



## Full wwPDB EM Validation Report ⓘ

Jun 9, 2024 – 08:26 PM EDT

PDB ID : 8FR8  
EMDB ID : EMD-29397  
Title : Structure of Mycobacterium smegmatis Rsh bound to a 70S translation initiation complex  
Authors : Majumdar, S.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.  
Deposited on : 2023-01-06  
Resolution : 2.76 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<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>.

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

EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

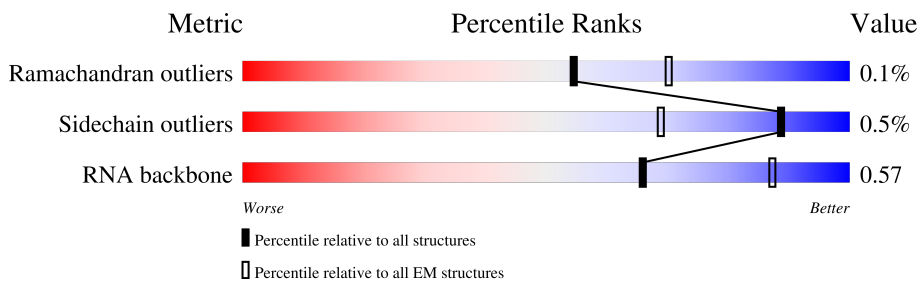
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.76 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.




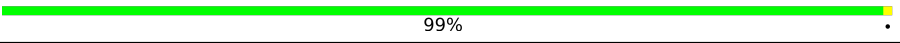
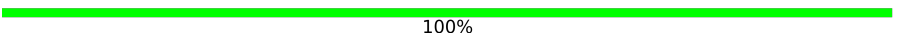
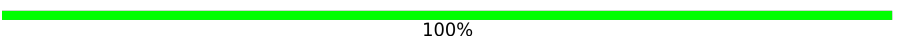
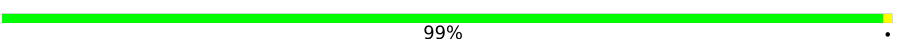
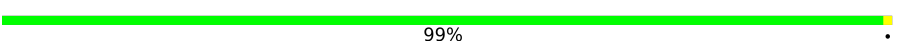
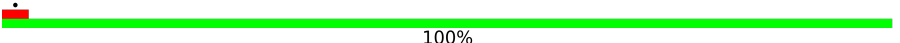
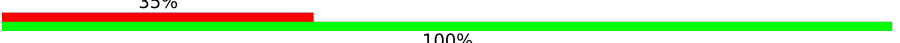
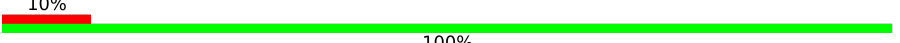
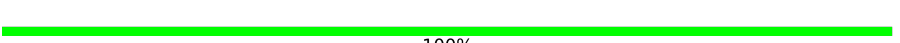

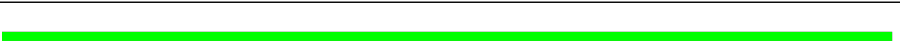



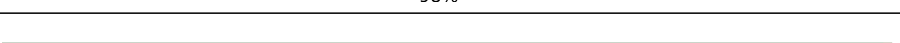
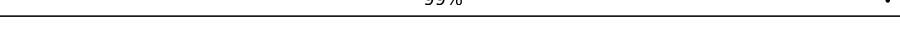
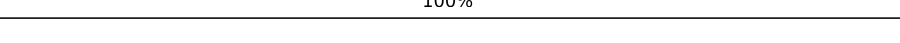
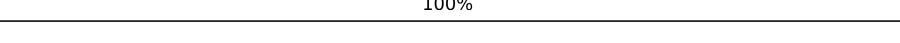
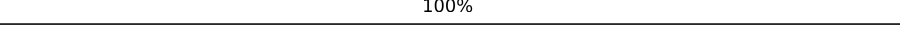
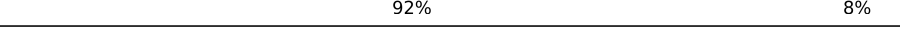
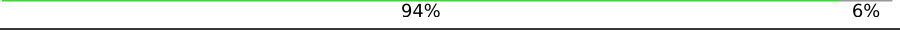
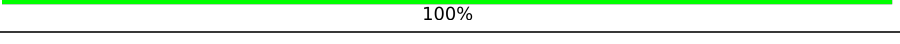
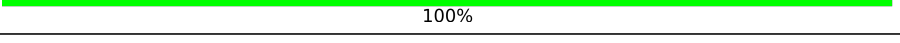
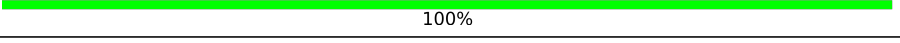
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	c	53	
2	y	77	
3	E	77	
4	d	82	
5	B	118	
6	j	116	
7	N	136	
8	3	23	
















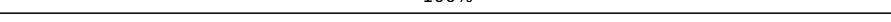
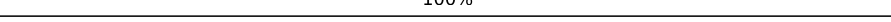
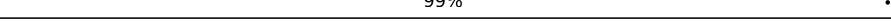

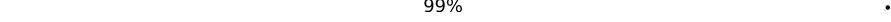
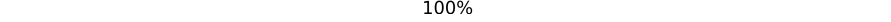




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Mol	Chain	Length	Quality of chain
9	A	3119	
10	K	275	
11	L	214	
12	M	209	
13	O	182	
14	P	176	
15	Q	151	
16	R	126	
17	S	133	
18	T	146	
19	U	122	
20	V	145	
21	J	118	
22	D	126	
23	C	113	
24	W	124	
25	X	100	
26	Y	114	
27	Z	97	
28	1	105	
29	2	192	
30	4	79	
31	6	64	
32	7	59	
33	8	54	

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Mol	Chain	Length	Quality of chain
34	0	46	 100%
35	x	63	 100%
36	F	37	 100%
37	a	1511	 78% 21%
38	b	32	 100%
39	G	208	 99%
40	e	200	 100%
41	f	180	 100%
42	g	96	 98% .
43	h	155	 100%
44	i	131	 100%
45	k	126	 98% .
46	l	99	 100%
47	m	115	 100%
48	n	122	 100%
49	p	88	 100%
50	q	113	 99% .
51	r	94	 100%
52	t	85	 99% .
53	u	228	 100%
54	v	20	 40% 50% 10%
55	I	797	 8% 19% 81%
56	H	82	 13% 91% 9%
57	o	84	 82% 18%
58	9	100	 100%

## 2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 152820 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 L33 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	c	49	Total	C	N	O	0	0
			423	263	89	71		

- Molecule 2 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	y	76	Total	C	N	O	S	0	0
			605	368	131	104	2		

- Molecule 3 is a RNA chain called fMet tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	77	Total	C	N	O	P	0	0
			1642	731	293	541	77		

- Molecule 4 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 5 is a RNA chain called 5S rRNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 6 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 7 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 8 is a protein called 50S ribosomal protein eL31.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 9 is a RNA chain called 23S rRNA (3119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 15 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 16 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 17 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 18 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 20 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	J	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	C	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	97	Total	C	N	O		0	0
			756	479	138	139			

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	180	Total	C	N	O		0	0
			1347	833	243	271			

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	79	Total	C	N	O		0	0
			586	361	123	102			

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	7	59	Total	C	N	O		0	0
			474	292	95	87			

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	8	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 34 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	0	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 35 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	x	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 36 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 37 is a RNA chain called 16S rRNA (1511-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 38 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	G	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	k	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	n	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	p	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	q	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	t	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 53 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 55 is a protein called GTP pyrophosphokinase RelA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	I	150	Total	C	N	O	S	0	0
			1126	700	200	221	5		

- Molecule 56 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	H	75	Total	C	N	O	S	0	0
			593	379	103	110	1		

- Molecule 57 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	o	69	Total	C	N	O	S	0	0
			543	338	107	96	2		


- Molecule 58 is a protein called 30S ribosomal protein S14.

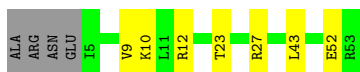
Mol	Chain	Residues	Atoms					AltConf	Trace
58	9	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

### 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.

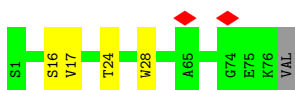
- Molecule 1: 50S ribosomal protein L33 2

Chain c: 



- Molecule 2: 50S ribosomal protein L28

Chain y: 



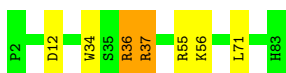
- Molecule 3: fMet tRNA (77-MER)

Chain E: 



- Molecule 4: 30S ribosomal protein S19

Chain d: 



- Molecule 5: 5S rRNA (118-MER)

Chain B: 



- Molecule 6: 30S ribosomal protein S13

Chain j:  98% ..



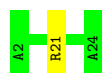
- Molecule 7: 50S ribosomal protein L16

Chain N:  100%


There are no outlier residues recorded for this chain.

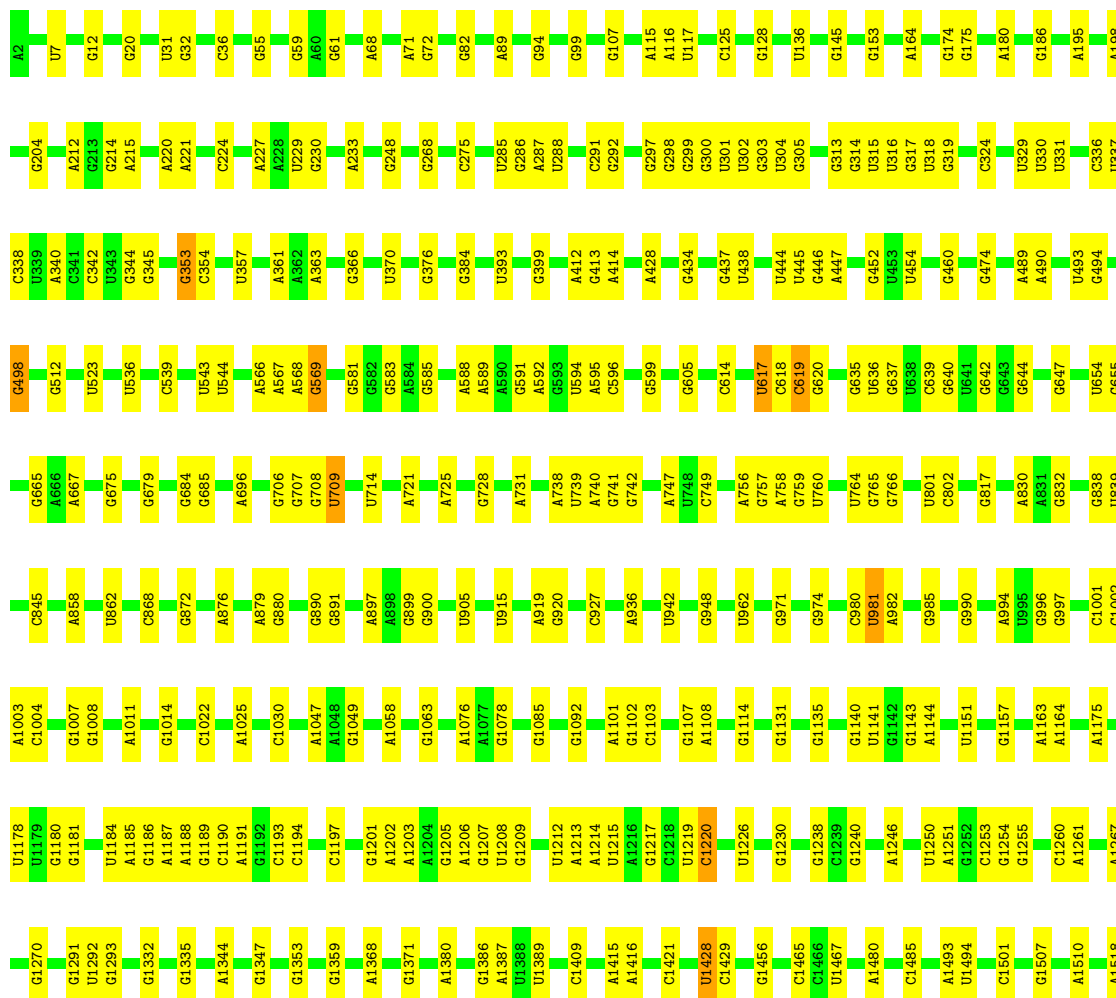
- Molecule 8: 50S ribosomal protein eL31

