



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:51 PM UTC

PDB ID : 8WHY / pdb_00008why
EMDB ID : EMD-37552
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-23
Resolution : 2.70 Å(reported)
Based on initial model : 8WHX

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

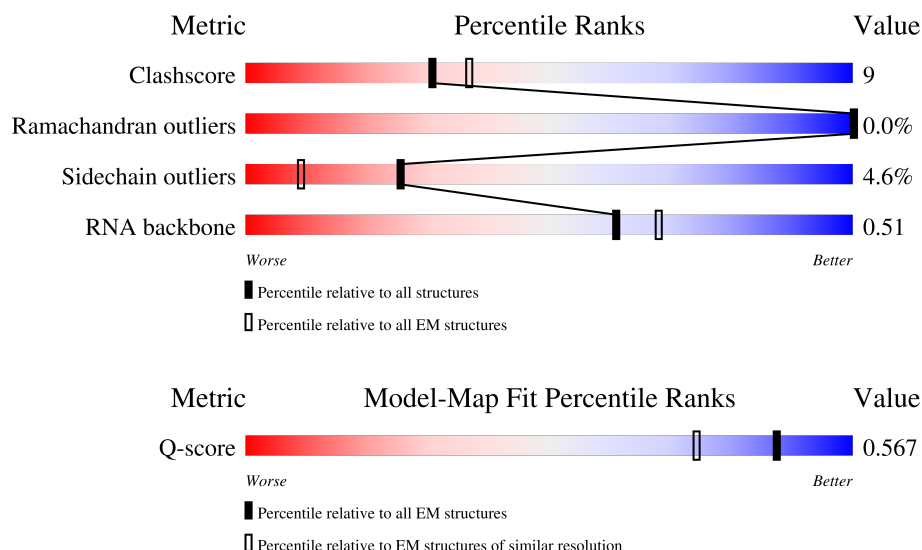
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	E	278	 85% 13% ..
2	F	217	 80% 19% .
3	G	215	 76% 20% ..

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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 89672 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 L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	181	Total	C	N	O	S	0	0
			1436	901	269	260	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L14.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

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

- Molecule 10 is a protein called 50S ribosomal protein L17.

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

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	124	Total	C	N	O	0	0
			941	577	195	169		

- Molecule 12 is a protein called 50S ribosomal protein L19.

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

- Molecule 13 is a protein called 50S ribosomal protein L20.

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

- Molecule 14 is a protein called 50S ribosomal protein L21.

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

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	113	Total	C	N	O	0	0
			864	538	170	156		

- Molecule 16 is a protein called 50S ribosomal protein L23.

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

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	93	Total	C	N	O	S	0	0
			710	443	133	132	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	77	Total	C	N	O	0	0
			574	355	121	98		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	58	Total	C	N	O	0	0
			470	290	94	86		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3017	Total	C	N	O	P	0	0
			64799	28881	11918	20983	3017		

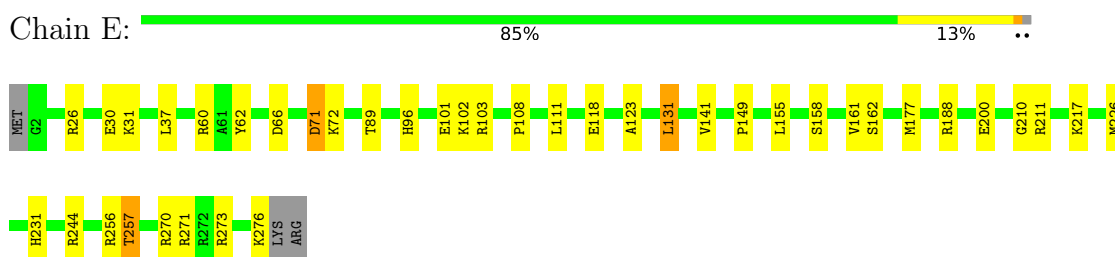
- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	B	117	2502	1117	465	803	117	0	0

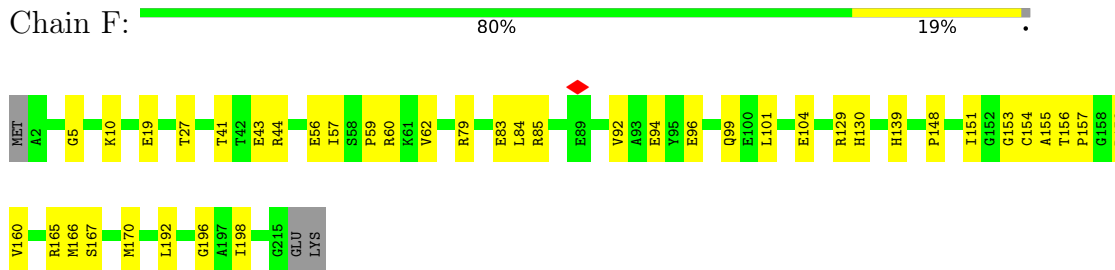
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

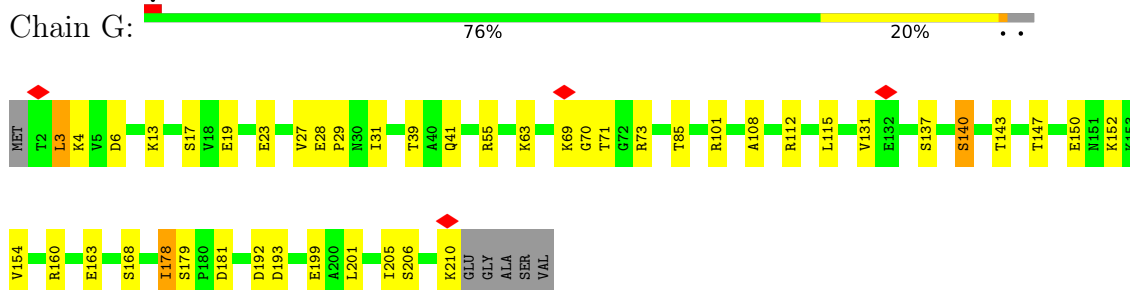
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



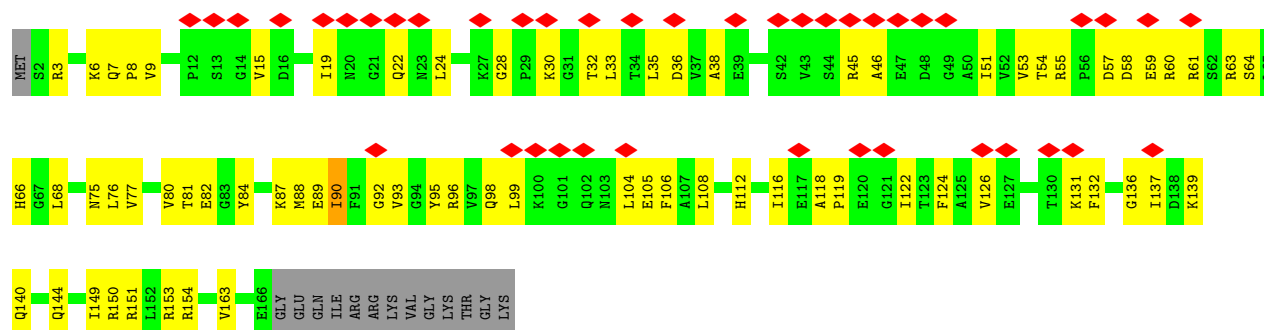
- Molecule 3: 50S ribosomal protein L4



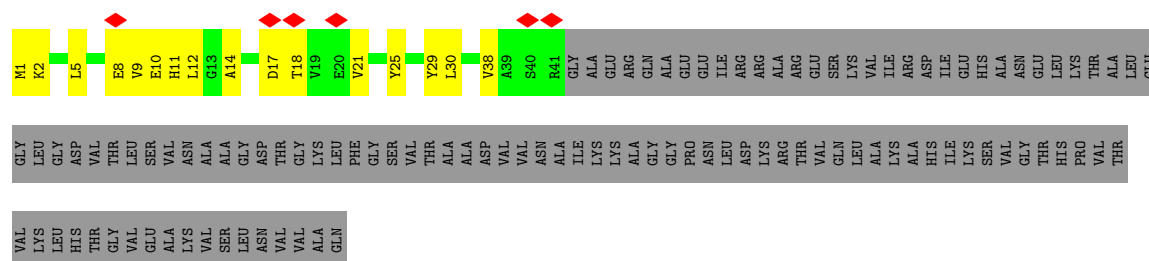
- Molecule 4: 50S ribosomal protein L5



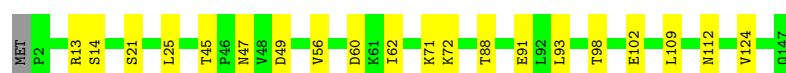
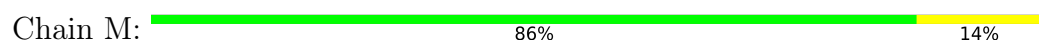
- Molecule 5: 50S ribosomal protein L6



