



Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 04:33 pm GMT

PDB ID : 6TNN
EMDB ID : EMD-10535
Title : Mini-RNase III (Mini-III) bound to 50S ribosome with precursor 23S rRNA
Authors : Oerum, S.; Dendooven, T.; Gilet, L.; Catala, M.; Degut, C.; Trinquier, A.; Barraud, P.; Luisi, B.; Condon, C.; Tisne, C.
Deposited on : 2019-12-09
Resolution : 3.07 Å(reported)
Based on initial model : 3J3V

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:

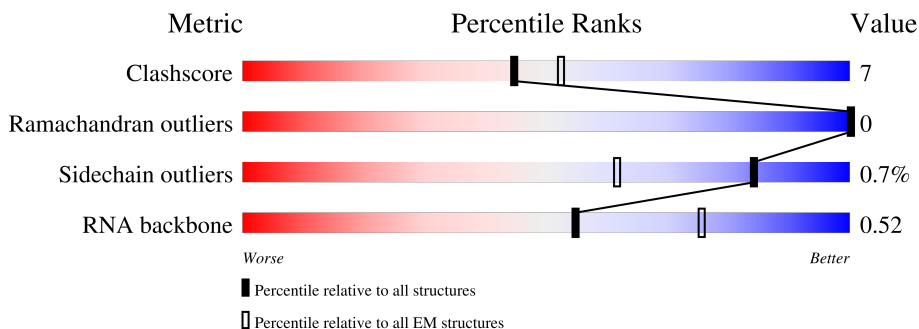
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.07 Å.

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





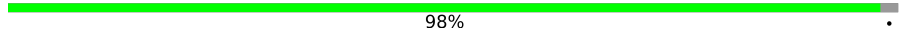
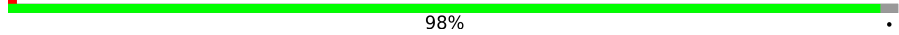
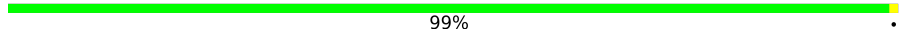
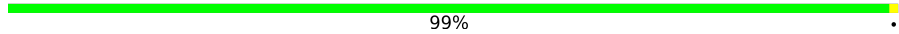
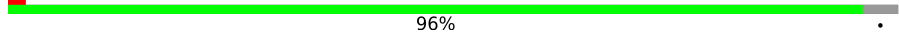
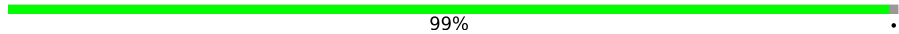
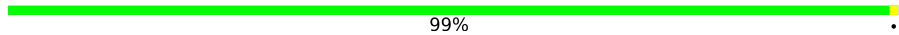
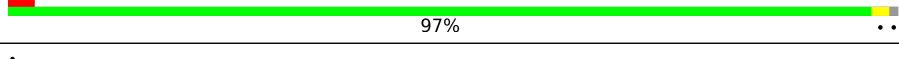
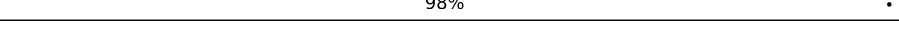
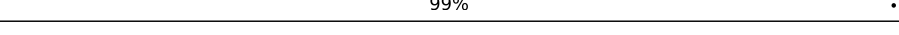
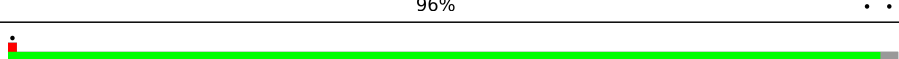


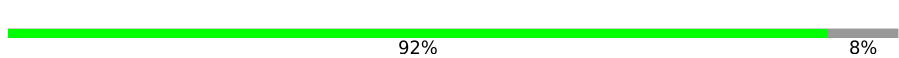
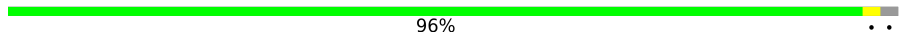
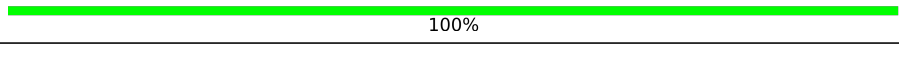
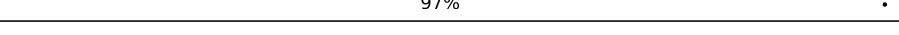
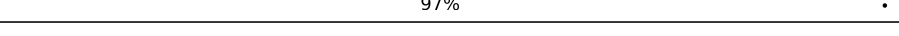
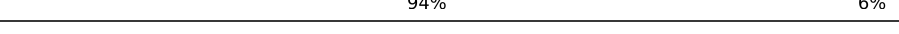
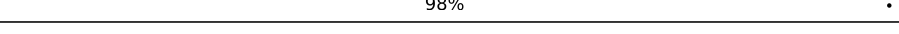
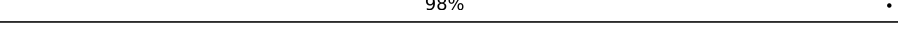

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	b	166	
2	H	143	
2	I	143	
3	U	2930	
4	V	116	
5	W	277	
6	X	209	

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Mol	Chain	Length	Quality of chain
7	Y	207	 80% 19%
8	Z	179	 11% 59% 39%
9	a	179	 98%
10	c	145	 98%
11	d	122	 99%
12	e	146	 99%
13	f	144	 96%
14	g	120	 99%
15	h	120	 99%
16	i	115	 97%
17	j	119	 98%
18	k	102	 99%
19	l	113	 96%
20	m	95	 98%
21	n	103	 98%
22	o	94	 86% 13%
23	p	59	 92% 8%
24	q	49	 96%
25	r	44	 100%
26	s	66	 97%
27	t	37	 97%
28	u	62	 94% 6%
29	v	66	 98%
30	w	59	 98%

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 91840 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 protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	b	123	955	602	163	189	1	0	0

- Molecule 2 is a protein called Mini-ribonuclease 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	H	132	1063	680	182	201	0	0
2	I	134	1079	691	184	203	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	23	ASN	ASP	conflict	UNP O31418
I	23	ASN	ASP	conflict	UNP O31418

- Molecule 3 is a RNA chain called pre-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	U	2930	62920	28070	11619	20301	2930	0	0

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	V	116	2475	1105	447	808	115	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	275	Total	C	N	O	S	0	0
			2110	1312	416	376	6		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	207	Total	C	N	O	S	0	0
			1574	988	290	291	5		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	205	Total	C	N	O	S	0	0
			1560	980	289	289	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	178	Total	C	N	O	S	0	0
			1403	893	245	258	7		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	175	Total	C	N	O	S	0	0
			1341	835	248	256	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	142	Total	C	N	O	S	0	0
			1122	710	206	201	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	122	Total	C	N	O	S	0	0
			919	571	173	171	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	146	Total	C	N	O	S	0	0
			1080	671	207	200	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	138	Total	C	N	O	S	0	0
			1096	703	208	180	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	119	Total	C	N	O	S	0	0
			952	583	186	179	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	120	Total	C	N	O	S	0	0
			911	564	176	170	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	i	114	Total	C	N	O	0	0
			935	595	184	156		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	j	117	Total	C	N	O	S	0	0
			939	591	189	155	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	101	Total	C	N	O	0	0
			785	501	139	145		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	109	Total	C	N	O	S	0	0
			841	525	164	149	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	93	Total	C	N	O	S	0	0
			751	472	137	138	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	101	Total	C	N	O	S	0	0
			761	478	142	137	4		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	o	82	Total	C	N	O	0	0
			629	390	123	116		

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	54	Total	C	N	O	S	0	0
			425	262	86	70	7		

- Molecule 24 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	q	48	Total	C	N	O	S	0	0
			400	244	80	72	4		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	44	Total	C	N	O	S	0	0
			366	222	89	53	2		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	s	64	511	321	107	81	2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	t	36	287	181	59	43	4	0	0

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	u	58	443	275	92	74	2	0	0

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	v	65	529	328	102	97	2	0	0

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	w	58	454	281	89	83	1	0	0

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	I	1	Total	Mg	0
			1	1	
31	U	214	Total	Mg	0
			214	214	
31	V	1	Total	Mg	0
			1	1	
31	W	2	Total	Mg	0
			2	2	
31	e	2	Total	Mg	0
			2	2	
31	u	1	Total	Mg	0
			1	1	

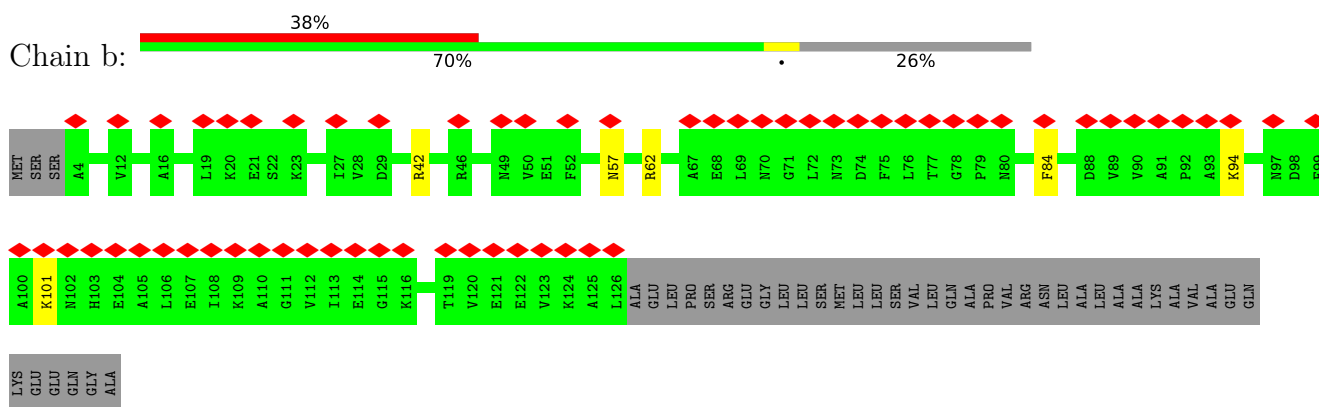
- Molecule 32 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	p	1	Total 1	Zn 1	0
32	q	1	Total 1	Zn 1	0
32	t	1	Total 1	Zn 1	0

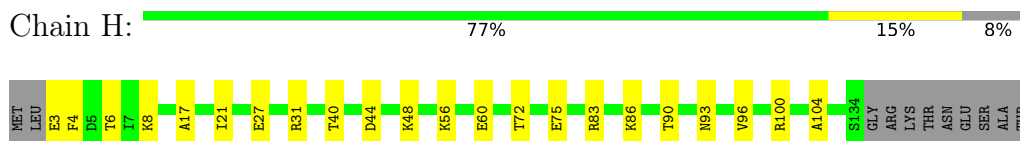
3 Residue-property plots [i](#)

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.

