



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:53 PM UTC

PDB ID : 9JMK / pdb_00009jmk
EMDB ID : EMD-61605
Title : 50S Ribosomal Subunit precursor state III
Authors : Sengupta, S.; Mukherjee, R.; Pilsl, M.; Bagale, S.; Adhikary, A.D.; Borkar, A.;
Pradeepkumar, P.I.; Engel, C.; Chowdhury, A.; Kaushal, P.S.; Anand, R.
Deposited on : 2024-09-20
Resolution : 4.00 Å(reported)
Based on initial model : 6GC8

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

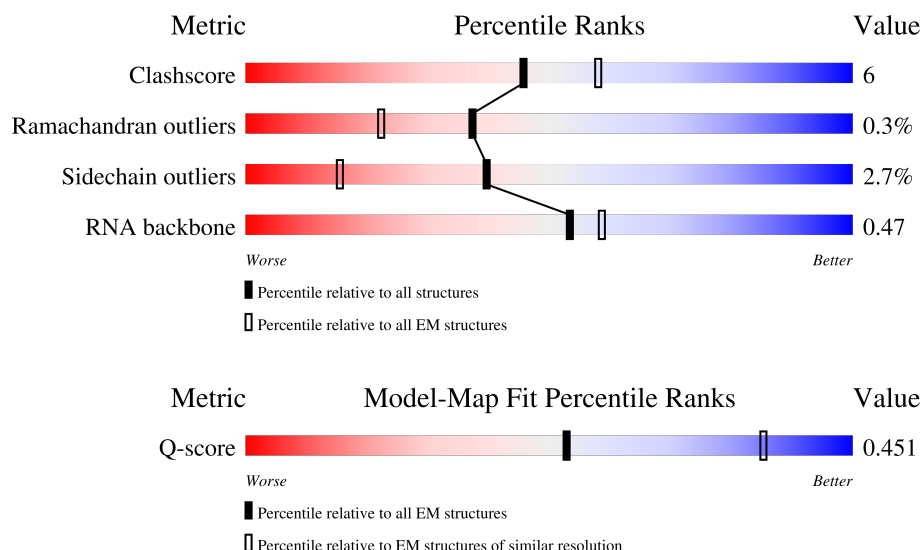
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.








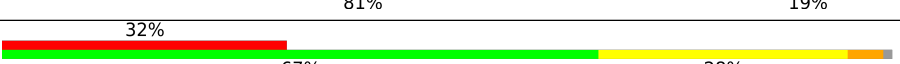
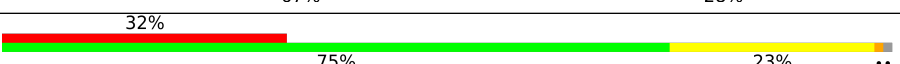



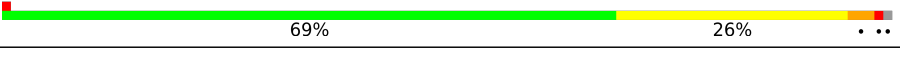
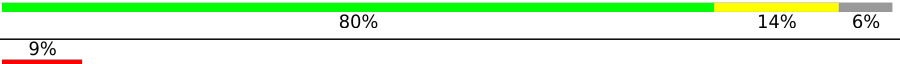

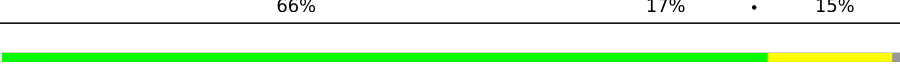
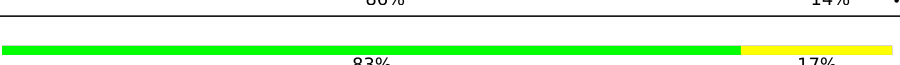










Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	0	57	<div> <div>5%</div> <div>77%</div> <div>21%</div> <div>.</div> </div>
2	1	55	<div> <div>75%</div> <div>13%</div> <div>13%</div> </div>
3	2	46	<div> <div>83%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
4	3	65	
5	A	2904	
6	B	120	
7	C	273	
8	D	209	
9	E	201	
10	F	179	
11	G	177	
12	H	149	
13	J	142	
14	K	123	
15	L	144	
16	N	127	
17	O	117	
18	P	115	
19	Q	118	
20	R	103	
21	S	110	
22	T	100	
23	U	104	
24	V	94	
25	W	85	
26	X	78	
27	Y	63	
28	Z	59	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 76537 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 L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	48	Total	C	N	O	0	0
			395	254	72	69		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2390	Total	C	N	O	P	0	0
			51353	22907	9498	16558	2390		

- Molecule 6 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	175	Total	C	N	O	S	0	0
			1317	829	242	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	32	Total	C	N	O	S	0	0
			241	155	42	43	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	98	Total	C	N	O	S	0	0
			783	494	148	140	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	87	Total	C	N	O	S	0	0
			686	434	128	123	1		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	76	Total	C	N	O	S	0	0
			581	360	117	103	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

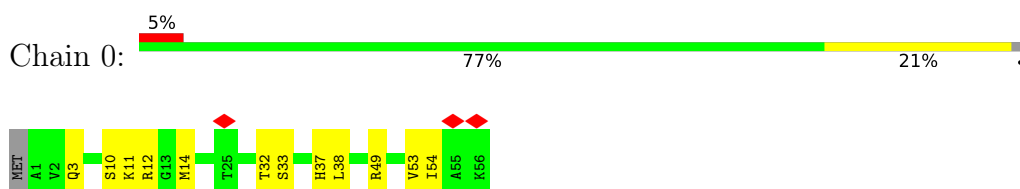
- Molecule 28 is a protein called 50S ribosomal protein L30.

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

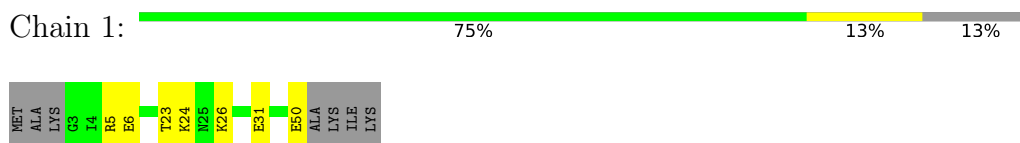
3 Residue-property plots

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.

