



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Aug 21, 2017 – 08:21 AM EDT

PDB ID : 4UE5  
EMDB ID: : EMD-2844  
Title : Structural basis for targeting and elongation arrest of Bacillus signal recognition particle  
Authors : Beckert, B.; Kedrov, A.; Sohmen, D.; Kempf, G.; Wild, K.; Sinning, I.; Stahlberg, H.; Wilson, D.N.; Beckmann, R.  
Deposited on : unknown  
Resolution : 9.00 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB 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/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

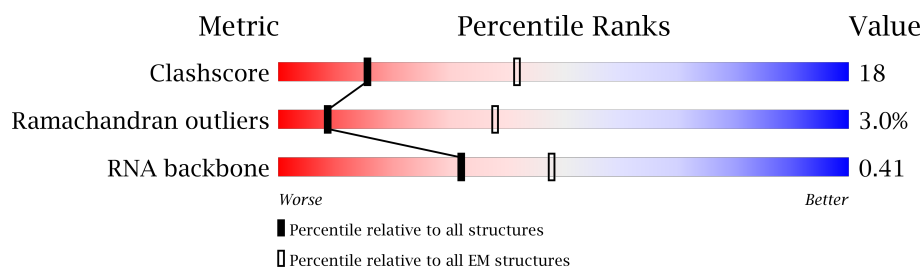
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	299	
2	B	75	
3	C	195	
4	D	433	
5	E	74	
6	F	107	
7	S	18	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9948 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 RNA chain called 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	299	Total	C	N	O	P	0	0
			6403	2852	1167	2086	298		

- Molecule 2 is a protein called SRP14.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	75	Total	C	N	O	0	0
			300	150	75	75		

- Molecule 3 is a protein called SIGNAL RECOGNITION PARTICLE SUBUNIT SRP68.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	179	Total	C	N	O	0	0
			716	358	179	179		

- Molecule 4 is a protein called SIGNAL RECOGNITION PARTICLE 54 KDA PROTEIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	433	Total	C	N	O	0	0
			1732	866	433	433		

- Molecule 5 is a protein called SRP9.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 6 is a protein called SIGNAL RECOGNITION PARTICLE 9 KDA PROTEIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	107	Total	C	N	O	0	0
			429	214	107	108		

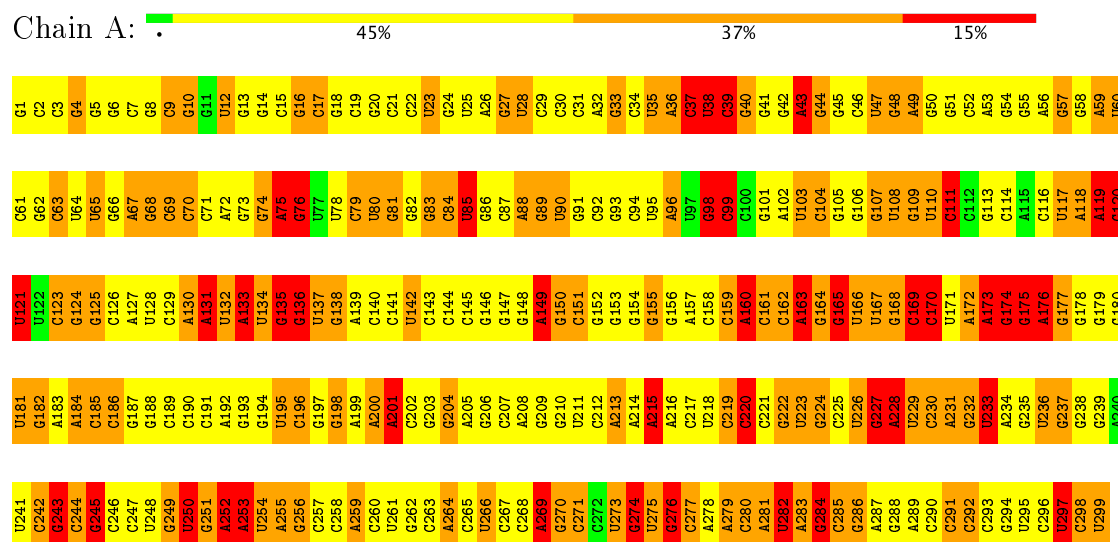
- Molecule 7 is a protein called SIGNAL SEQUENCE.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	S	18	72	36	18	18	0	0

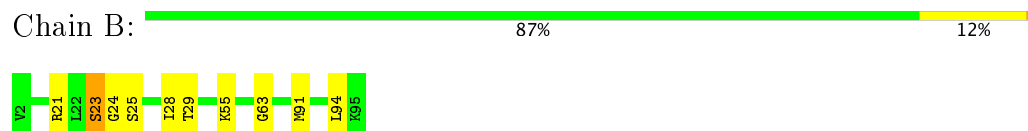
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

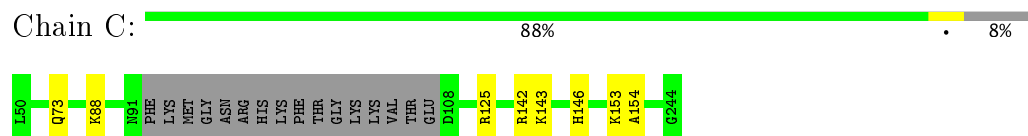
#### • Molecule 1: 7S RNA



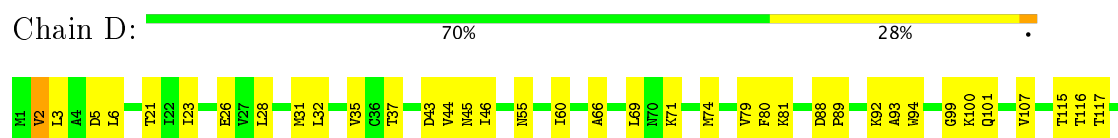
#### • Molecule 2: SRP14

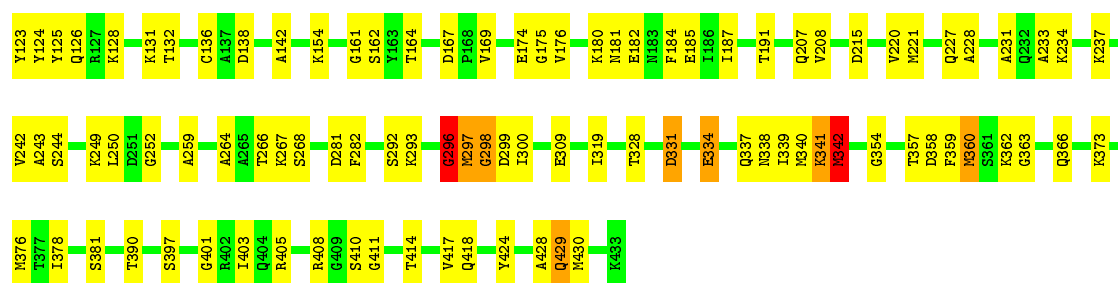


#### • Molecule 3: SIGNAL RECOGNITION PARTICLE SUBUNIT SRP68




#### • Molecule 4: SIGNAL RECOGNITION PARTICLE 54 KDA PROTEIN






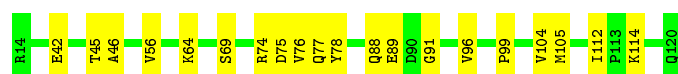
- Molecule 5: SRP9

Chain E:  81% 18%



- Molecule 6: SIGNAL RECOGNITION PARTICLE 9 KDA PROTEIN

Chain F:  81% 19%



- Molecule 7: SIGNAL SEQUENCE

Chain S:  100%

There are no outlier residues recorded for this chain.

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19096	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	MICROGRAPH	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	Depositor
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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  > 2	RMSZ	# Z  > 2
1	A	1.55	31/7161 (0.4%)	2.59	812/11171 (7.3%)
2	B	0.40	0/298	0.74	0/369
3	C	0.25	0/714	0.48	0/889
4	D	0.73	0/1731	0.94	0/2162
5	E	0.37	0/295	0.73	0/367
6	F	0.40	0/428	0.68	0/532
7	S	0.44	0/71	0.72	0/87
All	All	1.31	31/10698 (0.3%)	2.23	812/15577 (5.2%)

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	A	0	38
2	B	4	0
3	C	4	0
4	D	0	108
5	E	4	0
All	All	12	146

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	C	O3'-P	-8.07	1.51	1.61
1	A	229	U	O3'-P	-7.93	1.51	1.61
1	A	198	G	C2-N3	7.58	1.38	1.32
1	A	131	A	C6-N6	6.36	1.39	1.33
1	A	201	A	N7-C5	-6.30	1.35	1.39
1	A	118	A	C6-N6	6.09	1.38	1.33
1	A	88	A	C6-N6	5.93	1.38	1.33
1	A	283	A	C6-N6	5.79	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	A	C6-N6	5.76	1.38	1.33
1	A	287	A	C6-N6	5.67	1.38	1.33
1	A	133	A	N7-C5	-5.65	1.35	1.39
1	A	234	A	C6-N6	5.64	1.38	1.33
1	A	37	C	O3'-P	5.61	1.67	1.61
1	A	43	A	C6-N6	5.47	1.38	1.33
1	A	135	G	C2'-C1'	-5.36	1.47	1.53
1	A	255	A	C6-N6	5.30	1.38	1.33
1	A	96	A	C6-N6	5.29	1.38	1.33
1	A	253	A	C6-N6	5.24	1.38	1.33
1	A	130	A	C6-N6	5.22	1.38	1.33
1	A	48	G	C2'-C1'	-5.18	1.47	1.53
1	A	67	A	O3'-P	-5.16	1.54	1.61
1	A	251	G	C2-N3	5.09	1.36	1.32
1	A	243	G	C2-N3	5.09	1.36	1.32
1	A	72	A	C6-N6	5.08	1.38	1.33
1	A	187	G	C2-N3	5.07	1.36	1.32
1	A	96	A	N7-C5	-5.07	1.36	1.39
1	A	105	G	O3'-P	5.07	1.67	1.61
1	A	157	A	N9-C4	-5.06	1.34	1.37
1	A	280	C	O3'-P	5.04	1.67	1.61
1	A	237	G	C2-N3	5.00	1.36	1.32
1	A	49	A	C6-N6	5.00	1.38	1.33