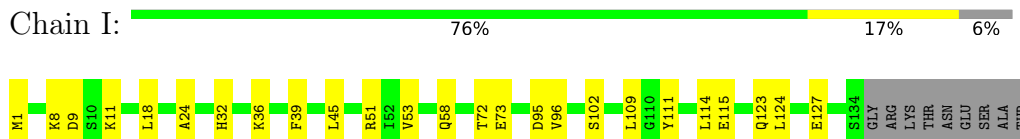
- Molecule 1: 50S ribosomal protein L10



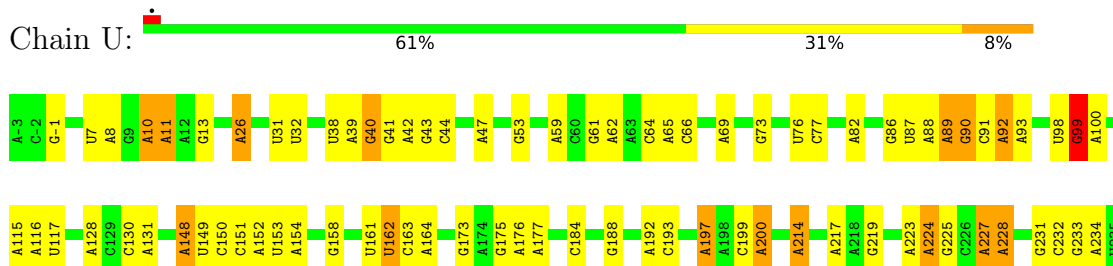
- Molecule 2: Mini-ribonuclease 3

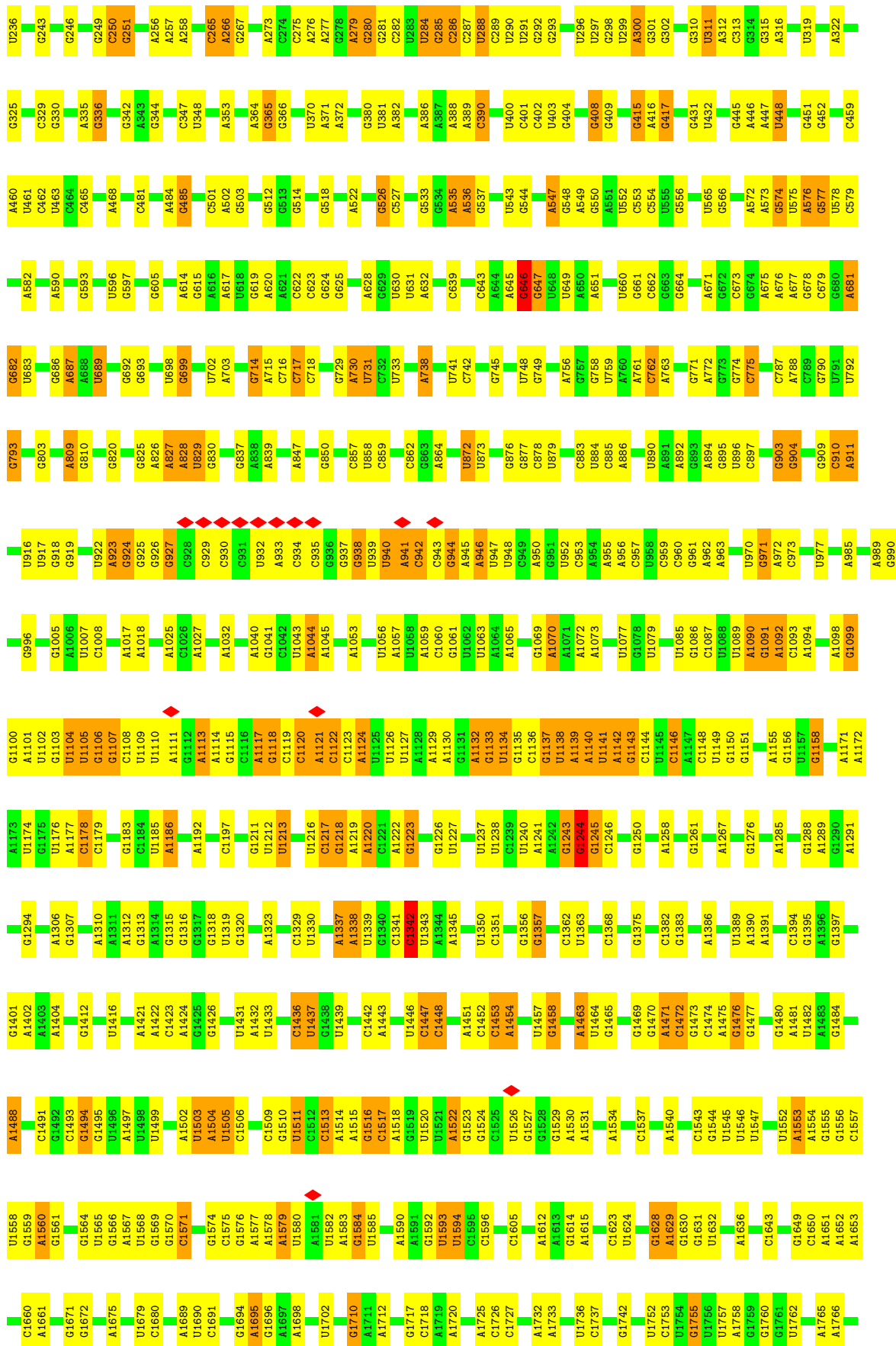


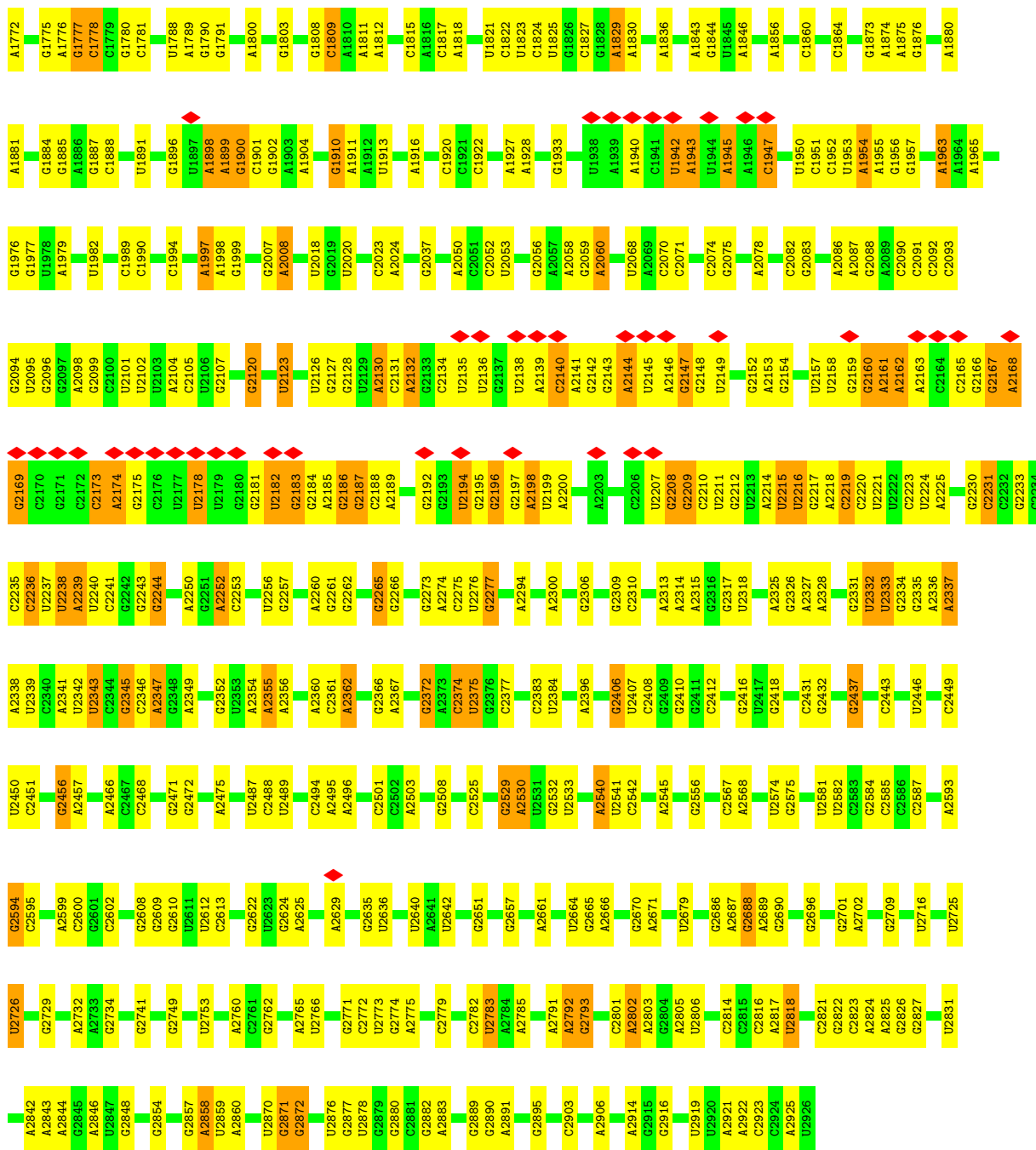
- Molecule 2: Mini-ribonuclease 3



- Molecule 3: pre-23S rRNA

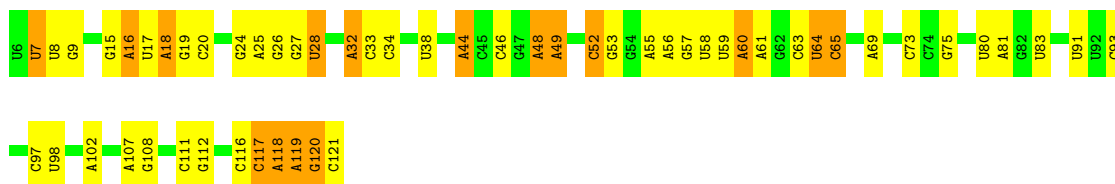




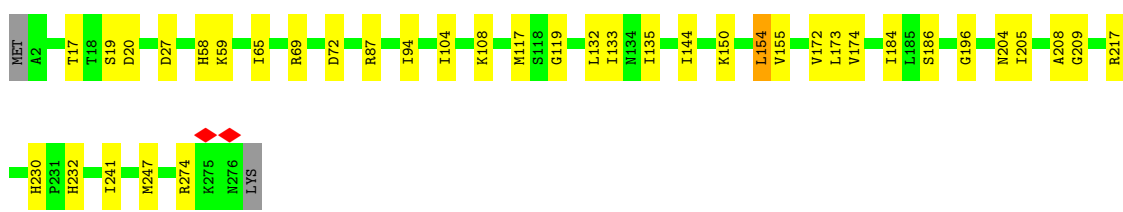
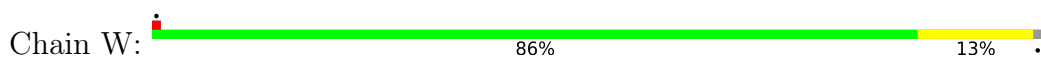


• Molecule 4: 5S rRNA

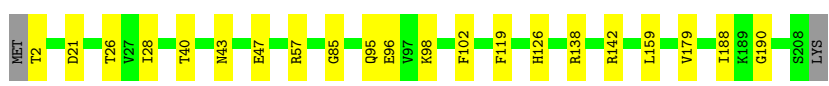
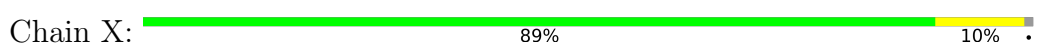
Chain V: 53% 34% 14%



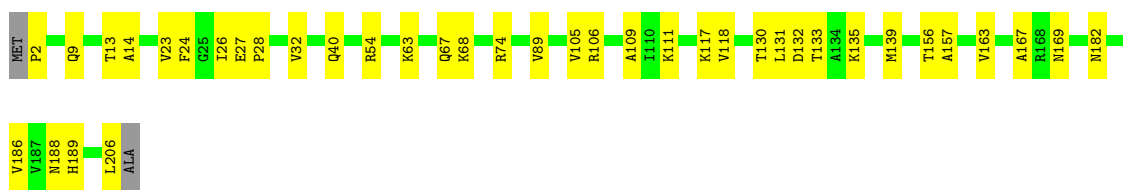
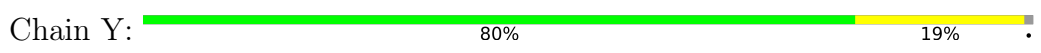
• Molecule 5: 50S ribosomal protein L2



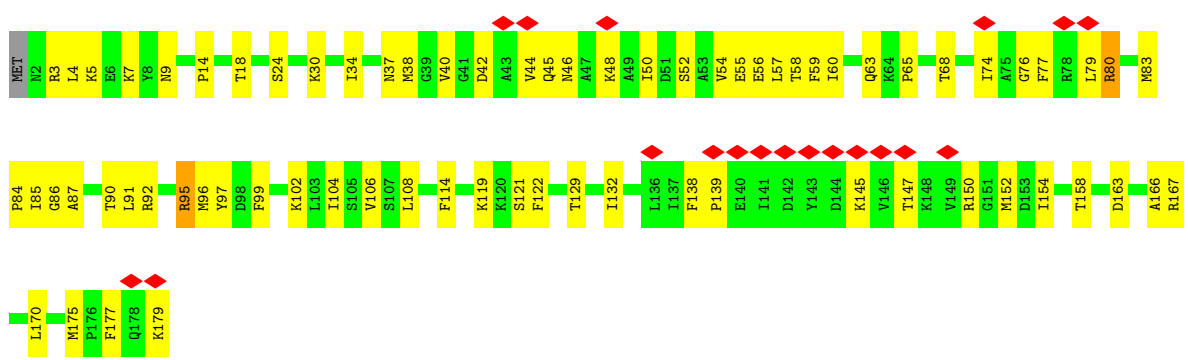
• Molecule 6: 50S ribosomal protein L3



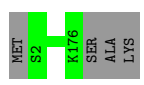
• Molecule 7: 50S ribosomal protein L4



• Molecule 8: 50S ribosomal protein L5

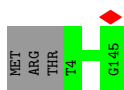


• Molecule 9: 50S ribosomal protein L6



• Molecule 10: 50S ribosomal protein L13

Chain c:  98%



- Molecule 11: 50S ribosomal protein L14

Chain d:  99%



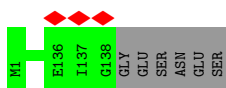
- Molecule 12: 50S ribosomal protein L15

Chain e:  99%



- Molecule 13: 50S ribosomal protein L16

Chain f:  96%



- Molecule 14: 50S ribosomal protein L17

Chain g:  99%



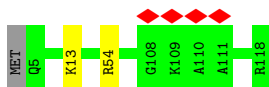
- Molecule 15: 50S ribosomal protein L18

Chain h:  99%



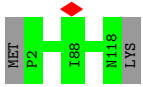
- Molecule 16: 50S ribosomal protein L19

Chain i:  97%



- Molecule 17: 50S ribosomal protein L20

Chain j:  98%



- Molecule 18: 50S ribosomal protein L21

Chain k:  99%



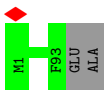
- Molecule 19: 50S ribosomal protein L22

Chain l:  96%



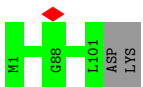
- Molecule 20: 50S ribosomal protein L23

Chain m:  98%




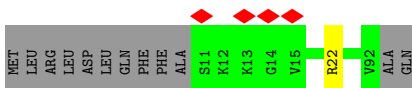
- Molecule 21: 50S ribosomal protein L24

Chain n:  98%

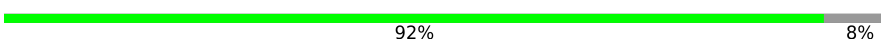


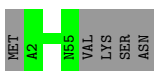
- Molecule 22: 50S ribosomal protein L27

Chain o:  86% 13%



- Molecule 23: 50S ribosomal protein L32

Chain p:  92% 8%



- Molecule 24: 50S ribosomal protein L33 1

Chain q:  96%



- Molecule 25: 50S ribosomal protein L34

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L35

Chain s:  97%



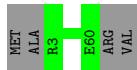
- Molecule 27: 50S ribosomal protein L36

Chain t:  97%



- Molecule 28: 50S ribosomal protein L28

Chain u:  94% 6%



- Molecule 29: 50S ribosomal protein L29

Chain v:  98%



- Molecule 30: 50S ribosomal protein L30

Chain w:  98%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57683	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23.94	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	9.780	Depositor
Minimum map value	-5.441	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.220	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	406.8, 406.8, 406.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.13, 1.13, 1.13	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	b	0.25	0/963	0.52	0/1298
2	H	0.26	0/1082	0.39	0/1454
2	I	0.26	0/1098	0.42	0/1475
3	U	0.41	0/70479	0.83	27/109956 (0.0%)
4	V	0.28	0/2767	0.82	1/4313 (0.0%)
5	W	0.29	0/2147	0.50	0/2880
6	X	0.29	0/1596	0.49	0/2139
7	Y	0.29	0/1579	0.46	0/2131
8	Z	0.26	0/1422	0.50	0/1909
9	a	0.26	0/1359	0.47	0/1831
10	c	0.29	0/1145	0.47	0/1541
11	d	0.28	0/926	0.47	0/1244
12	e	0.29	0/1092	0.49	0/1456
13	f	0.26	0/1119	0.44	0/1495
14	g	0.27	0/959	0.47	0/1283
15	h	0.25	0/920	0.45	0/1235
16	i	0.28	0/948	0.47	0/1268
17	j	0.32	0/951	0.45	0/1265
18	k	0.29	0/796	0.52	0/1069
19	l	0.28	0/850	0.47	0/1145
20	m	0.28	0/758	0.48	0/1010
21	n	0.28	0/771	0.50	0/1031
22	o	0.30	0/637	0.49	0/846
23	p	0.30	0/432	0.50	0/573
24	q	0.26	0/405	0.48	0/539
25	r	0.27	0/369	0.47	0/482
26	s	0.27	0/518	0.46	0/679
27	t	0.27	0/290	0.43	0/382
28	u	0.26	0/447	0.51	0/595
29	v	0.27	0/530	0.43	0/706
30	w	0.27	0/456	0.47	0/612
All	All	0.38	0/99811	0.76	28/149842 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	b	0	1
5	W	0	1
All	All	0	2

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	U	1431	U	C2-N1-C1'	8.67	128.10	117.70
3	U	1357	G	N3-C4-N9	-7.64	121.41	126.00
3	U	1431	U	N1-C2-O2	6.99	127.70	122.80
3	U	1350	U	C2-N1-C1'	6.91	126.00	117.70
3	U	1557	C	N3-C2-O2	-6.89	117.08	121.90
3	U	1431	U	C6-N1-C1'	-6.21	112.51	121.20
3	U	1431	U	N3-C2-O2	-5.88	118.08	122.20
3	U	1920	C	N3-C2-O2	-5.82	117.82	121.90
3	U	408	G	OP1-P-O3'	5.75	117.84	105.20
3	U	99	G	OP2-P-O3'	5.64	117.62	105.20
3	U	1920	C	N1-C2-O2	5.64	122.28	118.90
3	U	1342	C	O4'-C1'-N1	5.56	112.65	108.20
3	U	1357	G	N3-C4-C5	5.52	131.36	128.60
3	U	2818	U	C2-N1-C1'	5.52	124.32	117.70
3	U	1351	C	C2-N1-C1'	5.50	124.85	118.80
3	U	1520	U	N3-C2-O2	-5.50	118.35	122.20
3	U	1357	G	N3-C2-N2	-5.45	116.09	119.90
3	U	1244	G	O4'-C1'-N9	5.41	112.53	108.20
3	U	1386	A	O4'-C1'-N9	5.36	112.49	108.20
3	U	731	U	C2-N1-C1'	5.35	124.12	117.70
4	V	52	C	OP1-P-O3'	5.30	116.86	105.20
3	U	646	G	C3'-C2'-C1'	5.27	105.72	101.50
3	U	1557	C	N1-C2-O2	5.22	122.03	118.90
3	U	99	G	P-O3'-C3'	5.20	125.94	119.70
3	U	2487	U	N3-C2-O2	-5.17	118.58	122.20
3	U	1146	C	C2-N1-C1'	5.06	124.37	118.80
3	U	2236	C	N3-C2-O2	-5.04	118.37	121.90
3	U	381	U	C2-N1-C1'	5.02	123.72	117.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	W	154	LEU	Peptide
1	b	57	ASN	Peptide

5.2 Too-close contacts [i](#)

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	b	955	0	990	0	0
2	H	1063	0	1065	16	0
2	I	1079	0	1088	17	0
3	U	62920	0	31659	563	0
4	V	2475	0	1255	33	0
5	W	2110	0	2200	30	0
6	X	1574	0	1642	15	0
7	Y	1560	0	1647	25	0
8	Z	1403	0	1467	55	0
9	a	1341	0	1388	0	0
10	c	1122	0	1162	0	0
11	d	919	0	977	0	0
12	e	1080	0	1132	0	0
13	f	1096	0	1165	0	0
14	g	952	0	983	0	0
15	h	911	0	947	0	0
16	i	935	0	1008	0	0
17	j	939	0	1005	0	0
18	k	785	0	826	0	0
19	l	841	0	899	0	0
20	m	751	0	802	0	0
21	n	761	0	821	0	0
22	o	629	0	644	0	0
23	p	425	0	442	0	0
24	q	400	0	410	0	0
25	r	366	0	410	0	0
26	s	511	0	564	0	0
27	t	287	0	327	0	0
28	u	443	0	487	0	0
29	v	529	0	568	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	w	454	0	491	0	0
31	I	1	0	0	0	0
31	U	214	0	0	0	0
31	V	1	0	0	0	0
31	W	2	0	0	0	0
31	e	2	0	0	0	0
31	u	1	0	0	0	0
32	p	1	0	0	0	0
32	q	1	0	0	0	0
32	t	1	0	0	0	0
All	All	91840	0	60471	721	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 7.

