:HOH:O	1.92	0.67
3:B:135:PHE:CZ	3:B:147:SER:HB3	2.30	0.67
3:B:135:PHE:CE1	3:B:147:SER:HB3	2.30	0.67
1:C:9:DG:OP2	5:C:46:HOH:O	2.12	0.67
3:B:160:GLU:HG2	3:B:162:PRO:HD3	1.76	0.66
1:C:17:DG:H2''	1:C:18:DG:H5'	1.78	0.65
2:D:59:DC:OP2	5:D:67:HOH:O	2.15	0.64
3:B:171:LYS:HB3	5:B:71:HOH:O	1.99	0.62
1:C:1:DG:H2''	1:C:2:DT:C5'	2.30	0.60
1:C:21:DG:H2''	1:C:22:DT:H5'	1.82	0.60
2:D:43:DA:H2''	2:D:44:DC:H5'	1.84	0.59
3:B:114:ARG:NH1	3:B:114:ARG:CG	2.61	0.59
2:D:43:DA:C2'	2:D:44:DC:H5''	2.31	0.59
3:B:186:LEU:HG	5:B:100:HOH:O	2.02	0.59
3:A:137:CYS:O	3:A:141:MET:HA	2.04	0.57
1:C:3:DG:H5''	3:A:170:ARG:NH2	2.20	0.57
3:B:152:THR:HG21	5:B:17:HOH:O	2.04	0.57
3:B:165:CYS:HB2	3:B:181:HIS:CD2	2.39	0.57
2:D:60:DG:C2'	2:D:60:DG:O5'	2.45	0.56
3:B:167:ILE:HB	3:B:185:HIS:CD2	2.40	0.56
3:A:113:ASP:HB2	5:A:88:HOH:O	2.04	0.56
3:B:162:PRO:HB2	3:B:163:PHE:CD2	2.40	0.56
3:A:128:ILE:O	3:A:128:ILE:HD12	2.06	0.56
3:A:128:ILE:C	3:A:128:ILE:HD12	2.27	0.55
3:B:122:LEU:O	3:B:126:ILE:HG12	2.06	0.55
3:A:187:ARG:HH11	3:A:187:ARG:HA	1.72	0.54
3:A:103:ARG:O	3:A:115:ARG:NH1	2.40	0.54
3:B:161:LYS:CB	5:B:71:HOH:O	2.54	0.53
2:D:56:DC:H2''	2:D:57:DC:H5''	1.90	0.52
3:B:149:HIS:HB2	5:B:90:HOH:O	2.10	0.51
3:A:181:HIS:O	3:A:184:ILE:HG12	2.11	0.51
3:B:122:LEU:HD11	3:B:126:ILE:CD1	2.39	0.51
3:B:165:CYS:HB2	3:B:181:HIS:HD2	1.76	0.50
3:B:140:CYS:SG	3:B:142:ARG:HB3	2.51	0.50
3:B:135:PHE:CE2	3:B:146:ARG:HA	2.46	0.49
3:B:181:HIS:O	3:B:184:ILE:HG12	2.13	0.49
3:A:178:ARG:NE	5:A:32:HOH:O	2.39	0.49
2:D:53:DC:H2''	2:D:54:DG:O5'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:DT:H5'	5:C:29:HOH:O	2.13	0.48
3:B:167:ILE:HD12	3:B:185:HIS:CB	2.44	0.48
3:B:133:LYS:HB3	3:B:144:PHE:C	2.34	0.47
2:D:47:DC:H2''	2:D:48:DC:C5'	2.40	0.47
3:B:145:SER:C	3:B:146:ARG:HG3	2.36	0.46
1:C:2:DT:H2''	1:C:3:DG:O5'	2.15	0.46
1:C:18:DG:OP1	3:B:125:HIS:ND1	2.35	0.46
3:A:183:LYS:HD3	5:A:87:HOH:O	2.14	0.45
3:B:122:LEU:CD1	3:B:126:ILE:CD1	2.92	0.45
3:B:132:GLN:HG2	3:B:134:PRO:HD3	1.97	0.45
3:B:124:ARG:HD2	3:B:146:ARG:HD2	1.97	0.45
3:B:124:ARG:O	3:B:127:ARG:HB2	2.17	0.45
3:B:136:GLN:HG3	3:B:143:ASN:ND2	2.32	0.45
3:B:135:PHE:HB3	3:B:150:LEU:HD22	1.99	0.45
2:D:63:DA:O5'	2:D:63:DA:H2'	2.17	0.45
3:A:130:THR:O	3:A:132:GLN:N	2.50	0.44
3:B:138:ARG:HA	5:B:83:HOH:O	2.17	0.44
3:B:155:ARG:HB3	3:B:160:GLU:O	2.19	0.43
3:A:136:GLN:HG3	3:A:143:ASN:ND2	2.34	0.43
3:B:170:ARG:HD2	5:B:70:HOH:O	2.18	0.43
3:B:163:PHE:HZ	5:B:39:HOH:O	2.01	0.43
3:A:127:ARG:HH11	3:A:127:ARG:HD3	1.57	0.43
1:C:17:DG:H2''	1:C:18:DG:C5'	2.46	0.43
3:B:160:GLU:HB3	5:B:31:HOH:O	2.18	0.43
3:A:186:LEU:CD1	5:A:95:HOH:O	2.66	0.42
3:B:137:CYS:C	3:B:139:ILE:H	2.22	0.42
1:C:12:DG:H2''	1:C:13:DG:OP2	2.19	0.42
3:A:148:ASP:N	3:A:148:ASP:OD1	2.49	0.42
3:B:135:PHE:CE1	3:B:147:SER:CB	3.00	0.42
3:A:180:ARG:O	5:A:87:HOH:O	2.21	0.41
3:B:178:ARG:CD	5:B:64:HOH:O	2.52	0.41
3:B:153:HIS:C	3:B:153:HIS:CD2	2.93	0.41
3:B:126:ILE:HD12	3:B:126:ILE:HG23	1.76	0.41
3:B:144:PHE:HZ	3:B:153:HIS:CE1	2.38	0.41
3:A:125:HIS:O	3:A:128:ILE:HG23	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	85/87 (98%)	77 (91%)	4 (5%)	4 (5%)	3	1
3	B	82/87 (94%)	72 (88%)	7 (8%)	3 (4%)	4	1
All	All	167/174 (96%)	149 (89%)	11 (7%)	7 (4%)	3	1