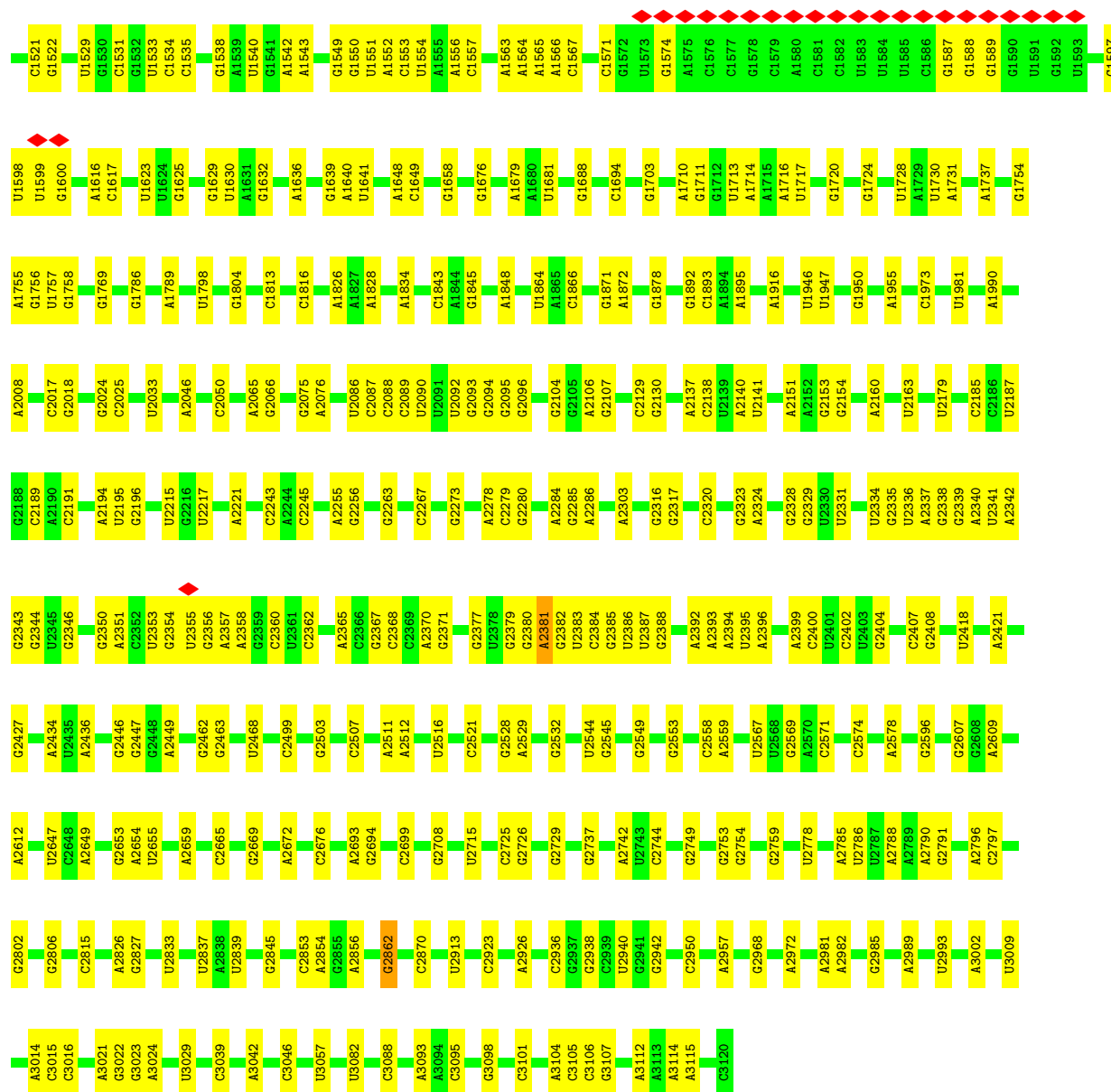
Chain 3:  96% .



- Molecule 9: 23S rRNA (3119-MER)

Chain A:  78% 21%





- Molecule 10: 50S ribosomal protein L2

Chain K: 99%




- Molecule 11: 50S ribosomal protein L3

Chain L: 100%

There are no outlier residues recorded for this chain.

- Molecule 12: 50S ribosomal protein L4

Chain M:  100%



- Molecule 13: 50S ribosomal protein L5

Chain O:  99%



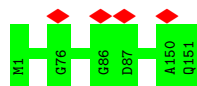
- Molecule 14: 50S ribosomal protein L6

Chain P:  99%



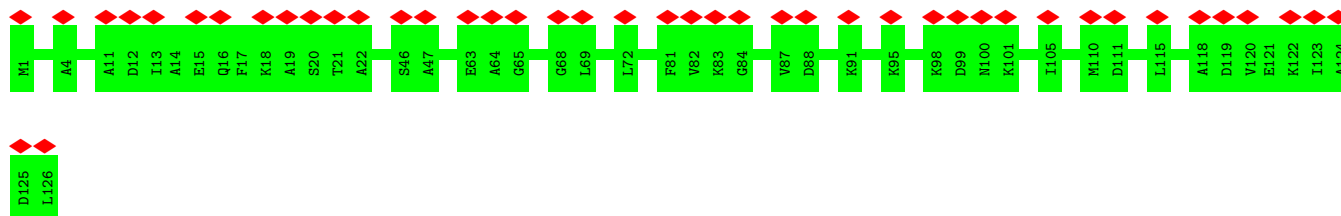
- Molecule 15: 50S ribosomal protein L9

Chain Q:  100%



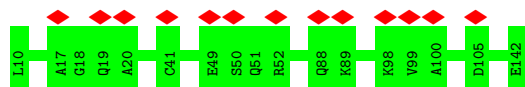
- Molecule 16: 50S ribosomal protein L10

Chain R:  35% 100%



- Molecule 17: 50S ribosomal protein L11

Chain S:  10% 100%



- Molecule 18: 50S ribosomal protein L13

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: 50S ribosomal protein L14

Chain U:  100%

There are no outlier residues recorded for this chain.

- Molecule 20: 50S ribosomal protein L15

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: 50S ribosomal protein L17

Chain J:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L18

Chain D:  98%



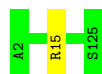
- Molecule 23: 50S ribosomal protein L19

Chain C:  98%



- Molecule 24: 50S ribosomal protein L20

Chain W:  99%



- Molecule 25: 50S ribosomal protein L21

Chain X:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L22

Chain Y:  100%

There are no outlier residues recorded for this chain.

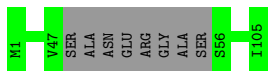
- Molecule 27: 50S ribosomal protein L23

Chain Z:  100%

There are no outlier residues recorded for this chain.

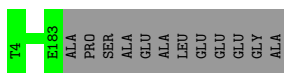
- Molecule 28: 50S ribosomal protein L24

Chain 1:  92% 8%



- Molecule 29: 50S ribosomal protein L25

Chain 2:  94% 6%



- Molecule 30: 50S ribosomal protein L27

Chain 4:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: 50S ribosomal protein L29

Chain 6:  100%

There are no outlier residues recorded for this chain.

- Molecule 32: 50S ribosomal protein L30

Chain 7:  100%

There are no outlier residues recorded for this chain.

- Molecule 33: 50S ribosomal protein L32

Chain 8:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: 50S ribosomal protein L34

Chain 0:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: 50S ribosomal protein L35

Chain x:  100%


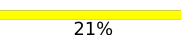
There are no outlier residues recorded for this chain.

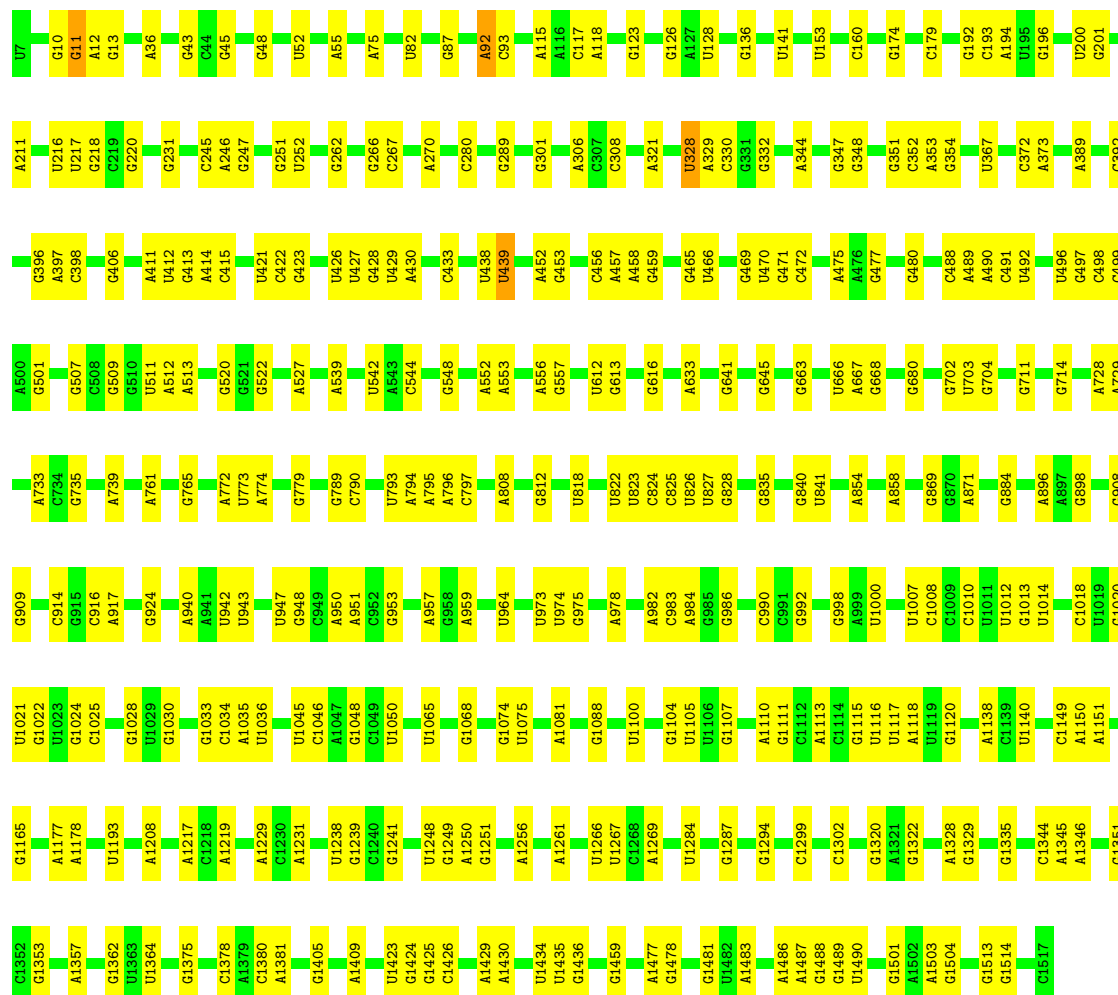
- Molecule 36: 50S ribosomal protein L36

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 37: 16S rRNA (1511-MER)

Chain a:  78%  21%



- Molecule 38: 30S ribosomal protein S22

Chain b:  100%

There are no outlier residues recorded for this chain.

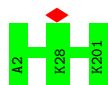
- Molecule 39: 30S ribosomal protein S3

Chain G:  99%



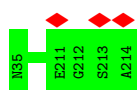
- Molecule 40: 30S ribosomal protein S4

Chain e:  100%



- Molecule 41: 30S ribosomal protein S5

Chain f:  100%



- Molecule 42: 30S ribosomal protein S6

Chain g:  98%



- Molecule 43: 30S ribosomal protein S7

Chain h:  100%

There are no outlier residues recorded for this chain.

- Molecule 44: 30S ribosomal protein S8

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 45: 30S ribosomal protein S9

Chain k:  98%



- Molecule 46: 30S ribosomal protein S10

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 30S ribosomal protein S11

Chain m:  100%

There are no outlier residues recorded for this chain.

- Molecule 48: 30S ribosomal protein S12

Chain n:  100%

There are no outlier residues recorded for this chain.

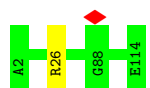
- Molecule 49: 30S ribosomal protein S15

Chain p:  100%

There are no outlier residues recorded for this chain.

- Molecule 50: 30S ribosomal protein S16

Chain q:  99%



- Molecule 51: 30S ribosomal protein S17

Chain r:  100%

There are no outlier residues recorded for this chain.

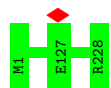
- Molecule 52: 30S ribosomal protein S20

Chain t:  99%



- Molecule 53: 30S ribosomal protein S2

Chain u:  100%

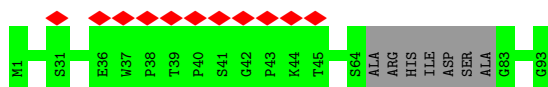
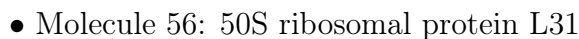



- Molecule 54: mRNA

Chain v:  40% 50% 10%



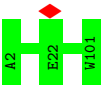
- Molecule 55: GTP pyrophosphokinase RelA



- Chain o:  82% 18%



- Molecule 58: 30S ribosomal protein S14



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	66.59	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.041	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	423.72, 423.72, 423.72	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84744, 0.84744, 0.84744	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	c	0.58	0/430	1.00	2/577 (0.3%)
2	y	0.62	1/616 (0.2%)	0.88	0/825
3	E	0.71	1/1833 (0.1%)	1.05	3/2854 (0.1%)
4	d	0.68	2/680 (0.3%)	0.91	3/915 (0.3%)
5	B	1.05	2/2821 (0.1%)	1.15	12/4396 (0.3%)
6	j	0.46	0/942	0.74	0/1260
7	N	0.69	0/1118	0.67	0/1506
8	3	0.69	0/191	0.82	1/247 (0.4%)
9	A	1.23	2/75001 (0.0%)	1.09	57/117027 (0.0%)
10	K	0.75	0/2153	0.73	1/2895 (0.0%)
11	L	0.75	0/1609	0.69	0/2165
12	M	0.70	1/1592 (0.1%)	0.61	0/2153
13	O	0.54	0/1467	0.64	0/1973
14	P	0.46	0/1369	0.61	0/1848
15	Q	0.34	0/1027	0.57	0/1398
16	R	0.31	0/925	0.58	0/1246
17	S	0.30	0/1006	0.58	0/1364
18	T	0.68	0/1157	0.60	0/1567
19	U	0.71	0/946	0.66	0/1268
20	V	0.69	0/1091	0.64	0/1457
21	J	0.70	0/945	0.65	0/1267
22	D	0.58	0/966	0.73	2/1298 (0.2%)
23	C	0.72	1/921 (0.1%)	0.68	1/1236 (0.1%)
24	W	0.77	0/1000	0.67	1/1341 (0.1%)
25	X	0.73	0/764	0.60	0/1030
26	Y	0.73	0/887	0.68	0/1204
27	Z	0.64	0/766	0.61	0/1030
28	1	0.58	0/738	0.61	0/987
29	2	0.42	0/1361	0.61	0/1858
30	4	0.76	0/595	0.66	0/798
31	6	0.59	0/534	0.66	0/713
32	7	0.66	0/477	0.68	0/640
33	8	0.74	0/427	0.70	0/572
34	0	0.75	0/380	0.83	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	x	0.70	0/507	0.74	0/672
36	F	0.69	0/303	0.71	0/401
37	a	1.08	1/36309 (0.0%)	1.05	25/56657 (0.0%)
38	b	0.57	0/280	0.85	0/359
39	G	0.49	0/1684	0.64	0/2261
40	e	0.48	0/1672	0.62	0/2251
41	f	0.57	0/1312	0.59	0/1772
42	g	0.56	0/782	0.65	0/1059
43	h	0.45	0/1252	0.61	0/1690
44	i	0.61	0/1025	0.64	0/1385
45	k	0.49	0/1012	0.63	0/1362
46	l	0.48	0/802	0.65	0/1086
47	m	0.55	0/873	0.62	0/1180
48	n	0.61	0/969	0.67	0/1294
49	p	0.58	0/729	0.62	0/977
50	q	0.55	0/908	0.64	0/1226
51	r	0.55	0/759	0.64	0/1016
52	t	0.51	1/663 (0.2%)	0.60	0/882
53	u	0.36	0/1822	0.56	0/2457
54	v	0.54	0/436	0.87	0/679
55	I	0.31	0/1144	0.61	0/1560
56	H	0.40	0/613	0.60	0/835
57	o	0.50	0/549	0.62	0/737
58	9	0.47	0/830	0.66	0/1106
All	All	1.04	12/165970 (0.0%)	0.98	108/248319 (0.0%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	501	C	OP3-P	-10.21	1.48	1.61
5	B	102	A	N9-C4	-5.86	1.34	1.37
23	C	72	THR	C-N	-5.69	1.21	1.34
37	a	1489	G	C2-N3	-5.31	1.28	1.32
5	B	94	G	N9-C4	-5.29	1.33	1.38
12	M	178	ILE	C-N	-5.23	1.22	1.34
4	d	71	LEU	C-N	5.18	1.42	1.33
52	t	67	ILE	C-N	-5.08	1.22	1.34
2	y	24	THR	C-N	5.08	1.44	1.34
4	d	34	TRP	CB-CG	-5.06	1.41	1.50
9	A	936	A	N9-C4	-5.03	1.34	1.37
9	A	876	A	N9-C4	-5.02	1.34	1.37