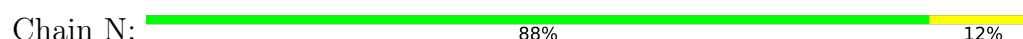
- Molecule 6: 50S ribosomal protein L9

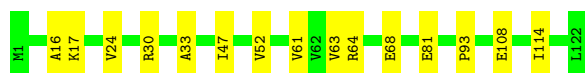


- Molecule 7: 50S ribosomal protein L13



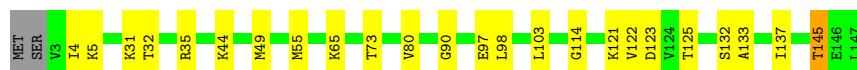
- Molecule 8: 50S ribosomal protein L14





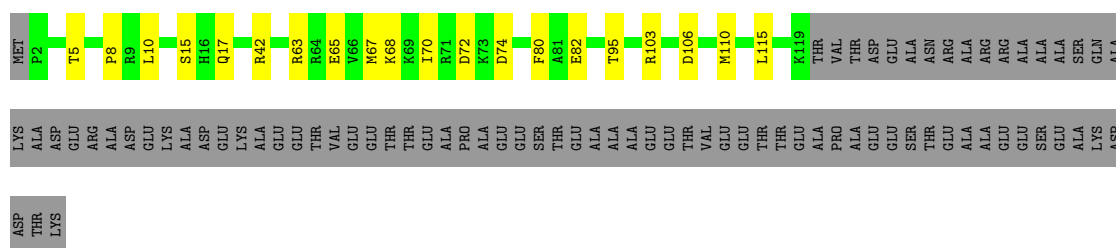
- Molecule 9: 50S ribosomal protein L15

Chain O: 82% 16% ..



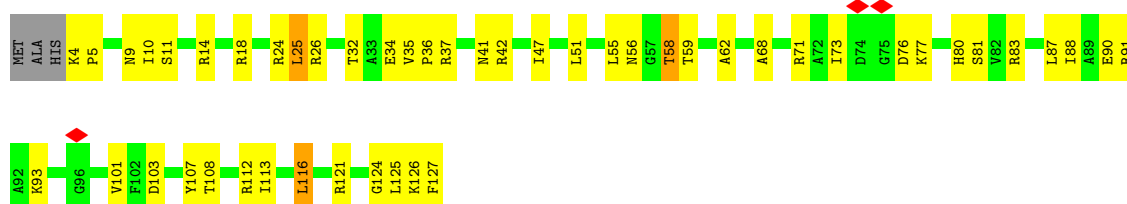
- Molecule 10: 50S ribosomal protein L17

Chain Q: 49% 10% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R: 59% 36% ..



- Molecule 12: 50S ribosomal protein L19

Chain S: 81% 17%



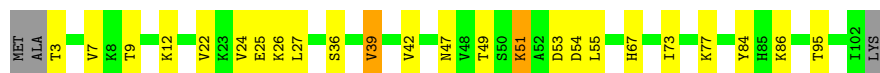
- Molecule 13: 50S ribosomal protein L20

Chain T: 79% 16%



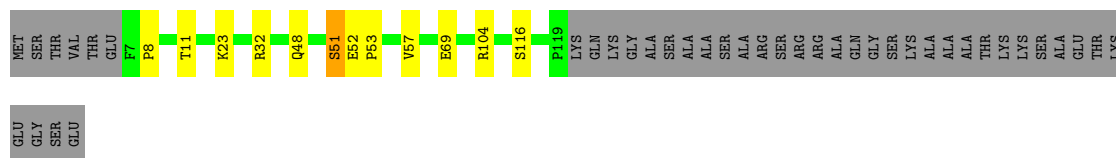
- Molecule 14: 50S ribosomal protein L21

Chain U:  74% 21% . .



- Molecule 15: 50S ribosomal protein L22

Chain V:  66% 7% . 26%



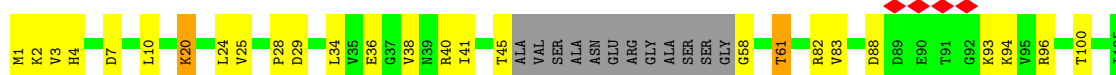
- Molecule 16: 50S ribosomal protein L23

Chain W:  80% 16% . .



- Molecule 17: 50S ribosomal protein L24

Chain X:  64% 23% . 11%



- Molecule 18: 50S ribosomal protein L27

Chain Z:  70% 16% . 13%



- Molecule 19: 50S ribosomal protein L28

Chain 1:  84% 12% . .



- Molecule 20: 50S ribosomal protein L29

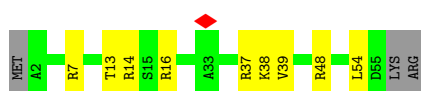
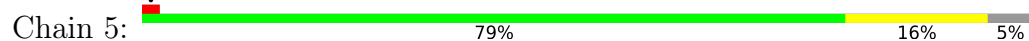
Chain 2:  62% 18% . 18%



- Molecule 21: 50S ribosomal protein L30



- Molecule 22: 50S ribosomal protein L32



- Molecule 23: 50S ribosomal protein L33A



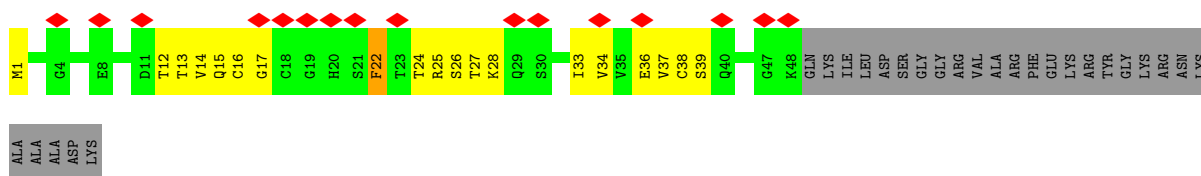
- Molecule 24: 50S ribosomal protein L34



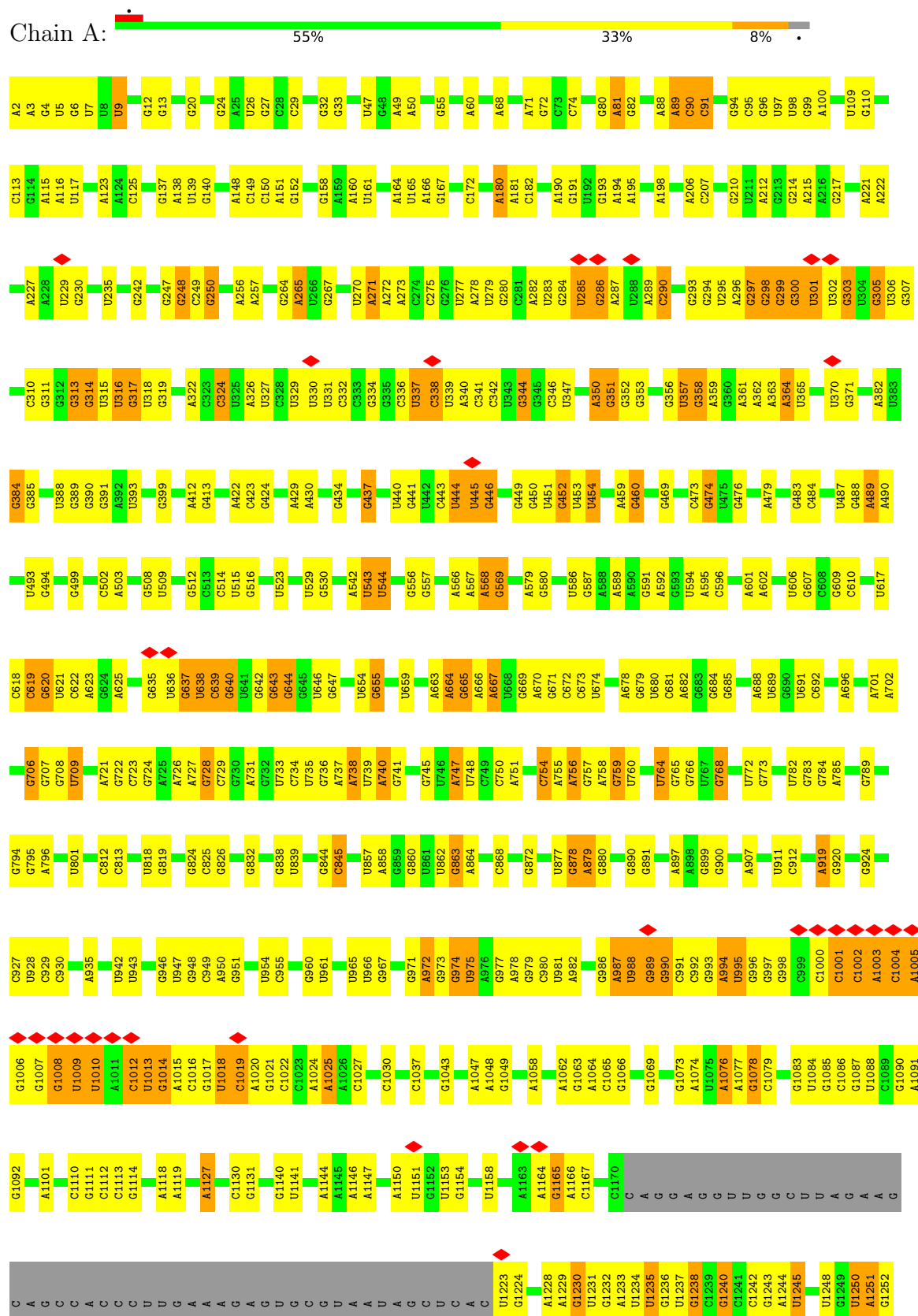
- Molecule 25: 50S ribosomal protein L35