All (812) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	G	O5'-P-OP2	-25.39	80.23	110.70
1	A	59	A	C4'-C3'-O3'	20.59	154.17	113.00
1	A	59	A	P-O3'-C3'	-18.37	97.66	119.70
1	A	201	A	N1-C6-N6	17.49	129.09	118.60
1	A	47	U	P-O3'-C3'	17.26	140.41	119.70
1	A	176	A	P-O3'-C3'	16.41	139.40	119.70
1	A	270	G	C4'-C3'-O3'	15.17	143.34	113.00
1	A	176	A	N1-C6-N6	14.93	127.56	118.60
1	A	215	A	N1-C6-N6	14.53	127.32	118.60
1	A	17	C	P-O5'-C5'	13.76	142.91	120.90
1	A	216	A	N1-C6-N6	13.64	126.79	118.60
1	A	270	G	O5'-P-OP1	13.58	127.00	110.70
1	A	83	G	N1-C6-O6	13.39	127.93	119.90
1	A	53	A	N1-C6-N6	13.29	126.57	118.60
1	A	149	A	N1-C6-N6	13.15	126.49	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	A	N1-C6-N6	12.99	126.39	118.60
1	A	57	G	C4'-C3'-O3'	12.98	138.97	113.00
1	A	253	A	N1-C6-N6	12.93	126.36	118.60
1	A	37	C	P-O5'-C5'	12.89	141.53	120.90
1	A	43	A	P-O3'-C3'	12.81	135.07	119.70
1	A	16	G	C4'-C3'-O3'	12.77	138.54	113.00
1	A	68	G	P-O5'-C5'	12.69	141.21	120.90
1	A	69	C	O4'-C1'-N1	12.58	118.26	108.20
1	A	60	U	O4'-C1'-N1	12.51	118.21	108.20
1	A	164	G	N1-C6-O6	12.50	127.40	119.90
1	A	172	A	P-O3'-C3'	12.49	134.69	119.70
1	A	252	A	P-O3'-C3'	12.48	134.68	119.70
1	A	200	A	N1-C6-N6	12.45	126.07	118.60
1	A	192	A	N1-C6-N6	12.42	126.05	118.60
1	A	36	A	C4'-C3'-O3'	-12.41	83.34	109.40
1	A	199	A	N1-C6-N6	12.37	126.02	118.60
1	A	96	A	N1-C6-N6	12.31	125.99	118.60
1	A	35	U	C4'-C3'-O3'	-12.27	83.63	109.40
1	A	166	U	O4'-C1'-N1	12.23	117.99	108.20
1	A	60	U	C4'-C3'-O3'	12.11	137.21	113.00
1	A	208	A	N1-C6-N6	12.10	125.86	118.60
1	A	173	A	N1-C6-N6	12.06	125.83	118.60
1	A	32	A	N1-C6-N6	11.95	125.77	118.60
1	A	185	C	P-O3'-C3'	11.94	134.02	119.70
1	A	76	G	C4'-C3'-O3'	11.91	136.82	113.00
1	A	49	A	N1-C6-N6	11.89	125.73	118.60
1	A	105	G	O4'-C1'-N9	11.78	117.62	108.20
1	A	58	G	O4'-C1'-N9	11.69	117.55	108.20
1	A	214	A	N1-C6-N6	11.64	125.58	118.60
1	A	139	A	N1-C6-N6	11.63	125.58	118.60
1	A	157	A	N1-C6-N6	11.61	125.57	118.60
1	A	61	C	P-O5'-C5'	-11.51	102.48	120.90
1	A	75	A	N1-C6-N6	11.50	125.50	118.60
1	A	183	A	N1-C6-N6	11.42	125.45	118.60
1	A	102	A	N1-C6-N6	11.36	125.42	118.60
1	A	294	G	N1-C6-O6	11.36	126.71	119.90
1	A	255	A	N1-C6-N6	11.35	125.41	118.60
1	A	160	A	N1-C6-N6	11.31	125.39	118.60
1	A	252	A	N1-C6-N6	11.28	125.37	118.60
1	A	259	A	N1-C6-N6	11.27	125.36	118.60
1	A	172	A	N1-C6-N6	11.22	125.33	118.60
1	A	83	G	C5-C6-O6	-11.21	121.88	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	26	A	N1-C6-N6	11.14	125.29	118.60
1	A	285	C	O4'-C1'-N1	11.13	117.10	108.20
1	A	205	A	N1-C6-N6	11.02	125.21	118.60
1	A	37	C	O5'-C5'-C4'	-11.02	90.77	111.70
1	A	213	A	N1-C6-N6	10.99	125.19	118.60
1	A	184	A	N1-C6-N6	10.97	125.19	118.60
1	A	283	A	N1-C6-N6	10.97	125.18	118.60
1	A	72	A	N1-C6-N6	10.96	125.17	118.60
1	A	24	G	N1-C6-O6	10.92	126.45	119.90
1	A	165	G	N1-C6-O6	10.91	126.45	119.90
1	A	86	G	N1-C6-O6	10.91	126.44	119.90
1	A	168	G	N1-C6-O6	10.88	126.43	119.90
1	A	234	A	N1-C6-N6	10.88	125.13	118.60
1	A	264	A	N1-C6-N6	10.82	125.09	118.60
1	A	161	C	O4'-C1'-N1	10.76	116.81	108.20
1	A	48	G	N1-C6-O6	10.65	126.29	119.90
1	A	88	A	N1-C6-N6	10.59	124.95	118.60
1	A	50	G	N1-C6-O6	10.58	126.25	119.90
1	A	51	G	N1-C6-O6	10.53	126.22	119.90
1	A	230	C	P-O5'-C5'	10.51	137.72	120.90
1	A	276	G	O4'-C1'-N9	10.39	116.51	108.20
1	A	81	G	N1-C6-O6	10.36	126.12	119.90
1	A	44	G	N1-C6-O6	10.35	126.11	119.90
1	A	282	U	O4'-C1'-N1	10.32	116.46	108.20
1	A	60	U	C5'-C4'-O4'	10.30	121.46	109.10
1	A	219	C	O4'-C1'-N1	10.29	116.43	108.20
1	A	159	C	O4'-C1'-N1	10.26	116.41	108.20
1	A	63	C	O4'-C1'-N1	10.24	116.39	108.20
1	A	131	A	C5-C6-N1	-10.21	112.60	117.70
1	A	237	G	N1-C6-O6	10.19	126.01	119.90
1	A	130	A	N1-C6-N6	10.16	124.69	118.60
1	A	187	G	N1-C6-O6	10.15	125.99	119.90
1	A	117	U	O4'-C1'-N1	10.11	116.29	108.20
1	A	61	C	O4'-C1'-N1	10.10	116.28	108.20
1	A	94	C	O4'-C1'-N1	10.00	116.20	108.20
1	A	254	U	O4'-C1'-N1	9.98	116.19	108.20
1	A	164	G	C5-C6-O6	-9.91	122.65	128.60
1	A	276	G	N1-C6-O6	9.88	125.83	119.90
1	A	162	C	O4'-C1'-N1	9.77	116.02	108.20
1	A	65	U	O4'-C1'-N1	9.77	116.02	108.20
1	A	227	G	N1-C6-O6	9.76	125.76	119.90
1	A	280	C	O3'-P-O5'	9.74	122.50	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	118	A	N1-C6-N6	9.70	124.42	118.60
1	A	242	C	C2'-C3'-O3'	9.66	130.75	109.50
1	A	243	G	N1-C6-O6	9.64	125.68	119.90
1	A	200	A	P-O3'-C3'	9.63	131.26	119.70
1	A	9	C	O4'-C1'-N1	9.58	115.87	108.20
1	A	257	C	O4'-C1'-N1	9.54	115.83	108.20
1	A	251	G	N1-C6-O6	9.53	125.62	119.90
1	A	20	G	N1-C6-O6	9.53	125.62	119.90
1	A	178	G	N1-C6-O6	9.52	125.61	119.90
1	A	286	G	O4'-C1'-N9	9.52	115.81	108.20
1	A	230	C	C5'-C4'-C3'	-9.51	100.78	116.00
1	A	87	C	O4'-C1'-N1	9.47	115.78	108.20
1	A	274	G	N1-C6-O6	9.45	125.57	119.90
1	A	140	C	O4'-C1'-N1	9.45	115.76	108.20
1	A	175	G	N1-C6-O6	9.41	125.55	119.90
1	A	201	A	C5-C6-N6	-9.39	116.19	123.70
1	A	52	C	O4'-C1'-N1	9.38	115.71	108.20
1	A	64	U	O4'-C1'-N1	9.37	115.70	108.20
1	A	223	U	O4'-C1'-N1	9.36	115.69	108.20
1	A	258	C	O4'-C1'-N1	9.35	115.68	108.20
1	A	105	G	C5'-C4'-O4'	9.32	120.28	109.10
1	A	209	G	N1-C6-O6	9.32	125.49	119.90
1	A	225	C	O4'-C1'-N1	9.31	115.65	108.20
1	A	43	A	N1-C6-N6	9.29	124.17	118.60
1	A	293	C	O4'-C1'-N1	9.27	115.62	108.20
1	A	4	G	N1-C6-O6	9.27	125.46	119.90
1	A	88	A	C5-C6-N1	-9.24	113.08	117.70
1	A	268	C	O4'-C1'-N1	9.22	115.58	108.20
1	A	158	C	O4'-C1'-N1	9.22	115.57	108.20
1	A	105	G	C5'-C4'-C3'	-9.21	101.26	116.00
1	A	118	A	C5-C6-N1	-9.21	113.09	117.70
1	A	287	A	N1-C6-N6	9.19	124.12	118.60
1	A	5	G	N1-C6-O6	9.13	125.38	119.90
1	A	24	G	C5-C6-O6	-9.11	123.13	128.60
1	A	167	U	O4'-C1'-N1	9.11	115.49	108.20
1	A	181	U	O4'-C1'-N1	9.10	115.48	108.20
1	A	215	A	C5-C6-N6	-9.10	116.42	123.70
1	A	6	G	N1-C6-O6	9.10	125.36	119.90
1	A	283	A	C5-C6-N1	-9.09	113.15	117.70
1	A	144	C	O4'-C1'-N1	9.07	115.46	108.20
1	A	207	C	O4'-C1'-N1	9.06	115.45	108.20
1	A	141	C	O4'-C1'-N1	9.06	115.45	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	G	N1-C6-O6	9.05	125.33	119.90
1	A	260	C	O4'-C1'-N1	9.04	115.43	108.20
1	A	96	A	C5-C6-N1	-9.03	113.18	117.70
1	A	150	G	N1-C6-O6	9.00	125.30	119.90
1	A	22	C	O4'-C1'-N1	8.99	115.39	108.20
1	A	40	G	N1-C6-O6	8.98	125.29	119.90
1	A	198	G	N1-C6-O6	8.98	125.29	119.90
1	A	234	A	C5-C6-N1	-8.97	113.22	117.70
1	A	106	G	N1-C6-O6	8.96	125.27	119.90
1	A	221	C	O4'-C1'-N1	8.95	115.36	108.20
1	A	95	U	O4'-C1'-N1	8.94	115.35	108.20
1	A	36	A	P-O5'-C5'	-8.93	106.61	120.90
1	A	152	G	N1-C6-O6	8.93	125.26	119.90
1	A	259	A	C5-C6-N1	-8.93	113.23	117.70
1	A	263	C	O4'-C1'-N1	8.92	115.34	108.20
1	A	91	G	O4'-C1'-N9	8.89	115.32	108.20
1	A	108	U	O4'-C1'-N1	8.89	115.31	108.20
1	A	147	G	N1-C6-O6	8.87	125.22	119.90
1	A	151	C	O4'-C1'-N1	8.87	115.30	108.20
1	A	206	G	N1-C6-O6	8.83	125.20	119.90
1	A	253	A	O4'-C1'-N9	8.83	115.27	108.20
1	A	28	U	O4'-C1'-N1	8.83	115.27	108.20
1	A	245	G	N1-C6-O6	8.83	125.20	119.90
1	A	182	G	N1-C6-O6	8.82	125.19	119.90
1	A	93	G	O4'-C1'-N9	8.81	115.25	108.20
1	A	266	U	O4'-C1'-N1	8.81	115.25	108.20
1	A	34	C	O4'-C1'-N1	8.80	115.24	108.20
1	A	217	C	O4'-C1'-N1	8.80	115.24	108.20
1	A	292	C	O4'-C1'-N1	8.80	115.24	108.20
1	A	232	G	N1-C6-O6	8.78	125.17	119.90
1	A	8	G	N1-C6-O6	8.75	125.15	119.90
1	A	284	G	O4'-C1'-N9	8.74	115.19	108.20
1	A	128	U	O4'-C1'-N1	8.73	115.19	108.20
1	A	135	G	O4'-C1'-N9	8.72	115.18	108.20
1	A	148	G	N1-C6-O6	8.72	125.13	119.90
1	A	60	U	C2'-C3'-O3'	-8.72	90.31	109.50
1	A	246	C	O4'-C1'-N1	8.71	115.17	108.20
1	A	41	G	N1-C6-O6	8.69	125.11	119.90
1	A	23	U	O4'-C1'-N1	8.69	115.15	108.20
1	A	267	C	O4'-C1'-N1	8.69	115.15	108.20
1	A	250	U	O4'-C1'-N1	8.67	115.14	108.20
1	A	287	A	C5-C6-N1	-8.65	113.37	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	C	O4'-C1'-N1	8.65	115.12	108.20
1	A	262	G	N1-C6-O6	8.64	125.08	119.90
1	A	33	G	N1-C6-O6	8.63	125.08	119.90
1	A	286	G	N1-C6-O6	8.62	125.07	119.90
1	A	92	C	O4'-C1'-N1	8.61	115.09	108.20
1	A	291	C	O4'-C1'-N1	8.60	115.08	108.20
1	A	126	C	O4'-C1'-N1	8.59	115.08	108.20
1	A	294	G	C5-C6-O6	-8.57	123.46	128.60
1	A	180	G	N1-C6-O6	8.56	125.04	119.90
1	A	228	A	C4'-C3'-O3'	8.56	130.12	113.00
1	A	284	G	N1-C6-O6	8.53	125.02	119.90
1	A	145	C	O4'-C1'-N1	8.52	115.02	108.20
1	A	18	G	N1-C6-O6	8.52	125.01	119.90
1	A	134	U	O4'-C1'-N1	8.50	115.00	108.20
1	A	107	G	O4'-C1'-N9	8.50	115.00	108.20
1	A	146	G	N1-C6-O6	8.50	125.00	119.90
1	A	226	U	O4'-C1'-N1	8.50	115.00	108.20
1	A	4	G	O4'-C1'-N9	8.45	114.96	108.20
1	A	42	G	N1-C6-O6	8.45	124.97	119.90
1	A	131	A	N1-C6-N6	8.44	123.67	118.60
1	A	1	G	N1-C6-O6	8.44	124.96	119.90
1	A	45	G	N1-C6-O6	8.44	124.96	119.90
1	A	19	C	O4'-C1'-N1	8.43	114.95	108.20
1	A	31	C	O4'-C1'-N1	8.42	114.94	108.20
1	A	79	C	P-O3'-C3'	-8.41	109.61	119.70
1	A	29	C	O4'-C1'-N1	8.39	114.91	108.20
1	A	244	C	O4'-C1'-N1	8.39	114.91	108.20
1	A	107	G	N1-C6-O6	8.37	124.92	119.90
1	A	296	C	O4'-C1'-N1	8.37	114.90	108.20
1	A	119	A	N1-C6-N6	8.37	123.62	118.60
1	A	54	G	N1-C6-O6	8.36	124.92	119.90
1	A	156	G	N1-C6-O6	8.36	124.92	119.90
1	A	58	G	C4'-C3'-O3'	-8.36	91.85	109.40
1	A	224	G	N1-C6-O6	8.36	124.92	119.90
1	A	21	C	O4'-C1'-N1	8.36	114.88	108.20
1	A	189	C	O4'-C1'-N1	8.34	114.87	108.20
1	A	277	C	O4'-C1'-N1	8.34	114.87	108.20
1	A	46	C	O4'-C1'-N1	8.32	114.85	108.20
1	A	70	C	O4'-C1'-N1	8.30	114.84	108.20
1	A	12	U	C4'-C3'-O3'	-8.28	92.02	109.40
1	A	220	C	O4'-C1'-N1	8.28	114.82	108.20
1	A	190	C	O4'-C1'-N1	8.28	114.82	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	G	N1-C6-O6	8.27	124.86	119.90
1	A	298	C	O4'-C1'-N1	8.27	114.82	108.20
1	A	218	U	O4'-C1'-N1	8.27	114.82	108.20
1	A	237	G	C5-C6-O6	-8.27	123.64	128.60
1	A	269	A	C4'-C3'-O3'	8.27	129.54	113.00
1	A	106	G	P-O5'-C5'	-8.26	107.68	120.90
1	A	252	A	O4'-C1'-N9	8.26	114.81	108.20
1	A	27	G	N1-C6-O6	8.25	124.85	119.90
1	A	177	G	N1-C6-O6	8.24	124.84	119.90
1	A	249	G	O4'-C1'-N9	8.24	114.79	108.20
1	A	39	C	O4'-C1'-N1	8.21	114.77	108.20
1	A	176	A	C5-C6-N6	-8.21	117.14	123.70
1	A	106	G	O4'-C1'-N9	8.20	114.76	108.20
1	A	93	G	N1-C6-O6	8.20	124.82	119.90
1	A	136	G	O4'-C1'-N9	8.20	114.76	108.20
1	A	62	G	N1-C6-O6	8.20	124.82	119.90
1	A	265	C	O4'-C1'-N1	8.19	114.75	108.20
1	A	74	G	N1-C6-O6	8.19	124.81	119.90
1	A	50	G	C5-C6-O6	-8.19	123.69	128.60
1	A	215	A	O4'-C1'-N9	8.18	114.74	108.20
1	A	129	C	O4'-C1'-N1	8.18	114.74	108.20
1	A	235	G	N1-C6-O6	8.18	124.81	119.90
1	A	188	G	N1-C6-O6	8.16	124.79	119.90
1	A	182	G	O4'-C1'-N9	8.15	114.72	108.20
1	A	248	U	O4'-C1'-N1	8.13	114.70	108.20
1	A	271	C	P-O5'-C5'	8.12	133.89	120.90
1	A	273	U	O4'-C1'-N1	8.11	114.69	108.20
1	A	295	U	O4'-C1'-N1	8.11	114.69	108.20
1	A	136	G	N1-C6-O6	8.09	124.76	119.90
1	A	203	G	N1-C6-O6	8.09	124.75	119.90
1	A	242	C	P-O3'-C3'	8.08	129.40	119.70
1	A	48	G	C5-C6-O6	-8.08	123.75	128.60
1	A	86	G	C5-C6-O6	-8.07	123.76	128.60
1	A	58	G	O4'-C4'-C3'	-8.06	95.94	104.00
1	A	62	G	O4'-C1'-N9	8.05	114.64	108.20
1	A	103	U	C4'-C3'-O3'	8.05	129.10	113.00
1	A	89	G	N1-C6-O6	8.04	124.72	119.90
1	A	253	A	C5-C6-N1	-8.04	113.68	117.70
1	A	37	C	C5'-C4'-C3'	8.03	128.85	116.00
1	A	82	G	N1-C6-O6	8.03	124.72	119.90
1	A	243	G	C5-C6-O6	-8.02	123.79	128.60
1	A	281	A	C4'-C3'-O3'	8.01	129.01	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	G	C5-C6-O6	-7.99	123.81	128.60
1	A	197	G	O4'-C1'-N9	7.99	114.59	108.20
1	A	256	G	O4'-C1'-N9	7.96	114.57	108.20
1	A	30	C	O4'-C1'-N1	7.96	114.56	108.20
1	A	154	G	O4'-C1'-N9	7.95	114.56	108.20
1	A	59	A	C2'-C3'-O3'	-7.95	92.01	109.50
1	A	120	G	O4'-C1'-N9	7.93	114.55	108.20
1	A	7	C	O4'-C1'-N1	7.92	114.53	108.20
1	A	283	A	O4'-C1'-N9	7.91	114.53	108.20
1	A	142	U	O4'-C1'-N1	7.90	114.52	108.20
1	A	290	C	O5'-C5'-C4'	7.90	126.71	111.70
1	A	79	C	C2'-C3'-O3'	7.90	126.88	109.50
1	A	71	C	O4'-C1'-N1	7.89	114.51	108.20
1	A	121	U	C4'-C3'-O3'	7.88	128.75	113.00
1	A	261	U	O4'-C1'-N1	7.88	114.50	108.20
1	A	255	A	O4'-C1'-N9	7.87	114.50	108.20
1	A	155	G	N1-C6-O6	7.87	124.62	119.90
1	A	90	U	O4'-C1'-N1	7.85	114.48	108.20
1	A	137	U	O4'-C1'-N1	7.85	114.48	108.20
1	A	160	A	O4'-C1'-N9	7.85	114.48	108.20
1	A	2	C	O4'-C1'-N1	7.85	114.48	108.20
1	A	125	G	N1-C6-O6	7.85	124.61	119.90
1	A	73	G	N1-C6-O6	7.84	124.60	119.90
1	A	33	G	O4'-C1'-N9	7.83	114.46	108.20
1	A	154	G	N1-C6-O6	7.82	124.59	119.90
1	A	290	C	P-O5'-C5'	-7.81	108.40	120.90
1	A	124	G	O4'-C1'-N9	7.81	114.45	108.20
1	A	256	G	N1-C6-O6	7.80	124.58	119.90
1	A	42	G	O4'-C1'-N9	7.80	114.44	108.20
1	A	210	G	N1-C6-O6	7.80	124.58	119.90
1	A	202	C	O4'-C1'-N1	7.77	114.42	108.20
1	A	193	G	O4'-C1'-N9	7.74	114.39	108.20
1	A	212	C	O4'-C1'-N1	7.73	114.38	108.20
1	A	236	U	O4'-C1'-N1	7.73	114.38	108.20
1	A	211	U	O4'-C1'-N1	7.72	114.38	108.20
1	A	119	A	O4'-C1'-N9	7.71	114.37	108.20
1	A	80	U	C4'-C3'-O3'	7.71	128.42	113.00
1	A	143	C	O4'-C1'-N1	7.70	114.36	108.20
1	A	3	C	O4'-C1'-N1	7.70	114.36	108.20
1	A	185	C	O4'-C1'-N1	7.70	114.36	108.20
1	A	165	G	O4'-C1'-N9	7.69	114.35	108.20
1	A	138	G	N1-C6-O6	7.69	124.51	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	G	O4'-C1'-N9	7.67	114.34	108.20
1	A	54	G	O4'-C1'-N9	7.67	114.34	108.20
1	A	224	G	O4'-C1'-N9	7.66	114.33	108.20
1	A	237	G	O4'-C1'-N9	7.61	114.29	108.20
1	A	198	G	O4'-C1'-N9	7.61	114.29	108.20
1	A	287	A	O4'-C1'-N9	7.61	114.29	108.20
1	A	168	G	C5-C6-O6	-7.59	124.04	128.60
1	A	195	U	O4'-C1'-N1	7.59	114.27	108.20
1	A	255	A	C5-C6-N1	-7.59	113.90	117.70
1	A	165	G	C5-C6-O6	-7.58	124.05	128.60
1	A	196	C	O4'-C1'-N1	7.58	114.27	108.20
1	A	55	G	N1-C6-O6	7.58	124.45	119.90
1	A	191	C	O4'-C1'-N1	7.56	114.25	108.20
1	A	153	G	N1-C6-O6	7.55	124.43	119.90
1	A	157	A	O4'-C1'-N9	7.54	114.23	108.20
1	A	251	G	C5-C6-O6	-7.53	124.08	128.60
1	A	200	A	O4'-C1'-N9	7.52	114.22	108.20
1	A	109	G	N1-C6-O6	7.51	124.41	119.90
1	A	73	G	O4'-C1'-N9	7.49	114.19	108.20
1	A	104	C	P-O3'-C3'	-7.48	110.72	119.70
1	A	170	C	O4'-C1'-N1	7.47	114.18	108.20
1	A	89	G	O4'-C1'-N9	7.47	114.17	108.20
1	A	98	G	C4'-C3'-O3'	7.45	127.90	113.00
1	A	88	A	O4'-C1'-N9	7.40	114.12	108.20
1	A	198	G	N3-C2-N2	7.39	125.07	119.90
1	A	36	A	O5'-C5'-C4'	7.39	125.73	111.70
1	A	39	C	N3-C4-N4	7.37	123.16	118.00
1	A	116	C	O4'-C1'-N1	7.37	114.10	108.20
1	A	17	C	C5'-C4'-C3'	-7.35	104.24	116.00
1	A	81	G	C5-C6-O6	-7.33	124.20	128.60
1	A	187	G	C5-C6-O6	-7.33	124.20	128.60
1	A	55	G	O4'-C1'-N9	7.30	114.04	108.20
1	A	155	G	O4'-C1'-N9	7.27	114.01	108.20
1	A	193	G	N1-C6-O6	7.26	124.26	119.90
1	A	44	G	C5-C6-O6	-7.25	124.25	128.60
1	A	91	G	N1-C6-O6	7.25	124.25	119.90
1	A	47	U	O4'-C1'-N1	7.23	113.98	108.20
1	A	233	U	O4'-C1'-N1	7.22	113.98	108.20
1	A	194	G	N1-C6-O6	7.21	124.23	119.90
1	A	74	G	O4'-C1'-N9	7.20	113.96	108.20
1	A	186	C	C2-N1-C1'	7.19	126.71	118.80
1	A	85	U	O4'-C1'-N1	7.19	113.95	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	A	C5-C6-N1	-7.16	114.12	117.70
1	A	71	C	N3-C4-N4	7.16	123.01	118.00
1	A	185	C	C2-N1-C1'	7.12	126.63	118.80
1	A	186	C	O4'-C1'-N1	7.12	113.89	108.20
1	A	130	A	C5-C6-N1	-7.11	114.14	117.70
1	A	204	G	C5-C6-O6	-7.11	124.33	128.60
1	A	201	A	O4'-C1'-N9	7.11	113.89	108.20
1	A	157	A	C5-C6-N1	-7.10	114.15	117.70
1	A	84	C	O4'-C1'-N1	7.09	113.88	108.20
1	A	153	G	O4'-C1'-N9	7.09	113.87	108.20
1	A	201	A	C4-C5-C6	7.08	120.54	117.00
1	A	133	A	O4'-C1'-N9	7.08	113.86	108.20
1	A	39	C	C5-C4-N4	-7.07	115.25	120.20
1	A	6	G	C5-C6-O6	-7.07	124.36	128.60
1	A	244	C	N3-C4-C5	-7.07	119.07	121.90
1	A	237	G	N1-C2-N3	-7.06	119.66	123.90
1	A	123	C	C4'-C3'-O3'	7.06	127.12	113.00
1	A	222	G	O4'-C1'-N9	7.05	113.84	108.20
1	A	242	C	P-O5'-C5'	-7.04	109.63	120.90
1	A	276	G	C5-C6-O6	-7.04	124.38	128.60
1	A	58	G	P-O5'-C5'	7.04	132.16	120.90
1	A	72	A	C5-C6-N1	-7.02	114.19	117.70
1	A	290	C	C5'-C4'-C3'	7.02	127.23	116.00
1	A	243	G	O4'-C1'-N9	6.98	113.78	108.20
1	A	127	A	C5-C6-N1	-6.98	114.21	117.70
1	A	16	G	C2'-C3'-O3'	-6.97	94.17	109.50
1	A	132	U	O4'-C1'-N1	6.96	113.77	108.20
1	A	20	G	C5-C6-O6	-6.96	124.42	128.60
1	A	8	G	O4'-C1'-N9	6.96	113.76	108.20
1	A	71	C	N3-C4-C5	-6.93	119.13	121.90
1	A	232	G	C5-C6-O6	-6.92	124.44	128.60
1	A	129	C	N3-C4-C5	-6.90	119.14	121.90
1	A	299	U	O4'-C1'-N1	6.89	113.71	108.20
1	A	285	C	N3-C4-C5	-6.88	119.15	121.90
1	A	222	G	N1-C6-O6	6.88	124.03	119.90
1	A	43	A	O4'-C1'-N9	6.88	113.70	108.20
1	A	174	G	N1-C6-O6	6.88	124.03	119.90
1	A	245	G	O4'-C1'-N9	6.87	113.70	108.20
1	A	25	U	O4'-C1'-N1	6.87	113.69	108.20
1	A	203	G	O4'-C1'-N9	6.86	113.69	108.20
1	A	177	G	O4'-C1'-N9	6.86	113.69	108.20
1	A	197	G	N1-C6-O6	6.85	124.01	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	C	N1-C1'-C2'	6.83	122.88	114.00
1	A	125	G	O4'-C1'-N9	6.83	113.66	108.20
1	A	51	G	O4'-C1'-N9	6.82	113.66	108.20
1	A	81	G	O4'-C1'-N9	6.82	113.66	108.20
1	A	259	A	O4'-C1'-N9	6.82	113.66	108.20
1	A	69	C	N3-C4-C5	-6.81	119.17	121.90
1	A	3	C	N3-C4-C5	-6.81	119.18	121.90
1	A	206	G	C5-C6-O6	-6.81	124.52	128.60
1	A	18	G	O4'-C1'-N9	6.81	113.64	108.20
1	A	140	C	N3-C4-N4	6.80	122.76	118.00