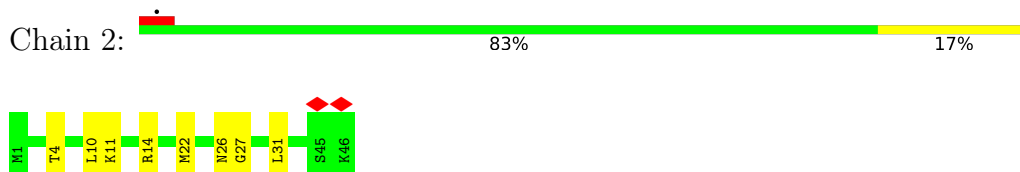
- Molecule 1: 50S ribosomal protein L32



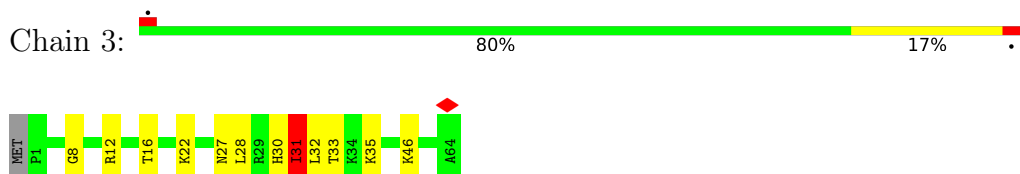
- Molecule 2: 50S ribosomal protein L33



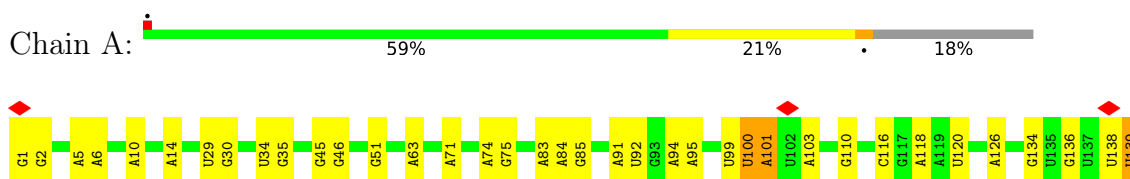
- Molecule 3: 50S ribosomal protein L34



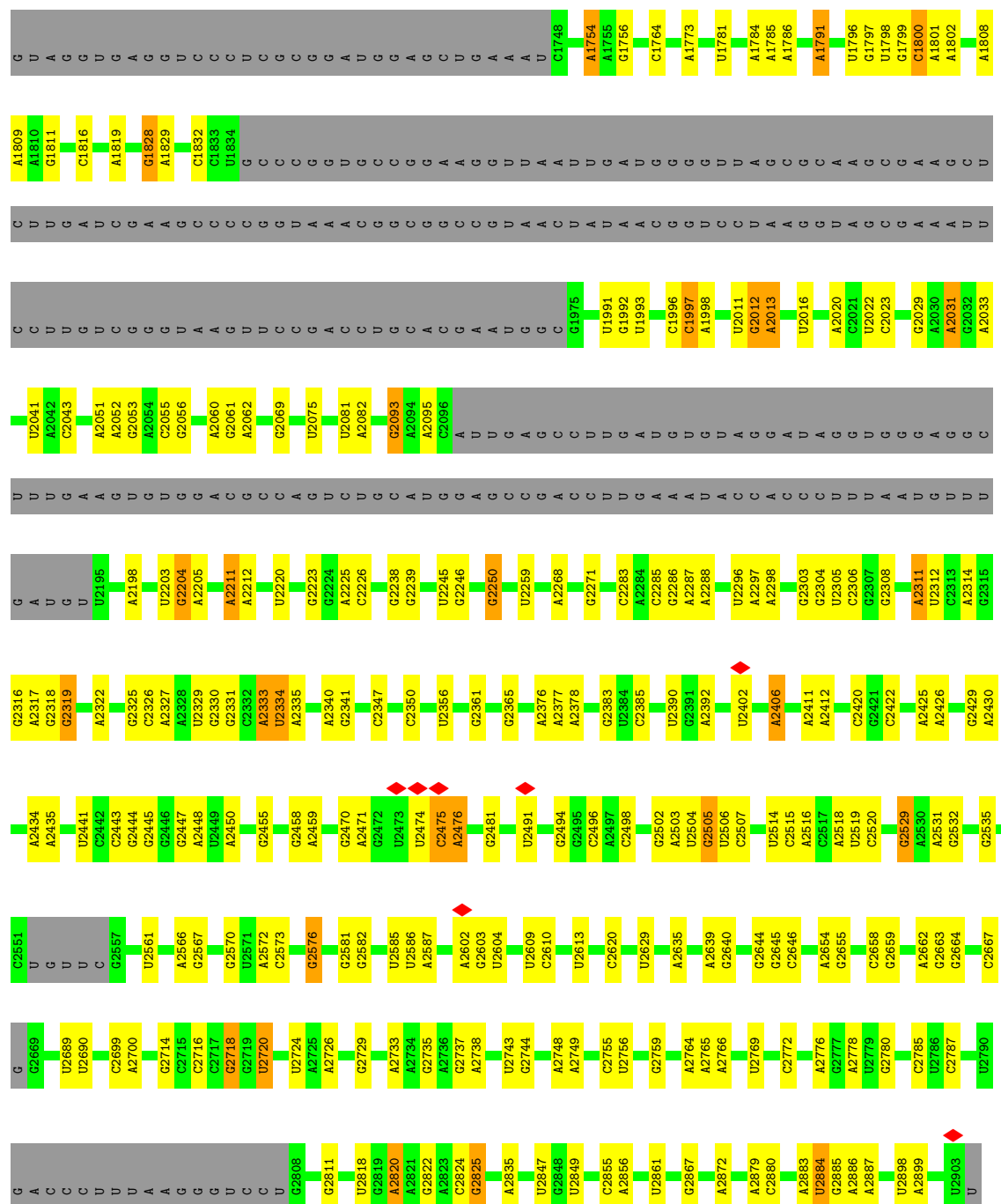
- Molecule 4: 50S ribosomal protein L35



- Molecule 5: 23S ribosomal RNA

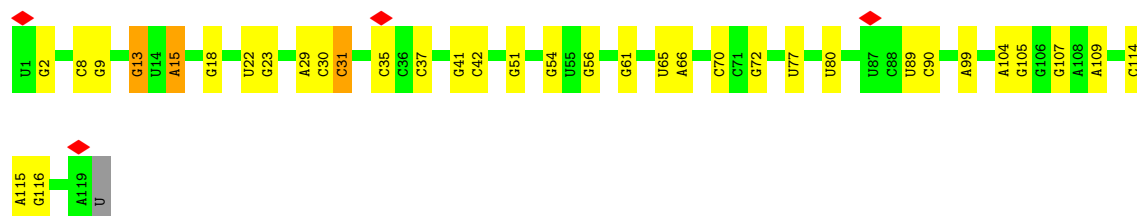







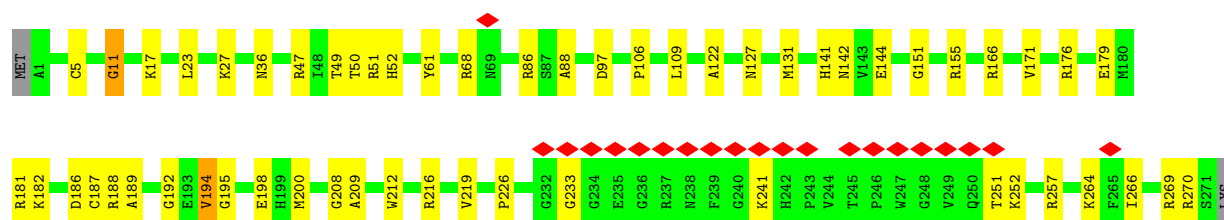
• Molecule 6: 5S ribosomal RNA

Chain B: 70% 27% ::




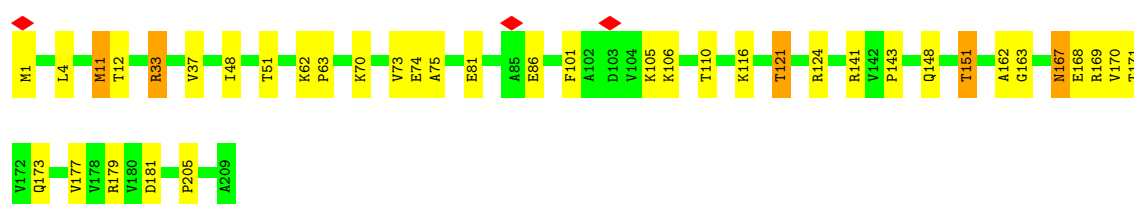
- Molecule 7: 50S ribosomal protein L2

Chain C: 