All (721) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2131:C:N4	3:U:2132:A:N6	2.04	1.04
3:U:2131:C:C4	3:U:2132:A:N6	2.35	0.92
3:U:1104:U:H3	3:U:1123:C:H42	1.01	0.92
3:U:927:G:H1	3:U:939:U:H3	1.23	0.87
3:U:1104:U:H3	3:U:1123:C:N4	1.73	0.86
3:U:1244:G:H1'	3:U:1245:G:H5'	1.59	0.85
3:U:1578:A:H3'	3:U:1579:A:H4'	1.60	0.83
3:U:2418:G:O2'	3:U:2456:G:N2	2.12	0.83
3:U:1578:A:H61	3:U:1583:A:H62	1.27	0.82
3:U:1950:U:C4	3:U:1951:C:N4	2.48	0.81
3:U:1494:G:H1	3:U:1505:U:H3	0.85	0.81
3:U:224:A:H8	3:U:452:G:H21	1.26	0.81
3:U:926:G:H1	3:U:942:C:H1'	1.48	0.78
3:U:1357:G:H22	3:U:1368:C:N4	1.82	0.78
3:U:2131:C:N4	3:U:2132:A:H62	1.76	0.77
3:U:1357:G:H22	3:U:1368:C:H41	1.33	0.77
3:U:2211:U:C4	3:U:2212:G:O6	2.40	0.75
8:Z:74:ILE:O	8:Z:80:ARG:NH1	2.19	0.75
7:Y:40:GLN:HE22	7:Y:182:ASN:HD22	1.33	0.74
3:U:2325:A:H62	3:U:2345:G:H8	1.34	0.74
3:U:2822:G:N2	3:U:2825:A:OP2	2.20	0.74
3:U:1884:G:N2	3:U:1913:U:O4	2.19	0.74
3:U:643:C:O2'	3:U:647:G:OP1	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1120:C:H5''	3:U:1122:C:H5''	1.70	0.73
3:U:628:A:H62	3:U:1289:A:H2	1.37	0.72
3:U:803:G:H21	3:U:2008:A:H62	1.36	0.72
3:U:2872:G:O2'	3:U:2889:G:N2	2.23	0.72
3:U:1488:A:H5'	3:U:1504:A:H62	1.52	0.72
3:U:526:G:H1'	3:U:550:G:H21	1.54	0.72
3:U:1120:C:H3'	3:U:1121:A:H5'	1.70	0.72
8:Z:4:LEU:HA	8:Z:7:LYS:HE2	1.72	0.72
3:U:1517:C:N4	3:U:1518:A:N1	2.37	0.72
3:U:2608:G:N2	3:U:2608:G:OP2	2.22	0.72
8:Z:34:ILE:HB	8:Z:96:MET:HE3	1.71	0.72
3:U:1943:A:OP1	3:U:1990:C:N4	2.24	0.71
3:U:1114:A:N7	3:U:1140:A:O2'	2.24	0.70
7:Y:139:MET:HG2	7:Y:167:ALA:HB2	1.73	0.70
3:U:1090:A:H3'	3:U:1091:G:H5'	1.73	0.70
5:W:230:HIS:HD2	5:W:232:HIS:H	1.39	0.70
8:Z:132:ILE:HD11	8:Z:154:ILE:HG22	1.74	0.70
3:U:1063:U:OP1	3:U:1079:U:O2'	2.10	0.69
3:U:730:A:H8	3:U:733:U:H3	1.41	0.69
3:U:2131:C:N4	3:U:2132:A:H61	1.91	0.68
3:U:909:G:HO2'	3:U:910:C:H6	1.38	0.68
7:Y:117:LYS:NZ	7:Y:186:VAL:O	2.26	0.68
5:W:132:LEU:HD23	5:W:135:ILE:HD12	1.75	0.67
3:U:2120:G:N3	3:U:2225:A:N6	2.43	0.67
3:U:2153:A:N6	3:U:2189:A:O2'	2.28	0.67
2:H:31:ARG:HH11	2:I:24:ALA:HB2	1.59	0.67
3:U:2921:A:H2'	3:U:2922:A:C8	2.29	0.67
6:X:2:THR:OG1	6:X:85:GLY:O	2.11	0.67
8:Z:119:LYS:HG3	8:Z:167:ARG:HE	1.59	0.67
3:U:2339:U:O2	8:Z:37:ASN:ND2	2.22	0.67
4:V:118:A:H2'	4:V:119:A:C8	2.30	0.67
3:U:2160:G:N2	3:U:2181:G:OP1	2.29	0.66
3:U:925:G:H2'	3:U:926:G:C8	2.30	0.66
3:U:2231:C:OP2	5:W:150:LYS:NZ	2.23	0.66
3:U:2338:A:H4'	8:Z:74:ILE:HG12	1.78	0.65
3:U:1106:G:N1	3:U:1122:C:O2'	2.29	0.65
5:W:94:ILE:HG13	5:W:104:ILE:HD12	1.77	0.65
8:Z:45:GLN:HE22	8:Z:79:LEU:HB3	1.60	0.65
8:Z:177:PHE:HB2	8:Z:179:LYS:HE3	1.77	0.65
3:U:1106:G:N2	3:U:1107:G:N7	2.44	0.65
3:U:1320:G:N2	3:U:1323:A:OP2	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1522:A:H61	3:U:1558:U:H3	1.44	0.65
3:U:1825:U:OP2	5:W:274:ARG:NH2	2.30	0.65
3:U:1480:G:H21	3:U:1560:A:H8	1.44	0.64
3:U:1150:G:H2'	3:U:1151:G:H8	1.62	0.64
3:U:1345:A:H62	3:U:1649:G:H8	1.45	0.64
3:U:2197:G:N2	3:U:2197:G:OP2	2.31	0.64
2:I:58:GLN:HE21	2:I:102:SER:HB2	1.63	0.63
3:U:1442:C:H2'	3:U:1443:A:H8	1.64	0.63
3:U:923:A:OP2	3:U:944:G:N2	2.32	0.63
3:U:2273:G:H2'	3:U:2274:A:H8	1.63	0.63
3:U:1614:G:H21	5:W:58:HIS:HE1	1.44	0.63
3:U:1514:A:H62	3:U:1566:G:H8	1.47	0.63
5:W:204:ASN:OD1	5:W:205:ILE:N	2.31	0.62
8:Z:104:ILE:HA	8:Z:108:LEU:HD13	1.81	0.62
8:Z:145:LYS:HG2	8:Z:147:THR:H	1.64	0.62
2:H:3:GLU:OE1	2:I:1:MET:N	2.32	0.62
3:U:924:G:H2'	3:U:925:G:C8	2.33	0.62
2:H:6:THR:O	2:I:36:LYS:NZ	2.30	0.62
7:Y:63:LYS:NZ	7:Y:67:GLN:OE1	2.32	0.62
3:U:2854:G:OP1	6:X:57:ARG:NH2	2.33	0.61
3:U:1211:G:H2'	3:U:1212:U:C6	2.35	0.61
3:U:749:G:H1'	3:U:772:A:H61	1.65	0.61
3:U:2056:G:N1	3:U:2060:A:OP2	2.24	0.61
3:U:2496:A:N6	3:U:2508:G:O2'	2.33	0.61
3:U:1137:G:N1	3:U:1143:G:O6	2.34	0.61
8:Z:77:PHE:O	8:Z:80:ARG:NH1	2.33	0.61
3:U:1114:A:OP2	3:U:1122:C:N4	2.34	0.61
3:U:1458:G:H1'	3:U:1629:A:H61	1.66	0.61
3:U:26:A:N6	3:U:556:G:O2'	2.33	0.61
3:U:1516:G:N2	3:U:1564:G:H22	1.97	0.61
3:U:1133:G:N2	3:U:1134:U:O4	2.33	0.60
4:V:46:C:H5'	8:Z:63:GLN:HG3	1.83	0.60
3:U:671:A:OP2	3:U:699:G:N2	2.34	0.60
3:U:2243:G:HO2'	3:U:2244:G:H8	1.49	0.60
4:V:48:A:C8	8:Z:92:ARG:HD2	2.36	0.60
3:U:1243:G:H1'	3:U:1244:G:H5'	1.84	0.60
3:U:2154:G:O6	3:U:2189:A:N6	2.34	0.60
3:U:926:G:N2	3:U:942:C:O2'	2.32	0.60
3:U:1954:A:H2'	3:U:1955:A:C8	2.36	0.60
3:U:631:U:H2'	3:U:632:A:H8	1.66	0.59
8:Z:30:LYS:O	8:Z:158:THR:OG1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:148:A:H61	3:U:177:A:H2	1.48	0.59
3:U:64:C:H2'	3:U:65:A:H8	1.66	0.59
8:Z:45:GLN:NE2	8:Z:79:LEU:O	2.35	0.59
3:U:1219:A:H2'	3:U:1220:A:C8	2.38	0.59
3:U:1494:G:O6	3:U:1505:U:O4	2.19	0.59
3:U:2166:G:OP1	3:U:2173:C:O2'	2.21	0.59
8:Z:44:VAL:HG23	8:Z:46:ASN:H	1.65	0.59
3:U:62:A:H61	3:U:88:A:H61	1.51	0.59
3:U:926:G:N7	3:U:940:U:N3	2.51	0.59
3:U:2921:A:H2'	3:U:2922:A:H8	1.67	0.59
8:Z:108:LEU:HB3	8:Z:114:PHE:HE1	1.68	0.59
3:U:197:A:H62	3:U:876:G:H21	1.49	0.59
3:U:227:A:H2'	3:U:228:A:C8	2.37	0.58
3:U:1694:G:HO2'	3:U:1695:A:H8	1.49	0.58
7:Y:131:LEU:HD12	7:Y:163:VAL:HG22	1.85	0.58
3:U:1899:A:O2'	3:U:1900:G:O4'	2.20	0.58
3:U:941:A:H4'	3:U:942:C:H5'	1.85	0.58
8:Z:37:ASN:OD1	8:Z:38:MET:N	2.35	0.58
3:U:2130:A:N1	3:U:2214:A:N6	2.48	0.58
3:U:1710:G:O2'	3:U:1712:A:N7	2.37	0.58
3:U:2152:G:O2'	3:U:2153:A:O4'	2.18	0.58
3:U:2858:A:OP1	6:X:57:ARG:NH1	2.36	0.58
3:U:903:G:O2'	3:U:904:G:OP1	2.21	0.58
3:U:1212:U:H2'	3:U:1213:U:C6	2.39	0.58
3:U:996:G:H21	3:U:2294:A:H2	1.52	0.58
3:U:2210:C:H2'	3:U:2211:U:C6	2.39	0.58
4:V:64:U:H2'	4:V:65:C:H6	1.69	0.58
5:W:117:MET:HE3	5:W:119:GLY:H	1.68	0.58
3:U:687:A:N6	3:U:2396:A:O2'	2.36	0.57
3:U:971:G:H2'	3:U:972:A:H8	1.67	0.57
3:U:2128:G:N1	3:U:2215:U:O2'	2.37	0.57
3:U:1357:G:N2	3:U:1368:C:H41	2.01	0.57
3:U:1394:C:H2'	3:U:1395:G:O4'	2.04	0.57
3:U:1566:G:OP2	3:U:1567:A:O2'	2.18	0.57
3:U:1777:G:O2'	3:U:1778:C:OP1	2.20	0.57
3:U:1891:U:OP1	3:U:2437:G:O2'	2.20	0.57
3:U:2355:A:H2'	3:U:2356:A:C8	2.40	0.57
3:U:417:G:N2	3:U:446:A:OP2	2.37	0.57
7:Y:9:GLN:NE2	7:Y:130:THR:O	2.37	0.57
8:Z:38:MET:HG3	8:Z:40:VAL:HG23	1.86	0.57
3:U:718:C:OP1	7:Y:54:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2238:U:O2'	3:U:2239:A:OP1	2.21	0.57
3:U:82:A:N6	3:U:99:G:H1'	2.19	0.56
3:U:535:A:O2'	3:U:536:A:OP1	2.24	0.56
3:U:749:G:H2'	3:U:771:G:H22	1.71	0.56
3:U:1063:U:HO2'	3:U:1065:A:H2	1.53	0.56
3:U:1108:C:H42	3:U:1113:A:H3'	1.70	0.56
3:U:1593:U:H2'	3:U:1594:U:C6	2.40	0.56
3:U:2273:G:H2'	3:U:2274:A:C8	2.40	0.56
3:U:2824:A:H2'	3:U:2825:A:C8	2.41	0.56
2:H:72:THR:OG1	2:H:75:GLU:OE1	2.17	0.56
3:U:788:A:O2'	3:U:1702:U:OP1	2.24	0.56
3:U:971:G:H2'	3:U:972:A:C8	2.41	0.56
3:U:1085:U:O2	3:U:1158:G:O6	2.23	0.56
3:U:275:C:H2'	3:U:276:A:H8	1.71	0.56
3:U:2211:U:O4	3:U:2212:G:O6	2.23	0.56
4:V:55:A:N3	4:V:56:A:N6	2.47	0.56
3:U:2341:A:H2'	3:U:2342:U:C6	2.41	0.56
5:W:230:HIS:CD2	5:W:232:HIS:H	2.21	0.56
3:U:826:A:OP1	5:W:217:ARG:NH2	2.39	0.56
3:U:1874:A:H2'	3:U:1875:A:H8	1.69	0.56
3:U:2472:G:OP1	7:Y:74:ARG:NH2	2.33	0.56
3:U:759:U:N3	3:U:762:C:OP2	2.39	0.56
4:V:16:A:O2'	4:V:18:A:OP2	2.23	0.55
2:H:90:THR:HG21	2:H:96:VAL:HA	1.88	0.55
3:U:459:C:H2'	3:U:460:A:C8	2.42	0.55
3:U:1401:G:N2	3:U:1404:A:OP2	2.36	0.55
3:U:1593:U:H2'	3:U:1594:U:H6	1.71	0.55
3:U:1942:U:H3	3:U:1963:A:H62	1.53	0.55
8:Z:4:LEU:HD21	8:Z:97:TYR:HB3	1.87	0.55
2:H:86:LYS:HZ2	2:H:100:ARG:HH12	1.53	0.55
3:U:1137:G:H2'	3:U:1138:U:C6	2.42	0.55
3:U:1570:G:O2'	3:U:1571:C:O5'	2.23	0.55
3:U:2126:U:O2	3:U:2217:G:O6	2.25	0.55
3:U:2136:U:N3	3:U:2207:U:O4	2.40	0.55
5:W:172:VAL:HG12	5:W:173:LEU:H	1.72	0.55
8:Z:14:PRO:O	8:Z:18:THR:HG23	2.06	0.55
3:U:1053:A:N3	3:U:1197:C:O2'	2.38	0.54
3:U:1950:U:N3	3:U:1951:C:N4	2.55	0.54
3:U:64:C:H2'	3:U:65:A:C8	2.42	0.54
3:U:2792:A:OP2	3:U:2793:G:N2	2.41	0.54
4:V:7:U:O4	4:V:121:C:N3	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:54:VAL:O	8:Z:58:THR:HG23	2.07	0.54
3:U:1424:A:H5'	3:U:1513:C:H1'	1.90	0.54
3:U:1540:A:N3	3:U:1623:C:O2'	2.38	0.54
3:U:82:A:H61	3:U:99:G:H1'	1.73	0.54
3:U:1120:C:N3	3:U:1122:C:O2'	2.38	0.54
3:U:1150:G:H2'	3:U:1151:G:C8	2.42	0.54
3:U:2871:G:O2'	3:U:2872:G:O5'	2.21	0.54
3:U:828:A:H2'	3:U:829:U:H4'	1.89	0.54
3:U:26:A:N6	3:U:556:G:H1'	2.23	0.54
3:U:1481:A:H2'	3:U:1482:U:H6	1.73	0.54
3:U:1671:G:H2'	3:U:1672:G:H8	1.73	0.54
3:U:219:G:H22	3:U:236:U:H4'	1.72	0.54
3:U:929:C:H2'	3:U:930:C:C6	2.43	0.54
3:U:631:U:H2'	3:U:632:A:C8	2.43	0.54
3:U:2123:U:O4	3:U:2220:C:N3	2.41	0.53
3:U:2842:A:O2'	3:U:2844:A:N7	2.38	0.53
3:U:275:C:H2'	3:U:276:A:C8	2.43	0.53
3:U:291:U:H2'	3:U:292:G:C8	2.43	0.53
3:U:329:C:H2'	3:U:330:G:H8	1.73	0.53
3:U:972:A:H2'	3:U:973:C:C6	2.44	0.53
3:U:1821:U:H2'	3:U:1822:C:C6	2.43	0.53
3:U:2471:G:OP2	7:Y:68:LYS:NZ	2.37	0.53
3:U:26:A:H61	3:U:556:G:H1'	1.72	0.53
3:U:92:A:H2'	3:U:93:A:C8	2.44	0.53
3:U:1105:U:C4	3:U:1115:G:H5'	2.43	0.53
3:U:1576:G:O6	3:U:1584:G:O2'	2.17	0.53
3:U:970:U:C2	3:U:971:G:C8	2.97	0.53
3:U:1515:A:H61	3:U:1565:U:H3	1.57	0.53
4:V:119:A:H2'	4:V:120:G:N7	2.23	0.53
3:U:909:G:O2'	3:U:910:C:H6	1.91	0.53
3:U:1452:C:H2'	3:U:1453:C:C2	2.44	0.53
3:U:1679:U:H2'	3:U:1680:C:C6	2.44	0.53
4:V:49:A:OP2	4:V:49:A:H8	1.92	0.53
3:U:447:A:H2'	3:U:448:U:O4'	2.08	0.52
8:Z:91:LEU:HD12	8:Z:95:ARG:HB3	1.91	0.52
8:Z:68:THR:OG1	8:Z:86:GLY:O	2.25	0.52
3:U:2140:C:H2'	3:U:2194:U:H3	1.75	0.52
3:U:257:A:H2'	3:U:258:A:C8	2.44	0.52
3:U:1091:G:H4'	3:U:1092:A:H5'	1.92	0.52
3:U:1098:A:N6	3:U:1099:G:O6	2.43	0.52
3:U:2276:U:H3'	3:U:2277:G:H5''	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2826:G:H2'	3:U:2827:G:H8	1.75	0.52
4:V:46:C:O2	8:Z:90:THR:OG1	2.27	0.52
3:U:90:G:H2'	3:U:91:C:C6	2.45	0.52
3:U:287:C:O2'	3:U:288:U:H5'	2.09	0.52
3:U:1829:A:H2'	3:U:1830:A:C8	2.45	0.52
3:U:1509:C:H2'	3:U:1510:G:C8	2.45	0.52
7:Y:24:PHE:HB3	7:Y:118:VAL:HG21	1.92	0.52
3:U:624:G:H2'	3:U:625:G:C8	2.44	0.52
3:U:1138:U:H5''	3:U:1139:A:H5''	1.91	0.52
4:V:49:A:OP2	4:V:49:A:H3'	2.09	0.52
3:U:1951:C:H2'	3:U:1952:C:C6	2.45	0.52
3:U:2214:A:H2'	3:U:2215:U:H4'	1.92	0.52
3:U:2822:G:O2'	3:U:2825:A:N6	2.43	0.52
3:U:2154:G:H21	3:U:2200:A:H1'	1.75	0.51
3:U:904:G:O2'	3:U:961:G:O6	2.16	0.51
3:U:2102:U:OP2	3:U:2265:G:O2'	2.23	0.51
8:Z:54:VAL:HG23	8:Z:65:PRO:HG2	1.93	0.51
3:U:401:C:H2'	3:U:402:C:C6	2.45	0.51
3:U:1463:A:H2'	3:U:1465:G:N7	2.25	0.51
3:U:89:A:H3'	3:U:90:G:C8	2.45	0.51
3:U:284:U:H3'	3:U:285:G:H8	1.75	0.51
3:U:872:U:O2'	3:U:2095:U:N3	2.43	0.51
3:U:2801:C:H2'	3:U:2802:A:O4'	2.11	0.51
5:W:72:ASP:OD1	5:W:72:ASP:N	2.43	0.51
2:I:123:GLN:O	2:I:127:GLU:HG2	2.11	0.51
3:U:1570:G:O2'	3:U:1571:C:H6	1.93	0.51
3:U:2326:G:H2'	3:U:2327:A:H8	1.75	0.51
5:W:27:ASP:N	5:W:27:ASP:OD1	2.44	0.51
3:U:758:G:O2'	3:U:763:A:N6	2.44	0.51
3:U:2871:G:HO2'	3:U:2872:G:P	2.34	0.51
4:V:48:A:H3'	4:V:49:A:N7	2.26	0.51
3:U:2877:G:H2'	3:U:2878:U:C6	2.46	0.51
3:U:1481:A:H2'	3:U:1482:U:C6	2.46	0.51
3:U:265:C:O2'	3:U:266:A:O5'	2.25	0.51
7:Y:156:THR:HG22	7:Y:157:ALA:H	1.76	0.51
3:U:622:C:H2'	3:U:623:C:C6	2.46	0.50
3:U:646:G:H2'	3:U:647:G:C8	2.46	0.50
3:U:1237:U:H2'	3:U:1238:U:C6	2.46	0.50
3:U:1442:C:H2'	3:U:1443:A:C8	2.43	0.50
3:U:1513:C:H2'	3:U:1514:A:H8	1.76	0.50
3:U:2162:A:C5	3:U:2186:G:H1'	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:702:U:H2'	3:U:703:A:C8	2.46	0.50
3:U:459:C:H2'	3:U:460:A:H8	1.77	0.50
8:Z:68:THR:OG1	8:Z:85:ILE:O	2.29	0.50
4:V:116:C:H2'	4:V:117:C:C6	2.46	0.50
7:Y:32:VAL:HG12	7:Y:109:ALA:HB2	1.93	0.50
3:U:738:A:O2'	3:U:1390:A:N3	2.44	0.50
3:U:1694:G:O2'	3:U:1695:A:H8	1.94	0.50
3:U:578:U:H2'	3:U:579:C:C6	2.47	0.50
3:U:790:G:O2'	3:U:793:G:O2'	2.24	0.50
3:U:2313:A:H4'	3:U:2314:A:O4'	2.11	0.50
3:U:315:G:H2'	3:U:316:A:C8	2.47	0.49
3:U:1122:C:H2'	3:U:1132:A:H2	1.77	0.49
3:U:2008:A:H2'	3:U:2008:A:N3	2.26	0.49
2:H:93:ASN:ND2	3:U:2923:C:OP2	2.41	0.49
3:U:2332:U:HO2'	3:U:2334:G:HO2'	1.50	0.49
7:Y:40:GLN:HE22	7:Y:182:ASN:ND2	2.04	0.49
3:U:415:G:OP2	3:U:468:A:N6	2.45	0.49
3:U:1523:G:H2'	3:U:1524:G:C8	2.48	0.49
3:U:2130:A:H2'	3:U:2131:C:C6	2.48	0.49
3:U:87:U:H5''	3:U:88:A:H2'	1.94	0.49
3:U:1137:G:H21	3:U:1142:A:H62	1.60	0.49
3:U:2529:G:H5''	3:U:2530:A:H5''	1.93	0.49
4:V:75:G:H21	4:V:107:A:H62	1.60	0.49
3:U:774:G:H5'	3:U:775:C:H5''	1.94	0.49
3:U:1426:G:H5'	3:U:1571:C:OP1	2.12	0.49
3:U:1452:C:H2'	3:U:1453:C:N3	2.28	0.49
3:U:1823:U:H2'	3:U:1824:C:C6	2.48	0.49
3:U:1217:C:H5''	3:U:1218:G:C8	2.47	0.49
5:W:17:THR:HG22	5:W:204:ASN:HB3	1.93	0.49
2:H:3:GLU:HB2	2:I:1:MET:HE3	1.95	0.49
3:U:624:G:H2'	3:U:625:G:H8	1.76	0.49
3:U:1390:A:H2'	3:U:1391:A:C8	2.48	0.49
3:U:1474:C:H2'	3:U:1475:A:C8	2.47	0.49
3:U:1628:G:O2'	3:U:1629:A:O5'	2.26	0.49
3:U:1880:A:H2'	3:U:1881:A:C8	2.48	0.49
3:U:2488:C:H2'	3:U:2489:U:C6	2.47	0.49
2:I:95:ASP:OD1	2:I:96:VAL:N	2.45	0.49
3:U:1927:A:H1'	3:U:1997:A:H2'	1.95	0.49
3:U:2337:A:H2'	8:Z:74:ILE:HG23	1.94	0.49
5:W:108:LYS:HB3	5:W:196:GLY:HA2	1.95	0.49
3:U:533:G:N2	3:U:535:A:H3'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2238:U:HO2'	3:U:2239:A:P	2.34	0.48
3:U:2792:A:H5''	3:U:2793:G:H21	1.78	0.48
5:W:232:HIS:CD2	5:W:241:ILE:HG12	2.48	0.48
5:W:232:HIS:HD2	5:W:241:ILE:HG12	1.77	0.48
3:U:149:U:H2'	3:U:150:C:C6	2.48	0.48
3:U:927:G:N2	3:U:939:U:O2	2.36	0.48
3:U:1105:U:H2'	3:U:1114:A:H4'	1.95	0.48
3:U:1809:C:O2	3:U:2635:G:O2'	2.24	0.48
3:U:1873:G:H1	3:U:1922:C:H42	1.60	0.48
3:U:2196:G:H21	3:U:2197:G:H22	1.60	0.48
3:U:544:G:N1	3:U:547:A:OP2	2.40	0.48
3:U:1474:C:H2'	3:U:1475:A:H8	1.78	0.48
3:U:1546:U:H2'	3:U:1547:U:C6	2.49	0.48
3:U:2166:G:HO2'	3:U:2167:G:H8	1.60	0.48
3:U:574:G:O2'	3:U:576:A:N7	2.46	0.48
3:U:809:A:H5''	5:W:209:GLY:HA3	1.96	0.48
3:U:2774:G:N1	3:U:2783:U:OP1	2.39	0.48
2:I:39:PHE:HB3	2:I:45:LEU:HD11	1.95	0.48
3:U:1451:A:H2'	3:U:1452:C:C6	2.48	0.48
3:U:526:G:H1'	3:U:550:G:N2	2.24	0.48
3:U:749:G:H1'	3:U:772:A:N6	2.28	0.48
3:U:1117:A:H5''	3:U:1118:G:C8	2.49	0.48
3:U:1129:A:O2'	3:U:1130:A:O4'	2.26	0.48
7:Y:23:VAL:HG13	7:Y:111:LYS:HG2	1.95	0.48
3:U:885:C:H2'	3:U:886:A:H8	1.78	0.48
5:W:65:ILE:HD12	5:W:87:ARG:CZ	2.43	0.48
3:U:2127:G:H22	3:U:2216:U:H2'	1.79	0.48
3:U:153:U:H2'	3:U:154:A:H8	1.79	0.48
6:X:28:ILE:HD12	6:X:188:ILE:HD12	1.95	0.48
3:U:1135:G:H2'	3:U:1136:C:C6	2.49	0.47
2:H:27:GLU:HG3	2:H:31:ARG:HD2	1.96	0.47
3:U:660:U:OP1	7:Y:106:ARG:HD3	2.13	0.47
3:U:2406:G:H2'	3:U:2407:U:C6	2.48	0.47
3:U:1122:C:H2'	3:U:1132:A:C2	2.50	0.47
3:U:1337:A:H4'	3:U:1338:A:O5'	2.14	0.47
3:U:1596:C:OP1	3:U:1762:U:O2'	2.25	0.47
3:U:2622:G:N2	3:U:2625:A:OP2	2.35	0.47
6:X:138:ARG:O	6:X:142:ARG:NH2	2.48	0.47
3:U:315:G:H2'	3:U:316:A:H8	1.80	0.47
3:U:462:C:H2'	3:U:463:U:C6	2.50	0.47
3:U:1817:C:H2'	3:U:1818:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:365:G:H5''	7:Y:169:ASN:OD1	2.14	0.47
3:U:1106:G:N2	3:U:1107:G:C5	2.83	0.47
3:U:1226:G:N2	3:U:1227:U:O4	2.48	0.47
3:U:2688:G:H2'	3:U:2689:A:O4'	2.15	0.47
3:U:291:U:H2'	3:U:292:G:H8	1.78	0.47
3:U:1091:G:O2'	3:U:1092:A:O5'	2.33	0.47
3:U:1329:C:H2'	3:U:1330:U:C6	2.49	0.47
5:W:232:HIS:HE1	5:W:247:MET:H	1.62	0.47
2:H:40:THR:HB	6:X:43:ASN:HD21	1.78	0.47
2:I:8:LYS:HD3	2:I:9:ASP:H	1.80	0.47
3:U:347:C:H2'	3:U:348:U:C6	2.50	0.47
3:U:446:A:H2'	3:U:447:A:C8	2.50	0.47
3:U:741:U:H2'	3:U:742:C:C6	2.50	0.47
3:U:1114:A:H5'	3:U:1115:G:H5''	1.96	0.47
3:U:1530:A:H2'	3:U:1531:A:H8	1.80	0.47
3:U:1578:A:N6	3:U:1583:A:H62	2.04	0.47
3:U:2235:C:H2'	3:U:2236:C:C6	2.50	0.47
3:U:2256:U:H2'	3:U:2257:G:H8	1.80	0.47
3:U:2922:A:H2'	3:U:2923:C:C6	2.50	0.47
4:V:59:U:H4'	4:V:60:A:H5'	1.97	0.47
6:X:21:ASP:OD1	6:X:21:ASP:N	2.47	0.47
3:U:364:A:H5'	3:U:382:A:H1'	1.97	0.47
3:U:2165:C:H2'	3:U:2166:G:O4'	2.13	0.47
4:V:17:U:OP2	4:V:73:C:O2'	2.33	0.47
3:U:929:C:H2'	3:U:930:C:H6	1.78	0.47
5:W:144:ILE:HB	5:W:154:LEU:HB2	1.97	0.47
3:U:227:A:O2'	3:U:228:A:O5'	2.27	0.46
3:U:1846:A:OP2	5:W:155:VAL:HA	2.16	0.46
3:U:681:A:H4'	3:U:682:G:O5'	2.15	0.46
3:U:2318:U:OP1	3:U:2407:U:O2'	2.33	0.46
6:X:102:PHE:O	6:X:179:VAL:HG21	2.15	0.46
3:U:2163:A:H2	3:U:2183:G:H2'	1.79	0.46
3:U:2366:G:H2'	3:U:2367:A:H8	1.80	0.46
2:H:17:ALA:O	2:H:21:ILE:HG12	2.16	0.46
3:U:162:U:H2'	3:U:163:C:C6	2.51	0.46
8:Z:46:ASN:HA	8:Z:48:LYS:HE2	1.96	0.46
3:U:1129:A:O2'	3:U:1148:C:O2'	2.22	0.46
3:U:1357:G:H8	3:U:1357:G:OP2	1.99	0.46
7:Y:32:VAL:HG13	7:Y:105:VAL:HG13	1.96	0.46
2:I:72:THR:OG1	2:I:73:GLU:N	2.48	0.46
3:U:279:A:O2'	3:U:280:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:923:A:C6	3:U:924:G:C6	3.04	0.46
5:W:174:VAL:HG21	5:W:184:ILE:HD12	1.97	0.46
5:W:232:HIS:CE1	5:W:247:MET:H	2.33	0.46