1	A	43	A	C5-C6-N1	-6.80	114.30	117.70
1	A	232	G	O4'-C1'-N9	6.79	113.63	108.20
1	A	298	C	N3-C4-C5	-6.79	119.19	121.90
1	A	147	G	C5-C6-O6	-6.78	124.53	128.60
1	A	179	G	N1-C6-O6	6.78	123.97	119.90
1	A	169	C	O4'-C1'-N1	6.78	113.62	108.20
1	A	148	G	C5-C6-O6	-6.77	124.54	128.60
1	A	274	G	N3-C2-N2	6.77	124.64	119.90
1	A	63	C	N3-C4-C5	-6.77	119.19	121.90
1	A	221	C	N3-C4-C5	-6.77	119.19	121.90
1	A	49	A	C5-C6-N1	-6.77	114.32	117.70
1	A	139	A	O4'-C1'-N9	6.76	113.61	108.20
1	A	291	C	N3-C4-C5	-6.76	119.19	121.90
1	A	27	G	O4'-C1'-N9	6.75	113.60	108.20
1	A	219	C	N3-C4-C5	-6.75	119.20	121.90
1	A	209	G	C5-C6-O6	-6.74	124.55	128.60
1	A	178	G	C5-C6-O6	-6.74	124.56	128.60
1	A	227	G	C5-C6-O6	-6.74	124.56	128.60
1	A	135	G	N1-C6-O6	6.72	123.93	119.90
1	A	130	A	O4'-C1'-N9	6.71	113.57	108.20
1	A	146	G	O4'-C1'-N9	6.71	113.57	108.20
1	A	175	G	O4'-C1'-N9	6.71	113.56	108.20
1	A	109	G	O4'-C1'-N9	6.70	113.56	108.20
1	A	5	G	C5-C6-O6	-6.70	124.58	128.60
1	A	216	A	O4'-C1'-N9	6.69	113.56	108.20
1	A	216	A	C5-C6-N6	-6.69	118.35	123.70
1	A	16	G	P-O5'-C5'	6.68	131.59	120.90
1	A	105	G	O4'-C4'-C3'	-6.67	97.33	104.00
1	A	48	G	O4'-C1'-N9	6.66	113.53	108.20
1	A	212	C	N3-C4-C5	-6.66	119.24	121.90
1	A	150	G	C5-C6-O6	-6.65	124.61	128.60
1	A	202	C	N3-C4-C5	-6.65	119.24	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	G	C5-C6-O6	-6.64	124.61	128.60
1	A	33	G	C5-C6-O6	-6.64	124.62	128.60
1	A	135	G	N3-C2-N2	6.63	124.54	119.90
1	A	124	G	O4'-C4'-C3'	-6.62	97.38	104.00
1	A	80	U	O5'-C5'-C4'	-6.61	99.14	111.70
1	A	149	A	C5-C6-N6	-6.61	118.41	123.70
1	A	118	A	C4-C5-C6	6.61	120.30	117.00
1	A	52	C	N3-C4-C5	-6.60	119.26	121.90
1	A	196	C	N3-C4-C5	-6.59	119.26	121.90
1	A	106	G	O5'-C5'-C4'	6.59	124.23	111.70
1	A	161	C	N3-C4-C5	-6.59	119.26	121.90
1	A	39	C	C4'-C3'-C2'	-6.58	96.02	102.60
1	A	41	G	O4'-C1'-N9	6.58	113.46	108.20
1	A	294	G	O4'-C1'-N9	6.57	113.46	108.20
1	A	159	C	N3-C4-C5	-6.56	119.28	121.90
1	A	124	G	O5'-C5'-C4'	6.56	124.16	111.70
1	A	225	C	N3-C4-C5	-6.56	119.28	121.90
1	A	192	A	O4'-C1'-N9	6.55	113.44	108.20
1	A	150	G	P-O5'-C5'	6.53	131.35	120.90
1	A	4	G	C5-C6-O6	-6.52	124.69	128.60
1	A	26	A	O4'-C1'-N9	6.51	113.41	108.20
1	A	267	C	N3-C4-C5	-6.49	119.30	121.90
1	A	180	G	O4'-C1'-N9	6.49	113.39	108.20
1	A	106	G	C5-C6-O6	-6.48	124.71	128.60
1	A	210	G	O4'-C1'-N9	6.47	113.38	108.20
1	A	38	U	C5'-C4'-C3'	6.46	126.34	116.00
1	A	264	A	C4-C5-C6	6.46	120.23	117.00
1	A	262	G	O4'-C1'-N9	6.45	113.36	108.20
1	A	274	G	P-O3'-C3'	6.45	127.44	119.70
1	A	175	G	C5-C6-O6	-6.45	124.73	128.60
1	A	8	G	C5-C6-O6	-6.44	124.74	128.60
1	A	263	C	N3-C4-C5	-6.43	119.33	121.90
1	A	59	A	P-O5'-C5'	-6.43	110.61	120.90
1	A	192	A	C5-C6-N6	-6.41	118.57	123.70
1	A	127	A	C4-C5-C6	6.41	120.20	117.00
1	A	268	C	N3-C4-C5	-6.40	119.34	121.90
1	A	40	G	C5-C6-O6	-6.39	124.76	128.60
1	A	143	C	N3-C4-N4	6.37	122.46	118.00
1	A	241	U	C4'-C3'-O3'	6.36	125.72	113.00
1	A	179	G	O4'-C1'-N9	6.35	113.28	108.20
1	A	58	G	C5'-C4'-O4'	6.35	116.72	109.10
1	A	258	C	N3-C4-C5	-6.35	119.36	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	C	C6-N1-C1'	-6.34	113.19	120.80
1	A	130	A	C4-C5-C6	6.34	120.17	117.00
1	A	216	A	C4-C5-C6	6.34	120.17	117.00
1	A	53	A	O4'-C1'-N9	6.32	113.26	108.20
1	A	244	C	N3-C4-N4	6.32	122.43	118.00
1	A	150	G	O4'-C1'-N9	6.32	113.25	108.20
1	A	207	C	N3-C4-N4	6.32	122.42	118.00
1	A	291	C	N3-C4-N4	6.31	122.42	118.00
1	A	162	C	N3-C4-C5	-6.30	119.38	121.90
1	A	72	A	O4'-C1'-N9	6.30	113.24	108.20
1	A	194	G	O4'-C1'-N9	6.30	113.24	108.20
1	A	180	G	C5-C6-O6	-6.29	124.82	128.60
1	A	205	A	O4'-C1'-N9	6.29	113.23	108.20
1	A	61	C	N3-C4-C5	-6.29	119.38	121.90
1	A	29	C	N3-C4-C5	-6.29	119.39	121.90
1	A	82	G	O4'-C1'-N9	6.29	113.23	108.20
1	A	200	A	C4-C5-C6	6.28	120.14	117.00
1	A	17	C	C5'-C4'-O4'	6.28	116.63	109.10
1	A	53	A	C5-C6-N6	-6.28	118.68	123.70
1	A	275	U	O4'-C1'-N1	6.28	113.22	108.20
1	A	7	C	N3-C4-N4	6.27	122.39	118.00
1	A	138	G	O4'-C1'-N9	6.27	113.21	108.20
1	A	44	G	O4'-C1'-N9	6.26	113.21	108.20
1	A	199	A	C4-C5-C6	6.26	120.13	117.00
1	A	184	A	C4-C5-C6	6.26	120.13	117.00
1	A	260	C	N3-C4-C5	-6.25	119.40	121.90
1	A	188	G	O4'-C1'-N9	6.25	113.20	108.20
1	A	165	G	O4'-C4'-C3'	-6.25	97.75	104.00
1	A	152	G	C5-C6-O6	-6.24	124.86	128.60
1	A	205	A	C5-C6-N1	-6.24	114.58	117.70
1	A	279	A	P-O3'-C3'	6.23	127.18	119.70
1	A	20	G	O4'-C1'-N9	6.23	113.19	108.20
1	A	38	U	P-O3'-C3'	6.23	127.18	119.70
1	A	144	C	N3-C4-C5	-6.23	119.41	121.90
1	A	41	G	C5-C6-O6	-6.23	124.86	128.60
1	A	249	G	N1-C6-O6	6.23	123.64	119.90
1	A	298	C	C2-N3-C4	6.22	123.01	119.90
1	A	276	G	C5'-C4'-C3'	-6.22	106.04	116.00
1	A	158	C	N3-C4-N4	6.21	122.35	118.00
1	A	293	C	N3-C4-N4	6.21	122.35	118.00
1	A	30	C	N3-C4-C5	-6.21	119.42	121.90
1	A	94	C	N3-C4-C5	-6.20	119.42	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	264	A	C5-C6-N1	-6.20	114.60	117.70
1	A	198	G	C5-C6-O6	-6.20	124.88	128.60
1	A	235	G	O4'-C1'-N9	6.19	113.16	108.20
1	A	31	C	N3-C4-C5	-6.19	119.42	121.90
1	A	151	C	N3-C4-C5	-6.19	119.42	121.90
1	A	96	A	O4'-C1'-N9	6.18	113.15	108.20
1	A	139	A	C5-C6-N1	-6.18	114.61	117.70
1	A	270	G	P-O3'-C3'	-6.18	112.29	119.70
1	A	156	G	O4'-C1'-N9	6.17	113.14	108.20
1	A	145	C	N3-C4-C5	-6.17	119.43	121.90
1	A	296	C	N3-C4-C5	-6.16	119.43	121.90
1	A	262	G	C5-C6-O6	-6.16	124.90	128.60
1	A	168	G	O4'-C1'-N9	6.16	113.13	108.20
1	A	27	G	C5-C6-O6	-6.15	124.91	128.60
1	A	292	C	N3-C4-C5	-6.15	119.44	121.90
1	A	131	A	C6-N1-C2	6.15	122.29	118.60
1	A	173	A	C4-C5-C6	6.14	120.07	117.00
1	A	257	C	N3-C4-C5	-6.14	119.44	121.90
1	A	141	C	N3-C4-C5	-6.13	119.45	121.90
1	A	171	U	O4'-C1'-N1	6.12	113.10	108.20
1	A	297	U	O4'-C1'-N1	6.12	113.10	108.20
1	A	286	G	C5-C6-O6	-6.12	124.93	128.60
1	A	264	A	O4'-C1'-N9	6.12	113.09	108.20
1	A	32	A	C4-C5-C6	6.12	120.06	117.00
1	A	18	G	C5-C6-O6	-6.11	124.93	128.60
1	A	205	A	C4-C5-C6	6.11	120.06	117.00
1	A	255	A	C4-C5-C6	6.11	120.06	117.00
1	A	49	A	C4-C5-C6	6.11	120.05	117.00
1	A	283	A	C4-C5-C6	6.10	120.05	117.00
1	A	289	A	C4'-C3'-O3'	-6.09	96.62	109.40
1	A	277	C	N3-C4-C5	-6.08	119.47	121.90
1	A	206	G	O4'-C1'-N9	6.08	113.06	108.20
1	A	42	G	C5-C6-O6	-6.07	124.96	128.60
1	A	253	A	C4-C5-C6	6.07	120.04	117.00
1	A	102	A	C4-C5-C6	6.07	120.03	117.00
1	A	96	A	C4-C5-C6	6.06	120.03	117.00
1	A	178	G	O4'-C1'-N9	6.06	113.05	108.20
1	A	204	G	O4'-C1'-N9	6.06	113.05	108.20
1	A	208	A	C5-C6-N6	-6.04	118.87	123.70
1	A	47	U	C2'-C3'-O3'	6.04	123.36	113.70
1	A	173	A	C5-C6-N1	-6.03	114.69	117.70
1	A	45	G	O4'-C1'-N9	6.03	113.02	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	C	N3-C4-N4	6.03	122.22	118.00
1	A	72	A	C4-C5-C6	6.02	120.01	117.00
1	A	220	C	N3-C4-C5	-6.02	119.49	121.90
1	A	169	C	N3-C4-N4	6.02	122.21	118.00
1	A	199	A	C5-C6-N6	-6.01	118.89	123.70
1	A	186	C	C6-N1-C1'	-6.01	113.59	120.80
1	A	146	G	C5-C6-O6	-6.00	125.00	128.60
1	A	6	G	O4'-C1'-N9	6.00	113.00	108.20
1	A	192	A	C4-C5-C6	6.00	120.00	117.00
1	A	200	A	C5-C6-N6	-6.00	118.90	123.70
1	A	79	C	P-O5'-C5'	5.99	130.49	120.90
1	A	92	C	N3-C4-N4	5.99	122.19	118.00
1	A	183	A	C4-C5-C6	5.99	119.99	117.00
1	A	45	G	C5-C6-O6	-5.99	125.01	128.60
1	A	7	C	N3-C4-C5	-5.98	119.51	121.90
1	A	71	C	C2-N3-C4	5.98	122.89	119.90
1	A	261	U	C2-N3-C4	5.98	130.59	127.00
1	A	102	A	C5-C6-N1	-5.97	114.71	117.70
1	A	93	G	C5-C6-O6	-5.97	125.02	128.60
1	A	63	C	C2-N3-C4	5.97	122.89	119.90
1	A	201	A	C5-C6-N1	-5.97	114.72	117.70
1	A	46	C	N3-C4-C5	-5.96	119.52	121.90
1	A	3	C	C2-N3-C4	5.96	122.88	119.90
1	A	53	A	C4-C5-C6	5.95	119.98	117.00
1	A	160	A	C4-C5-C6	5.94	119.97	117.00
1	A	208	A	O4'-C1'-N9	5.94	112.95	108.20
1	A	292	C	N3-C4-N4	5.93	122.15	118.00
1	A	15	C	P-O5'-C5'	-5.93	111.41	120.90
1	A	227	G	O4'-C1'-N9	5.93	112.94	108.20
1	A	43	A	C4-C5-C6	5.93	119.96	117.00
1	A	58	G	O3'-P-O5'	-5.93	92.74	104.00
1	A	231	A	P-O5'-C5'	-5.93	111.42	120.90
1	A	17	C	O4'-C1'-N1	5.92	112.94	108.20
1	A	107	G	C5-C6-O6	-5.92	125.05	128.60
1	A	143	C	N3-C4-C5	-5.92	119.53	121.90
1	A	9	C	N3-C4-C5	-5.92	119.53	121.90
1	A	87	C	N3-C4-C5	-5.92	119.53	121.90
1	A	246	C	N3-C4-C5	-5.92	119.53	121.90
1	A	287	A	C4-C5-C6	5.92	119.96	117.00
1	A	189	C	N3-C4-C5	-5.91	119.53	121.90
1	A	19	C	N3-C4-C5	-5.91	119.54	121.90
1	A	32	A	O4'-C1'-N9	5.90	112.92	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	G	P-O5'-C5'	5.90	130.34	120.90
1	A	53	A	C5-C6-N1	-5.90	114.75	117.70
1	A	126	C	N3-C4-C5	-5.90	119.54	121.90
1	A	213	A	C4-C5-C6	5.90	119.95	117.00
1	A	119	A	C5-C6-N1	-5.90	114.75	117.70
1	A	258	C	N3-C4-N4	5.89	122.12	118.00
1	A	208	A	C4-C5-C6	5.89	119.94	117.00
1	A	22	C	N3-C4-N4	5.89	122.12	118.00
1	A	259	A	C6-N1-C2	5.89	122.13	118.60
1	A	17	C	O4'-C4'-C3'	-5.87	98.13	104.00
1	A	48	G	P-O3'-C3'	5.87	126.75	119.70
1	A	229	U	O4'-C4'-C3'	-5.87	98.13	104.00
1	A	64	U	C2-N3-C4	5.86	130.52	127.00
1	A	224	G	C5-C6-O6	-5.86	125.08	128.60
1	A	234	A	C4-C5-C6	5.86	119.93	117.00
1	A	187	G	O4'-C1'-N9	5.86	112.88	108.20
1	A	274	G	C5-C6-O6	-5.86	125.09	128.60
1	A	96	A	C6-N1-C2	5.85	122.11	118.60
1	A	75	A	C4-C5-C6	5.84	119.92	117.00
1	A	190	C	N3-C4-C5	-5.84	119.56	121.90
1	A	281	A	C2'-C3'-O3'	-5.83	96.67	109.50
1	A	140	C	N3-C4-C5	-5.83	119.57	121.90
1	A	21	C	N3-C4-N4	5.83	122.08	118.00
1	A	101	G	C5'-C4'-C3'	5.83	125.32	116.00
1	A	235	G	C5-C6-O6	-5.83	125.11	128.60
1	A	209	G	O4'-C1'-N9	5.81	112.85	108.20
1	A	88	A	C6-N1-C2	5.81	122.08	118.60
1	A	152	G	O4'-C1'-N9	5.80	112.84	108.20
1	A	1	G	C5-C6-O6	-5.79	125.12	128.60
1	A	101	G	P-O5'-C5'	-5.79	111.64	120.90
1	A	188	G	C5-C6-O6	-5.79	125.13	128.60
1	A	214	A	C4-C5-C6	5.77	119.89	117.00
1	A	201	A	C4'-C3'-C2'	-5.76	96.84	102.60
1	A	118	A	C6-N1-C2	5.76	122.06	118.60
1	A	2	C	N3-C4-C5	-5.75	119.60	121.90
1	A	279	A	C4'-C3'-O3'	5.75	124.50	113.00
1	A	1	G	O4'-C1'-N9	5.74	112.79	108.20
1	A	176	A	C4-C5-C6	5.74	119.87	117.00
1	A	216	A	C5-C6-N1	-5.73	114.83	117.70
1	A	26	A	C4-C5-C6	5.72	119.86	117.00
1	A	252	A	C5-C6-N6	-5.71	119.13	123.70
1	A	217	C	N3-C4-C5	-5.70	119.62	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	U	C4'-C3'-C2'	-5.69	96.91	102.60
1	A	138	G	N3-C2-N2	5.69	123.89	119.90
1	A	48	G	N1-C2-N3	-5.69	120.49	123.90
1	A	217	C	N3-C4-N4	5.69	121.98	118.00
1	A	247	C	N3-C4-N4	5.68	121.98	118.00
1	A	34	C	N3-C4-N4	5.68	121.98	118.00
1	A	196	C	N3-C4-N4	5.68	121.97	118.00
1	A	191	C	N3-C4-N4	5.67	121.97	118.00
1	A	212	C	C2-N3-C4	5.67	122.73	119.90
1	A	247	C	N3-C4-C5	-5.67	119.63	121.90
1	A	186	C	N3-C4-C5	-5.67	119.63	121.90
1	A	214	A	C5-C6-N1	-5.67	114.87	117.70
1	A	283	A	C6-N1-C2	5.67	122.00	118.60
1	A	185	C	N3-C4-N4	5.66	121.96	118.00
1	A	57	G	O3'-P-O5'	5.65	114.74	104.00
1	A	118	A	O4'-C1'-N9	5.65	112.72	108.20
1	A	22	C	N3-C4-C5	-5.64	119.64	121.90
1	A	245	G	C5-C6-O6	-5.63	125.22	128.60
1	A	259	A	C4-C5-C6	5.63	119.81	117.00
1	A	242	C	C5'-C4'-O4'	-5.62	102.35	109.10
1	A	177	G	C5-C6-O6	-5.62	125.23	128.60
1	A	172	A	C4-C5-C6	5.62	119.81	117.00
1	A	155	G	C5-C6-O6	-5.61	125.23	128.60
1	A	257	C	N3-C4-N4	5.61	121.93	118.00
1	A	148	G	O4'-C1'-N9	5.61	112.69	108.20
1	A	52	C	C2-N3-C4	5.61	122.70	119.90
1	A	83	G	O4'-C1'-N9	5.61	112.69	108.20
1	A	184	A	O4'-C1'-N9	5.61	112.68	108.20
1	A	133	A	C5-C6-N1	-5.60	114.90	117.70
1	A	156	G	C5-C6-O6	-5.60	125.24	128.60
1	A	32	A	C5-C6-N6	-5.60	119.22	123.70
1	A	149	A	O4'-C1'-N9	5.59	112.68	108.20
1	A	24	G	O4'-C1'-N9	5.59	112.67	108.20
1	A	296	C	N3-C4-N4	5.59	121.91	118.00
1	A	198	G	C6-C5-N7	-5.59	127.05	130.40
1	A	246	C	N3-C4-N4	5.58	121.91	118.00
1	A	199	A	O4'-C1'-N9	5.58	112.67	108.20
1	A	37	C	P-O3'-C3'	5.57	126.39	119.70
1	A	263	C	C2-N3-C4	5.57	122.69	119.90
1	A	69	C	C2-N3-C4	5.56	122.68	119.90
1	A	293	C	N3-C4-C5	-5.56	119.67	121.90
1	A	92	C	N3-C4-C5	-5.55	119.68	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	G	O4'-C1'-N9	5.55	112.64	108.20
1	A	99	C	O4'-C1'-N1	5.54	112.63	108.20
1	A	149	A	C4-C5-C6	5.54	119.77	117.00
1	A	73	G	C5-C6-O6	-5.54	125.28	128.60
1	A	75	A	C5-C6-N6	-5.54	119.27	123.70
1	A	86	G	O4'-C1'-N9	5.53	112.62	108.20
1	A	38	U	O4'-C1'-N1	5.52	112.62	108.20
1	A	131	A	C4-C5-C6	5.52	119.76	117.00
1	A	164	G	O4'-C1'-N9	5.50	112.60	108.20
1	A	231	A	C4-C5-C6	5.50	119.75	117.00
1	A	280	C	N1-C1'-C2'	5.50	121.15	114.00
1	A	139	A	C4-C5-C6	5.49	119.75	117.00
1	A	44	G	N1-C2-N3	-5.48	120.61	123.90
1	A	186	C	N3-C4-N4	5.48	121.83	118.00
1	A	50	G	O4'-C1'-N9	5.48	112.58	108.20
1	A	21	C	N3-C4-C5	-5.47	119.71	121.90
1	A	189	C	N3-C4-N4	5.47	121.83	118.00
1	A	119	A	P-O3'-C3'	5.46	126.26	119.70
1	A	281	A	P-O5'-C5'	5.46	129.64	120.90
1	A	277	C	N3-C4-N4	5.46	121.82	118.00
1	A	131	A	O4'-C1'-N9	5.45	112.56	108.20
1	A	127	A	C5-C6-N6	-5.45	119.34	123.70
1	A	288	G	C4'-C3'-O3'	5.45	123.90	113.00
1	A	9	C	N3-C4-N4	5.44	121.81	118.00
1	A	119	A	C4-C5-C6	5.43	119.72	117.00
1	A	89	G	C5-C6-O6	-5.43	125.34	128.60
1	A	30	C	N3-C4-N4	5.43	121.80	118.00
1	A	68	G	O5'-C5'-C4'	-5.43	101.39	111.70
1	A	81	G	N1-C2-N3	-5.43	120.64	123.90
1	A	270	G	C2'-C3'-O3'	-5.43	97.56	109.50
1	A	193	G	C5-C6-O6	-5.41	125.36	128.60
1	A	158	C	N3-C4-C5	-5.41	119.74	121.90
1	A	269	A	P-O3'-C3'	-5.40	113.22	119.70
1	A	32	A	C5-C6-N1	-5.39	115.00	117.70
1	A	228	A	P-O3'-C3'	5.38	126.16	119.70
1	A	111	C	P-O5'-C5'	5.38	129.51	120.90
1	A	184	A	C5-C6-N1	-5.38	115.01	117.70
1	A	185	C	N3-C4-C5	-5.38	119.75	121.90
1	A	86	G	N1-C2-N3	-5.38	120.67	123.90
1	A	120	G	C5-C6-O6	-5.38	125.37	128.60
1	A	219	C	C2-N3-C4	5.37	122.59	119.90
1	A	280	C	C5'-C4'-O4'	5.37	115.55	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	A	P-O3'-C3'	5.37	126.14	119.70
1	A	187	G	N1-C2-N3	-5.37	120.68	123.90
1	A	251	G	P-O5'-C5'	5.37	129.48	120.90
1	A	169	C	N3-C4-C5	-5.36	119.75	121.90
1	A	284	G	C5-C6-O6	-5.36	125.38	128.60
1	A	151	C	N3-C4-N4	5.36	121.75	118.00
1	A	200	A	C5-C6-N1	-5.35	115.03	117.70
1	A	84	C	N3-C4-C5	-5.35	119.76	121.90
1	A	183	A	C5-C6-N6	-5.33	119.44	123.70
1	A	170	C	N3-C4-N4	5.31	121.72	118.00
1	A	176	A	C5-C6-N1	-5.30	115.05	117.70
1	A	116	C	N3-C4-C5	-5.29	119.78	121.90
1	A	82	G	C5-C6-O6	-5.29	125.42	128.60
1	A	294	G	N1-C2-N3	-5.29	120.73	123.90
1	A	234	A	O4'-C1'-N9	5.29	112.43	108.20
1	A	1	G	N3-C2-N2	5.29	123.60	119.90
1	A	70	C	N3-C4-C5	-5.29	119.79	121.90
1	A	88	A	C4-C5-C6	5.28	119.64	117.00
1	A	173	A	C5-C6-N6	-5.28	119.48	123.70
1	A	34	C	N3-C4-C5	-5.25	119.80	121.90
1	A	210	G	C5-C6-O6	-5.25	125.45	128.60
1	A	172	A	C5-C6-N6	-5.25	119.50	123.70
1	A	221	C	N3-C4-N4	5.25	121.67	118.00
1	A	46	C	N3-C4-N4	5.24	121.67	118.00
1	A	170	C	N3-C4-C5	-5.24	119.80	121.90
1	A	54	G	C5-C6-O6	-5.24	125.46	128.60
1	A	116	C	N3-C4-N4	5.24	121.66	118.00
1	A	199	A	C5-C6-N1	-5.24	115.08	117.70
1	A	281	A	C5'-C4'-O4'	5.24	115.38	109.10
1	A	229	U	N1-C1'-C2'	-5.23	106.25	112.00
1	A	230	C	O4'-C1'-N1	5.23	112.38	108.20
1	A	285	C	C2-N3-C4	5.22	122.51	119.90
1	A	168	G	N1-C2-N3	-5.22	120.77	123.90
1	A	276	G	N1-C2-N3	-5.21	120.77	123.90
1	A	291	C	C2-N3-C4	5.21	122.50	119.90
1	A	149	A	C5-C6-N1	-5.21	115.10	117.70
1	A	166	U	N3-C4-C5	-5.20	111.48	114.60
1	A	234	A	C6-N1-C2	5.20	121.72	118.60
1	A	147	G	O4'-C1'-N9	5.20	112.36	108.20
1	A	274	G	O4'-C1'-N9	5.19	112.35	108.20
1	A	214	A	C5-C6-N6	-5.19	119.55	123.70
1	A	256	G	C5-C6-O6	-5.19	125.48	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	183	A	C5-C6-N1	-5.18	115.11	117.70
1	A	227	G	N1-C2-N3	-5.18	120.79	123.90
1	A	26	A	C5-C6-N1	-5.16	115.12	117.70
1	A	19	C	N3-C4-N4	5.16	121.61	118.00
1	A	15	C	C4'-C3'-O3'	-5.13	98.62	109.40
1	A	26	A	C5-C6-N6	-5.13	119.59	123.70
1	A	268	C	C2-N3-C4	5.13	122.47	119.90
1	A	191	C	N3-C4-C5	-5.13	119.85	121.90
1	A	265	C	N3-C4-C5	-5.12	119.85	121.90
1	A	105	G	P-O3'-C3'	-5.12	113.56	119.70
1	A	49	A	O4'-C1'-N9	5.12	112.29	108.20
1	A	74	G	C5-C6-O6	-5.11	125.53	128.60
1	A	75	A	C5-C6-N1	-5.11	115.14	117.70
1	A	136	G	C5-C6-O6	-5.11	125.53	128.60
1	A	105	G	C1'-O4'-C4'	-5.11	105.81	109.90
1	A	62	G	C5-C6-O6	-5.10	125.54	128.60
1	A	190	C	N3-C4-N4	5.10	121.57	118.00
1	A	60	U	N1-C1'-C2'	5.10	120.63	114.00
1	A	159	C	C2-N3-C4	5.09	122.45	119.90
1	A	213	A	C5-C6-N6	-5.09	119.63	123.70
1	A	60	U	C1'-O4'-C4'	-5.09	105.83	109.90
1	A	172	A	C5-C6-N1	-5.09	115.16	117.70
1	A	174	G	C5-C6-O6	-5.09	125.55	128.60
1	A	55	G	N3-C2-N2	5.08	123.45	119.90
1	A	125	G	C5-C6-O6	-5.08	125.55	128.60
1	A	29	C	N3-C4-N4	5.07	121.55	118.00
1	A	76	G	C2'-C3'-O3'	-5.07	98.36	109.50
1	A	265	C	N3-C4-N4	5.05	121.54	118.00
1	A	213	A	C5-C6-N1	-5.05	115.18	117.70
1	A	129	C	C2-N3-C4	5.04	122.42	119.90
1	A	105	G	C2'-C3'-O3'	-5.03	98.43	109.50
1	A	225	C	C2-N3-C4	5.03	122.41	119.90
1	A	163	A	C5-C6-N1	-5.03	115.19	117.70
1	A	267	C	C2-N3-C4	5.03	122.41	119.90
1	A	274	G	C4'-C3'-C2'	-5.02	97.58	102.60
1	A	2	C	N3-C4-N4	5.02	121.51	118.00
1	A	163	A	O4'-C1'-N9	5.02	112.22	108.20
1	A	166	U	C5-C4-O4	5.01	128.91	125.90
1	A	203	G	C5-C6-O6	-5.01	125.59	128.60
1	A	260	C	N3-C4-N4	5.01	121.51	118.00
1	A	182	G	P-O3'-C3'	5.01	125.71	119.70