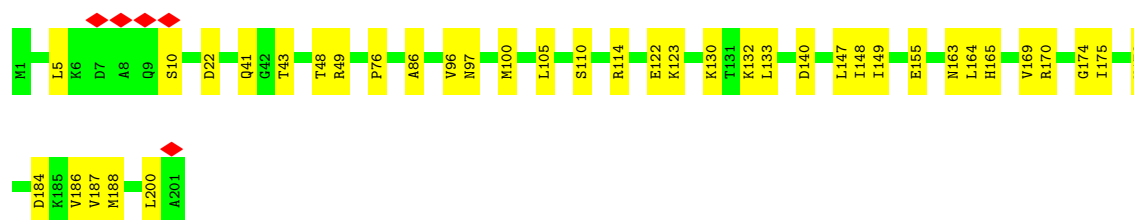
- Molecule 8: 50S ribosomal protein L3

Chain D: 



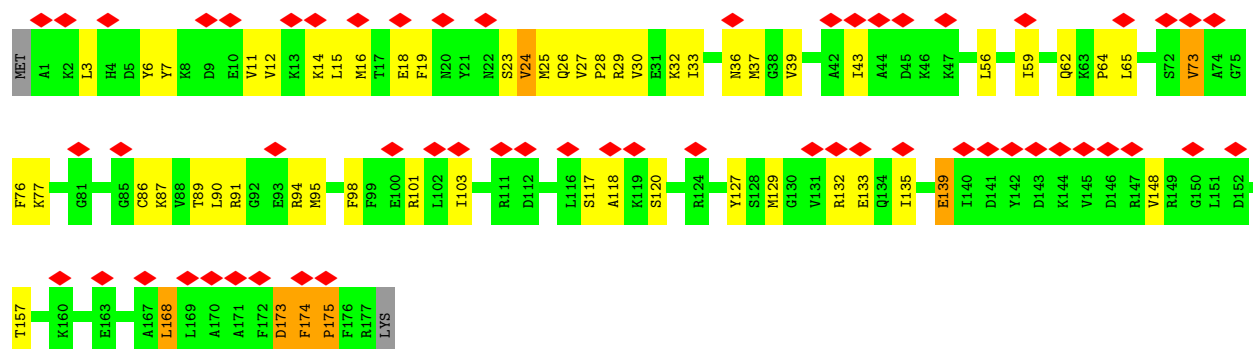
- Molecule 9: 50S ribosomal protein L4

Chain E: 

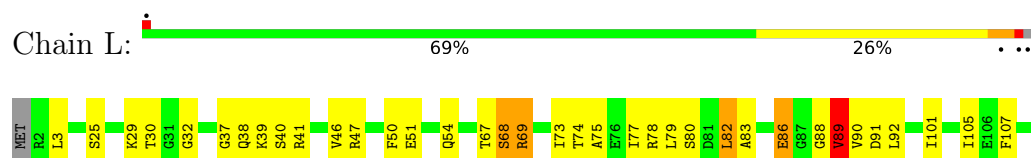


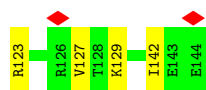
- Molecule 10: 50S ribosomal protein L5

Chain F: 



- Molecule 11: 50S ribosomal protein L6





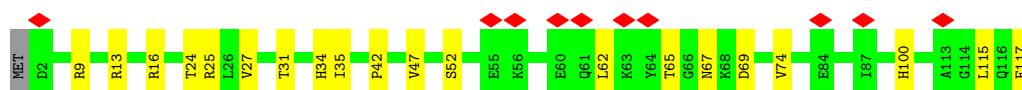
- Molecule 16: 50S ribosomal protein L17

Chain N: 80% 14% 6%



- Molecule 17: 50S ribosomal protein L18

Chain O: 9% 82% 17%



- Molecule 18: 50S ribosomal protein L19

Chain P: 66% 17% 15%



- Molecule 19: 50S ribosomal protein L20

Chain Q: 86% 14%



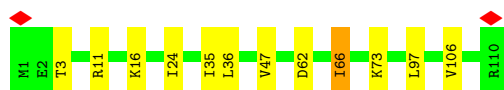
- Molecule 20: 50S ribosomal protein L21

Chain R: 83% 17%

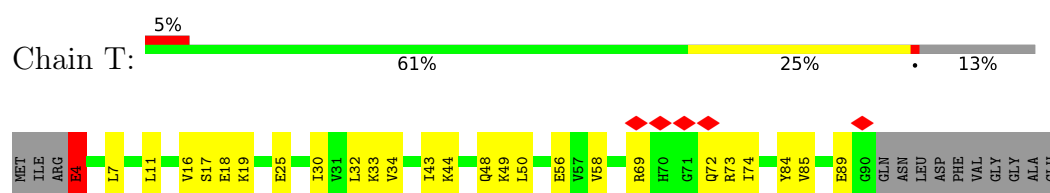


- Molecule 21: 50S ribosomal protein L22

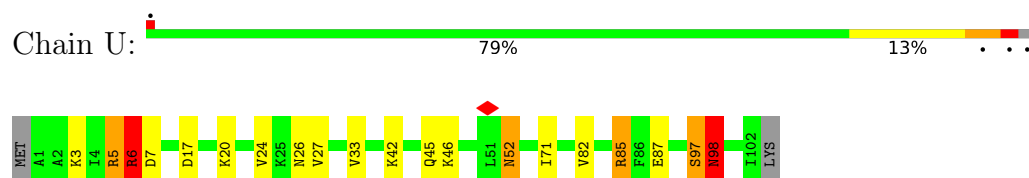
Chain S: 89% 10%



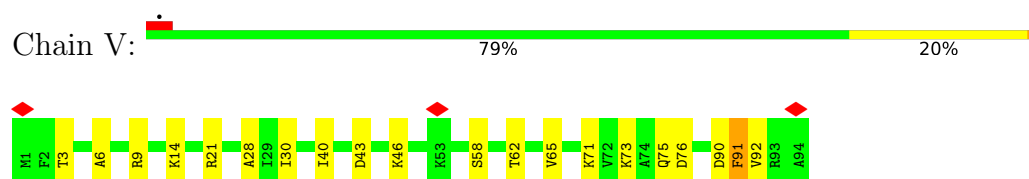
- Molecule 22: 50S ribosomal protein L23



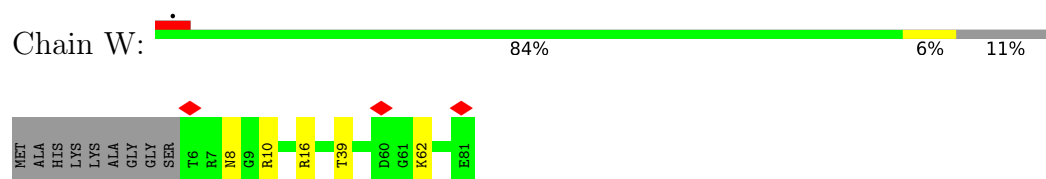
- Molecule 23: 50S ribosomal protein L24



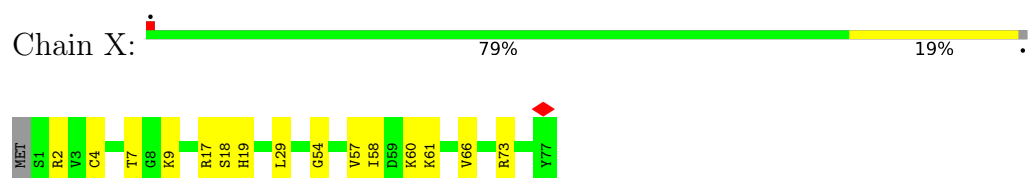
- Molecule 24: 50S ribosomal protein L25



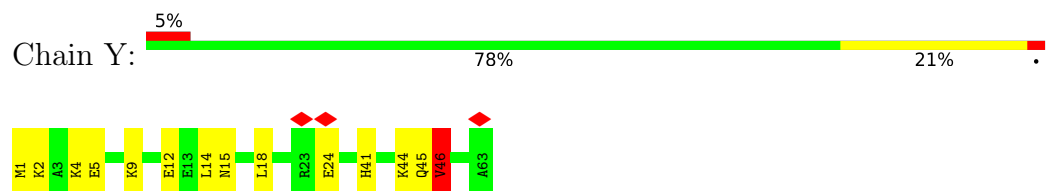
- Molecule 25: 50S ribosomal protein L27