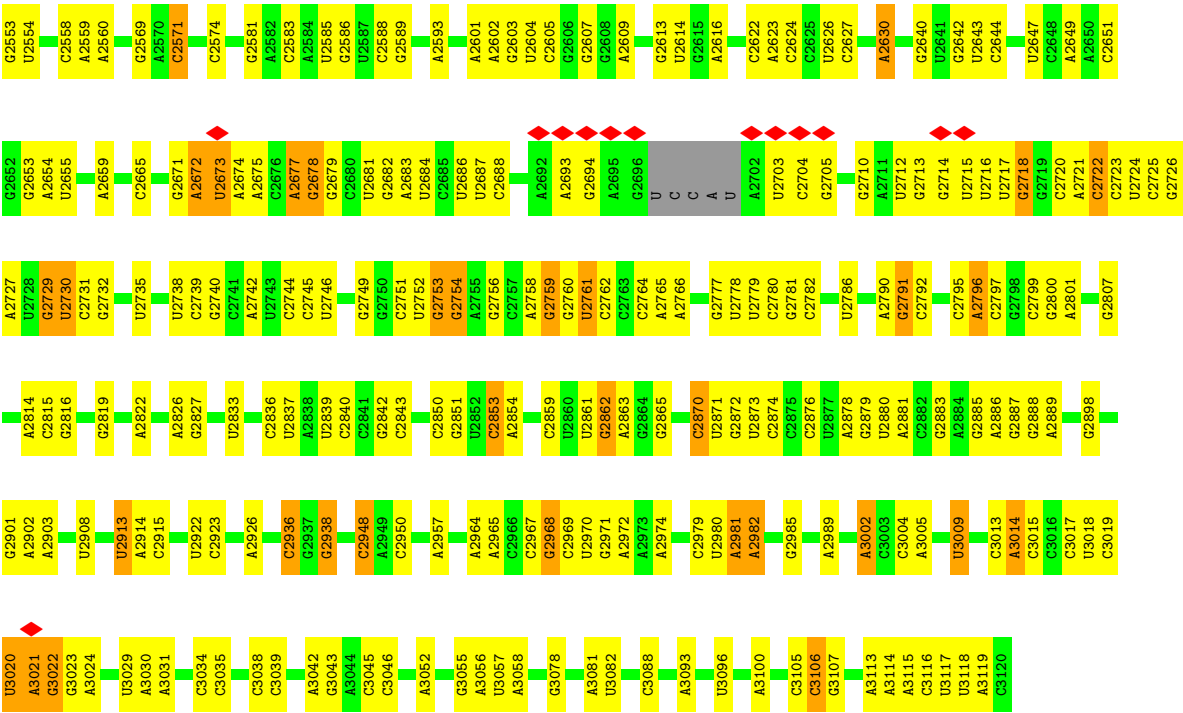
- Molecule 26: 50S ribosomal protein L31



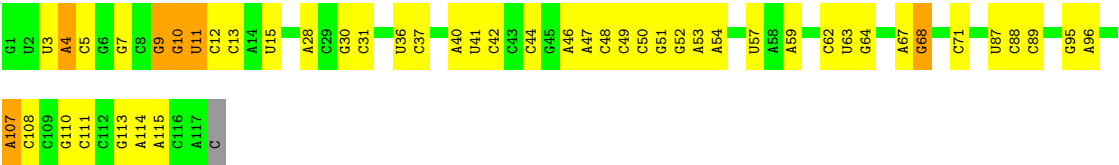
- Molecule 27: 23S rRNA







● Molecule 28: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion 3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.280	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	E	0.20	0/2153	0.27	0/2895
2	F	0.21	0/1609	0.35	0/2165
3	G	0.20	0/1592	0.34	0/2153
4	H	0.14	0/1458	0.35	0/1962
5	I	0.13	0/1281	0.34	0/1733
6	J	0.17	0/311	0.47	0/419
7	M	0.19	0/1157	0.29	0/1567
8	N	0.19	0/946	0.27	0/1268
9	O	0.17	0/1091	0.37	0/1457
10	Q	0.21	0/945	0.35	0/1267
11	R	0.19	0/950	0.47	0/1276
12	S	0.19	0/921	0.37	0/1236
13	T	0.21	0/1000	0.30	0/1341
14	U	0.19	0/764	0.24	0/1030
15	V	0.21	0/878	0.32	0/1192
16	W	0.22	0/766	0.38	0/1030
17	X	0.17	0/716	0.33	0/957
18	Z	0.18	0/583	0.32	0/782
19	1	0.16	0/478	0.32	0/641
20	2	0.19	0/530	0.37	0/708
21	3	0.20	0/473	0.38	0/635
22	5	0.15	0/427	0.26	0/572
23	6	0.25	0/413	0.59	1/553 (0.2%)
24	7	0.20	0/375	0.28	0/493
25	8	0.13	0/507	0.25	0/672
26	4	0.14	0/372	0.35	0/503
27	A	0.22	0/72557	0.30	0/113208
28	B	0.15	0/2799	0.27	0/4362
All	All	0.21	0/98052	0.31	1/148077 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	6	18	CYS	CB-CA-C	-5.33	110.42	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	23	0
2	F	1587	0	1630	33	0
3	G	1569	0	1607	30	0
4	H	1436	0	1463	46	0
5	I	1260	0	1300	57	0
6	J	308	0	323	10	0
7	M	1130	0	1167	11	0
8	N	938	0	1000	9	0
9	O	1078	0	1151	15	0
10	Q	928	0	972	14	0
11	R	941	0	979	35	0
12	S	907	0	938	13	0
13	T	988	0	1038	15	0
14	U	754	0	802	13	0
15	V	864	0	903	8	0
16	W	756	0	802	11	0
17	X	710	0	760	16	0
18	Z	574	0	591	11	0
19	1	470	0	484	9	0
20	2	527	0	538	11	0
21	3	470	0	497	8	0
22	5	423	0	463	6	0
23	6	405	0	411	50	0
24	7	372	0	406	7	0
25	8	502	0	541	13	0
26	4	364	0	352	16	0
27	A	64799	0	32602	886	0
28	B	2502	0	1274	27	0
All	All	89672	0	57159	1269	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 1269 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:6:19:LYS:HE3	23:6:45:CYS:SG	1.61	1.39
23:6:6:ASP:O	23:6:7:VAL:HG13	1.22	1.28
23:6:20:HIS:CG	27:A:2624:C:H5'	1.78	1.18
23:6:20:HIS:CD2	27:A:2624:C:H5'	1.93	1.03
23:6:19:LYS:CE	23:6:45:CYS:SG	2.46	1.02

