



Full wwPDB EM Validation Report ⓘ

Jun 20, 2026 – 08:28 pm BST

PDB ID : 6XZ7 / pdb_00006xz7
EMDB ID : EMD-10655
Title : E. coli 50S ribosomal subunit in complex with dirithromycin, fMet-Phe-tRNA(Phe) and deacylated tRNA(iMet).
Authors : Pichkur, E.B.; Polikanov, Y.S.; Myasnikov, A.G.; Konevega, A.L.
Deposited on : 2020-02-03
Resolution : 2.10 Å(reported)
Based on initial model : 4YBB

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

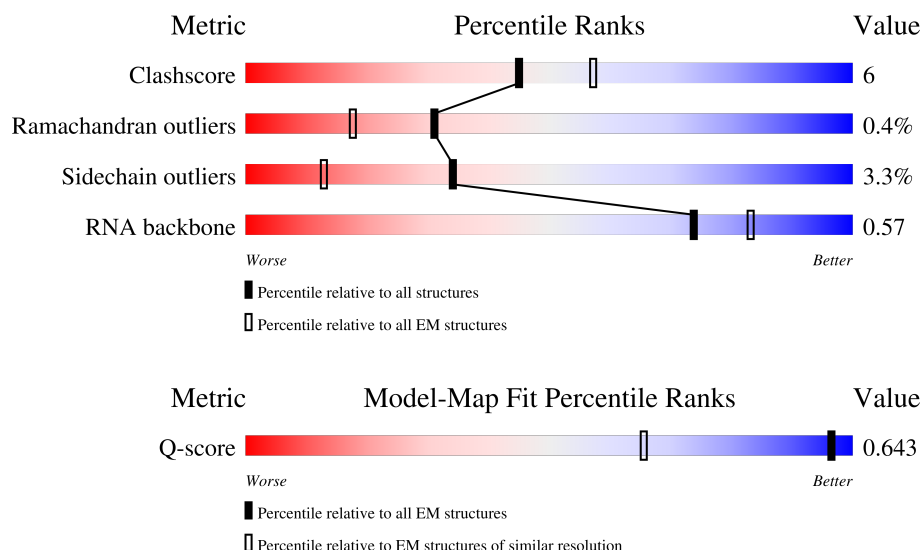
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.10 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.



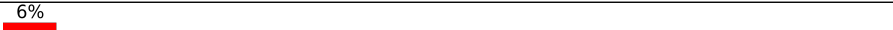
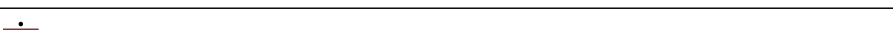
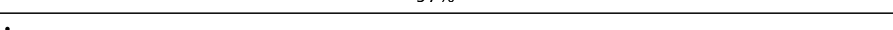
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2317 (1.60 - 2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2897	
2	B	120	
3	C	271	

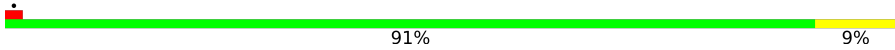
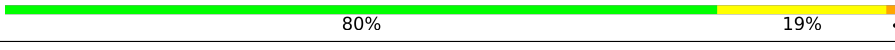
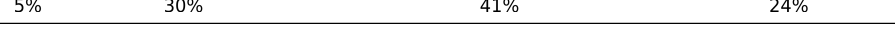
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Mol	Chain	Length	Quality of chain
4	D	209	 89% 11%
5	E	201	 89% 10% .
6	F	177	 40% 56% 37% 6% .
7	G	176	 19% 69% 27% .
8	H	135	 100% 68% 28% . .
9	I	134	 100% 73% 22% 5%
10	J	142	 85% 14% .
11	K	123	 84% 16%
12	L	144	 85% 15%
13	M	136	 88% 11% .
14	N	125	 6% 93% 6% .
15	O	117	 79% 21%
16	P	114	 85% 14% .
17	Q	117	 97% .
18	R	103	 88% 9% . .
19	S	110	 90% 10%
20	T	93	 84% 16%
21	U	102	 5% 86% 14%
22	V	94	 79% 19% .
23	W	76	 87% 13%
24	X	77	 88% 12%
25	Y	62	 6% 90% 6% .
26	Z	58	 91% 7% .
27	a	56	 91% 9%
28	b	51	 88% 12%

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Mol	Chain	Length	Quality of chain
29	c	46	 91% 9%
30	d	64	 80% 19%
31	e	38	 87% 13%
32	f	76	 14% 22% 54% 9%
33	g	76	 5% 30% 41% 24%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 94915 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2897	Total	C	N	O	P	3	0
			62252	27778	11454	20121	2899		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	209	Total	C	N	O	S	1	0
			1566	980	288	294	4		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	135	Total	C	N	O	S	0	0
			1023	649	179	192	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	85	VAL	SER	conflict	UNP P0A7J3
H	86	THR	MET	conflict	UNP P0A7J3

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	1	0
			1075	686	205	178	6		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	76	Total	C	N	O	S	1	0
			580	359	117	103	1		

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	58	Total	C	N	O	S	2	0
			449	281	87	79	2		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	51	Total	C	N	O		0	0
			414	266	76	72			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a RNA chain called Deacylated tRNAi(Met).

Mol	Chain	Residues	Atoms						AltConf	Trace
32	f	76	Total	C	N	O	P	S	0	0
			1625	725	294	529	76	1		

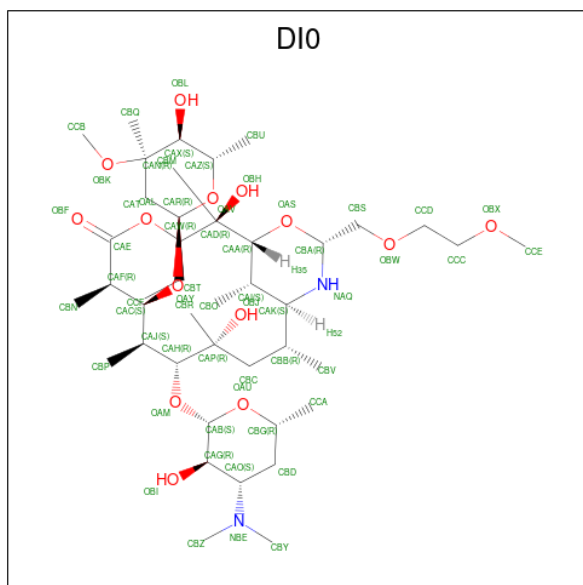
- Molecule 33 is a RNA chain called fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
33	g	76	Total	C	N	O	P	S	0	0
			1667	760	297	534	75	1		

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
34	A	174	Total Mg 174 174	0
34	B	3	Total Mg 3 3	0
34	U	1	Total Mg 1 1	0

- Molecule 35 is Dirithromycin (CCD ID: DI0) (formula: $\text{C}_{42}\text{H}_{78}\text{N}_2\text{O}_{14}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
35	A	1	Total	C	N	O	0
			58	42	2	14	

- Molecule 36 is water.

Mol	Chain	Residues	Atoms	AltConf
36	A	498	Total O 498 498	0
36	B	9	Total O 9 9	0
36	C	7	Total O 7 7	0
36	D	1	Total O 1 1	0
36	E	1	Total O 1 1	0

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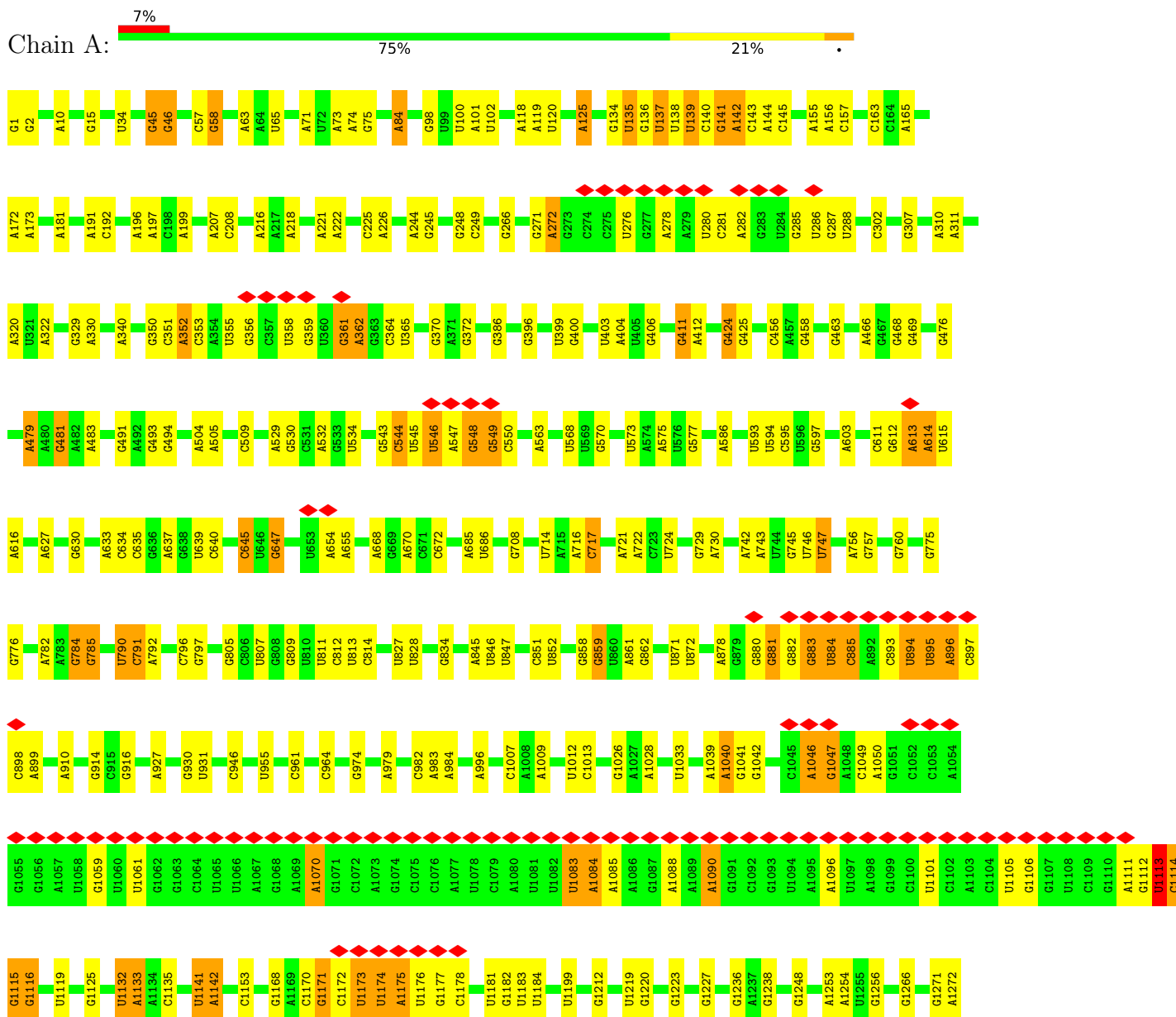
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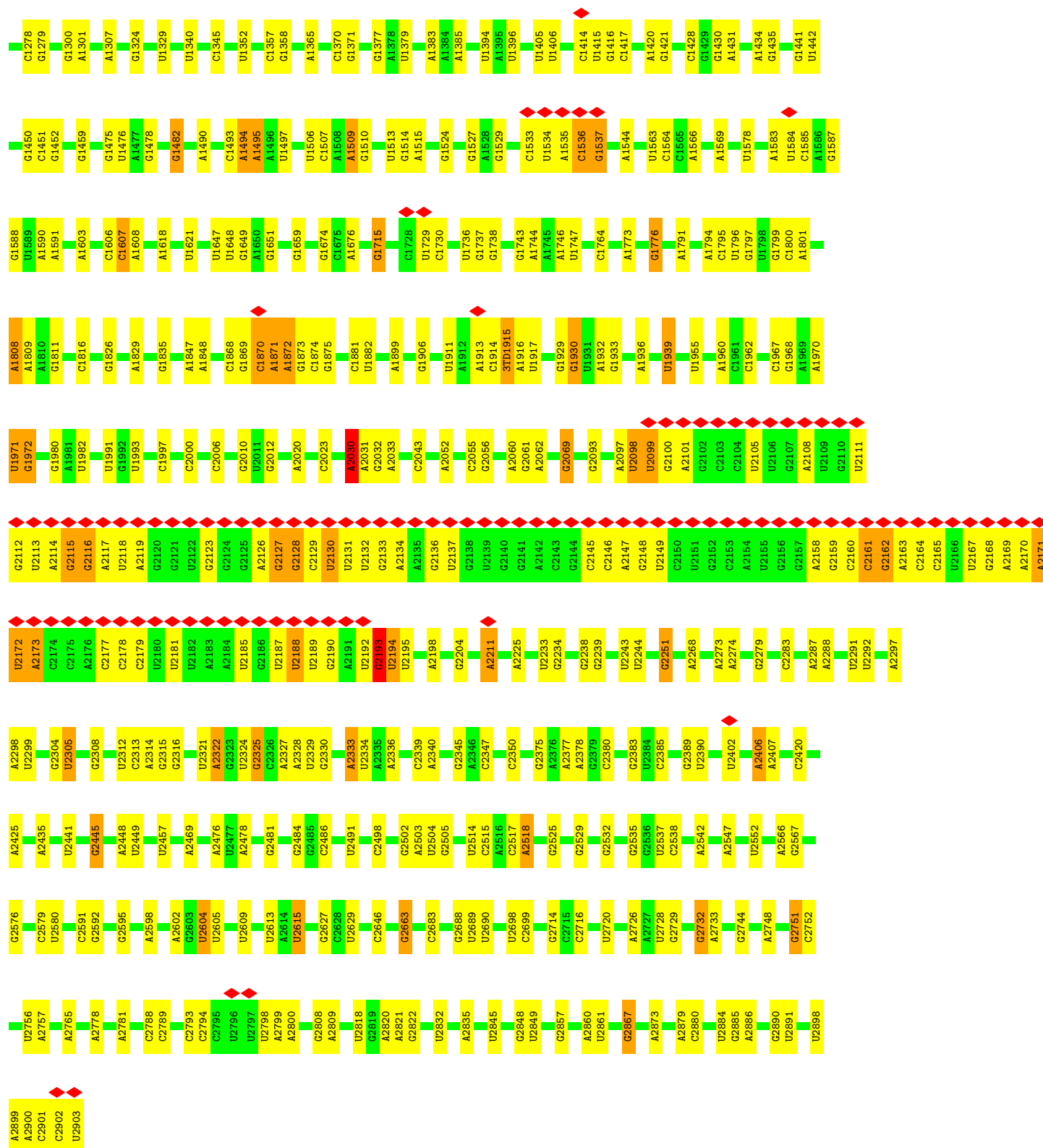
Mol	Chain	Residues	Atoms		AltConf
36	L	6	Total 6	O 6	0
36	N	1	Total 1	O 1	0
36	T	1	Total 1	O 1	0
36	d	4	Total 4	O 4	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

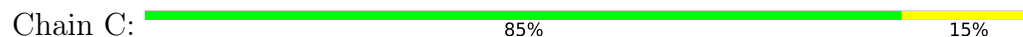
• Molecule 1: 23S rRNA



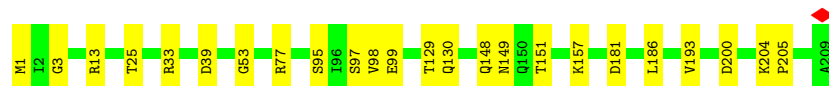
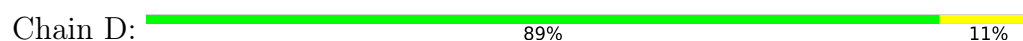




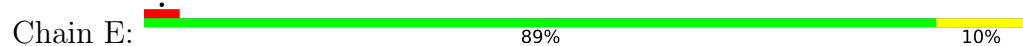
- Molecule 3: 50S ribosomal protein L2



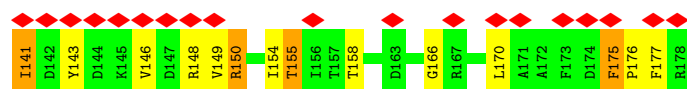
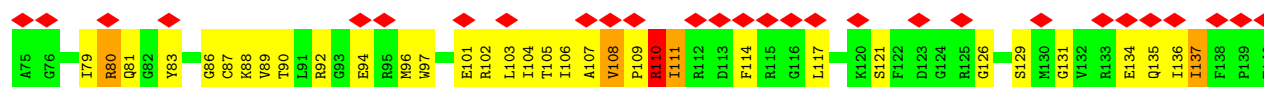
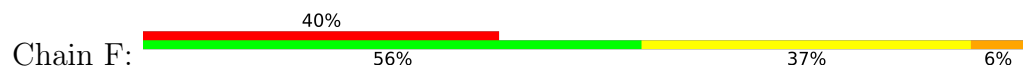
- Molecule 4: 50S ribosomal protein L3



- Molecule 5: 50S ribosomal protein L4

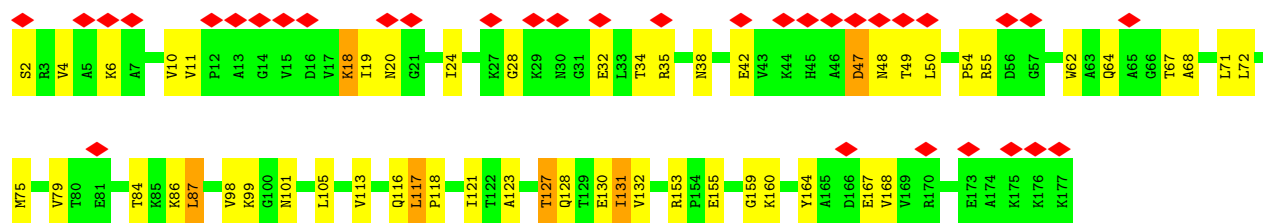


- Molecule 6: 50S ribosomal protein L5

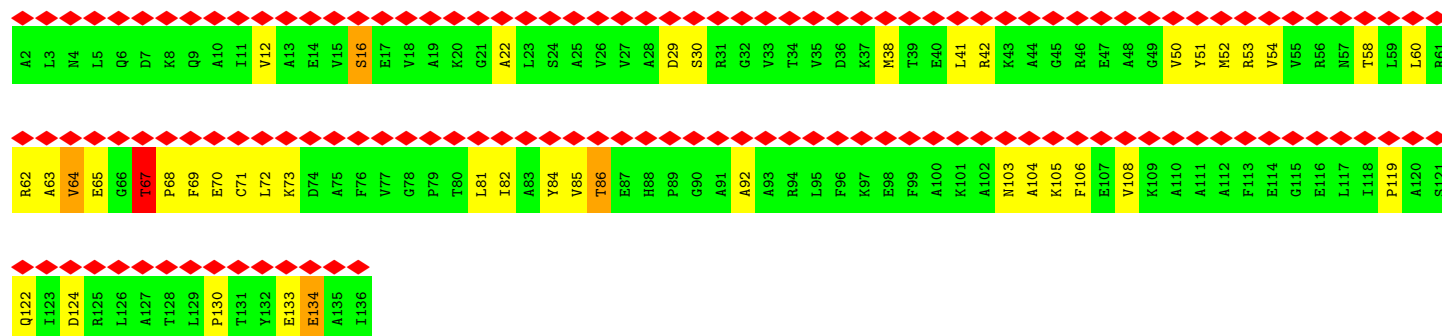


- Molecule 7: 50S ribosomal protein L6

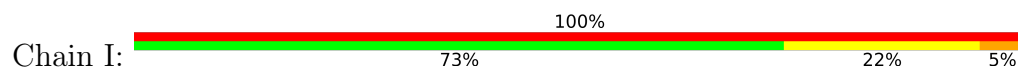




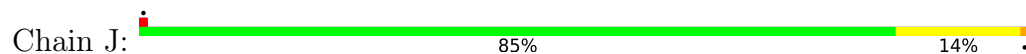
• Molecule 8: 50S ribosomal protein L10



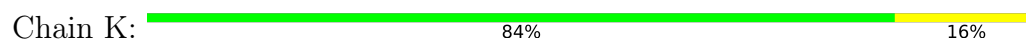
• Molecule 9: 50S ribosomal protein L11



• Molecule 10: 50S ribosomal protein L13



• Molecule 11: 50S ribosomal protein L14



- Molecule 12: 50S ribosomal protein L15

Chain L:  85% 15%



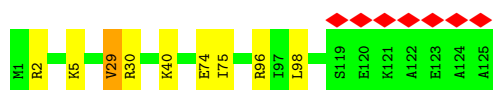
- Molecule 13: 50S ribosomal protein L16

Chain M:  88% 11%



- Molecule 14: 50S ribosomal protein L17

Chain N:  6% 93% 6%



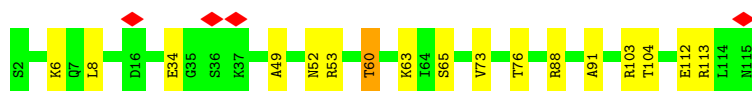
- Molecule 15: 50S ribosomal protein L18

Chain O:  79% 21%

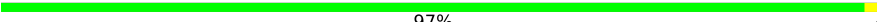


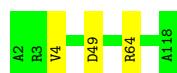
- Molecule 16: 50S ribosomal protein L19

Chain P:  85% 14%



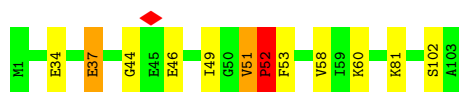
- Molecule 17: 50S ribosomal protein L20

Chain Q:  97%



- Molecule 18: 50S ribosomal protein L21

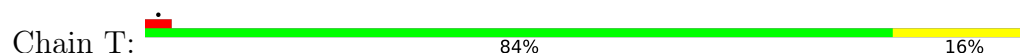
Chain R:  88% 9%



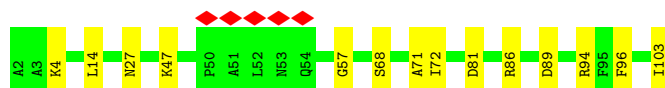
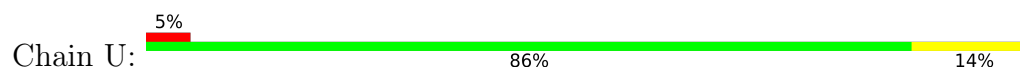
- Molecule 19: 50S ribosomal protein L22



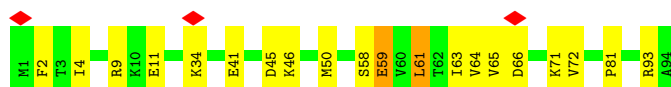
- Molecule 20: 50S ribosomal protein L23



- Molecule 21: 50S ribosomal protein L24



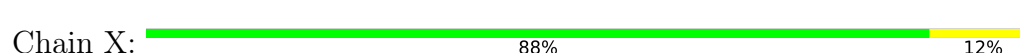
- Molecule 22: 50S ribosomal protein L25



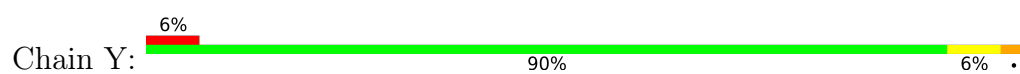
- Molecule 23: 50S ribosomal protein L27



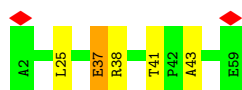
- Molecule 24: 50S ribosomal protein L28



- Molecule 25: 50S ribosomal protein L29



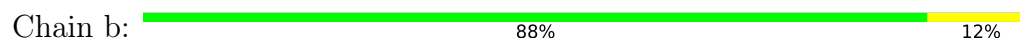
- Molecule 26: 50S ribosomal protein L30



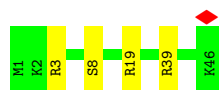
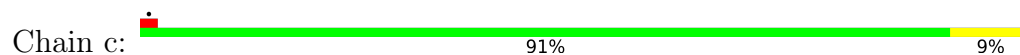
- Molecule 27: 50S ribosomal protein L32



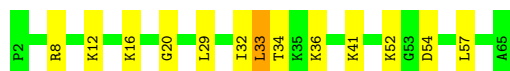
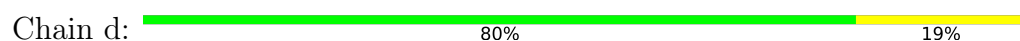
- Molecule 28: 50S ribosomal protein L33



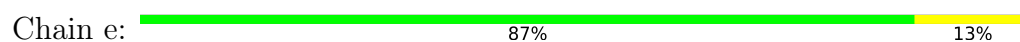
- Molecule 29: 50S ribosomal protein L34



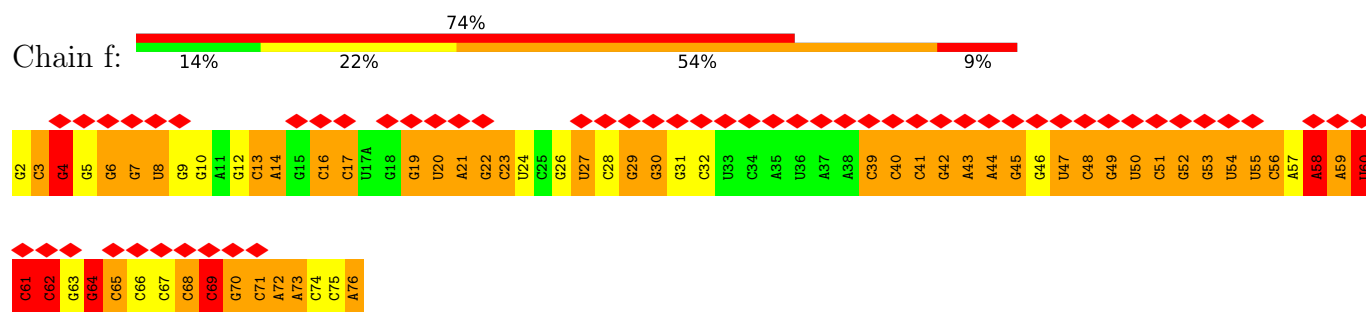
- Molecule 30: 50S ribosomal protein L35



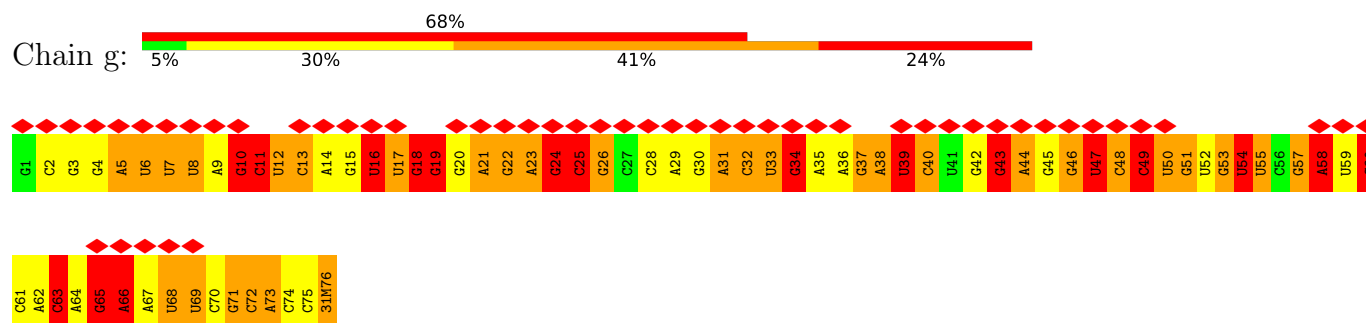
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: Deacylated tRNAⁱ(Met)



• Molecule 33: fMet-Phe-tRNA(Phe)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	401905	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.709	Depositor
Minimum map value	-1.212	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	440.32, 440.32, 440.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 4SU, 1MA, OMG, H2U, DI0, 3TD, YYG, 4D4, 5MU, OMC, 6MZ, G7M, M2G, 7MG, 2MG, OMU, MEQ, MG, 31M, PSU, 1MG, 5MC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.34	0/69172	0.28	5/107908 (0.0%)
2	B	0.25	0/2872	0.20	0/4478
3	C	0.30	0/2122	0.34	0/2852
4	D	0.28	0/1576	0.31	0/2119
5	E	0.26	0/1571	0.31	0/2113
6	F	0.22	0/1435	0.44	0/1926
7	G	0.19	0/1343	0.32	0/1816
8	H	0.55	0/1037	0.86	0/1402
9	I	0.70	0/993	0.99	4/1341 (0.3%)
10	J	0.28	0/1152	0.30	0/1551
11	K	0.29	0/955	0.35	0/1279
12	L	0.28	0/1062	0.34	0/1413
13	M	0.28	0/1081	0.34	0/1443
14	N	0.30	0/1006	0.37	0/1345
15	O	0.22	0/910	0.33	0/1219
16	P	0.28	0/929	0.35	0/1242
17	Q	0.32	0/960	0.32	0/1278
18	R	0.40	0/829	0.60	3/1107 (0.3%)
19	S	0.37	1/864 (0.1%)	0.35	0/1156
20	T	0.25	0/745	0.35	0/994
21	U	0.24	0/788	0.33	0/1051
22	V	0.24	0/766	0.30	0/1025
23	W	0.29	0/587	0.34	0/776
24	X	0.30	0/635	0.37	0/848
25	Y	0.22	0/502	0.30	0/667
26	Z	0.26	0/453	0.31	0/605
27	a	0.28	0/450	0.32	0/599
28	b	0.21	0/421	0.30	0/561
29	c	0.33	0/380	0.40	0/498
30	d	0.40	0/513	0.47	0/676
31	e	0.29	0/303	0.33	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	f	0.67	2/1725 (0.1%)	1.85	87/2689 (3.2%)
33	g	0.62	0/1458	1.58	45/2272 (2.0%)
All	All	0.35	3/101595 (0.0%)	0.44	144/152646 (0.1%)

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
18	R	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	S	92	ARG	C-O	-6.36	1.16	1.23
32	f	59	A	O3'-P	-5.20	1.53	1.61
32	f	39	C	O3'-P	-5.00	1.53	1.61