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2245	C	C2-N1-C1'	9.87	129.66	118.80
37	a	1486	A	C8-N9-C4	-8.56	102.38	105.80
5	B	20	G	N1-C6-O6	-8.07	115.06	119.90
9	A	2245	C	N1-C2-O2	7.92	123.65	118.90
9	A	905	U	C2-N1-C1'	7.87	127.14	117.70
23	C	15	ASP	CB-CG-OD1	7.84	125.36	118.30
9	A	1220	C	C6-N1-C2	-7.75	117.20	120.30
9	A	2245	C	C6-N1-C1'	-7.70	111.56	120.80
37	a	1486	A	N7-C8-N9	7.66	117.63	113.80
9	A	617	U	C2-N1-C1'	7.61	126.83	117.70
37	a	1489	G	N3-C2-N2	-7.45	114.69	119.90
4	d	37	ARG	N-CA-C	7.16	130.32	111.00
37	a	415	C	N1-C2-O2	7.11	123.16	118.90
37	a	1489	G	N3-C4-N9	-7.07	121.76	126.00
5	B	82	A	N1-C6-N6	6.97	122.78	118.60
37	a	415	C	N3-C2-O2	-6.96	117.02	121.90
9	A	3046	C	N3-C2-O2	-6.83	117.12	121.90
9	A	654	U	C5-C6-N1	6.78	126.09	122.70
3	E	567	C	C6-N1-C2	-6.76	117.60	120.30
9	A	2025	C	N3-C2-O2	-6.74	117.18	121.90
9	A	599	G	O4'-C1'-N9	6.65	113.52	108.20
5	B	74	A	N1-C6-N6	6.58	122.55	118.60
5	B	94	G	N3-C4-C5	6.58	131.89	128.60
5	B	20	G	C5-C6-O6	6.56	132.53	128.60
4	d	37	ARG	CB-CA-C	-6.53	97.34	110.40
9	A	1535	C	N1-C2-O2	6.48	122.79	118.90
5	B	94	G	N3-C4-N9	-6.48	122.11	126.00
1	c	27	ARG	NE-CZ-NH1	6.47	123.53	120.30
9	A	619	C	C2-N1-C1'	6.47	125.92	118.80
3	E	531	G	N3-C4-N9	-6.39	122.16	126.00
37	a	439	U	N3-C2-O2	-6.35	117.75	122.20
37	a	1489	G	N1-C2-N2	6.34	121.91	116.20
37	a	1486	A	C5-N7-C8	-6.34	100.73	103.90
37	a	308	C	N1-C2-O2	6.29	122.67	118.90
9	A	2468	U	N3-C4-O4	6.28	123.80	119.40
37	a	439	U	C6-N1-C2	-6.24	117.25	121.00
9	A	962	U	C2-N1-C1'	6.22	125.16	117.70
9	A	2025	C	N1-C2-O2	6.19	122.61	118.90
9	A	1428	U	C2-N1-C1'	6.14	125.07	117.70
9	A	353	G	C4-N9-C1'	6.14	134.48	126.50
37	a	328	U	C2-N1-C1'	6.13	125.06	117.70
5	B	87	U	N3-C2-O2	-6.09	117.94	122.20

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2870	C	C5-C6-N1	6.02	124.01	121.00
9	A	617	U	N1-C2-O2	6.01	127.01	122.80
9	A	2245	C	N3-C2-O2	-5.95	117.73	121.90
9	A	2400	C	N3-C2-O2	-5.82	117.83	121.90
9	A	619	C	C6-N1-C1'	-5.79	113.85	120.80
1	c	23	THR	O-C-N	-5.78	113.46	122.70
9	A	2468	U	C5-C4-O4	-5.77	122.44	125.90
8	3	21	ARG	NE-CZ-NH1	5.76	123.18	120.30
37	a	1477	A	P-O3'-C3'	5.74	126.59	119.70
9	A	619	C	N1-C2-O2	5.73	122.34	118.90
9	A	2025	C	C2-N1-C1'	5.71	125.08	118.80
22	D	24	ARG	NE-CZ-NH1	5.69	123.15	120.30
37	a	1489	G	N3-C4-C5	5.65	131.43	128.60
37	a	790	C	C6-N1-C2	-5.63	118.05	120.30
9	A	3046	C	C6-N1-C2	-5.62	118.05	120.30
37	a	415	C	C2-N1-C1'	5.62	124.98	118.80
9	A	1429	C	C6-N1-C2	-5.62	118.05	120.30
9	A	569	G	O4'-C1'-N9	5.54	112.63	108.20
37	a	415	C	C6-N1-C2	-5.54	118.08	120.30
37	a	1375	G	C2-N3-C4	-5.53	109.14	111.90
5	B	31	C	C6-N1-C2	-5.52	118.09	120.30
9	A	2185	C	N1-C2-O2	5.51	122.21	118.90
9	A	2725	C	N1-C2-O2	5.50	122.20	118.90
9	A	858	A	C5-N7-C8	-5.45	101.18	103.90
9	A	1973	C	C6-N1-C2	-5.44	118.12	120.30
9	A	617	U	C6-N1-C1'	-5.43	113.60	121.20
9	A	353	G	C8-N9-C1'	-5.42	119.96	127.00
9	A	2870	C	C6-N1-C2	-5.41	118.14	120.30
9	A	3046	C	C2-N1-C1'	5.40	124.74	118.80
9	A	2923	C	C5-C6-N1	5.38	123.69	121.00
9	A	1220	C	C2-N1-C1'	5.34	124.67	118.80
37	a	11	G	O4'-C1'-N9	5.34	112.47	108.20
9	A	2381	A	P-O3'-C3'	5.33	126.10	119.70
9	A	498	G	N7-C8-N9	5.33	115.76	113.10
10	K	88	ARG	NE-CZ-NH2	-5.33	117.64	120.30
37	a	92	A	P-O3'-C3'	5.32	126.08	119.70
24	W	15	ARG	NE-CZ-NH1	5.31	122.95	120.30
9	A	948	G	N7-C8-N9	5.30	115.75	113.10
3	E	575	C	C6-N1-C2	-5.29	118.18	120.30
5	B	94	G	N3-C2-N2	-5.29	116.19	119.90
37	a	998	G	O5'-P-OP1	-5.29	100.94	105.70
9	A	204	G	O4'-C1'-N9	5.28	112.43	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	82	A	C5-C6-N6	-5.28	119.48	123.70
5	B	87	U	N1-C2-O2	5.27	126.49	122.80
4	d	36	ARG	NE-CZ-NH1	5.26	122.93	120.30
37	a	270	A	N9-C4-C5	-5.25	103.70	105.80
9	A	2243	C	C5-C4-N4	-5.24	116.53	120.20
9	A	1535	C	C2-N1-C1'	5.24	124.56	118.80
9	A	1535	C	N3-C2-O2	-5.19	118.27	121.90
9	A	2862	G	O4'-C1'-N9	5.19	112.35	108.20
9	A	709	U	C2-N1-C1'	5.18	123.92	117.70
9	A	2516	U	C5-C6-N1	5.17	125.29	122.70
37	a	439	U	C5-C6-N1	5.16	125.28	122.70
9	A	1429	C	C2-N1-C1'	5.14	124.46	118.80
9	A	2521	C	C6-N1-C2	-5.14	118.24	120.30
22	D	14	ARG	NE-CZ-NH1	5.12	122.86	120.30
37	a	179	C	C2-N1-C1'	5.11	124.42	118.80
37	a	328	U	N3-C2-O2	-5.09	118.64	122.20
9	A	802	C	C5-C4-N4	-5.09	116.64	120.20
9	A	981	U	C6-N1-C2	-5.08	117.95	121.00
9	A	2815	C	C6-N1-C2	-5.08	118.27	120.30
9	A	2499	C	N1-C2-O2	5.08	121.95	118.90
9	A	2553	G	N7-C8-N9	5.07	115.63	113.10
5	B	66	C	C6-N1-C2	-5.06	118.28	120.30
9	A	2870	C	N3-C4-N4	5.05	121.54	118.00
9	A	1816	C	C6-N1-C2	-5.01	118.30	120.30

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	c	47/53 (89%)	36 (77%)	11 (23%)	0	100	100
2	y	74/77 (96%)	63 (85%)	11 (15%)	0	100	100
4	d	80/82 (98%)	73 (91%)	6 (8%)	1 (1%)	12	21
6	j	114/116 (98%)	94 (82%)	18 (16%)	2 (2%)	8	15
7	N	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
8	3	21/23 (91%)	21 (100%)	0	0	100	100
10	K	273/275 (99%)	259 (95%)	14 (5%)	0	100	100
11	L	212/214 (99%)	194 (92%)	18 (8%)	0	100	100
12	M	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
13	O	180/182 (99%)	167 (93%)	13 (7%)	0	100	100
14	P	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
15	Q	149/151 (99%)	132 (89%)	17 (11%)	0	100	100
16	R	124/126 (98%)	108 (87%)	16 (13%)	0	100	100
17	S	131/133 (98%)	104 (79%)	27 (21%)	0	100	100
18	T	144/146 (99%)	138 (96%)	6 (4%)	0	100	100
19	U	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
20	V	143/145 (99%)	133 (93%)	10 (7%)	0	100	100
21	J	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
22	D	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
23	C	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
24	W	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
25	X	98/100 (98%)	98 (100%)	0	0	100	100
26	Y	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
27	Z	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
28	1	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
29	2	178/192 (93%)	164 (92%)	14 (8%)	0	100	100
30	4	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
31	6	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
32	7	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
33	8	52/54 (96%)	48 (92%)	4 (8%)	0	100	100
34	0	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
35	x	61/63 (97%)	61 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	F	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
38	b	30/32 (94%)	30 (100%)	0	0	100	100
39	G	206/208 (99%)	179 (87%)	26 (13%)	1 (0%)	29	47
40	e	198/200 (99%)	177 (89%)	21 (11%)	0	100	100
41	f	178/180 (99%)	165 (93%)	13 (7%)	0	100	100
42	g	94/96 (98%)	87 (93%)	7 (7%)	0	100	100
43	h	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
44	i	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
45	k	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
46	l	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
47	m	113/115 (98%)	101 (89%)	12 (11%)	0	100	100
48	n	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
49	p	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
50	q	111/113 (98%)	95 (86%)	16 (14%)	0	100	100
51	r	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
52	t	83/85 (98%)	83 (100%)	0	0	100	100
53	u	226/228 (99%)	213 (94%)	13 (6%)	0	100	100
55	I	148/797 (19%)	112 (76%)	36 (24%)	0	100	100
56	H	71/82 (87%)	63 (89%)	8 (11%)	0	100	100
57	o	67/84 (80%)	61 (91%)	6 (9%)	0	100	100
58	9	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
All	All	6188/6992 (88%)	5721 (92%)	463 (8%)	4 (0%)	54	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	d	37	ARG
6	j	83	GLU
39	G	126	ARG
6	j	82	ILE