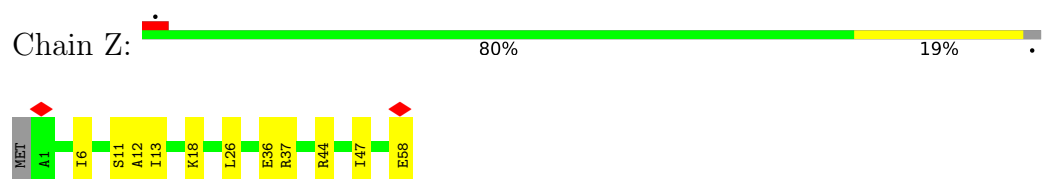
- Molecule 26: 50S ribosomal protein L28



- Molecule 27: 50S ribosomal protein L29



- Molecule 28: 50S ribosomal protein L30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6081	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.25	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0033	Depositor
Map size (Å)	331.2, 331.2, 331.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.69, 0.69, 0.69	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	0	0.36	0/450	0.63	0/599
2	1	0.24	0/402	0.56	0/536
3	2	0.26	0/380	0.43	0/498
4	3	0.35	0/513	0.75	1/676 (0.1%)
5	A	0.26	0/57514	0.39	6/89699 (0.0%)
6	B	0.18	0/2847	0.31	0/4440
7	C	0.27	0/2121	0.57	2/2852 (0.1%)
8	D	0.36	0/1586	0.66	3/2134 (0.1%)
9	E	0.25	0/1571	0.51	0/2113
10	F	0.27	0/1434	0.68	0/1926
11	G	0.33	0/1336	0.72	3/1805 (0.2%)
12	H	0.57	0/243	0.80	0/328
13	J	0.30	0/1152	0.66	2/1551 (0.1%)
14	K	0.28	0/947	0.75	2/1268 (0.2%)
15	L	0.36	0/1054	1.18	11/1403 (0.8%)
16	N	0.31	0/973	0.68	0/1301
17	O	0.26	0/902	0.56	0/1209
18	P	0.32	0/795	0.63	1/1067 (0.1%)
19	Q	0.30	0/960	0.51	0/1278
20	R	0.30	0/829	0.57	0/1107
21	S	0.37	0/864	0.62	0/1156
22	T	0.33	0/692	1.00	5/925 (0.5%)
23	U	0.44	0/787	0.83	5/1051 (0.5%)
24	V	0.27	0/766	0.70	0/1025
25	W	0.32	0/588	0.46	0/779
26	X	0.21	0/635	0.49	0/848
27	Y	0.37	0/510	0.80	0/677
28	Z	0.24	0/453	0.51	0/605
All	All	0.27	0/83304	0.47	41/124856 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	3	0	1
7	C	0	1
8	D	0	1
11	G	0	1
14	K	0	1
15	L	0	1
18	P	0	2
22	T	0	1
23	U	0	4
All	All	0	13

There are no bond length outliers.

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	L	69	ARG	N-CA-C	15.91	128.09	111.07
15	L	68	SER	N-CA-C	-13.10	90.11	109.63
4	3	31	ILE	N-CA-C	12.93	136.24	109.34
13	J	81	ILE	N-CA-C	11.80	122.75	110.36
22	T	4	GLU	N-CA-C	-11.52	78.74	111.00

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	3	31	ILE	Peptide
7	C	11	GLY	Peptide
8	D	33	ARG	Sidechain
11	G	34	ARG	Sidechain
14	K	92	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	8	0
2	1	395	0	422	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	2	377	0	418	5	0
4	3	504	0	574	33	0
5	A	51353	0	25840	247	0
6	B	2548	0	1292	15	0
7	C	2082	0	2157	67	0
8	D	1565	0	1616	38	0
9	E	1552	0	1619	23	0
10	F	1410	0	1447	70	0
11	G	1317	0	1368	50	0
12	H	241	0	257	12	0
13	J	1129	0	1162	31	0
14	K	938	0	1012	22	0
15	L	1045	0	1117	31	0
16	N	960	0	999	18	0
17	O	892	0	923	15	0
18	P	783	0	816	12	0
19	Q	947	0	1022	30	0
20	R	816	0	839	49	0
21	S	857	0	922	6	0
22	T	686	0	746	15	0
23	U	779	0	834	18	0
24	V	753	0	780	12	0
25	W	581	0	599	4	0
26	X	625	0	655	21	0
27	Y	509	0	543	11	0
28	Z	449	0	491	6	0
All	All	76537	0	50931	776	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 776 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)
8:D:33:ARG:HH21	8:D:51:THR:CG2	1.08	1.67
4:3:22:LYS:CE	4:3:46:LYS:HZ1	1.30	1.43
11:G:84:LYS:NZ	11:G:144:ALA:HB2	1.31	1.43
10:F:64:PRO:HB2	10:F:86:CYS:SG	1.59	1.42
4:3:22:LYS:CE	4:3:46:LYS:NZ	1.82	1.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
2	1	46/55 (84%)	44 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
4	3	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
7	C	269/273 (98%)	245 (91%)	23 (9%)	1 (0%)	30	65
8	D	207/209 (99%)	189 (91%)	17 (8%)	1 (0%)	24	60
9	E	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
10	F	175/179 (98%)	156 (89%)	18 (10%)	1 (1%)	21	57
11	G	171/177 (97%)	154 (90%)	16 (9%)	1 (1%)	21	57
12	H	30/149 (20%)	21 (70%)	9 (30%)	0	100	100
13	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
14	K	120/123 (98%)	107 (89%)	13 (11%)	0	100	100
15	L	141/144 (98%)	118 (84%)	20 (14%)	3 (2%)	5	32
16	N	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
17	O	114/117 (97%)	106 (93%)	8 (7%)	0	100	100
18	P	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
19	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
20	R	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
21	S	108/110 (98%)	102 (94%)	5 (5%)	1 (1%)	14	48
22	T	85/100 (85%)	73 (86%)	12 (14%)	0	100	100
23	U	100/104 (96%)	87 (87%)	13 (13%)	0	100	100
24	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
25	W	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
26	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
27	Y	61/63 (97%)	54 (88%)	6 (10%)	1 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
All	All	2853/3093 (92%)	2610 (92%)	234 (8%)	9 (0%)	37	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	F	175	PRO
15	L	89	VAL
21	S	66	ILE
27	Y	46	VAL
7	C	194	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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	44/49 (90%)	43 (98%)	1 (2%)	44	64
3	2	38/38 (100%)	37 (97%)	1 (3%)	40	61
4	3	51/52 (98%)	51 (100%)	0	100	100
7	C	216/218 (99%)	214 (99%)	2 (1%)	70	76
8	D	164/164 (100%)	158 (96%)	6 (4%)	30	52
9	E	165/165 (100%)	159 (96%)	6 (4%)	31	53
10	F	148/150 (99%)	141 (95%)	7 (5%)	23	46
11	G	136/138 (99%)	132 (97%)	4 (3%)	37	58
12	H	26/114 (23%)	23 (88%)	3 (12%)	5	22
13	J	116/116 (100%)	113 (97%)	3 (3%)	40	61
14	K	103/104 (99%)	101 (98%)	2 (2%)	50	67
15	L	102/103 (99%)	99 (97%)	3 (3%)	37	58
16	N	100/103 (97%)	98 (98%)	2 (2%)	48	66
17	O	86/87 (99%)	83 (96%)	3 (4%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	P	86/100 (86%)	83 (96%)	3 (4%)	32	54
19	Q	89/90 (99%)	88 (99%)	1 (1%)	65	74
20	R	84/84 (100%)	83 (99%)	1 (1%)	63	73
21	S	93/93 (100%)	89 (96%)	4 (4%)	26	48
22	T	74/84 (88%)	73 (99%)	1 (1%)	59	71
23	U	83/85 (98%)	79 (95%)	4 (5%)	23	46
24	V	78/78 (100%)	76 (97%)	2 (3%)	40	61
25	W	58/63 (92%)	58 (100%)	0	100	100
26	X	67/68 (98%)	67 (100%)	0	100	100
27	Y	55/55 (100%)	52 (94%)	3 (6%)	19	44
28	Z	48/49 (98%)	47 (98%)	1 (2%)	47	65
All	All	2357/2498 (94%)	2294 (97%)	63 (3%)	40	60