All (144) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	51	C	C1'-C2'-O2'	-14.28	86.98	108.40
32	f	40	C	C1'-C2'-O2'	-13.62	87.97	108.40
33	g	47	U	C4'-C3'-O3'	13.55	129.72	109.40
33	g	13	C	C4'-C3'-O3'	13.11	132.66	113.00
32	f	23	C	C1'-C2'-O2'	-12.91	89.03	108.40
33	g	57	G	C1'-C2'-O2'	-12.41	89.79	108.40
32	f	64	G	C1'-C2'-O2'	-12.33	89.90	108.40
32	f	22	G	C1'-C2'-O2'	-12.28	89.97	108.40
33	g	51	G	C1'-C2'-O2'	-11.99	90.42	108.40
32	f	26	G	C1'-C2'-O2'	-11.96	90.45	108.40
32	f	23	C	C4'-C3'-O3'	11.68	130.52	113.00
33	g	50	U	C1'-C2'-O2'	-11.16	91.66	108.40
32	f	65	C	C4'-C3'-O3'	11.02	129.53	113.00
32	f	42	G	C1'-C2'-O2'	-10.66	92.40	108.40
32	f	3	C	C1'-C2'-O2'	-10.42	92.77	108.40
32	f	29	G	C4'-C3'-O3'	10.41	128.61	113.00
33	g	13	C	C1'-C2'-O2'	-10.41	92.78	108.40
32	f	29	G	C1'-C2'-O2'	-10.25	93.03	108.40
32	f	72	A	C4'-C3'-O3'	10.21	128.31	113.00
32	f	12	G	C4'-C3'-O3'	9.80	127.69	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	42	G	C4'-C3'-O3'	9.68	127.52	113.00
33	g	18	G	C1'-C2'-O2'	9.62	126.23	111.80
32	f	74	C	C1'-C2'-O2'	-9.57	94.04	108.40
32	f	27	U	C1'-C2'-O2'	-9.42	94.27	108.40
32	f	71	C	C4'-C3'-O3'	9.12	126.68	113.00
32	f	64	G	C4'-C3'-O3'	9.03	126.54	113.00
32	f	43	A	C1'-C2'-O2'	-9.00	94.90	108.40
32	f	62	C	N1-C1'-C2'	-8.82	98.76	112.00
32	f	4	G	C1'-C2'-O2'	-8.79	95.22	108.40
33	g	69	U	C4'-C3'-O3'	8.78	126.17	113.00
33	g	50	U	C4'-C3'-O3'	8.75	126.12	113.00
33	g	22	G	C2'-C3'-O3'	8.68	126.72	113.70
9	I	116	ASP	N-CA-C	8.67	123.58	112.92
32	f	2	G	C4'-C3'-O3'	8.55	125.83	113.00
33	g	18	G	C4'-C3'-O3'	-8.51	96.63	109.40
33	g	69	U	C1'-C2'-O2'	-8.39	95.81	108.40
32	f	12	G	C1'-C2'-O2'	-8.37	95.84	108.40
32	f	5	G	C1'-C2'-O2'	-8.35	95.87	108.40
32	f	6	G	C1'-C2'-O2'	-8.29	95.97	108.40
32	f	42	G	C2'-C3'-O3'	-8.21	101.39	113.70
32	f	13	C	C1'-C2'-O2'	-8.12	96.21	108.40
32	f	69	C	C4'-C3'-O3'	8.10	125.16	113.00
33	g	19	G	C4'-C3'-O3'	-8.09	97.27	109.40
33	g	60	C	C4'-C3'-O3'	8.08	121.52	109.40
32	f	48	C	C4'-C3'-O3'	-8.04	97.35	109.40
32	f	52	G	C4'-C3'-O3'	8.02	125.02	113.00
32	f	40	C	C4'-C3'-O3'	7.99	124.98	113.00
32	f	30	G	N9-C1'-C2'	-7.98	100.03	112.00
32	f	45	G	C1'-C2'-O2'	-7.97	96.44	108.40
32	f	53	G	C4'-C3'-O3'	7.82	124.73	113.00
32	f	13	C	C4'-C3'-O3'	7.80	124.70	113.00
33	g	5	A	C4'-C3'-O3'	7.75	124.63	113.00
32	f	27	U	C4'-C3'-O3'	7.72	124.58	113.00
33	g	68	U	C4'-C3'-O3'	7.70	124.55	113.00
32	f	59	A	C1'-C2'-O2'	-7.61	96.99	108.40
33	g	44	A	C3'-C2'-O2'	7.36	121.74	110.70
32	f	51	C	C4'-C3'-O3'	7.30	123.95	113.00
32	f	43	A	C4'-C3'-O3'	7.25	123.88	113.00
32	f	41	C	C1'-C2'-O2'	-7.19	97.61	108.40
33	g	13	C	N1-C1'-C2'	-7.15	101.27	112.00
33	g	24	G	N9-C1'-C2'	-7.15	101.28	112.00
32	f	65	C	N1-C1'-C2'	-7.14	101.29	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2193	G	C2'-C3'-O3'	7.10	124.36	113.70
32	f	52	G	N9-C1'-C2'	-7.07	101.39	112.00
32	f	74	C	C4'-C3'-O3'	7.04	123.55	113.00
9	I	21	SER	CA-C-N	-7.03	113.14	120.38
9	I	21	SER	C-N-CA	-7.03	113.14	120.38
1	A	1113	U	C2'-C3'-O3'	6.98	124.17	113.70
33	g	5	A	C1'-C2'-O2'	-6.97	97.94	108.40
32	f	5	G	C4'-C3'-O3'	6.94	123.41	113.00
33	g	48	C	C4'-C3'-O3'	-6.92	99.01	109.40
32	f	4	G	C4'-C3'-O3'	6.91	123.37	113.00
32	f	50	U	C4'-C3'-O3'	6.80	123.20	113.00
32	f	72	A	C1'-C2'-O2'	-6.79	98.22	108.40
33	g	65	G	N9-C1'-C2'	-6.75	101.87	112.00
32	f	59	A	C4'-C3'-O3'	6.58	122.88	113.00
1	A	1113	U	C3'-C2'-O2'	6.55	120.52	110.70
32	f	60	U	C4'-C3'-O3'	-6.53	99.61	109.40
32	f	21	A	C1'-C2'-O2'	-6.52	98.62	108.40
33	g	25	C	C3'-C2'-O2'	6.48	120.42	110.70
32	f	71	C	C1'-C2'-O2'	-6.44	98.73	108.40
32	f	12	G	N9-C1'-C2'	-6.31	102.53	112.00
32	f	52	G	C2'-C3'-O3'	-6.30	104.25	113.70
32	f	64	G	C2'-C3'-O3'	-6.29	104.26	113.70
32	f	42	G	N9-C1'-C2'	-6.27	102.59	112.00
32	f	44	A	C1'-C2'-O2'	-6.25	99.02	108.40
32	f	12	G	C2'-C3'-O3'	-6.21	104.39	113.70
33	g	23	A	C1'-C2'-O2'	-6.18	99.12	108.40
32	f	51	C	N1-C1'-C2'	-6.13	102.80	112.00
32	f	72	A	N9-C1'-C2'	-6.13	102.80	112.00
33	g	57	G	C4'-C3'-O3'	6.13	122.19	113.00
32	f	23	C	C2'-C3'-O3'	-6.12	104.53	113.70
32	f	52	G	C3'-C2'-O2'	6.12	119.87	110.70
33	g	65	G	C1'-C2'-O2'	-6.10	99.25	108.40
33	g	51	G	C4'-C3'-O3'	6.10	122.15	113.00
33	g	47	U	C1'-C2'-O2'	-6.06	102.71	111.80
18	R	49	ILE	CA-C-N	-6.05	116.93	122.80
18	R	49	ILE	C-N-CA	-6.05	116.93	122.80
33	g	24	G	C4'-C3'-O3'	6.04	122.07	113.00
33	g	12	U	C4'-C3'-O3'	6.04	122.06	113.00
18	R	52	PRO	CA-N-CD	-5.99	103.61	112.00
1	A	2193	G	C3'-C2'-O2'	5.97	119.66	110.70
32	f	6	G	C2'-C3'-O3'	-5.97	104.75	113.70
32	f	43	A	N9-C1'-C2'	-5.95	103.07	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	66	A	C1'-C2'-O2'	5.92	117.28	108.40
32	f	58	A	C1'-C2'-O2'	5.92	120.68	111.80
32	f	5	G	N9-C1'-C2'	-5.91	103.14	112.00
32	f	29	G	N9-C1'-C2'	-5.87	103.19	112.00
33	g	22	G	P-O3'-C3'	5.78	128.87	120.20
32	f	44	A	C4'-C3'-O3'	5.75	121.63	113.00
32	f	43	A	P-O5'-C5'	-5.74	112.29	120.90
32	f	5	G	C2'-C3'-O3'	-5.72	105.12	113.70
33	g	63	C	C4'-C3'-O3'	-5.70	104.45	113.00
32	f	58	A	C4'-C3'-O3'	-5.68	100.88	109.40
33	g	43	G	C2'-C3'-O3'	-5.66	105.21	113.70
33	g	51	G	N9-C1'-C2'	-5.66	103.51	112.00
32	f	30	G	C1'-C2'-O2'	-5.61	99.99	108.40
33	g	68	U	N1-C1'-C2'	-5.59	103.62	112.00
33	g	50	U	N1-C1'-C2'	-5.58	103.62	112.00
32	f	73	A	N9-C1'-C2'	-5.55	103.68	112.00
33	g	5	A	N9-C1'-C2'	-5.50	103.75	112.00
33	g	65	G	C4'-C3'-O3'	5.50	121.25	113.00
32	f	6	G	N9-C1'-C2'	-5.50	103.76	112.00
32	f	14	A	C1'-C2'-O2'	-5.46	100.21	108.40
32	f	2	G	N9-C1'-C2'	-5.44	103.84	112.00
32	f	13	C	N1-C1'-C2'	-5.41	103.88	112.00
33	g	9	A	C2'-C3'-O3'	-5.41	101.39	109.50
9	I	99	GLY	CA-C-O	-5.41	118.25	122.52
33	g	25	C	C1'-C2'-O2'	5.38	116.48	108.40
32	f	14	A	N9-C1'-C2'	-5.31	104.03	112.00
33	g	11	C	N1-C1'-C2'	-5.31	104.04	112.00
32	f	6	G	C4'-C3'-O3'	5.31	120.96	113.00
1	A	404	A	O4'-C1'-C2'	-5.26	100.54	105.80
33	g	11	C	C4'-C3'-O3'	5.25	120.88	113.00
32	f	45	G	C4'-C3'-O3'	5.23	120.85	113.00
33	g	24	G	C1'-C2'-O2'	-5.22	100.57	108.40
32	f	61	C	C4'-C3'-O3'	5.21	120.81	113.00
33	g	57	G	N9-C1'-C2'	-5.19	104.22	112.00
32	f	22	G	C4'-C3'-O3'	5.18	120.77	113.00
32	f	14	A	C4'-C3'-O3'	5.13	120.69	113.00
32	f	30	G	C4'-C3'-O3'	5.11	120.67	113.00
32	f	47	U	P-O3'-C3'	5.11	127.87	120.20
32	f	59	A	N9-C1'-C2'	-5.10	104.36	112.00
32	f	26	G	C4'-C3'-O3'	5.05	120.57	113.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	R	51	VAL	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	62252	0	31324	412	0
2	B	2569	0	1301	14	0
3	C	2083	0	2154	23	0
4	D	1566	0	1617	14	0
5	E	1552	0	1619	15	0
6	F	1411	0	1444	97	0
7	G	1323	0	1371	32	0
8	H	1023	0	1052	37	0
9	I	979	0	1028	33	0
10	J	1129	0	1162	13	0
11	K	946	0	1023	11	0
12	L	1053	0	1129	14	0
13	M	1075	0	1155	10	0
14	N	993	0	1034	6	0
15	O	900	0	935	18	0
16	P	917	0	962	11	0
17	Q	947	0	1019	3	0
18	R	816	0	839	8	0
19	S	857	0	922	7	0
20	T	739	0	807	17	0
21	U	780	0	830	7	0
22	V	753	0	780	11	0
23	W	580	0	593	5	0
24	X	625	0	652	4	0
25	Y	501	0	531	4	0
26	Z	449	0	487	3	0
27	a	444	0	458	4	0
28	b	414	0	442	3	0
29	c	377	0	418	3	0
30	d	504	0	572	12	0
31	e	302	0	343	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	f	1625	0	829	52	0
33	g	1667	0	880	93	0
34	A	174	0	0	0	0
34	B	3	0	0	0	0
34	U	1	0	0	0	0
35	A	58	0	0	1	0
36	A	498	0	0	13	0
36	B	9	0	0	0	0
36	C	7	0	0	1	0
36	D	1	0	0	0	0
36	E	1	0	0	0	0
36	L	6	0	0	0	0
36	N	1	0	0	0	0
36	T	1	0	0	0	0
36	d	4	0	0	0	0
All	All	94915	0	61712	916	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 6.