3:U:917:U:H2'	3:U:918:G:C8	2.51	0.46
3:U:2225:A:N7	3:U:2252:A:N6	2.57	0.46
3:U:2360:A:H5'	3:U:2362:A:H1'	1.97	0.46
4:V:26:G:N2	4:V:64:U:C2	2.84	0.46
2:H:44:ASP:O	2:H:48:LYS:HG2	2.16	0.46
3:U:1725:A:H2'	3:U:1726:C:C6	2.50	0.46
3:U:2078:A:H8	3:U:2078:A:OP2	1.99	0.46
3:U:2670:G:H2'	3:U:2671:A:H8	1.81	0.46
3:U:2679:U:O2	3:U:2696:G:C2	2.69	0.46
4:V:9:G:C2	4:V:118:A:C2	3.04	0.46
3:U:2135:U:O2	3:U:2208:G:N2	2.49	0.46
3:U:2265:G:H2'	3:U:2265:G:N3	2.31	0.46
3:U:2383:C:H2'	3:U:2384:U:O4'	2.15	0.46
8:Z:42:ASP:C	8:Z:44:VAL:H	2.19	0.46
2:H:4:PHE:HB3	2:I:32:HIS:CE1	2.50	0.46
2:H:83:ARG:HG3	2:H:104:ALA:HB2	1.98	0.46
3:U:335:A:O2'	3:U:336:G:O4'	2.33	0.46
3:U:1553:A:H1'	3:U:1554:A:C8	2.51	0.46
3:U:2146:A:N1	3:U:2198:A:O2'	2.46	0.46
3:U:2338:A:O2'	3:U:2339:U:O4'	2.29	0.46
3:U:2876:U:H2'	3:U:2877:G:H8	1.81	0.46
4:V:120:G:H2'	4:V:121:C:C6	2.51	0.46
7:Y:27:GLU:HG2	7:Y:28:PRO:HD2	1.98	0.46
3:U:76:U:H2'	3:U:77:C:C6	2.52	0.45
3:U:630:U:H2'	3:U:631:U:C6	2.51	0.45
3:U:748:U:H2'	3:U:749:G:O4'	2.15	0.45
3:U:2826:G:H2'	3:U:2827:G:C8	2.50	0.45
8:Z:50:ILE:HG12	8:Z:150:ARG:HH22	1.80	0.45
3:U:1120:C:H3'	3:U:1121:A:C5'	2.43	0.45
8:Z:34:ILE:HD11	8:Z:154:ILE:HD11	1.98	0.45
8:Z:56:GLU:HA	8:Z:59:PHE:CZ	2.52	0.45
2:I:11:LYS:HE3	2:I:115:GLU:HG3	1.99	0.45
3:U:1356:G:H2'	3:U:1357:G:C8	2.51	0.45
3:U:1458:G:H1'	3:U:1629:A:N6	2.29	0.45
3:U:2374:C:O2'	3:U:2375:U:H6	2.00	0.45
3:U:543:U:H2'	3:U:544:G:O4'	2.16	0.45
3:U:2859:U:H2'	3:U:2860:A:C8	2.52	0.45
3:U:1185:U:H4'	3:U:1186:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1495:G:H22	3:U:1503:U:H3	1.63	0.45
3:U:1846:A:N1	5:W:274:ARG:NH1	2.65	0.45
3:U:38:U:H2'	3:U:39:A:H8	1.81	0.45
3:U:678:G:H2'	3:U:679:C:C6	2.52	0.45
3:U:714:G:H2'	3:U:714:G:N3	2.32	0.45
3:U:1017:A:H5'	3:U:1227:U:H1'	1.99	0.45
3:U:1447:C:H3'	3:U:1448:C:H5''	1.97	0.45
3:U:1942:U:O4	3:U:1989:C:O2'	2.29	0.45
3:U:2052:C:H2'	3:U:2053:U:C6	2.51	0.45
2:H:86:LYS:NZ	2:H:100:ARG:HH12	2.15	0.45
3:U:1341:C:HO2'	3:U:1342:C:C5'	2.29	0.45
3:U:2374:C:HO2'	3:U:2375:U:P	2.38	0.45
6:X:26:THR:OG1	6:X:190:GLY:O	2.29	0.45
3:U:692:G:H2'	3:U:693:G:H8	1.81	0.45
3:U:1516:G:H22	3:U:1564:G:H1	1.65	0.45
3:U:702:U:H2'	3:U:703:A:H8	1.81	0.45
3:U:885:C:H2'	3:U:886:A:C8	2.52	0.45
3:U:2725:U:H2'	3:U:2726:U:C6	2.52	0.45
3:U:192:A:H2'	3:U:193:C:C6	2.52	0.45
3:U:686:G:N2	3:U:689:U:OP2	2.36	0.45
3:U:947:U:H2'	3:U:948:U:C6	2.52	0.45
3:U:2132:A:N1	3:U:2212:G:C6	2.85	0.45
3:U:2274:A:H2'	3:U:2275:C:H6	1.82	0.45
3:U:646:G:H2'	3:U:647:G:H8	1.82	0.44
3:U:963:A:N3	4:V:83:U:O2'	2.50	0.44
3:U:1357:G:N2	3:U:1368:C:N4	2.59	0.44
3:U:2314:A:O2'	3:U:2315:A:H2'	2.16	0.44
3:U:925:G:H2'	3:U:926:G:H8	1.79	0.44
3:U:1120:C:C6	3:U:1122:C:H4'	2.52	0.44
3:U:1135:G:H2'	3:U:1136:C:H6	1.81	0.44
3:U:1885:G:H2'	3:U:1910:G:H22	1.82	0.44
3:U:2584:G:H2'	3:U:2585:C:C6	2.53	0.44
4:V:64:U:H2'	4:V:65:C:C6	2.50	0.44
7:Y:2:PRO:HD2	7:Y:118:VAL:HG11	1.99	0.44
3:U:1059:A:H2'	3:U:1060:C:C6	2.52	0.44
3:U:1091:G:HO2'	3:U:1092:A:H8	1.63	0.44
3:U:1901:C:H2'	3:U:1902:G:O4'	2.17	0.44
3:U:2098:A:H2'	3:U:2099:G:C8	2.53	0.44
3:U:2374:C:O2'	3:U:2375:U:O5'	2.25	0.44
8:Z:42:ASP:HA	8:Z:50:ILE:HG21	2.00	0.44
3:U:892:A:H62	3:U:977:U:H3	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2161:A:N6	3:U:2185:A:O4'	2.51	0.44
6:X:98:LYS:HE2	6:X:98:LYS:HB2	1.81	0.44
3:U:1446:U:H1'	3:U:1447:C:H5	1.82	0.44
3:U:1898:A:H5''	3:U:1899:A:N7	2.33	0.44
3:U:2189:A:H5''	3:U:2199:U:C5	2.52	0.44
8:Z:166:ALA:O	8:Z:170:LEU:HG	2.17	0.44
3:U:265:C:H4'	3:U:266:A:OP1	2.17	0.44
3:U:292:G:C6	3:U:293:G:N7	2.85	0.44
3:U:596:U:H2'	3:U:597:G:O4'	2.17	0.44
3:U:858:U:H2'	3:U:859:C:C6	2.52	0.44
3:U:1142:A:H3'	3:U:1143:G:H8	1.82	0.44
3:U:1451:A:H2'	3:U:1452:C:H6	1.83	0.44
3:U:1516:G:H22	3:U:1564:G:H22	1.66	0.44
3:U:1976:G:H2'	3:U:1977:G:C8	2.52	0.44
3:U:2007:G:H3'	3:U:2008:A:H5''	1.99	0.44
3:U:2104:A:H2'	3:U:2105:C:C6	2.52	0.44
3:U:2327:A:H2'	3:U:2328:A:C8	2.52	0.44
7:Y:132:ASP:OD1	7:Y:133:THR:N	2.44	0.44
3:U:762:C:H5''	3:U:763:A:H2	1.83	0.44
3:U:2243:G:O2'	3:U:2244:G:H8	1.99	0.44
3:U:2540:A:H2'	3:U:2541:U:C6	2.53	0.44
3:U:2877:G:H2'	3:U:2878:U:H6	1.82	0.44
4:V:32:A:O2'	4:V:61:A:N1	2.48	0.44
6:X:40:THR:HA	6:X:47:GLU:OE2	2.18	0.44
8:Z:57:LEU:HD23	8:Z:60:ILE:HD11	1.98	0.44
3:U:1044:A:H2'	3:U:1045:A:C8	2.53	0.44
3:U:1491:C:O2'	3:U:1590:A:N3	2.50	0.44
3:U:2333:U:H5''	3:U:2334:G:H3'	2.00	0.44
5:W:19:SER:OG	5:W:20:ASP:N	2.51	0.44
3:U:716:C:HO2'	3:U:717:C:H6	1.63	0.44
3:U:787:C:H2'	3:U:788:A:C8	2.53	0.44
3:U:1896:G:C2	3:U:1900:G:C6	3.06	0.44
3:U:576:A:H4'	3:U:577:G:C8	2.53	0.43
3:U:1072:A:H2'	3:U:1073:A:C8	2.53	0.43
3:U:2209:G:H2'	3:U:2210:C:C6	2.54	0.43
3:U:2309:G:H4'	3:U:2416:G:O2'	2.18	0.43
6:X:95:GLN:HG2	6:X:96:GLU:H	1.83	0.43
8:Z:119:LYS:HA	8:Z:122:PHE:HE1	1.82	0.43
3:U:310:G:H2'	3:U:311:U:O4'	2.18	0.43
8:Z:9:ASN:HD21	8:Z:30:LYS:HE2	1.82	0.43
3:U:153:U:H2'	3:U:154:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:862:C:O2'	3:U:884:U:OP1	2.34	0.43
3:U:878:C:H2'	3:U:879:U:C6	2.53	0.43
3:U:1008:C:O2'	3:U:2300:A:N3	2.43	0.43
3:U:1104:U:N3	3:U:1106:G:C8	2.86	0.43
3:U:1511:U:C5	3:U:1592:G:H2'	2.53	0.43
3:U:1752:U:H2'	3:U:1753:C:C6	2.53	0.43
3:U:2870:U:H2'	3:U:2871:G:O4'	2.17	0.43
8:Z:52:SER:HA	8:Z:55:GLU:CD	2.38	0.43
8:Z:99:PHE:HD1	8:Z:102:LYS:NZ	2.16	0.43
3:U:276:A:H2'	3:U:277:A:H8	1.83	0.43
3:U:628:A:H5'	7:Y:89:VAL:HG21	2.00	0.43
3:U:745:G:O2'	3:U:1675:A:N3	2.34	0.43
3:U:1243:G:H1'	3:U:1244:G:C5'	2.48	0.43
3:U:1505:U:H2'	3:U:1506:C:C6	2.54	0.43
3:U:2567:C:H2'	3:U:2568:A:O4'	2.18	0.43
3:U:2670:G:H2'	3:U:2671:A:C8	2.54	0.43
3:U:400:U:H2'	3:U:401:C:C6	2.53	0.43
3:U:681:A:H1'	3:U:682:G:OP2	2.19	0.43
3:U:1123:C:H2'	3:U:1124:A:C8	2.54	0.43
3:U:1577:A:H2'	3:U:1578:A:C8	2.53	0.43
3:U:2260:A:H2'	3:U:2261:G:H8	1.83	0.43
4:V:48:A:H3'	4:V:49:A:C8	2.53	0.43
3:U:76:U:H2'	3:U:77:C:H6	1.83	0.43
3:U:290:U:H2'	3:U:291:U:C6	2.54	0.43
3:U:1864:C:O2'	3:U:1954:A:N3	2.47	0.43
5:W:133:ILE:HG12	5:W:186:SER:HB2	2.00	0.43
8:Z:104:ILE:HD12	8:Z:108:LEU:HD13	1.99	0.43
3:U:65:A:H1'	3:U:86:G:N2	2.34	0.43
3:U:285:G:OP2	3:U:286:C:N4	2.46	0.43
3:U:300:A:H2'	3:U:301:G:H8	1.84	0.43
3:U:676:A:H2'	3:U:677:A:C8	2.54	0.43
3:U:1222:A:H2'	3:U:1223:G:O4'	2.19	0.43
3:U:1476:G:H2'	3:U:1477:G:C8	2.53	0.43
3:U:1945:A:O2'	3:U:1947:C:N4	2.51	0.43
3:U:2431:C:H2'	3:U:2432:G:O4'	2.17	0.43
3:U:2772:C:H2'	3:U:2773:U:C6	2.54	0.43
4:V:48:A:H2'	4:V:48:A:N3	2.34	0.43
8:Z:106:VAL:HG21	8:Z:139:PRO:HD3	1.99	0.43
3:U:7:U:H2'	3:U:8:A:H8	1.83	0.43
3:U:289:C:H2'	3:U:290:U:H6	1.84	0.43
3:U:2134:C:H2'	3:U:2135:U:C2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:2679:U:C2	3:U:2696:G:N1	2.87	0.43
8:Z:74:ILE:HG22	8:Z:76:GLY:H	1.83	0.43
3:U:619:G:H2'	3:U:620:A:C8	2.53	0.43
3:U:927:G:N1	3:U:939:U:N3	2.45	0.43
3:U:1085:U:H2'	3:U:1086:G:H8	1.84	0.43
3:U:1513:C:H2'	3:U:1514:A:C8	2.54	0.43
3:U:1671:G:H2'	3:U:1672:G:C8	2.52	0.43
3:U:2145:U:O4	3:U:2174:A:O2'	2.31	0.43
3:U:2342:U:H2'	3:U:2343:U:C6	2.53	0.43
3:U:2347:A:N3	3:U:2347:A:H2'	2.34	0.43
3:U:288:U:C2	3:U:289:C:C5	3.07	0.43
3:U:946:A:H2'	3:U:947:U:O4'	2.19	0.43
3:U:2147:G:H2'	3:U:2148:G:C8	2.53	0.43
8:Z:163:ASP:O	8:Z:167:ARG:HG3	2.19	0.43
3:U:484:A:H2'	3:U:485:G:O4'	2.19	0.42
3:U:877:G:H2'	3:U:878:C:C6	2.54	0.42
3:U:909:G:N2	3:U:911:A:H61	2.17	0.42
3:U:1085:U:H2'	3:U:1086:G:C8	2.54	0.42
3:U:1530:A:H2'	3:U:1531:A:C8	2.54	0.42
3:U:2187:G:H2'	3:U:2188:C:C6	2.54	0.42
3:U:2687:A:H2'	3:U:2688:G:O4'	2.19	0.42
3:U:2876:U:H2'	3:U:2877:G:C8	2.54	0.42
4:V:7:U:H5'	4:V:8:U:OP2	2.19	0.42
4:V:26:G:H1	4:V:63:C:H42	1.67	0.42
7:Y:188:ASN:C	7:Y:189:HIS:HD1	2.22	0.42
2:I:53:VAL:HG12	2:I:53:VAL:O	2.19	0.42
3:U:232:C:H3'	3:U:233:G:C8	2.54	0.42
3:U:285:G:P	3:U:286:C:H41	2.41	0.42
3:U:660:U:H2'	3:U:661:G:H8	1.85	0.42
3:U:2169:G:OP1	3:U:2208:G:O2'	2.34	0.42
2:I:18:LEU:HD13	2:I:111:TYR:HB2	2.02	0.42
3:U:673:C:O2	3:U:683:U:O2'	2.36	0.42
3:U:2168:A:H2'	3:U:2208:G:H21	1.84	0.42
3:U:2494:C:H2'	3:U:2495:A:O4'	2.19	0.42
3:U:2871:G:H1'	3:U:2891:A:H61	1.83	0.42
3:U:281:G:H2'	3:U:282:C:O4'	2.19	0.42
3:U:909:G:O2'	3:U:910:C:O5'	2.37	0.42
3:U:1138:U:H5''	3:U:1139:A:C5'	2.49	0.42
3:U:1823:U:H2'	3:U:1824:C:H6	1.84	0.42
3:U:2168:A:N6	3:U:2178:U:H3	2.17	0.42
3:U:10:A:O2'	3:U:11:A:OP1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:199:C:O2'	3:U:200:A:H5'	2.19	0.42
3:U:1143:G:H2'	3:U:1144:C:C6	2.54	0.42
3:U:1817:C:O2'	5:W:208:ALA:HB2	2.18	0.42
3:U:1952:C:H2'	3:U:1953:U:C6	2.55	0.42
8:Z:132:ILE:HG21	8:Z:152:MET:H	1.84	0.42
3:U:-1:G:O6	3:U:2925:A:N6	2.52	0.42
3:U:825:G:H2'	3:U:827:A:N7	2.35	0.42
3:U:1495:G:H1	3:U:1503:U:H3	1.67	0.42
3:U:1555:G:H3'	3:U:1556:G:H8	1.85	0.42
3:U:2157:U:H4'	3:U:2161:A:H2	1.84	0.42
3:U:2211:U:H2'	3:U:2212:G:C8	2.55	0.42
3:U:2326:G:H2'	3:U:2327:A:C8	2.55	0.42
3:U:2846:A:OP1	6:X:119:PHE:HB2	2.18	0.42
6:X:126:HIS:CE1	6:X:159:LEU:HD22	2.55	0.42
3:U:945:A:H3'	3:U:946:A:H5''	2.02	0.42
3:U:1136:C:N4	3:U:1137:G:C6	2.88	0.42
3:U:1217:C:H3'	3:U:1218:G:O4'	2.19	0.42
3:U:2574:U:O2'	3:U:2575:G:H5''	2.20	0.42
8:Z:42:ASP:OD1	8:Z:50:ILE:HG22	2.20	0.42
3:U:1306:A:H2'	3:U:1307:G:O4'	2.20	0.42
4:V:58:U:O3'	8:Z:24:SER:OG	2.37	0.42
4:V:80:U:H2'	4:V:81:A:C8	2.55	0.42
3:U:1436:C:HO2'	3:U:1437:U:P	2.41	0.42
3:U:1732:A:H2'	3:U:1733:A:C8	2.55	0.42
3:U:2594:G:H2'	3:U:2595:C:C6	2.55	0.42
5:W:69:ARG:HE	5:W:69:ARG:HB3	1.76	0.42
3:U:937:G:N1	3:U:938:G:O6	2.53	0.42
3:U:1363:U:HO2'	3:U:2037:G:HO2'	1.51	0.42
3:U:2327:A:H2'	3:U:2328:A:H8	1.83	0.42
3:U:2880:G:N2	3:U:2883:A:OP2	2.46	0.42
3:U:2882:G:O5'	3:U:2882:G:H8	2.03	0.42
3:U:280:G:C2	3:U:281:G:C5	3.08	0.41
3:U:280:G:C2	3:U:288:U:C2	3.08	0.41
3:U:389:A:H2'	3:U:390:C:C6	2.55	0.41
3:U:1887:G:H2'	3:U:1888:C:C6	2.55	0.41
3:U:2223:C:H2'	3:U:2224:U:C6	2.55	0.41
3:U:894:A:H2'	3:U:895:G:H8	1.84	0.41
3:U:2092:C:H2'	3:U:2093:C:H6	1.85	0.41
4:V:44:A:OP1	4:V:46:C:N4	2.53	0.41
8:Z:38:MET:HB3	8:Z:87:ALA:H	1.85	0.41
3:U:39:A:H2'	3:U:40:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1529:G:H2'	3:U:1530:A:H8	1.85	0.41
3:U:1821:U:H2'	3:U:1822:C:H6	1.85	0.41
3:U:2093:C:H2'	3:U:2094:G:C8	2.55	0.41
3:U:2218:A:H2'	3:U:2219:C:H6	1.85	0.41
3:U:250:C:H4'	3:U:251:G:O5'	2.20	0.41
3:U:1243:G:O2'	3:U:1244:G:O5'	2.38	0.41
3:U:1453:C:O2'	3:U:1454:A:O5'	2.25	0.41
3:U:1631:G:H2'	3:U:1632:U:C6	2.54	0.41
3:U:2341:A:H2'	3:U:2342:U:H6	1.84	0.41
4:V:80:U:H2'	4:V:81:A:H8	1.84	0.41
6:X:95:GLN:HG2	6:X:96:GLU:N	2.35	0.41
8:Z:175:MET:HB2	8:Z:177:PHE:CE2	2.55	0.41
3:U:184:C:H42	3:U:214:A:N6	2.19	0.41
3:U:896:U:H2'	3:U:897:C:H6	1.86	0.41
3:U:1423:C:H2'	3:U:1424:A:H8	1.84	0.41
3:U:1517:C:C4	3:U:1518:A:N1	2.88	0.41
3:U:1315:G:H2'	3:U:1316:G:H8	1.86	0.41
3:U:1726:C:H2'	3:U:1727:C:H6	1.86	0.41
3:U:1788:U:H3	3:U:1789:A:N6	2.19	0.41
3:U:2144:A:HO2'	3:U:2145:U:H5	1.68	0.41
8:Z:83:MET:HB3	8:Z:84:PRO:HD2	2.03	0.41
2:I:109:LEU:HD21	2:I:124:LEU:HD22	2.01	0.41
3:U:1007:U:H2'	3:U:1008:C:C6	2.56	0.41
3:U:1695:A:H2'	3:U:1696:G:O4'	2.20	0.41
3:U:1725:A:OP2	3:U:1742:G:N2	2.52	0.41
3:U:2701:G:H2'	3:U:2702:A:C8	2.55	0.41
4:V:48:A:H8	8:Z:92:ARG:HD2	1.85	0.41
8:Z:108:LEU:H	8:Z:108:LEU:HD12	1.84	0.41
3:U:87:U:H3'	3:U:88:A:H8	1.85	0.41
3:U:292:G:C4	3:U:293:G:C8	3.09	0.41
3:U:536:A:H2'	3:U:537:G:O4'	2.21	0.41
3:U:1070:A:C4	3:U:1178:C:H5	2.39	0.41
3:U:1086:G:H2'	3:U:1087:C:H6	1.86	0.41
3:U:2182:U:H5''	3:U:2184:G:N1	2.35	0.41
3:U:2317:G:H2'	3:U:2318:U:C6	2.55	0.41
7:Y:135:LYS:HE3	7:Y:135:LYS:HB3	1.88	0.41
2:H:56:LYS:O	2:H:60:GLU:HG2	2.20	0.41
3:U:276:A:C6	3:U:292:G:C6	3.09	0.41
3:U:749:G:H2'	3:U:771:G:N2	2.35	0.41
3:U:1114:A:C6	3:U:1141:U:H1'	2.55	0.41
3:U:1240:U:H2'	3:U:1241:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1240:U:H2'	3:U:1241:A:H8	1.86	0.41
3:U:1471:A:H4'	3:U:1472:C:O5'	2.20	0.41
3:U:1545:U:H2'	3:U:1546:U:H6	1.86	0.41
3:U:1755:G:O4'	3:U:1757:U:H5'	2.20	0.41
3:U:1765:A:H2'	3:U:1766:A:C8	2.56	0.41
3:U:1777:G:O2'	3:U:1778:C:P	2.79	0.41
3:U:2074:C:H2'	3:U:2075:G:H8	1.86	0.41
3:U:2101:U:H2'	3:U:2102:U:C6	2.56	0.41
3:U:2142:G:N1	3:U:2146:A:N7	2.69	0.41
3:U:2541:U:H2'	3:U:2542:C:H6	1.85	0.41
3:U:2859:U:H2'	3:U:2860:A:H8	1.86	0.41
4:V:27:G:H4'	4:V:28:U:H5	1.86	0.41
4:V:97:C:H2'	4:V:98:U:C6	2.56	0.41
8:Z:138:PHE:CG	8:Z:139:PRO:HD2	2.56	0.41
3:U:503:G:O2'	3:U:514:G:O6	2.32	0.41
3:U:1757:U:H2'	3:U:1758:A:H8	1.85	0.41
3:U:2260:A:H2'	3:U:2261:G:C8	2.56	0.41
7:Y:13:THR:HG22	7:Y:14:ALA:N	2.36	0.41
8:Z:121:SER:HB2	8:Z:129:THR:HG22	2.02	0.41
3:U:1726:C:H2'	3:U:1727:C:C6	2.56	0.40
3:U:2372:G:N3	3:U:2408:C:H2'	2.36	0.40
5:W:58:HIS:CD2	5:W:59:LYS:H	2.38	0.40
3:U:1543:C:H2'	3:U:1544:G:H8	1.86	0.40
3:U:1900:G:H2'	3:U:1901:C:C6	2.57	0.40
7:Y:26:ILE:HG12	7:Y:27:GLU:N	2.36	0.40
3:U:130:C:H2'	3:U:131:A:H8	1.87	0.40
3:U:1090:A:H4'	3:U:1091:G:OP2	2.22	0.40
3:U:2664:U:H2'	3:U:2665:G:O4'	2.21	0.40
2:I:114:LEU:HD23	2:I:114:LEU:HA	1.89	0.40
3:U:290:U:H2'	3:U:291:U:H6	1.85	0.40
3:U:1219:A:H2'	3:U:1220:A:H8	1.85	0.40
3:U:1318:G:H2'	3:U:1319:U:C6	2.57	0.40
3:U:2218:A:H2'	3:U:2219:C:C6	2.57	0.40
2:I:51:ARG:NE	2:I:51:ARG:HA	2.37	0.40
3:U:151:C:C2	3:U:152:A:C8	3.10	0.40
3:U:285:G:H3'	3:U:286:C:C5	2.56	0.40
3:U:417:G:O2'	3:U:445:G:O6	2.27	0.40
3:U:1093:C:C2	3:U:1094:A:C8	3.09	0.40
3:U:1469:G:H2'	3:U:1470:G:C8	2.57	0.40
3:U:1527:G:P	3:U:1527:G:H8	2.45	0.40
3:U:1942:U:H3	3:U:1963:A:N6	2.18	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:1979:A:N3	3:U:2587:C:O2'	2.48	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	121/166 (73%)	101 (84%)	20 (16%)	0	100	100
2	H	130/143 (91%)	127 (98%)	3 (2%)	0	100	100
2	I	132/143 (92%)	128 (97%)	4 (3%)	0	100	100
5	W	273/277 (99%)	252 (92%)	21 (8%)	0	100	100
6	X	205/209 (98%)	194 (95%)	11 (5%)	0	100	100
7	Y	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
8	Z	176/179 (98%)	159 (90%)	17 (10%)	0	100	100
9	a	173/179 (97%)	160 (92%)	13 (8%)	0	100	100
10	c	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
11	d	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
12	e	144/146 (99%)	132 (92%)	12 (8%)	0	100	100
13	f	136/144 (94%)	130 (96%)	6 (4%)	0	100	100
14	g	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
15	h	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
16	i	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
17	j	115/119 (97%)	107 (93%)	8 (7%)	0	100	100
18	k	99/102 (97%)	85 (86%)	14 (14%)	0	100	100
19	l	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
20	m	91/95 (96%)	88 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	n	99/103 (96%)	88 (89%)	11 (11%)	0	100	100
22	o	80/94 (85%)	75 (94%)	5 (6%)	0	100	100
23	p	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
24	q	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
25	r	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
26	s	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
27	t	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
28	u	56/62 (90%)	51 (91%)	5 (9%)	0	100	100
29	v	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
30	w	56/59 (95%)	56 (100%)	0	0	100	100
All	All	3302/3483 (95%)	3080 (93%)	222 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
1	b	105/138 (76%)	100 (95%)	5 (5%)	25	57
2	H	114/123 (93%)	113 (99%)	1 (1%)	78	90
2	I	116/123 (94%)	116 (100%)	0	100	100
5	W	223/225 (99%)	223 (100%)	0	100	100
6	X	168/170 (99%)	168 (100%)	0	100	100
7	Y	169/170 (99%)	168 (99%)	1 (1%)	86	93
8	Z	153/154 (99%)	149 (97%)	4 (3%)	46	72
9	a	148/151 (98%)	148 (100%)	0	100	100
10	c	120/123 (98%)	120 (100%)	0	100	100
11	d	101/101 (100%)	100 (99%)	1 (1%)	76	89
12	e	110/110 (100%)	109 (99%)	1 (1%)	78	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	f	111/116 (96%)	111 (100%)	0	100	100
14	g	99/100 (99%)	99 (100%)	0	100	100
15	h	93/93 (100%)	92 (99%)	1 (1%)	73	88
16	i	99/100 (99%)	97 (98%)	2 (2%)	55	78
17	j	96/98 (98%)	96 (100%)	0	100	100
18	k	83/84 (99%)	83 (100%)	0	100	100
19	l	90/93 (97%)	89 (99%)	1 (1%)	73	88
20	m	84/85 (99%)	84 (100%)	0	100	100
21	n	85/87 (98%)	85 (100%)	0	100	100
22	o	64/74 (86%)	63 (98%)	1 (2%)	62	83
23	p	48/53 (91%)	48 (100%)	0	100	100
24	q	46/47 (98%)	45 (98%)	1 (2%)	52	76
25	r	39/39 (100%)	39 (100%)	0	100	100
26	s	54/56 (96%)	54 (100%)	0	100	100
27	t	34/35 (97%)	34 (100%)	0	100	100
28	u	47/50 (94%)	47 (100%)	0	100	100
29	v	56/57 (98%)	56 (100%)	0	100	100
30	w	52/53 (98%)	52 (100%)	0	100	100
All	All	2807/2908 (96%)	2788 (99%)	19 (1%)	84	92