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	H	11	ASN
23	U	85	ARG
15	L	89	VAL
23	U	6	ARG
27	Y	9	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
13	J	138	GLN
27	Y	45	GLN
16	N	3	HIS
24	V	5	ASN
14	K	90	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A	2374/2904 (81%)	430 (18%)	7 (0%)
6	B	118/120 (98%)	15 (12%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	2492/3024 (82%)	445 (17%)	7 (0%)

5 of 445 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	10	A
5	A	14	A
5	A	34	U
5	A	35	G
5	A	45	G

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	2211	A
5	A	2304	G
5	A	2425	A
5	A	2326	C
5	A	1378	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 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.

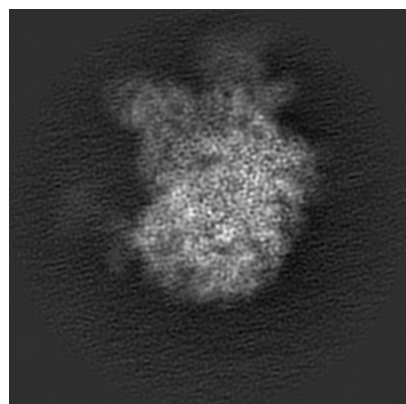
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61605. These allow visual inspection of the internal detail of the map and identification of artifacts.

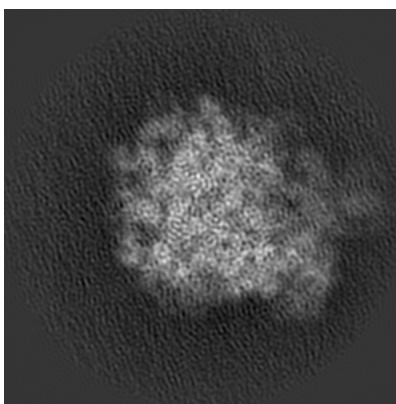
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

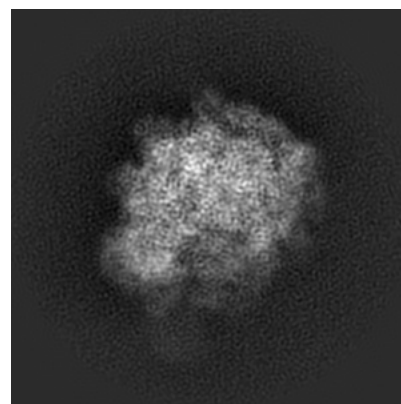
6.1.1 Primary map



X

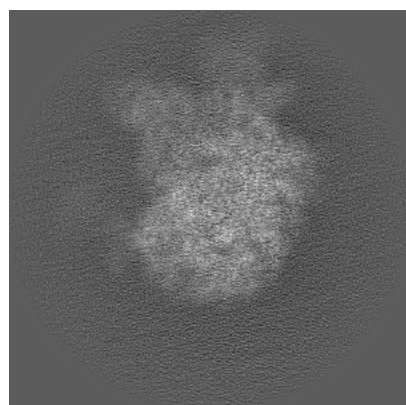


Y

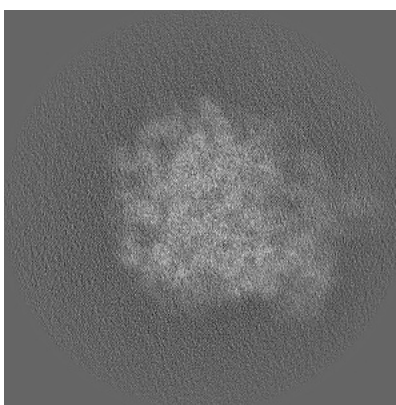


Z

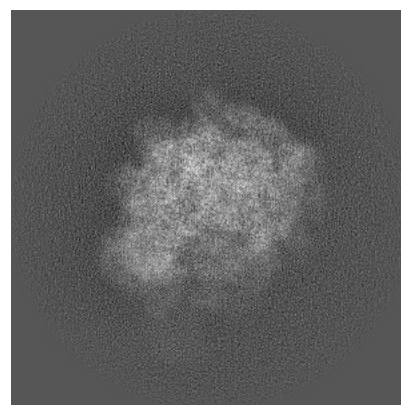
6.1.2 Raw map



X



Y

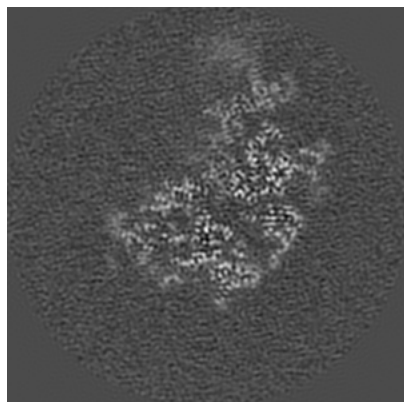


Z

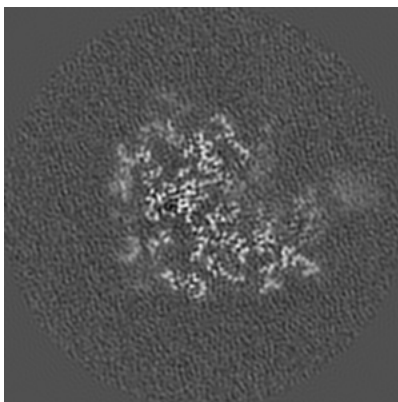
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