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	c	46/49 (94%)	41 (89%)	5 (11%)	6	10
2	y	63/64 (98%)	60 (95%)	3 (5%)	25	44
4	d	73/73 (100%)	69 (94%)	4 (6%)	21	37
6	j	99/99 (100%)	98 (99%)	1 (1%)	76	85
7	N	114/114 (100%)	114 (100%)	0	100	100
8	3	18/18 (100%)	18 (100%)	0	100	100
10	K	215/215 (100%)	214 (100%)	1 (0%)	88	92
11	L	160/160 (100%)	160 (100%)	0	100	100
12	M	169/169 (100%)	169 (100%)	0	100	100
13	O	151/151 (100%)	149 (99%)	2 (1%)	69	81
14	P	148/148 (100%)	147 (99%)	1 (1%)	84	89
15	Q	90/116 (78%)	90 (100%)	0	100	100
16	R	89/89 (100%)	89 (100%)	0	100	100
17	S	102/102 (100%)	102 (100%)	0	100	100
18	T	119/119 (100%)	119 (100%)	0	100	100
19	U	100/100 (100%)	100 (100%)	0	100	100
20	V	112/112 (100%)	112 (100%)	0	100	100
21	J	97/97 (100%)	97 (100%)	0	100	100
22	D	93/93 (100%)	93 (100%)	0	100	100
23	C	100/100 (100%)	100 (100%)	0	100	100
24	W	97/97 (100%)	97 (100%)	0	100	100
25	X	81/81 (100%)	81 (100%)	0	100	100
26	Y	90/90 (100%)	90 (100%)	0	100	100
27	Z	83/83 (100%)	83 (100%)	0	100	100
28	1	81/86 (94%)	81 (100%)	0	100	100
29	2	148/155 (96%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	4	58/58 (100%)	58 (100%)	0	100	100
31	6	58/58 (100%)	58 (100%)	0	100	100
32	7	52/52 (100%)	52 (100%)	0	100	100
33	8	43/43 (100%)	43 (100%)	0	100	100
34	0	35/35 (100%)	35 (100%)	0	100	100
35	x	53/53 (100%)	53 (100%)	0	100	100
36	F	35/35 (100%)	35 (100%)	0	100	100
38	b	30/30 (100%)	30 (100%)	0	100	100
39	G	170/170 (100%)	168 (99%)	2 (1%)	71	82
40	e	175/175 (100%)	175 (100%)	0	100	100
41	f	127/127 (100%)	127 (100%)	0	100	100
42	g	85/85 (100%)	83 (98%)	2 (2%)	49	68
43	h	131/131 (100%)	131 (100%)	0	100	100
44	i	107/107 (100%)	107 (100%)	0	100	100
45	k	102/102 (100%)	100 (98%)	2 (2%)	55	72
46	l	89/89 (100%)	89 (100%)	0	100	100
47	m	89/89 (100%)	89 (100%)	0	100	100
48	n	103/103 (100%)	103 (100%)	0	100	100
49	p	76/76 (100%)	76 (100%)	0	100	100
50	q	92/92 (100%)	91 (99%)	1 (1%)	73	84
51	r	80/80 (100%)	80 (100%)	0	100	100
52	t	69/69 (100%)	69 (100%)	0	100	100
53	u	191/191 (100%)	191 (100%)	0	100	100
55	I	128/653 (20%)	128 (100%)	0	100	100
56	H	64/70 (91%)	64 (100%)	0	100	100
57	o	58/70 (83%)	58 (100%)	0	100	100
58	9	85/85 (100%)	85 (100%)	0	100	100
All	All	5123/5708 (90%)	5099 (100%)	24 (0%)	89	92

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	c	9	VAL

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Mol	Chain	Res	Type
1	c	10	LYS
1	c	12	ARG
1	c	43	LEU
1	c	52	GLU
2	y	16	SER
2	y	17	VAL
2	y	28	TRP
4	d	12	ASP
4	d	36	ARG
4	d	55	ARG
4	d	56	LYS
6	j	83	GLU
10	K	188	ARG
13	O	119	ARG
13	O	144	MET
14	P	70	ARG
39	G	123	LEU
39	G	126	ARG
42	g	17	ARG
42	g	47	ARG
45	k	32	ARG
45	k	126	ARG
50	q	26	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
4	d	47	HIS
4	d	57	HIS
13	O	62	ASN
21	J	17	GLN
29	2	76	GLN
31	6	31	ASN
39	G	125	ASN
39	G	143	GLN
48	n	112	GLN
50	q	57	GLN
55	I	701	GLN
56	H	15	GLN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	E	76/77 (98%)	40 (52%)	4 (5%)
37	a	1510/1511 (99%)	318 (21%)	0
5	B	117/118 (99%)	27 (23%)	2 (1%)
54	v	17/20 (85%)	10 (58%)	0
9	A	3118/3119 (99%)	632 (20%)	15 (0%)
All	All	4838/4845 (99%)	1027 (21%)	21 (0%)

All (1027) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	E	502	G
3	E	503	C
3	E	504	G
3	E	505	G
3	E	508	U
3	E	514	A
3	E	515	G
3	E	516	C
3	E	518	U
3	E	518(A)	C
3	E	518(B)	G
3	E	519	G
3	E	520	U
3	E	521	A
3	E	522	G
3	E	534	C
3	E	535	A
3	E	537	A
3	E	538	A
3	E	542	A
3	E	543	G
3	E	548	C
3	E	549	G
3	E	554	U
3	E	555	U
3	E	557	G
3	E	558	A
3	E	559	A
3	E	563	U
3	E	564	G
3	E	566	C
3	E	567	C
3	E	568	C

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Mol	Chain	Res	Type
3	E	569	C
3	E	570	G
3	E	571	C
3	E	572	U
3	E	573	A
3	E	574	C
3	E	576	A
5	B	3	U
5	B	4	A
5	B	5	C
5	B	6	G
5	B	12	C
5	B	13	C
5	B	20	G
5	B	22	A
5	B	26	A
5	B	31	C
5	B	35	G
5	B	36	U
5	B	42	C
5	B	43	C
5	B	54	A
5	B	56	C
5	B	57	U
5	B	58	A
5	B	66	C
5	B	67	A
5	B	74	A
5	B	87	U
5	B	88	C
5	B	90	G
5	B	107	A
5	B	115	A
5	B	116	C
9	A	7	U
9	A	12	G
9	A	20	G
9	A	31	U
9	A	32	G
9	A	36	C
9	A	55	G
9	A	59	G

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Mol	Chain	Res	Type
9	A	61	G
9	A	68	A
9	A	71	A
9	A	72	G
9	A	82	G
9	A	89	A
9	A	94	G
9	A	99	G
9	A	107	G
9	A	115	A
9	A	116	A
9	A	117	U
9	A	125	C
9	A	128	G
9	A	136	U
9	A	145	G
9	A	153	G
9	A	164	A
9	A	174	G
9	A	175	G
9	A	180	A
9	A	186	G
9	A	195	A
9	A	198	A
9	A	212	A
9	A	214	G
9	A	215	A
9	A	220	A
9	A	221	A
9	A	224	C
9	A	227	A
9	A	229	U
9	A	230	G
9	A	233	A
9	A	248	G
9	A	268	G
9	A	275	C
9	A	285	U
9	A	286	G
9	A	287	A
9	A	288	U
9	A	291	C

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Mol	Chain	Res	Type
9	A	292	G
9	A	297	G
9	A	298	G
9	A	299	G
9	A	300	G
9	A	301	U
9	A	302	U
9	A	303	G
9	A	304	U
9	A	305	G
9	A	313	G
9	A	314	G
9	A	315	U
9	A	317	G
9	A	318	U
9	A	319	G
9	A	324	C
9	A	329	U
9	A	330	U
9	A	331	U
9	A	336	C
9	A	337	U
9	A	338	C
9	A	340	A
9	A	342	C
9	A	344	G
9	A	345	G
9	A	353	G
9	A	354	C
9	A	357	U
9	A	361	A
9	A	363	A
9	A	366	G
9	A	370	U
9	A	376	G
9	A	384	G
9	A	393	U
9	A	399	G
9	A	412	A
9	A	413	G
9	A	414	A
9	A	428	A

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Mol	Chain	Res	Type
9	A	434	G
9	A	437	G
9	A	438	U
9	A	444	U
9	A	445	U
9	A	446	G
9	A	447	A
9	A	452	G
9	A	454	U
9	A	460	G
9	A	474	G
9	A	489	A
9	A	490	A
9	A	493	U
9	A	494	G
9	A	498	G
9	A	512	G
9	A	523	U
9	A	536	U
9	A	539	C
9	A	543	U
9	A	544	U
9	A	566	A
9	A	567	A
9	A	568	A
9	A	569	G
9	A	581	G
9	A	583	G
9	A	585	G
9	A	588	A
9	A	589	A
9	A	591	G
9	A	592	A
9	A	594	U
9	A	595	A
9	A	596	C
9	A	605	G
9	A	614	C
9	A	617	U
9	A	618	C
9	A	619	C
9	A	620	G

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Mol	Chain	Res	Type
9	A	635	G
9	A	636	U
9	A	637	G
9	A	639	C
9	A	640	G
9	A	642	G
9	A	644	G
9	A	647	G
9	A	655	G
9	A	665	G
9	A	667	A
9	A	675	G
9	A	679	G
9	A	684	G
9	A	685	G
9	A	696	A
9	A	706	G
9	A	707	G
9	A	708	G
9	A	709	U
9	A	714	U
9	A	721	A
9	A	725	A
9	A	728	G
9	A	731	A
9	A	738	A
9	A	739	U
9	A	740	A
9	A	741	G
9	A	742	G
9	A	747	A
9	A	749	C
9	A	756	A
9	A	757	G
9	A	758	A
9	A	759	G
9	A	760	U
9	A	764	U
9	A	765	G
9	A	766	G
9	A	801	U
9	A	817	G

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Mol	Chain	Res	Type
9	A	830	A
9	A	832	G
9	A	838	G
9	A	839	U
9	A	845	C
9	A	862	U
9	A	868	C
9	A	872	G
9	A	879	A
9	A	880	G
9	A	890	G
9	A	891	G
9	A	897	A
9	A	899	G
9	A	900	G
9	A	915	U
9	A	920	G
9	A	927	C
9	A	942	U
9	A	971	G
9	A	974	G
9	A	981	U
9	A	982	A
9	A	985	G
9	A	990	G
9	A	994	A
9	A	996	G
9	A	997	G
9	A	1001	C
9	A	1002	C
9	A	1003	A
9	A	1004	C
9	A	1007	G
9	A	1008	G
9	A	1011	A
9	A	1014	G
9	A	1022	C
9	A	1025	A
9	A	1030	C
9	A	1047	A
9	A	1049	G
9	A	1058	A

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Mol	Chain	Res	Type
9	A	1063	G
9	A	1076	A
9	A	1078	G
9	A	1085	G
9	A	1092	G
9	A	1101	A
9	A	1103	C
9	A	1107	G
9	A	1108	A
9	A	1114	G
9	A	1131	G
9	A	1135	G
9	A	1140	G
9	A	1141	U
9	A	1143	G
9	A	1144	A
9	A	1151	U
9	A	1157	G
9	A	1163	A
9	A	1164	A
9	A	1175	A
9	A	1178	U
9	A	1180	G
9	A	1181	G
9	A	1184	U
9	A	1185	A
9	A	1186	G
9	A	1187	A
9	A	1188	A
9	A	1189	G
9	A	1190	C
9	A	1191	A
9	A	1193	C
9	A	1194	C
9	A	1197	C
9	A	1201	G
9	A	1202	A
9	A	1203	A
9	A	1205	G
9	A	1206	A
9	A	1207	G
9	A	1208	U

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Mol	Chain	Res	Type
9	A	1209	G
9	A	1212	U
9	A	1213	A
9	A	1214	A
9	A	1215	U
9	A	1217	G
9	A	1219	U
9	A	1220	C
9	A	1226	U
9	A	1230	G
9	A	1238	G
9	A	1240	G
9	A	1246	A
9	A	1250	U
9	A	1251	A
9	A	1253	C
9	A	1254	G
9	A	1260	C
9	A	1261	A
9	A	1267	A
9	A	1270	G
9	A	1292	U
9	A	1293	G
9	A	1332	G
9	A	1335	G
9	A	1344	A
9	A	1347	G
9	A	1353	G
9	A	1359	G
9	A	1368	A
9	A	1371	G
9	A	1380	A
9	A	1386	G
9	A	1387	A
9	A	1389	U
9	A	1409	C
9	A	1415	A
9	A	1416	A
9	A	1421	C
9	A	1428	U
9	A	1456	G
9	A	1465	C

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Mol	Chain	Res	Type
9	A	1467	U
9	A	1480	A
9	A	1485	C
9	A	1493	A
9	A	1494	U
9	A	1501	C
9	A	1507	G
9	A	1510	A
9	A	1518	A
9	A	1521	C
9	A	1522	G
9	A	1529	U
9	A	1531	C
9	A	1533	U
9	A	1534	C
9	A	1538	G
9	A	1540	U
9	A	1542	A
9	A	1543	A
9	A	1549	G
9	A	1550	G
9	A	1551	U
9	A	1552	A
9	A	1553	C
9	A	1554	U
9	A	1556	A
9	A	1557	C
9	A	1563	A
9	A	1564	A
9	A	1565	A
9	A	1566	A
9	A	1567	C
9	A	1571	C
9	A	1574	G
9	A	1587	G
9	A	1588	G
9	A	1589	G
9	A	1597	G
9	A	1598	U
9	A	1599	U
9	A	1600	G
9	A	1617	C

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Mol	Chain	Res	Type
9	A	1623	U
9	A	1625	G
9	A	1629	G
9	A	1630	U
9	A	1632	G
9	A	1636	A
9	A	1639	G
9	A	1640	A
9	A	1641	U
9	A	1648	A
9	A	1649	C
9	A	1658	G
9	A	1676	G
9	A	1679	A
9	A	1681	U
9	A	1688	G
9	A	1694	C
9	A	1703	G
9	A	1710	A
9	A	1711	G
9	A	1713	U
9	A	1714	A
9	A	1716	A
9	A	1717	U
9	A	1720	G
9	A	1724	G
9	A	1728	U
9	A	1731	A
9	A	1737	A
9	A	1754	G
9	A	1755	A
9	A	1756	G
9	A	1757	U
9	A	1758	G
9	A	1769	G
9	A	1786	G
9	A	1789	A
9	A	1798	U
9	A	1804	G
9	A	1813	C
9	A	1826	A
9	A	1828	A

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Mol	Chain	Res	Type
9	A	1834	A
9	A	1843	C
9	A	1845	G
9	A	1848	A
9	A	1864	U
9	A	1866	C
9	A	1871	G
9	A	1872	A
9	A	1878	G
9	A	1892	G
9	A	1893	C
9	A	1895	A
9	A	1916	A
9	A	1946	U
9	A	1947	U
9	A	1950	G
9	A	1955	A
9	A	1981	U
9	A	1990	A
9	A	2008	A
9	A	2017	C
9	A	2018	G
9	A	2024	G
9	A	2033	U
9	A	2046	A
9	A	2050	C
9	A	2065	A
9	A	2066	G
9	A	2075	G
9	A	2076	A
9	A	2086	U
9	A	2087	C
9	A	2088	C
9	A	2089	C
9	A	2090	U
9	A	2092	U
9	A	2093	G
9	A	2094	G
9	A	2095	G
9	A	2096	G
9	A	2104	G
9	A	2106	A

