



Full wwPDB EM Validation Report ⓘ

Dec 12, 2022 – 02:42 am GMT

PDB ID : 6TPQ
EMDB ID : EMD-10543
Title : RNase M5 bound to 50S ribosome with precursor 5S rRNA
Authors : Oerum, S.; Dendooven, T.; Gilet, L.; Catala, M.; Degut, C.; Trinquier, A.;
Barraud, P.; Luisi, B.; Condon, C.; Tisne, C.
Deposited on : 2019-12-13
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:

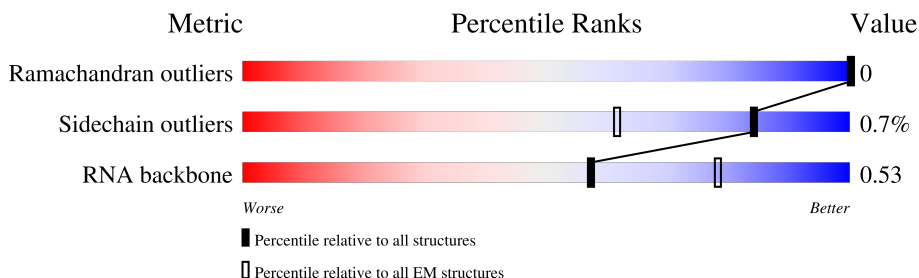
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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.



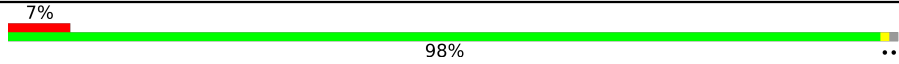
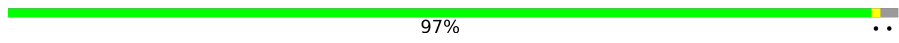
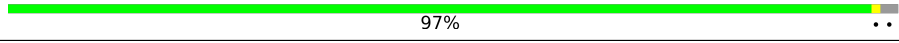


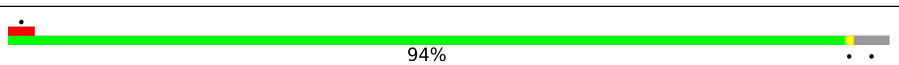
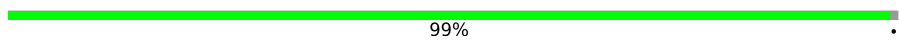
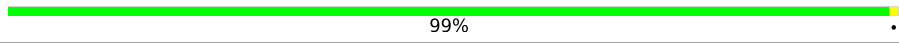
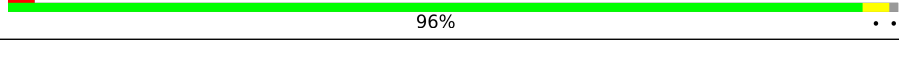
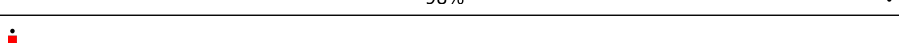
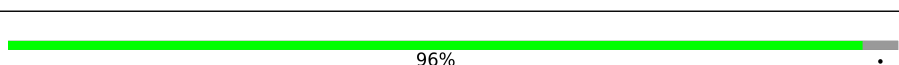
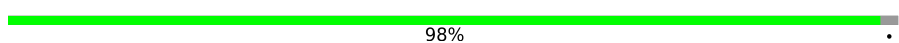
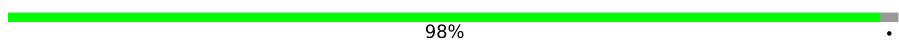

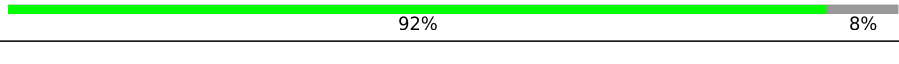
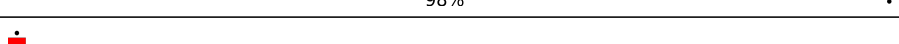
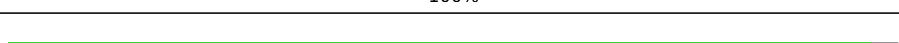

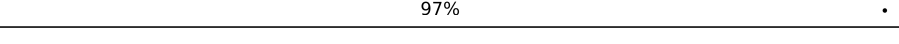
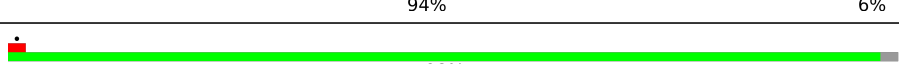
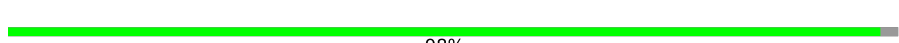


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	A	187	
1	B	187	
2	V	123	
3	b	166	
4	U	2924	
5	W	277	
6	X	209	
7	Y	207	

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Mol	Chain	Length	Quality of chain
8	Z	179	 98%
9	a	179	 97%
10	c	145	 97%
11	d	122	 100%
12	e	146	 100%
13	f	144	 94%
14	g	120	 99%
15	h	120	 99%
16	i	115	 96%
17	j	119	 98%
18	k	102	 98%
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	 98%
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 91728 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 Ribonuclease M5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	183	Total	C	N	O	S	0	0
			1425	887	269	266	3		
1	A	69	Total	C	N	O	S	0	0
			548	343	108	95	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	58	ALA	ASP	engineered mutation	UNP A0A087LGV4
A	58	ALA	ASP	engineered mutation	UNP A0A087LGV4

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	V	123	Total	C	N	O	P	0	0
			2628	1172	473	860	123		

- Molecule 3 is a protein called 50S ribosomal protein L10.

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

- Molecule 4 is a RNA chain called pre-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	U	2924	Total	C	N	O	P	0	0
			62790	28012	11594	20260	2924		

- 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
			2111	1312	416	377	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
			1575	988	290	292	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
			1561	980	289	290	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
			1404	893	245	259	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
			1342	835	248	257	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
			1124	710	206	203	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
			921	571	173	173	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	e	146	1082	671	207	202	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	f	138	1097	703	208	181	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	g	119	954	583	186	181	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	h	120	913	564	176	172	1	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	i	114	937	595	184	158	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	j	117	940	591	189	156	4	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	k	101	787	501	139	147	0	0

- 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
			842	525	164	150	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
			752	472	137	139	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
			762	478	142	138	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
			630	390	123	117		

- 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
			426	262	86	71	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
			401	244	80	73	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
			368	222	89	55	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	36	Total	C	N	O	S	0	0
			289	181	59	45	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	w	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

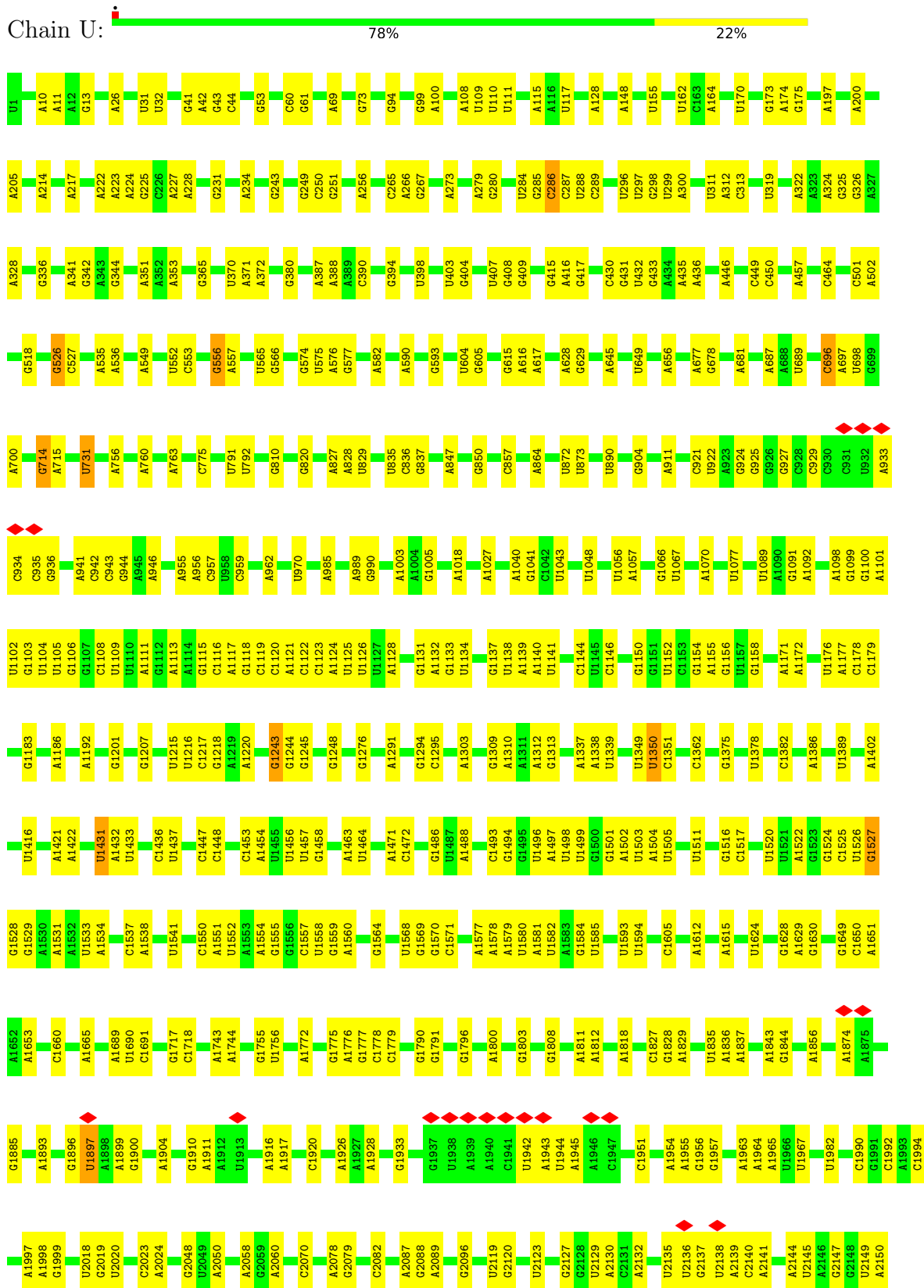
- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