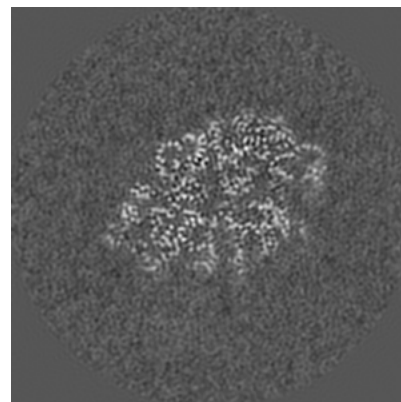
6.2.1 Primary map



X Index: 240

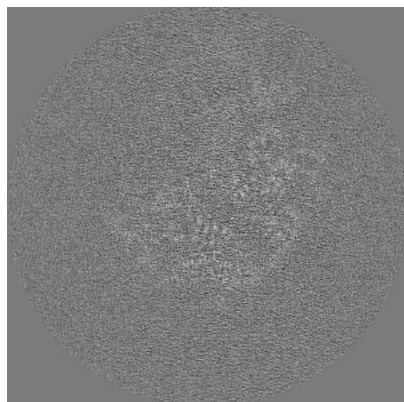


Y Index: 240

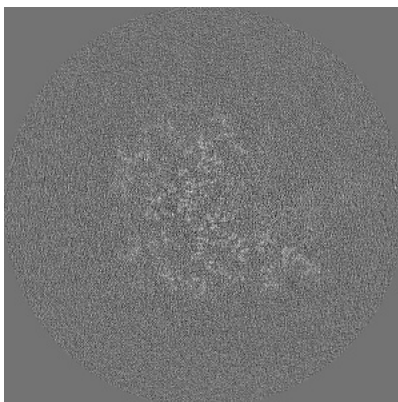


Z Index: 240

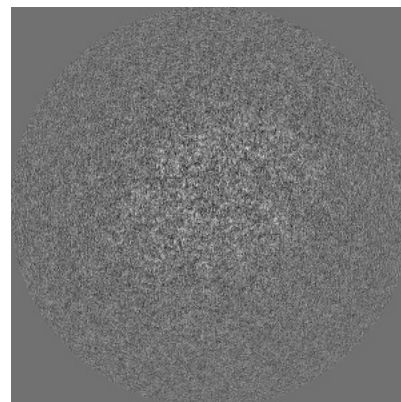
6.2.2 Raw map



X Index: 240



Y Index: 240

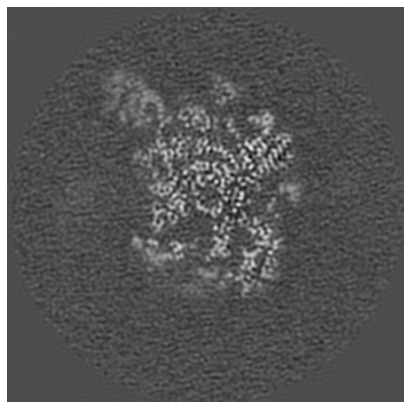


Z Index: 240

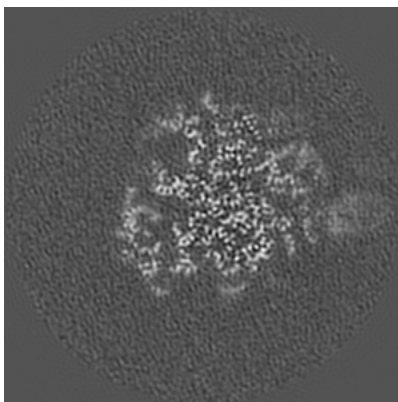
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

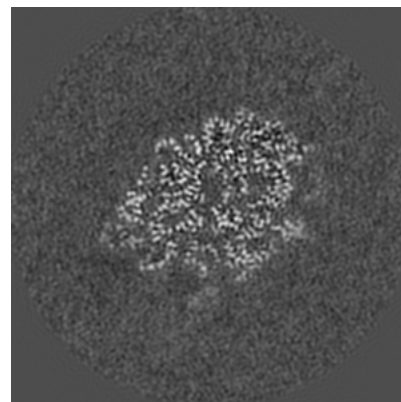
6.3.1 Primary map



X Index: 188

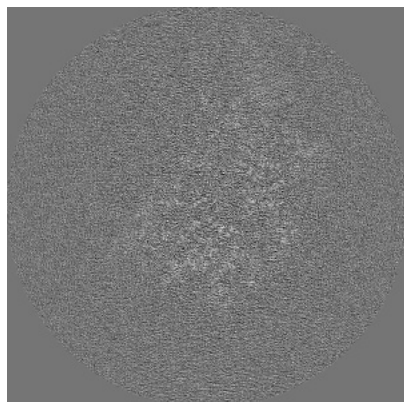


Y Index: 292

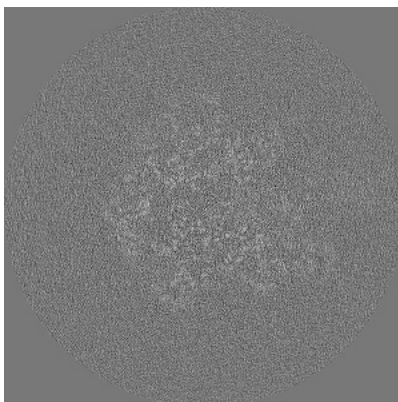


Z Index: 233

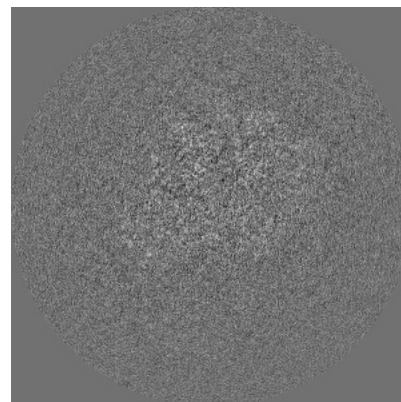
6.3.2 Raw map



X Index: 232



Y Index: 261

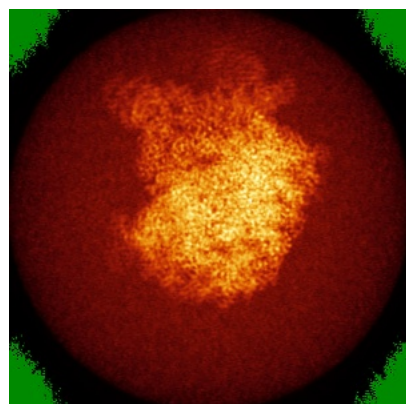


Z Index: 260

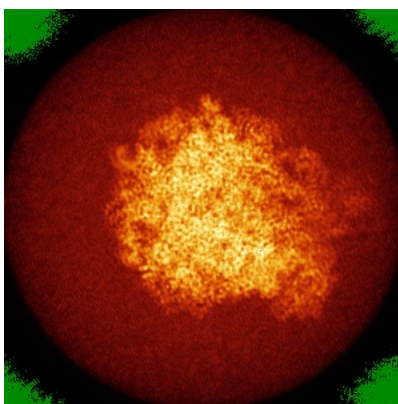
The images above show the largest variance slices of the map in three orthogonal directions.