All (916) 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)
33:g:75:C:O3'	33:g:76:31M:P	1.09	1.47
1:A:883:G:N2	1:A:894:U:O2	1.56	1.37
1:A:1:G:N2	1:A:2902:C:O2	1.64	1.30
32:f:76:A:O3'	33:g:76:31M:HAM	1.15	1.30
9:I:98:VAL:O	9:I:138:LEU:HD23	1.22	1.25
1:A:1:G:N1	1:A:2902:C:N3	1.92	1.17
1:A:1050:A:N3	1:A:2751:G:C2	2.13	1.17
6:F:108:VAL:CG1	6:F:109:PRO:HD3	1.76	1.16
6:F:108:VAL:HG13	6:F:109:PRO:CD	1.78	1.14
8:H:67:THR:HG22	8:H:68:PRO:CD	1.76	1.14
6:F:103:LEU:HB2	6:F:107:ALA:CB	1.79	1.12
18:R:51:VAL:HG12	18:R:52:PRO:HD2	1.29	1.11
32:f:76:A:O3'	33:g:76:31M:CAM	2.00	1.10
1:A:884:U:O4	1:A:893:C:C4	2.07	1.08
8:H:12:VAL:CG1	8:H:63:ALA:HB2	1.84	1.07
8:H:67:THR:HG22	8:H:68:PRO:HD3	1.04	1.03
1:A:2898:U:H2'	1:A:2899:A:C8	1.92	1.03
1:A:882:G:N1	1:A:895:U:O2	1.90	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:67:THR:HB	8:H:68:PRO:HD2	1.38	1.02
1:A:2898:U:H2'	1:A:2899:A:H8	1.24	1.00
6:F:103:LEU:HB2	6:F:107:ALA:HB3	1.38	1.00
33:g:75:C:C3'	33:g:76:31M:P	2.49	0.99
1:A:884:U:O4	1:A:893:C:N3	1.96	0.99
9:I:100:LYS:HB2	9:I:141:GLU:HB2	1.46	0.98
1:A:1050:A:C4	1:A:2751:G:C2	2.51	0.98
8:H:67:THR:CG2	8:H:68:PRO:HD3	1.94	0.98
8:H:67:THR:CG2	8:H:68:PRO:CD	2.41	0.97
1:A:894:U:O2'	1:A:895:U:OP1	1.82	0.97
8:H:12:VAL:HG13	8:H:63:ALA:HB2	1.42	0.97
33:g:75:C:O3'	33:g:76:31M:OP2	1.80	0.96
1:A:1050:A:H1'	1:A:2751:G:N2	1.79	0.96
33:g:39:PSU:H5'	33:g:39:PSU:C6	2.01	0.95
1:A:1:G:N1	1:A:2902:C:C2	2.34	0.95
33:g:75:C:HO3'	33:g:76:31M:P	1.19	0.94
33:g:2:C:N4	33:g:71:G:O6	2.01	0.94
1:A:1050:A:C4	1:A:2751:G:N2	2.36	0.94
6:F:110:ARG:HB3	6:F:137:ILE:HG23	1.48	0.94
1:A:884:U:C4	1:A:893:C:N3	2.35	0.93
6:F:103:LEU:CB	6:F:107:ALA:HB3	1.98	0.92
1:A:2469:A:H4'	13:M:55:ARG:HD2	1.51	0.92
33:g:54:5MU:H5'	33:g:54:5MU:H6	1.35	0.92
8:H:67:THR:CB	8:H:68:PRO:HD2	2.00	0.90
1:A:1:G:C2	1:A:2902:C:O2	2.24	0.90
1:A:1847:A:HO2'	1:A:1848:A:H8	0.98	0.90
1:A:1050:A:C2	1:A:2751:G:C2	2.59	0.90
6:F:103:LEU:CB	6:F:107:ALA:CB	2.50	0.89
1:A:883:G:H1	1:A:894:U:H3	0.89	0.89
1:A:2116:G:O6	1:A:2171:A:N6	2.06	0.89
33:g:16:H2U:H62	33:g:16:H2U:H5''	1.55	0.88
6:F:103:LEU:CA	6:F:107:ALA:HB3	2.03	0.88
9:I:98:VAL:O	9:I:138:LEU:CD2	2.17	0.88
6:F:150:ARG:HG2	6:F:150:ARG:HH11	1.38	0.88
1:A:134:G:C6	1:A:135:U:C4	2.62	0.87
1:A:884:U:O4	1:A:893:C:N4	2.08	0.86
6:F:103:LEU:HA	6:F:107:ALA:CB	2.06	0.86
8:H:67:THR:CB	8:H:68:PRO:CD	2.53	0.85
6:F:103:LEU:CA	6:F:107:ALA:CB	2.54	0.85
1:A:1:G:C6	1:A:2902:C:N3	2.45	0.85
32:f:76:A:H4'	33:g:76:31M:HGM2	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1049:C:H1'	1:A:1113:U:O2'	1.78	0.84
33:g:39:PSU:H5'	33:g:39:PSU:H6	1.38	0.83
32:f:76:A:HO3'	33:g:76:31M:HAM	1.44	0.82
8:H:64:VAL:HG22	8:H:69:PHE:HB3	1.60	0.82
7:G:118:PRO:HG2	7:G:121:ILE:HD13	1.60	0.82
33:g:32:OMC:O2	33:g:32:OMC:HM23	1.80	0.82
33:g:54:5MU:H6	33:g:54:5MU:C5'	1.92	0.81
8:H:16:SER:OG	8:H:63:ALA:HB1	1.79	0.81
8:H:67:THR:CG2	8:H:68:PRO:HD2	2.11	0.81
8:H:67:THR:HB	8:H:68:PRO:CD	2.12	0.80
33:g:76:31M:H8	33:g:76:31M:H5'	1.64	0.80
6:F:136:ILE:HG22	6:F:136:ILE:O	1.81	0.80
8:H:60:LEU:O	8:H:64:VAL:HB	1.82	0.80
32:f:76:A:O3'	33:g:76:31M:CGM	2.30	0.80
1:A:884:U:H3'	1:A:885:C:H4'	1.64	0.80
1:A:2006:C:OP2	36:A:3201:HOH:O	1.98	0.80
1:A:894:U:H2'	1:A:895:U:H6	1.47	0.79
6:F:135:GLN:O	6:F:141:ILE:HG21	1.80	0.79
33:g:72:C:H6	33:g:72:C:C5'	1.95	0.78
1:A:2099:U:H2'	1:A:2100:G:H8	1.47	0.78
6:F:134:GLU:CD	6:F:149:VAL:HG13	2.08	0.78
1:A:1:G:O6	1:A:2902:C:N4	2.17	0.78
1:A:1050:A:H1'	1:A:2751:G:H21	1.47	0.78
1:A:1050:A:N3	1:A:2751:G:N2	2.31	0.78
1:A:883:G:C2	1:A:894:U:O2	2.36	0.78
6:F:104:ILE:O	6:F:108:VAL:HG11	1.84	0.78
8:H:12:VAL:HG12	8:H:63:ALA:HB2	1.65	0.77
1:A:2010:G:O6	36:A:3202:HOH:O	2.02	0.77
1:A:894:U:H2'	1:A:895:U:C6	2.19	0.77
6:F:103:LEU:HA	6:F:107:ALA:HB2	1.63	0.77
6:F:111:ILE:HG13	6:F:111:ILE:O	1.83	0.77
32:f:70:G:H4'	32:f:70:G:OP1	1.84	0.77
1:A:1:G:N1	1:A:2902:C:O2	2.18	0.76
1:A:1050:A:C1'	1:A:2751:G:N2	2.48	0.76
6:F:135:GLN:NE2	6:F:148:ARG:O	2.18	0.76
9:I:117:MET:HA	9:I:117:MET:HE2	1.67	0.75
1:A:882:G:C6	1:A:883:G:N7	2.54	0.75
18:R:51:VAL:CG1	18:R:52:PRO:HD2	2.13	0.75
1:A:1050:A:C2	1:A:2751:G:C4	2.74	0.75
33:g:72:C:H6	33:g:72:C:H5''	1.51	0.75
5:E:7:ASP:OD1	5:E:7:ASP:N	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:31:C:O2	2:B:53:A:N6	2.20	0.74
6:F:134:GLU:OE2	6:F:149:VAL:HG13	1.87	0.74
6:F:111:ILE:HD11	6:F:114:PHE:HA	1.69	0.74
1:A:2751:G:H2'	1:A:2751:G:N3	2.02	0.74
1:A:142:A:C2	1:A:143:C:C2	2.75	0.74
1:A:63:A:H2	20:T:70:HIS:CE1	2.05	0.74
32:f:53:G:H2'	32:f:54:5MU:H73	1.68	0.73
32:f:16:C:O3'	32:f:60:U:O2'	2.05	0.73
1:A:611:C:C4	1:A:612:G:C5	2.77	0.73
1:A:2683:C:O2	11:K:70:ARG:NH2	2.22	0.73
6:F:80:ARG:HB2	6:F:83:TYR:CZ	2.24	0.72
6:F:149:VAL:O	6:F:149:VAL:HG12	1.88	0.72
1:A:611:C:N4	1:A:612:G:C6	2.58	0.72
3:C:133:ARG:HB3	3:C:186:ALA:HB1	1.71	0.72
30:d:29:LEU:O	30:d:29:LEU:HG	1.89	0.72
32:f:61:C:O2'	32:f:62:C:O4'	2.08	0.72
6:F:102:ARG:O	6:F:106:ILE:HB	1.90	0.72
1:A:883:G:N2	1:A:894:U:C2	2.56	0.72
9:I:113:LYS:O	9:I:117:MET:N	2.23	0.71
10:J:6:ALA:H	10:J:45:THR:HG21	1.55	0.71
1:A:611:C:C4	1:A:612:G:C6	2.77	0.71
1:A:884:U:H4'	1:A:884:U:OP1	1.91	0.71
1:A:1307:A:N6	1:A:1606:C:O2	2.19	0.71
33:g:37:YYG:H141	33:g:37:YYG:C10	2.20	0.71
1:A:1050:A:C2	1:A:2751:G:N3	2.58	0.71
6:F:80:ARG:NH1	6:F:80:ARG:HG3	2.05	0.71
6:F:80:ARG:HG3	6:F:80:ARG:HH11	1.56	0.70
1:A:760:G:H4'	1:A:1776:G:OP1	1.92	0.70
6:F:108:VAL:HG13	6:F:109:PRO:HD3	0.84	0.69
1:A:1869:G:H21	1:A:1872:A:H2	1.38	0.69
1:A:1478:G:H1	1:A:1513:U:H3	1.39	0.69
1:A:2099:U:H2'	1:A:2100:G:C8	2.27	0.69
1:A:881:G:H2'	1:A:882:G:C8	2.27	0.69
33:g:10:2MG:N1	33:g:25:C:O2	2.23	0.69
1:A:756:A:N7	36:A:3210:HOH:O	2.25	0.69
1:A:468:G:N7	29:c:39:ARG:NH2	2.42	0.68
3:C:2:ALA:N	3:C:20:VAL:O	2.27	0.68
1:A:141:G:N3	1:A:141:G:H3'	2.09	0.68
6:F:111:ILE:HA	6:F:137:ILE:CD1	2.23	0.68
1:A:1324:G:N7	36:A:3214:HOH:O	2.28	0.67
6:F:103:LEU:O	6:F:107:ALA:N	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:85:VAL:HG11	12:L:90:VAL:HG12	1.77	0.67
12:L:56:PRO:HG2	12:L:59:ARG:HG3	1.76	0.67
9:I:113:LYS:HB3	9:I:117:MET:HE3	1.76	0.67
1:A:139:U:C6	20:T:1:MET:SD	2.88	0.67
9:I:98:VAL:O	9:I:138:LEU:HA	1.95	0.66
1:A:136:G:C6	1:A:137:U:C5	2.83	0.66
1:A:894:U:C4	1:A:895:U:C4	2.83	0.66
1:A:1039:A:H2	1:A:1116:G:H22	1.42	0.66
1:A:1050:A:N9	1:A:2751:G:N2	2.43	0.66
30:d:32:ILE:O	30:d:36:LYS:HE2	1.96	0.66
1:A:611:C:C5	1:A:612:G:C5	2.83	0.66
2:B:43:C:O2	6:F:92:ARG:NH2	2.29	0.66
1:A:1113:U:O5'	1:A:1113:U:H6	1.79	0.66
8:H:12:VAL:HG13	8:H:63:ALA:CB	2.22	0.66
1:A:811:U:OP1	36:A:3204:HOH:O	2.14	0.66
1:A:2127:G:O2'	1:A:2128:G:O4'	2.13	0.66
33:g:8:U:H6	33:g:8:U:O5'	1.79	0.66
1:A:1972:G:OP2	36:A:3203:HOH:O	2.13	0.65
10:J:88:THR:OG1	10:J:90:GLU:OE2	2.14	0.65
32:f:76:A:C4'	33:g:76:31M:HGM2	2.25	0.65
1:A:611:C:C5	1:A:612:G:C6	2.84	0.65
1:A:1377:G:N7	36:A:3216:HOH:O	2.29	0.65
30:d:33:LEU:HB3	30:d:41:LYS:HD3	1.79	0.65
6:F:103:LEU:C	6:F:107:ALA:HB3	2.22	0.65
6:F:134:GLU:OE1	6:F:149:VAL:CG1	2.45	0.64
32:f:76:A:H4'	33:g:76:31M:CGM	2.26	0.64
1:A:1482:G:H1'	1:A:1509:A:H61	1.62	0.64
25:Y:11:VAL:O	25:Y:15:ASN:ND2	2.29	0.64
32:f:61:C:O2'	32:f:62:C:H5'	1.98	0.64
6:F:150:ARG:HG2	6:F:150:ARG:NH1	2.10	0.64
8:H:16:SER:CB	8:H:63:ALA:HB1	2.28	0.64
1:A:1871:A:O2'	1:A:1872:A:N3	2.25	0.64
6:F:47:LYS:H	6:F:47:LYS:HD2	1.62	0.64
1:A:881:G:H3'	1:A:882:G:C8	2.33	0.64
1:A:2900:A:O5'	1:A:2900:A:H8	1.80	0.64
3:C:236:GLU:OE2	36:C:301:HOH:O	2.15	0.64
6:F:104:ILE:O	6:F:108:VAL:CG1	2.46	0.64
1:A:1899:A:N7	36:A:3217:HOH:O	2.29	0.64
1:A:1061:U:OP2	9:I:10:LYS:NZ	2.31	0.63
1:A:1050:A:N3	1:A:2751:G:N3	2.46	0.63
1:A:882:G:H22	1:A:895:U:H2'	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:47:ASP:O	7:G:49:THR:N	2.29	0.63
1:A:2127:G:O2'	1:A:2128:G:O5'	2.15	0.63
1:A:134:G:C5	1:A:135:U:C4	2.86	0.63
6:F:134:GLU:CD	6:F:149:VAL:CG1	2.72	0.63
1:A:568:U:H1'	1:A:2030:6MZ:H9C1	1.81	0.62
1:A:790:U:O2'	1:A:791:C:C5	2.53	0.62
11:K:121:GLU:OE1	16:P:65:SER:OG	2.17	0.62
1:A:1:G:O6	1:A:2902:C:N3	2.32	0.62
1:A:1050:A:C4	1:A:2751:G:N1	2.67	0.62
33:g:31:A:H8	33:g:31:A:OP2	1.82	0.62
1:A:1248:G:OP1	5:E:44:ARG:NH2	2.33	0.62
6:F:136:ILE:HD13	6:F:143:TYR:HD1	1.64	0.62
16:P:91:ALA:HB2	16:P:113:ARG:HA	1.80	0.62
1:A:125:A:OP2	29:c:19:ARG:NH2	2.32	0.62
6:F:4:LEU:HA	6:F:7:TYR:HB3	1.81	0.62
1:A:139:U:C5	20:T:1:MET:CE	2.83	0.62
1:A:881:G:C6	1:A:882:G:C6	2.87	0.62
18:R:37:GLU:OE2	18:R:37:GLU:HA	1.98	0.62
33:g:37:YYG:H31	33:g:37:YYG:H1'	1.81	0.62
6:F:103:LEU:CA	6:F:107:ALA:HB2	2.28	0.61
1:A:1826:G:O2'	1:A:1971:U:OP2	2.18	0.61
4:D:33:ARG:NH1	4:D:53:GLY:O	2.33	0.61
1:A:355:U:H2'	1:A:356:G:H8	1.65	0.61
1:A:881:G:H3'	1:A:882:G:H8	1.66	0.61
8:H:70:GLU:O	8:H:73:LYS:HG3	2.01	0.61
9:I:100:LYS:HA	9:I:139:VAL:O	1.99	0.61
10:J:114:LEU:HG	10:J:118:MET:HE3	1.81	0.61
6:F:103:LEU:CB	6:F:107:ALA:HB2	2.31	0.61
20:T:11:LEU:O	25:Y:29:ARG:NH1	2.31	0.61
1:A:862:G:N7	36:A:3222:HOH:O	2.31	0.60
1:A:84:A:N1	1:A:98:G:O2'	2.32	0.60
1:A:144:A:H2'	1:A:145:C:C6	2.36	0.60
6:F:80:ARG:HH11	6:F:80:ARG:CG	2.14	0.60
32:f:76:A:O3'	33:g:76:31M:CBM	2.49	0.60
8:H:134:GLU:O	8:H:134:GLU:HG3	2.00	0.60
9:I:110:ALA:O	9:I:114:ALA:N	2.34	0.60
1:A:136:G:C5	1:A:137:U:C5	2.89	0.60
7:G:35:ARG:HD3	7:G:71:LEU:HD23	1.82	0.59
1:A:63:A:C2	20:T:70:HIS:CE1	2.90	0.59
1:A:2324:U:H3'	1:A:2325:G:C5'	2.32	0.59
6:F:101:GLU:HA	6:F:104:ILE:HG22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:41:THR:HG22	26:Z:43:ALA:H	1.67	0.59
32:f:55:PSU:O2'	32:f:57:A:N7	2.33	0.59
2:B:54:G:H21	6:F:26:MET:HE3	1.67	0.59
7:G:87:LEU:HB2	7:G:131:ILE:HG23	1.85	0.59
14:N:29:VAL:HG21	14:N:75:ILE:HG23	1.84	0.59
1:A:2752:C:H6	1:A:2752:C:O5'	1.86	0.59
3:C:29:PRO:HG2	3:C:34:LEU:HD11	1.85	0.59
28:b:9:ILE:HD12	28:b:51:GLU:HG3	1.83	0.59
6:F:136:ILE:O	6:F:136:ILE:CG2	2.48	0.59
1:A:45:G:H5'	1:A:46:G:H5'	1.85	0.59
1:A:894:U:N3	1:A:895:U:C4	2.70	0.59
7:G:127:THR:HG23	7:G:130:GLU:HB2	1.85	0.59
1:A:143:C:H6	1:A:143:C:O5'	1.86	0.59
7:G:127:THR:OG1	7:G:128:GLN:N	2.35	0.59
1:A:807:U:OP2	12:L:41:ARG:NH1	2.36	0.58
6:F:65:PRO:HA	6:F:89:VAL:HG22	1.85	0.58
33:g:72:C:C5'	33:g:72:C:C6	2.83	0.58
1:A:134:G:C5	1:A:135:U:C5	2.92	0.58
32:f:76:A:O3'	33:g:76:31M:HGM3	2.02	0.58
8:H:16:SER:HG	8:H:63:ALA:HB1	1.69	0.58
1:A:884:U:N3	1:A:893:C:C2	2.68	0.58
1:A:1527:G:N1	1:A:1544:A:OP2	2.32	0.58
1:A:2420:C:OP1	30:d:34:THR:OG1	2.20	0.58
1:A:894:U:C2	1:A:895:U:C5	2.92	0.58
32:f:23:C:H2'	32:f:24:U:C6	2.39	0.58
30:d:29:LEU:HD12	30:d:33:LEU:CD2	2.34	0.58
1:A:320:A:N3	5:E:163:ASN:ND2	2.50	0.57
13:M:20:LEU:HD13	22:V:81:PRO:HG2	1.86	0.57
33:g:54:5MU:H5'	33:g:54:5MU:C6	2.30	0.57
8:H:103:ASN:O	8:H:105:LYS:N	2.37	0.57
32:f:7:G:H1	32:f:66:C:H42	1.51	0.57
1:A:139:U:C4	20:T:1:MET:HE3	2.39	0.57
1:A:883:G:N1	1:A:894:U:N3	2.35	0.57
2:B:51:G:OP1	15:O:63:LYS:NZ	2.37	0.57
1:A:2518:A:H2'	1:A:2518:A:N3	2.20	0.57
33:g:39:PSU:C6	33:g:39:PSU:C5'	2.84	0.57
7:G:19:ILE:HG13	7:G:24:ILE:HD12	1.87	0.57
6:F:134:GLU:OE2	6:F:149:VAL:CG1	2.52	0.57
22:V:58:SER:OG	22:V:59:GLU:OE1	2.20	0.57
33:g:32:OMC:H6	33:g:32:OMC:O5'	1.88	0.57
1:A:2517:C:C6	1:A:2542:A:N7	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:89:GLU:H	20:T:89:GLU:CD	2.13	0.57
1:A:757:G:O6	36:A:3205:HOH:O	2.14	0.56
1:A:2315:G:H2'	1:A:2316:G:H8	1.69	0.56
6:F:35:THR:HG23	6:F:155:THR:HG23	1.87	0.56
15:O:99:TYR:OH	15:O:111:ARG:NH1	2.38	0.56
6:F:117:LEU:HB2	6:F:176:PRO:O	2.05	0.56
6:F:141:ILE:O	6:F:141:ILE:HG23	2.04	0.56
7:G:42:GLU:HB3	7:G:55:ARG:HE	1.70	0.56
8:H:22:ALA:HA	8:H:86:THR:HA	1.88	0.56
33:g:2:C:H2'	33:g:2:C:O2	2.06	0.56
1:A:271:G:O2'	1:A:272:A:O5'	2.22	0.56
3:C:227:PRO:HA	3:C:233:GLY:HA2	1.87	0.56
13:M:77:PRO:HG2	13:M:80:VAL:HG21	1.88	0.56
6:F:110:ARG:HB3	6:F:137:ILE:CG2	2.28	0.56
13:M:75:GLU:HB2	13:M:90:GLU:HG3	1.86	0.56
1:A:218:A:N7	36:A:3224:HOH:O	2.32	0.56
1:A:1715:G:O2'	1:A:1743:G:O6	2.20	0.56
3:C:79:GLU:OE2	3:C:101:ARG:NE	2.39	0.56
7:G:155:GLU:OE1	7:G:160:LYS:N	2.33	0.56
9:I:19:ASN:HA	9:I:39:CYS:SG	2.46	0.56
9:I:119:GLY:O	9:I:125:MET:HE3	2.06	0.56
5:E:136:GLN:NE2	5:E:140:ASP:OD1	2.38	0.56
33:g:68:U:H2'	33:g:69:U:C6	2.41	0.56
1:A:1041:G:C2	1:A:1115:G:C2	2.93	0.56
9:I:99:GLY:HA3	9:I:138:LEU:HD22	1.87	0.56
33:g:21:A:O5'	33:g:21:A:H8	1.89	0.56
1:A:2898:U:O2'	1:A:2899:A:H5'	2.06	0.55
19:S:4:ILE:HG12	19:S:106:VAL:HG22	1.89	0.55
19:S:83:LYS:HD2	19:S:95:ARG:HE	1.71	0.55
6:F:111:ILE:HA	6:F:137:ILE:HD12	1.87	0.55
26:Z:37:GLU:O	26:Z:38:ARG:NH1	2.39	0.55
1:A:1059:G:H4'	9:I:117:MET:HE1	1.88	0.55
6:F:126:GLY:O	6:F:158:THR:OG1	2.23	0.55
13:M:25:ASP:N	13:M:25:ASP:OD1	2.38	0.55
6:F:104:ILE:HG23	6:F:105:THR:HG23	1.88	0.55
13:M:66:ARG:NH1	13:M:104:GLU:OE1	2.39	0.55
32:f:19:G:H4'	32:f:20:U:OP2	2.06	0.55
1:A:2756:U:OP2	31:e:19:ARG:NE	2.38	0.55
11:K:110:GLU:HA	11:K:113:MET:HG2	1.89	0.55
33:g:37:YYG:C10	33:g:37:YYG:C14	2.85	0.55
33:g:54:5MU:C5'	33:g:54:5MU:C6	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:597:G:O2'	12:L:11:GLY:O	2.24	0.55
32:f:76:A:C3'	33:g:76:31M:HGM2	2.37	0.55
1:A:134:G:C6	1:A:135:U:N3	2.76	0.54
1:A:2314:A:OP1	6:F:88:LYS:NZ	2.41	0.54
33:g:54:5MU:HN3	33:g:58:1MA:H2	1.56	0.54
1:A:1266:G:O2'	1:A:2012:G:O6	2.21	0.54
35:A:3175:DI0:CBN	35:A:3175:DI0:CAR	2.86	0.54
1:A:370:G:O2'	1:A:424:G:OP1	2.20	0.54
1:A:2032:G:N2	4:D:151:THR:OG1	2.40	0.54
5:E:157:LEU:HG	5:E:169:VAL:HG11	1.89	0.54
33:g:37:YYG:C14	33:g:37:YYG:H101	2.37	0.54
1:A:790:U:O2'	1:A:791:C:C6	2.61	0.54
5:E:118:LEU:HD11	5:E:188:MET:HG3	1.90	0.54
1:A:141:G:N3	1:A:141:G:H5''	2.23	0.54
13:M:110:GLU:OE2	13:M:114:ARG:NH2	2.41	0.54
1:A:668:A:H2'	1:A:670:A:H62	1.73	0.54
10:J:45:THR:HG22	17:Q:64:ARG:HH21	1.73	0.54
1:A:1494:A:O2'	1:A:1495:A:OP1	2.26	0.54
1:A:2646:C:OP2	1:A:2732:G:O2'	2.25	0.54
33:g:76:31M:H5''	33:g:76:31M:O	2.07	0.54
5:E:17:THR:O	5:E:21:ARG:NH2	2.41	0.53
2:B:40:U:N3	2:B:44:G:OP2	2.29	0.53
1:A:714:U:O2'	1:A:716:A:N7	2.41	0.53
1:A:1050:A:C1'	1:A:2751:G:H22	2.18	0.53
1:A:1651:G:OP1	14:N:40:LYS:NZ	2.41	0.53
1:A:2172:U:H4'	1:A:2173:A:H5'	1.90	0.53
1:A:1871:A:O2'	1:A:1872:A:O5'	2.27	0.53
3:C:5:LYS:NZ	3:C:14:ARG:O	2.40	0.53
33:g:16:H2U:H62	33:g:16:H2U:C5'	2.33	0.53
21:U:81:ASP:OD2	21:U:96:PHE:HB3	2.09	0.53
32:f:61:C:H2'	32:f:62:C:C6	2.43	0.53
33:g:73:A:C8	33:g:73:A:H5''	2.44	0.53
1:A:882:G:C6	1:A:883:G:C8	2.97	0.53
1:A:894:U:C4	1:A:895:U:O4	2.62	0.53
1:A:896:A:N1	33:g:19:G:O2'	2.31	0.53
22:V:45:ASP:OD1	22:V:45:ASP:N	2.42	0.53
1:A:1007:C:OP1	10:J:37:ARG:NH2	2.42	0.53
16:P:63:LYS:HE2	16:P:65:SER:HB2	1.91	0.53
22:V:11:GLU:N	22:V:11:GLU:OE1	2.42	0.53
1:A:1:G:O6	1:A:2902:C:C4	2.62	0.52
1:A:881:G:C2'	1:A:882:G:C8	2.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:39:C:H2'	32:f:40:C:C6	2.44	0.52
33:g:43:G:H2'	33:g:44:A:C8	2.43	0.52
1:A:142:A:H2'	1:A:143:C:C6	2.44	0.52
32:f:42:G:H2'	32:f:43:A:H8	1.75	0.52
1:A:136:G:O5'	1:A:136:G:H8	1.91	0.52
1:A:155:A:H2'	1:A:156:A:C8	2.45	0.52
1:A:1141:U:H4'	1:A:1142:A:O4'	2.10	0.52
32:f:27:U:H2'	32:f:28:C:C6	2.45	0.52
1:A:1105:U:H2'	1:A:1106:G:H8	1.75	0.52
1:A:1796:U:H2'	1:A:1797:G:C8	2.45	0.52
1:A:2291:U:OP1	1:A:2380:C:O2'	2.26	0.52
1:A:2751:G:N3	1:A:2751:G:C2'	2.73	0.52
3:C:107:PRO:HD2	3:C:110:LEU:HD22	1.91	0.52
7:G:123:ALA:HB1	7:G:131:ILE:HD11	1.92	0.52
18:R:37:GLU:HG3	18:R:53:PHE:CE1	2.43	0.52
1:A:2857:G:N2	1:A:2860:A:OP2	2.35	0.52
23:W:65:GLY:HA2	23:W:85:GLU:HG2	1.92	0.52
32:f:39:C:H2'	32:f:40:C:H6	1.75	0.52
33:g:65:G:H2'	33:g:66:A:C8	2.44	0.52
1:A:141:G:N3	1:A:141:G:C3'	2.73	0.52
1:A:2788:C:O2'	1:A:2809:A:N3	2.38	0.52
1:A:2469:A:H4'	13:M:55:ARG:CD	2.33	0.52
32:f:49:G:H2'	32:f:50:U:C6	2.44	0.52
1:A:881:G:C3'	1:A:882:G:C8	2.93	0.52
1:A:882:G:H22	1:A:895:U:C2'	2.23	0.52
6:F:34:ILE:HG12	6:F:96:MET:HG3	1.90	0.52
11:K:7:MET:HE1	11:K:44:LYS:HG3	1.92	0.52
1:A:894:U:O2'	1:A:895:U:P	2.68	0.51
32:f:56:C:O5'	32:f:56:C:H6	1.92	0.51
1:A:143:C:H2'	1:A:144:A:C8	2.45	0.51
1:A:2406:A:OP2	1:A:2406:A:H2'	2.10	0.51
33:g:51:G:H2'	33:g:52:U:C6	2.45	0.51
1:A:1049:C:C1'	1:A:1113:U:O2'	2.55	0.51
1:A:1007:C:OP2	36:A:3206:HOH:O	2.19	0.51
1:A:2757:A:N1	7:G:67:THR:HG21	2.26	0.51
1:A:139:U:C5	20:T:1:MET:HE3	2.45	0.51
1:A:894:U:C2	1:A:895:U:C6	2.98	0.51
1:A:463:G:N2	1:A:466:A:OP2	2.37	0.51
1:A:2315:G:H2'	1:A:2316:G:C8	2.44	0.51
32:f:58:A:O2'	32:f:60:U:OP2	2.22	0.51
33:g:25:C:H2'	33:g:26:M2G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:108:VAL:CG1	6:F:109:PRO:CD	2.61	0.51
20:T:28:ASN:ND2	20:T:88:LYS:O	2.43	0.51
33:g:71:G:H2'	33:g:72:C:H5''	1.93	0.51
1:A:612:G:H2'	1:A:614:A:C8	2.45	0.51
2:B:66:A:H61	2:B:107:G:H2'	1.76	0.51
22:V:4:ILE:HG12	22:V:50:MET:HE1	1.92	0.51
1:A:743:A:O2'	1:A:1659:G:OP1	2.28	0.51
1:A:896:A:C2	33:g:19:G:O2'	2.56	0.51
1:A:1046:A:H4'	8:H:58:THR:HG21	1.91	0.51
1:A:1172:C:C5	1:A:1173:U:H1'	2.46	0.51
32:f:64:G:H2'	32:f:65:C:C6	2.45	0.51
12:L:91:ASP:OD1	12:L:93:ASN:N	2.43	0.51
11:K:107:LEU:HB2	11:K:116:ILE:HD11	1.93	0.50
33:g:26:M2G:HM12	33:g:44:A:H2	1.77	0.50
1:A:1796:U:H2'	1:A:1797:G:H8	1.76	0.50
4:D:3:GLY:HA3	4:D:204:LYS:HG2	1.93	0.50
6:F:104:ILE:C	6:F:108:VAL:HG12	2.36	0.50
33:g:10:2MG:O6	33:g:25:C:N3	2.43	0.50
1:A:534:U:O2'	17:Q:49:ASP:OD2	2.25	0.50
1:A:2469:A:N6	1:A:2481:G:O2'	2.44	0.50
3:C:133:ARG:O	3:C:167:ARG:NH2	2.45	0.50
3:C:245:VAL:HG12	3:C:251:GLN:HA	1.94	0.50
33:g:5:A:H2'	33:g:6:U:C6	2.47	0.50
1:A:611:C:N4	1:A:612:G:N1	2.59	0.50
1:A:1799:G:O2'	3:C:180:GLU:OE2	2.24	0.50
1:A:1808:A:H3'	1:A:1809:A:C8	2.47	0.50
1:A:2052:A:H4'	4:D:148:GLN:O	2.11	0.50
4:D:77:ARG:NH2	4:D:200:ASP:OD1	2.45	0.50
32:f:61:C:H2'	32:f:62:C:H6	1.77	0.50
1:A:278:A:OP2	1:A:361:G:N1	2.45	0.50
1:A:613:A:H4'	1:A:614:A:H5''	1.94	0.50
1:A:1047:G:H1'	1:A:1111:A:H61	1.76	0.50
1:A:1506:U:H2'	1:A:1507:C:C6	2.46	0.50
1:A:611:C:C6	1:A:612:G:N7	2.79	0.50
1:A:2848:G:O2'	1:A:2867:G:N2	2.33	0.50
1:A:2899:A:H2'	1:A:2900:A:C8	2.46	0.50
1:A:1090:A:N1	1:A:1101:U:O2	2.45	0.50
1:A:1587:G:H2'	1:A:1588:G:H8	1.77	0.50
6:F:73:SER:OG	6:F:81:GLN:N	2.39	0.50
33:g:49:5MC:O2	33:g:49:5MC:H2'	2.10	0.50
1:A:2591:C:H2'	1:A:2592:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:18:ALA:C	9:I:20:PRO:HD2	2.37	0.49
1:A:2898:U:C2	1:A:2899:A:N7	2.80	0.49
6:F:121:SER:OG	6:F:129:SER:O	2.29	0.49
1:A:244:A:OP2	30:d:8:ARG:NH2	2.45	0.49
1:A:784:G:H5'	1:A:785:G:OP1	2.12	0.49
16:P:49:ALA:HB3	16:P:60:THR:HG23	1.92	0.49
32:f:70:G:H2'	32:f:71:C:C6	2.46	0.49
33:g:75:C:H2'	33:g:76:31M:C8	2.42	0.49
1:A:355:U:H2'	1:A:356:G:C8	2.47	0.49
22:V:9:ARG:HG2	22:V:41:GLU:HG3	1.94	0.49
3:C:72:ASP:OD2	3:C:189:ARG:NH1	2.33	0.49
1:A:136:G:C6	1:A:137:U:C4	3.01	0.49
1:A:191:A:H2'	1:A:192:C:C6	2.47	0.49
1:A:249:C:O2	30:d:12:LYS:NZ	2.46	0.49
1:A:729:G:C6	3:C:207:LYS:HB2	2.47	0.49
1:A:1172:C:C6	1:A:1173:U:H1'	2.48	0.49
15:O:15:ARG:NH2	15:O:95:SER:HB2	2.27	0.49
1:A:1340:U:OP1	20:T:19:LYS:NZ	2.45	0.49
1:A:1590:A:H2'	1:A:1591:A:C8	2.48	0.49
6:F:44:ILE:HG21	6:F:79:ILE:HG22	1.94	0.49
6:F:103:LEU:C	6:F:107:ALA:H	2.20	0.49
1:A:1794:A:H2'	1:A:1795:C:C6	2.48	0.49
1:A:2313:C:H5''	6:F:88:LYS:HD3	1.95	0.49
6:F:129:SER:HA	6:F:155:THR:HA	1.94	0.49
1:A:58:G:O2'	1:A:73:A:N1	2.44	0.49
1:A:1170:C:H2'	1:A:1171:G:O4'	2.13	0.49
11:K:40:LYS:HE3	11:K:57:VAL:HG12	1.94	0.49
33:g:37:YYG:HN20	33:g:37:YYG:H132	1.45	0.49
1:A:1046:A:C8	8:H:62:ARG:NH2	2.81	0.49
1:A:2627:G:O2'	1:A:2781:A:N1	2.42	0.49
1:A:134:G:H2'	1:A:135:U:O4'	2.13	0.48
1:A:144:A:H2'	1:A:145:C:H6	1.77	0.48
32:f:61:C:HO2'	32:f:62:C:H6	1.58	0.48
1:A:141:G:N3	1:A:141:G:C5'	2.76	0.48
1:A:1916:A:O5'	1:A:1916:A:H8	1.96	0.48
3:C:232:HIS:HA	3:C:242:LYS:HD2	1.95	0.48
6:F:4:LEU:HD13	6:F:97:TRP:HE3	1.79	0.48
6:F:108:VAL:N	6:F:109:PRO:CD	2.77	0.48
12:L:132:ARG:HG3	12:L:142:ILE:HD12	1.94	0.48
33:g:53:G:H2'	33:g:54:5MU:H5'	1.95	0.48
1:A:612:G:O5'	1:A:612:G:H8	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:885:C:O2	1:A:885:C:O2'	2.30	0.48
1:A:896:A:C8	1:A:896:A:H3'	2.48	0.48
1:A:1590:A:H2'	1:A:1591:A:H8	1.77	0.48
3:C:123:ALA:O	3:C:128:ASN:ND2	2.41	0.48
10:J:125:TYR:OH	10:J:132:HIS:NE2	2.45	0.48
22:V:72:VAL:HG12	22:V:93:ARG:HA	1.95	0.48
1:A:2000:C:OP1	14:N:5:LYS:NZ	2.35	0.48
33:g:70:C:H2'	33:g:71:G:H5''	1.95	0.48
1:A:1083:U:H4'	8:H:42:ARG:NH1	2.28	0.48
9:I:21:SER:HB3	9:I:22:PRO:HD3	1.96	0.48
1:A:1113:U:H2'	1:A:1114:C:C6	2.48	0.48
1:A:2514:U:H2'	1:A:2515:C:C6	2.48	0.48
1:A:2808:G:O2'	1:A:2890:G:O6	2.29	0.48
6:F:136:ILE:HD11	6:F:146:VAL:HG21	1.95	0.48
7:G:101:ASN:ND2	7:G:116:GLN:OE1	2.47	0.48
32:f:50:U:H2'	32:f:51:C:C6	2.49	0.48
1:A:245:G:O6	30:d:8:ARG:NH1	2.46	0.48
1:A:1050:A:C5	1:A:2751:G:N1	2.82	0.48
6:F:79:ILE:HD12	6:F:79:ILE:O	2.14	0.48
1:A:546:U:O2'	1:A:548:G:OP2	2.27	0.47
1:A:1177:G:H2'	1:A:1178:C:C6	2.49	0.47
1:A:2243:U:H2'	1:A:2244:U:C6	2.49	0.47
6:F:80:ARG:HD3	32:f:56:C:C4	2.49	0.47
24:X:6:GLN:O	24:X:74:ARG:NH1	2.47	0.47
1:A:630:G:N2	1:A:633:A:OP2	2.33	0.47
5:E:119:ILE:HB	5:E:187:VAL:HG22	1.97	0.47
6:F:108:VAL:N	6:F:109:PRO:HD2	2.29	0.47
22:V:2:PHE:HB2	22:V:61:LEU:HD22	1.95	0.47
23:W:26:PHE:N	23:W:29:GLU:OE1	2.36	0.47
1:A:2162:G:H5''	1:A:2171:A:H2'	1.95	0.47
1:A:2751:G:H4'	7:G:4:VAL:CG2	2.45	0.47
9:I:22:PRO:HB2	9:I:23:PRO:HD3	1.96	0.47
33:g:39:PSU:O4	33:g:39:PSU:H2'	2.14	0.47
1:A:2251:OMG:HM23	1:A:2251:OMG:H1'	1.70	0.47
20:T:33:LYS:HG2	20:T:80:TRP:CZ3	2.49	0.47
32:f:75:C:H6	32:f:75:C:O5'	1.96	0.47
33:g:37:YYG:H31	33:g:37:YYG:C1'	2.42	0.47
1:A:859:G:O2'	1:A:916:G:O6	2.29	0.47
1:A:1113:U:H2'	1:A:1114:C:H6	1.80	0.47
5:E:171:ASP:OD1	5:E:172:ALA:N	2.45	0.47
32:f:16:C:H5''	32:f:17:C:C5	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:38:A:O5'	33:g:38:A:H8	1.98	0.47
33:g:73:A:C8	33:g:73:A:C5'	2.97	0.47
1:A:307:G:N1	1:A:310:A:OP2	2.45	0.47
1:A:340:A:O2'	5:E:162:ARG:NH1	2.47	0.47
1:A:476:G:N1	1:A:479:A:OP2	2.48	0.47
1:A:568:U:O4	18:R:81:LYS:NZ	2.48	0.47
1:A:611:C:C5	1:A:612:G:N7	2.82	0.47
1:A:896:A:H3'	1:A:896:A:H8	1.80	0.47
1:A:1105:U:H2'	1:A:1106:G:C8	2.49	0.47
1:A:2576:G:O2'	1:A:2579:C:OP2	2.25	0.47
3:C:163:GLN:OE1	3:C:175:ARG:NH1	2.40	0.47
4:D:129:THR:HG22	4:D:130:GLN:O	2.15	0.47
6:F:68:THR:N	6:F:86:GLY:O	2.37	0.47
6:F:103:LEU:O	6:F:107:ALA:HB3	2.14	0.47
7:G:38:ASN:HD22	7:G:64:GLN:CD	2.23	0.47
9:I:20:PRO:HB2	9:I:23:PRO:HD2	1.97	0.47
9:I:100:LYS:O	9:I:100:LYS:HG3	2.15	0.47
9:I:113:LYS:O	9:I:117:MET:HG2	2.15	0.47
12:L:123:ARG:NE	12:L:143:GLU:OE2	2.46	0.47
24:X:3:ARG:O	24:X:12:PRO:HD3	2.15	0.47
1:A:400:G:N7	24:X:57:ARG:NH1	2.54	0.47
1:A:881:G:C3'	1:A:882:G:H8	2.26	0.47
1:A:1915:3TD:H6	1:A:1915:3TD:O5'	2.15	0.47
1:A:2099:U:O2'	1:A:2100:G:H5'	2.14	0.47
1:A:2532:G:N2	1:A:2663:G:O2'	2.48	0.47
32:f:63:G:H2'	32:f:64:G:C8	2.50	0.47
33:g:24:G:H2'	33:g:25:C:C6	2.50	0.47
33:g:62:A:H2'	33:g:63:C:C6	2.50	0.47
33:g:64:A:H3'	33:g:65:G:H5''	1.96	0.47
1:A:881:G:C5	1:A:882:G:C6	3.02	0.47
1:A:2377:A:H2'	1:A:2378:A:C8	2.50	0.47
7:G:68:ALA:O	7:G:72:LEU:HD12	2.15	0.47
7:G:164:TYR:HB2	7:G:167:GLU:HG2	1.97	0.47
9:I:19:ASN:N	9:I:20:PRO:HD2	2.29	0.47
1:A:2305:U:H5''	6:F:131:GLY:HA3	1.97	0.47
1:A:1870:C:O2'	1:A:1871:A:N3	2.36	0.46
9:I:12:GLN:HA	9:I:56:PRO:HA	1.96	0.46
30:d:16:LYS:HD2	30:d:20:GLY:HA2	1.97	0.46
33:g:42:G:C2'	33:g:43:G:H5'	2.46	0.46
1:A:2720:U:OP1	16:P:53:ARG:NH2	2.48	0.46
8:H:29:ASP:OD1	8:H:30:SER:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:C:H2'	1:A:282:A:C8	2.49	0.46
15:O:52:SER:OG	15:O:54:VAL:HG22	2.15	0.46
15:O:64:TYR:HB3	15:O:67:ASN:ND2	2.31	0.46
1:A:593:U:H2'	1:A:594:U:C6	2.51	0.46
1:A:1870:C:O2'	1:A:1871:A:O5'	2.34	0.46
33:g:11:C:OP2	33:g:11:C:C6	2.69	0.46
1:A:882:G:C5	1:A:883:G:C8	3.03	0.46
4:D:181:ASP:HB3	4:D:186:LEU:HB2	1.98	0.46
6:F:166:GLY:O	6:F:170:LEU:HD12	2.15	0.46
8:H:54:VAL:HG22	8:H:81:LEU:HD13	1.96	0.46
10:J:58:ASN:HD21	10:J:128:ASN:ND2	2.13	0.46
22:V:65:VAL:HG22	22:V:66:ASP:OD1	2.15	0.46
1:A:287:G:H2'	1:A:288:U:C6	2.51	0.46
1:A:350:G:H2'	1:A:351:C:O4'	2.15	0.46
1:A:479:A:N3	1:A:481:G:H5''	2.30	0.46
1:A:577:G:O2'	1:A:1254:A:OP1	2.33	0.46
1:A:811:U:H2'	12:L:21:ARG:HA	1.98	0.46
1:A:1405:U:H2'	1:A:1406:U:C6	2.50	0.46
1:A:2314:A:H2'	1:A:2315:G:H8	1.81	0.46
7:G:2:SER:O	7:G:6:LYS:N	2.44	0.46
15:O:95:SER:O	15:O:95:SER:OG	2.26	0.46
1:A:144:A:O2'	1:A:145:C:H5'	2.14	0.46
1:A:1041:G:N1	1:A:1115:G:N1	2.63	0.46
1:A:1736:U:H2'	1:A:1737:G:O4'	2.16	0.46
1:A:2097:A:C2'	1:A:2098:U:H5'	2.45	0.46
8:H:85:VAL:HG22	8:H:92:ALA:HB2	1.98	0.46
9:I:99:GLY:HA3	9:I:138:LEU:CD2	2.46	0.46
1:A:1049:C:H1'	1:A:1113:U:HO2'	1.77	0.46
1:A:1183:U:H2'	1:A:1184:U:C6	2.51	0.46
1:A:1219:U:H2'	1:A:1220:G:C8	2.51	0.46
9:I:35:ILE:CG2	9:I:36:MET:N	2.79	0.46
33:g:10:2MG:C2	33:g:25:C:O2	2.69	0.46
1:A:1028:A:N3	1:A:2486:C:O2'	2.43	0.46
1:A:1874:C:H2'	1:A:1875:G:O4'	2.16	0.46
1:A:2291:U:H2'	1:A:2292:U:C6	2.51	0.46
6:F:150:ARG:NH1	6:F:150:ARG:CG	2.74	0.46
32:f:42:G:H2'	32:f:43:A:C8	2.51	0.46
33:g:18:G:H4'	33:g:60:C:C5	2.51	0.46
1:A:851:C:H2'	1:A:852:U:C6	2.51	0.46
1:A:964:C:O2'	1:A:2273:A:N3	2.42	0.46
3:C:252:THR:OG1	3:C:253:LYS:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:33:ALA:N	23:W:64:ASP:OD1	2.48	0.46
1:A:278:A:N1	1:A:361:G:O2'	2.49	0.45
1:A:286:U:H2'	1:A:287:G:C8	2.51	0.45
1:A:1563:U:H2'	1:A:1564:C:C6	2.51	0.45
8:H:82:ILE:HD12	8:H:84:TYR:CE2	2.51	0.45
9:I:86:ILE:HD13	9:I:138:LEU:HD21	1.97	0.45
11:K:10:VAL:HG12	11:K:12:ASP:H	1.80	0.45
15:O:15:ARG:HH21	15:O:95:SER:HB2	1.81	0.45
1:A:2298:A:H2'	1:A:2299:U:O4'	2.16	0.45
8:H:103:ASN:C	8:H:105:LYS:H	2.24	0.45
1:A:896:A:C8	1:A:896:A:C3'	2.99	0.45
1:A:2799:A:O2'	1:A:2800:A:H5''	2.16	0.45
6:F:136:ILE:HD13	6:F:143:TYR:CD1	2.47	0.45
7:G:86:LYS:HG2	7:G:132:VAL:HG22	1.98	0.45
1:A:281:C:H2'	1:A:282:A:H8	1.81	0.45
1:A:570:G:H2'	1:A:2030:6MZ:N7	2.31	0.45
1:A:2020:A:H5'	27:a:9:THR:CG2	2.46	0.45
4:D:1:MET:HB3	4:D:205:PRO:HG2	1.99	0.45
33:g:43:G:C8	33:g:43:G:OP2	2.70	0.45
1:A:930:G:H1'	26:Z:25:LEU:HD21	1.99	0.45
1:A:1009:A:N3	1:A:1153:C:O2'	2.48	0.45
6:F:40:VAL:HG11	6:F:43:ALA:HB2	1.99	0.45
19:S:83:LYS:HD2	19:S:95:ARG:HH11	1.81	0.45
1:A:280:U:H2'	1:A:281:C:C6	2.52	0.45
1:A:548:G:H5''	1:A:549:G:H5'	1.98	0.45
1:A:1607:C:N4	1:A:1621:U:OP2	2.50	0.45
21:U:89:ASP:OD1	21:U:89:ASP:N	2.49	0.45
33:g:29:A:H2'	33:g:30:G:C8	2.51	0.45
1:A:1050:A:C2	1:A:2751:G:C5	3.04	0.45
6:F:43:ALA:HA	6:F:49:LEU:HD11	1.99	0.45
31:e:16:ILE:HD13	31:e:25:VAL:HG22	1.99	0.45
1:A:172:A:H2'	1:A:173:A:C8	2.52	0.45
1:A:639:U:H2'	1:A:640:C:C6	2.52	0.45
1:A:2098:U:C2'	1:A:2099:U:H5'	2.47	0.45
1:A:2304:G:H22	1:A:2312:U:H3	1.65	0.45
15:O:88:LYS:HB2	15:O:88:LYS:HE2	1.71	0.45
32:f:29:G:H2'	32:f:30:G:H8	1.81	0.45
1:A:65:U:O2'	1:A:456:C:N3	2.48	0.45
1:A:1182:G:H2'	1:A:1183:U:O4'	2.17	0.45
1:A:2233:U:H2'	1:A:2234:G:C8	2.52	0.45
3:C:16:VAL:HG22	3:C:206:GLY:HA3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:125:TYR:HH	10:J:132:HIS:CD2	2.34	0.45
20:T:18:GLU:O	20:T:22:THR:HG22	2.17	0.45
1:A:1916:A:O5'	1:A:1916:A:C8	2.70	0.45
1:A:2788:C:H2'	1:A:2789:C:C6	2.52	0.45
19:S:84:ARG:O	19:S:96:ILE:N	2.44	0.45
1:A:1494:A:H2'	1:A:1495:A:C8	2.52	0.44
1:A:1868:C:H2'	1:A:1869:G:O4'	2.16	0.44
1:A:2537:U:H2'	1:A:2538:C:C6	2.52	0.44
1:A:2793:C:H2'	1:A:2794:C:C6	2.52	0.44
32:f:72:A:H2'	32:f:73:A:H8	1.80	0.44
1:A:286:U:H2'	1:A:287:G:H8	1.82	0.44
1:A:2193:G:H2'	1:A:2194:U:C6	2.51	0.44
1:A:2328:A:H2'	1:A:2329:U:C6	2.52	0.44
2:B:48:U:H4'	15:O:100:HIS:HD2	1.82	0.44
3:C:37:ASN:HB2	3:C:62:TYR:HB2	1.99	0.44
6:F:36:LEU:HD22	6:F:154:ILE:HG12	1.99	0.44
15:O:59:ALA:HA	15:O:62:LEU:HD12	1.98	0.44
32:f:51:C:H2'	32:f:52:G:H8	1.83	0.44
1:A:883:G:C4	1:A:895:U:O2	2.70	0.44
1:A:1028:A:N6	1:A:1125:G:H2'	2.33	0.44
1:A:1050:A:C2	1:A:2751:G:N1	2.85	0.44
1:A:2615:U:C2	27:a:4:GLN:HA	2.53	0.44
3:C:28:LYS:HA	3:C:28:LYS:HD2	1.82	0.44
7:G:28:GLY:HA3	7:G:79:VAL:HB	2.00	0.44
8:H:50:VAL:HG22	8:H:85:VAL:HG13	1.98	0.44
15:O:33:ARG:O	15:O:65:THR:HG23	2.18	0.44
1:A:351:C:H2'	1:A:352:A:O4'	2.17	0.44
1:A:543:G:H2'	1:A:544:C:O4'	2.18	0.44
16:P:60:THR:HB	16:P:73:VAL:HG22	1.98	0.44
19:S:1:MET:HE3	19:S:1:MET:HA	1.99	0.44
33:g:42:G:H2'	33:g:43:G:H5'	1.98	0.44
33:g:44:A:O5'	33:g:44:A:H8	2.00	0.44
1:A:134:G:C2	1:A:135:U:C2	3.05	0.44
1:A:137:U:O2	1:A:137:U:H2'	2.18	0.44
1:A:2822:G:O6	14:N:2:ARG:NH1	2.50	0.44
8:H:119:PRO:HG2	8:H:122:GLN:HB2	1.98	0.44
31:e:2:LYS:HE2	31:e:32:LYS:O	2.18	0.44
33:g:34:OMG:HM23	33:g:34:OMG:H1'	1.48	0.44
1:A:411:G:OP2	1:A:2406:A:O2'	2.30	0.44
1:A:1746:A:H2'	1:A:1747:U:C6	2.53	0.44
6:F:30:ARG:HG3	6:F:30:ARG:HH11	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:69:ARG:O	20:T:69:ARG:HG2	2.18	0.44
32:f:27:U:H2'	32:f:28:C:H6	1.81	0.44
33:g:33:U:H2'	33:g:34:OMG:H3'	1.99	0.44
33:g:52:U:H2'	33:g:53:G:H5''	2.00	0.44
1:A:2161:C:H4'	1:A:2173:A:P	2.58	0.44
1:A:2845:U:H5''	16:P:52:ASN:O	2.18	0.44
4:D:25:THR:HG21	4:D:193:VAL:HG22	1.99	0.44
14:N:30:ARG:NH2	14:N:74:GLU:OE1	2.40	0.44
15:O:2:ASP:OD1	15:O:2:ASP:N	2.51	0.44
1:A:796:C:H2'	1:A:797:G:C8	2.53	0.44
1:A:871:U:H2'	1:A:872:U:C6	2.53	0.44
9:I:80:LEU:CD2	9:I:101:ILE:HD13	2.48	0.44
18:R:34:GLU:OE1	18:R:60:LYS:HG2	2.17	0.44
16:P:34:GLU:N	16:P:34:GLU:OE1	2.50	0.43
28:b:7:GLU:HB2	28:b:27:LYS:HE3	2.00	0.43
1:A:1181:U:H2'	1:A:1182:G:C8	2.54	0.43
3:C:161:TYR:HB3	3:C:194:GLU:HB2	1.98	0.43
9:I:20:PRO:HB2	9:I:23:PRO:CG	2.47	0.43
14:N:96:ARG:HD3	14:N:98:LEU:HD21	2.00	0.43
33:g:37:YYG:H141	33:g:37:YYG:H101	1.96	0.43
1:A:898:C:H2'	1:A:899:A:O4'	2.18	0.43
1:A:1847:A:O2'	1:A:1848:A:H8	1.79	0.43
1:A:2595:G:N2	1:A:2598:A:OP2	2.40	0.43
4:D:39:ASP:N	4:D:39:ASP:OD1	2.51	0.43
8:H:72:LEU:O	8:H:73:LYS:C	2.62	0.43
12:L:90:VAL:HG22	12:L:122:VAL:HA	1.99	0.43
21:U:96:PHE:CE2	21:U:103:ILE:HG12	2.53	0.43
33:g:37:YYG:H131	33:g:38:A:C2	2.54	0.43
1:A:672:C:OP2	12:L:42:SER:OG	2.29	0.43
1:A:1536:C:H4'	1:A:1537:G:C4	2.54	0.43
1:A:2688:G:N1	1:A:2720:U:OP2	2.32	0.43
1:A:2329:U:H2'	1:A:2330:G:C8	2.53	0.43
2:B:24:G:N7	2:B:56:G:H2'	2.33	0.43
16:P:88:ARG:HH21	16:P:112:GLU:HB2	1.82	0.43
33:g:6:U:H2'	33:g:7:U:C6	2.54	0.43
33:g:49:5MC:H2'	33:g:50:U:C6	2.53	0.43
1:A:1939:5MU:OP1	1:A:2604:PSU:O2'	2.37	0.43
4:D:97:SER:OG	4:D:98:VAL:N	2.51	0.43
9:I:18:ALA:O	9:I:19:ASN:CB	2.67	0.43
1:A:813:U:H2'	1:A:814:C:C6	2.54	0.43
6:F:104:ILE:HD11	6:F:176:PRO:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:155:GLU:OE1	7:G:159:GLY:N	2.52	0.43
11:K:71:ARG:HD3	11:K:71:ARG:HA	1.85	0.43
1:A:136:G:O5'	1:A:136:G:C8	2.70	0.43
1:A:143:C:O5'	1:A:143:C:C6	2.70	0.43
1:A:586:A:N1	1:A:809:G:O2'	2.46	0.43
1:A:1050:A:C6	1:A:2751:G:C6	3.06	0.43
1:A:2188:U:H2'	1:A:2189:U:O4'	2.19	0.43
1:A:2273:A:H2'	1:A:2274:A:C8	2.54	0.43
6:F:35:THR:HA	6:F:90:THR:HA	2.01	0.43
11:K:24:VAL:HG13	11:K:33:ALA:HB2	2.01	0.43
19:S:11:ARG:HD2	19:S:100:THR:HG22	2.00	0.43
32:f:53:G:H2'	32:f:54:5MU:C6	2.53	0.43
32:f:72:A:H2'	32:f:73:A:C8	2.54	0.43
1:A:134:G:O6	1:A:135:U:O4	2.36	0.43
1:A:1676:A:N7	36:A:3236:HOH:O	2.37	0.43
1:A:2339:C:H2'	1:A:2340:A:C8	2.53	0.43
2:B:1:U:H2'	2:B:2:G:H8	1.83	0.43
2:B:48:U:H4'	15:O:100:HIS:CD2	2.54	0.43
6:F:54:ALA:HB1	6:F:65:PRO:HG2	2.01	0.43
15:O:108:ASP:HA	15:O:111:ARG:HB2	2.00	0.43
1:A:1980:G:O2'	1:A:1982:U:OP2	2.35	0.43
2:B:42:C:N3	6:F:90:THR:HG22	2.33	0.43
9:I:56:PRO:HG2	9:I:72:LYS:HB2	2.01	0.43
15:O:115:LEU:HD12	15:O:115:LEU:HA	1.85	0.43
25:Y:42:LEU:O	25:Y:46:VAL:HG12	2.19	0.43
33:g:53:G:H5''	33:g:53:G:H8	1.84	0.43
1:A:594:U:H2'	1:A:595:C:C6	2.54	0.42
1:A:1040:A:N1	1:A:1115:G:N2	2.66	0.42
1:A:1199:U:H1'	17:Q:4:VAL:HG22	2.01	0.42
1:A:1441:G:H2'	1:A:1442:U:C6	2.54	0.42
6:F:150:ARG:H	6:F:150:ARG:HG3	1.46	0.42
7:G:105:LEU:HB2	7:G:113:VAL:HG13	2.01	0.42
1:A:57:C:H2'	1:A:58:G:O4'	2.19	0.42
1:A:708:G:N2	1:A:724:U:H1'	2.34	0.42
1:A:1041:G:C2	1:A:1115:G:N1	2.87	0.42
1:A:2314:A:H2'	1:A:2315:G:C8	2.53	0.42
9:I:20:PRO:HB2	9:I:23:PRO:HG2	2.01	0.42
9:I:86:ILE:CD1	9:I:138:LEU:HD21	2.49	0.42
9:I:114:ALA:CB	9:I:125:MET:SD	3.07	0.42
1:A:544:C:H2'	1:A:545:U:O4'	2.19	0.42
1:A:1420:A:C5	1:A:2211:A:C6	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1915:3TD:H2'	1:A:1916:A:H8	1.84	0.42
1:A:2333:A:P	23:W:77:ARG:HH22	2.42	0.42
1:A:2389:G:H5''	1:A:2390:U:O4'	2.19	0.42
7:G:153:ARG:HB2	7:G:153:ARG:CZ	2.49	0.42
21:U:14:LEU:HD11	21:U:71:ALA:HB2	2.01	0.42
24:X:65:ASP:OD1	24:X:66:THR:N	2.53	0.42
32:f:19:G:H3'	32:f:20:U:H6	1.84	0.42
33:g:10:2MG:C6	33:g:25:C:N3	2.87	0.42
1:A:207:A:H2'	1:A:208:C:O4'	2.18	0.42
1:A:1172:C:H3'	1:A:1173:U:C4'	2.49	0.42
1:A:2728:U:O2'	1:A:2729:G:H8	2.03	0.42
10:J:9:GLU:H	10:J:9:GLU:CD	2.28	0.42
21:U:47:LYS:HE2	21:U:47:LYS:HB3	1.88	0.42
1:A:2698:U:H2'	1:A:2699:C:C6	2.54	0.42
2:B:48:U:H2'	2:B:49:C:C6	2.54	0.42
5:E:155:GLU:H	5:E:155:GLU:CD	2.28	0.42
6:F:175:PHE:HB3	6:F:177:PHE:CE1	2.55	0.42
32:f:63:G:H2'	32:f:64:G:H8	1.84	0.42
33:g:70:C:C2'	33:g:71:G:H5''	2.50	0.42
1:A:483:A:O2'	21:U:57:GLY:N	2.49	0.42
1:A:721:A:H2'	1:A:722:A:C8	2.55	0.42
1:A:1915:3TD:H2'	1:A:1916:A:C8	2.55	0.42
7:G:72:LEU:HA	7:G:75:MET:HB2	2.01	0.42
32:f:4:G:H1	32:f:69:C:H42	1.68	0.42
12:L:77:ILE:HD13	12:L:108:ALA:HB1	2.02	0.42
23:W:17:GLU:O	23:W:19:LYS:NZ	2.52	0.42
33:g:10:2MG:C4	33:g:26:M2G:HM22	2.55	0.42
1:A:139:U:C5	20:T:1:MET:SD	3.13	0.42
1:A:612:G:H1'	1:A:616:A:H61	1.84	0.42
6:F:121:SER:OG	6:F:121:SER:O	2.35	0.42
7:G:155:GLU:H	7:G:155:GLU:HG3	1.68	0.42
12:L:57:LEU:HD22	30:d:54:ASP:HB3	2.02	0.42
33:g:47:U:O2	33:g:47:U:C2'	2.67	0.42
20:T:1:MET:HE2	20:T:1:MET:HB2	1.83	0.42
22:V:46:LYS:HE3	22:V:46:LYS:HB2	1.79	0.42
1:A:225:C:H2'	1:A:226:A:O4'	2.20	0.42
1:A:458:G:O2'	1:A:469:G:O6	2.32	0.42
1:A:1930:G:O2'	1:A:1968:G:O6	2.33	0.42
5:E:122:GLU:CD	5:E:122:GLU:H	2.28	0.42
6:F:56:ASP:O	6:F:60:ILE:HG12	2.20	0.42
7:G:50:LEU:HA	7:G:50:LEU:HD23	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:117:ALA:HA	10:J:120:ARG:HH21	1.85	0.42
22:V:63:ILE:HD12	22:V:72:VAL:HG21	2.01	0.42
32:f:29:G:H2'	32:f:30:G:C8	2.55	0.42
32:f:49:G:H2'	32:f:50:U:H6	1.85	0.42
33:g:6:U:H2'	33:g:7:U:H6	1.85	0.42
7:G:54:PRO:HG3	7:G:62:TRP:CE2	2.54	0.41
8:H:38:MET:O	8:H:41:LEU:N	2.53	0.41
16:P:6:LYS:HD2	16:P:6:LYS:C	2.44	0.41
18:R:58:VAL:HB	18:R:102:SER:OG	2.19	0.41
33:g:51:G:H2'	33:g:52:U:H6	1.85	0.41
1:A:714:U:H1'	1:A:717:C:H5	1.86	0.41
1:A:1047:G:H1'	1:A:1111:A:N6	2.35	0.41
1:A:2375:G:N2	1:A:2378:A:OP2	2.47	0.41
7:G:10:VAL:HA	7:G:49:THR:HA	2.02	0.41
33:g:67:A:H2'	33:g:68:U:C6	2.55	0.41
1:A:364:C:H2'	1:A:365:U:C6	2.56	0.41
1:A:1070:A:N7	1:A:1096:A:O2'	2.47	0.41
1:A:2162:G:OP1	1:A:2171:A:H2'	2.20	0.41
8:H:51:TYR:OH	8:H:53:ARG:NH1	2.53	0.41
11:K:38:ILE:HD11	11:K:112:PHE:HZ	1.85	0.41
32:f:76:A:C3'	33:g:76:31M:CGM	2.98	0.41
1:A:358:U:H2'	1:A:359:G:C8	2.55	0.41
1:A:834:G:H5'	30:d:57:LEU:HD21	2.02	0.41
1:A:1084:A:C6	1:A:1085:A:C6	3.08	0.41
1:A:1385:A:O2'	1:A:1396:U:O2	2.39	0.41
1:A:1475:G:O2'	1:A:1514:G:O6	2.34	0.41
1:A:2129:C:N4	1:A:2130:U:O4	2.54	0.41
6:F:8:TYR:HA	6:F:12:VAL:HG22	2.03	0.41
6:F:175:PHE:HB3	6:F:177:PHE:HE1	1.85	0.41
10:J:31:GLU:OE2	10:J:35:ARG:NE	2.51	0.41
18:R:44:GLY:C	18:R:46:GLU:H	2.28	0.41
1:A:742:A:H2'	1:A:743:A:C8	2.56	0.41
1:A:984:A:N3	1:A:984:A:H2'	2.35	0.41
1:A:1042:G:N2	1:A:1114:C:H1'	2.35	0.41
6:F:80:ARG:HB2	6:F:83:TYR:CE2	2.55	0.41
8:H:65:GLU:O	8:H:65:GLU:HG3	2.20	0.41
13:M:50:ARG:O	13:M:53:MET:HG2	2.20	0.41
19:S:23:LEU:HD22	27:a:24:ALA:HB2	2.02	0.41
32:f:44:A:H2'	32:f:45:G:C8	2.55	0.41
1:A:1174:U:H5'	1:A:1175:A:OP2	2.20	0.41
1:A:1278:C:H2'	1:A:1279:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1482:G:H1'	1:A:1509:A:N6	2.32	0.41
1:A:2321:U:H5'	1:A:2322:A:OP2	2.21	0.41
15:O:43:ASN:OD1	15:O:45:SER:OG	2.29	0.41
15:O:60:GLU:H	15:O:60:GLU:HG2	1.72	0.41
1:A:287:G:H2'	1:A:288:U:H6	1.85	0.41
6:F:67:ILE:HD13	6:F:87:CYS:HB3	2.02	0.41
6:F:94:GLU:HA	6:F:97:TRP:HD1	1.85	0.41
7:G:64:GLN:O	7:G:67:THR:OG1	2.36	0.41
10:J:110:PRO:O	10:J:115:GLY:HA3	2.21	0.41
29:c:3:ARG:HD3	29:c:3:ARG:HA	1.85	0.41
32:f:41:C:H2'	32:f:42:G:C8	2.56	0.41
1:A:278:A:N6	1:A:362:A:N7	2.69	0.41
1:A:322:A:OP2	5:E:163:ASN:HB2	2.21	0.41
1:A:1223:G:C6	1:A:1227:G:C6	3.08	0.41
1:A:2114:A:OP2	1:A:2115:G:C6	2.73	0.41
7:G:18:LYS:NZ	7:G:20:ASN:HB2	2.36	0.41
33:g:18:G:N2	33:g:57:G:H2'	2.36	0.41
33:g:25:C:H2'	33:g:26:M2G:H8	1.85	0.41
1:A:882:G:C2	1:A:883:G:C8	3.08	0.41
1:A:1050:A:N1	1:A:2751:G:C6	2.88	0.41
1:A:1278:C:H2'	1:A:1279:G:H8	1.86	0.41
1:A:1932:A:H2'	1:A:1933:G:O4'	2.21	0.41
2:B:78:A:H2'	2:B:79:G:O4'	2.21	0.41
2:B:118:C:H2'	2:B:119:A:C8	2.56	0.41
3:C:155:ALA:HB2	3:C:162:VAL:HG23	2.03	0.41
5:E:2:GLU:HB3	5:E:11:ALA:HB1	2.03	0.41
5:E:6:LYS:HE2	5:E:6:LYS:HA	2.02	0.41
6:F:32:GLU:OE2	6:F:32:GLU:N	2.53	0.41
6:F:42:GLU:H	6:F:42:GLU:HG3	1.72	0.41
6:F:103:LEU:HA	6:F:107:ALA:H	1.85	0.41
7:G:117:LEU:HD13	7:G:117:LEU:HA	1.88	0.41
20:T:33:LYS:HE2	20:T:80:TRP:CE3	2.56	0.41
25:Y:5:GLU:CD	25:Y:5:GLU:H	2.29	0.41
28:b:32:GLU:H	28:b:32:GLU:CD	2.29	0.41
1:A:634:C:H2'	1:A:635:C:C6	2.56	0.41
1:A:880:G:C2	1:A:881:G:H1'	2.56	0.41
1:A:979:A:H2'	1:A:982:C:H42	1.85	0.41
1:A:1049:C:HO2'	1:A:1114:C:P	2.43	0.41
1:A:1394:U:H4'	1:A:1603:A:H4'	2.03	0.41
1:A:2484:G:OP1	13:M:44:ARG:NH2	2.49	0.41
3:C:199:GLU:H	3:C:199:GLU:CD	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:103:LEU:O	6:F:108:VAL:N	2.54	0.41
12:L:77:ILE:CD1	12:L:108:ALA:HB1	2.51	0.41
20:T:26:LYS:HE2	20:T:26:LYS:HA	2.02	0.41
27:a:43:ILE:HG22	27:a:49:TYR:HB2	2.03	0.41
30:d:52:LYS:HB3	30:d:52:LYS:HE2	1.72	0.41
1:A:861:A:H2'	1:A:862:G:O4'	2.20	0.40
1:A:1357:C:H2'	1:A:1358:G:O4'	2.20	0.40
1:A:1871:A:H1'	1:A:1872:A:H5'	2.02	0.40
1:A:1881:C:H2'	1:A:1882:U:O4'	2.21	0.40
1:A:2116:G:C6	1:A:2171:A:N6	2.84	0.40
4:D:99:GLU:H	4:D:99:GLU:HG3	1.74	0.40
4:D:157:LYS:HE3	4:D:157:LYS:HB2	1.85	0.40
6:F:38:MET:HE2	6:F:87:CYS:SG	2.61	0.40
11:K:63:VAL:HG12	11:K:107:LEU:HD11	2.03	0.40
12:L:1:MET:HE2	12:L:1:MET:HB3	1.82	0.40
33:g:43:G:OP2	33:g:43:G:H8	2.03	0.40
1:A:493:G:H2'	1:A:494:G:O4'	2.21	0.40
1:A:1370:C:H2'	1:A:1371:G:O4'	2.22	0.40
1:A:1430:G:H2'	1:A:1431:A:O4'	2.21	0.40
1:A:1450:G:C6	1:A:1451:C:N4	2.89	0.40
4:D:186:LEU:HD13	16:P:8:LEU:HD11	2.04	0.40
9:I:90:SER:HB2	9:I:98:VAL:CG2	2.51	0.40
10:J:58:ASN:HD21	10:J:128:ASN:HD22	1.69	0.40
32:f:68:C:H2'	32:f:69:C:H5''	2.03	0.40
33:g:21:A:O5'	33:g:21:A:C8	2.74	0.40
1:A:1414:C:H2'	1:A:1415:U:O4'	2.21	0.40
6:F:10:ASP:OD1	6:F:11:GLU:N	2.54	0.40
8:H:52:MET:HE1	8:H:81:LEU:HG	2.04	0.40
1:A:1:G:H2'	1:A:2:G:H8	1.85	0.40
1:A:882:G:C6	1:A:883:G:C5	3.10	0.40
7:G:48:ASN:O	7:G:48:ASN:ND2	2.54	0.40
15:O:89:ASP:OD1	15:O:89:ASP:N	2.54	0.40
1:A:645:C:H2'	1:A:647:G:C8	2.57	0.40
1:A:1132:U:H3'	1:A:1133:A:H5''	2.04	0.40
7:G:121:ILE:N	7:G:121:ILE:HD12	2.35	0.40
21:U:4:LYS:O	21:U:94:ARG:NH2	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	C	269/271 (99%)	265 (98%)	4 (2%)	0	100	100
4	D	206/209 (99%)	201 (98%)	4 (2%)	1 (0%)	24	22
5	E	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
6	F	175/177 (99%)	163 (93%)	11 (6%)	1 (1%)	21	18
7	G	174/176 (99%)	168 (97%)	5 (3%)	1 (1%)	21	18
8	H	133/135 (98%)	109 (82%)	18 (14%)	6 (4%)	2	0
9	I	132/134 (98%)	117 (89%)	11 (8%)	4 (3%)	3	1
10	J	140/142 (99%)	140 (100%)	0	0	100	100
11	K	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
12	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
13	M	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
14	N	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
15	O	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
16	P	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
17	Q	115/117 (98%)	115 (100%)	0	0	100	100
18	R	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	9
19	S	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
20	T	91/93 (98%)	90 (99%)	1 (1%)	0	100	100
21	U	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
22	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
23	W	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
24	X	75/77 (97%)	75 (100%)	0	0	100	100
25	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
26	Z	56/58 (97%)	56 (100%)	0	0	100	100
27	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	b	49/51 (96%)	49 (100%)	0	0	100	100
29	c	44/46 (96%)	44 (100%)	0	0	100	100
30	d	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
31	e	36/38 (95%)	36 (100%)	0	0	100	100
All	All	3291/3351 (98%)	3184 (97%)	93 (3%)	14 (0%)	31	28