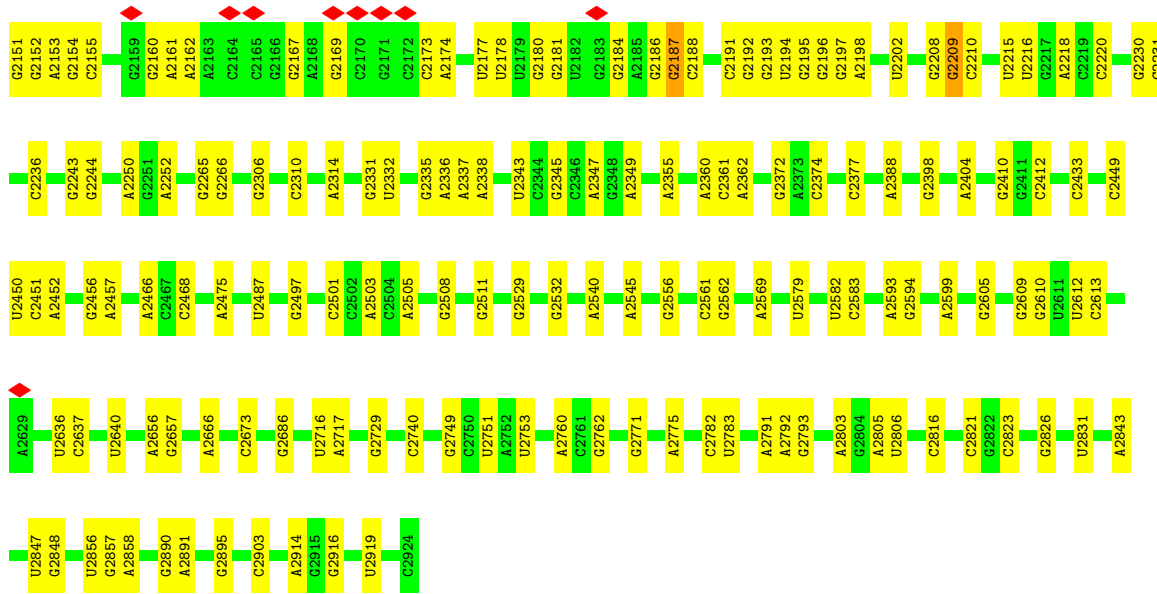
Mol	Chain	Residues	Atoms		AltConf
31	V	1	Total	Mg	0
			1	1	
31	U	214	Total	Mg	0
			214	214	
31	W	2	Total	Mg	0
			2	2	
31	e	1	Total	Mg	0
			1	1	
31	u	1	Total	Mg	0
			1	1	

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

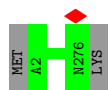
Mol	Chain	Residues	Atoms		AltConf
32	p	1	Total 1	Zn 1	0
32	q	1	Total 1	Zn 1	0
32	t	1	Total 1	Zn 1	0

● Molecule 4: pre-23S rRNA

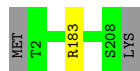




• Molecule 5: 50S ribosomal protein L2



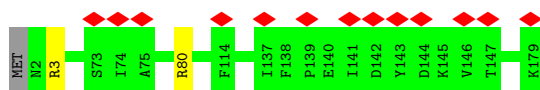
• Molecule 6: 50S ribosomal protein L3



• Molecule 7: 50S ribosomal protein L4



• Molecule 8: 50S ribosomal protein L5



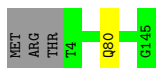
• Molecule 9: 50S ribosomal protein L6





- Molecule 10: 50S ribosomal protein L13

Chain c: 97%



- Molecule 11: 50S ribosomal protein L14

Chain d: 100%

There are no outlier residues recorded for this chain.

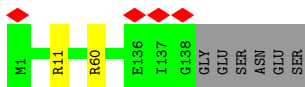
- Molecule 12: 50S ribosomal protein L15

Chain e: 100%

There are no outlier residues recorded for this chain.

- Molecule 13: 50S ribosomal protein L16

Chain f: 94%



- 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: 96%



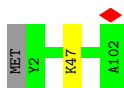
- Molecule 17: 50S ribosomal protein L20

Chain j:  98%



- Molecule 18: 50S ribosomal protein L21

Chain k:  98%



- Molecule 19: 50S ribosomal protein L22

Chain l:  96%



- Molecule 20: 50S ribosomal protein L23

Chain m:  98%




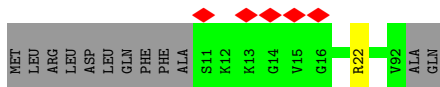
- Molecule 21: 50S ribosomal protein L24

Chain n:  98%



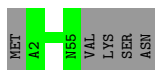
- Molecule 22: 50S ribosomal protein L27

Chain o:  5% 86% 13%



- Molecule 23: 50S ribosomal protein L32

Chain p:  92% 8%



- Molecule 24: 50S ribosomal protein L33 1

Chain q:  98%



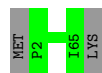
- Molecule 25: 50S ribosomal protein L34

Chain r:  100%



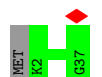
- Molecule 26: 50S ribosomal protein L35

Chain s:  97%



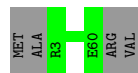
- Molecule 27: 50S ribosomal protein L36

Chain t:  97%



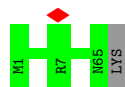
- Molecule 28: 50S ribosomal protein L28

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, Not provided	
Number of particles used	92799	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	2.791	Depositor
Minimum map value	-1.113	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.135	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	A	0.30	0/554	0.44	0/736
1	B	0.27	0/1444	0.44	0/1939
2	V	0.64	0/2938	0.84	0/4579
3	b	0.27	0/963	0.51	0/1298
4	U	0.90	0/70333	0.89	61/109728 (0.1%)
5	W	0.43	0/2148	0.51	0/2881
6	X	0.45	0/1597	0.49	0/2140
7	Y	0.43	0/1580	0.48	0/2132
8	Z	0.31	0/1423	0.50	0/1910
9	a	0.34	0/1360	0.47	0/1832
10	c	0.48	1/1147 (0.1%)	0.50	0/1542
11	d	0.42	0/928	0.51	0/1245
12	e	0.43	0/1094	0.52	0/1457
13	f	0.42	0/1120	0.47	0/1496
14	g	0.43	0/961	0.48	0/1284
15	h	0.33	0/922	0.46	0/1236
16	i	0.45	0/950	0.49	0/1269
17	j	0.53	0/952	0.50	0/1266
18	k	0.48	0/798	0.52	0/1070
19	l	0.44	0/851	0.46	0/1146
20	m	0.45	0/759	0.49	0/1011
21	n	0.40	0/772	0.49	0/1032
22	o	0.46	0/638	0.52	0/847
23	p	0.45	0/433	0.47	0/574
24	q	0.41	0/406	0.49	0/540
25	r	0.46	0/371	0.47	0/483
26	s	0.41	0/519	0.45	0/680
27	t	0.40	0/292	0.45	0/383
28	u	0.37	0/448	0.50	0/596
29	v	0.36	0/531	0.45	0/707
30	w	0.41	0/458	0.49	0/613
All	All	0.80	1/99690 (0.0%)	0.81	61/149652 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	c	80	GLN	C-N	-5.04	1.22	1.34