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Mol	Chain	Res	Type
9	A	2107	G
9	A	2129	C
9	A	2130	G
9	A	2137	A
9	A	2138	C
9	A	2140	A
9	A	2141	U
9	A	2151	A
9	A	2153	G
9	A	2154	G
9	A	2160	A
9	A	2163	U
9	A	2179	U
9	A	2187	U
9	A	2189	C
9	A	2191	C
9	A	2194	A
9	A	2195	U
9	A	2196	G
9	A	2215	U
9	A	2217	U
9	A	2221	A
9	A	2255	A
9	A	2256	G
9	A	2263	G
9	A	2267	C
9	A	2273	G
9	A	2278	A
9	A	2279	C
9	A	2280	G
9	A	2284	A
9	A	2285	G
9	A	2286	A
9	A	2303	A
9	A	2316	G
9	A	2317	G
9	A	2320	C
9	A	2323	G
9	A	2324	A
9	A	2328	G
9	A	2329	G
9	A	2331	U

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Mol	Chain	Res	Type
9	A	2334	U
9	A	2335	G
9	A	2336	U
9	A	2337	A
9	A	2338	G
9	A	2339	G
9	A	2340	A
9	A	2341	U
9	A	2342	A
9	A	2343	G
9	A	2344	G
9	A	2346	G
9	A	2351	A
9	A	2353	U
9	A	2354	G
9	A	2355	U
9	A	2357	A
9	A	2358	A
9	A	2360	C
9	A	2362	C
9	A	2365	A
9	A	2367	G
9	A	2368	C
9	A	2370	A
9	A	2371	G
9	A	2377	G
9	A	2379	G
9	A	2380	G
9	A	2381	A
9	A	2382	G
9	A	2383	U
9	A	2384	C
9	A	2385	G
9	A	2386	U
9	A	2387	U
9	A	2388	G
9	A	2392	A
9	A	2393	A
9	A	2394	A
9	A	2395	U
9	A	2396	A
9	A	2399	A

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Mol	Chain	Res	Type
9	A	2402	C
9	A	2404	G
9	A	2407	C
9	A	2408	G
9	A	2418	U
9	A	2421	A
9	A	2427	G
9	A	2434	A
9	A	2436	A
9	A	2446	G
9	A	2447	G
9	A	2449	A
9	A	2462	G
9	A	2463	G
9	A	2503	G
9	A	2507	C
9	A	2511	A
9	A	2512	A
9	A	2528	G
9	A	2529	A
9	A	2532	G
9	A	2544	U
9	A	2545	G
9	A	2549	G
9	A	2558	C
9	A	2559	A
9	A	2567	U
9	A	2569	G
9	A	2571	C
9	A	2574	C
9	A	2578	A
9	A	2596	G
9	A	2607	G
9	A	2609	A
9	A	2612	A
9	A	2647	U
9	A	2649	A
9	A	2653	G
9	A	2654	A
9	A	2655	U
9	A	2659	A
9	A	2665	C

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Mol	Chain	Res	Type
9	A	2669	G
9	A	2672	A
9	A	2676	C
9	A	2693	A
9	A	2694	G
9	A	2699	C
9	A	2708	G
9	A	2715	U
9	A	2726	G
9	A	2729	G
9	A	2737	G
9	A	2742	A
9	A	2744	C
9	A	2749	G
9	A	2753	G
9	A	2754	G
9	A	2759	G
9	A	2778	U
9	A	2785	A
9	A	2786	U
9	A	2788	A
9	A	2790	A
9	A	2791	G
9	A	2796	A
9	A	2797	C
9	A	2802	G
9	A	2806	G
9	A	2826	A
9	A	2827	G
9	A	2833	U
9	A	2837	U
9	A	2839	U
9	A	2845	G
9	A	2853	C
9	A	2854	A
9	A	2856	A
9	A	2862	G
9	A	2913	U
9	A	2926	A
9	A	2936	C
9	A	2938	G
9	A	2940	U

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Mol	Chain	Res	Type
9	A	2942	G
9	A	2950	C
9	A	2957	A
9	A	2968	G
9	A	2972	A
9	A	2981	A
9	A	2982	A
9	A	2985	G
9	A	2989	A
9	A	2993	U
9	A	3002	A
9	A	3009	U
9	A	3014	A
9	A	3015	C
9	A	3016	C
9	A	3021	A
9	A	3022	G
9	A	3023	G
9	A	3024	A
9	A	3029	U
9	A	3039	C
9	A	3042	A
9	A	3057	U
9	A	3082	U
9	A	3088	C
9	A	3093	A
9	A	3095	C
9	A	3098	G
9	A	3101	C
9	A	3104	A
9	A	3105	C
9	A	3106	C
9	A	3107	G
9	A	3112	A
9	A	3114	A
9	A	3115	A
37	a	10	G
37	a	11	G
37	a	12	A
37	a	13	G
37	a	36	A
37	a	43	G

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Mol	Chain	Res	Type
37	a	45	G
37	a	48	G
37	a	52	U
37	a	55	A
37	a	75	A
37	a	82	U
37	a	87	G
37	a	92	A
37	a	93	C
37	a	115	A
37	a	117	C
37	a	118	A
37	a	123	G
37	a	126	G
37	a	128	U
37	a	136	G
37	a	141	U
37	a	153	U
37	a	160	C
37	a	174	G
37	a	192	G
37	a	193	C
37	a	194	A
37	a	196	G
37	a	200	U
37	a	201	G
37	a	211	A
37	a	216	U
37	a	217	U
37	a	218	G
37	a	220	G
37	a	231	G
37	a	245	C
37	a	246	A
37	a	247	G
37	a	251	G
37	a	252	U
37	a	262	G
37	a	266	G
37	a	267	C
37	a	280	C
37	a	289	G

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Mol	Chain	Res	Type
37	a	301	G
37	a	306	A
37	a	321	A
37	a	328	U
37	a	329	A
37	a	330	C
37	a	332	G
37	a	344	A
37	a	347	G
37	a	348	G
37	a	351	G
37	a	352	C
37	a	353	A
37	a	354	G
37	a	367	U
37	a	372	C
37	a	373	A
37	a	389	A
37	a	392	C
37	a	396	G
37	a	397	A
37	a	398	C
37	a	406	G
37	a	411	A
37	a	412	U
37	a	413	G
37	a	414	A
37	a	421	U
37	a	422	C
37	a	423	G
37	a	426	U
37	a	427	U
37	a	428	G
37	a	429	U
37	a	430	A
37	a	433	C
37	a	438	U
37	a	439	U
37	a	452	A
37	a	453	G
37	a	456	C
37	a	457	A

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Mol	Chain	Res	Type
37	a	458	A
37	a	459	G
37	a	465	G
37	a	466	U
37	a	469	G
37	a	470	U
37	a	471	G
37	a	472	C
37	a	475	A
37	a	477	G
37	a	480	G
37	a	488	C
37	a	489	A
37	a	490	A
37	a	491	C
37	a	492	U
37	a	496	U
37	a	497	G
37	a	498	C
37	a	499	C
37	a	501	G
37	a	507	G
37	a	509	G
37	a	511	U
37	a	512	A
37	a	513	A
37	a	520	G
37	a	522	G
37	a	527	A
37	a	539	A
37	a	542	U
37	a	544	C
37	a	548	G
37	a	552	A
37	a	553	A
37	a	556	A
37	a	557	G
37	a	612	U
37	a	613	G
37	a	616	G
37	a	633	A
37	a	641	G

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Mol	Chain	Res	Type
37	a	645	G
37	a	663	G
37	a	666	U
37	a	667	A
37	a	668	G
37	a	680	G
37	a	702	G
37	a	703	U
37	a	704	G
37	a	711	G
37	a	714	G
37	a	728	A
37	a	729	A
37	a	733	A
37	a	735	G
37	a	739	A
37	a	761	A
37	a	765	G
37	a	772	A
37	a	773	U
37	a	774	A
37	a	779	G
37	a	789	G
37	a	793	U
37	a	794	A
37	a	795	A
37	a	796	A
37	a	797	C
37	a	808	A
37	a	812	G
37	a	818	U
37	a	822	U
37	a	823	U
37	a	824	C
37	a	825	C
37	a	826	U
37	a	827	U
37	a	828	G
37	a	835	G
37	a	840	G
37	a	841	U
37	a	854	A

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Mol	Chain	Res	Type
37	a	858	A
37	a	869	G
37	a	871	A
37	a	884	G
37	a	896	A
37	a	898	G
37	a	908	G
37	a	909	G
37	a	914	C
37	a	916	C
37	a	917	A
37	a	924	G
37	a	940	A
37	a	942	U
37	a	943	U
37	a	947	U
37	a	948	G
37	a	950	A
37	a	951	A
37	a	953	G
37	a	957	A
37	a	959	A
37	a	964	U
37	a	973	U
37	a	974	U
37	a	975	G
37	a	978	A
37	a	982	A
37	a	983	C
37	a	984	A
37	a	986	G
37	a	990	C
37	a	992	G
37	a	1000	U
37	a	1007	U
37	a	1008	C
37	a	1010	C
37	a	1012	U
37	a	1013	G
37	a	1014	U
37	a	1018	C
37	a	1020	G

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Mol	Chain	Res	Type
37	a	1021	U
37	a	1022	G
37	a	1024	G
37	a	1025	C
37	a	1028	G
37	a	1030	G
37	a	1033	G
37	a	1034	C
37	a	1035	A
37	a	1036	U
37	a	1045	U
37	a	1046	C
37	a	1048	G
37	a	1050	U
37	a	1065	U
37	a	1068	G
37	a	1074	G
37	a	1075	U
37	a	1081	A
37	a	1088	G
37	a	1100	U
37	a	1104	G
37	a	1105	U
37	a	1107	G
37	a	1110	A
37	a	1111	G
37	a	1113	A
37	a	1115	G
37	a	1116	U
37	a	1117	U
37	a	1118	A
37	a	1120	G
37	a	1138	A
37	a	1140	U
37	a	1149	C
37	a	1150	A
37	a	1151	A
37	a	1165	G
37	a	1177	A
37	a	1178	A
37	a	1193	U
37	a	1208	A

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Mol	Chain	Res	Type
37	a	1217	A
37	a	1219	A
37	a	1229	A
37	a	1231	A
37	a	1238	U
37	a	1239	G
37	a	1241	G
37	a	1248	U
37	a	1249	G
37	a	1250	A
37	a	1251	G
37	a	1256	A
37	a	1261	A
37	a	1266	U
37	a	1267	U
37	a	1269	A
37	a	1284	U
37	a	1287	G
37	a	1294	G
37	a	1299	C
37	a	1302	C
37	a	1320	G
37	a	1322	G
37	a	1328	A
37	a	1329	G
37	a	1335	G
37	a	1344	C
37	a	1345	A
37	a	1346	A
37	a	1351	G
37	a	1353	G
37	a	1357	A
37	a	1362	G
37	a	1364	U
37	a	1378	C
37	a	1380	C
37	a	1381	A
37	a	1405	G
37	a	1409	A
37	a	1423	U
37	a	1424	G
37	a	1425	G

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Mol	Chain	Res	Type
37	a	1426	C
37	a	1429	A
37	a	1430	A
37	a	1434	U
37	a	1435	U
37	a	1436	G
37	a	1459	G
37	a	1478	G
37	a	1481	G
37	a	1483	A
37	a	1487	A
37	a	1488	G
37	a	1490	U
37	a	1501	G
37	a	1503	A
37	a	1504	G
37	a	1513	G
37	a	1514	G
54	v	6	G
54	v	7	G
54	v	8	A
54	v	9	G
54	v	10	G
54	v	11	U
54	v	13	A
54	v	19	U
54	v	21	C
54	v	22	A

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	E	534	C
3	E	546	U
3	E	565	U
3	E	572	U
5	B	2	U
5	B	53	A
9	A	316	U
9	A	438	U
9	A	919	A
9	A	980	C

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Mol	Chain	Res	Type
9	A	981	U
9	A	1102	G
9	A	1255	G
9	A	1291	G
9	A	1616	A
9	A	1730	U
9	A	2075	G
9	A	2094	G
9	A	2350	G
9	A	2356	G
9	A	2381	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

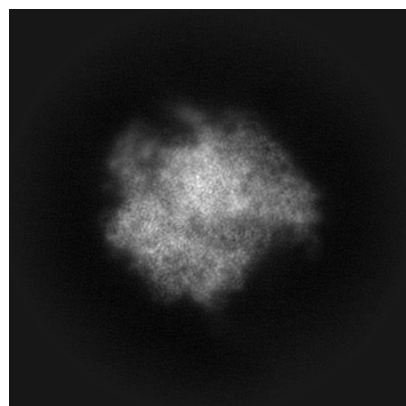
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29397. These allow visual inspection of the internal detail of the map and identification of artifacts.