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	42	ARG
1	b	62	ARG
1	b	84	PHE
1	b	94	LYS
1	b	101	LYS
2	H	8	LYS
7	Y	206	LEU
8	Z	3	ARG
8	Z	5	LYS
8	Z	80	ARG
8	Z	95	ARG
11	d	122	ILE
12	e	71	ARG

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Mol	Chain	Res	Type
15	h	61	LYS
16	i	13	LYS
16	i	54	ARG
19	l	92	ARG
22	o	22	ARG
24	q	48	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	97	ASN
1	b	102	ASN
2	H	23	ASN
2	H	58	GLN
2	H	68	GLN
2	I	32	HIS
2	I	33	HIS
2	I	43	ASN
2	I	46	HIS
2	I	58	GLN
2	I	93	ASN
5	W	58	HIS
5	W	230	HIS
6	X	43	ASN
6	X	126	HIS
6	X	173	ASN
7	Y	40	GLN
8	Z	9	ASN
8	Z	45	GLN
8	Z	63	GLN
8	Z	161	ASN
9	a	20	ASN
9	a	23	ASN
9	a	62	HIS
10	c	8	ASN
10	c	59	ASN
10	c	96	ASN
10	c	118	GLN
11	d	4	GLN
12	e	38	GLN
12	e	39	ASN
12	e	78	ASN