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	696	C	N1-C2-O2	9.20	124.42	118.90
4	U	1243	G	O4'-C1'-N9	9.03	115.43	108.20
4	U	1525	C	C2-N1-C1'	-8.69	109.25	118.80
4	U	696	C	C2-N1-C1'	8.28	127.91	118.80
4	U	696	C	N3-C2-O2	-7.78	116.46	121.90
4	U	2236	C	N3-C2-O2	-7.71	116.50	121.90
4	U	1525	C	C6-N1-C1'	7.31	129.57	120.80
4	U	1351	C	C2-N1-C1'	7.08	126.59	118.80
4	U	1431	U	C2-N1-C1'	7.06	126.17	117.70
4	U	1550	C	C6-N1-C1'	6.94	129.13	120.80
4	U	1557	C	N3-C2-O2	-6.91	117.06	121.90
4	U	286	C	N1-C2-O2	6.81	122.99	118.90
4	U	1550	C	N3-C2-O2	-6.63	117.26	121.90
4	U	696	C	C6-N1-C1'	-6.56	112.93	120.80
4	U	1527	G	N3-C4-N9	-6.54	122.08	126.00
4	U	2155	C	N1-C2-O2	6.39	122.73	118.90
4	U	526	G	O4'-C1'-N9	6.35	113.28	108.20
4	U	1550	C	C5-C4-N4	6.34	124.64	120.20
4	U	1520	U	N3-C2-O2	-6.21	117.86	122.20
4	U	1578	A	C6-C5-N7	-6.19	127.97	132.30
4	U	1818	A	N1-C2-N3	6.18	132.39	129.30
4	U	1350	U	C2-N1-C1'	6.11	125.03	117.70
4	U	1920	C	N3-C2-O2	-6.10	117.63	121.90
4	U	2155	C	N3-C2-O2	-6.03	117.68	121.90
4	U	1431	U	N3-C2-O2	-6.00	118.00	122.20
4	U	1431	U	N1-C2-O2	5.87	126.91	122.80
4	U	1550	C	C2-N1-C1'	-5.81	112.41	118.80
4	U	1550	C	N1-C2-N3	5.74	123.22	119.20
4	U	1525	C	O4'-C1'-N1	5.67	112.74	108.20
4	U	1564	G	C5-C6-O6	5.67	132.00	128.60
4	U	1351	C	C6-N1-C1'	-5.65	114.02	120.80
4	U	1818	A	C2-N3-C4	-5.64	107.78	110.60
4	U	2209	G	N3-C4-N9	-5.45	122.73	126.00
4	U	1524	G	N3-C4-N9	-5.45	122.73	126.00
4	U	287	C	N3-C2-O2	-5.44	118.09	121.90
4	U	1146	C	C2-N1-C1'	5.38	124.72	118.80
4	U	2187	G	N1-C2-N2	-5.32	111.41	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	1201	G	N3-C4-N9	5.30	129.18	126.00
4	U	714	G	C4-N9-C1'	5.29	133.37	126.50
4	U	1201	G	C8-N9-C1'	-5.28	120.13	127.00
4	U	2487	U	N3-C2-O2	-5.27	118.51	122.20
4	U	1386	A	O4'-C1'-N9	5.26	112.41	108.20
4	U	1528	G	C5-C6-O6	5.25	131.75	128.60
4	U	526	G	C4-N9-C1'	5.24	133.31	126.50
4	U	556	G	P-O3'-C3'	5.21	125.95	119.70
4	U	1525	C	N3-C4-N4	-5.20	114.36	118.00
4	U	1520	U	N1-C2-O2	5.18	126.43	122.80
4	U	1649	G	O4'-C1'-N9	5.18	112.35	108.20
4	U	111	U	C2-N1-C1'	5.17	123.91	117.70
4	U	1550	C	N3-C4-N4	-5.17	114.38	118.00
4	U	526	G	C8-N9-C1'	-5.17	120.28	127.00
4	U	1527	G	N3-C4-C5	5.16	131.18	128.60
4	U	1201	G	C4-N9-C1'	5.12	133.15	126.50
4	U	731	U	N3-C2-O2	-5.11	118.62	122.20
4	U	2243	G	C5-C6-O6	5.08	131.65	128.60
4	U	1897	U	N1-C2-O2	5.08	126.35	122.80
4	U	731	U	C2-N1-C1'	5.06	123.77	117.70
4	U	1564	G	N3-C4-N9	-5.01	122.99	126.00
4	U	1578	A	N9-C4-C5	-5.01	103.80	105.80
4	U	1243	G	OP1-P-O3'	5.01	116.22	105.20
4	U	1578	A	N3-C4-N9	5.01	131.41	127.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A	67/187 (36%)	63 (94%)	4 (6%)	0	100	100
1	B	181/187 (97%)	169 (93%)	12 (7%)	0	100	100
3	b	121/166 (73%)	97 (80%)	24 (20%)	0	100	100
5	W	273/277 (99%)	242 (89%)	31 (11%)	0	100	100
6	X	205/209 (98%)	183 (89%)	22 (11%)	0	100	100
7	Y	203/207 (98%)	178 (88%)	25 (12%)	0	100	100
8	Z	176/179 (98%)	149 (85%)	27 (15%)	0	100	100
9	a	173/179 (97%)	151 (87%)	22 (13%)	0	100	100
10	c	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
11	d	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
12	e	144/146 (99%)	129 (90%)	15 (10%)	0	100	100
13	f	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	g	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
15	h	118/120 (98%)	108 (92%)	10 (8%)	0	100	100
16	i	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
17	j	115/119 (97%)	109 (95%)	6 (5%)	0	100	100
18	k	99/102 (97%)	83 (84%)	16 (16%)	0	100	100
19	l	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
20	m	91/95 (96%)	84 (92%)	7 (8%)	0	100	100
21	n	99/103 (96%)	90 (91%)	9 (9%)	0	100	100
22	o	80/94 (85%)	73 (91%)	7 (9%)	0	100	100
23	p	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
24	q	46/49 (94%)	42 (91%)	4 (9%)	0	100	100
25	r	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
26	s	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
27	t	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
28	u	56/62 (90%)	50 (89%)	6 (11%)	0	100	100
29	v	63/66 (96%)	56 (89%)	7 (11%)	0	100	100
30	w	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
All	All	3288/3571 (92%)	2974 (90%)	314 (10%)	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	A	50/143 (35%)	50 (100%)	0	100	100
1	B	139/143 (97%)	138 (99%)	1 (1%)	84	92
3	b	105/138 (76%)	103 (98%)	2 (2%)	57	79
5	W	223/225 (99%)	223 (100%)	0	100	100
6	X	168/170 (99%)	167 (99%)	1 (1%)	86	93
7	Y	169/170 (99%)	168 (99%)	1 (1%)	86	93
8	Z	153/154 (99%)	151 (99%)	2 (1%)	69	86
9	a	148/151 (98%)	146 (99%)	2 (1%)	67	84
10	c	120/123 (98%)	120 (100%)	0	100	100
11	d	101/101 (100%)	101 (100%)	0	100	100
12	e	110/110 (100%)	110 (100%)	0	100	100
13	f	111/116 (96%)	109 (98%)	2 (2%)	59	80
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%)	95 (96%)	4 (4%)	31	63
17	j	96/98 (98%)	96 (100%)	0	100	100
18	k	83/84 (99%)	82 (99%)	1 (1%)	71	87
19	l	90/93 (97%)	90 (100%)	0	100	100
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%)	46 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	2766/2948 (94%)	2748 (99%)	18 (1%)	84	92

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

Mol	Chain	Res	Type
1	B	88	ARG
3	b	62	ARG
3	b	101	LYS
6	X	183	ARG
7	Y	151	LYS
8	Z	3	ARG
8	Z	80	ARG
9	a	96	ARG
9	a	165	TYR
13	f	11	ARG
13	f	60	ARG
15	h	61	LYS
16	i	13	LYS
16	i	40	ARG
16	i	54	ARG
16	i	107	ARG
18	k	47	LYS
22	o	22	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	142	GLN
1	B	159	HIS
5	W	11	ASN
5	W	45	ASN
5	W	58	HIS
5	W	199	GLN
5	W	230	HIS
5	W	232	HIS
6	X	33	ASN
6	X	173	ASN