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	104	ALA
8	H	106	PHE
9	I	15	ALA
9	I	19	ASN
18	R	52	PRO
4	D	149	ASN
8	H	67	THR
8	H	108	VAL
9	I	25	GLY
8	H	124	ASP
9	I	23	PRO
8	H	130	PRO
7	G	47	ASP
6	F	110	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	C	216/216 (100%)	216 (100%)	0	100	100
4	D	163/163 (100%)	161 (99%)	2 (1%)	63	72
5	E	165/165 (100%)	161 (98%)	4 (2%)	43	49
6	F	148/148 (100%)	132 (89%)	16 (11%)	6	4
7	G	137/137 (100%)	125 (91%)	12 (9%)	9	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	103/103 (100%)	96 (93%)	7 (7%)	14	12
9	I	104/104 (100%)	97 (93%)	7 (7%)	15	12
10	J	116/116 (100%)	112 (97%)	4 (3%)	32	35
11	K	104/104 (100%)	102 (98%)	2 (2%)	50	58
12	L	103/103 (100%)	101 (98%)	2 (2%)	50	58
13	M	108/108 (100%)	104 (96%)	4 (4%)	30	33
14	N	102/102 (100%)	101 (99%)	1 (1%)	68	76
15	O	87/87 (100%)	85 (98%)	2 (2%)	44	51
16	P	99/99 (100%)	95 (96%)	4 (4%)	28	29
17	Q	89/89 (100%)	89 (100%)	0	100	100
18	R	84/84 (100%)	83 (99%)	1 (1%)	63	72
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	80/80 (100%)	78 (98%)	2 (2%)	42	48
21	U	83/83 (100%)	79 (95%)	4 (5%)	23	23
22	V	78/78 (100%)	73 (94%)	5 (6%)	16	14
23	W	57/58 (98%)	56 (98%)	1 (2%)	51	60
24	X	67/67 (100%)	65 (97%)	2 (3%)	36	41
25	Y	54/54 (100%)	52 (96%)	2 (4%)	30	33
26	Z	48/48 (100%)	47 (98%)	1 (2%)	47	54
27	a	47/47 (100%)	47 (100%)	0	100	100
28	b	45/46 (98%)	44 (98%)	1 (2%)	45	53
29	c	38/38 (100%)	37 (97%)	1 (3%)	40	46
30	d	51/51 (100%)	50 (98%)	1 (2%)	48	56
31	e	34/34 (100%)	34 (100%)	0	100	100
All	All	2703/2705 (100%)	2615 (97%)	88 (3%)	34	37

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	13	ARG
4	D	95	SER
5	E	7	ASP
5	E	21	ARG
5	E	80	SER