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	273/278 (98%)	262 (96%)	11 (4%)	0	100	100
2	F	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
3	G	207/215 (96%)	201 (97%)	6 (3%)	0	100	100
4	H	179/187 (96%)	167 (93%)	12 (7%)	0	100	100
5	I	163/179 (91%)	161 (99%)	2 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
8	N	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
9	O	143/147 (97%)	131 (92%)	12 (8%)	0	100	100
10	Q	116/199 (58%)	112 (97%)	4 (3%)	0	100	100
11	R	122/127 (96%)	121 (99%)	1 (1%)	0	100	100
12	S	111/113 (98%)	103 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	T	122/129 (95%)	119 (98%)	3 (2%)	0	100	100
14	U	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
15	V	111/153 (72%)	108 (97%)	3 (3%)	0	100	100
16	W	95/100 (95%)	93 (98%)	2 (2%)	0	100	100
17	X	89/105 (85%)	86 (97%)	3 (3%)	0	100	100
18	Z	75/88 (85%)	69 (92%)	6 (8%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
21	3	56/61 (92%)	55 (98%)	1 (2%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	47/55 (86%)	42 (89%)	4 (8%)	1 (2%)	5	15
24	7	43/47 (92%)	43 (100%)	0	0	100	100
25	8	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
26	4	46/75 (61%)	44 (96%)	2 (4%)	0	100	100
All	All	2846/3260 (87%)	2736 (96%)	109 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	6	7	VAL

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	E	215/218 (99%)	206 (96%)	9 (4%)	26	55
2	F	160/163 (98%)	154 (96%)	6 (4%)	29	58
3	G	169/173 (98%)	161 (95%)	8 (5%)	23	51
4	H	150/156 (96%)	145 (97%)	5 (3%)	33	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	I	139/150 (93%)	132 (95%)	7 (5%)	22	48
6	J	31/116 (27%)	28 (90%)	3 (10%)	8	20
7	M	119/120 (99%)	115 (97%)	4 (3%)	32	62
8	N	100/100 (100%)	98 (98%)	2 (2%)	48	76
9	O	112/114 (98%)	109 (97%)	3 (3%)	39	69
10	Q	97/158 (61%)	96 (99%)	1 (1%)	68	86
11	R	92/94 (98%)	85 (92%)	7 (8%)	12	30
12	S	100/100 (100%)	93 (93%)	7 (7%)	14	34
13	T	97/99 (98%)	94 (97%)	3 (3%)	35	65
14	U	81/83 (98%)	71 (88%)	10 (12%)	4	12
15	V	89/117 (76%)	87 (98%)	2 (2%)	45	74
16	W	83/85 (98%)	79 (95%)	4 (5%)	23	50
17	X	79/86 (92%)	72 (91%)	7 (9%)	9	23
18	Z	56/63 (89%)	50 (89%)	6 (11%)	6	16
19	1	50/51 (98%)	49 (98%)	1 (2%)	48	76
20	2	58/66 (88%)	55 (95%)	3 (5%)	21	47
21	3	52/54 (96%)	49 (94%)	3 (6%)	18	42
22	5	43/46 (94%)	41 (95%)	2 (5%)	23	51
23	6	47/52 (90%)	47 (100%)	0	100	100
24	7	35/36 (97%)	34 (97%)	1 (3%)	37	67
25	8	53/54 (98%)	49 (92%)	4 (8%)	12	31
26	4	43/63 (68%)	42 (98%)	1 (2%)	44	73
All	All	2350/2617 (90%)	2241 (95%)	109 (5%)	25	51

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	S	69	VAL
14	U	39	VAL
21	3	28	LEU
12	S	84	ASP
14	U	3	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
8	N	3	GLN
13	T	39	GLN
25	8	63	ASN
23	6	22	ASN
25	8	25	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3013/3119 (96%)	568 (18%)	15 (0%)
28	B	116/118 (98%)	17 (14%)	1 (0%)
All	All	3129/3237 (96%)	585 (18%)	16 (0%)

5 of 585 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	9	U
27	A	12	G
27	A	20	G
27	A	24	G

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	2729	G
27	A	2381	A
27	A	1002	C
27	A	2350	G
27	A	974	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 oligosaccharides 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.

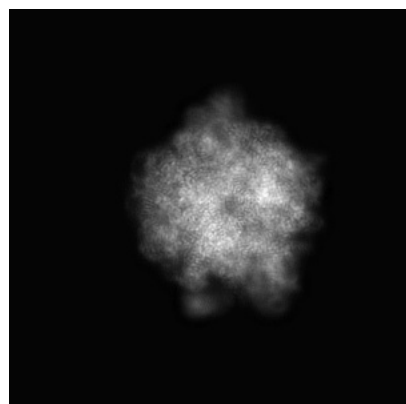
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37552. These allow visual inspection of the internal detail of the map and identification of artifacts.

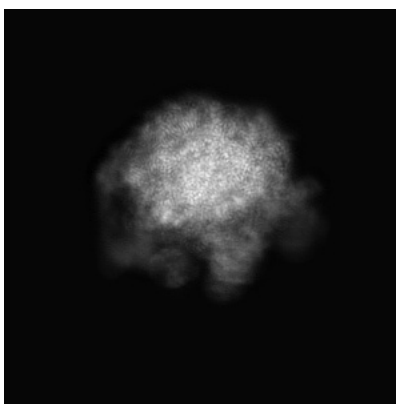
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

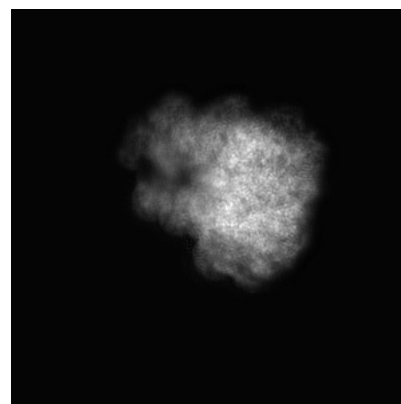
6.1.1 Primary map



X

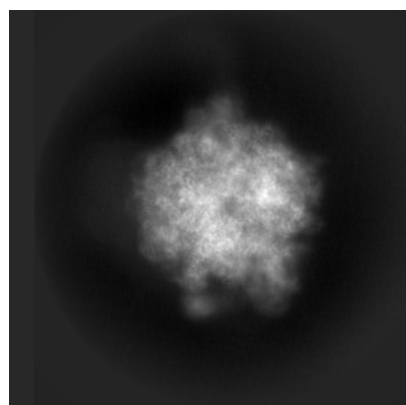


Y

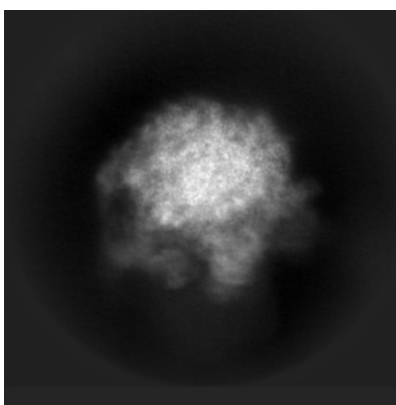


Z

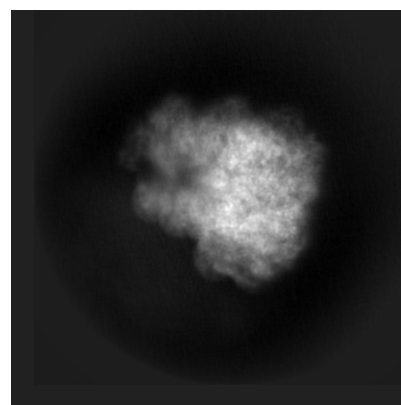
6.1.2 Raw map



X



Y

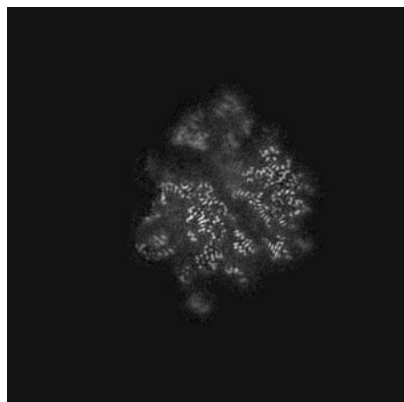


Z

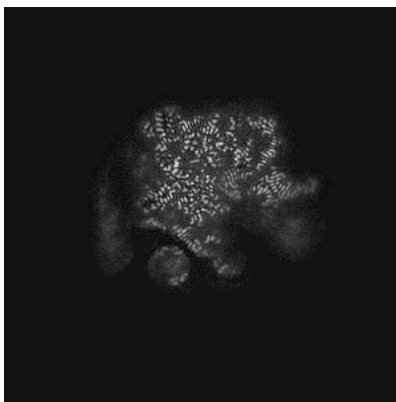
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