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Mol	Chain	Res	Type
14	g	61	GLN
15	h	43	GLN
17	j	29	HIS
17	j	37	GLN
17	j	52	GLN
17	j	107	ASN
18	k	86	GLN
19	l	28	GLN
21	n	64	HIS
21	n	99	GLN
23	p	40	HIS
24	q	25	ASN
28	u	20	HIS
28	u	41	ASN
29	v	65	ASN
30	w	33	GLN
30	w	37	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	U	2929/2930 (99%)	618 (21%)	29 (0%)
4	V	115/116 (99%)	30 (26%)	3 (2%)
All	All	3044/3046 (99%)	648 (21%)	32 (1%)

All (648) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	U	11	A
3	U	13	G
3	U	26	A
3	U	31	U
3	U	32	U
3	U	40	G
3	U	42	A
3	U	43	G
3	U	44	C
3	U	47	A
3	U	53	G
3	U	59	A
3	U	61	G

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Mol	Chain	Res	Type
3	U	66	C
3	U	69	A
3	U	73	G
3	U	89	A
3	U	90	G
3	U	92	A
3	U	98	U
3	U	100	A
3	U	115	A
3	U	116	A
3	U	117	U
3	U	128	A
3	U	148	A
3	U	158	G
3	U	161	U
3	U	162	U
3	U	164	A
3	U	173	G
3	U	175	G
3	U	176	A
3	U	188	G
3	U	197	A
3	U	200	A
3	U	214	A
3	U	217	A
3	U	223	A
3	U	224	A
3	U	225	G
3	U	228	A
3	U	231	G
3	U	234	A
3	U	243	G
3	U	246	G
3	U	249	G
3	U	251	G
3	U	256	A
3	U	266	A
3	U	267	G
3	U	273	A
3	U	279	A
3	U	280	G
3	U	284	U

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Mol	Chain	Res	Type
3	U	285	G
3	U	286	C
3	U	288	U
3	U	296	U
3	U	297	U
3	U	298	G
3	U	299	U
3	U	300	A
3	U	302	G
3	U	311	U
3	U	312	A
3	U	313	C
3	U	319	U
3	U	322	A
3	U	325	G
3	U	336	G
3	U	342	G
3	U	344	G
3	U	353	A
3	U	365	G
3	U	366	G
3	U	370	U
3	U	371	A
3	U	372	A
3	U	380	G
3	U	386	A
3	U	388	A
3	U	390	C
3	U	403	U
3	U	404	G
3	U	409	G
3	U	415	G
3	U	416	A
3	U	417	G
3	U	431	G
3	U	432	U
3	U	448	U
3	U	451	G
3	U	461	U
3	U	465	C
3	U	481	C
3	U	485	G

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Mol	Chain	Res	Type
3	U	501	C
3	U	502	A
3	U	512	G
3	U	518	G
3	U	522	A
3	U	526	G
3	U	527	C
3	U	535	A
3	U	536	A
3	U	548	G
3	U	549	A
3	U	552	U
3	U	553	C
3	U	554	C
3	U	565	U
3	U	566	G
3	U	572	A
3	U	573	A
3	U	574	G
3	U	575	U
3	U	576	A
3	U	577	G
3	U	582	A
3	U	590	A
3	U	593	G
3	U	605	G
3	U	614	A
3	U	615	G
3	U	617	A
3	U	639	C
3	U	645	A
3	U	646	G
3	U	647	G
3	U	649	U
3	U	651	A
3	U	662	C
3	U	664	G
3	U	675	A
3	U	681	A
3	U	682	G
3	U	687	A
3	U	689	U

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Mol	Chain	Res	Type
3	U	698	U
3	U	699	G
3	U	714	G
3	U	715	A
3	U	717	C
3	U	729	G
3	U	730	A
3	U	731	U
3	U	738	A
3	U	756	A
3	U	761	A
3	U	762	C
3	U	775	C
3	U	792	U
3	U	793	G
3	U	809	A
3	U	810	G
3	U	820	G
3	U	827	A
3	U	828	A
3	U	829	U
3	U	830	G
3	U	837	G
3	U	839	A
3	U	847	A
3	U	850	G
3	U	857	C
3	U	864	A
3	U	872	U
3	U	873	U
3	U	883	C
3	U	890	U
3	U	904	G
3	U	910	C
3	U	911	A
3	U	916	U
3	U	919	G
3	U	922	U
3	U	923	A
3	U	924	G
3	U	927	G
3	U	932	U

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Mol	Chain	Res	Type
3	U	933	A
3	U	934	C
3	U	935	C
3	U	938	G
3	U	940	U
3	U	941	A
3	U	942	C
3	U	943	C
3	U	944	G
3	U	946	A
3	U	950	A
3	U	952	U
3	U	953	C
3	U	955	A
3	U	956	A
3	U	957	C
3	U	959	C
3	U	960	C
3	U	962	A
3	U	971	G
3	U	985	A
3	U	989	A
3	U	990	G
3	U	1005	G
3	U	1018	A
3	U	1025	A
3	U	1027	A
3	U	1032	A
3	U	1040	A
3	U	1041	G
3	U	1043	U
3	U	1044	A
3	U	1056	U
3	U	1057	A
3	U	1061	G
3	U	1069	G
3	U	1070	A
3	U	1077	U
3	U	1089	U
3	U	1090	A
3	U	1091	G
3	U	1092	A

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Mol	Chain	Res	Type
3	U	1099	G
3	U	1100	G
3	U	1101	A
3	U	1102	U
3	U	1103	G
3	U	1104	U
3	U	1105	U
3	U	1106	G
3	U	1107	G
3	U	1109	U
3	U	1110	U
3	U	1111	A
3	U	1113	A
3	U	1117	A
3	U	1118	G
3	U	1119	C
3	U	1120	C
3	U	1121	A
3	U	1122	C
3	U	1124	A
3	U	1126	U
3	U	1127	U
3	U	1132	A
3	U	1133	G
3	U	1134	U
3	U	1137	G
3	U	1138	U
3	U	1139	A
3	U	1140	A
3	U	1141	U
3	U	1142	A
3	U	1143	G
3	U	1146	C
3	U	1149	U
3	U	1155	A
3	U	1156	G
3	U	1158	G
3	U	1171	A
3	U	1172	A
3	U	1174	U
3	U	1176	U
3	U	1177	A

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Mol	Chain	Res	Type
3	U	1178	C
3	U	1179	C
3	U	1183	G
3	U	1186	A
3	U	1192	A
3	U	1213	U
3	U	1216	U
3	U	1217	C
3	U	1218	G
3	U	1220	A
3	U	1223	G
3	U	1244	G
3	U	1245	G
3	U	1246	C
3	U	1250	G
3	U	1258	A
3	U	1261	G
3	U	1267	A
3	U	1276	G
3	U	1285	A
3	U	1288	G
3	U	1291	A
3	U	1294	G
3	U	1310	A
3	U	1312	A
3	U	1313	G
3	U	1337	A
3	U	1338	A
3	U	1339	U
3	U	1342	C
3	U	1343	U
3	U	1362	C
3	U	1375	G
3	U	1382	C
3	U	1383	G
3	U	1389	U
3	U	1397	G
3	U	1402	A
3	U	1412	G
3	U	1416	U
3	U	1421	A
3	U	1422	A

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Mol	Chain	Res	Type
3	U	1432	A
3	U	1433	U
3	U	1437	U
3	U	1439	U
3	U	1447	C
3	U	1448	C
3	U	1454	A
3	U	1457	U
3	U	1458	G
3	U	1463	A
3	U	1464	U
3	U	1471	A
3	U	1472	C
3	U	1473	G
3	U	1476	G
3	U	1484	G
3	U	1488	A
3	U	1493	C
3	U	1494	G
3	U	1497	A
3	U	1499	U
3	U	1502	A
3	U	1503	U
3	U	1504	A
3	U	1505	U
3	U	1511	U
3	U	1513	C
3	U	1517	C
3	U	1522	A
3	U	1526	U
3	U	1534	A
3	U	1537	C
3	U	1552	U
3	U	1553	A
3	U	1559	G
3	U	1560	A
3	U	1561	G
3	U	1568	U
3	U	1569	G
3	U	1571	C
3	U	1574	G
3	U	1575	C