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Mol	Chain	Res	Type
5	E	197	GLU
6	F	4	LEU
6	F	14	LYS
6	F	24	SER
6	F	33	LYS
6	F	35	THR
6	F	38	MET
6	F	51	ASP
6	F	80	ARG
6	F	108	VAL
6	F	110	ARG
6	F	111	ILE
6	F	137	ILE
6	F	141	ILE
6	F	150	ARG
6	F	155	THR
6	F	175	PHE
7	G	11	VAL
7	G	18	LYS
7	G	32	GLU
7	G	34	THR
7	G	84	THR
7	G	87	LEU
7	G	98	VAL
7	G	99	LYS
7	G	117	LEU
7	G	127	THR
7	G	131	ILE
7	G	168	VAL
8	H	16	SER
8	H	64	VAL
8	H	67	THR
8	H	71	CYS
8	H	86	THR
8	H	133	GLU
8	H	134	GLU
9	I	24	VAL
9	I	35	ILE
9	I	59	ILE
9	I	61	VAL
9	I	98	VAL
9	I	103	ARG

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Mol	Chain	Res	Type
9	I	113	LYS
10	J	5	THR
10	J	17	VAL
10	J	90	GLU
10	J	142	ILE
11	K	92	GLU
11	K	109	SER
12	L	30	THR
12	L	118	THR
13	M	53	MET
13	M	55	ARG
13	M	58	LYS
13	M	59	ARG
14	N	29	VAL
15	O	24	THR
15	O	35	ILE
16	P	60	THR
16	P	76	THR
16	P	103	ARG
16	P	104	THR
18	R	37	GLU
20	T	16	VAL
20	T	93	LEU
21	U	27	ASN
21	U	68	SER
21	U	72	ILE
21	U	86	ARG
22	V	34	LYS
22	V	59	GLU
22	V	61	LEU
22	V	64	VAL
22	V	71	LYS
23	W	67	VAL
24	X	42	SER
24	X	48	THR
25	Y	5	GLU
25	Y	11	VAL
26	Z	37	GLU
28	b	17	THR
29	c	8	SER
30	d	33	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34)

such sidechains are listed below:

Mol	Chain	Res	Type
3	C	142	HIS
3	C	243	HIS
4	D	42	ASN
4	D	173	GLN
5	E	9	GLN
5	E	90	GLN
5	E	136	GLN
6	F	21	ASN
6	F	27	GLN
7	G	104	ASN
7	G	111	HIS
7	G	115	HIS
8	H	9	GLN
10	J	47	HIS
10	J	58	ASN
10	J	128	ASN
12	L	35	HIS
13	M	3	GLN
13	M	13	HIS
13	M	60	GLN
14	N	73	ASN
15	O	19	GLN
15	O	100	HIS
16	P	41	GLN
17	Q	81	ASN
19	S	7	HIS
20	T	70	HIS
21	U	27	ASN
21	U	46	GLN
24	X	36	HIS
26	Z	9	GLN
29	c	29	GLN
30	d	43	HIS
31	e	13	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2892/2897 (99%)	383 (13%)	16 (0%)
2	B	119/120 (99%)	7 (5%)	0
32	f	75/76 (98%)	32 (42%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	g	74/76 (97%)	50 (67%)	0
All	All	3160/3169 (99%)	472 (14%)	16 (0%)

All (472) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	15	G
1	A	34	U
1	A	45	G
1	A	46	G
1	A	58	G
1	A	71	A
1	A	74	A
1	A	75	G
1	A	84	A
1	A	101	A
1	A	102	U
1	A	118	A
1	A	119	A
1	A	120	U
1	A	125	A
1	A	135	U
1	A	137	U
1	A	138	U
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	157	C
1	A	163	C
1	A	165	A
1	A	181	A
1	A	196	A
1	A	199	A
1	A	216	A
1	A	221	A
1	A	222	A
1	A	248	G
1	A	266	G
1	A	272	A
1	A	276	U

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Mol	Chain	Res	Type
1	A	285	G
1	A	302	C
1	A	311	A
1	A	329	G
1	A	330	A
1	A	352	A
1	A	353	C
1	A	361	G
1	A	362	A
1	A	372	G
1	A	386	G
1	A	396	G
1	A	399	U
1	A	403	U
1	A	406	G
1	A	411	G
1	A	412	A
1	A	424	G
1	A	425	G
1	A	479	A
1	A	481	G
1	A	491	G
1	A	504	A
1	A	505	A
1	A	509	C
1	A	529	A
1	A	530	G
1	A	532	A
1	A	544	C
1	A	546	U
1	A	547	A
1	A	548	G
1	A	549	G
1	A	550	C
1	A	563	A
1	A	573	U
1	A	575	A
1	A	603	A
1	A	613	A
1	A	614	A
1	A	615	U
1	A	627	A

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Mol	Chain	Res	Type
1	A	637	A
1	A	645	C
1	A	647	G
1	A	654	A
1	A	655	A
1	A	685	A
1	A	686	U
1	A	717	C
1	A	730	A
1	A	747	5MU
1	A	775	G
1	A	776	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	790	U
1	A	791	C
1	A	792	A
1	A	805	G
1	A	812	C
1	A	827	U
1	A	828	U
1	A	845	A
1	A	846	U
1	A	847	U
1	A	858	G
1	A	859	G
1	A	878	A
1	A	881	G
1	A	883	G
1	A	884	U
1	A	885	C
1	A	895	U
1	A	896	A
1	A	897	C
1	A	910	A
1	A	914	G
1	A	927	A
1	A	931	U
1	A	946	C
1	A	961	C
1	A	974	G

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Mol	Chain	Res	Type
1	A	983	A
1	A	996	A
1	A	1012	U
1	A	1013	C
1	A	1026	G
1	A	1033	U
1	A	1040	A
1	A	1046	A
1	A	1047	G
1	A	1070	A
1	A	1083	U
1	A	1084	A
1	A	1088	A
1	A	1090	A
1	A	1112	G
1	A	1114	C
1	A	1115	G
1	A	1116	G
1	A	1119	U
1	A	1132	U
1	A	1133	A
1	A	1135	C
1	A	1141	U
1	A	1142	A
1	A	1168	G
1	A	1171	G
1	A	1173	U
1	A	1174	U
1	A	1175	A
1	A	1176	U
1	A	1212	G
1	A	1236	G
1	A	1238	G
1	A	1253	A
1	A	1256	G
1	A	1271	G
1	A	1272	A
1	A	1300	G
1	A	1301	A
1	A	1329	U
1	A	1345	C
1	A	1352	U

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Mol	Chain	Res	Type
1	A	1365	A
1	A	1379	U
1	A	1383	A
1	A	1416	G
1	A	1417	C
1	A	1421	G
1	A	1428	C
1	A	1434	A
1	A	1435	G
1	A	1452	G
1	A	1459	G
1	A	1476	U
1	A	1482	G
1	A	1490	A
1	A	1493	C
1	A	1494	A
1	A	1495	A
1	A	1497	U
1	A	1509	A
1	A	1510	G
1	A	1515	A
1	A	1524	G
1	A	1529	G
1	A	1533	C
1	A	1534	U
1	A	1535	A
1	A	1536	C
1	A	1537	G
1	A	1566	A
1	A	1569	A
1	A	1578	U
1	A	1583	A
1	A	1584	U
1	A	1585	C
1	A	1607	C
1	A	1608	A
1	A	1647	U
1	A	1648	U
1	A	1649	G
1	A	1674	G
1	A	1715	G
1	A	1729	U

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Mol	Chain	Res	Type
1	A	1730	C
1	A	1738	G
1	A	1744	A
1	A	1764	C
1	A	1773	A
1	A	1776	G
1	A	1791	A
1	A	1800	C
1	A	1801	A
1	A	1808	A
1	A	1811	G
1	A	1816	C
1	A	1829	A
1	A	1870	C
1	A	1871	A
1	A	1872	A
1	A	1873	G
1	A	1906	G
1	A	1913	A
1	A	1914	C
1	A	1929	G
1	A	1930	G
1	A	1936	A
1	A	1955	U
1	A	1960	A
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1991	U
1	A	1993	U
1	A	1997	C
1	A	2023	C
1	A	2030	6MZ
1	A	2031	A
1	A	2033	A
1	A	2043	C
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A

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Mol	Chain	Res	Type
1	A	2069	G7M
1	A	2093	G
1	A	2098	U
1	A	2099	U
1	A	2101	A
1	A	2105	U
1	A	2108	A
1	A	2111	U
1	A	2112	G
1	A	2113	U
1	A	2115	G
1	A	2116	G
1	A	2117	A
1	A	2118	U
1	A	2119	A
1	A	2123	G
1	A	2126	A
1	A	2127	G
1	A	2128	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2134	A
1	A	2136	G
1	A	2137	U
1	A	2145	C
1	A	2146	C
1	A	2147	A
1	A	2148	G
1	A	2149	U
1	A	2159	G
1	A	2160	C
1	A	2161	C
1	A	2162	G
1	A	2163	A
1	A	2164	C
1	A	2165	C
1	A	2167	U
1	A	2168	G
1	A	2169	A
1	A	2170	A
1	A	2171	A

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Mol	Chain	Res	Type
1	A	2172	U
1	A	2173	A
1	A	2177	C
1	A	2178	C
1	A	2179	C
1	A	2181	U
1	A	2185	U
1	A	2187	U
1	A	2188	U
1	A	2190	G
1	A	2192	U
1	A	2193	G
1	A	2194	U
1	A	2195	U
1	A	2198	A
1	A	2204	G
1	A	2211	A
1	A	2225	A
1	A	2238	G
1	A	2239	G
1	A	2268	A
1	A	2279	G
1	A	2283	C
1	A	2287	A
1	A	2288	A
1	A	2297	A
1	A	2305	U
1	A	2308	G
1	A	2322	A
1	A	2325	G
1	A	2327	A
1	A	2333	A
1	A	2334	U
1	A	2336	A
1	A	2345	G
1	A	2347	C
1	A	2350	C
1	A	2383	G
1	A	2385	C
1	A	2402	U
1	A	2406	A
1	A	2407	A

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Mol	Chain	Res	Type
1	A	2425	A
1	A	2435	A
1	A	2441	U
1	A	2445	2MG
1	A	2448	A
1	A	2476	A
1	A	2478	A
1	A	2491	U
1	A	2502	G
1	A	2505	G
1	A	2518	A
1	A	2525	G
1	A	2529	G
1	A	2535	G
1	A	2547	A
1	A	2566	A
1	A	2567	G
1	A	2602	A
1	A	2609	U
1	A	2613	U
1	A	2615	U
1	A	2629	U
1	A	2663	G
1	A	2689	U
1	A	2690	U
1	A	2714	G
1	A	2716	C
1	A	2726	A
1	A	2732	G
1	A	2733	A
1	A	2744	G
1	A	2748	A
1	A	2751	G
1	A	2765	A
1	A	2778	A
1	A	2798	U
1	A	2818	U
1	A	2820	A
1	A	2821	A
1	A	2832	U
1	A	2835	A
1	A	2849	U

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Mol	Chain	Res	Type
1	A	2861	U
1	A	2867	G
1	A	2873	A
1	A	2879	A
1	A	2880	C
1	A	2884	U
1	A	2885	G
1	A	2886	A
1	A	2891	U
1	A	2901	C
1	A	2903	U
2	B	9	G
2	B	35	C
2	B	42	C
2	B	56	G
2	B	89	U
2	B	90	C
2	B	109	A
32	f	3	C
32	f	4	G
32	f	6	G
32	f	7	G
32	f	8	4SU
32	f	9	G
32	f	10	G
32	f	13	C
32	f	14	A
32	f	16	C
32	f	17	C
32	f	19	G
32	f	20	U
32	f	21	A
32	f	22	G
32	f	31	G
32	f	46	G
32	f	47	U
32	f	48	C
32	f	49	G
32	f	56	C
32	f	58	A
32	f	59	A
32	f	60	U

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Mol	Chain	Res	Type
32	f	61	C
32	f	62	C
32	f	64	G
32	f	67	C
32	f	68	C
32	f	69	C
32	f	70	G
32	f	76	A
33	g	3	G
33	g	4	G
33	g	6	U
33	g	7	U
33	g	8	U
33	g	10	2MG
33	g	11	C
33	g	12	U
33	g	13	C
33	g	14	A
33	g	15	G
33	g	16	H2U
33	g	17	H2U
33	g	18	G
33	g	19	G
33	g	20	G
33	g	21	A
33	g	22	G
33	g	23	A
33	g	24	G
33	g	25	C
33	g	28	C
33	g	31	A
33	g	33	U
33	g	34	OMG
33	g	35	A
33	g	36	A
33	g	38	A
33	g	39	PSU
33	g	40	5MC
33	g	43	G
33	g	45	G
33	g	46	7MG
33	g	47	U

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Mol	Chain	Res	Type
33	g	48	C
33	g	49	5MC
33	g	53	G
33	g	54	5MU
33	g	55	PSU
33	g	58	1MA
33	g	59	U
33	g	60	C
33	g	61	C
33	g	63	C
33	g	65	G
33	g	66	A
33	g	71	G
33	g	72	C
33	g	73	A
33	g	74	C

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	100	U
1	A	549	G
1	A	784	G
1	A	790	U
1	A	894	U
1	A	1046	A
1	A	1113	U
1	A	1494	A
1	A	1535	A
1	A	2099	U
1	A	2118	U
1	A	2127	G
1	A	2130	U
1	A	2158	A
1	A	2193	G
1	A	2406	A

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

45 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	PSU	A	2580	1	18,21,22	2.47	10 (55%)	22,30,33	1.90	5 (22%)
1	OMU	A	2552	1	19,22,23	2.68	7 (36%)	26,31,34	1.86	6 (23%)
33	M2G	g	26	33	24,27,28	1.32	4 (16%)	35,40,43	1.92	7 (20%)
33	7MG	g	46	33	22,26,27	2.13	4 (18%)	29,39,42	3.15	10 (34%)
33	5MU	g	54	33	19,22,23	1.54	3 (15%)	28,32,35	2.42	7 (25%)
1	G7M	A	2069	1	23,26,27	2.22	5 (21%)	35,39,42	1.60	6 (17%)
1	2MA	A	2503	1,34	22,25,26	1.69	4 (18%)	33,37,40	2.02	8 (24%)
33	5MC	g	40	33	18,22,23	1.27	1 (5%)	26,32,35	2.12	10 (38%)
32	4SU	f	8	32	18,21,22	3.20	5 (27%)	26,30,33	3.64	10 (38%)
1	OMG	A	2251	1,32	23,26,27	2.14	5 (21%)	33,38,41	1.79	8 (24%)
1	5MU	A	1939	1	19,22,23	2.67	7 (36%)	28,32,35	3.95	10 (35%)
1	PSU	A	1917	1	18,21,22	2.32	8 (44%)	22,30,33	1.82	4 (18%)
1	3TD	A	1915	1	18,22,23	6.42	12 (66%)	22,32,35	1.93	4 (18%)
1	6MZ	A	1618	1	22,25,26	2.87	3 (13%)	30,36,39	2.30	10 (33%)
33	YYG	g	37	33	37,42,43	2.39	10 (27%)	45,62,65	1.90	14 (31%)
33	OMC	g	32	33	19,22,23	1.39	3 (15%)	26,31,34	2.13	2 (7%)
4	MEQ	D	150[A]	4	8,9,10	0.95	0	5,10,12	0.66	0
1	2MG	A	2445	1	23,26,27	2.93	5 (21%)	32,38,41	2.11	11 (34%)
1	PSU	A	1911	1	18,21,22	2.32	8 (44%)	22,30,33	1.84	4 (18%)
33	5MC	g	49	33	18,22,23	1.07	2 (11%)	26,32,35	1.72	4 (15%)
32	5MU	f	54	32	19,22,23	1.65	3 (15%)	28,32,35	2.93	11 (39%)
33	2MG	g	10	33	23,26,27	1.66	6 (26%)	32,38,41	2.65	11 (34%)
1	2MG	A	1835	1	23,26,27	2.92	5 (21%)	32,38,41	2.17	11 (34%)
1	PSU	A	2605	1	18,21,22	2.39	8 (44%)	22,30,33	1.87	4 (18%)
1	5MC	A	1962	1	18,22,23	2.01	6 (33%)	26,32,35	1.16	2 (7%)
32	5MC	f	32	32	18,22,23	0.97	2 (11%)	26,32,35	1.29	3 (11%)
1	OMC	A	2498	1,34	19,22,23	1.90	6 (31%)	26,31,34	0.96	1 (3%)
33	31M	g	76	1	41,44,45	3.29	21 (51%)	51,61,64	2.62	20 (39%)
1	PSU	A	955	1	18,21,22	2.44	8 (44%)	22,30,33	1.85	4 (18%)
1	6MZ	A	2030	1	22,25,26	2.86	3 (13%)	30,36,39	2.50	10 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	PSU	g	39	33	18,21,22	1.84	5 (27%)	22,30,33	2.49	7 (31%)
1	PSU	A	2504	1	18,21,22	2.39	8 (44%)	22,30,33	1.89	4 (18%)
13	4D4	M	81	13	9,11,12	2.03	2 (22%)	8,13,15	2.10	4 (50%)
1	H2U	A	2449	1	18,21,22	4.07	5 (27%)	21,30,33	5.20	7 (33%)
33	1MA	g	58	33	21,25,26	1.90	6 (28%)	31,37,40	2.74	11 (35%)
32	PSU	f	55	32	18,21,22	1.31	2 (11%)	22,30,33	1.91	4 (18%)
1	PSU	A	2457	1	18,21,22	2.46	8 (44%)	22,30,33	1.90	4 (18%)
1	PSU	A	2604	1	18,21,22	2.40	8 (44%)	22,30,33	1.87	4 (18%)
1	PSU	A	746	1,34	18,21,22	2.37	9 (50%)	22,30,33	1.80	4 (18%)
1	5MU	A	747	1	19,22,23	2.58	7 (36%)	28,32,35	3.81	11 (39%)
33	H2U	g	16	33	18,21,22	0.99	2 (11%)	21,30,33	1.90	2 (9%)
33	PSU	g	55	33	18,21,22	2.22	6 (33%)	22,30,33	2.47	8 (36%)
33	H2U	g	17	33	18,21,22	1.01	2 (11%)	21,30,33	3.29	5 (23%)
1	1MG	A	745	1	22,26,27	2.41	5 (22%)	33,39,42	1.71	7 (21%)
33	OMG	g	34	33	23,26,27	1.61	5 (21%)	33,38,41	2.13	10 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	2580	1	-	0/7/25/26	0/2/2/2
1	OMU	A	2552	1	-	0/9/27/28	0/2/2/2
33	M2G	g	26	33	-	0/11/29/30	0/3/3/3
33	7MG	g	46	33	-	3/7/37/38	0/3/3/3
33	5MU	g	54	33	-	2/7/25/26	0/2/2/2
1	G7M	A	2069	1	-	1/7/25/26	0/3/3/3
1	2MA	A	2503	1,34	-	1/7/25/26	0/3/3/3
33	5MC	g	40	33	-	0/7/25/26	0/2/2/2
32	4SU	f	8	32	-	0/7/25/26	0/2/2/2
1	OMG	A	2251	1,32	-	1/9/27/28	0/3/3/3
1	5MU	A	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1917	1	-	0/7/25/26	0/2/2/2
1	3TD	A	1915	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	1618	1	-	0/9/27/28	0/3/3/3
33	YYG	g	37	33	-	16/24/42/43	0/4/4/4
33	OMC	g	32	33	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MEQ	D	150[A]	4	-	4/8/9/11	-
1	2MG	A	2445	1	-	2/9/27/28	0/3/3/3
1	PSU	A	1911	1	-	0/7/25/26	0/2/2/2
33	5MC	g	49	33	-	3/7/25/26	0/2/2/2
32	5MU	f	54	32	-	1/7/25/26	0/2/2/2
33	2MG	g	10	33	-	1/9/27/28	0/3/3/3
1	2MG	A	1835	1	-	0/9/27/28	0/3/3/3
1	PSU	A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	A	1962	1	-	2/7/25/26	0/2/2/2
32	5MC	f	32	32	-	0/7/25/26	0/2/2/2
1	OMC	A	2498	1,34	-	0/9/27/28	0/2/2/2
33	31M	g	76	1	-	6/31/49/50	0/4/4/4
1	PSU	A	955	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	2030	1	-	2/9/27/28	0/3/3/3
33	PSU	g	39	33	-	3/7/25/26	0/2/2/2
1	PSU	A	2504	1	-	2/7/25/26	0/2/2/2
13	4D4	M	81	13	-	3/11/12/14	-
1	H2U	A	2449	1	-	0/7/38/39	0/2/2/2
33	1MA	g	58	33	-	4/7/25/26	0/3/3/3
32	PSU	f	55	32	-	0/7/25/26	0/2/2/2
1	PSU	A	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2604	1	-	0/7/25/26	0/2/2/2
1	PSU	A	746	1,34	-	2/7/25/26	0/2/2/2
1	5MU	A	747	1	-	0/7/25/26	0/2/2/2
33	H2U	g	16	33	-	3/7/38/39	0/2/2/2
33	PSU	g	55	33	-	0/7/25/26	0/2/2/2
33	H2U	g	17	33	-	5/7/38/39	0/2/2/2
1	1MG	A	745	1	-	0/7/25/26	0/3/3/3
33	OMG	g	34	33	-	3/9/27/28	0/3/3/3