All (12) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	21	ARG	CA
2	B	23	SER	CA
2	B	26	VAL	CA
2	B	27	PHE	CA
3	C	143	LYS	CA
3	C	146	HIS	CA
3	C	149	SER	CA
3	C	150	ARG	CA
5	E	29	LEU	CA
5	E	30	LYS	CA
5	E	31	TYR	CA
5	E	34	SER	CA

All (146) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	U	Sidechain
1	A	119	A	Sidechain
1	A	131	A	Sidechain
1	A	133	A	Sidechain
1	A	134	U	Sidechain
1	A	135	G	Sidechain
1	A	136	G	Sidechain
1	A	137	U	Sidechain
1	A	138	G	Sidechain
1	A	149	A	Sidechain
1	A	163	A	Sidechain
1	A	165	G	Sidechain
1	A	166	U	Sidechain
1	A	167	U	Sidechain
1	A	168	G	Sidechain
1	A	175	G	Sidechain
1	A	201	A	Sidechain
1	A	215	A	Sidechain
1	A	233	U	Sidechain
1	A	237	G	Sidechain
1	A	245	G	Sidechain
1	A	250	U	Sidechain
1	A	251	G	Sidechain
1	A	252	A	Sidechain
1	A	253	A	Sidechain
1	A	254	U	Sidechain
1	A	255	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	274	G	Sidechain
1	A	276	G	Sidechain
1	A	282	U	Sidechain
1	A	284	G	Sidechain
1	A	297	U	Sidechain
1	A	39	C	Sidechain
1	A	43	A	Sidechain
1	A	75	A	Sidechain
1	A	83	G	Sidechain
1	A	85	U	Sidechain
1	A	96	A	Sidechain
4	D	100	LYS	Mainchain
4	D	107	VAL	Mainchain
4	D	115	THR	Mainchain
4	D	116	THR	Mainchain
4	D	117	THR	Mainchain
4	D	123	TYR	Mainchain
4	D	124	TYR	Mainchain
4	D	125	TYR	Mainchain
4	D	126	GLN	Mainchain
4	D	128	LYS	Mainchain
4	D	131	LYS	Mainchain
4	D	132	THR	Mainchain
4	D	136	CYS	Mainchain
4	D	138	ASP	Mainchain
4	D	142	ALA	Mainchain
4	D	154	LYS	Mainchain
4	D	162	SER	Mainchain
4	D	167	ASP	Mainchain
4	D	169	VAL	Mainchain
4	D	174	GLU	Mainchain
4	D	175	GLY	Mainchain
4	D	176	VAL	Mainchain
4	D	180	LYS	Mainchain
4	D	181	ASN	Mainchain
4	D	182	GLU	Mainchain
4	D	184	PHE	Mainchain
4	D	185	GLU	Mainchain
4	D	187	ILE	Mainchain
4	D	191	THR	Mainchain
4	D	2	VAL	Mainchain
4	D	207	GLN	Mainchain