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Mol	Chain	Res	Type
7	Y	40	GLN
8	Z	45	GLN
8	Z	46	ASN
8	Z	135	GLN
8	Z	161	ASN
9	a	62	HIS
9	a	148	ASN
10	c	48	HIS
10	c	81	HIS
12	e	78	ASN
12	e	126	ASN
13	f	13	HIS
13	f	123	HIS
14	g	76	ASN
14	g	81	GLN
15	h	37	ASN
16	i	39	ASN
17	j	37	GLN
17	j	72	ASN
17	j	91	ASN
17	j	108	GLN
17	j	118	ASN
19	l	97	ASN
19	l	102	HIS
20	m	55	ASN
21	n	64	HIS
23	p	40	HIS
24	q	16	ASN
24	q	25	ASN
24	q	45	HIS
25	r	6	GLN
28	u	41	ASN
29	v	65	ASN
30	w	32	ASN
30	w	33	GLN
30	w	37	HIS
30	w	40	ASN

5.3.3 RNA

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	V	122/123 (99%)	27 (22%)	4 (3%)
4	U	2923/2924 (99%)	607 (20%)	41 (1%)
All	All	3045/3047 (99%)	634 (20%)	45 (1%)

All (634) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	V	4	G
2	V	10	G
2	V	13	A
2	V	14	G
2	V	15	C
2	V	19	G
2	V	20	A
2	V	22	G
2	V	23	U
2	V	24	C
2	V	28	C
2	V	40	C
2	V	47	C
2	V	48	G
2	V	49	G
2	V	51	A
2	V	55	A
2	V	60	C
2	V	63	C
2	V	64	A
2	V	85	U
2	V	86	U
2	V	87	U
2	V	88	C
2	V	97	A
2	V	103	G
2	V	107	G
4	U	11	A
4	U	13	G
4	U	26	A
4	U	31	U
4	U	32	U
4	U	41	G
4	U	42	A

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Mol	Chain	Res	Type
4	U	43	G
4	U	44	C
4	U	53	G
4	U	60	C
4	U	61	G
4	U	69	A
4	U	73	G
4	U	94	G
4	U	99	G
4	U	100	A
4	U	108	A
4	U	109	U
4	U	110	U
4	U	115	A
4	U	117	U
4	U	128	A
4	U	148	A
4	U	155	U
4	U	162	U
4	U	164	A
4	U	170	U
4	U	173	G
4	U	174	A
4	U	175	G
4	U	197	A
4	U	200	A
4	U	205	A
4	U	214	A
4	U	217	A
4	U	222	A
4	U	223	A
4	U	224	A
4	U	225	G
4	U	228	A
4	U	231	G
4	U	234	A
4	U	243	G
4	U	249	G
4	U	251	G
4	U	256	A
4	U	266	A
4	U	267	G

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Mol	Chain	Res	Type
4	U	273	A
4	U	279	A
4	U	280	G
4	U	284	U
4	U	285	G
4	U	286	C
4	U	288	U
4	U	289	C
4	U	296	U
4	U	297	U
4	U	298	G
4	U	299	U
4	U	300	A
4	U	311	U
4	U	312	A
4	U	313	C
4	U	319	U
4	U	322	A
4	U	324	A
4	U	325	G
4	U	326	G
4	U	328	A
4	U	336	G
4	U	341	A
4	U	342	G
4	U	344	G
4	U	351	A
4	U	353	A
4	U	365	G
4	U	370	U
4	U	371	A
4	U	372	A
4	U	380	G
4	U	387	A
4	U	388	A
4	U	390	C
4	U	394	G
4	U	398	U
4	U	403	U
4	U	404	G
4	U	407	U
4	U	409	G

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Mol	Chain	Res	Type
4	U	415	G
4	U	416	A
4	U	417	G
4	U	430	C
4	U	431	G
4	U	432	U
4	U	433	G
4	U	436	A
4	U	446	A
4	U	449	C
4	U	450	C
4	U	457	A
4	U	464	C
4	U	501	C
4	U	502	A
4	U	518	G
4	U	526	G
4	U	527	C
4	U	535	A
4	U	536	A
4	U	549	A
4	U	552	U
4	U	553	C
4	U	557	A
4	U	565	U
4	U	566	G
4	U	574	G
4	U	575	U
4	U	576	A
4	U	577	G
4	U	582	A
4	U	590	A
4	U	593	G
4	U	604	U
4	U	605	G
4	U	615	G
4	U	616	A
4	U	617	A
4	U	628	A
4	U	629	G
4	U	645	A
4	U	649	U

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Mol	Chain	Res	Type
4	U	656	A
4	U	677	A
4	U	678	G
4	U	681	A
4	U	687	A
4	U	689	U
4	U	696	C
4	U	697	A
4	U	698	U
4	U	700	A
4	U	714	G
4	U	715	A
4	U	731	U
4	U	756	A
4	U	760	A
4	U	763	A
4	U	775	C
4	U	792	U
4	U	810	G
4	U	820	G
4	U	827	A
4	U	828	A
4	U	829	U
4	U	835	U
4	U	836	C
4	U	837	G
4	U	847	A
4	U	850	G
4	U	857	C
4	U	864	A
4	U	872	U
4	U	873	U
4	U	890	U
4	U	904	G
4	U	911	A
4	U	921	C
4	U	922	U
4	U	924	G
4	U	925	G
4	U	927	G
4	U	929	C
4	U	933	A

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Mol	Chain	Res	Type
4	U	934	C
4	U	935	C
4	U	936	G
4	U	941	A
4	U	942	C
4	U	943	C
4	U	944	G
4	U	946	A
4	U	955	A
4	U	956	A
4	U	957	C
4	U	959	C
4	U	962	A
4	U	970	U
4	U	985	A
4	U	989	A
4	U	990	G
4	U	1003	A
4	U	1005	G
4	U	1018	A
4	U	1027	A
4	U	1040	A
4	U	1041	G
4	U	1043	U
4	U	1048	U
4	U	1056	U
4	U	1057	A
4	U	1066	G
4	U	1067	U
4	U	1070	A
4	U	1077	U
4	U	1089	U
4	U	1091	G
4	U	1092	A
4	U	1098	A
4	U	1099	G
4	U	1100	G
4	U	1101	A
4	U	1102	U
4	U	1103	G
4	U	1104	U
4	U	1105	U

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Mol	Chain	Res	Type
4	U	1106	G
4	U	1108	C
4	U	1109	U
4	U	1111	A
4	U	1113	A
4	U	1116	C
4	U	1117	A
4	U	1118	G
4	U	1119	C
4	U	1120	C
4	U	1121	A
4	U	1122	C
4	U	1123	C
4	U	1124	A
4	U	1125	U
4	U	1126	U
4	U	1128	A
4	U	1131	G
4	U	1132	A
4	U	1133	G
4	U	1134	U
4	U	1137	G
4	U	1138	U
4	U	1139	A
4	U	1140	A
4	U	1141	U
4	U	1144	C
4	U	1150	G
4	U	1152	U
4	U	1155	A
4	U	1156	G
4	U	1158	G
4	U	1171	A
4	U	1172	A
4	U	1176	U
4	U	1177	A
4	U	1178	C
4	U	1179	C
4	U	1183	G
4	U	1186	A
4	U	1192	A
4	U	1207	G

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Mol	Chain	Res	Type
4	U	1215	U
4	U	1216	U
4	U	1217	C
4	U	1218	G
4	U	1220	A
4	U	1244	G
4	U	1245	G
4	U	1248	G
4	U	1276	G
4	U	1291	A
4	U	1294	G
4	U	1295	C
4	U	1303	A
4	U	1309	G
4	U	1310	A
4	U	1312	A
4	U	1313	G
4	U	1337	A
4	U	1338	A
4	U	1339	U
4	U	1349	U
4	U	1350	U
4	U	1362	C
4	U	1375	G
4	U	1378	U
4	U	1382	C
4	U	1389	U
4	U	1402	A
4	U	1416	U
4	U	1421	A
4	U	1422	A
4	U	1431	U
4	U	1432	A
4	U	1433	U
4	U	1437	U
4	U	1447	C
4	U	1448	C
4	U	1453	C
4	U	1454	A
4	U	1456	U
4	U	1457	U
4	U	1458	G

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Mol	Chain	Res	Type
4	U	1463	A
4	U	1464	U
4	U	1471	A
4	U	1472	C
4	U	1486	G
4	U	1488	A
4	U	1493	C
4	U	1494	G
4	U	1496	U
4	U	1497	A
4	U	1498	U
4	U	1499	U
4	U	1501	G
4	U	1502	A
4	U	1503	U
4	U	1504	A
4	U	1505	U
4	U	1511	U
4	U	1517	C
4	U	1522	A
4	U	1526	U
4	U	1527	G
4	U	1529	G
4	U	1531	A
4	U	1533	U
4	U	1534	A
4	U	1537	C
4	U	1538	A
4	U	1541	U
4	U	1551	A
4	U	1552	U
4	U	1554	A
4	U	1555	G
4	U	1558	U
4	U	1559	G
4	U	1560	A
4	U	1568	U
4	U	1569	G
4	U	1570	G
4	U	1571	C
4	U	1577	A
4	U	1579	A