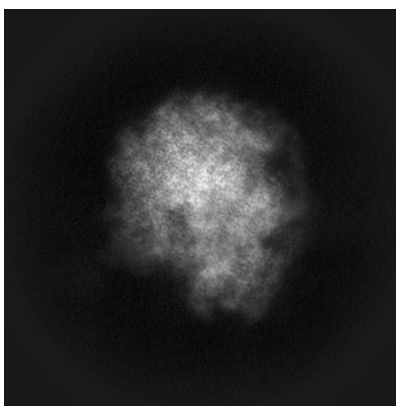
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

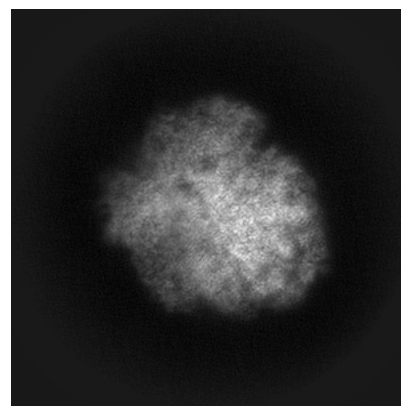
#### 6.1.1 Primary map



X

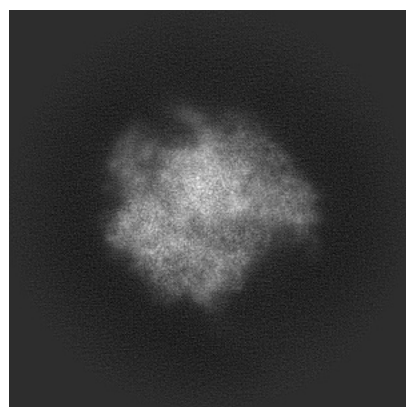


Y

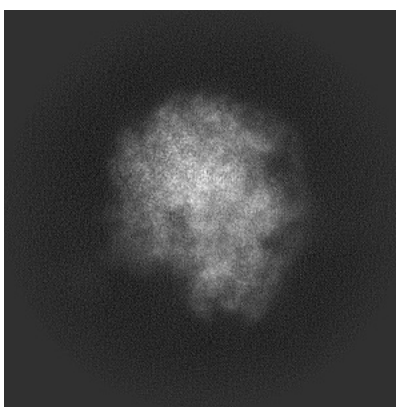


Z

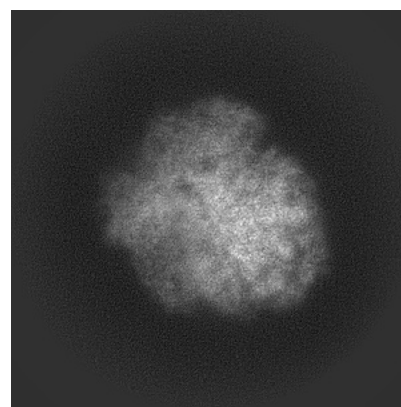
#### 6.1.2 Raw map



X



Y

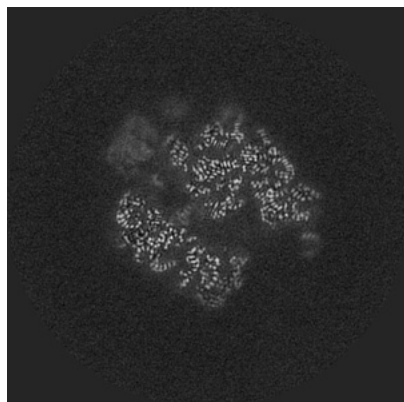


Z

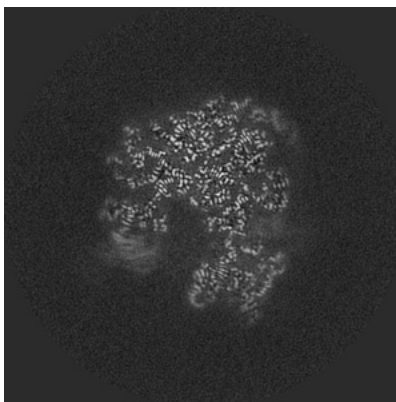
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

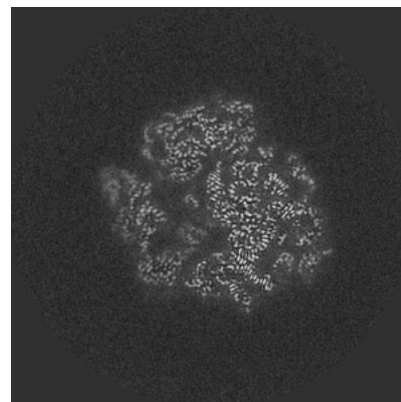
### 6.2.1 Primary map



X Index: 250

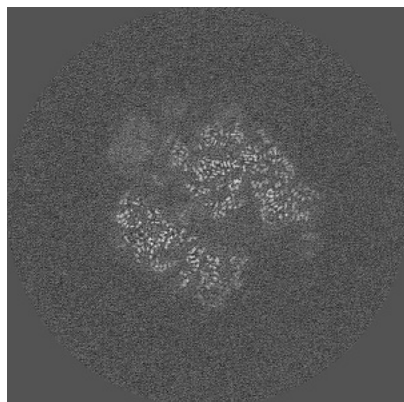


Y Index: 250

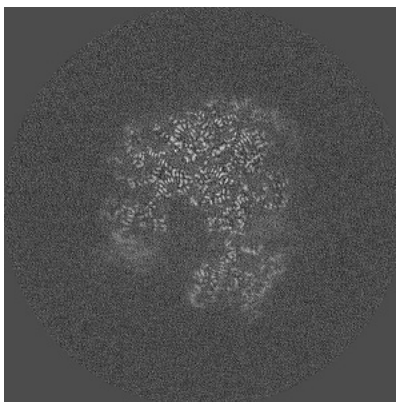


Z Index: 250

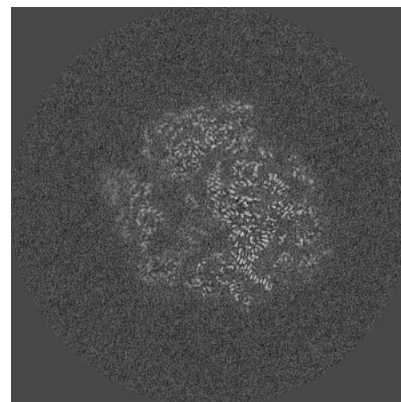
### 6.2.2 Raw map



X Index: 250



Y Index: 250

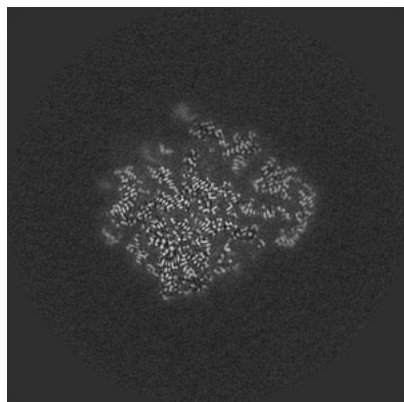


Z Index: 250

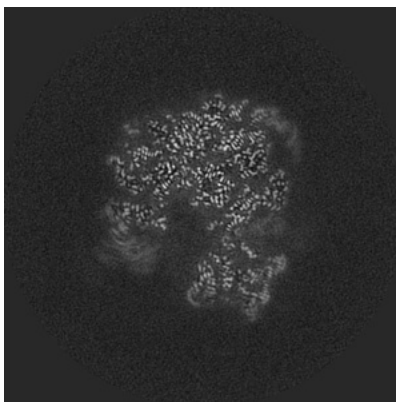
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

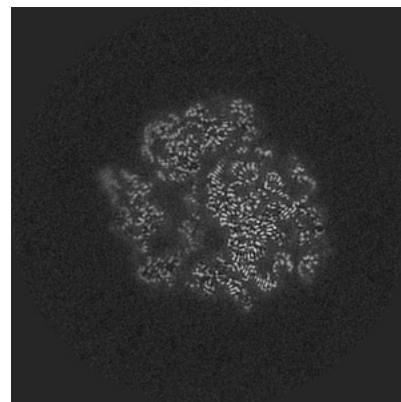
### 6.3.1 Primary map



X Index: 281

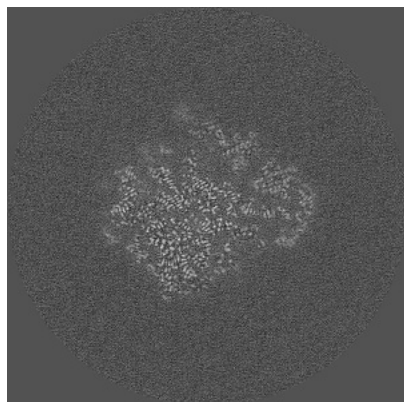


Y Index: 246

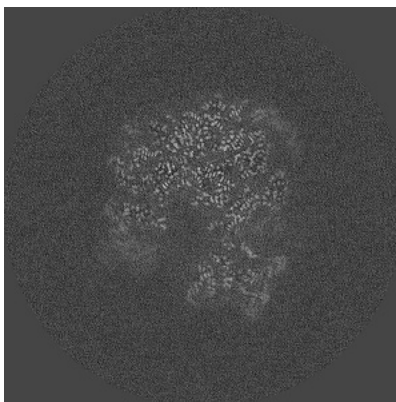


Z Index: 252

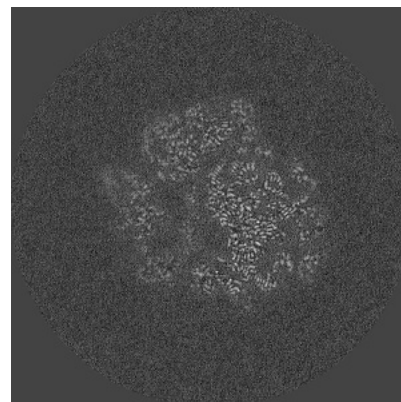
### 6.3.2 Raw map



X Index: 281



Y Index: 246



Z Index: 252

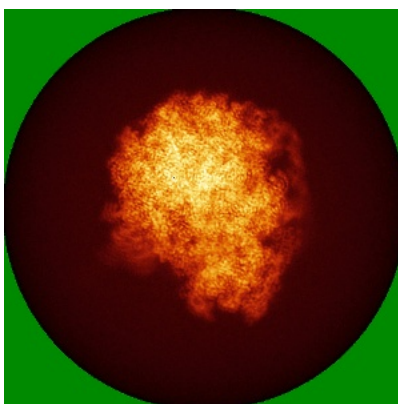
The images above show the largest variance slices of the map in three orthogonal directions.

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

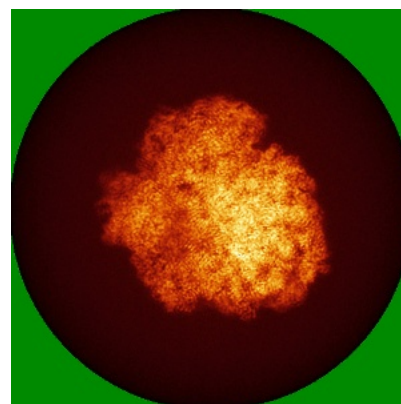
### 6.4.1 Primary map



X

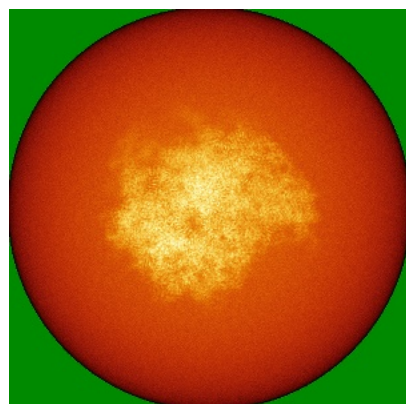


Y

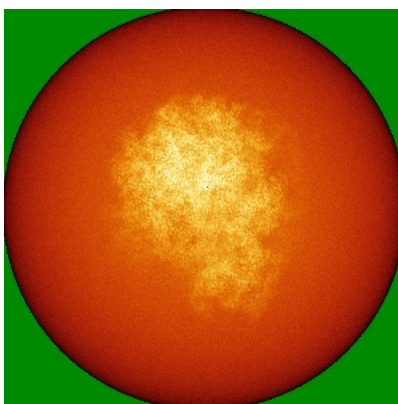


Z

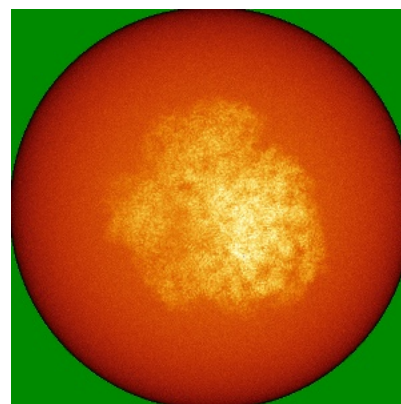
### 6.4.2 Raw map



X



Y

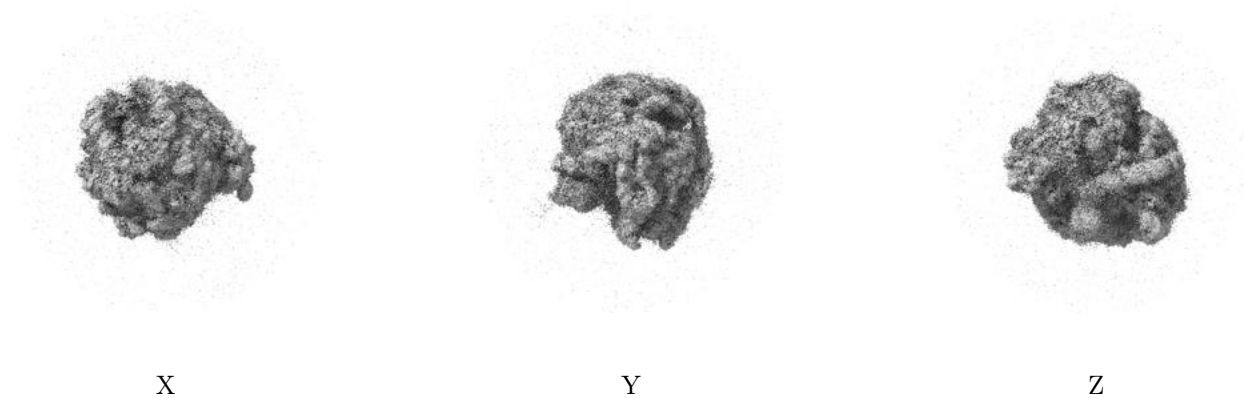


Z

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

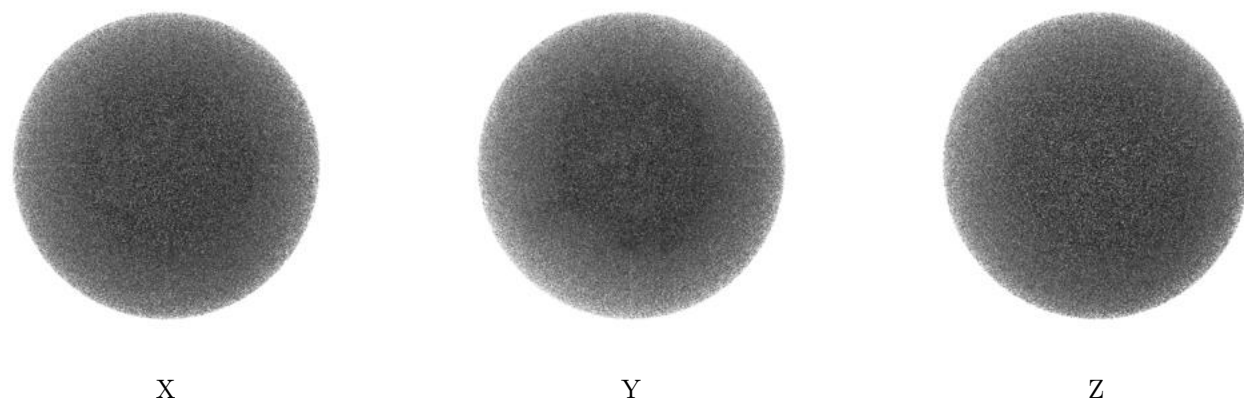
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