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Mol	Chain	Res	Type	Group
4	D	208	VAL	Mainchain
4	D	21	THR	Mainchain
4	D	215	ASP	Mainchain
4	D	220	VAL	Mainchain
4	D	221	MET	Mainchain
4	D	227	GLN	Mainchain
4	D	228	ALA	Mainchain
4	D	23	ILE	Mainchain
4	D	231	ALA	Mainchain
4	D	237	LYS	Mainchain
4	D	242	VAL	Mainchain
4	D	243	ALA	Mainchain
4	D	244	SER	Mainchain
4	D	249	LYS	Mainchain
4	D	250	LEU	Mainchain
4	D	252	GLY	Mainchain
4	D	259	ALA	Mainchain
4	D	26	GLU	Mainchain
4	D	264	ALA	Mainchain
4	D	266	THR	Mainchain
4	D	268	SER	Mainchain
4	D	28	LEU	Mainchain
4	D	281	ASP	Mainchain
4	D	282	PHE	Mainchain
4	D	292	SER	Mainchain
4	D	293	LYS	Mainchain
4	D	296	GLY	Mainchain
4	D	298	GLY	Mainchain,Peptide
4	D	3	LEU	Mainchain
4	D	309	GLU	Mainchain
4	D	31	MET	Mainchain
4	D	319	ILE	Mainchain
4	D	32	LEU	Mainchain
4	D	331	ASP	Mainchain
4	D	334	GLU	Mainchain
4	D	342	MET	Peptide
4	D	35	VAL	Mainchain
4	D	357	THR	Mainchain
4	D	358	ASP	Mainchain
4	D	360	MET	Mainchain
4	D	366	GLN	Mainchain
4	D	37	THR	Mainchain