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Mol	Chain	Res	Type
4	U	1580	U
4	U	1581	A
4	U	1582	U
4	U	1584	G
4	U	1585	U
4	U	1594	U
4	U	1605	C
4	U	1612	A
4	U	1615	A
4	U	1624	U
4	U	1629	A
4	U	1630	G
4	U	1650	C
4	U	1651	A
4	U	1653	A
4	U	1660	C
4	U	1665	A
4	U	1690	U
4	U	1691	C
4	U	1717	G
4	U	1718	C
4	U	1743	A
4	U	1744	A
4	U	1755	G
4	U	1756	U
4	U	1772	A
4	U	1775	G
4	U	1776	A
4	U	1777	G
4	U	1778	C
4	U	1779	C
4	U	1790	G
4	U	1791	G
4	U	1796	G
4	U	1800	A
4	U	1803	G
4	U	1808	G
4	U	1812	A
4	U	1827	C
4	U	1828	G
4	U	1829	A
4	U	1835	U

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Mol	Chain	Res	Type
4	U	1836	A
4	U	1837	A
4	U	1843	A
4	U	1844	G
4	U	1856	A
4	U	1874	A
4	U	1885	G
4	U	1893	A
4	U	1896	G
4	U	1897	U
4	U	1899	A
4	U	1900	G
4	U	1904	A
4	U	1910	G
4	U	1911	A
4	U	1916	A
4	U	1917	A
4	U	1926	A
4	U	1928	A
4	U	1933	G
4	U	1942	U
4	U	1943	A
4	U	1944	U
4	U	1945	A
4	U	1951	C
4	U	1954	A
4	U	1955	A
4	U	1956	G
4	U	1957	G
4	U	1963	A
4	U	1964	A
4	U	1965	A
4	U	1967	U
4	U	1982	U
4	U	1990	C
4	U	1992	C
4	U	1994	C
4	U	1997	A
4	U	1998	A
4	U	1999	G
4	U	2018	U
4	U	2019	G

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Mol	Chain	Res	Type
4	U	2020	U
4	U	2023	C
4	U	2024	A
4	U	2048	G
4	U	2050	A
4	U	2058	A
4	U	2060	A
4	U	2070	C
4	U	2078	A
4	U	2079	G
4	U	2082	C
4	U	2087	A
4	U	2088	G
4	U	2089	A
4	U	2096	G
4	U	2119	U
4	U	2120	G
4	U	2123	U
4	U	2127	G
4	U	2129	U
4	U	2130	A
4	U	2132	A
4	U	2135	U
4	U	2136	U
4	U	2137	G
4	U	2138	U
4	U	2139	A
4	U	2140	C
4	U	2141	A
4	U	2144	A
4	U	2145	U
4	U	2147	G
4	U	2149	U
4	U	2150	A
4	U	2151	G
4	U	2152	G
4	U	2153	A
4	U	2154	G
4	U	2160	G
4	U	2161	A
4	U	2162	A
4	U	2167	G

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Mol	Chain	Res	Type
4	U	2169	G
4	U	2173	C
4	U	2174	A
4	U	2177	U
4	U	2178	U
4	U	2180	G
4	U	2181	G
4	U	2184	G
4	U	2186	G
4	U	2187	G
4	U	2188	C
4	U	2191	C
4	U	2192	G
4	U	2193	G
4	U	2194	U
4	U	2195	G
4	U	2196	G
4	U	2197	G
4	U	2198	A
4	U	2202	U
4	U	2208	G
4	U	2209	G
4	U	2210	C
4	U	2215	U
4	U	2216	U
4	U	2218	A
4	U	2220	C
4	U	2230	G
4	U	2231	C
4	U	2244	G
4	U	2250	A
4	U	2252	A
4	U	2265	G
4	U	2266	G
4	U	2306	G
4	U	2310	C
4	U	2314	A
4	U	2331	G
4	U	2332	U
4	U	2335	G
4	U	2336	A
4	U	2337	A

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Mol	Chain	Res	Type
4	U	2338	A
4	U	2343	U
4	U	2345	G
4	U	2347	A
4	U	2349	A
4	U	2355	A
4	U	2360	A
4	U	2361	C
4	U	2362	A
4	U	2372	G
4	U	2374	C
4	U	2377	C
4	U	2388	A
4	U	2398	G
4	U	2404	A
4	U	2410	G
4	U	2412	C
4	U	2433	C
4	U	2449	C
4	U	2450	U
4	U	2451	C
4	U	2452	A
4	U	2456	G
4	U	2457	A
4	U	2466	A
4	U	2468	C
4	U	2475	A
4	U	2497	G
4	U	2501	C
4	U	2503	A
4	U	2505	A
4	U	2508	G
4	U	2511	G
4	U	2529	G
4	U	2532	G
4	U	2540	A
4	U	2545	A
4	U	2556	G
4	U	2561	C
4	U	2562	G
4	U	2569	A
4	U	2579	U

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Mol	Chain	Res	Type
4	U	2582	U
4	U	2583	C
4	U	2593	A
4	U	2594	G
4	U	2599	A
4	U	2605	G
4	U	2609	G
4	U	2610	G
4	U	2612	U
4	U	2613	C
4	U	2636	U
4	U	2637	C
4	U	2640	U
4	U	2656	A
4	U	2657	G
4	U	2666	A
4	U	2673	C
4	U	2686	G
4	U	2716	U
4	U	2717	A
4	U	2729	G
4	U	2740	C
4	U	2749	G
4	U	2751	U
4	U	2753	U
4	U	2760	A
4	U	2762	G
4	U	2771	G
4	U	2775	A
4	U	2783	U
4	U	2791	A
4	U	2792	A
4	U	2793	G
4	U	2803	A
4	U	2805	A
4	U	2806	U
4	U	2816	C
4	U	2821	C
4	U	2823	C
4	U	2826	G
4	U	2831	U
4	U	2843	A

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Mol	Chain	Res	Type
4	U	2847	U
4	U	2848	G
4	U	2856	U
4	U	2857	G
4	U	2858	A
4	U	2890	G
4	U	2891	A
4	U	2895	G
4	U	2903	C
4	U	2914	A
4	U	2916	G
4	U	2919	U

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	V	3	U
2	V	19	G
2	V	47	C
2	V	59	U
4	U	10	A
4	U	41	G
4	U	108	A
4	U	109	U
4	U	173	G
4	U	227	A
4	U	250	C
4	U	265	C
4	U	403	U
4	U	408	G
4	U	435	A
4	U	526	G
4	U	535	A
4	U	556	G
4	U	791	U
4	U	835	U
4	U	921	C
4	U	1091	G
4	U	1115	G
4	U	1122	C
4	U	1133	G
4	U	1154	G

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Mol	Chain	Res	Type
4	U	1216	U
4	U	1243	G
4	U	1337	A
4	U	1349	U
4	U	1436	C
4	U	1456	U
4	U	1516	G
4	U	1554	A
4	U	1579	A
4	U	1593	U
4	U	1628	G
4	U	1689	A
4	U	1777	G
4	U	1811	A
4	U	1835	U
4	U	2161	A
4	U	2186	G
4	U	2782	C
4	U	2890	G

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 222 ligands modelled in this entry, 222 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.

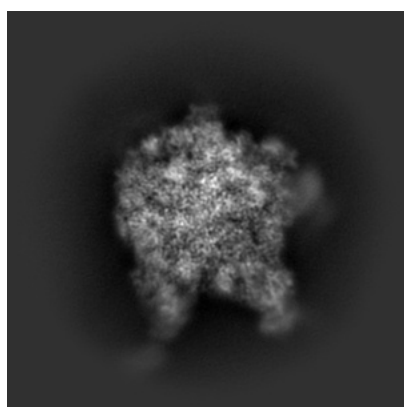
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10543. These allow visual inspection of the internal detail of the map and identification of artifacts.