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	141	MET
3	B	110	GLU
3	B	162	PRO
3	A	110	GLU
3	A	131	GLY
3	B	163	PHE
3	A	103	ARG

### 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	81/81 (100%)	73 (90%)	8 (10%)	10	9
3	B	78/81 (96%)	68 (87%)	10 (13%)	5	4
All	All	159/162 (98%)	141 (89%)	18 (11%)	7	6

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	104	PRO
3	A	114	ARG
3	A	128	ILE
3	A	130	THR
3	A	166	ASP
3	A	170	ARG
3	A	186	LEU
3	A	187	ARG
3	B	103	ARG
3	B	110	GLU
3	B	114	ARG
3	B	117	SER
3	B	118	ARG
3	B	141	MET
3	B	146	ARG
3	B	154	ILE
3	B	161	LYS
3	B	175	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	143	ASN
3	B	143	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	C	22/22 (100%)	-0.33	0 100 100	45, 56, 63, 71	0
2	D	22/22 (100%)	-0.31	0 100 100	41, 61, 71, 74	0
3	A	87/87 (100%)	0.24	4 (4%) 36 35	39, 61, 97, 102	0
3	B	84/87 (96%)	0.94	15 (17%) 2 2	59, 80, 103, 107	0
All	All	215/218 (98%)	0.40	19 (8%) 12 11	39, 64, 100, 107	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	186	LEU	5.6
3	B	110	GLU	5.0
3	B	141	MET	4.4
3	A	113	ASP	3.4
3	A	102	GLU	3.4
3	A	187	ARG	2.9
3	B	111	SER	2.8
3	B	103	ARG	2.7
3	A	111	SER	2.6
3	B	139	ILE	2.6
3	B	113	ASP	2.4
3	B	168	CYS	2.3
3	B	112	CYS	2.3
3	B	109	VAL	2.2
3	B	135	PHE	2.2
3	B	130	THR	2.2
3	B	105	TYR	2.1
3	B	144	PHE	2.1
3	B	167	ILE	2.0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	ZN	A	203	1/1	0.99	0.14	0.24	55,55,55,55	0
4	ZN	B	205	1/1	0.98	0.09	-1.76	82,82,82,82	0
4	ZN	B	204	1/1	0.99	0.07	-2.51	78,78,78,78	0
4	ZN	B	206	1/1	0.94	0.08	-3.45	71,71,71,71	0
4	ZN	A	202	1/1	0.98	0.15	-	51,51,51,51	0
4	ZN	A	201	1/1	0.98	0.14	-	83,83,83,83	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.