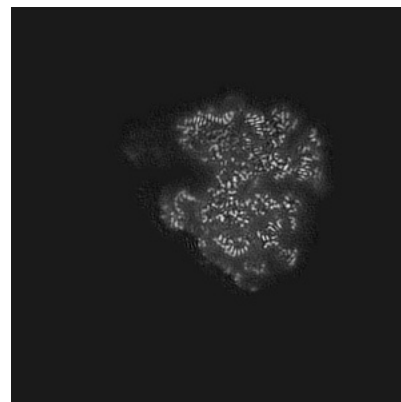
6.2.1 Primary map



X Index: 190

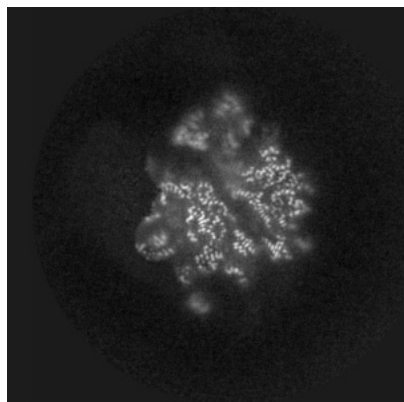


Y Index: 190

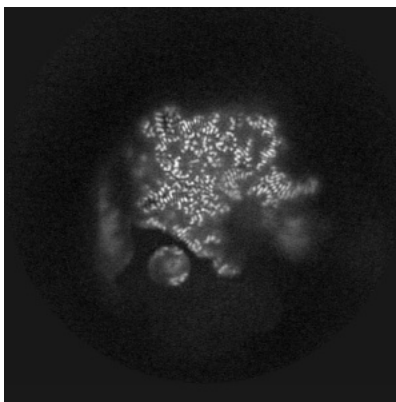


Z Index: 190

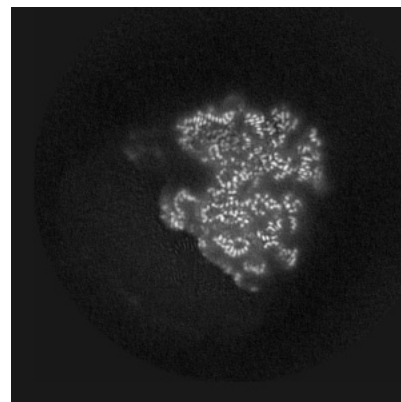
6.2.2 Raw map



X Index: 190



Y Index: 190

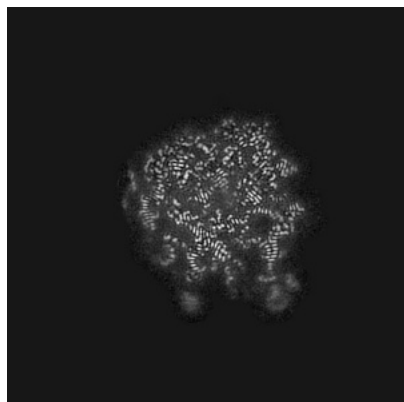


Z Index: 190

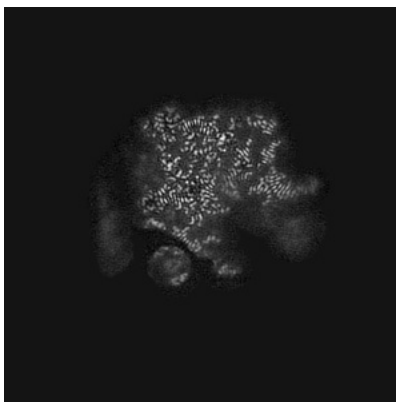
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

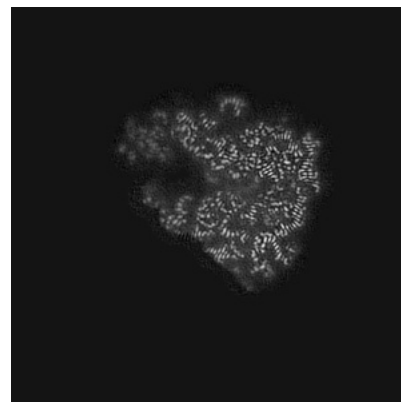
6.3.1 Primary map



X Index: 230

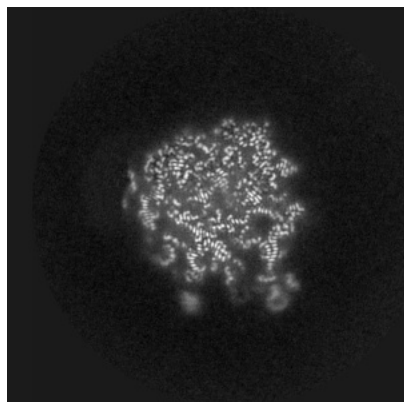


Y Index: 191

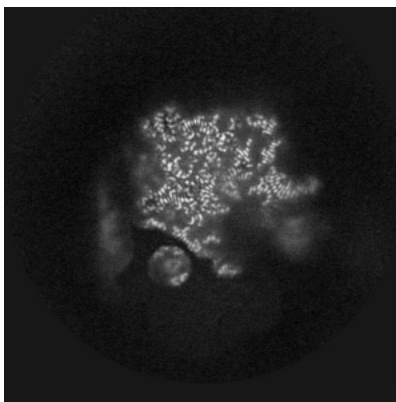


Z Index: 199

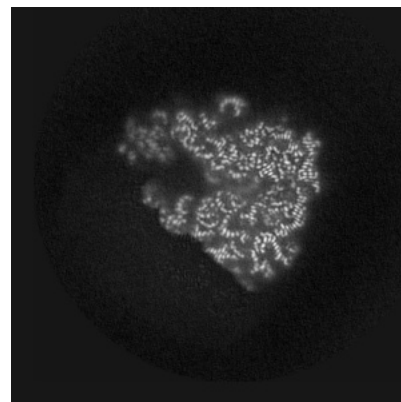
6.3.2 Raw map



X Index: 230



Y Index: 191

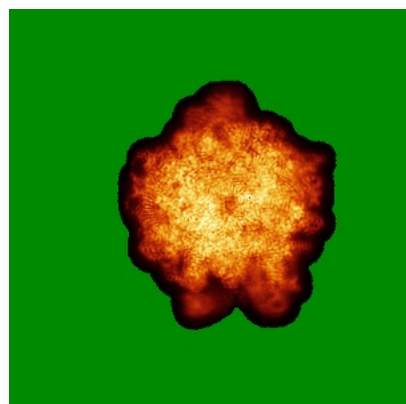


Z Index: 199

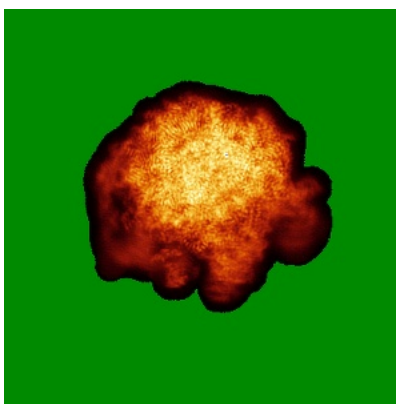
The images above show the largest variance slices of the map in three orthogonal directions.