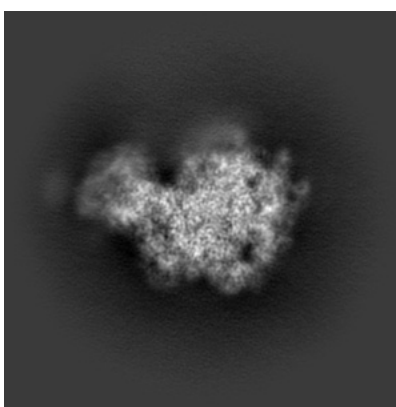
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

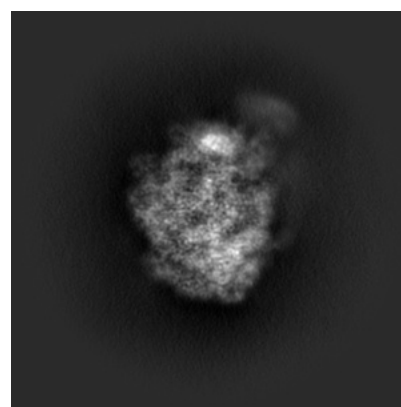
6.1.1 Primary map



X



Y

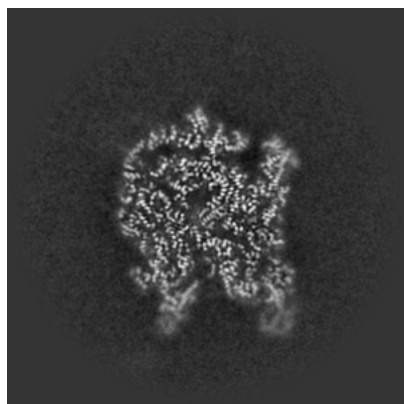


Z

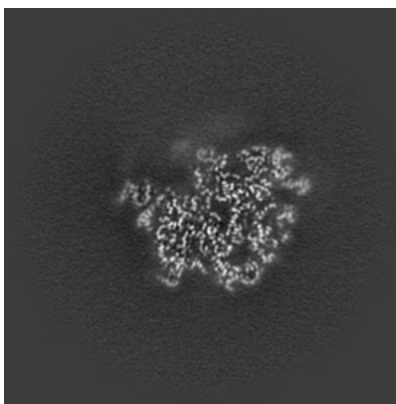
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

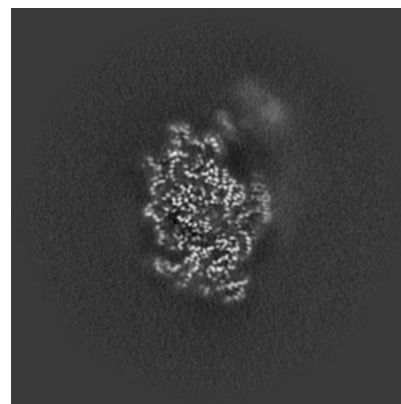
6.2.1 Primary map



X Index: 180



Y Index: 180

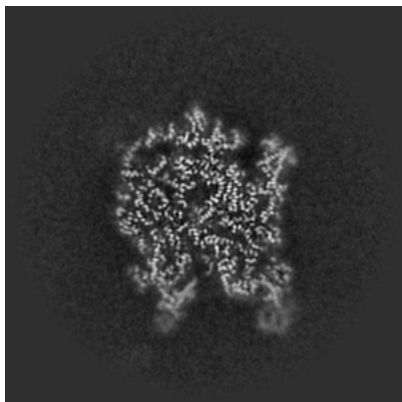


Z Index: 180

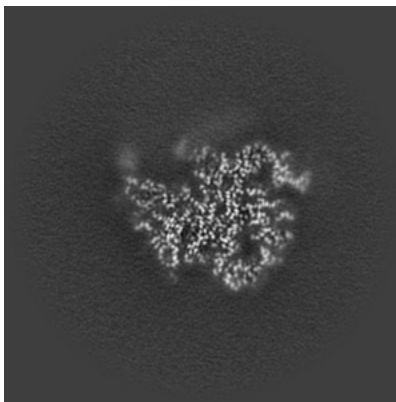
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

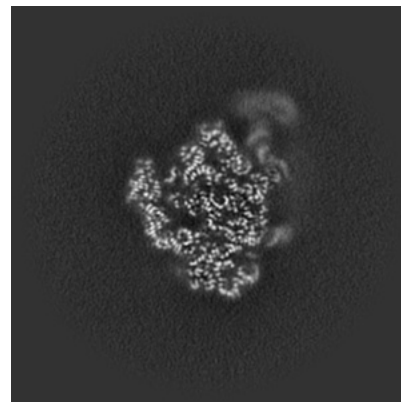
6.3.1 Primary map



X Index: 179



Y Index: 186



Z Index: 210

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.