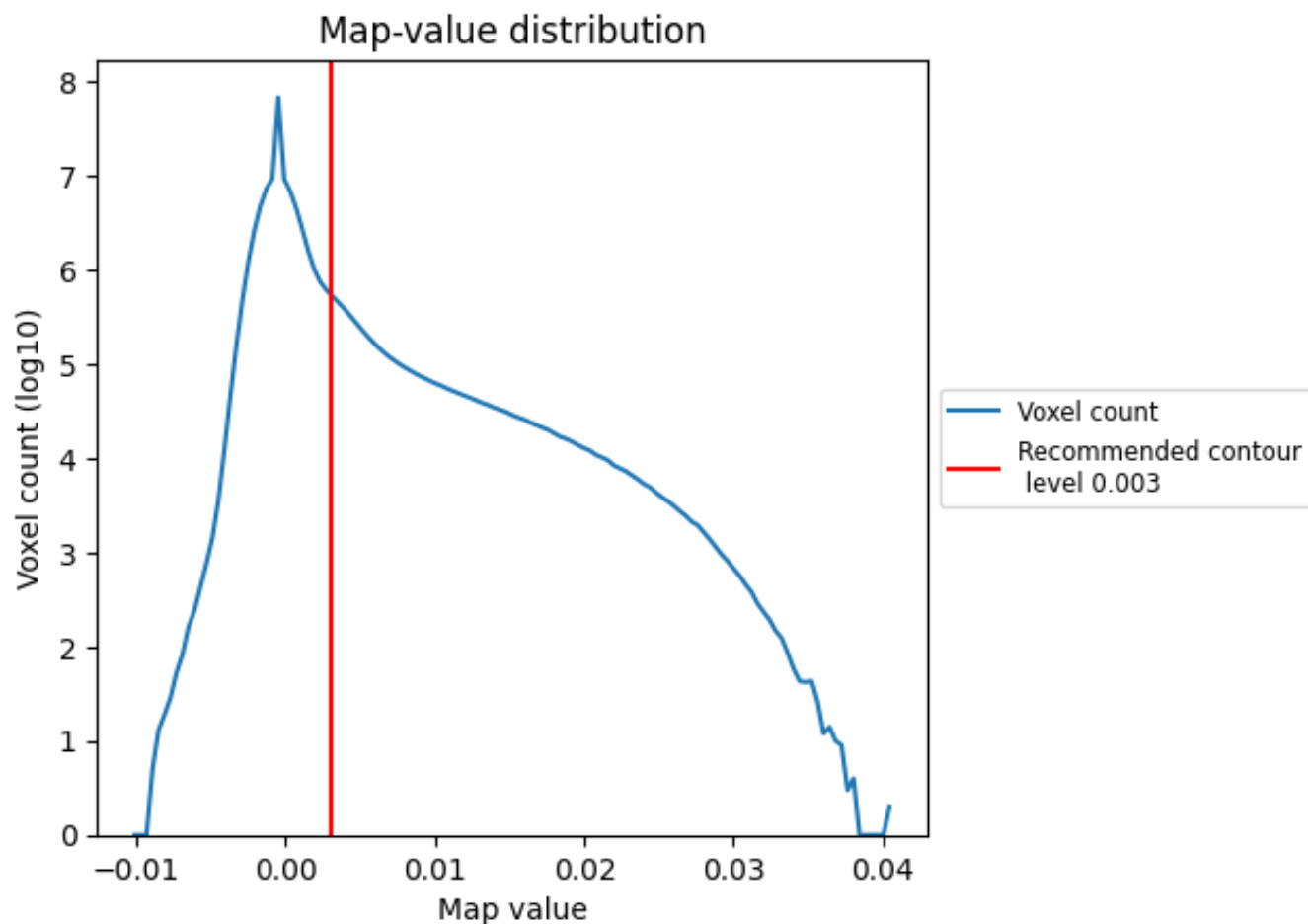
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

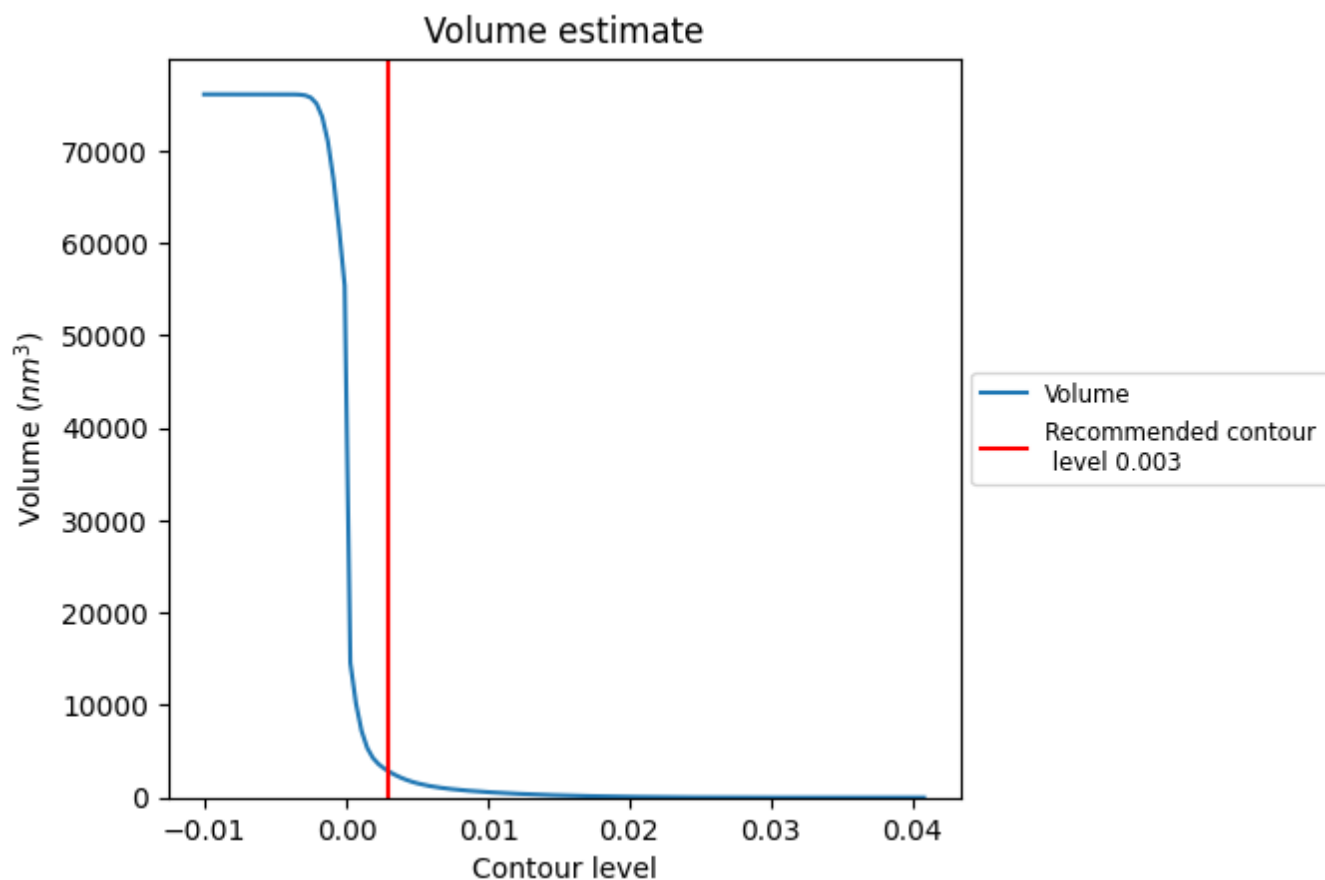
This section contains the results of statistical analysis of the map.

### 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.

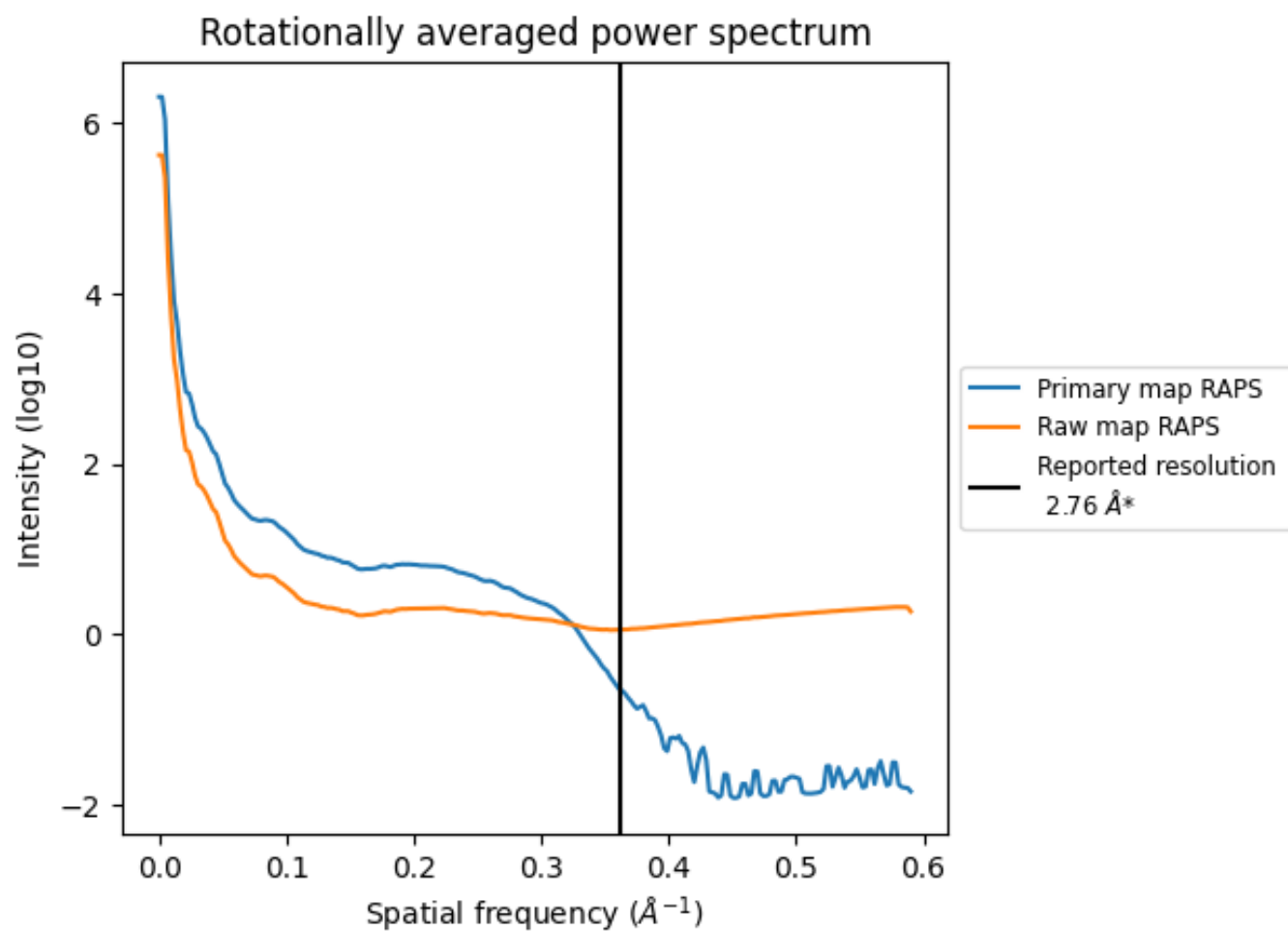
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2823 nm<sup>3</sup>; this corresponds to an approximate mass of 2550 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