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

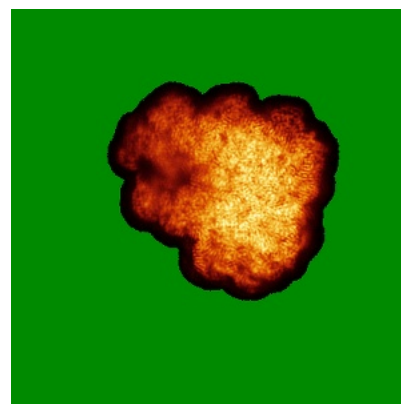
6.4.1 Primary map



X

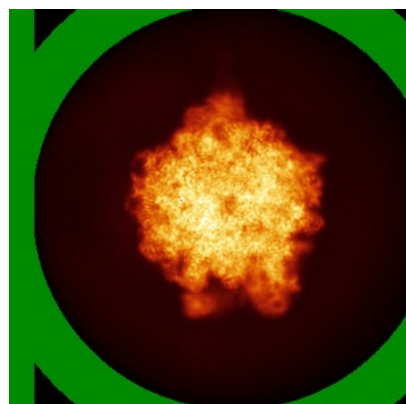


Y

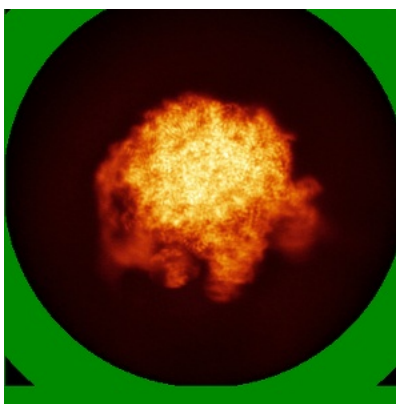


Z

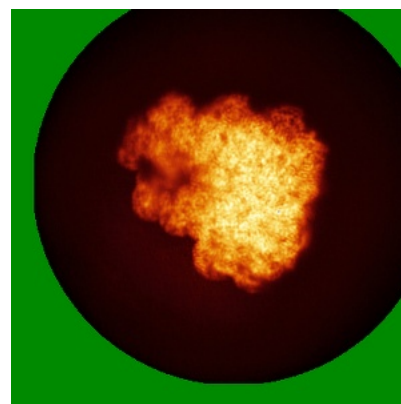
6.4.2 Raw map



X



Y

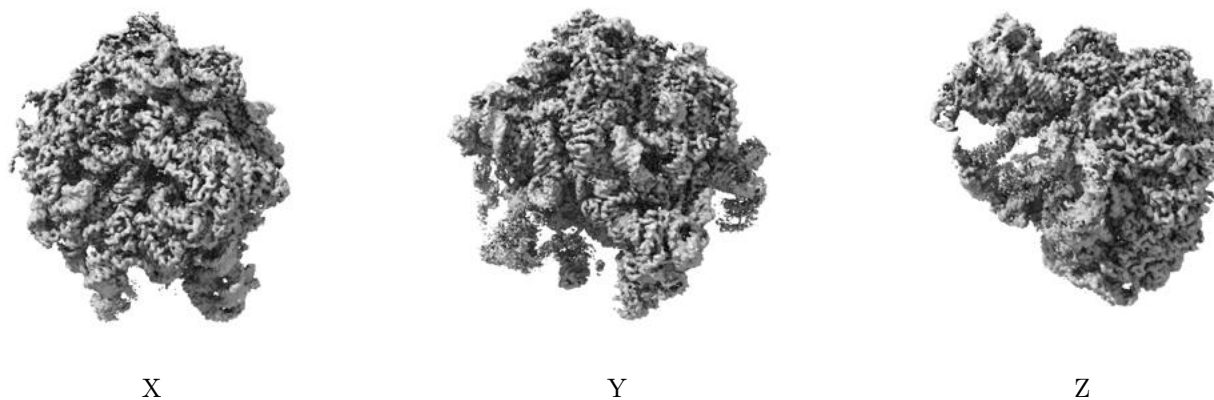


Z

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.

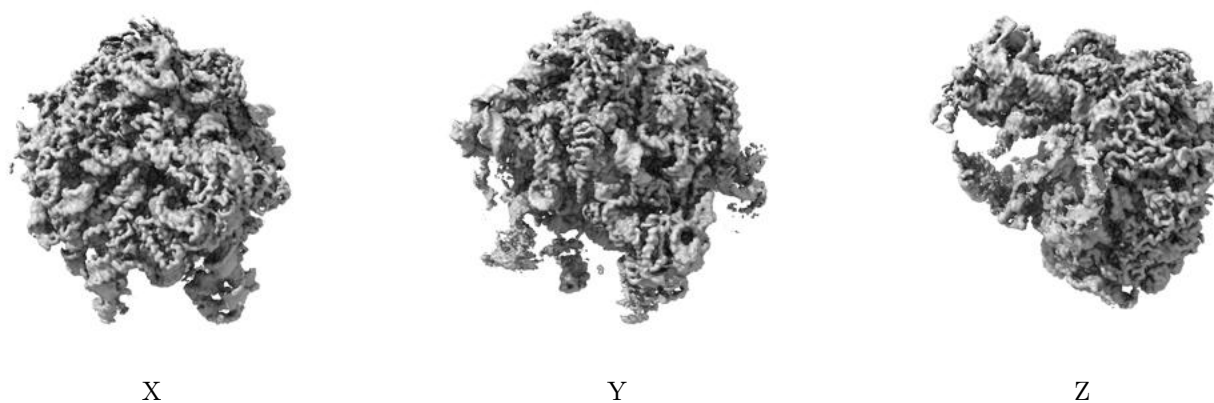
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. 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.

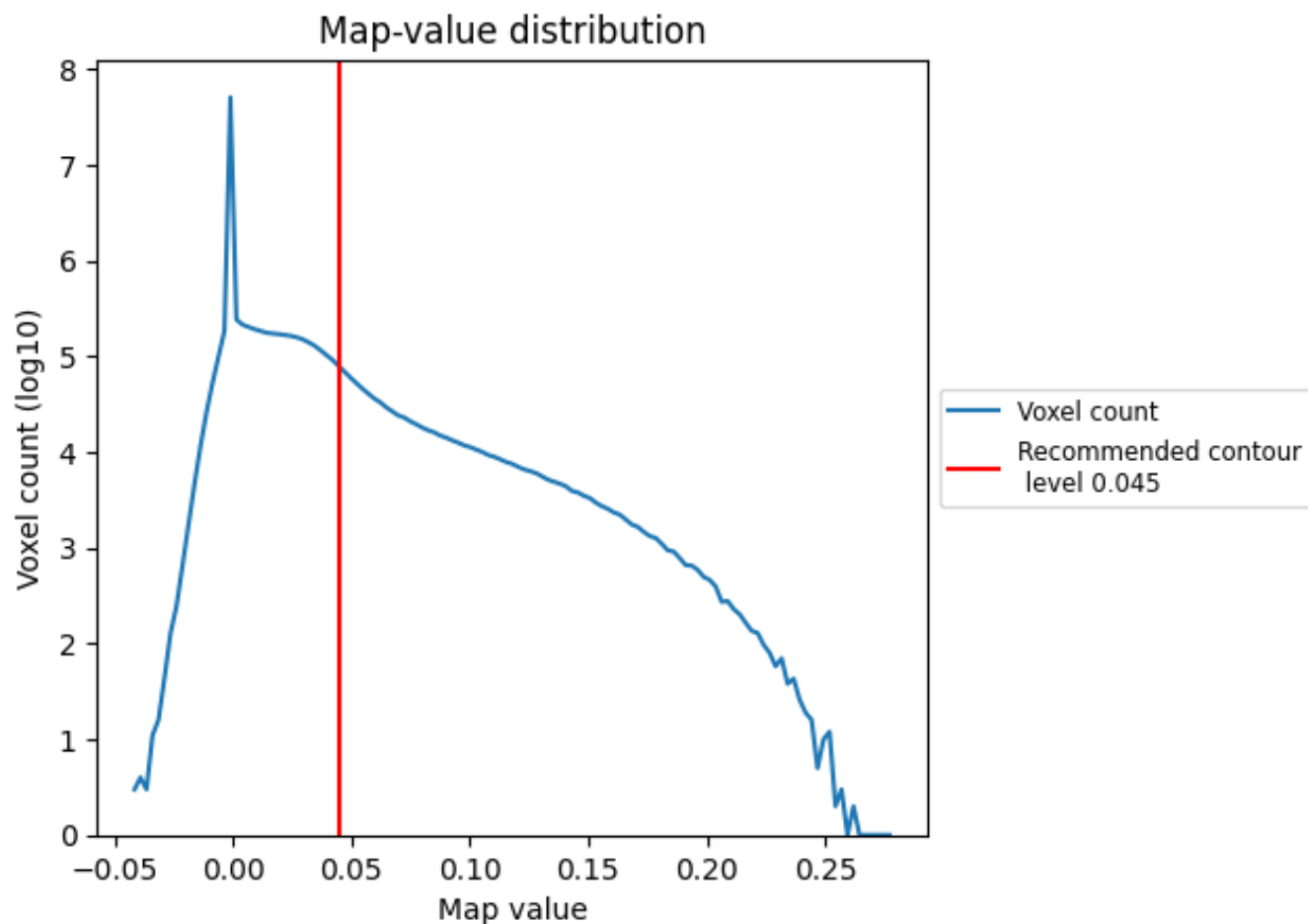
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