All (254) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1915	3TD	C2'-C1'	-18.07	1.30	1.53
1	A	1915	3TD	O4'-C1'	14.21	1.63	1.43
1	A	1618	6MZ	C6-N6	12.69	1.47	1.34
1	A	2030	6MZ	C6-N6	12.49	1.47	1.34
1	A	2449	H2U	O4-C4	10.10	1.43	1.23
1	A	1835	2MG	O6-C6	9.72	1.42	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2445	2MG	O6-C6	9.64	1.41	1.23
33	g	76	31M	O4'-C4'	-9.47	1.23	1.45
1	A	1915	3TD	O4-C4	8.29	1.40	1.23
32	f	8	4SU	C4-S4	-8.15	1.53	1.68
1	A	745	1MG	O6-C6	8.15	1.40	1.23
1	A	2449	H2U	C2-N1	8.08	1.47	1.35
1	A	2449	H2U	O2-C2	8.07	1.37	1.23
33	g	76	31M	C2'-C1'	-7.94	1.28	1.53
1	A	2552	OMU	O4-C4	7.89	1.39	1.24
1	A	1915	3TD	O4'-C4'	-7.63	1.28	1.45
32	f	8	4SU	C4-N3	-6.86	1.30	1.37
33	g	76	31M	O4'-C1'	6.71	1.57	1.42
1	A	2251	OMG	O6-C6	6.70	1.36	1.23
33	g	37	YYG	O23-C21	6.69	1.46	1.34
1	A	2069	G7M	O6-C6	6.60	1.36	1.23
1	A	1939	5MU	C2-N1	-6.47	1.28	1.38
33	g	46	7MG	C5-N7	-6.47	1.28	1.35
1	A	2449	H2U	C2-N3	6.14	1.48	1.38
1	A	747	5MU	C2-N1	-6.10	1.28	1.38
33	g	76	31M	C8-N9	-5.80	1.27	1.37
1	A	1835	2MG	C2-N2	5.69	1.46	1.33
1	A	2445	2MG	C2-N2	5.64	1.45	1.33
33	g	37	YYG	C6-N1	-5.50	1.29	1.42
32	f	8	4SU	C5-C4	-5.44	1.35	1.42
1	A	2503	2MA	C6-N6	5.41	1.47	1.34
1	A	1835	2MG	CM2-N2	5.35	1.55	1.45
33	g	37	YYG	O18-C16	5.25	1.46	1.33
1	A	2445	2MG	CM2-N2	5.22	1.54	1.45
33	g	58	1MA	C5-N7	-5.14	1.29	1.39
33	g	76	31M	O-C	-5.10	1.13	1.23
1	A	745	1MG	C2-N2	5.06	1.43	1.34
33	g	76	31M	O5'-C5'	-4.93	1.32	1.44
33	g	37	YYG	C2-N1	-4.89	1.31	1.38
33	g	76	31M	C5-N7	-4.86	1.29	1.39
1	A	2580	PSU	C1'-C5	-4.84	1.39	1.50
1	A	2604	PSU	C1'-C5	-4.81	1.39	1.50
1	A	2457	PSU	C1'-C5	-4.80	1.39	1.50
1	A	2069	G7M	C2-N2	4.76	1.45	1.34
13	M	81	4D4	CZ-NE	4.74	1.42	1.33
1	A	1939	5MU	C2-N3	-4.73	1.29	1.38
1	A	2449	H2U	C4-N3	4.73	1.45	1.37
33	g	55	PSU	C4-N3	-4.73	1.30	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1917	PSU	C1'-C5	-4.71	1.39	1.50
1	A	955	PSU	C1'-C5	-4.70	1.39	1.50
1	A	2605	PSU	C1'-C5	-4.69	1.39	1.50
1	A	746	PSU	C1'-C5	-4.68	1.39	1.50
1	A	2504	PSU	C1'-C5	-4.67	1.39	1.50
1	A	1911	PSU	C1'-C5	-4.66	1.39	1.50
32	f	8	4SU	C2-N3	-4.66	1.29	1.38
1	A	2498	OMC	C4-N4	4.65	1.44	1.33
1	A	1939	5MU	C6-N1	-4.62	1.30	1.38
33	g	37	YYG	C2-N3	-4.59	1.31	1.39
1	A	747	5MU	C2-N3	-4.58	1.29	1.38
1	A	2251	OMG	C6-N1	-4.57	1.30	1.38
1	A	2552	OMU	C2-N1	-4.55	1.31	1.38
1	A	2251	OMG	C2-N2	4.53	1.45	1.34
1	A	747	5MU	C6-N1	-4.46	1.30	1.38
33	g	76	31M	CTM-N	4.38	1.43	1.34
1	A	2445	2MG	C6-N1	-4.37	1.30	1.38
33	g	34	OMG	C6-N1	-4.36	1.30	1.38
33	g	46	7MG	C4-N9	-4.33	1.32	1.37
33	g	37	YYG	C5-N7	-4.31	1.30	1.39
33	g	55	PSU	C2-N3	-4.23	1.30	1.37
1	A	1835	2MG	C6-N1	-4.21	1.31	1.38
1	A	1962	5MC	C4-N4	4.17	1.45	1.34
32	f	54	5MU	C6-N1	-4.15	1.31	1.38
33	g	39	PSU	C2-N1	-4.13	1.31	1.36
33	g	46	7MG	C6-N1	-4.08	1.31	1.38
33	g	76	31M	C3'-N3'	-4.08	1.39	1.45
1	A	2457	PSU	C4-N3	-4.03	1.31	1.38
1	A	2580	PSU	C4-N3	-4.03	1.31	1.38
1	A	1962	5MC	C2-N1	-4.02	1.31	1.40
1	A	955	PSU	C2-N1	-4.01	1.31	1.36
1	A	2457	PSU	C2-N1	-3.96	1.31	1.36
1	A	955	PSU	C4-N3	-3.96	1.31	1.38
1	A	2605	PSU	C4-N3	-3.93	1.31	1.38
1	A	2069	G7M	C5-N7	-3.90	1.34	1.39
1	A	2504	PSU	C4-N3	-3.89	1.31	1.38
1	A	2580	PSU	C2-N1	-3.89	1.31	1.36
33	g	40	5MC	C6-N1	-3.88	1.31	1.38
1	A	2604	PSU	C4-N3	-3.86	1.31	1.38
1	A	2069	G7M	C6-N1	-3.86	1.31	1.38
1	A	2552	OMU	C4-N3	-3.83	1.31	1.38
1	A	1962	5MC	C6-N1	-3.83	1.31	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2504	PSU	C2-N1	-3.82	1.31	1.36
33	g	10	2MG	C5-N7	-3.80	1.31	1.39
1	A	2604	PSU	C2-N1	-3.80	1.31	1.36
1	A	2605	PSU	C2-N1	-3.79	1.31	1.36
1	A	746	PSU	C4-N3	-3.77	1.31	1.38
1	A	2457	PSU	C2-N3	-3.75	1.31	1.37
1	A	1911	PSU	C4-N3	-3.75	1.31	1.38
1	A	2605	PSU	C2-N3	-3.74	1.31	1.37
1	A	2552	OMU	C2-N3	-3.73	1.31	1.38
1	A	2498	OMC	C2-N1	-3.72	1.31	1.40
1	A	1917	PSU	C4-N3	-3.72	1.31	1.38
1	A	1915	3TD	O2'-C2'	3.71	1.51	1.43
1	A	746	PSU	C2-N1	-3.70	1.31	1.36
1	A	955	PSU	C2-N3	-3.69	1.31	1.37
1	A	2503	2MA	C8-N9	-3.67	1.30	1.37
1	A	2580	PSU	C2-N3	-3.66	1.31	1.37
1	A	1915	3TD	C4-N3	-3.66	1.32	1.40
1	A	2604	PSU	C2-N3	-3.65	1.31	1.37
1	A	1911	PSU	C2-N1	-3.64	1.31	1.36
33	g	58	1MA	C5-C4	3.63	1.48	1.38
1	A	2504	PSU	C2-N3	-3.63	1.31	1.37
1	A	745	1MG	C6-N1	-3.63	1.32	1.40
1	A	1917	PSU	C2-N1	-3.63	1.31	1.36
1	A	1915	3TD	C2-N1	-3.60	1.32	1.37
1	A	1939	5MU	C4-N3	-3.59	1.32	1.38
33	g	10	2MG	C6-N1	-3.57	1.32	1.38
1	A	746	PSU	C2-N3	-3.53	1.31	1.37
1	A	747	5MU	C6-C5	3.52	1.40	1.34
32	f	54	5MU	C4-N3	-3.52	1.32	1.38
1	A	1939	5MU	C6-C5	3.51	1.40	1.34
1	A	1917	PSU	C2-N3	-3.48	1.31	1.37
1	A	747	5MU	C4-N3	-3.47	1.32	1.38
1	A	2445	2MG	C2-N1	-3.46	1.31	1.36
33	g	55	PSU	C2-N1	-3.43	1.32	1.36
1	A	1911	PSU	C2-N3	-3.42	1.31	1.37
33	g	39	PSU	C4-N3	-3.40	1.32	1.38
1	A	1915	3TD	C6-C5	3.34	1.39	1.35
32	f	54	5MU	C2-N3	-3.31	1.32	1.38
33	g	76	31M	C4-N9	-3.29	1.30	1.37
33	g	54	5MU	C4-N3	-3.28	1.32	1.38
1	A	1835	2MG	C2-N1	-3.27	1.31	1.36
33	g	76	31M	C-N3'	3.25	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	g	34	OMG	C5-N7	-3.13	1.33	1.39
33	g	55	PSU	C6-N1	-3.08	1.31	1.36
33	g	54	5MU	C6-N1	-3.07	1.32	1.38
33	g	37	YYG	C4-N3	-3.05	1.31	1.38
33	g	54	5MU	C2-N3	-3.04	1.32	1.38
13	M	81	4D4	CZ-NH2	3.03	1.44	1.32
1	A	1962	5MC	O2-C2	-3.02	1.18	1.23
1	A	1939	5MU	O4-C4	-3.00	1.17	1.23
1	A	1939	5MU	O2-C2	-3.00	1.17	1.23
1	A	2498	OMC	O2-C2	-2.99	1.18	1.23
1	A	2605	PSU	O4-C4	-2.99	1.17	1.23
33	g	32	OMC	C6-N1	-2.98	1.30	1.38
1	A	2457	PSU	O4-C4	-2.98	1.17	1.23
33	g	46	7MG	C8-N9	-2.97	1.44	1.46
33	g	76	31M	C2-N3	-2.97	1.28	1.33
1	A	955	PSU	O4-C4	-2.97	1.17	1.23
1	A	747	5MU	O4-C4	-2.97	1.17	1.23
1	A	1911	PSU	C6-C5	2.95	1.38	1.35
33	g	55	PSU	C2'-C1'	-2.95	1.49	1.53
1	A	2580	PSU	O4-C4	-2.93	1.18	1.23
1	A	2030	6MZ	C8-N9	-2.93	1.32	1.37
33	g	26	M2G	C5-C4	2.93	1.46	1.38
1	A	1917	PSU	C6-C5	2.90	1.38	1.35
1	A	2504	PSU	C6-C5	2.90	1.38	1.35
1	A	747	5MU	O2-C2	-2.89	1.17	1.23
1	A	2503	2MA	C5-N7	-2.89	1.33	1.39
1	A	2604	PSU	O4-C4	-2.89	1.18	1.23
1	A	746	PSU	C6-C5	2.89	1.38	1.35
1	A	2504	PSU	O4-C4	-2.88	1.18	1.23
32	f	55	PSU	C6-C5	2.87	1.38	1.35
1	A	746	PSU	O4-C4	-2.85	1.18	1.23
33	g	76	31M	C2'-C3'	-2.84	1.48	1.53
1	A	2604	PSU	C6-C5	2.81	1.38	1.35
1	A	1618	6MZ	C8-N9	-2.79	1.32	1.37
1	A	2069	G7M	C2-N1	-2.78	1.30	1.37
1	A	955	PSU	C6-C5	2.77	1.38	1.35
1	A	1915	3TD	O3'-C3'	-2.75	1.36	1.43
33	g	26	M2G	C6-N1	-2.75	1.33	1.38
1	A	1911	PSU	O4-C4	-2.75	1.18	1.23
1	A	2580	PSU	C6-N1	-2.75	1.31	1.36
1	A	1915	3TD	C2-N3	-2.75	1.32	1.38
1	A	2580	PSU	C6-C5	2.74	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2457	PSU	C6-C5	2.74	1.38	1.35
1	A	2552	OMU	O2-C2	-2.72	1.18	1.23
1	A	2605	PSU	C6-C5	2.72	1.38	1.35
1	A	955	PSU	C6-N1	-2.72	1.31	1.36
33	g	76	31M	C6-N6	2.72	1.41	1.34
33	g	10	2MG	C2-N1	-2.71	1.32	1.36
32	f	32	5MC	C6-N1	-2.70	1.33	1.38
33	g	49	5MC	C6-N1	-2.66	1.33	1.38
1	A	2457	PSU	C6-N1	-2.65	1.31	1.36
1	A	1917	PSU	O4-C4	-2.64	1.18	1.23
33	g	17	H2U	C4-N3	-2.63	1.33	1.37
1	A	2605	PSU	C6-N1	-2.61	1.31	1.36
1	A	2604	PSU	C6-N1	-2.60	1.31	1.36
1	A	2457	PSU	O2-C2	-2.59	1.18	1.23
1	A	2504	PSU	C6-N1	-2.59	1.31	1.36
33	g	26	M2G	C2-N2	2.58	1.40	1.35
32	f	8	4SU	C6-N1	-2.58	1.31	1.38
33	g	39	PSU	C2-N3	-2.58	1.33	1.37
33	g	32	OMC	C5-C4	-2.58	1.37	1.42
33	g	58	1MA	C2-N1	-2.57	1.31	1.35
33	g	76	31M	C5-C4	-2.57	1.34	1.39
1	A	2580	PSU	O2-C2	-2.56	1.18	1.23
1	A	2552	OMU	C6-N1	-2.55	1.31	1.38
1	A	955	PSU	O2-C2	-2.55	1.18	1.23
1	A	1917	PSU	C6-N1	-2.54	1.32	1.36
1	A	2251	OMG	C8-N9	-2.53	1.31	1.37
33	g	16	H2U	C2-N3	-2.52	1.33	1.38
33	g	10	2MG	C2-N3	2.51	1.36	1.31
1	A	2498	OMC	C6-N1	-2.51	1.31	1.38
33	g	76	31M	C6-N1	-2.50	1.28	1.35
33	g	39	PSU	C6-N1	-2.49	1.32	1.36
1	A	1911	PSU	C6-N1	-2.49	1.32	1.36
33	g	39	PSU	C2'-C1'	-2.47	1.50	1.53
32	f	55	PSU	C4-N3	-2.47	1.34	1.38
33	g	16	H2U	C4-N3	-2.47	1.33	1.37
1	A	2605	PSU	O2-C2	-2.47	1.18	1.23
1	A	2504	PSU	O2-C2	-2.45	1.18	1.23
1	A	1962	5MC	C2-N3	-2.44	1.31	1.36
1	A	2604	PSU	O2-C2	-2.44	1.18	1.23
33	g	37	YYG	C11-N2	-2.43	1.33	1.38
1	A	2498	OMC	C2-N3	-2.42	1.31	1.36
1	A	746	PSU	C6-N1	-2.41	1.32	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2552	OMU	C5-C4	-2.41	1.38	1.43
33	g	76	31M	OTM-CTM	-2.40	1.18	1.23
1	A	745	1MG	C5-C6	-2.38	1.39	1.45
1	A	1917	PSU	O2-C2	-2.38	1.18	1.23
33	g	10	2MG	C8-N9	-2.37	1.32	1.37
32	f	32	5MC	C6-C5	2.35	1.38	1.34
1	A	745	1MG	C5-N7	-2.35	1.34	1.39
1	A	1911	PSU	O2-C2	-2.34	1.18	1.23
33	g	34	OMG	C4-N9	-2.34	1.32	1.38
33	g	17	H2U	C2-N3	-2.34	1.33	1.38
1	A	746	PSU	O2-C2	-2.34	1.18	1.23
1	A	2580	PSU	O4'-C1'	-2.30	1.40	1.43
33	g	10	2MG	C5-C4	2.28	1.45	1.38
33	g	34	OMG	C2-N1	-2.28	1.32	1.37
33	g	58	1MA	C6-N6	2.27	1.33	1.28
33	g	58	1MA	C4-N9	-2.27	1.32	1.38
33	g	58	1MA	C4-N3	-2.27	1.31	1.35
1	A	1915	3TD	C6-N1	-2.25	1.32	1.36
33	g	76	31M	C8-N7	-2.24	1.27	1.31
33	g	55	PSU	C1'-C5	-2.23	1.45	1.50
1	A	1962	5MC	C6-C5	2.22	1.38	1.34
1	A	1915	3TD	O2-C2	-2.22	1.19	1.23
33	g	32	OMC	C2-N3	-2.21	1.31	1.36
33	g	37	YYG	C5-C4	2.20	1.45	1.38
33	g	26	M2G	C5-N7	-2.18	1.34	1.39
1	A	746	PSU	O4'-C1'	-2.18	1.40	1.43
33	g	34	OMG	C5-C4	2.17	1.44	1.38
1	A	2503	2MA	C6-N1	-2.15	1.31	1.35
33	g	37	YYG	C4-N9	-2.14	1.31	1.38
33	g	76	31M	CE1-CD1	-2.11	1.34	1.38
33	g	49	5MC	C6-C5	2.11	1.38	1.34
1	A	2030	6MZ	C5-N7	-2.10	1.35	1.39
33	g	76	31M	O2'-C2'	2.09	1.47	1.43
33	g	76	31M	C2-N1	-2.08	1.30	1.33
1	A	2251	OMG	C5-N7	-2.05	1.35	1.39
1	A	1618	6MZ	C5-N7	-2.03	1.35	1.39
1	A	2580	PSU	C4-C5	-2.01	1.38	1.44
1	A	2498	OMC	C5-C4	-2.00	1.38	1.42

All (309) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2449	H2U	C4-N3-C2	-15.23	113.16	125.79
33	g	17	H2U	C4-N3-C2	-13.77	114.37	125.79
1	A	2449	H2U	O2-C2-N1	-11.49	108.68	123.11
33	g	46	7MG	N9-C4-N3	10.82	141.66	125.47
32	f	8	4SU	C4-N3-C2	-10.44	117.20	127.34
32	f	8	4SU	C5-C4-N3	10.31	124.25	114.69
33	g	32	OMC	C2'-C1'-N1	-9.28	96.21	114.22
1	A	1939	5MU	C4-N3-C2	-9.13	115.53	127.35
32	f	54	5MU	O4-C4-C5	-8.97	114.50	124.90
1	A	747	5MU	C4-N3-C2	-8.56	116.27	127.35
1	A	747	5MU	C5M-C5-C4	8.48	128.10	118.77
1	A	1939	5MU	N3-C2-N1	8.44	126.09	114.89
1	A	1939	5MU	C5-C6-N1	-8.33	114.77	123.34
1	A	747	5MU	N3-C2-N1	8.22	125.80	114.89
1	A	1939	5MU	C5M-C5-C4	8.09	127.67	118.77
1	A	2449	H2U	O4-C4-N3	-7.92	107.72	120.28
33	g	10	2MG	C5-C4-N3	-7.51	116.27	128.46
33	g	10	2MG	C2-N3-C4	7.44	121.26	112.04
33	g	55	PSU	N1-C2-N3	7.43	123.55	115.13
1	A	2503	2MA	C5-C4-N3	-7.37	118.90	127.19
1	A	747	5MU	C5-C6-N1	-7.32	115.81	123.34
1	A	2449	H2U	O2-C2-N3	-7.19	108.11	121.50
33	g	58	1MA	C2'-C1'-N9	7.04	133.16	113.22
33	g	16	H2U	C4-N3-C2	-6.92	120.05	125.79
1	A	1939	5MU	C5-C4-N3	6.87	121.18	115.31
1	A	1915	3TD	N1-C2-N3	6.71	121.43	116.14
1	A	1835	2MG	C2-N3-C4	6.64	120.27	112.04
33	g	10	2MG	N9-C4-N3	6.61	139.20	125.94
33	g	46	7MG	N9-C8-N7	-6.57	93.97	103.38
1	A	747	5MU	C5M-C5-C6	-6.57	114.07	122.85
1	A	2449	H2U	O4-C4-C5	-6.54	108.19	122.17
1	A	1939	5MU	C5M-C5-C6	-6.51	114.16	122.85
1	A	2030	6MZ	C9-N6-C6	-6.46	117.30	122.87
1	A	747	5MU	C5-C4-N3	6.46	120.83	115.31
33	g	34	OMG	C5-C4-N3	-6.41	118.06	128.46
1	A	2445	2MG	C2-N3-C4	6.38	119.94	112.04
33	g	26	M2G	C5-C4-N3	-6.33	118.19	128.46
33	g	46	7MG	C5-C4-N3	-6.33	116.07	128.13
33	g	76	31M	C5-C4-N3	-6.31	118.52	126.75
32	f	8	4SU	C5-C4-S4	-6.21	116.46	124.47
32	f	54	5MU	C4-N3-C2	-6.08	119.48	127.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2449	H2U	N3-C2-N1	-6.07	110.24	116.65
33	g	54	5MU	C5-C4-N3	5.97	120.40	115.31
33	g	54	5MU	C4-N3-C2	-5.93	119.68	127.35
33	g	58	1MA	C5-C4-N3	-5.90	118.47	127.26
32	f	55	PSU	N1-C2-N3	5.78	121.68	115.13
1	A	2580	PSU	N1-C2-N3	5.74	121.64	115.13
1	A	2504	PSU	N1-C2-N3	5.72	121.61	115.13
1	A	2457	PSU	N1-C2-N3	5.71	121.60	115.13
1	A	2251	OMG	C5-C4-N3	-5.70	119.22	128.46
1	A	1835	2MG	C5-C4-N3	-5.68	119.24	128.46
32	f	54	5MU	N3-C2-N1	5.67	122.42	114.89
1	A	2445	2MG	C5-C4-N3	-5.62	119.34	128.46
1	A	2604	PSU	N1-C2-N3	5.62	121.50	115.13
1	A	955	PSU	N1-C2-N3	5.57	121.44	115.13
1	A	1917	PSU	N1-C2-N3	5.56	121.44	115.13
1	A	2605	PSU	N1-C2-N3	5.56	121.42	115.13
33	g	76	31M	C5-N7-C8	5.55	111.39	103.51
1	A	2552	OMU	N3-C2-N1	5.51	122.21	114.89
1	A	1911	PSU	N1-C2-N3	5.51	121.37	115.13
1	A	2503	2MA	N3-C4-N9	5.50	134.62	126.99
33	g	39	PSU	N1-C2-N3	5.44	121.29	115.13
32	f	8	4SU	N3-C2-N1	5.43	122.10	114.89
1	A	746	PSU	N1-C2-N3	5.43	121.28	115.13
33	g	76	31M	C4-C5-N7	-5.41	104.03	110.62
33	g	76	31M	N1-C2-N3	-5.40	120.15	128.60
32	f	54	5MU	C5-C4-N3	5.40	119.92	115.31
1	A	1618	6MZ	C5-C4-N3	-5.40	119.71	126.75
1	A	745	1MG	C5-C4-N3	-5.31	119.85	128.46
33	g	76	31M	O4'-C1'-N9	5.29	118.48	108.06
33	g	58	1MA	C1'-N9-C4	5.16	141.83	126.50
33	g	54	5MU	N3-C2-N1	5.05	121.60	114.89
33	g	40	5MC	O2-C2-N3	-5.02	114.16	122.33
33	g	34	OMG	N9-C4-N3	5.01	136.00	125.94
1	A	2030	6MZ	C5-C4-N3	-4.99	120.24	126.75
33	g	26	M2G	N9-C4-N3	4.92	135.81	125.94
33	g	54	5MU	O4-C4-C5	-4.90	119.23	124.90
33	g	39	PSU	O2-C2-N1	-4.88	117.41	122.79
1	A	2030	6MZ	N1-C2-N3	-4.87	120.99	128.60
33	g	55	PSU	C4-N3-C2	-4.76	119.48	126.34
1	A	2552	OMU	C4-N3-C2	-4.76	120.31	126.58
1	A	1618	6MZ	C9-N6-C6	-4.75	118.78	122.87
33	g	49	5MC	C5-C6-N1	-4.69	118.51	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	76	31M	C2-N3-C4	4.68	122.81	111.75
33	g	58	1MA	C1'-N9-C8	-4.67	113.42	126.70
1	A	1618	6MZ	N1-C2-N3	-4.66	121.31	128.60
33	g	39	PSU	C4-N3-C2	-4.66	119.63	126.34
33	g	34	OMG	C2-N3-C4	4.56	120.43	112.30
33	g	39	PSU	C6-C5-C4	-4.53	115.03	118.20
33	g	58	1MA	N1-C2-N3	4.47	131.30	126.00
33	g	26	M2G	C2-N3-C4	4.44	120.71	112.51
33	g	76	31M	CB-CA-C	-4.38	98.88	110.25
33	g	37	YYG	N9-C4-N3	4.38	136.68	129.44
33	g	76	31M	N9-C8-N7	-4.36	107.96	113.91
1	A	2069	G7M	C2-N3-C4	4.33	120.01	112.30
33	g	46	7MG	C2-N3-C4	4.32	120.00	112.30
32	f	32	5MC	C5-C6-N1	-4.29	118.92	123.34
1	A	1939	5MU	O2-C2-N1	-4.24	117.15	122.79
1	A	1962	5MC	C5-C6-N1	-4.23	118.99	123.34
1	A	2251	OMG	C2-N3-C4	4.22	119.82	112.30
33	g	58	1MA	O4'-C1'-C2'	-4.16	97.57	106.64
1	A	2605	PSU	C4-N3-C2	-4.12	120.40	126.34
1	A	745	1MG	N9-C4-N3	4.11	134.19	125.94
1	A	2457	PSU	C4-N3-C2	-4.09	120.44	126.34
1	A	1835	2MG	N9-C4-N3	4.09	134.15	125.94
1	A	746	PSU	C4-N3-C2	-4.06	120.50	126.34
1	A	2604	PSU	C4-N3-C2	-4.05	120.50	126.34
1	A	2504	PSU	C4-N3-C2	-4.04	120.51	126.34
1	A	2445	2MG	N9-C4-N3	4.03	134.02	125.94
32	f	55	PSU	C4-N3-C2	-4.02	120.54	126.34
1	A	2251	OMG	N9-C4-N3	4.02	134.02	125.94
1	A	1939	5MU	O4-C4-N3	-4.00	112.44	120.12
1	A	955	PSU	C4-N3-C2	-3.92	120.68	126.34
1	A	1911	PSU	C4-N3-C2	-3.92	120.69	126.34
1	A	1917	PSU	C4-N3-C2	-3.90	120.72	126.34
1	A	2580	PSU	C4-N3-C2	-3.89	120.73	126.34
33	g	76	31M	N3-C4-N9	3.89	133.49	127.08
1	A	747	5MU	O4-C4-N3	-3.87	112.69	120.12
1	A	1618	6MZ	C2-N3-C4	3.86	120.87	111.75
1	A	1618	6MZ	N3-C4-N9	3.85	133.43	127.08
1	A	2030	6MZ	C2-N3-C4	3.85	120.84	111.75
1	A	2030	6MZ	N9-C8-N7	-3.84	108.66	113.91
1	A	2069	G7M	C5-C4-N3	-3.76	120.94	128.15
33	g	49	5MC	O2-C2-N3	-3.72	116.28	122.33
33	g	49	5MC	C2'-C1'-N1	-3.68	102.80	113.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	g	76	31M	CA-C-N3'	3.67	124.74	116.70
1	A	2030	6MZ	C5-N7-C8	3.66	108.72	103.51
1	A	1835	2MG	C2-N1-C6	-3.66	120.27	124.48
33	g	58	1MA	N9-C4-N3	3.65	135.45	126.94
33	g	54	5MU	C5-C6-N1	-3.65	119.58	123.34
1	A	2069	G7M	C6-C5-N7	3.63	136.63	132.25
1	A	1915	3TD	C4-N3-C2	-3.63	120.67	124.61
33	g	37	YYG	C10-C11-N2	3.62	126.73	119.38
13	M	81	4D4	NE-CZ-NH2	-3.60	114.37	120.70
32	f	54	5MU	O2-C2-N1	-3.60	118.01	122.79
1	A	2030	6MZ	C6-C5-N7	3.57	136.25	132.39
33	g	58	1MA	C2'-C3'-C4'	-3.52	95.80	102.64
33	g	37	YYG	C24-O23-C21	3.52	119.82	115.66
33	g	46	7MG	C5-C6-N1	3.48	117.12	110.99
1	A	747	5MU	O2-C2-N1	-3.46	118.19	122.79
1	A	745	1MG	C2-N3-C4	3.44	119.72	111.98
1	A	2445	2MG	C2-N1-C6	-3.44	120.52	124.48
33	g	76	31M	O-C-N3'	-3.42	116.60	122.93
32	f	55	PSU	O2-C2-N1	-3.42	119.03	122.79
33	g	37	YYG	C2'-C3'-C4'	-3.40	96.04	102.64
33	g	55	PSU	O2-C2-N1	-3.39	119.06	122.79
1	A	1618	6MZ	N9-C8-N7	-3.35	109.33	113.91
33	g	37	YYG	O18-C16-C15	3.35	120.09	111.52
1	A	2030	6MZ	N3-C4-N9	3.31	132.54	127.08
33	g	17	H2U	C5-C4-N3	-3.31	112.93	116.65
1	A	1618	6MZ	C5-N7-C8	3.30	108.19	103.51
33	g	55	PSU	C3'-C2'-C1'	3.30	105.48	101.64
1	A	2504	PSU	O2-C2-N1	-3.29	119.17	122.79
1	A	2030	6MZ	C4-C5-N7	-3.28	106.62	110.62
33	g	39	PSU	O4-C4-C5	-3.25	115.53	124.05
1	A	2069	G7M	C5-C6-N1	3.24	118.55	111.79
1	A	955	PSU	O2-C2-N1	-3.24	119.23	122.79
33	g	40	5MC	O4'-C1'-N1	3.23	115.75	108.36
33	g	10	2MG	O2'-C2'-C3'	-3.18	101.54	111.82
1	A	2580	PSU	O2-C2-N1	-3.17	119.30	122.79
33	g	37	YYG	C19-O18-C16	3.17	123.11	115.94
13	M	81	4D4	NH1-CZ-NE	3.16	126.48	119.19
33	g	46	7MG	C5-C4-N9	-3.15	102.26	106.35
1	A	2457	PSU	O2-C2-N1	-3.14	119.34	122.79
32	f	8	4SU	O2'-C2'-C1'	-3.09	99.69	110.02
33	g	76	31M	C6-C5-N7	3.07	137.74	132.02
33	g	40	5MC	C5-C6-N1	-3.07	120.18	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1911	PSU	O2-C2-N1	-3.05	119.44	122.79
1	A	2552	OMU	O2-C2-N1	-3.04	118.74	122.79
1	A	746	PSU	O2-C2-N1	-3.03	119.45	122.79
1	A	1917	PSU	O2-C2-N1	-3.01	119.48	122.79
1	A	747	5MU	C1'-N1-C6	-2.98	116.17	121.12
33	g	10	2MG	C2-N1-C6	-2.96	121.07	124.48
1	A	747	5MU	O2-C2-N3	-2.95	116.01	121.50
1	A	2069	G7M	N9-C4-N3	2.95	131.86	125.94
33	g	55	PSU	C5-C6-N1	-2.94	117.70	122.11
1	A	1939	5MU	C6-N1-C2	2.93	124.27	121.30
32	f	8	4SU	C3'-C2'-C1'	2.92	106.98	101.43
1	A	2604	PSU	O2-C2-N1	-2.92	119.58	122.79
33	g	46	7MG	C2-N1-C6	-2.89	119.82	125.10
1	A	2498	OMC	O2-C2-N3	-2.89	117.62	122.33
1	A	2069	G7M	O6-C6-C5	-2.89	121.53	128.06
33	g	46	7MG	O6-C6-C5	-2.89	120.45	127.54
33	g	34	OMG	C4'-O4'-C1'	2.89	115.84	109.47
32	f	54	5MU	O4-C4-N3	2.85	125.57	120.12
1	A	1618	6MZ	C4-C5-N7	-2.84	107.16	110.62
1	A	1915	3TD	C3'-C2'-C1'	2.84	104.94	101.64
33	g	40	5MC	C1'-N1-C2	2.83	124.74	118.42
33	g	40	5MC	C1'-N1-C6	-2.82	116.42	121.12
32	f	54	5MU	O3'-C3'-C2'	2.82	120.96	111.82
1	A	2605	PSU	O2-C2-N1	-2.81	119.69	122.79
1	A	2030	6MZ	C4-N9-C8	2.81	108.77	105.73
33	g	26	M2G	C6-C5-N7	2.78	135.43	130.25
33	g	55	PSU	O2'-C2'-C1'	-2.75	104.68	111.23
33	g	37	YYG	C2'-C1'-N9	-2.75	105.43	113.22
33	g	37	YYG	O4'-C1'-C2'	-2.74	100.67	106.64
33	g	32	OMC	C5-C6-N1	-2.74	117.22	121.81
33	g	49	5MC	C5'-C4'-C3'	-2.74	104.93	115.18
33	g	46	7MG	O4'-C1'-N9	2.73	113.01	109.30
32	f	8	4SU	C6-C5-C4	-2.71	117.60	119.95
33	g	76	31M	C4-N9-C8	2.69	108.65	105.73
33	g	58	1MA	O4'-C1'-N9	-2.68	102.24	108.36
1	A	2552	OMU	C5-C6-N1	-2.67	117.33	121.81
1	A	1618	6MZ	C6-C5-N7	2.66	135.27	132.39
33	g	10	2MG	O3'-C3'-C4'	2.65	118.72	111.05
33	g	76	31M	CEM-SDM-CGM	2.64	109.48	100.40
33	g	17	H2U	C2'-C3'-C4'	2.64	107.77	102.64
32	f	8	4SU	O2-C2-N3	-2.63	116.60	121.50
1	A	2503	2MA	N6-C6-N1	2.62	120.73	117.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2552	OMU	C5-C4-N3	2.62	118.76	114.84
33	g	39	PSU	C5'-C4'-C3'	-2.62	105.38	115.18
33	g	37	YYG	N1-C2-N2	-2.61	110.30	114.03
32	f	32	5MC	C5-C4-N3	-2.61	118.86	121.67
33	g	26	M2G	C2'-C1'-N9	-2.60	105.86	113.22
33	g	34	OMG	C3'-C2'-C1'	2.60	107.77	102.89
33	g	26	M2G	C4-C5-N7	-2.57	106.65	110.72
33	g	37	YYG	C3'-C2'-C1'	2.56	106.28	101.43
1	A	1939	5MU	O2-C2-N3	-2.55	116.75	121.50
33	g	76	31M	CB-CA-N	-2.53	105.46	110.79
1	A	1618	6MZ	C4-N9-C8	2.53	108.47	105.73
1	A	2503	2MA	C5-N7-C8	2.51	107.08	103.51
33	g	10	2MG	C1'-N9-C8	-2.51	119.56	126.70
1	A	2552	OMU	O4-C4-C5	-2.51	120.75	125.16
1	A	1835	2MG	C5-C6-N1	2.51	119.56	113.19
1	A	2457	PSU	C5-C6-N1	-2.51	118.35	122.11
33	g	16	H2U	C3'-C2'-C1'	2.50	106.17	101.43
33	g	17	H2U	O4-C4-N3	2.49	124.23	120.28
33	g	76	31M	C2'-C1'-N9	-2.48	107.01	113.30
1	A	745	1MG	N9-C8-N7	-2.48	108.72	113.39
1	A	2503	2MA	N9-C8-N7	-2.47	110.54	113.91
1	A	2604	PSU	C5-C6-N1	-2.47	118.41	122.11
1	A	746	PSU	C5-C6-N1	-2.46	118.42	122.11
1	A	2605	PSU	C5-C6-N1	-2.46	118.42	122.11
1	A	1835	2MG	C6-C5-N7	2.46	134.82	130.25
13	M	81	4D4	CB-CA-C	-2.45	107.85	111.77
33	g	37	YYG	O23-C21-N20	2.44	115.08	110.80
33	g	34	OMG	O4'-C1'-C2'	-2.43	102.31	106.57
1	A	2445	2MG	C6-C5-N7	2.41	134.73	130.25
33	g	40	5MC	C5-C4-N3	-2.41	119.08	121.67
33	g	40	5MC	O4'-C4'-C5'	2.40	117.27	109.37
33	g	34	OMG	C2-N1-C6	-2.38	120.75	125.10
1	A	2445	2MG	C5-C6-N1	2.38	119.24	113.19
33	g	37	YYG	O18-C16-O17	-2.37	119.20	123.84
33	g	55	PSU	O2-C2-N3	-2.35	117.39	121.82
1	A	2251	OMG	C4-C5-N7	-2.33	107.03	110.72
1	A	1911	PSU	C5-C6-N1	-2.33	118.61	122.11
1	A	2449	H2U	C5-C4-N3	-2.33	114.03	116.65
33	g	40	5MC	O2'-C2'-C1'	-2.33	102.24	110.02
33	g	39	PSU	O5'-C5'-C4'	2.32	116.90	108.99
33	g	10	2MG	C8-N7-C5	2.32	108.44	104.24
33	g	34	OMG	C6-C5-N7	2.32	134.56	130.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2504	PSU	C5-C6-N1	-2.30	118.65	122.11
1	A	1835	2MG	O6-C6-C5	-2.30	120.49	126.60
1	A	2445	2MG	C4-C5-N7	-2.30	107.08	110.72
1	A	2251	OMG	C8-N7-C5	2.30	108.40	104.24
33	g	40	5MC	N1-C2-N3	2.28	122.96	118.81
1	A	1835	2MG	N9-C8-N7	-2.27	109.12	113.39
33	g	34	OMG	O6-C6-C5	-2.26	120.61	126.60
1	A	1835	2MG	C4-C5-N7	-2.26	107.15	110.72
1	A	1917	PSU	C5-C6-N1	-2.25	118.73	122.11
1	A	2445	2MG	N9-C8-N7	-2.25	109.15	113.39
32	f	54	5MU	C5-C6-N1	-2.25	121.03	123.34
32	f	32	5MC	CM5-C5-C6	-2.25	119.85	122.85
1	A	2445	2MG	CM2-N2-C2	-2.24	118.91	123.86
32	f	54	5MU	C6-N1-C2	-2.24	119.03	121.30
1	A	2445	2MG	O6-C6-C5	-2.23	120.67	126.60
33	g	37	YYG	C14-C13-C12	-2.23	108.38	113.32
33	g	58	1MA	O2'-C2'-C3'	-2.23	104.61	111.82
1	A	2580	PSU	C5-C6-N1	-2.21	118.79	122.11
33	g	40	5MC	O4'-C4'-C3'	-2.21	100.74	105.11
1	A	955	PSU	C5-C6-N1	-2.21	118.80	122.11
1	A	2503	2MA	C4-C5-N7	-2.20	107.94	110.62
1	A	1835	2MG	CM2-N2-C2	-2.20	119.00	123.86
33	g	10	2MG	C4-C5-N7	-2.19	107.26	110.72
1	A	2503	2MA	N3-C2-N1	-2.19	121.70	125.72
1	A	2580	PSU	O4'-C1'-C2'	2.19	108.23	105.14
1	A	1835	2MG	C8-N7-C5	2.18	108.19	104.24
1	A	745	1MG	C8-N7-C5	2.18	108.19	104.24
33	g	26	M2G	O6-C6-C5	-2.16	120.86	126.60
1	A	2445	2MG	C8-N7-C5	2.16	108.14	104.24
1	A	2251	OMG	N9-C8-N7	-2.16	109.33	113.39
33	g	76	31M	OTM-CTM-N	-2.15	118.94	122.93
33	g	76	31M	C2-N1-C6	2.15	122.46	118.77
32	f	55	PSU	C5-C6-N1	-2.14	118.90	122.11
1	A	747	5MU	C6-N1-C2	2.13	123.45	121.30
33	g	10	2MG	C5-C6-N1	2.13	118.59	113.19
33	g	55	PSU	O4'-C4'-C3'	-2.13	100.91	105.11
33	g	34	OMG	C5-C6-N1	2.12	118.57	113.19
33	g	10	2MG	O6-C6-C5	-2.12	120.98	126.60
33	g	46	7MG	C5'-C4'-C3'	-2.12	107.25	115.18
33	g	54	5MU	O2-C2-N1	-2.12	119.97	122.79
1	A	745	1MG	C6-C5-N7	2.11	134.13	129.35
1	A	2251	OMG	O6-C6-C5	-2.11	121.00	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	745	1MG	C5-C6-N1	2.11	118.98	114.91
33	g	37	YYG	O23-C21-O22	-2.10	121.49	124.58
13	M	81	4D4	O-C-CA	-2.10	119.27	124.78
32	f	54	5MU	C1'-N1-C2	2.10	121.38	117.57
33	g	76	31M	CBM-CAM-CTM	2.08	115.35	110.85
33	g	17	H2U	C4'-O4'-C1'	2.08	114.06	109.47
1	A	2503	2MA	C4-N9-C8	2.07	107.97	105.73
32	f	8	4SU	C2'-C1'-N1	-2.05	107.41	113.22
33	g	58	1MA	C3'-C2'-C1'	-2.04	97.55	101.43
1	A	2251	OMG	C2-N1-C6	-2.03	121.40	125.10
1	A	1915	3TD	C5-C6-N1	-2.03	119.06	122.11
32	f	54	5MU	O2'-C2'-C1'	-2.03	103.24	110.02
32	f	8	4SU	O5'-C5'-C4'	2.03	115.89	108.99
1	A	1962	5MC	C5-C4-N3	-2.02	119.50	121.67
33	g	54	5MU	C2'-C1'-N1	-2.01	107.51	113.22
33	g	76	31M	C-CA-N	2.01	116.63	111.16