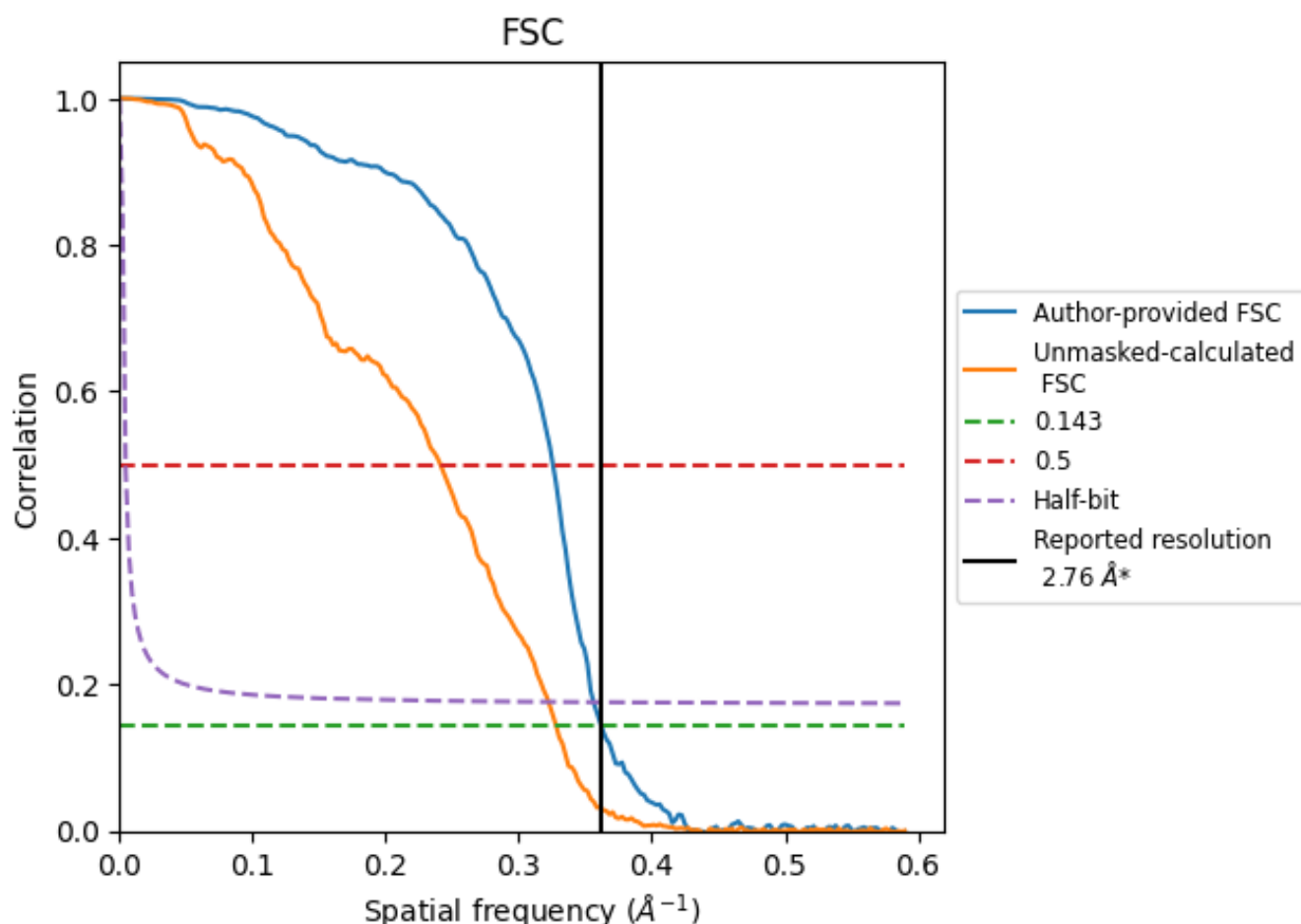


\*Reported resolution corresponds to spatial frequency of 0.362 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.362  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

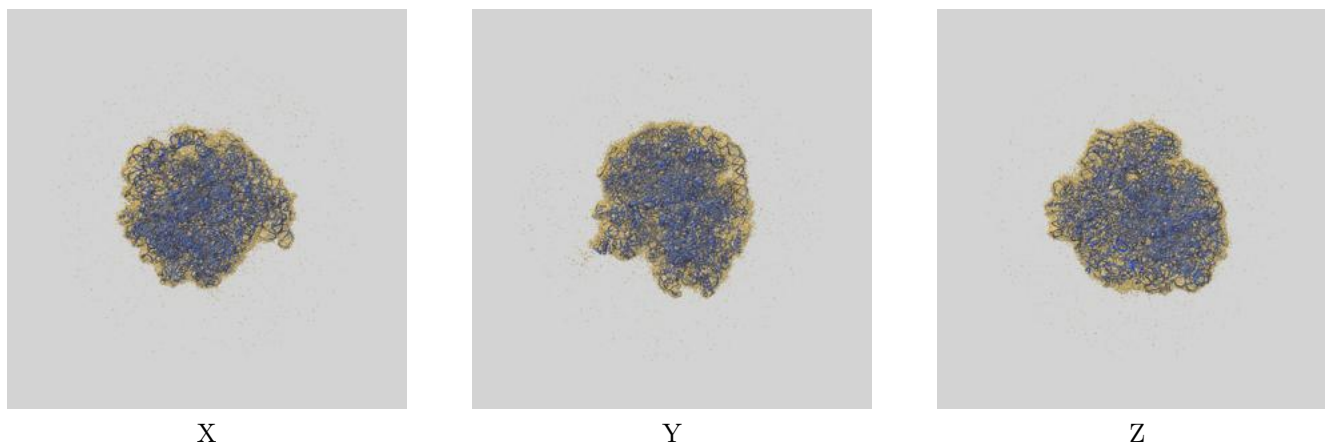
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.76	3.07	2.81
Unmasked-calculated*	3.05	4.15	3.10

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.05 differs from the reported value 2.76 by more than 10 %

## 9 Map-model fit [i](#)

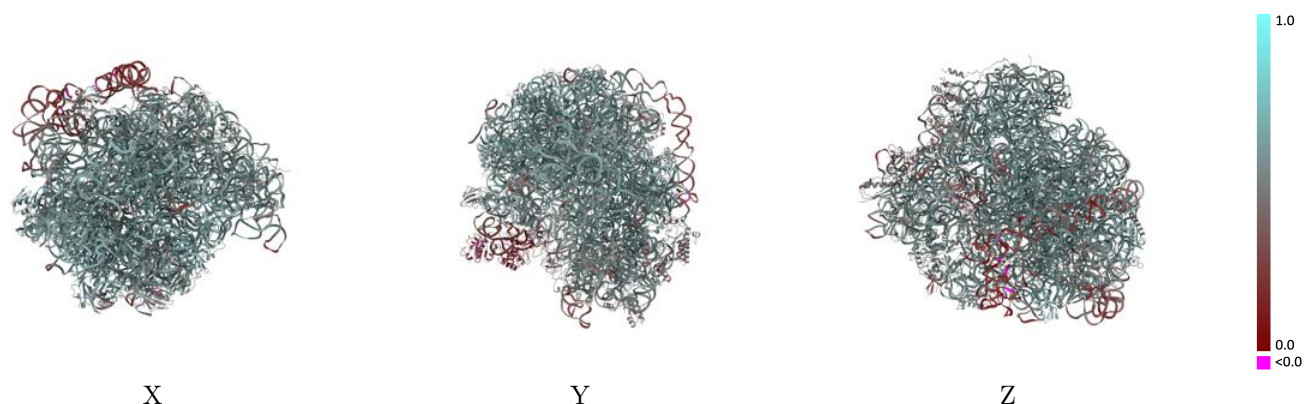
This section contains information regarding the fit between EMDB map EMD-29397 and PDB model 8FR8. Per-residue inclusion information can be found in section [3](#) on page [14](#).

### 9.1 Map-model overlay [i](#)



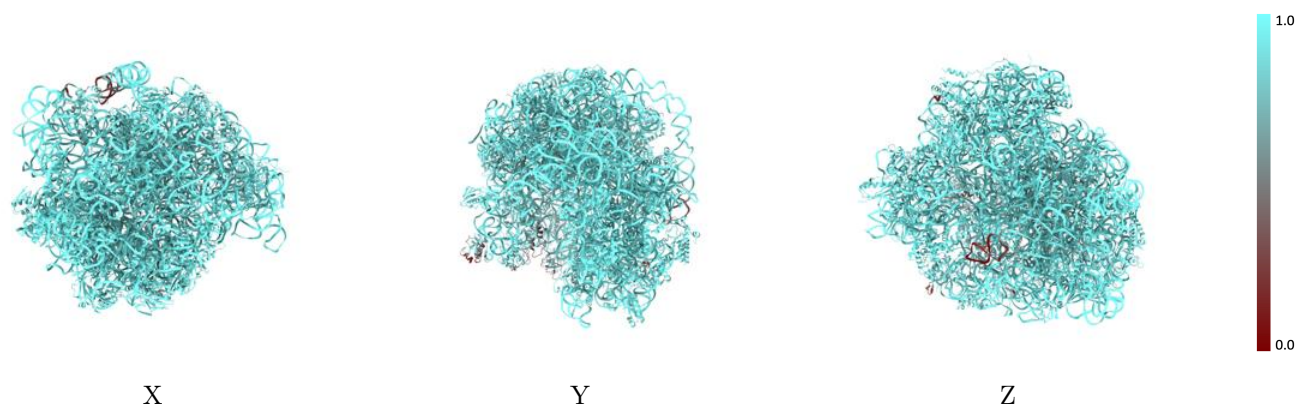
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



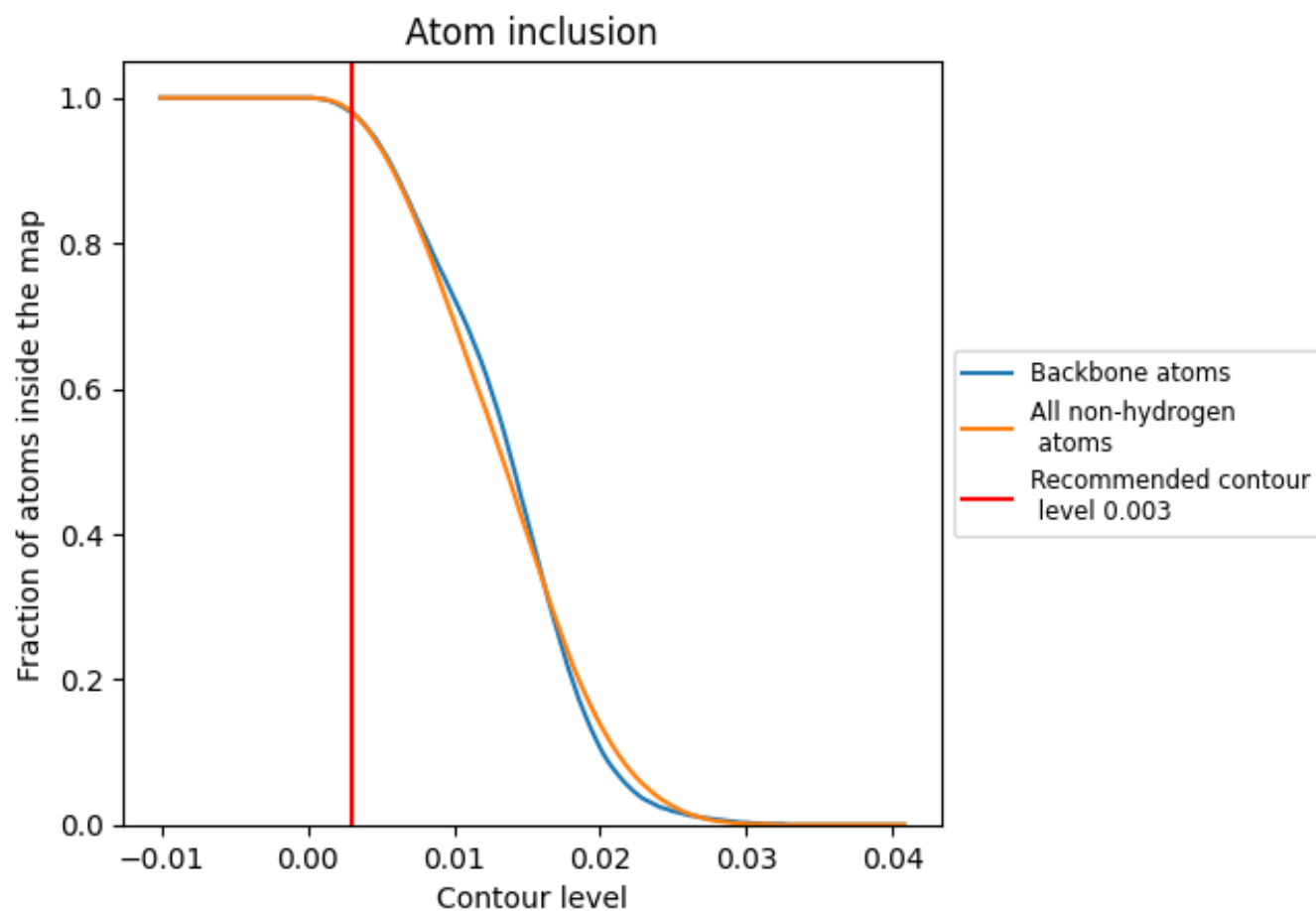
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9810	 0.5490
0	 1.0000	 0.6150
1	 0.9900	 0.5600
2	 0.9720	 0.5300
3	 0.9940	 0.6180
4	 1.0000	 0.6180
6	 0.9800	 0.5630
7	 0.9850	 0.5920
8	 0.9980	 0.5770
9	 0.9480	 0.4960
A	 0.9880	 0.5560
B	 0.9960	 0.5520
C	 0.9980	 0.5970
D	 0.9940	 0.5670
E	 0.9810	 0.4200
F	 1.0000	 0.6080
G	 0.9820	 0.5030
H	 0.8040	 0.4030
I	 0.4750	 0.2710
J	 0.9980	 0.6020
K	 0.9980	 0.6150
L	 0.9940	 0.5970
M	 0.9910	 0.5820
N	 0.9940	 0.5810
O	 0.9820	 0.5430
P	 0.9830	 0.5140
Q	 0.8880	 0.4680
R	 0.6230	 0.2390
S	 0.7840	 0.1930
T	 0.9950	 0.5960
U	 0.9980	 0.6000
V	 0.9970	 0.6010
W	 0.9910	 0.5960
X	 0.9880	 0.6000
Y	 0.9960	 0.5950



*Continued on next page...*

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Chain	Atom inclusion	Q-score
Z	 0.9910	 0.5620
a	 0.9980	 0.5680
b	 1.0000	 0.5870
c	 0.9700	 0.4690
d	 0.9800	 0.4800
e	 0.9830	 0.5000
f	 0.9760	 0.5450
g	 0.9800	 0.5400
h	 0.9950	 0.5260
i	 0.9960	 0.5800
j	 0.9800	 0.4960
k	 0.9910	 0.5440
l	 0.9640	 0.5090
m	 0.9950	 0.5600
n	 0.9940	 0.5660
o	 0.9940	 0.5030
p	 0.9910	 0.5700
q	 0.9790	 0.5400
r	 0.9930	 0.5620
t	 0.9890	 0.5430
u	 0.9440	 0.4680
v	 0.9850	 0.3500
x	 1.0000	 0.6210
y	 0.9220	 0.4750