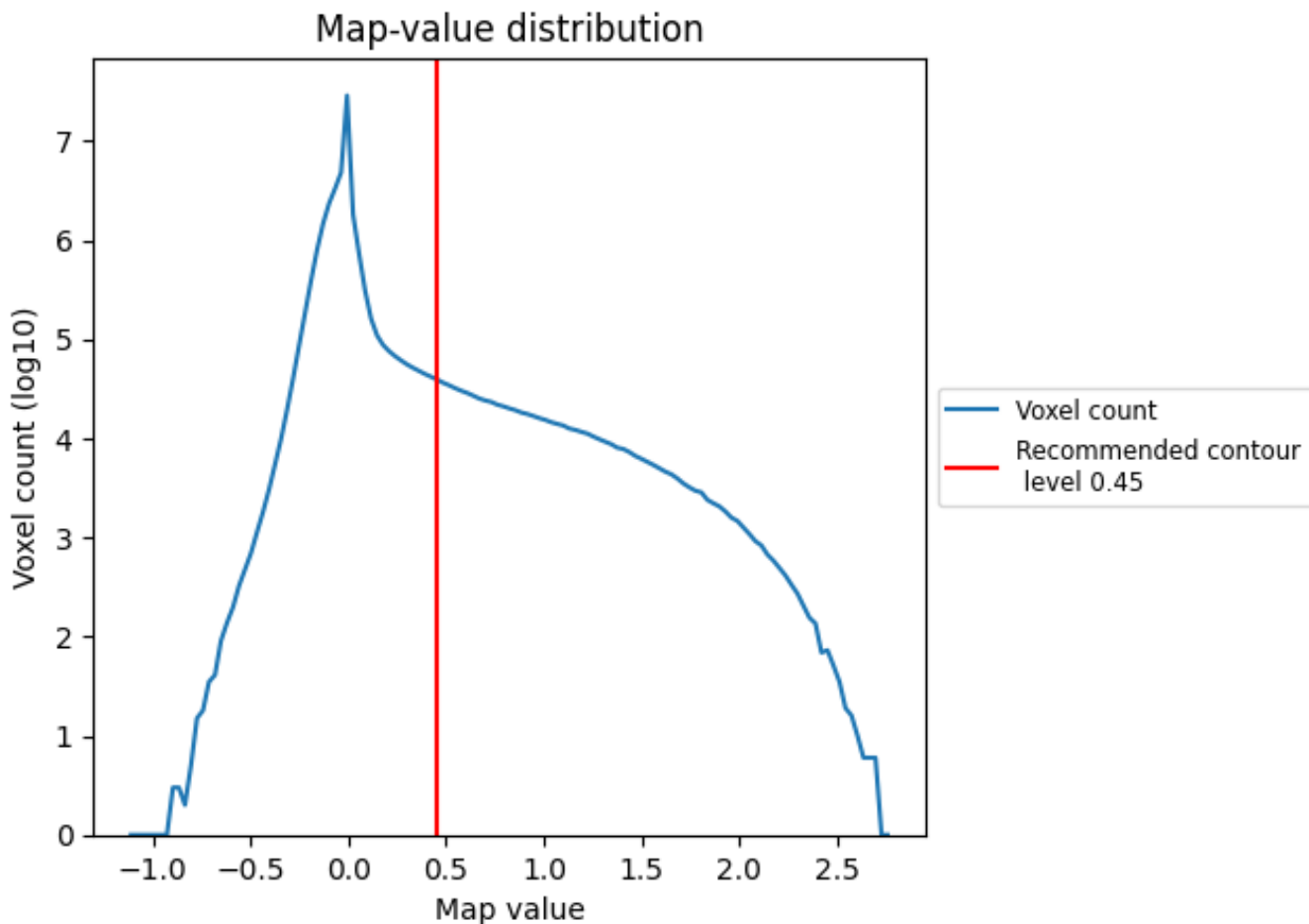
6.5 Mask visualisation

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

7 Map analysis [i](#)

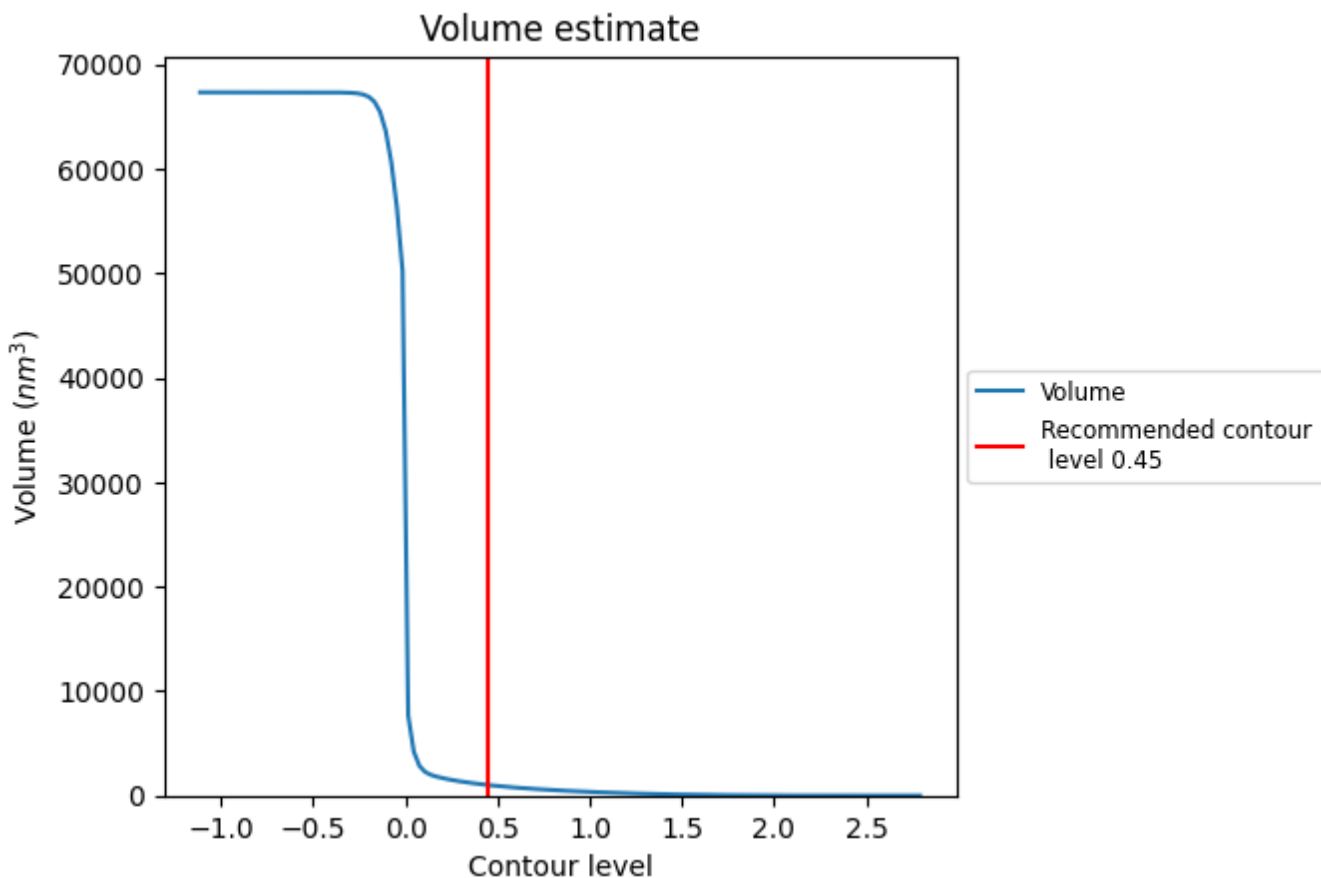
This section contains the results of statistical analysis of the map.

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.

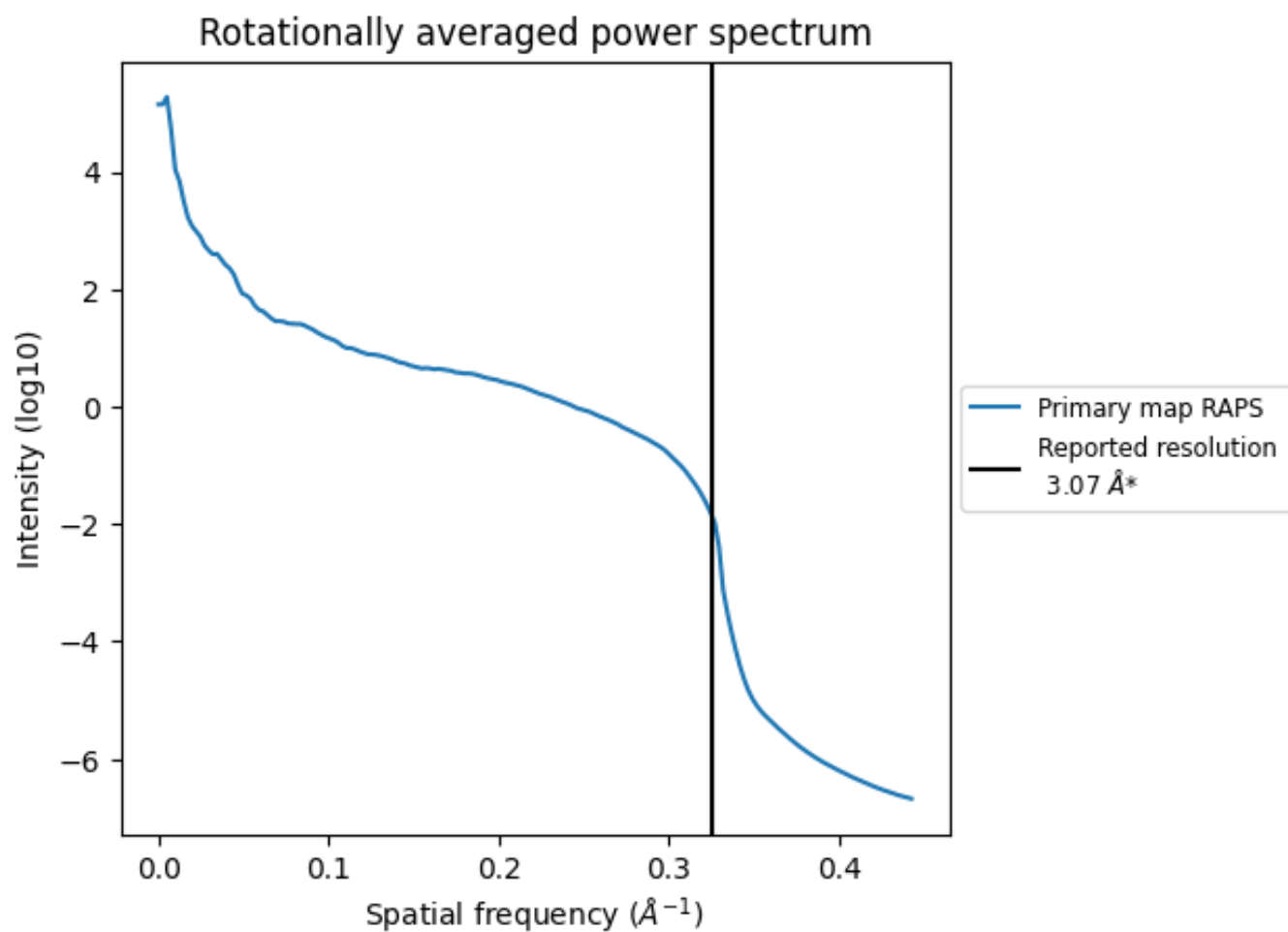
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1008 nm³; this corresponds to an approximate mass of 910 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

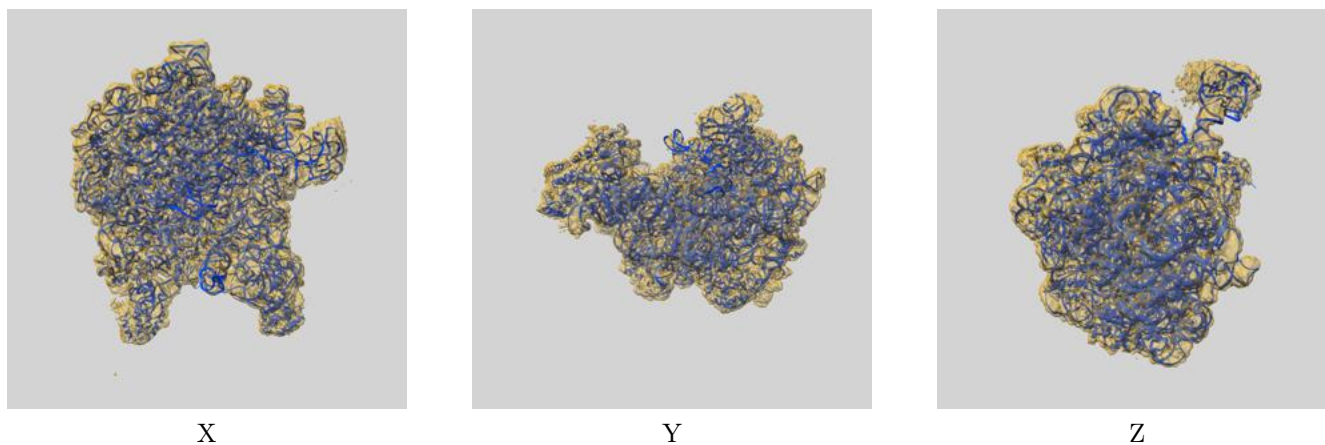
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