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

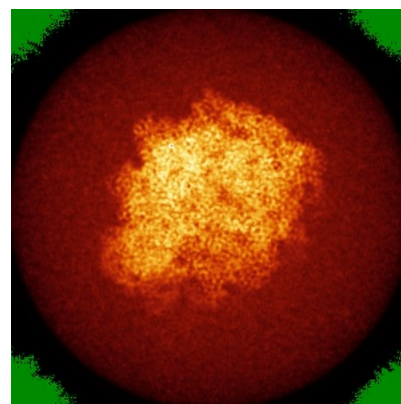
6.4.1 Primary map



X

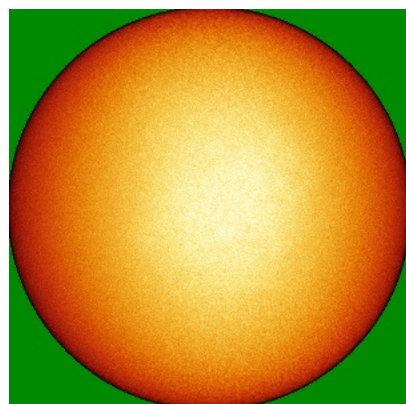


Y

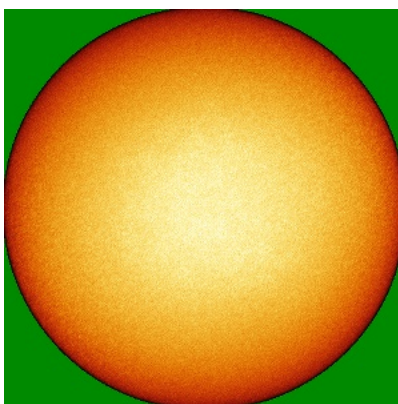


Z

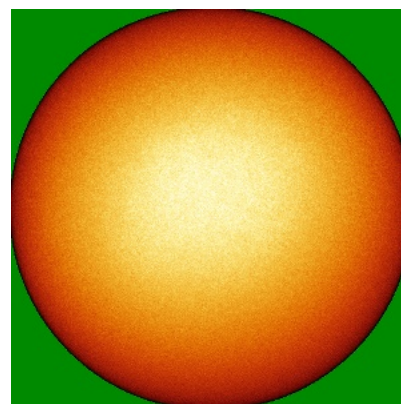
6.4.2 Raw map



X



Y

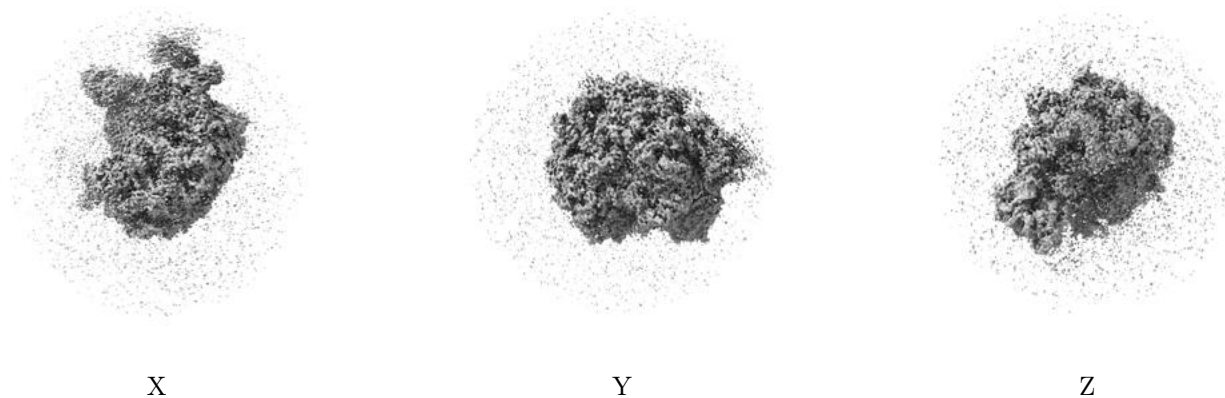


Z

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.

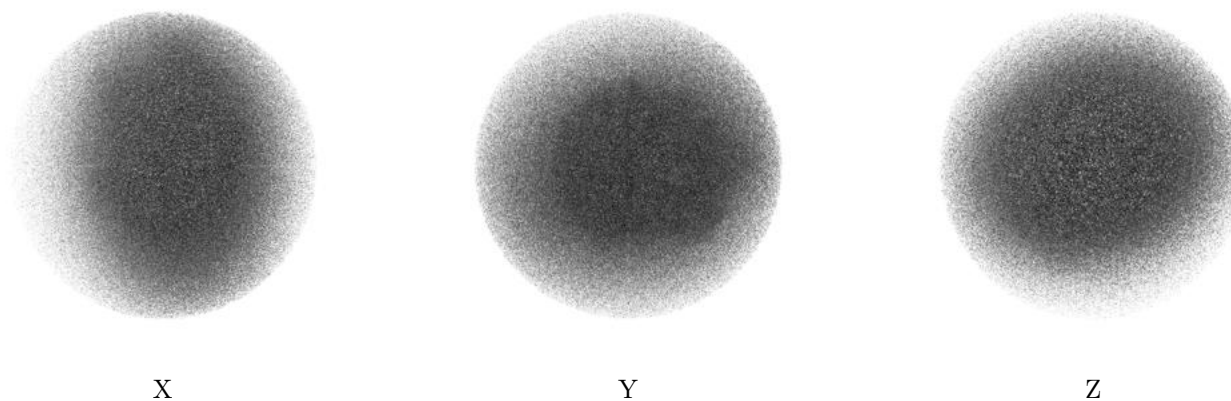
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0033. 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.

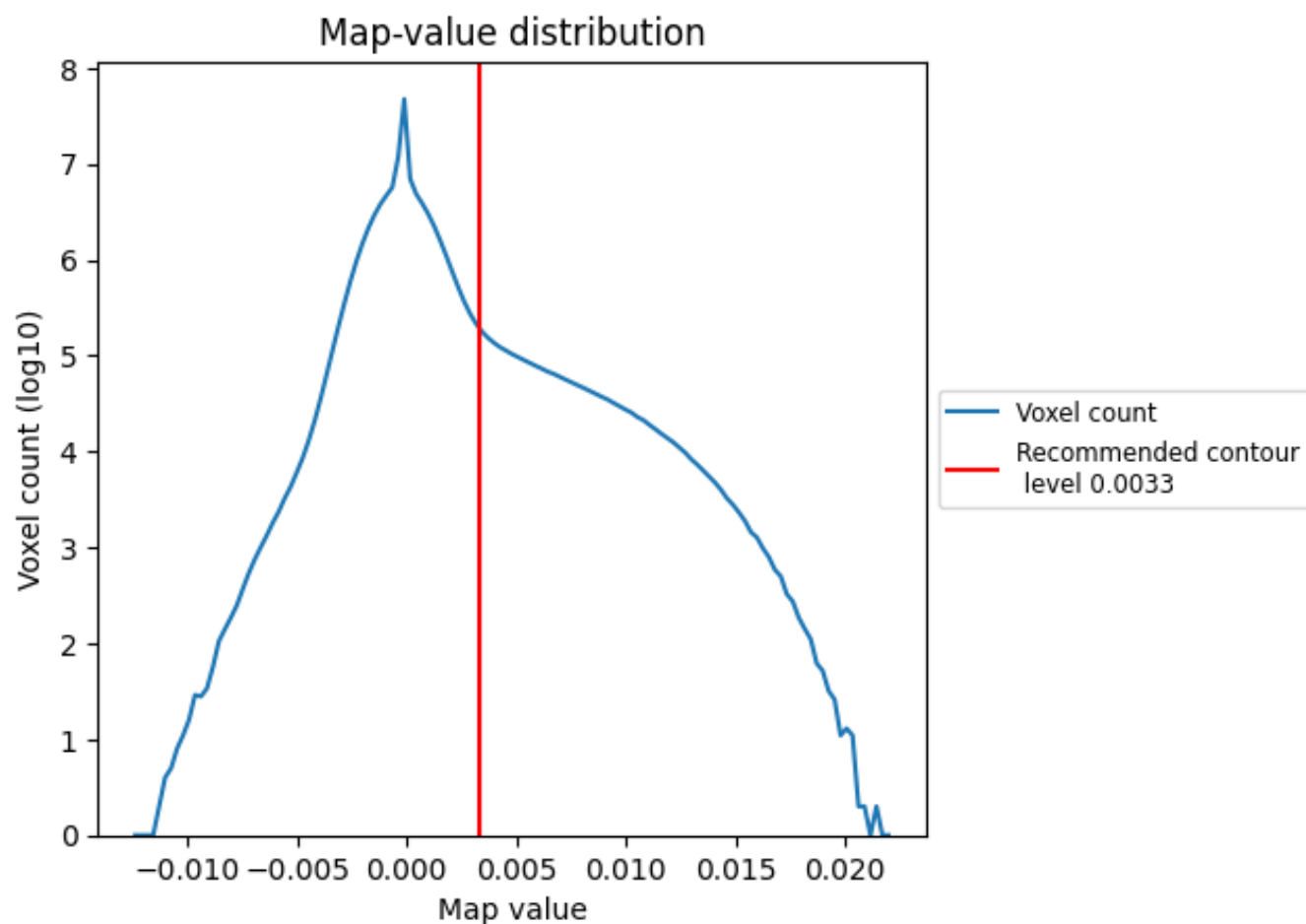
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