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Mol	Chain	Res	Type	Group
4	D	376	MET	Mainchain
4	D	378	ILE	Mainchain
4	D	381	SER	Mainchain
4	D	390	THR	Mainchain
4	D	397	SER	Mainchain
4	D	401	GLY	Mainchain
4	D	403	ILE	Mainchain
4	D	405	ARG	Mainchain
4	D	408	ARG	Mainchain
4	D	417	VAL	Mainchain
4	D	418	GLN	Mainchain
4	D	424	TYR	Mainchain
4	D	428	ALA	Mainchain
4	D	429	GLN	Mainchain
4	D	43	ASP	Mainchain
4	D	44	VAL	Mainchain
4	D	45	ASN	Mainchain
4	D	46	ILE	Mainchain
4	D	5	ASP	Mainchain
4	D	55	ASN	Mainchain
4	D	6	LEU	Mainchain
4	D	60	ILE	Mainchain
4	D	66	ALA	Mainchain
4	D	69	LEU	Mainchain
4	D	71	LYS	Mainchain
4	D	74	MET	Mainchain
4	D	79	VAL	Mainchain
4	D	80	PHE	Mainchain
4	D	81	LYS	Mainchain
4	D	89	PRO	Mainchain
4	D	92	LYS	Mainchain
4	D	93	ALA	Mainchain
4	D	94	TRP	Mainchain
4	D	99	GLY	Mainchain