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	150[A]	MEQ	N-CA-CB-CG
13	M	81	4D4	NE-CD-CG-CB
1	A	746	PSU	C2'-C1'-C5-C4
1	A	2251	OMG	C1'-C2'-O2'-CM2
33	g	17	H2U	O4'-C1'-N1-C6
33	g	34	OMG	O4'-C4'-C5'-O5'
33	g	34	OMG	C1'-C2'-O2'-CM2
33	g	37	YYG	C13-C14-C15-N20
33	g	37	YYG	C15-C16-O18-C19
33	g	37	YYG	O23-C21-N20-C15
33	g	37	YYG	N20-C21-O23-C24
33	g	37	YYG	O22-C21-O23-C24
33	g	39	PSU	C3'-C4'-C5'-O5'
33	g	46	7MG	O4'-C4'-C5'-O5'
33	g	49	5MC	O4'-C4'-C5'-O5'
33	g	49	5MC	C3'-C4'-C5'-O5'
33	g	54	5MU	C3'-C4'-C5'-O5'
33	g	54	5MU	O4'-C4'-C5'-O5'
33	g	76	31M	CTM-CAM-CBM-CGM
33	g	76	31M	NM-CAM-CBM-CGM
33	g	37	YYG	O17-C16-O18-C19

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Mol	Chain	Res	Type	Atoms
33	g	37	YYG	O22-C21-N20-C15
1	A	2030	6MZ	O4'-C4'-C5'-O5'
1	A	2030	6MZ	C3'-C4'-C5'-O5'
1	A	2445	2MG	C3'-C4'-C5'-O5'
1	A	2504	PSU	O4'-C4'-C5'-O5'
33	g	16	H2U	C3'-C4'-C5'-O5'
33	g	34	OMG	C3'-C4'-C5'-O5'
33	g	46	7MG	C3'-C4'-C5'-O5'
33	g	58	1MA	O4'-C4'-C5'-O5'
33	g	76	31M	CBM-CGM-SDM-CEM
1	A	2504	PSU	C3'-C4'-C5'-O5'
33	g	39	PSU	O4'-C4'-C5'-O5'
33	g	37	YYG	C12-C13-C14-C15
33	g	58	1MA	C3'-C4'-C5'-O5'
33	g	58	1MA	C2'-C1'-N9-C4
1	A	2445	2MG	O4'-C4'-C5'-O5'
33	g	37	YYG	O4'-C4'-C5'-O5'
13	M	81	4D4	OB-CB-CG-CD
33	g	37	YYG	C13-C14-C15-C16
4	D	150[A]	MEQ	C-CA-CB-CG
13	M	81	4D4	CA-CB-CG-CD
33	g	37	YYG	N20-C15-C16-O17
33	g	37	YYG	C16-C15-N20-C21
33	g	16	H2U	O4'-C4'-C5'-O5'
33	g	37	YYG	C3'-C4'-C5'-O5'
4	D	150[A]	MEQ	OE1-CD-CG-CB
33	g	37	YYG	N20-C15-C16-O18
33	g	17	H2U	C4'-C5'-O5'-P
4	D	150[A]	MEQ	NE2-CD-CG-CB
33	g	46	7MG	C2'-C1'-N9-C8
33	g	16	H2U	C4'-C5'-O5'-P
33	g	39	PSU	C4'-C5'-O5'-P
33	g	58	1MA	C2'-C1'-N9-C8
33	g	76	31M	CAM-CBM-CGM-SDM
33	g	76	31M	CA-CB-CG-CD1
33	g	17	H2U	O4'-C1'-N1-C2
1	A	1962	5MC	C2'-C1'-N1-C6
1	A	2503	2MA	O4'-C4'-C5'-O5'
1	A	1962	5MC	O4'-C1'-N1-C6
32	f	54	5MU	O4'-C4'-C5'-O5'
33	g	17	H2U	C3'-C4'-C5'-O5'
33	g	76	31M	CA-CB-CG-CD2

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Mol	Chain	Res	Type	Atoms
33	g	37	YYG	N1-C12-C13-C14
33	g	37	YYG	C11-C12-C13-C14
1	A	746	PSU	O4'-C1'-C5-C6
33	g	10	2MG	C2'-C1'-N9-C4
1	A	2069	G7M	O4'-C4'-C5'-O5'
33	g	17	H2U	C2'-C1'-N1-C2
33	g	49	5MC	C2'-C1'-N1-C2

There are no ring outliers.

18 monomers are involved in 62 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	g	26	M2G	4	0
33	g	54	5MU	6	0
1	A	2251	OMG	1	0
1	A	1939	5MU	1	0
1	A	1915	3TD	3	0
33	g	37	YYG	8	0
33	g	32	OMC	2	0
33	g	49	5MC	2	0
32	f	54	5MU	2	0
33	g	10	2MG	5	0
33	g	76	31M	18	0
1	A	2030	6MZ	2	0
33	g	39	PSU	4	0
33	g	58	1MA	1	0
32	f	55	PSU	1	0
1	A	2604	PSU	1	0
33	g	16	H2U	2	0
33	g	34	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 179 ligands modelled in this entry, 178 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	DI0	A	3175	-	58,61,61	1.62	11 (18%)	77,92,92	1.65	20 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	DI0	A	3175	-	-	10/70/121/121	0/3/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	A	3175	DI0	CAF-CAE	-5.60	1.39	1.51
35	A	3175	DI0	OBI-CAG	-4.12	1.33	1.43
35	A	3175	DI0	OAU-CBG	-3.41	1.38	1.44
35	A	3175	DI0	OAY-CAC	-3.13	1.35	1.43
35	A	3175	DI0	CBC-CBB	2.86	1.58	1.54
35	A	3175	DI0	OAU-CAB	-2.79	1.34	1.41
35	A	3175	DI0	CAP-CAH	2.66	1.60	1.55
35	A	3175	DI0	CAI-CAK	2.49	1.57	1.54
35	A	3175	DI0	CAD-CAW	-2.49	1.50	1.54
35	A	3175	DI0	OBJ-CAP	-2.28	1.40	1.44
35	A	3175	DI0	OBL-CAX	-2.25	1.38	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	3175	DI0	OAL-CAW-CBT	4.88	116.70	107.40
35	A	3175	DI0	CBT-CAW-CAD	-4.69	106.31	115.20
35	A	3175	DI0	OBK-CAN-CAX	4.22	110.07	103.81
35	A	3175	DI0	CAP-CAH-CAJ	-3.35	109.30	114.05
35	A	3175	DI0	CBR-CAP-CBC	-2.75	106.45	111.09
35	A	3175	DI0	CCB-OBK-CAN	-2.68	111.95	117.55
35	A	3175	DI0	CBV-CBB-CBC	-2.64	106.45	112.45
35	A	3175	DI0	CBP-CAJ-CAC	-2.51	106.89	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	3175	DI0	CAF-CAC-CAJ	-2.37	106.20	113.05
35	A	3175	DI0	OBI-CAG-CAO	-2.35	105.59	109.77
35	A	3175	DI0	OBJ-CAP-CAH	2.22	111.80	107.59
35	A	3175	DI0	OBK-CAN-CAT	-2.22	109.41	112.96
35	A	3175	DI0	OAY-CAR-CAT	2.13	112.68	109.01
35	A	3175	DI0	CBO-CAI-CAA	-2.12	107.97	112.94
35	A	3175	DI0	CBO-CAI-CAK	-2.11	109.52	112.02
35	A	3175	DI0	OAU-CAB-CAG	-2.08	105.95	110.35
35	A	3175	DI0	OBK-CAN-CBQ	-2.07	107.48	110.92
35	A	3175	DI0	CAN-CAX-CAZ	-2.06	107.98	111.14
35	A	3175	DI0	OAM-CAH-CAJ	-2.04	108.48	111.54
35	A	3175	DI0	OAM-CAB-OAU	-2.03	105.02	110.67

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	A	3175	DI0	NAQ-CBA-CBS-OBW
35	A	3175	DI0	NAQ-CAK-CBB-CBC
35	A	3175	DI0	CAJ-CAH-CAP-OBJ
35	A	3175	DI0	OBX-CCC-CCD-OBW
35	A	3175	DI0	OAL-CAW-CBT-CCF
35	A	3175	DI0	CAD-CAW-OAL-CAE
35	A	3175	DI0	CBA-CBS-OBW-CCD
35	A	3175	DI0	CAJ-CAC-CAF-CBN
35	A	3175	DI0	CAD-CAW-CBT-CCF
35	A	3175	DI0	NAQ-CAK-CBB-CBV

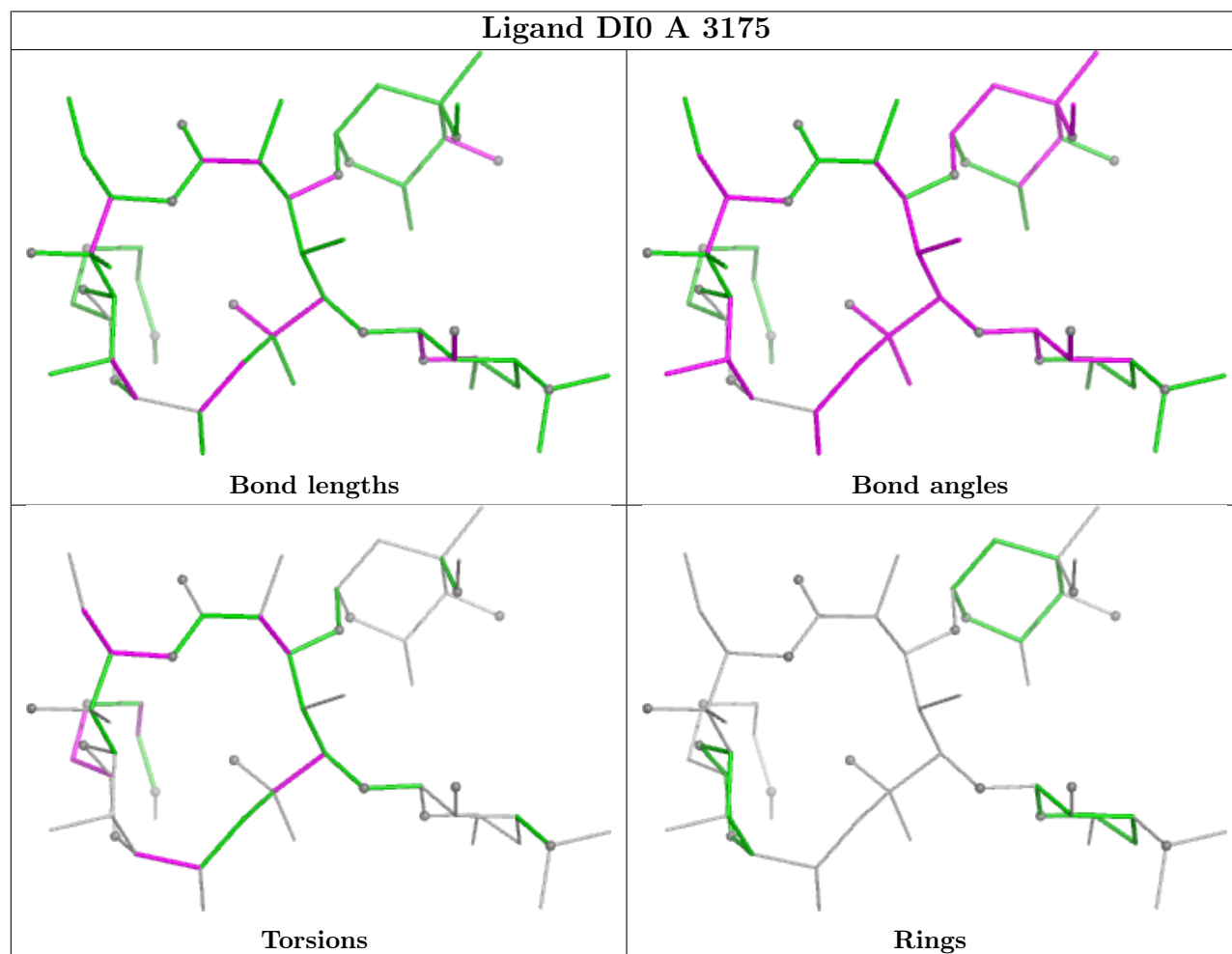
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	A	3175	DI0	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
33	g	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	885:C	O3'	892:A	P	11.25
1	A	1915:3TD	O3'	1916:A	P	1.31
1	g	75:C	O3'	76:31M	P	1.09

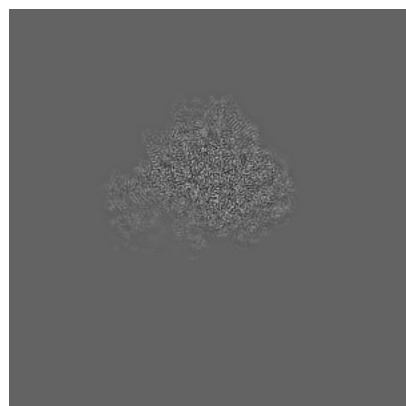
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10655. These allow visual inspection of the internal detail of the map and identification of artifacts.

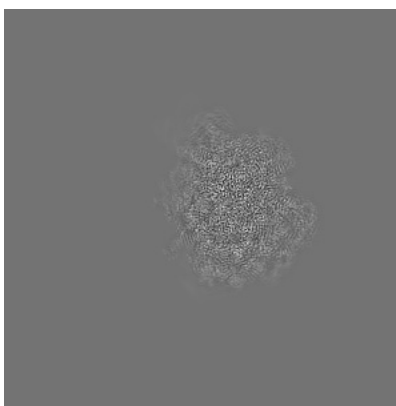
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

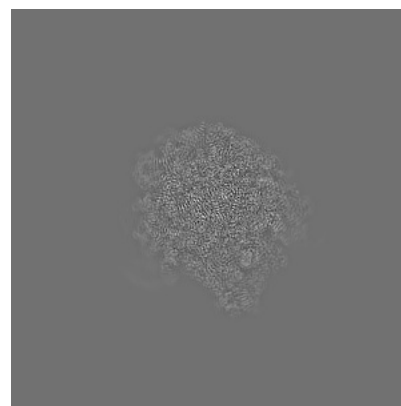
6.1.1 Primary map



X

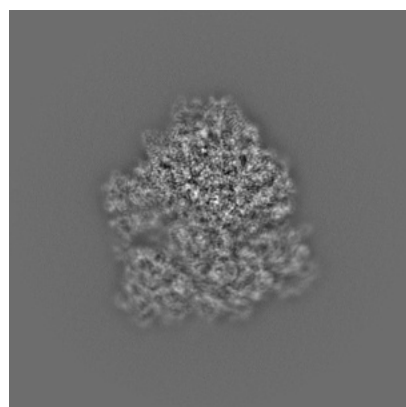


Y

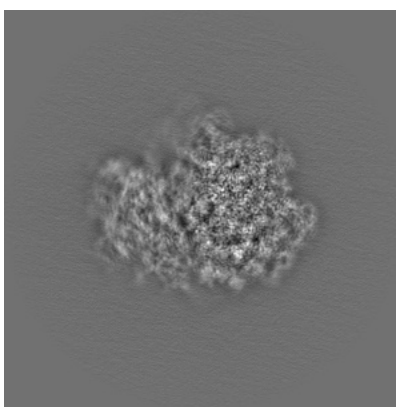


Z

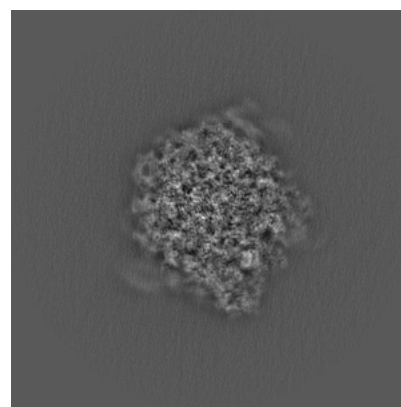
6.1.2 Raw map



X



Y

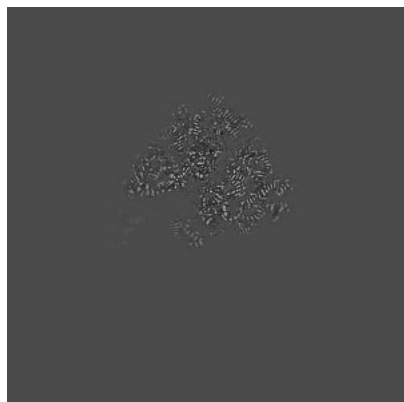


Z

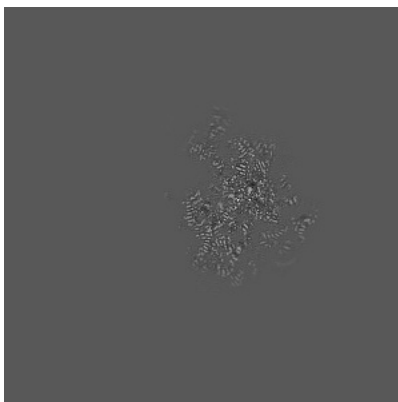
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

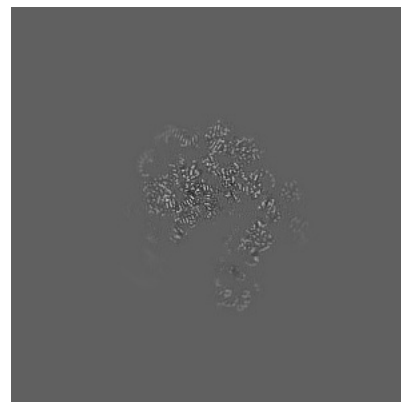
6.2.1 Primary map



X Index: 256

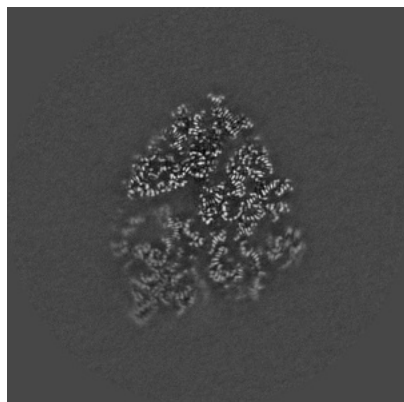


Y Index: 256

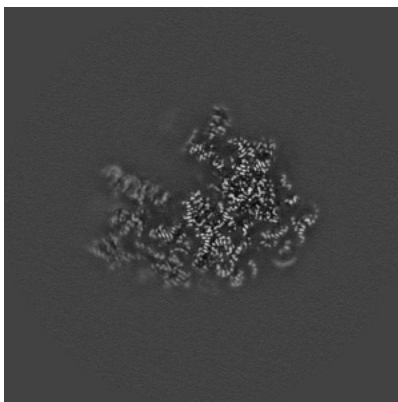


Z Index: 256

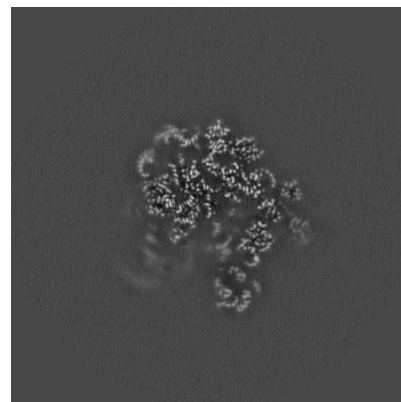
6.2.2 Raw map



X Index: 256



Y Index: 256

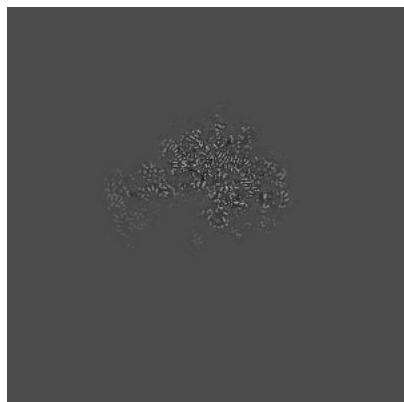


Z Index: 256

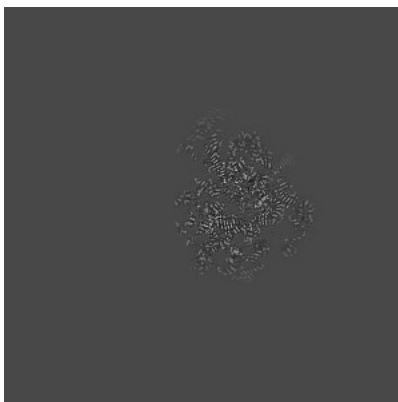
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

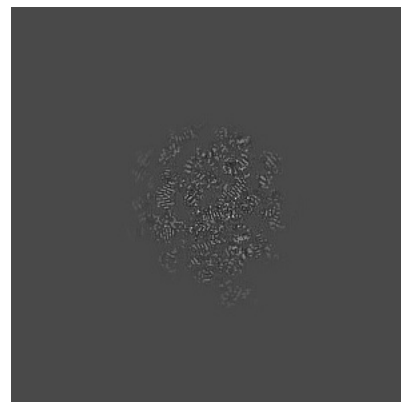
6.3.1 Primary map



X Index: 274

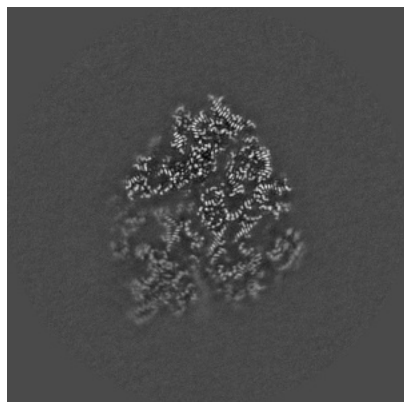


Y Index: 267

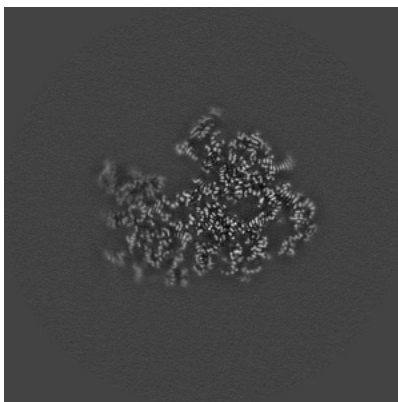


Z Index: 297

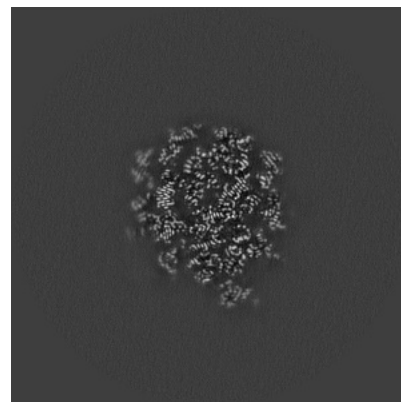
6.3.2 Raw map



X Index: 259



Y Index: 271

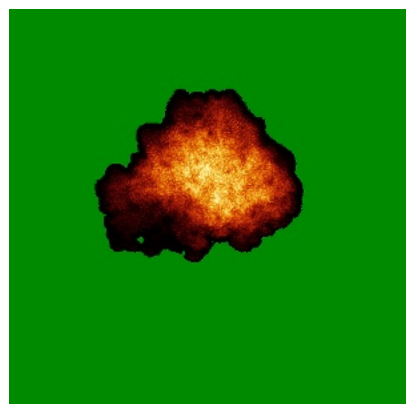


Z Index: 297

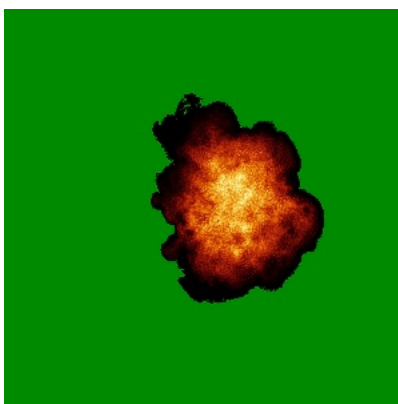
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

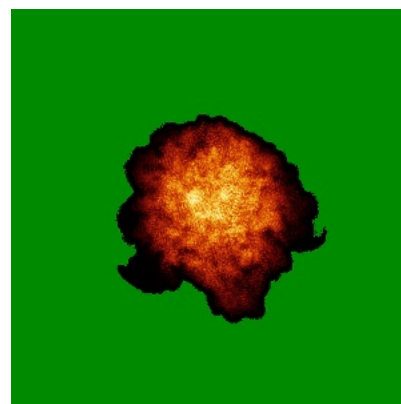
6.4.1 Primary map



X

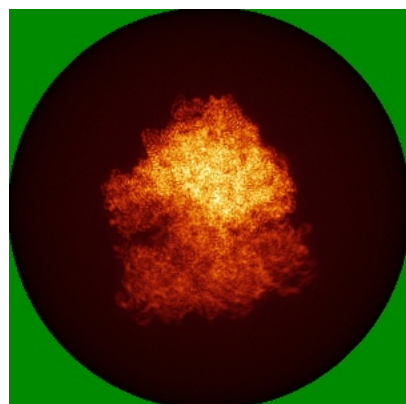


Y

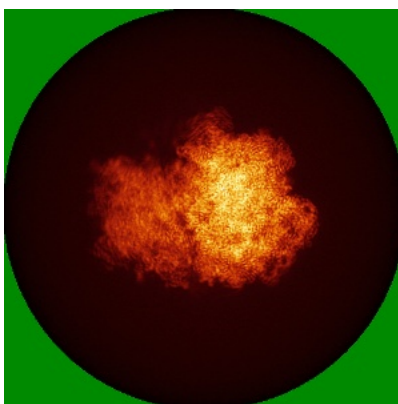


Z

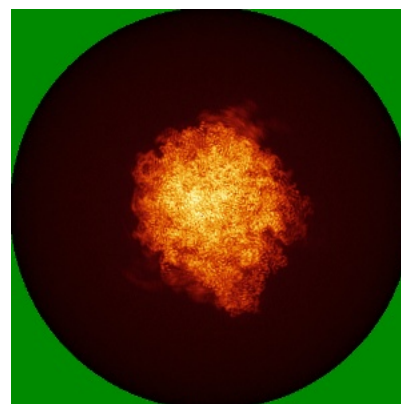
6.4.2 Raw map



X



Y

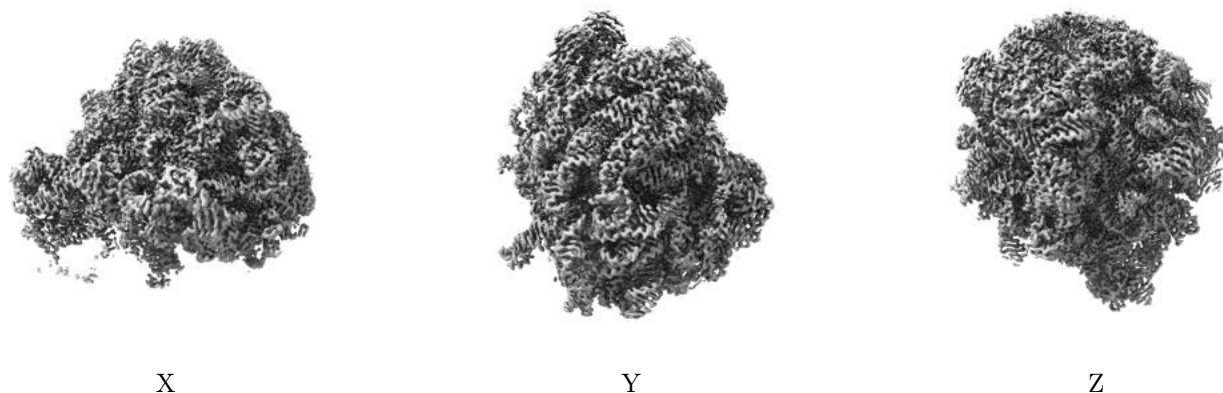


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

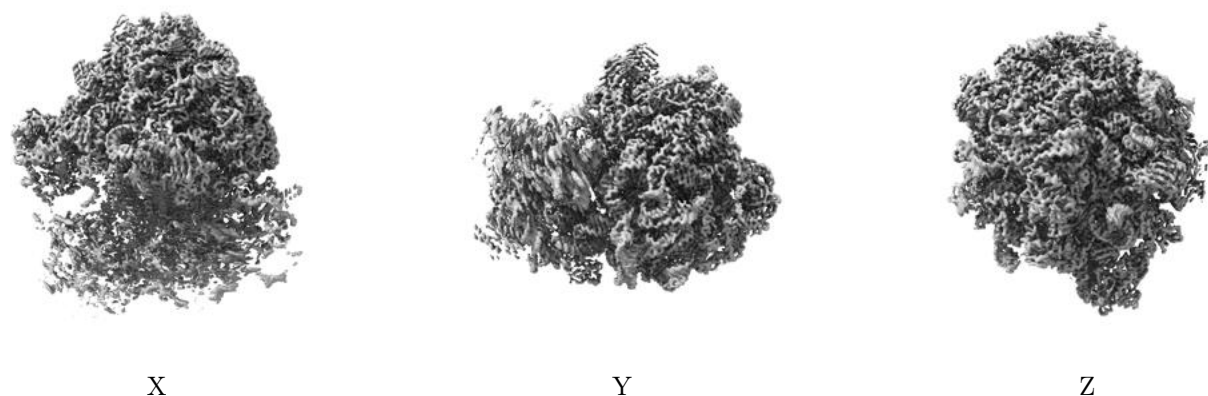
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