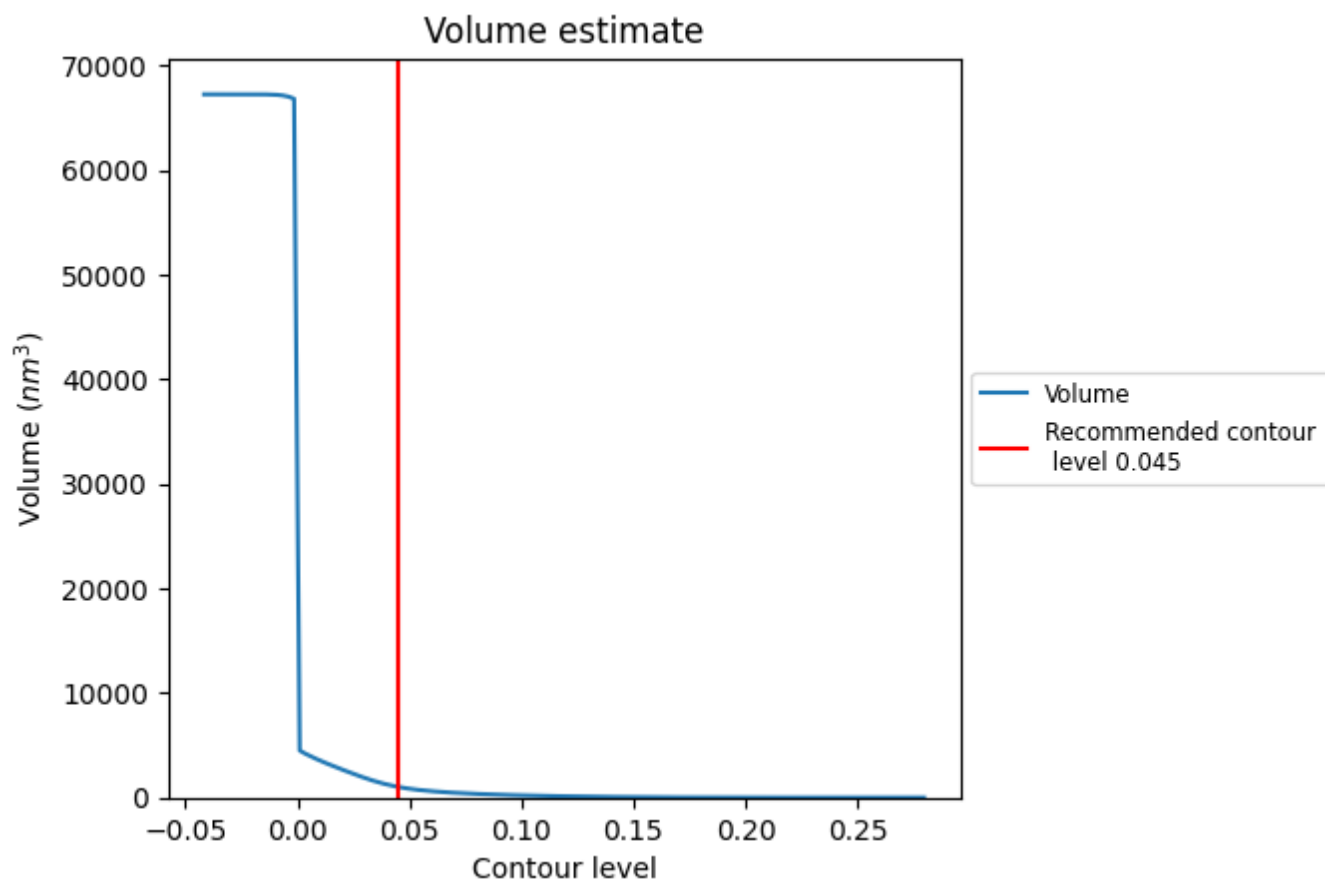
This section contains the results of statistical analysis of the map.

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.

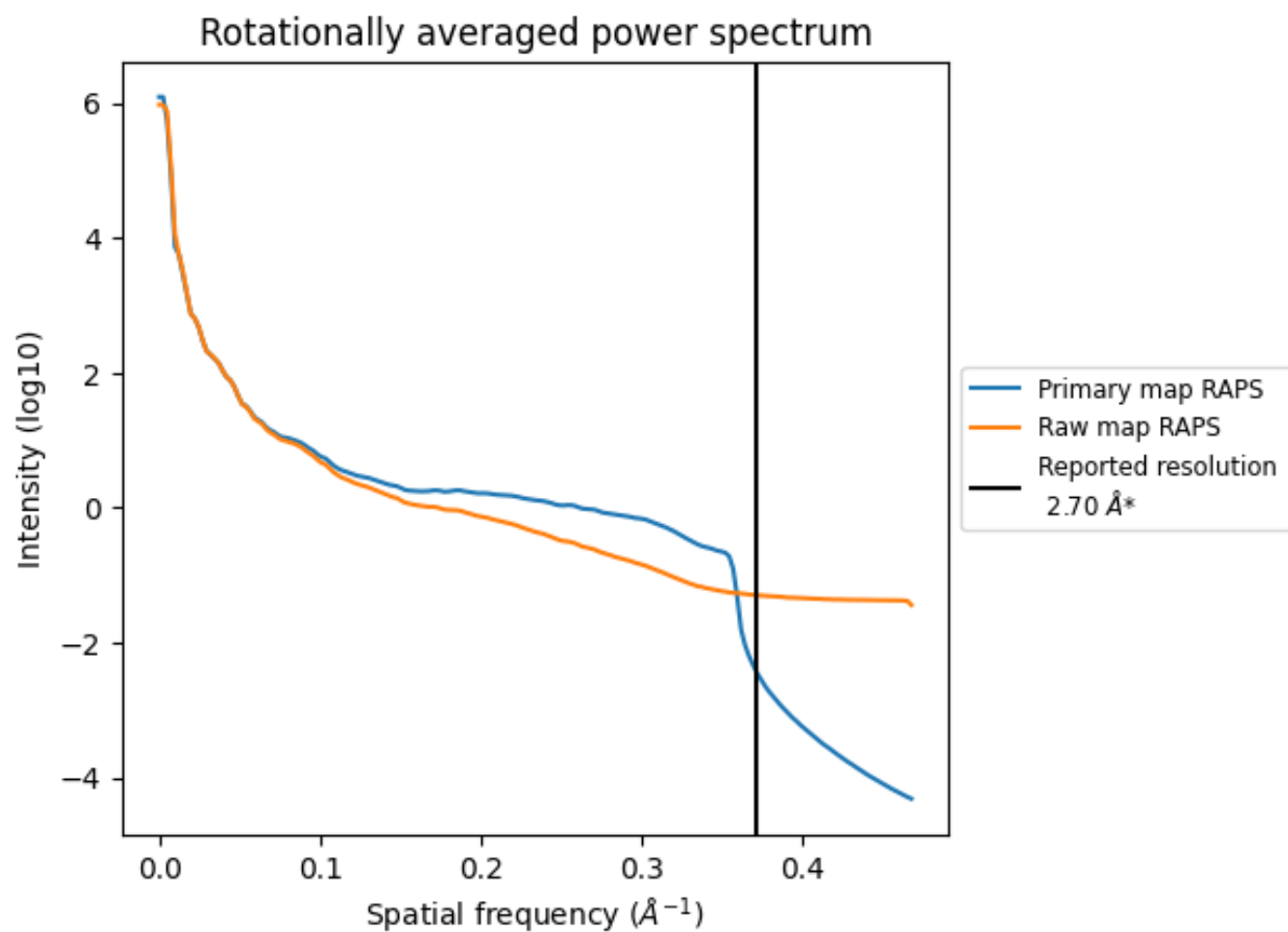
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1020 nm³; this corresponds to an approximate mass of 922 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 ⓘ