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Mol	Chain	Res	Type
3	U	1579	A
3	U	1580	U
3	U	1582	U
3	U	1584	G
3	U	1585	U
3	U	1594	U
3	U	1605	C
3	U	1612	A
3	U	1615	A
3	U	1624	U
3	U	1629	A
3	U	1630	G
3	U	1636	A
3	U	1643	C
3	U	1650	C
3	U	1651	A
3	U	1652	A
3	U	1653	A
3	U	1660	C
3	U	1661	A
3	U	1689	A
3	U	1690	U
3	U	1691	C
3	U	1695	A
3	U	1698	A
3	U	1710	G
3	U	1717	G
3	U	1718	C
3	U	1720	A
3	U	1736	U
3	U	1737	C
3	U	1755	G
3	U	1760	G
3	U	1772	A
3	U	1775	G
3	U	1776	A
3	U	1777	G
3	U	1778	C
3	U	1780	G
3	U	1781	C
3	U	1790	G
3	U	1791	G

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Mol	Chain	Res	Type
3	U	1800	A
3	U	1803	G
3	U	1808	G
3	U	1809	C
3	U	1811	A
3	U	1812	A
3	U	1815	C
3	U	1827	C
3	U	1829	A
3	U	1836	A
3	U	1843	A
3	U	1844	G
3	U	1856	A
3	U	1860	C
3	U	1876	G
3	U	1898	A
3	U	1899	A
3	U	1900	G
3	U	1904	A
3	U	1910	G
3	U	1911	A
3	U	1916	A
3	U	1928	A
3	U	1933	G
3	U	1940	A
3	U	1942	U
3	U	1943	A
3	U	1945	A
3	U	1947	C
3	U	1954	A
3	U	1956	G
3	U	1957	G
3	U	1963	A
3	U	1965	A
3	U	1982	U
3	U	1994	C
3	U	1997	A
3	U	1998	A
3	U	1999	G
3	U	2008	A
3	U	2018	U
3	U	2020	U

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Mol	Chain	Res	Type
3	U	2023	C
3	U	2024	A
3	U	2050	A
3	U	2058	A
3	U	2059	G
3	U	2060	A
3	U	2068	U
3	U	2070	C
3	U	2071	C
3	U	2082	C
3	U	2083	G
3	U	2086	A
3	U	2087	A
3	U	2088	G
3	U	2090	C
3	U	2091	C
3	U	2096	G
3	U	2107	G
3	U	2120	G
3	U	2123	U
3	U	2130	A
3	U	2132	A
3	U	2138	U
3	U	2139	A
3	U	2140	C
3	U	2141	A
3	U	2143	G
3	U	2144	A
3	U	2147	G
3	U	2149	U
3	U	2158	U
3	U	2159	G
3	U	2160	G
3	U	2162	A
3	U	2167	G
3	U	2168	A
3	U	2169	G
3	U	2173	C
3	U	2174	A
3	U	2175	G
3	U	2178	U
3	U	2182	U

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Mol	Chain	Res	Type
3	U	2183	G
3	U	2186	G
3	U	2187	G
3	U	2192	G
3	U	2194	U
3	U	2195	G
3	U	2196	G
3	U	2198	A
3	U	2208	G
3	U	2209	G
3	U	2215	U
3	U	2216	U
3	U	2219	C
3	U	2221	U
3	U	2230	G
3	U	2231	C
3	U	2233	G
3	U	2237	U
3	U	2238	U
3	U	2239	A
3	U	2240	U
3	U	2241	C
3	U	2244	G
3	U	2250	A
3	U	2252	A
3	U	2253	C
3	U	2262	G
3	U	2265	G
3	U	2266	G
3	U	2277	G
3	U	2306	G
3	U	2310	C
3	U	2331	G
3	U	2332	U
3	U	2333	U
3	U	2335	G
3	U	2336	A
3	U	2337	A
3	U	2343	U
3	U	2345	G
3	U	2346	C
3	U	2347	A

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Mol	Chain	Res	Type
3	U	2349	A
3	U	2352	G
3	U	2354	A
3	U	2355	A
3	U	2361	C
3	U	2362	A
3	U	2372	G
3	U	2374	C
3	U	2375	U
3	U	2377	C
3	U	2406	G
3	U	2410	G
3	U	2412	C
3	U	2437	G
3	U	2443	C
3	U	2446	U
3	U	2449	C
3	U	2450	U
3	U	2451	C
3	U	2456	G
3	U	2457	A
3	U	2466	A
3	U	2468	C
3	U	2475	A
3	U	2501	C
3	U	2503	A
3	U	2525	C
3	U	2529	G
3	U	2530	A
3	U	2532	G
3	U	2533	U
3	U	2540	A
3	U	2545	A
3	U	2556	G
3	U	2581	U
3	U	2582	U
3	U	2593	A
3	U	2594	G
3	U	2599	A
3	U	2600	C
3	U	2602	C
3	U	2609	G

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Mol	Chain	Res	Type
3	U	2610	G
3	U	2612	U
3	U	2613	C
3	U	2624	G
3	U	2629	A
3	U	2636	U
3	U	2640	U
3	U	2642	U
3	U	2651	G
3	U	2657	G
3	U	2661	A
3	U	2666	A
3	U	2686	G
3	U	2688	G
3	U	2690	G
3	U	2709	G
3	U	2716	U
3	U	2726	U
3	U	2729	G
3	U	2732	A
3	U	2734	G
3	U	2741	G
3	U	2749	G
3	U	2753	U
3	U	2760	A
3	U	2762	G
3	U	2765	A
3	U	2766	U
3	U	2771	G
3	U	2775	A
3	U	2779	C
3	U	2783	U
3	U	2785	A
3	U	2791	A
3	U	2792	A
3	U	2793	G
3	U	2802	A
3	U	2803	A
3	U	2805	A
3	U	2806	U
3	U	2814	C
3	U	2816	C

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Mol	Chain	Res	Type
3	U	2817	A
3	U	2818	U
3	U	2821	C
3	U	2823	C
3	U	2831	U
3	U	2843	A
3	U	2848	G
3	U	2857	G
3	U	2858	A
3	U	2872	G
3	U	2890	G
3	U	2895	G
3	U	2903	C
3	U	2906	A
3	U	2914	A
3	U	2916	G
3	U	2919	U
4	V	7	U
4	V	15	G
4	V	16	A
4	V	18	A
4	V	19	G
4	V	20	C
4	V	25	A
4	V	28	U
4	V	32	A
4	V	33	C
4	V	34	C
4	V	38	U
4	V	44	A
4	V	48	A
4	V	49	A
4	V	53	G
4	V	57	G
4	V	60	A
4	V	65	C
4	V	69	A
4	V	91	U
4	V	93	C
4	V	102	A
4	V	108	G
4	V	111	C

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Mol	Chain	Res	Type
4	V	112	G
4	V	117	C
4	V	118	A
4	V	119	A
4	V	120	G

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	U	10	A
3	U	41	G
3	U	99	G
3	U	227	A
3	U	250	C
3	U	265	C
3	U	403	U
3	U	408	G
3	U	526	G
3	U	535	A
3	U	547	A
3	U	646	G
3	U	681	A
3	U	903	G
3	U	1091	G
3	U	1243	G
3	U	1337	A
3	U	1436	C
3	U	1453	C
3	U	1516	G
3	U	1593	U
3	U	1628	G
3	U	1777	G
3	U	1811	A
3	U	2161	A
3	U	2238	U
3	U	2374	C
3	U	2782	C
3	U	2871	G
4	V	24	G
4	V	52	C
4	V	64	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 224 ligands modelled in this entry, 224 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

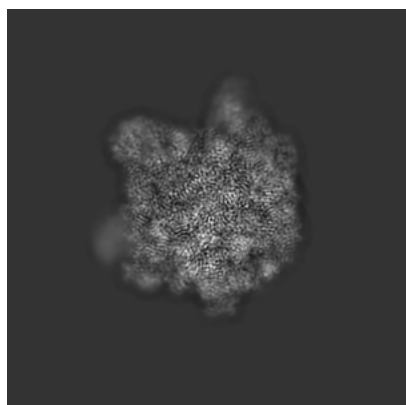
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10535. These allow visual inspection of the internal detail of the map and identification of artifacts.

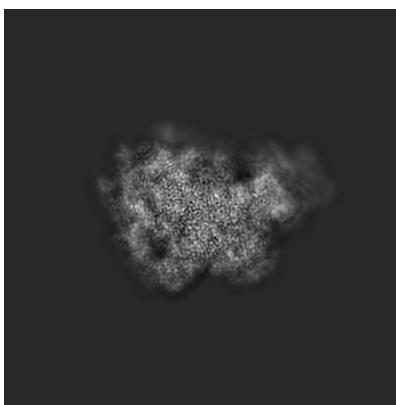
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

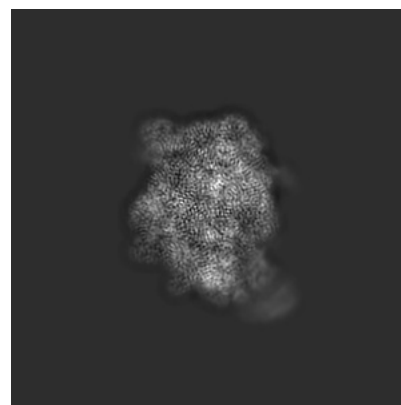
6.1.1 Primary map



X



Y

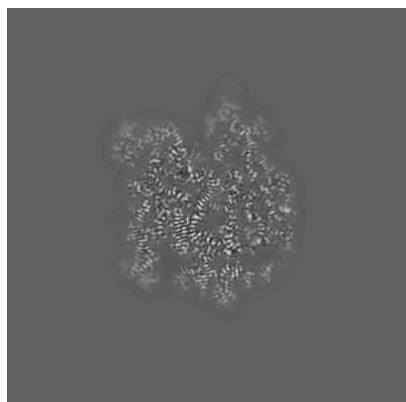


Z

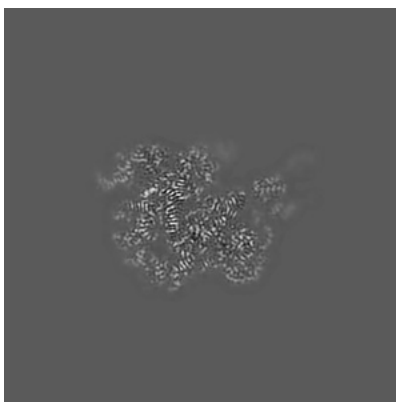
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

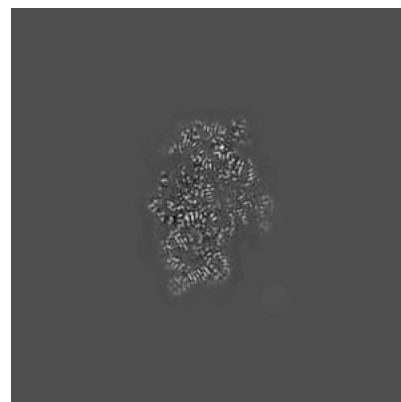
6.2.1 Primary map



X Index: 180



Y Index: 180

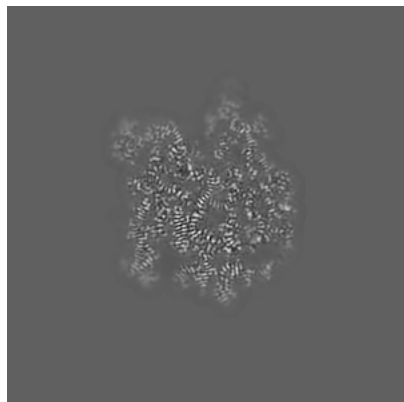


Z Index: 180

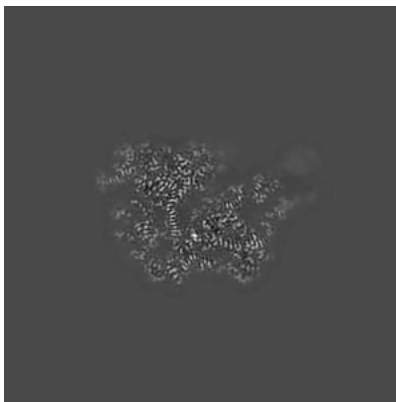
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

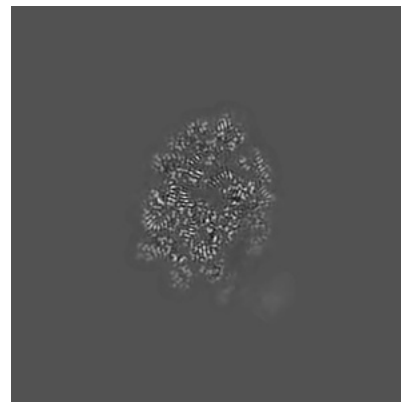
6.3.1 Primary map



X Index: 180



Y Index: 185



Z Index: 168

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

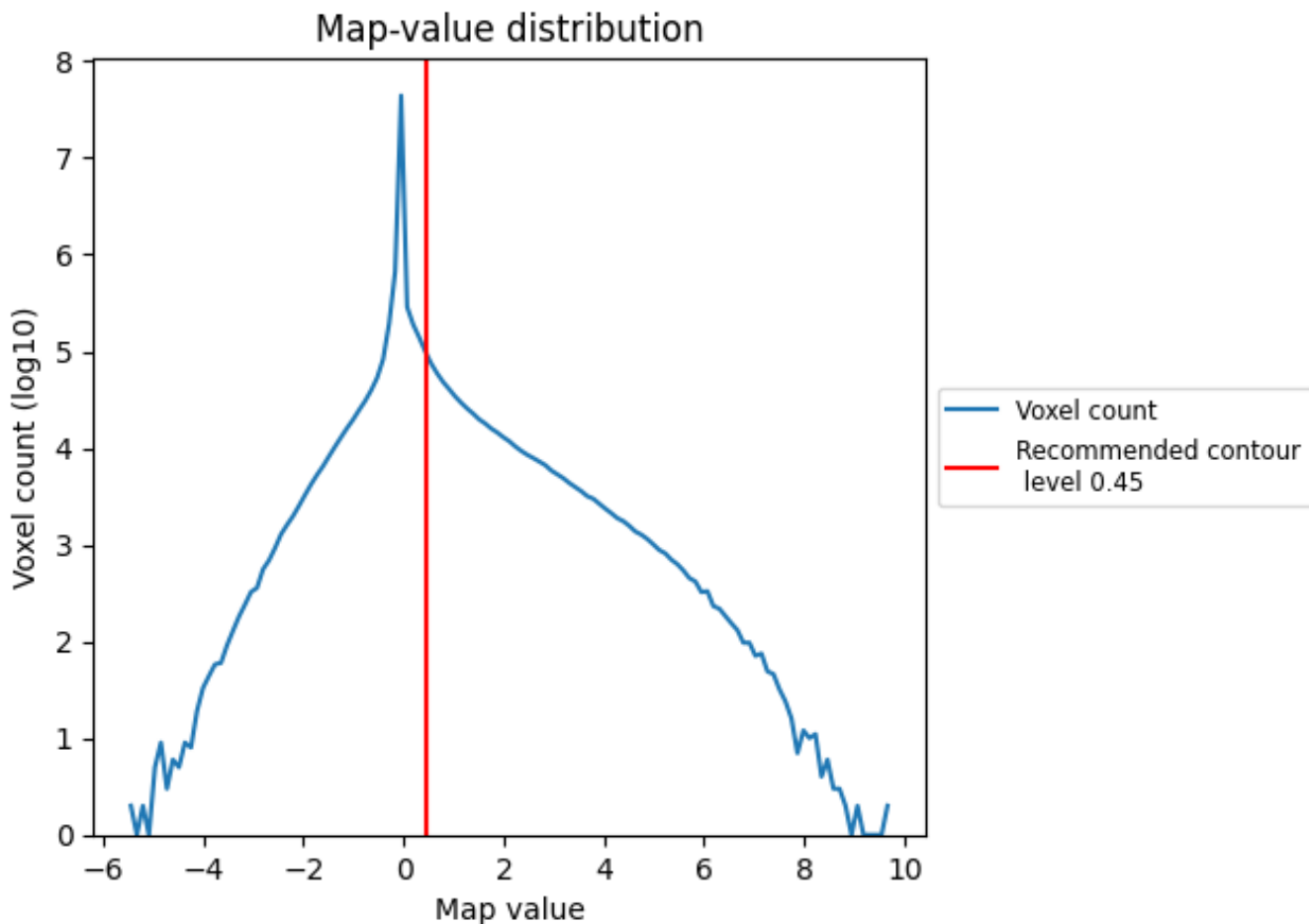
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