## 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	6403	0	3239	206	0
2	B	300	0	74	22	0
3	C	716	0	184	27	0
4	D	1732	0	488	27	0
5	E	296	0	71	26	0
6	F	429	0	109	11	0
7	S	72	0	18	0	0
All	All	9948	0	4183	255	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 18.

All (255) 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:B:94:LEU:CA	5:E:55:GLN:CA	1.96	1.43
2:B:94:LEU:N	5:E:56:ALA:H	1.26	1.31
2:B:94:LEU:H	5:E:56:ALA:N	1.30	1.28
1:A:196:C:H4'	6:F:69:SER:CA	1.65	1.26
2:B:94:LEU:CA	5:E:56:ALA:H	1.49	1.25
2:B:94:LEU:N	5:E:56:ALA:N	1.84	1.22
1:A:174:G:H5''	3:C:146:HIS:O	1.08	1.21
1:A:195:U:C5'	4:D:411:GLY:HA3	1.71	1.20
2:B:94:LEU:CA	5:E:56:ALA:N	2.03	1.19
1:A:195:U:H5''	4:D:411:GLY:HA3	1.20	1.15
1:A:174:G:C5'	3:C:146:HIS:O	1.93	1.15
1:A:175:G:C5'	3:C:146:HIS:H	1.62	1.12
1:A:175:G:C5'	3:C:143:LYS:O	2.03	1.07
1:A:175:G:H5'	3:C:146:HIS:N	1.68	1.07
1:A:175:G:H5'	3:C:146:HIS:H	1.16	1.06
1:A:278:A:C2	1:A:280:C:N4	2.24	1.06
1:A:278:A:H2	1:A:280:C:N4	1.56	1.04
1:A:174:G:H5''	3:C:146:HIS:C	1.80	1.01
2:B:94:LEU:CA	5:E:55:GLN:C	2.31	0.99
1:A:175:G:H5'	3:C:143:LYS:O	1.64	0.95
1:A:175:G:H5'	3:C:146:HIS:CA	1.98	0.93
1:A:195:U:H4'	4:D:411:GLY:HA2	1.49	0.93
2:B:23:SER:CA	5:E:35:ASP:CA	2.34	0.92
1:A:175:G:H4'	3:C:143:LYS:O	1.67	0.92
1:A:67:A:C2	1:A:281:A:N6	2.38	0.91
1:A:173:A:OP2	3:C:153:LYS:CA	2.19	0.91
1:A:66:G:N2	1:A:283:A:C1'	2.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:A:OP2	3:C:153:LYS:C	2.10	0.90
1:A:16:G:H5''	1:A:17:C:C5	2.07	0.90
1:A:66:G:H21	1:A:283:A:C1'	1.86	0.89
1:A:196:C:C4'	6:F:69:SER:CA	2.50	0.87
1:A:109:G:P	1:A:238:G:OP2	2.32	0.87
1:A:79:C:H42	1:A:270:G:H1	1.16	0.86
1:A:110:U:H3'	1:A:111:C:H5	1.41	0.86
1:A:124:G:O2'	1:A:125:G:H5'	1.76	0.86
1:A:175:G:C5'	3:C:146:HIS:N	2.34	0.85
1:A:195:U:C5'	4:D:411:GLY:CA	2.54	0.84
4:D:362:LYS:N	4:D:363:GLY:HA3	1.92	0.84
1:A:173:A:OP2	3:C:154:ALA:N	2.09	0.84
1:A:175:G:C4'	3:C:143:LYS:O	2.25	0.83
1:A:79:C:N4	1:A:270:G:H1	1.75	0.82
1:A:59:A:N3	1:A:59:A:H2'	1.95	0.81
1:A:278:A:N6	1:A:279:A:N1	2.27	0.81
1:A:67:A:N3	1:A:281:A:N6	2.28	0.81
1:A:74:G:H1	1:A:271:C:H42	1.25	0.81
1:A:174:G:C3'	3:C:146:HIS:CA	2.60	0.80
1:A:195:U:H4'	4:D:411:GLY:CA	2.12	0.80
2:B:28:ILE:C	5:E:28:VAL:C	2.40	0.79
1:A:278:A:H2	1:A:280:C:C4	2.01	0.79
1:A:59:A:C2	1:A:60:U:H5'	2.17	0.79
1:A:291:C:O4'	5:E:46:LEU:CA	2.31	0.78
2:B:21:ARG:O	5:E:34:SER:C	2.25	0.75
1:A:111:C:N4	1:A:239:G:O6	2.20	0.75
1:A:37:C:O2'	1:A:38:U:H5'	1.86	0.74
1:A:229:U:H3'	1:A:230:C:H6	1.52	0.74
4:D:296:GLY:HA2	4:D:297:MET:C	2.09	0.74
1:A:66:G:N2	1:A:283:A:N9	2.37	0.73
1:A:37:C:H2'	1:A:38:U:O4'	1.89	0.73
1:A:226:U:H2'	1:A:227:G:H5''	1.71	0.72
2:B:91:MET:O	5:E:56:ALA:CA	2.37	0.72
1:A:109:G:OP2	1:A:238:G:OP2	2.08	0.72
1:A:74:G:H1	1:A:271:C:N4	1.88	0.72
1:A:123:C:O2'	1:A:124:G:H5'	1.89	0.72
1:A:16:G:H5''	1:A:17:C:H5	1.51	0.72
1:A:66:G:N2	1:A:283:A:C8	2.58	0.71
1:A:110:U:C2'	1:A:111:C:OP1	2.39	0.71
1:A:98:G:H5''	1:A:98:G:C8	2.25	0.71
2:B:21:ARG:O	5:E:35:ASP:N	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:G:C5'	3:C:146:HIS:CA	2.69	0.70
1:A:13:G:H1	1:A:37:C:H42	1.40	0.69
1:A:278:A:O2'	1:A:279:A:H5'	1.93	0.69
1:A:175:G:C5'	3:C:143:LYS:C	2.49	0.68
1:A:175:G:H5''	3:C:143:LYS:C	2.14	0.68
1:A:281:A:C5	1:A:282:U:H1'	2.30	0.67
1:A:37:C:C2'	1:A:38:U:H5'	2.25	0.67
1:A:195:U:H5'	4:D:410:SER:O	1.95	0.66
2:B:24:GLY:C	5:E:32:ARG:CA	2.64	0.66
1:A:23:U:O4	2:B:63:GLY:O	2.13	0.66
2:B:55:LYS:N	5:E:73:MET:O	2.29	0.66
1:A:110:U:H2'	1:A:111:C:OP1	1.95	0.65
1:A:124:G:HO2'	1:A:125:G:H5'	1.61	0.64
2:B:29:THR:N	5:E:28:VAL:CA	2.61	0.63
1:A:223:U:OP1	3:C:73:GLN:CA	2.46	0.63
1:A:226:U:C2'	1:A:227:G:H5''	2.29	0.63
4:D:339:ILE:O	4:D:342:MET:N	2.30	0.62
1:A:181:U:H2'	1:A:182:G:H5'	1.79	0.62
1:A:66:G:H21	1:A:283:A:H1'	1.63	0.62
1:A:103:U:C6	1:A:104:C:C6	2.88	0.61
1:A:103:U:C5	1:A:104:C:C5	2.88	0.61
1:A:111:C:O5'	1:A:111:C:H6	1.83	0.61
1:A:195:U:C4'	4:D:411:GLY:CA	2.79	0.61
1:A:135:G:H2'	1:A:136:G:H5'	1.81	0.61
1:A:9:C:C2'	1:A:10:G:H5'	2.31	0.61
1:A:37:C:H2'	1:A:38:U:C5'	2.31	0.61
1:A:59:A:N3	1:A:60:U:H5'	2.16	0.60
4:D:296:GLY:CA	4:D:297:MET:C	2.69	0.60
1:A:66:G:N2	1:A:283:A:H1'	2.13	0.60
1:A:242:C:H5''	1:A:242:C:O2	2.02	0.60
1:A:269:A:H2'	1:A:270:G:O5'	2.01	0.60
1:A:229:U:C6	1:A:230:C:C6	2.90	0.60
1:A:278:A:N6	1:A:279:A:C6	2.70	0.60
1:A:67:A:C2	1:A:281:A:C6	2.90	0.59
1:A:66:G:N2	1:A:283:A:O4'	2.32	0.59
4:D:340:MET:C	4:D:342:MET:N	2.56	0.59
1:A:78:U:H2'	1:A:78:U:O2	2.02	0.59
1:A:291:C:C1'	5:E:46:LEU:CA	2.80	0.59
1:A:280:C:O2	1:A:280:C:H2'	2.02	0.59
1:A:278:A:C6	1:A:279:A:C2	2.90	0.59
1:A:175:G:H5''	3:C:142:ARG:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:C:H2'	1:A:163:A:H5'	1.84	0.59
1:A:195:U:H5'	4:D:411:GLY:HA3	1.74	0.58
2:B:25:SER:C	5:E:31:TYR:C	2.60	0.58
1:A:68:G:H2'	1:A:69:C:O4'	2.04	0.58
1:A:278:A:H2'	1:A:279:A:O4'	2.03	0.58
4:D:340:MET:C	4:D:342:MET:H	2.06	0.58
1:A:175:G:H5''	3:C:146:HIS:H	1.62	0.58
1:A:278:A:N6	1:A:279:A:C2	2.72	0.58
1:A:163:A:H2'	1:A:164:G:C8	2.39	0.57
1:A:227:G:C2	1:A:228:A:H1'	2.39	0.57
1:A:104:C:O2	1:A:104:C:H2'	2.04	0.57
1:A:14:G:H1'	1:A:38:U:H3	1.69	0.56
1:A:195:U:H5''	4:D:411:GLY:CA	2.13	0.56
1:A:37:C:C2'	1:A:38:U:C5'	2.83	0.56
1:A:224:G:H5''	3:C:125:ARG:CA	2.35	0.55
1:A:278:A:C5	1:A:279:A:C5	2.94	0.55
1:A:291:C:H1'	5:E:46:LEU:CA	2.36	0.55
1:A:16:G:H5''	1:A:17:C:C6	2.42	0.55
1:A:79:C:H5'	1:A:80:U:OP2	2.08	0.54
4:D:337:GLN:O	4:D:340:MET:N	2.40	0.54
1:A:76:G:N3	1:A:76:G:H2'	2.23	0.54
1:A:67:A:N3	1:A:281:A:C6	2.76	0.54
1:A:269:A:H2'	1:A:270:G:C5'	2.38	0.54
1:A:98:G:C2	1:A:253:A:C5	2.96	0.53
1:A:103:U:C6	1:A:104:C:C5	2.96	0.53
1:A:79:C:P	1:A:264:A:H5''	2.48	0.53
1:A:67:A:H3'	1:A:68:G:H8	1.73	0.53
1:A:182:G:H1'	1:A:215:A:H61	1.73	0.53
1:A:103:U:C5	1:A:104:C:C6	2.97	0.52
1:A:113:G:OP2	1:A:114:C:H5	1.92	0.52
2:B:94:LEU:N	5:E:55:GLN:CA	2.70	0.52
1:A:229:U:O5'	1:A:230:C:H5	1.93	0.51
6:F:88:GLN:O	6:F:91:GLY:N	2.42	0.51
1:A:133:A:N1	1:A:163:A:N1	2.58	0.51
1:A:75:A:C5	1:A:76:G:H1'	2.45	0.51
6:F:112:ILE:C	6:F:114:LYS:H	2.13	0.51
1:A:162:C:C2'	1:A:163:A:H5'	2.41	0.51
1:A:278:A:C2	1:A:280:C:C4	2.86	0.51
1:A:198:G:H1'	1:A:201:A:N6	2.25	0.51
1:A:135:G:C2'	1:A:136:G:H5'	2.41	0.51
1:A:150:G:H2'	1:A:151:C:H5'	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:C:H2'	1:A:79:C:O2	2.10	0.50
1:A:67:A:H3'	1:A:68:G:C8	2.47	0.50
1:A:249:G:H2'	1:A:250:U:C6	2.47	0.50
1:A:270:G:OP2	1:A:271:C:C5	2.65	0.50
2:B:94:LEU:N	5:E:55:GLN:C	2.52	0.49
1:A:229:U:H3'	1:A:230:C:C6	2.40	0.49
1:A:67:A:C6	1:A:68:G:C2	3.00	0.49
1:A:119:A:H3'	1:A:120:G:H5''	1.95	0.49
1:A:56:A:N6	1:A:57:G:C2	2.81	0.49
1:A:59:A:N3	1:A:59:A:C2'	2.72	0.49
1:A:131:A:C2	1:A:132:U:H1'	2.48	0.49
1:A:229:U:P	1:A:230:C:H5	2.36	0.49
4:D:360:MET:O	4:D:362:LYS:N	2.41	0.48
1:A:159:C:H2'	1:A:160:A:H5'	1.95	0.48
1:A:123:C:C2'	1:A:124:G:H5'	2.43	0.48
1:A:110:U:H3'	1:A:111:C:C5	2.33	0.48
1:A:67:A:N6	1:A:68:G:N1	2.62	0.48
4:D:337:GLN:C	4:D:340:MET:H	2.17	0.48
1:A:111:C:C6	1:A:111:C:O5'	2.65	0.47
4:D:340:MET:O	4:D:342:MET:N	2.47	0.47
4:D:341:LYS:O	4:D:342:MET:O	2.32	0.47
1:A:160:A:H2'	1:A:161:C:O4'	2.14	0.47
1:A:9:C:H2'	1:A:10:G:H5'	1.95	0.47
1:A:98:G:H8	1:A:98:G:H5''	1.72	0.47
1:A:67:A:C5	1:A:68:G:C5	3.02	0.47
1:A:270:G:OP2	1:A:271:C:H5	1.98	0.47
1:A:227:G:H2'	1:A:228:A:O4'	2.14	0.47
1:A:35:U:O2'	1:A:36:A:H5'	2.15	0.47
4:D:429:GLN:O	4:D:430:MET:C	2.53	0.47
1:A:75:A:C4	1:A:76:G:H1'	2.50	0.47
1:A:79:C:OP1	1:A:264:A:H5''	2.16	0.46
1:A:173:A:P	3:C:153:LYS:C	2.93	0.46
1:A:67:A:N6	1:A:68:G:C2	2.83	0.46
1:A:228:A:OP2	3:C:88:LYS:CA	2.64	0.46
1:A:277:C:H2'	1:A:278:A:C8	2.50	0.46
2:B:94:LEU:H	5:E:56:ALA:CA	2.18	0.46
6:F:76:VAL:C	6:F:78:TYR:N	2.69	0.46
1:A:278:A:H2'	1:A:279:A:O5'	2.16	0.46
1:A:110:U:O2'	1:A:111:C:OP1	2.32	0.46
1:A:124:G:C2'	1:A:125:G:H5'	2.46	0.45
1:A:181:U:C2'	1:A:182:G:H5'	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:A:H2'	1:A:270:G:H5'	1.98	0.45
1:A:278:A:N7	1:A:279:A:C5	2.84	0.45
2:B:25:SER:CA	5:E:32:ARG:N	2.79	0.45
1:A:281:A:C4	1:A:282:U:H1'	2.51	0.45
6:F:76:VAL:O	6:F:78:TYR:N	2.50	0.45
1:A:119:A:N1	1:A:231:A:C2	2.85	0.45
1:A:281:A:C6	1:A:282:U:H1'	2.52	0.45
1:A:79:C:C5'	1:A:80:U:OP2	2.65	0.45
1:A:113:G:OP2	1:A:114:C:C5	2.70	0.45
4:D:362:LYS:N	4:D:363:GLY:CA	2.72	0.45
1:A:169:C:H3'	1:A:170:C:C5'	2.47	0.45
1:A:242:C:H4'	1:A:243:G:H8	1.82	0.45
1:A:98:G:C5'	1:A:98:G:C8	2.99	0.44
1:A:164:G:C5	1:A:165:G:C8	3.05	0.44
1:A:79:C:OP1	1:A:264:A:OP1	2.35	0.44
1:A:198:G:H1'	1:A:201:A:H61	1.82	0.44
1:A:229:U:OP2	1:A:230:C:C5	2.70	0.44
6:F:45:THR:O	6:F:46:ALA:C	2.56	0.44
4:D:233:ALA:O	4:D:234:LYS:C	2.56	0.44
1:A:229:U:OP2	1:A:230:C:H5	2.01	0.44
1:A:230:C:H2'	1:A:231:A:O5'	2.18	0.44
1:A:108:U:O3'	1:A:238:G:OP2	2.35	0.44
5:E:12:ARG:O	5:E:13:ALA:C	2.57	0.43
1:A:75:A:C6	1:A:76:G:H1'	2.53	0.43
1:A:163:A:C2	1:A:164:G:C6	3.06	0.43
1:A:16:G:H1'	1:A:39:C:N4	2.33	0.43
1:A:79:C:N3	1:A:270:G:N1	2.67	0.43
1:A:123:C:H2'	1:A:124:G:C5'	2.49	0.42
1:A:243:G:H2'	1:A:244:C:C6	2.53	0.42
1:A:13:G:H1	1:A:37:C:N4	2.12	0.42
4:D:414:THR:H	6:F:74:ARG:CA	2.32	0.42
1:A:12:U:O2'	1:A:14:G:N7	2.45	0.42
1:A:182:G:H1'	1:A:215:A:N6	2.32	0.42
1:A:219:C:C2'	1:A:220:C:H5'	2.49	0.42
1:A:37:C:H3'	1:A:37:C:O2	2.20	0.42
1:A:174:G:H3'	3:C:146:HIS:CA	2.47	0.42
4:D:334:GLU:O	4:D:338:ASN:N	2.48	0.42
4:D:337:GLN:C	4:D:339:ILE:N	2.73	0.42
1:A:159:C:C2'	1:A:160:A:H5'	2.49	0.42
1:A:269:A:C2'	1:A:270:G:O5'	2.68	0.41
1:A:273:U:H2'	1:A:274:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:328:THR:O	4:D:331:ASP:N	2.34	0.41
1:A:65:U:O2'	1:A:66:G:H5'	2.20	0.41
1:A:164:G:C6	1:A:165:G:C8	3.08	0.41
6:F:88:GLN:O	6:F:89:GLU:C	2.58	0.41
1:A:222:G:H2'	1:A:223:U:H5'	2.03	0.41
1:A:56:A:N6	1:A:57:G:N1	2.69	0.41
1:A:252:A:H4'	1:A:253:A:H5'	2.03	0.41
1:A:278:A:O5'	1:A:278:A:H8	2.04	0.41
1:A:278:A:C6	1:A:279:A:C6	3.09	0.41
1:A:297:U:H2'	1:A:298:C:C6	2.56	0.41
1:A:99:C:C5	1:A:252:A:N6	2.89	0.41
6:F:112:ILE:C	6:F:114:LYS:N	2.74	0.41
6:F:104:VAL:O	6:F:105:MET:C	2.60	0.41
1:A:276:G:H2'	1:A:277:C:C6	2.56	0.41
5:E:62:ILE:C	5:E:64:LYS:N	2.74	0.41
1:A:224:G:H5'	3:C:125:ARG:C	2.41	0.40
1:A:80:U:H2'	1:A:81:G:C8	2.56	0.40
1:A:120:G:O2'	1:A:121:U:H5'	2.22	0.40
1:A:79:C:C2'	1:A:79:C:O2	2.68	0.40
1:A:110:U:O2'	1:A:111:C:P	2.79	0.40
1:A:132:U:H2'	1:A:133:A:C8	2.57	0.40
2:B:25:SER:N	5:E:32:ARG:CA	2.84	0.40
1:A:165:G:N7	1:A:176:A:C6	2.89	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 PDB entries followed by that with respect to all EM entries.