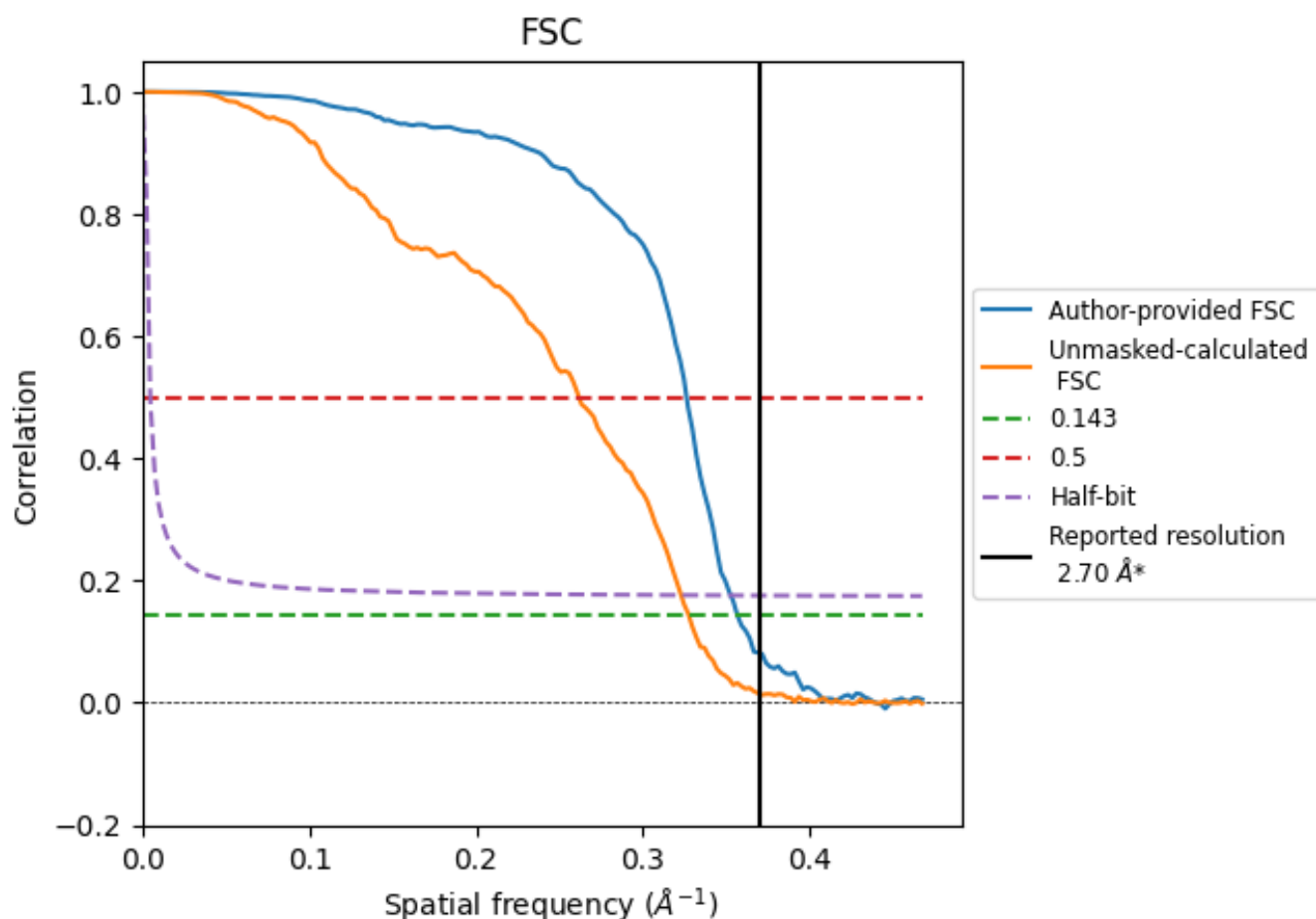


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.80	3.07	2.84
Unmasked-calculated*	3.05	3.82	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 2.7 by more than 10 %

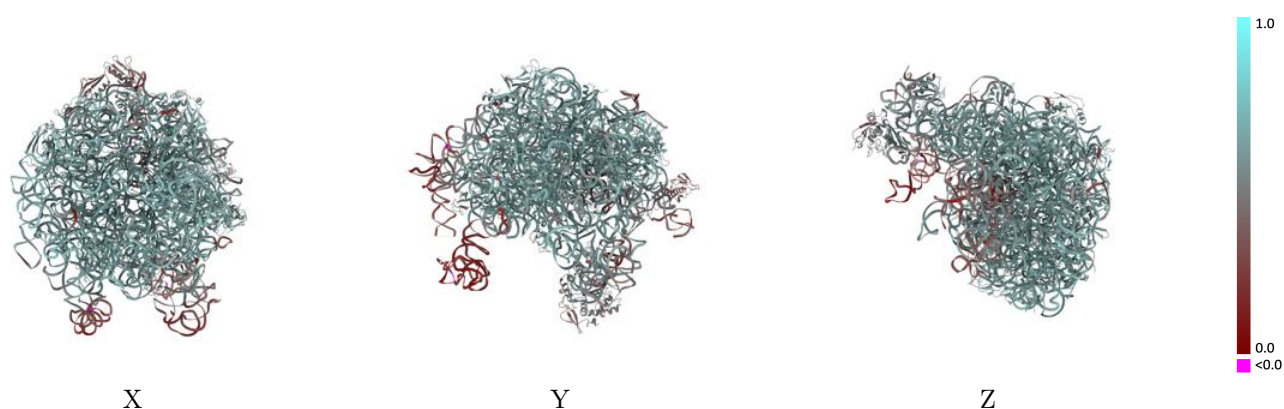
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37552 and PDB model 8WHY. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

This section was not generated.

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

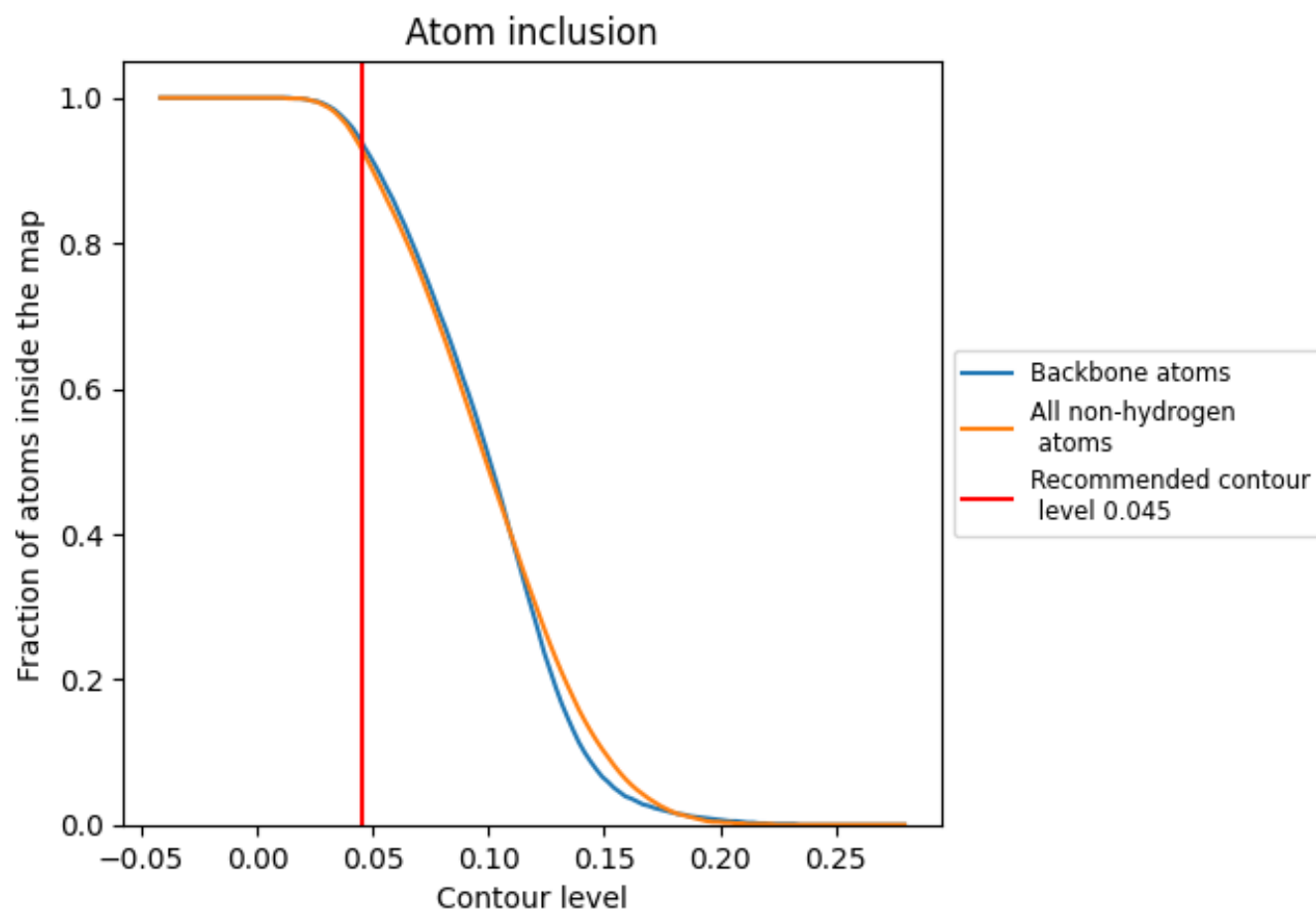


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.5670
1	 0.9120	 0.5730
2	 0.9230	 0.5780
3	 0.9470	 0.6130
4	 0.5250	 0.3830
5	 0.9030	 0.6140
6	 0.8050	 0.5260
7	 1.0000	 0.6400
8	 0.9630	 0.6210
A	 0.9370	 0.5640
B	 0.9700	 0.5290
E	 0.9840	 0.6320
F	 0.9520	 0.6110
G	 0.9210	 0.5910
H	 0.8120	 0.4940
I	 0.6060	 0.3740
J	 0.6900	 0.5240
M	 0.9600	 0.6130
N	 0.9660	 0.6130
O	 0.9370	 0.6040
Q	 0.9800	 0.6250
R	 0.8810	 0.5310
S	 0.9590	 0.5980
T	 0.9720	 0.6180
U	 0.9380	 0.6220
V	 0.9780	 0.6230
W	 0.9310	 0.6040
X	 0.8750	 0.5790
Z	 0.9660	 0.6050