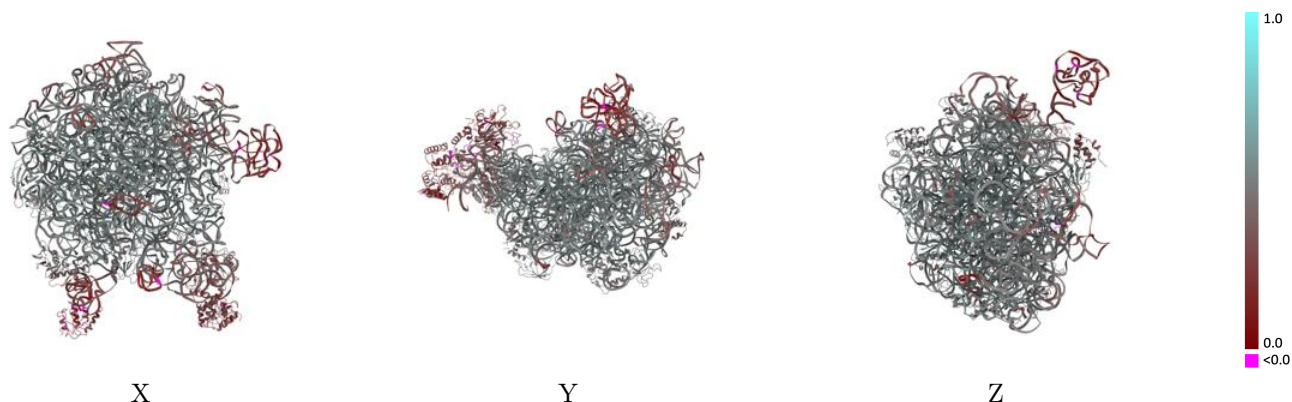
This section contains information regarding the fit between EMDB map EMD-10543 and PDB model 6TPQ. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



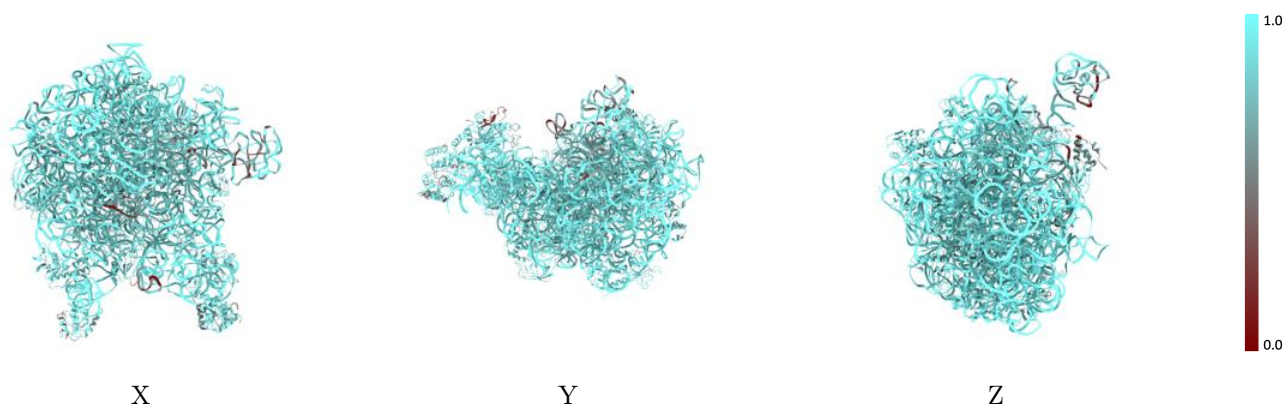
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



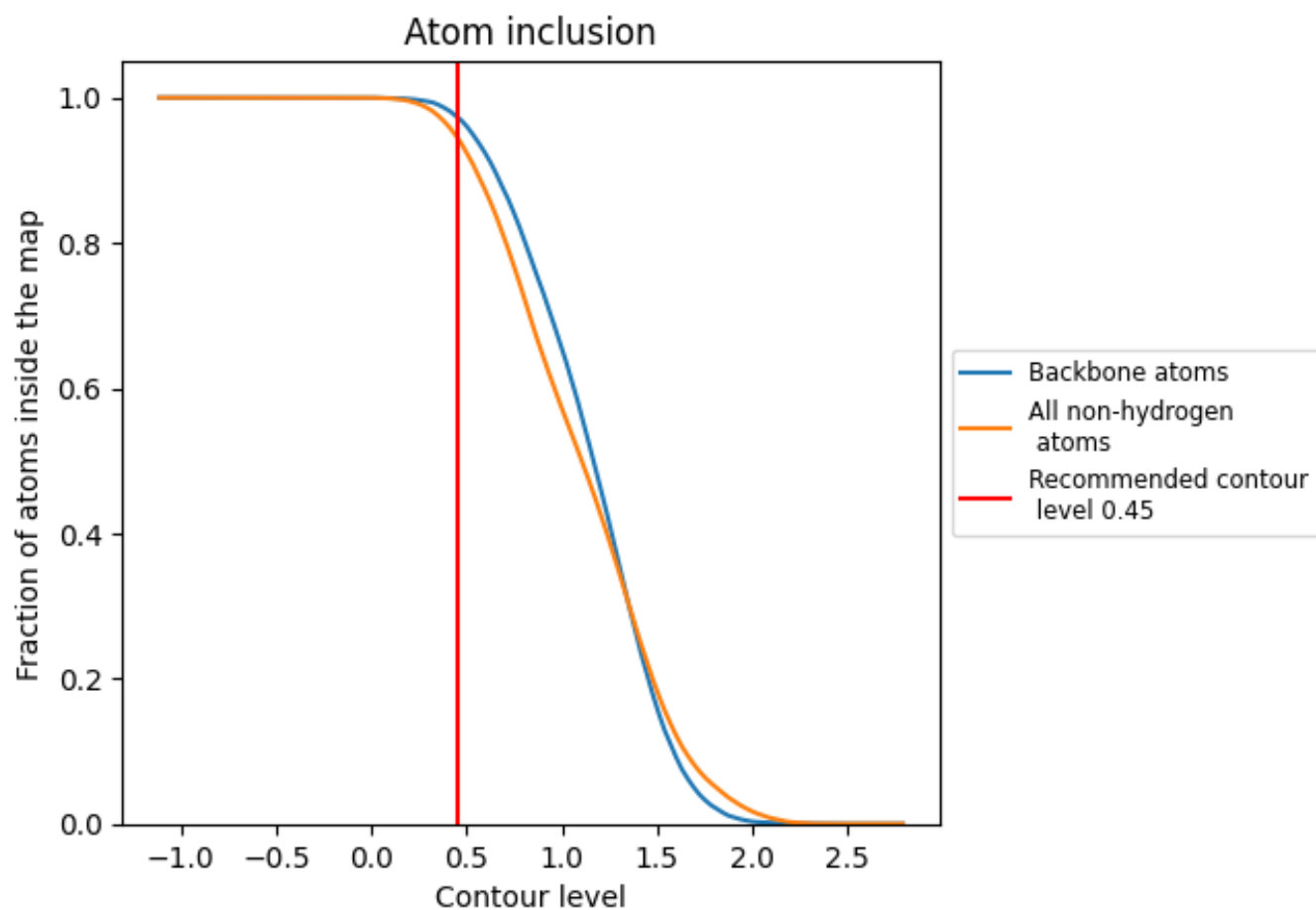
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% of all backbone atoms, 95% 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	 0.9455	 0.4740
A	 0.5970	 0.3500
B	 0.7748	 0.2700
U	 0.9710	 0.4820
V	 0.9924	 0.4310
W	 0.8979	 0.5220
X	 0.9302	 0.5250
Y	 0.9260	 0.4970
Z	 0.8065	 0.3060
a	 0.9192	 0.4240
b	 0.7614	 0.1840
c	 0.9181	 0.5130
d	 0.8931	 0.5000
e	 0.9013	 0.5030
f	 0.8523	 0.4960
g	 0.9085	 0.5080
h	 0.8806	 0.4220
i	 0.8687	 0.4780
j	 0.9230	 0.5090
k	 0.9228	 0.5030
l	 0.8913	 0.5150
m	 0.8755	 0.4860
n	 0.9325	 0.4860
o	 0.8637	 0.5090
p	 0.9203	 0.5240
q	 0.9124	 0.5000
r	 0.9104	 0.5500
s	 0.8818	 0.5480
t	 0.8803	 0.5150
u	 0.8568	 0.5150
v	 0.8716	 0.4320
w	 0.8991	 0.5010