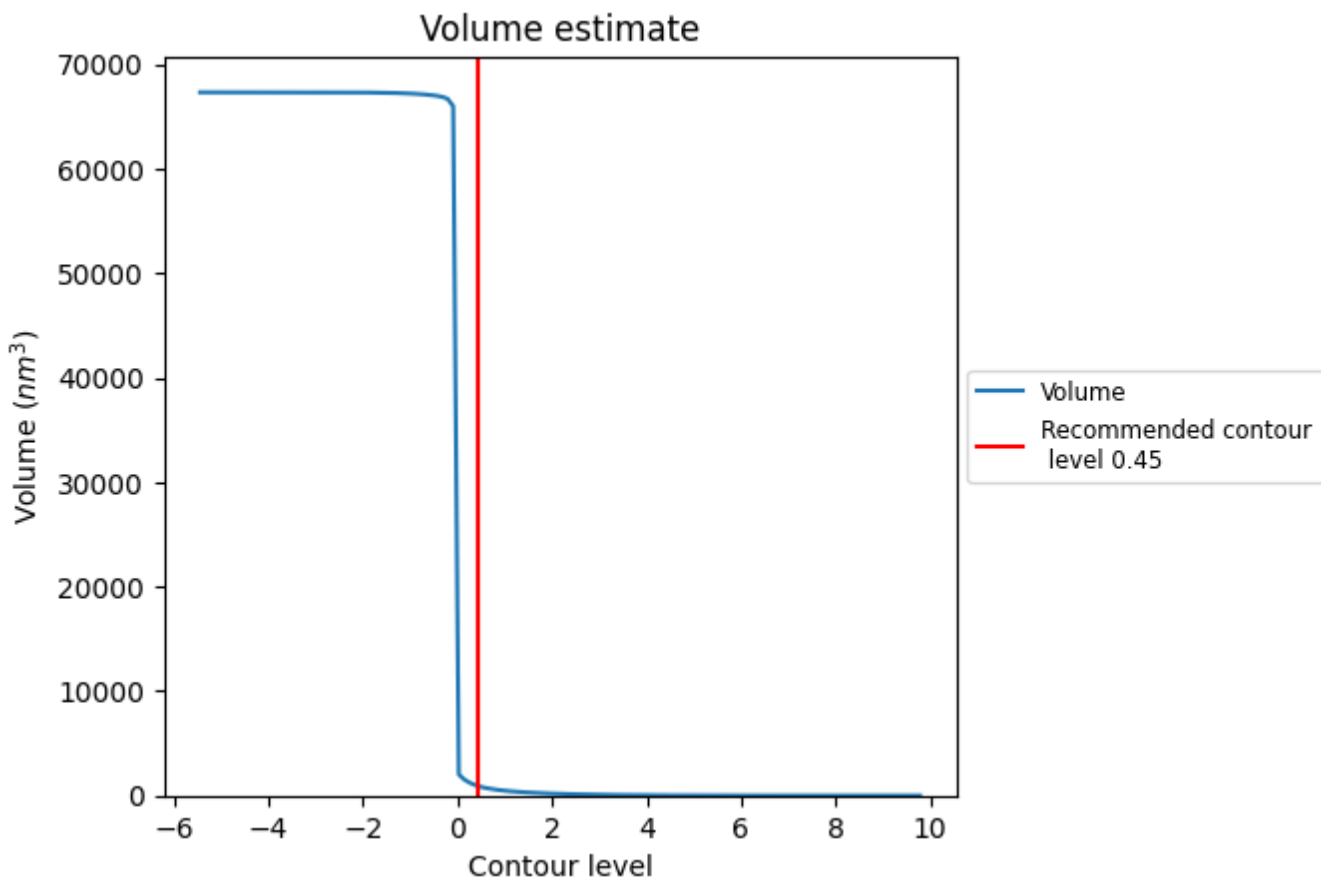
This section contains the results of statistical analysis of the map.

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.

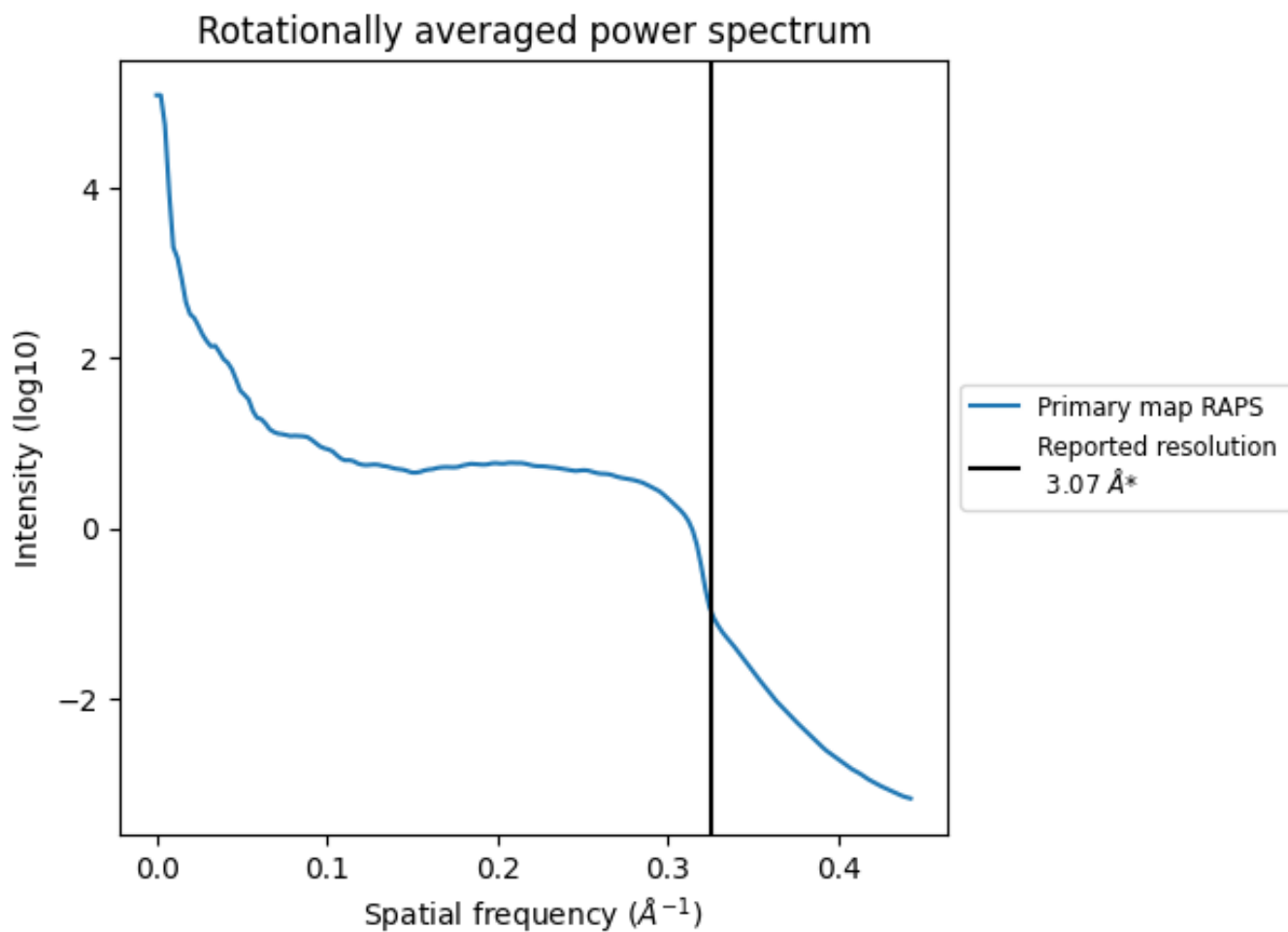
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 899 nm³; this corresponds to an approximate mass of 812 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 i



*Reported resolution corresponds to spatial frequency of 0.326 Å⁻¹

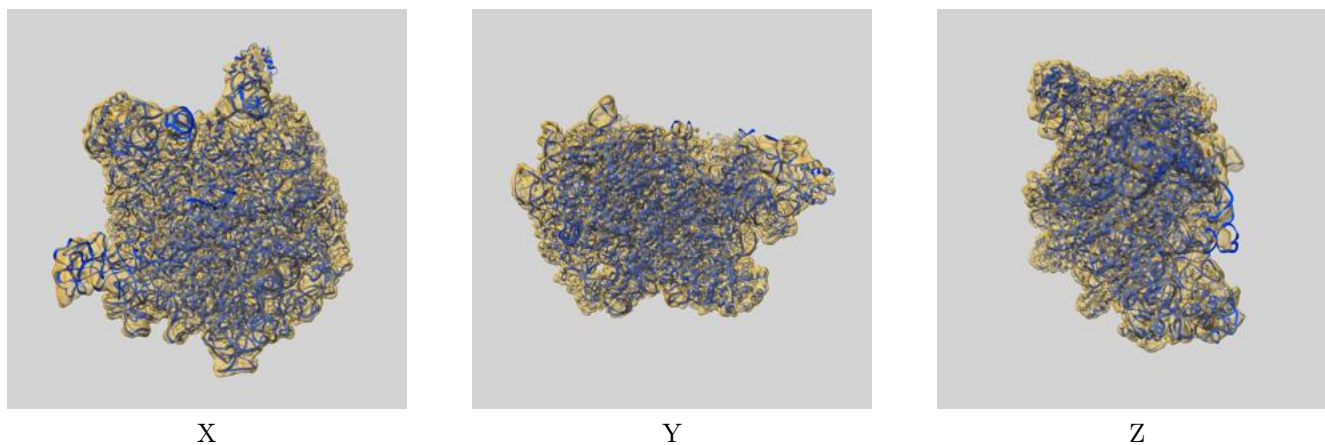
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

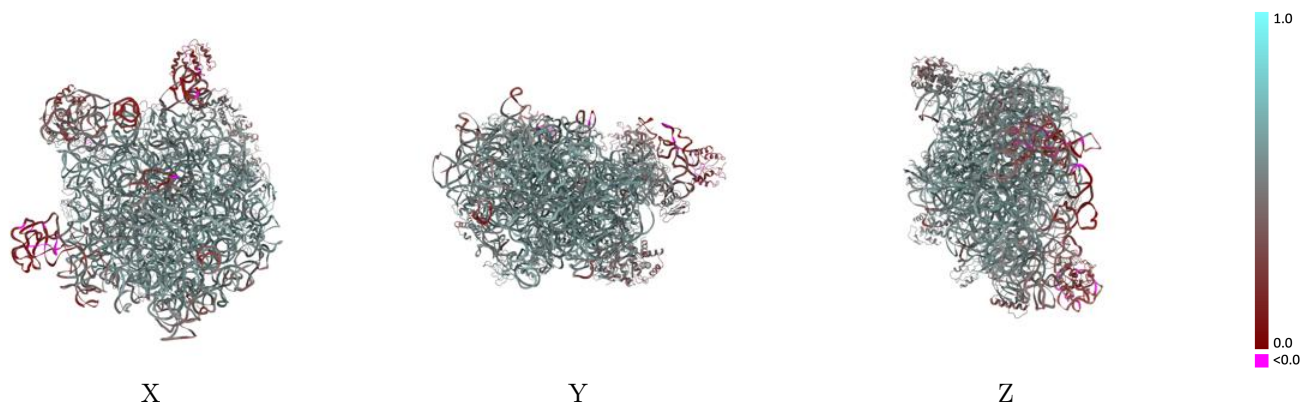
This section contains information regarding the fit between EMDB map EMD-10535 and PDB model 6TNN. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



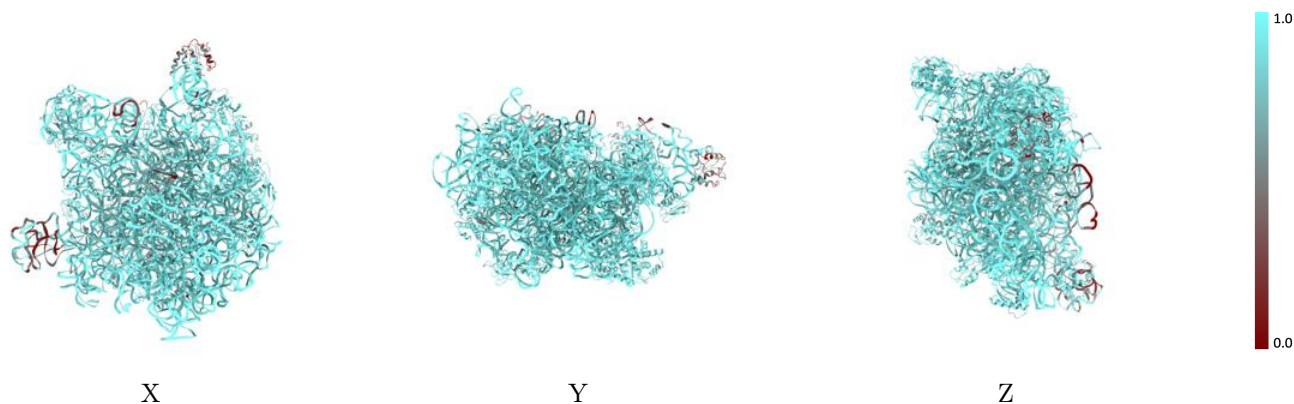
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



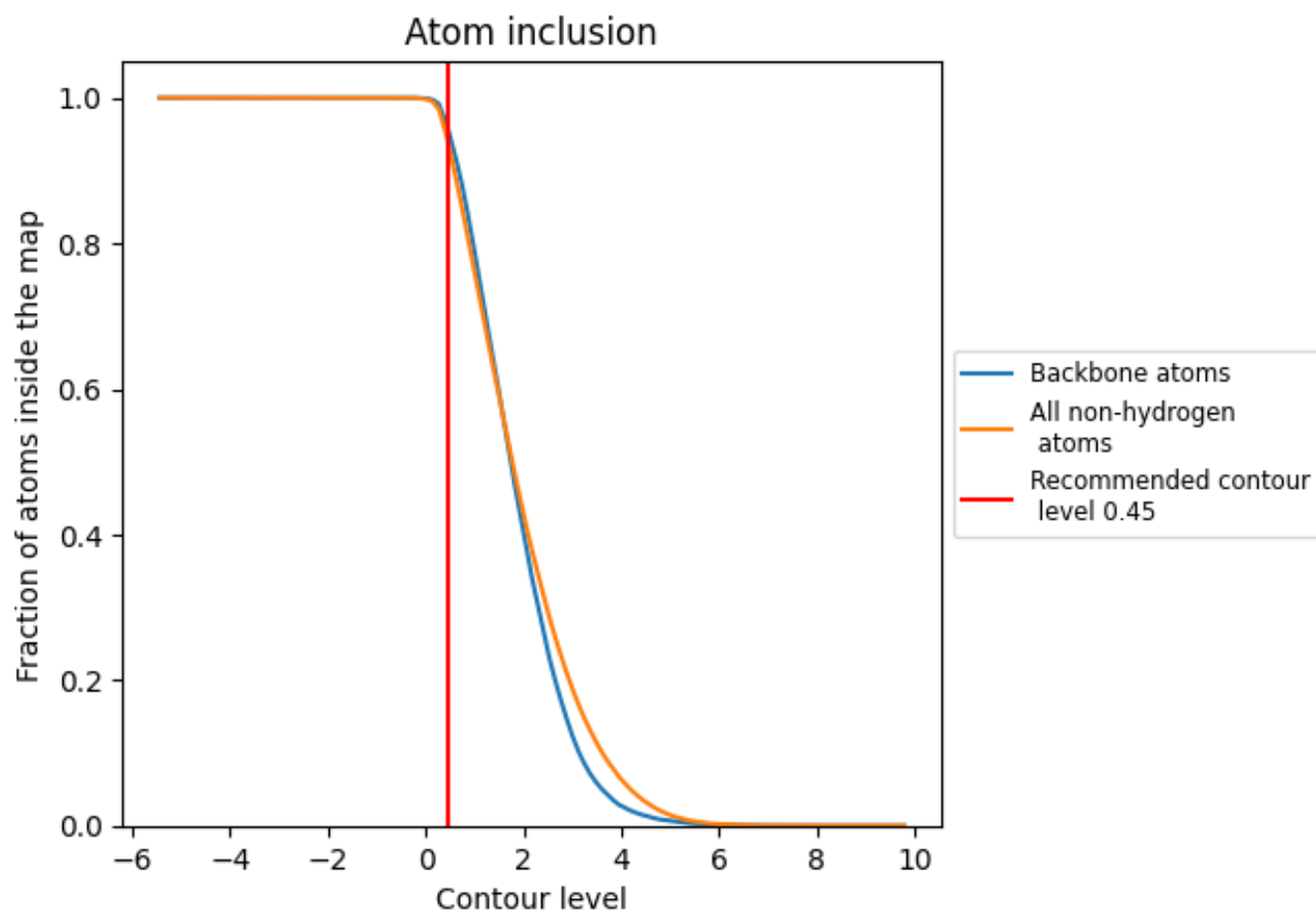
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9415	 0.5220
H	 0.8815	 0.4300
I	 0.9106	 0.4700
U	 0.9563	 0.5300
V	 0.9818	 0.4600
W	 0.9436	 0.5680
X	 0.9573	 0.5680
Y	 0.9332	 0.5380
Z	 0.7671	 0.2910
a	 0.9123	 0.4560
b	 0.4062	 0.1490
c	 0.9344	 0.5690
d	 0.9420	 0.5490
e	 0.9426	 0.5440
f	 0.8964	 0.5390
g	 0.9356	 0.5570
h	 0.9086	 0.4700
i	 0.8963	 0.5160
j	 0.9526	 0.5710
k	 0.9510	 0.5470
l	 0.9499	 0.5670
m	 0.9041	 0.5290
n	 0.9218	 0.5050
o	 0.9145	 0.5620
p	 0.9564	 0.5760
q	 0.9406	 0.5360
r	 0.9797	 0.6050
s	 0.9659	 0.5920
t	 0.9220	 0.5670
u	 0.8889	 0.5460
v	 0.9220	 0.4900
w	 0.9347	 0.5530