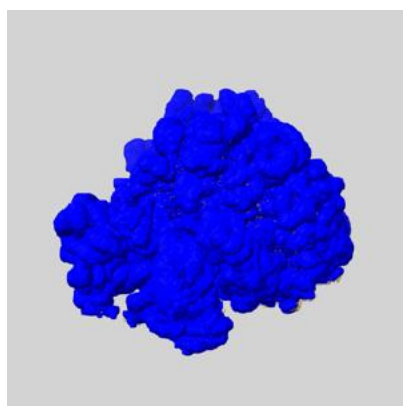
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

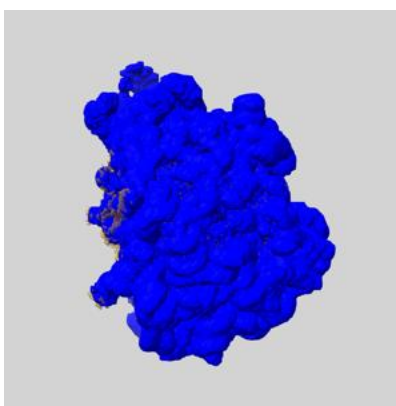
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

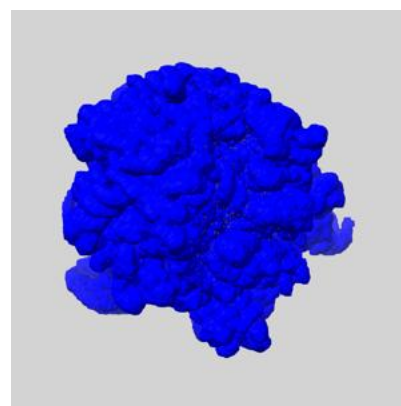
6.6.1 emd_10655_msk_1.map [i](#)



X



Y

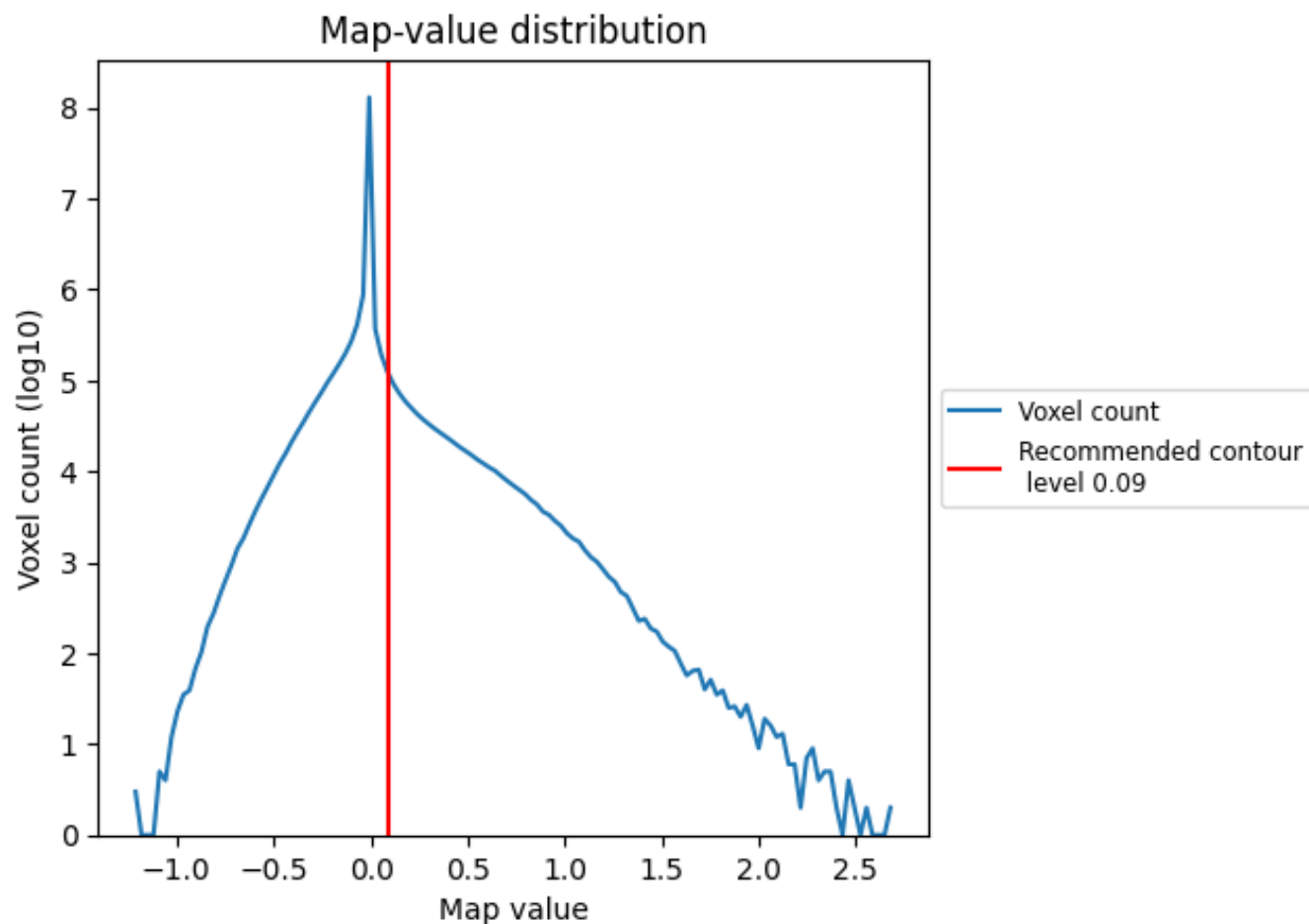


Z

7 Map analysis [i](#)

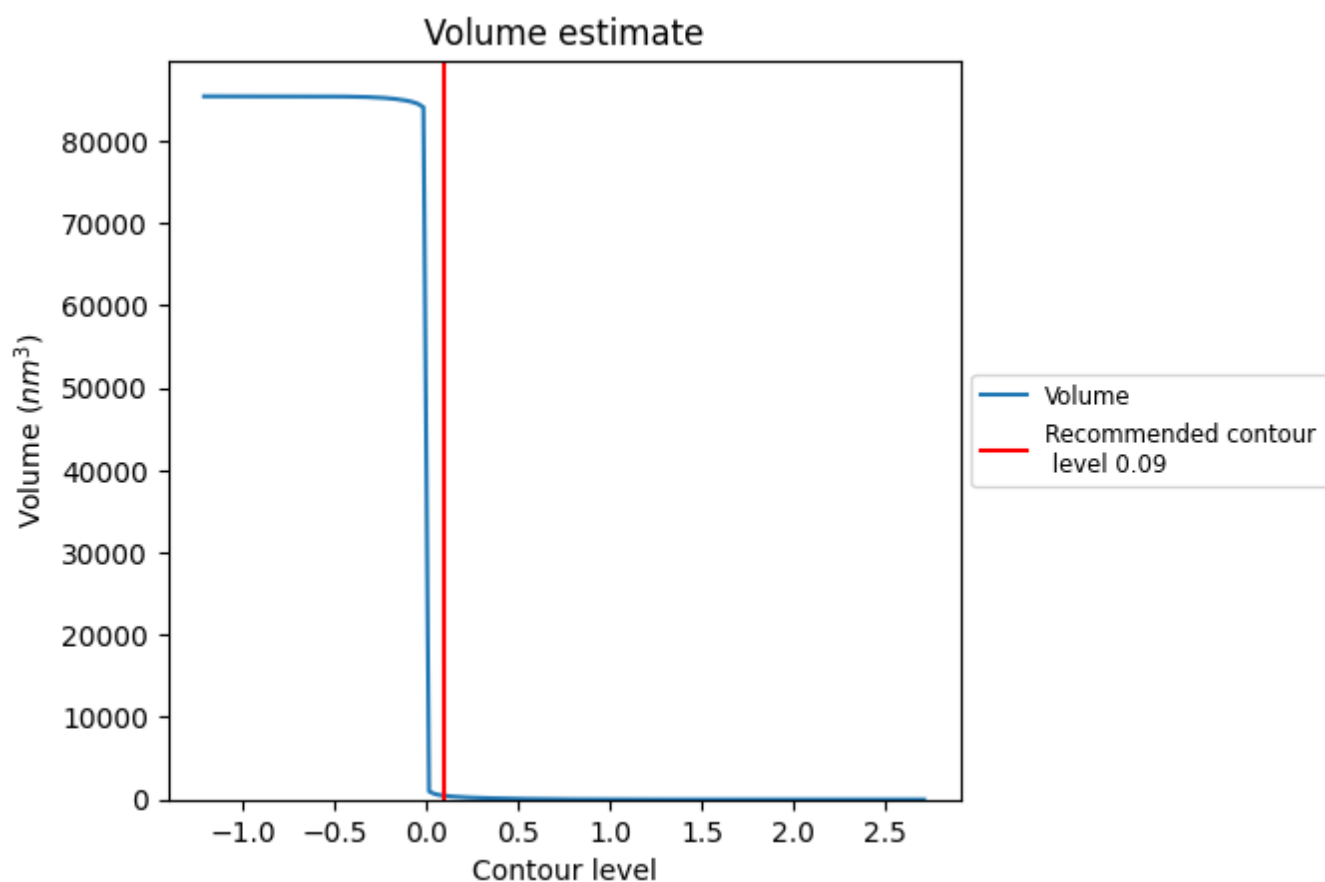
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

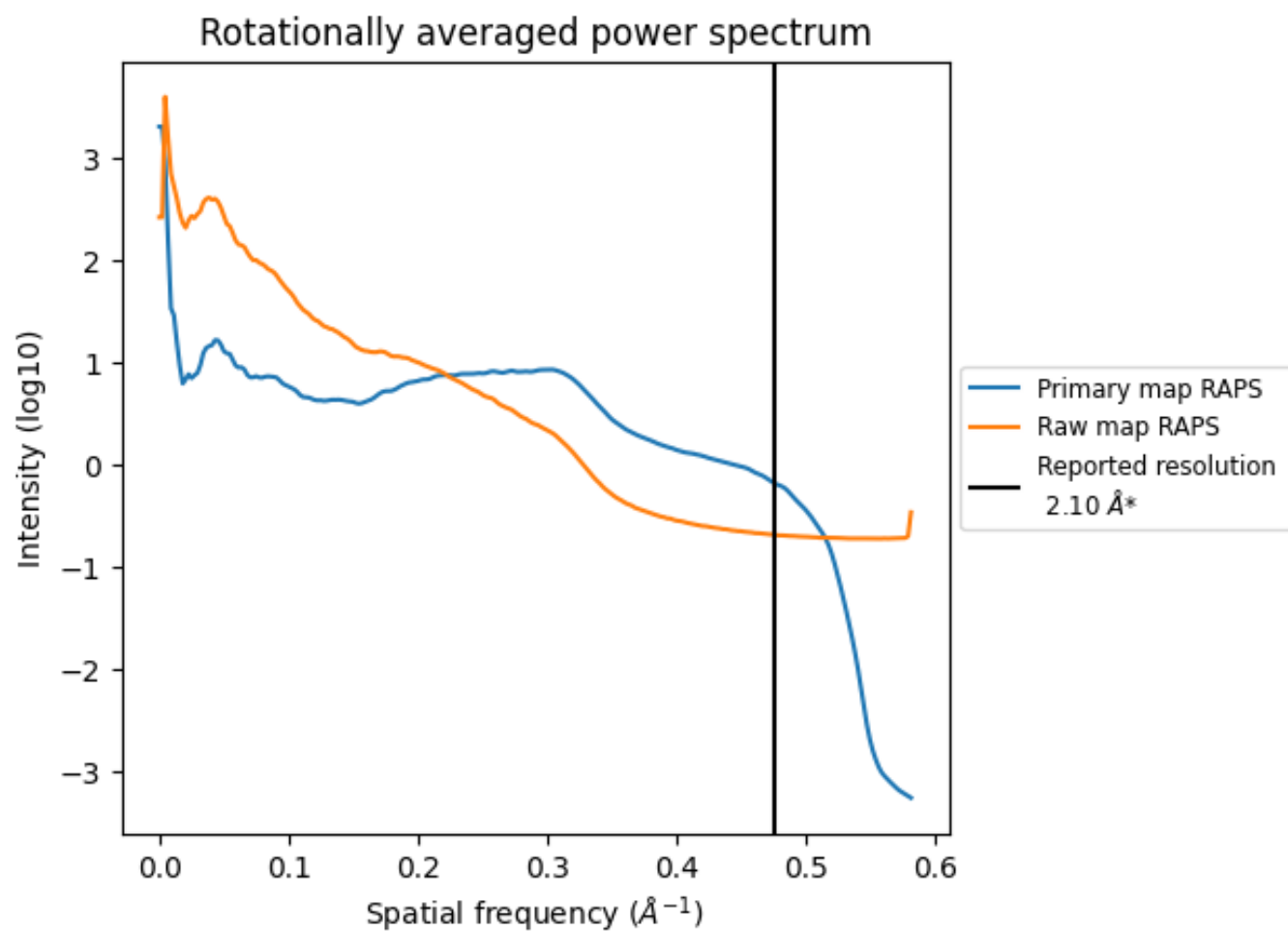
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 487 nm^3 ; this corresponds to an approximate mass of 440 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

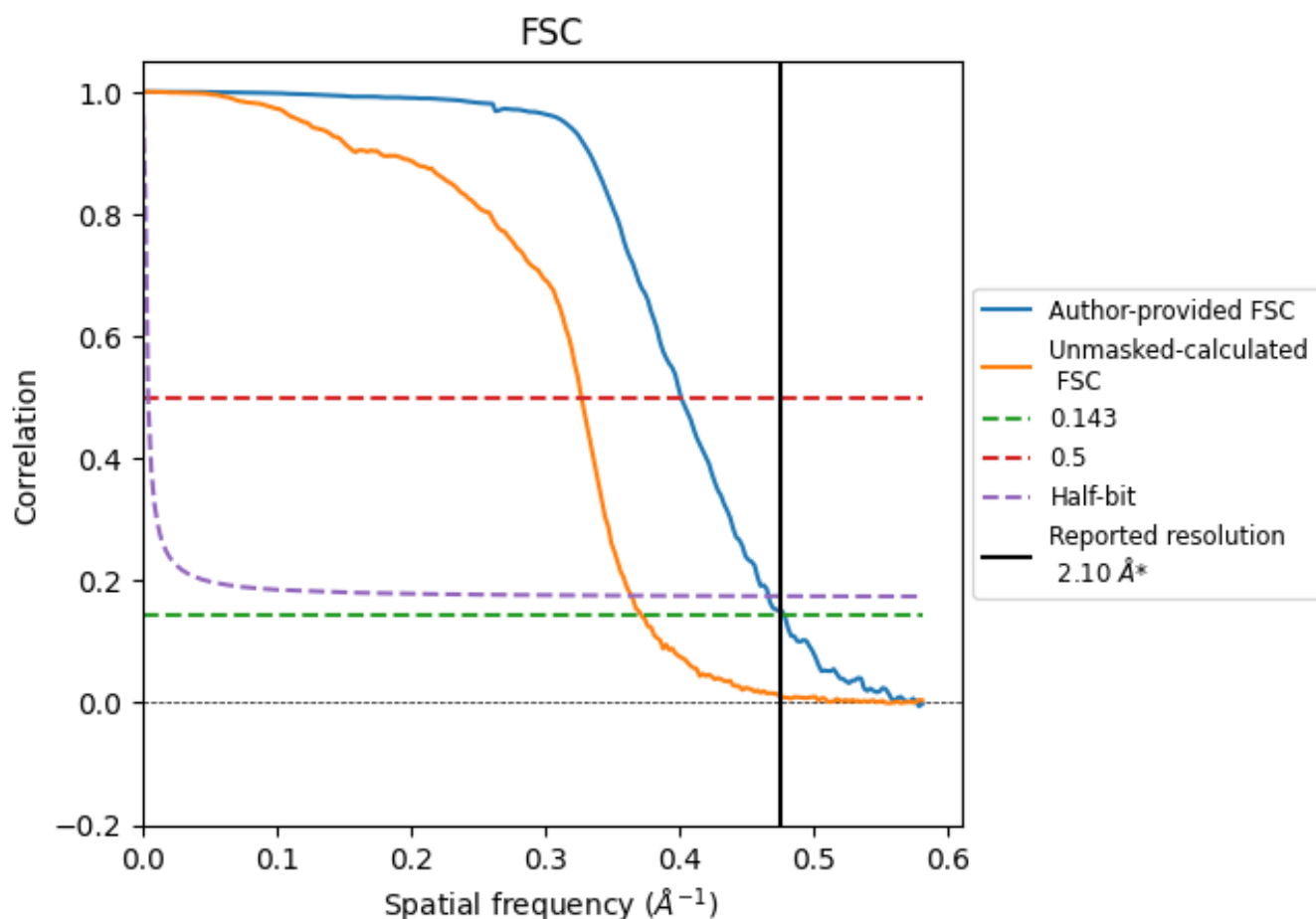


*Reported resolution corresponds to spatial frequency of 0.476 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.476 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

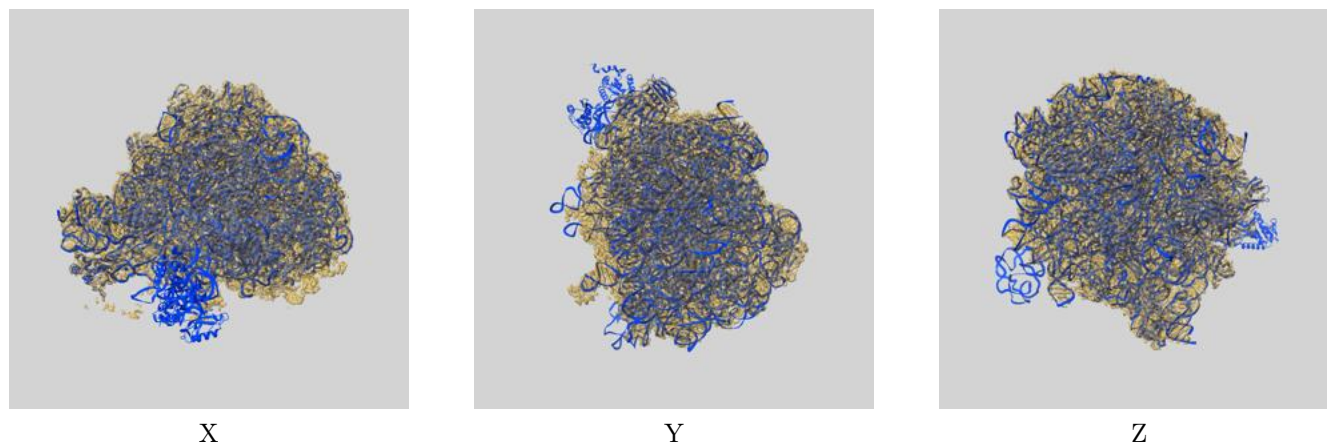
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.10	-	-
Author-provided FSC curve	2.09	2.49	2.14
Unmasked-calculated*	2.69	3.05	2.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.69 differs from the reported value 2.1 by more than 10 %

9 Map-model fit [i](#)

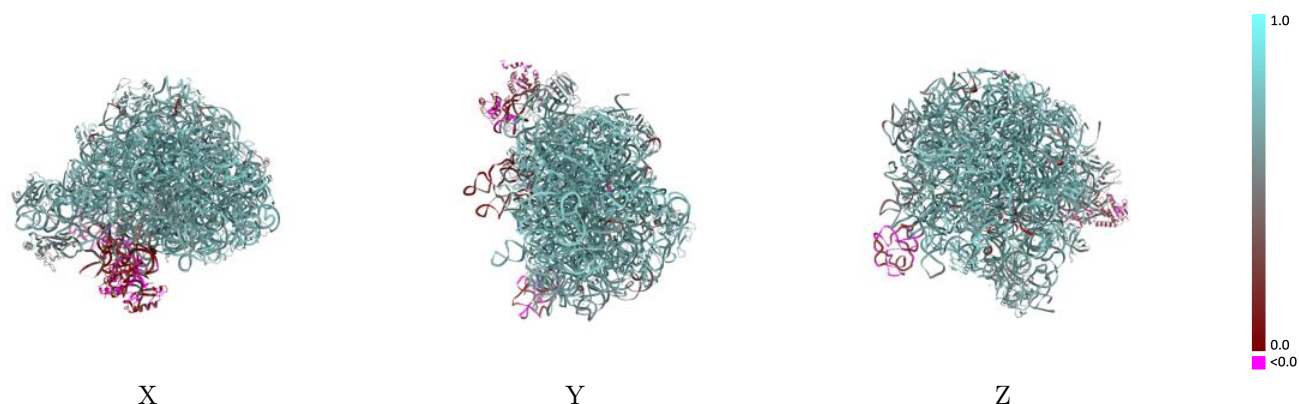
This section contains information regarding the fit between EMDB map EMD-10655 and PDB model 6XZ7. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



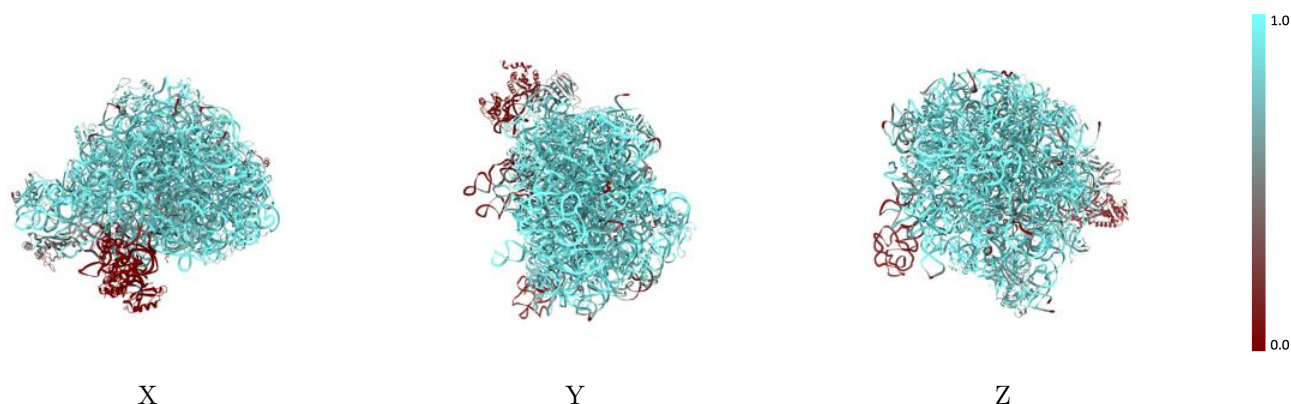
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



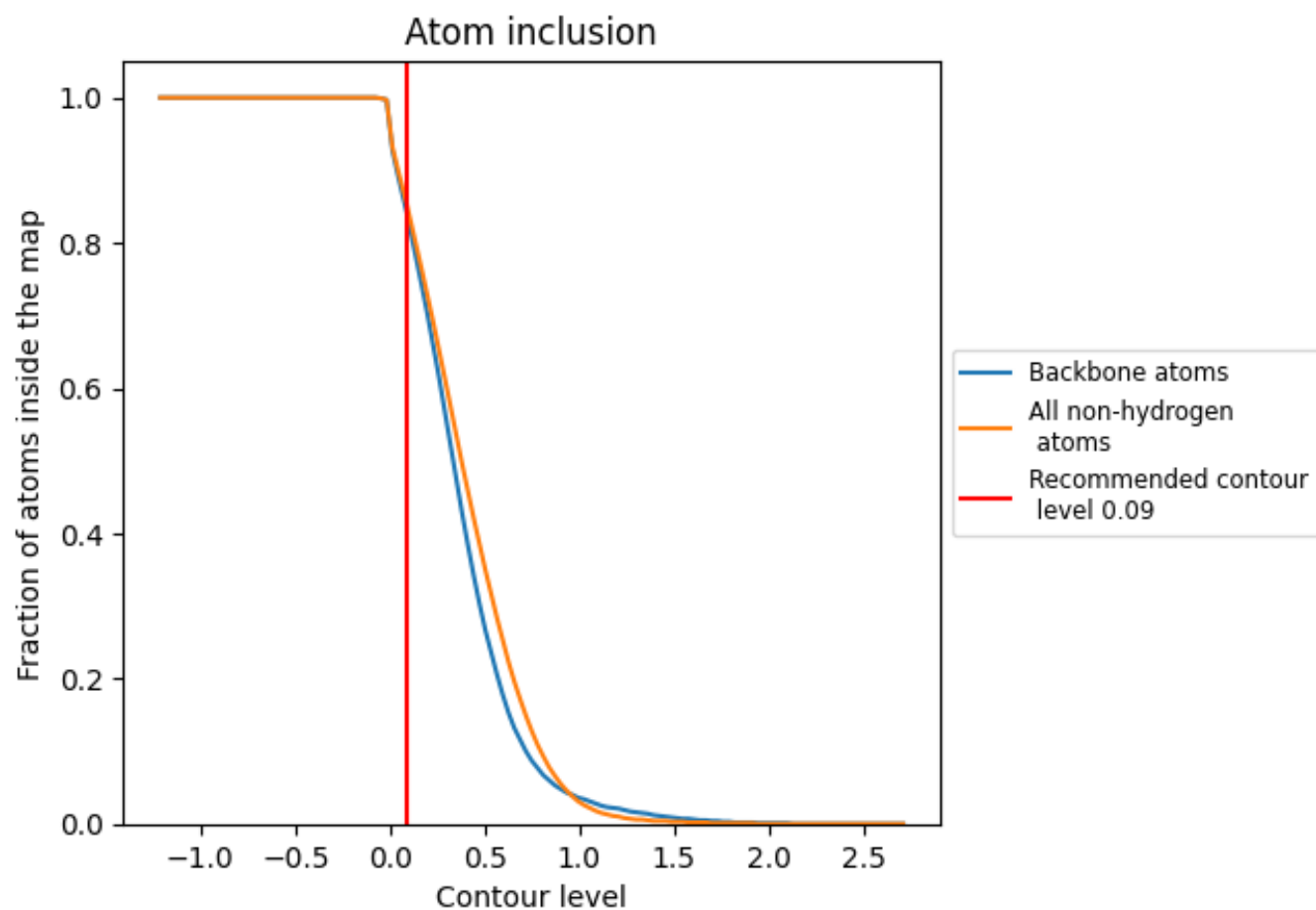
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.6430
A	 0.9030	 0.6720
B	 0.9090	 0.6460
C	 0.9500	 0.7170
D	 0.9340	 0.7080
E	 0.8780	 0.6770
F	 0.4670	 0.4930
G	 0.6220	 0.5550
H	 0.0000	 0.1280
I	 0.0000	 0.0590
J	 0.9370	 0.7070
K	 0.9340	 0.7020
L	 0.9280	 0.6990
M	 0.9410	 0.7050
N	 0.9260	 0.7040
O	 0.8060	 0.6160
P	 0.8930	 0.6750
Q	 0.9660	 0.7490
R	 0.8820	 0.6700
S	 0.9220	 0.7070
T	 0.8730	 0.6540
U	 0.8440	 0.6310
V	 0.8440	 0.6340
W	 0.9220	 0.6990
X	 0.9350	 0.6880
Y	 0.7970	 0.6110
Z	 0.8970	 0.6860
a	 0.9180	 0.7040
b	 0.8450	 0.6480
c	 0.9580	 0.7370
d	 0.9780	 0.7360
e	 0.9490	 0.6900
f	 0.2320	 0.2270
g	 0.2570	 0.2550