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	
2	B	71/75 (95%)	61 (86%)	9 (13%)	1 (1%)	13	54
3	C	175/195 (90%)	168 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	431/433 (100%)	360 (84%)	55 (13%)	16 (4%)	4	33
5	E	72/74 (97%)	61 (85%)	9 (12%)	2 (3%)	6	39
6	F	105/107 (98%)	87 (83%)	11 (10%)	7 (7%)	1	21
7	S	16/18 (89%)	14 (88%)	2 (12%)	0	100	100
All	All	870/902 (96%)	751 (86%)	93 (11%)	26 (3%)	9	37

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	342	MET
6	F	42	GLU
6	F	75	ASP
4	D	296	GLY
4	D	297	MET
4	D	298	GLY
4	D	299	ASP
6	F	99	PRO
2	B	23	SER
4	D	2	VAL
4	D	88	ASP
4	D	161	GLY
4	D	300	ILE
4	D	359	PHE
5	E	46	LEU
4	D	267	LYS
6	F	64	LYS
6	F	77	GLN
4	D	164	THR
4	D	341	LYS
4	D	373	LYS
4	D	101	GLN
4	D	354	GLY
5	E	21	ASP
6	F	56	VAL
6	F	96	VAL

### 5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.



## 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	298/299 (99%)	69 (23%)	10 (3%)

All (69) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	G
1	A	10	G
1	A	27	G
1	A	28	U
1	A	33	G
1	A	38	U
1	A	40	G
1	A	43	A
1	A	44	G
1	A	47	U
1	A	48	G
1	A	49	A
1	A	63	C
1	A	70	C
1	A	75	A
1	A	76	G
1	A	84	C
1	A	85	U
1	A	88	A
1	A	89	G
1	A	90	U
1	A	99	C
1	A	107	G
1	A	111	C
1	A	118	A
1	A	119	A
1	A	120	G
1	A	121	U
1	A	130	A
1	A	136	G
1	A	142	U
1	A	149	A
1	A	155	G
1	A	160	A
1	A	163	A
1	A	169	C

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Mol	Chain	Res	Type
1	A	170	C
1	A	173	A
1	A	174	G
1	A	175	G
1	A	176	A
1	A	177	G
1	A	184	A
1	A	185	C
1	A	186	C
1	A	201	A
1	A	204	G
1	A	213	A
1	A	220	C
1	A	227	G
1	A	228	A
1	A	232	G
1	A	233	U
1	A	236	U
1	A	243	G
1	A	245	G
1	A	253	A
1	A	256	G
1	A	259	A
1	A	266	U
1	A	269	A
1	A	275	U
1	A	276	G
1	A	282	U
1	A	284	G
1	A	285	C
1	A	286	G
1	A	292	C
1	A	299	U

All (10) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	37	C
1	A	43	A
1	A	47	U
1	A	98	G
1	A	110	U

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Mol	Chain	Res	Type
1	A	172	A
1	A	176	A
1	A	185	C
1	A	200	A
1	A	252	A

## 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	34:ASP	C	54:ASN	N	9.50