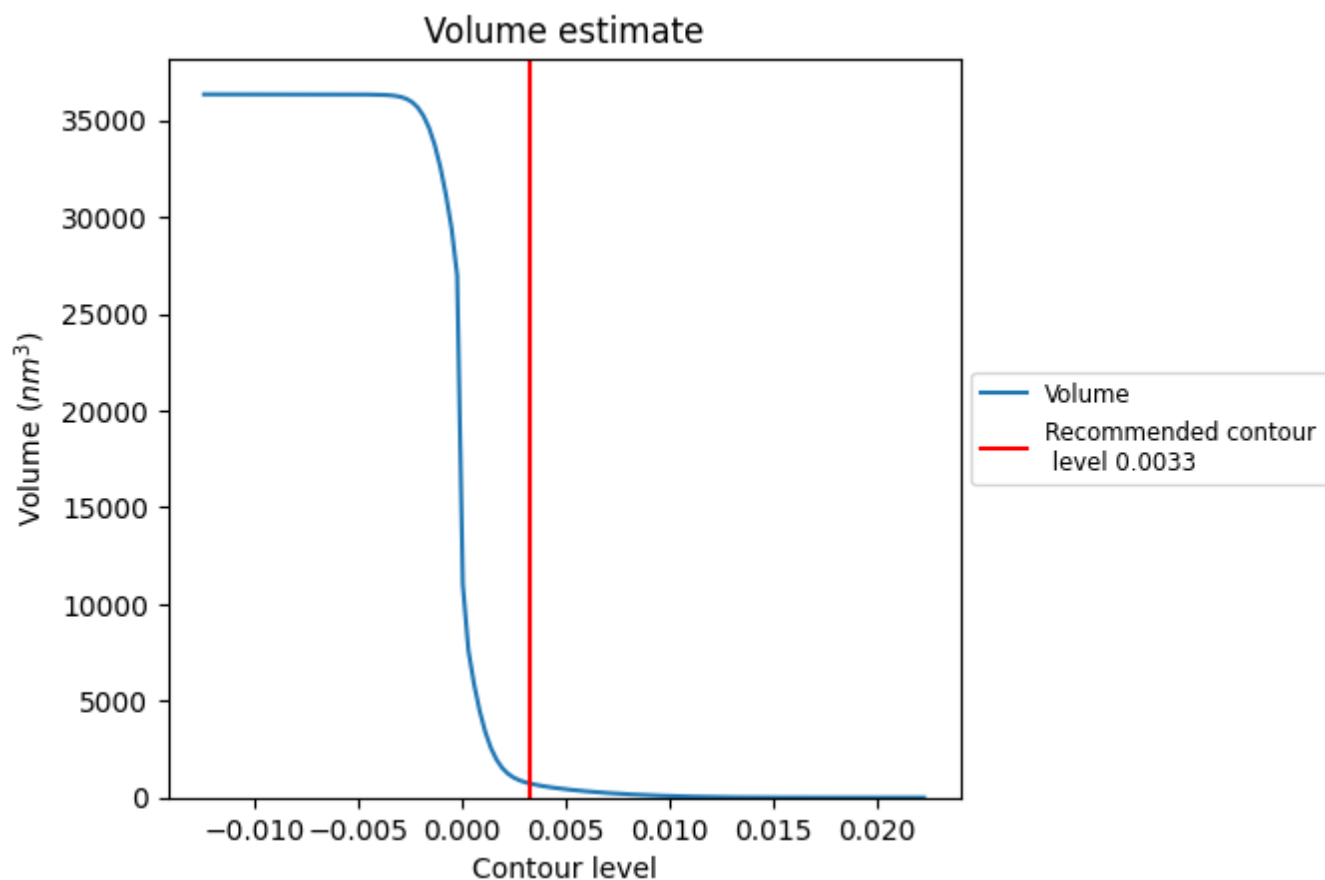
This section contains the results of statistical analysis of the map.

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.

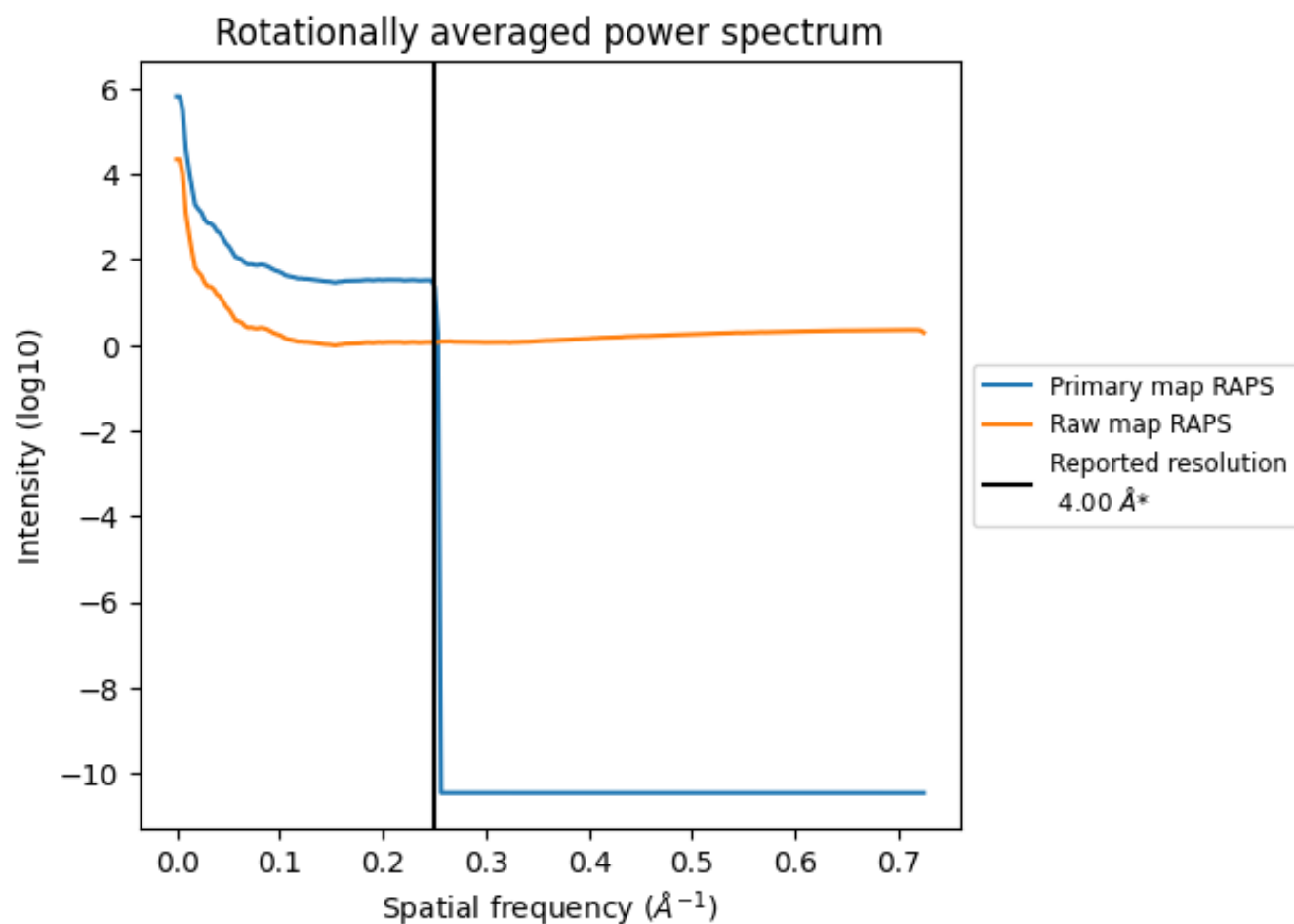
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 723 nm³; this corresponds to an approximate mass of 653 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 ⓘ

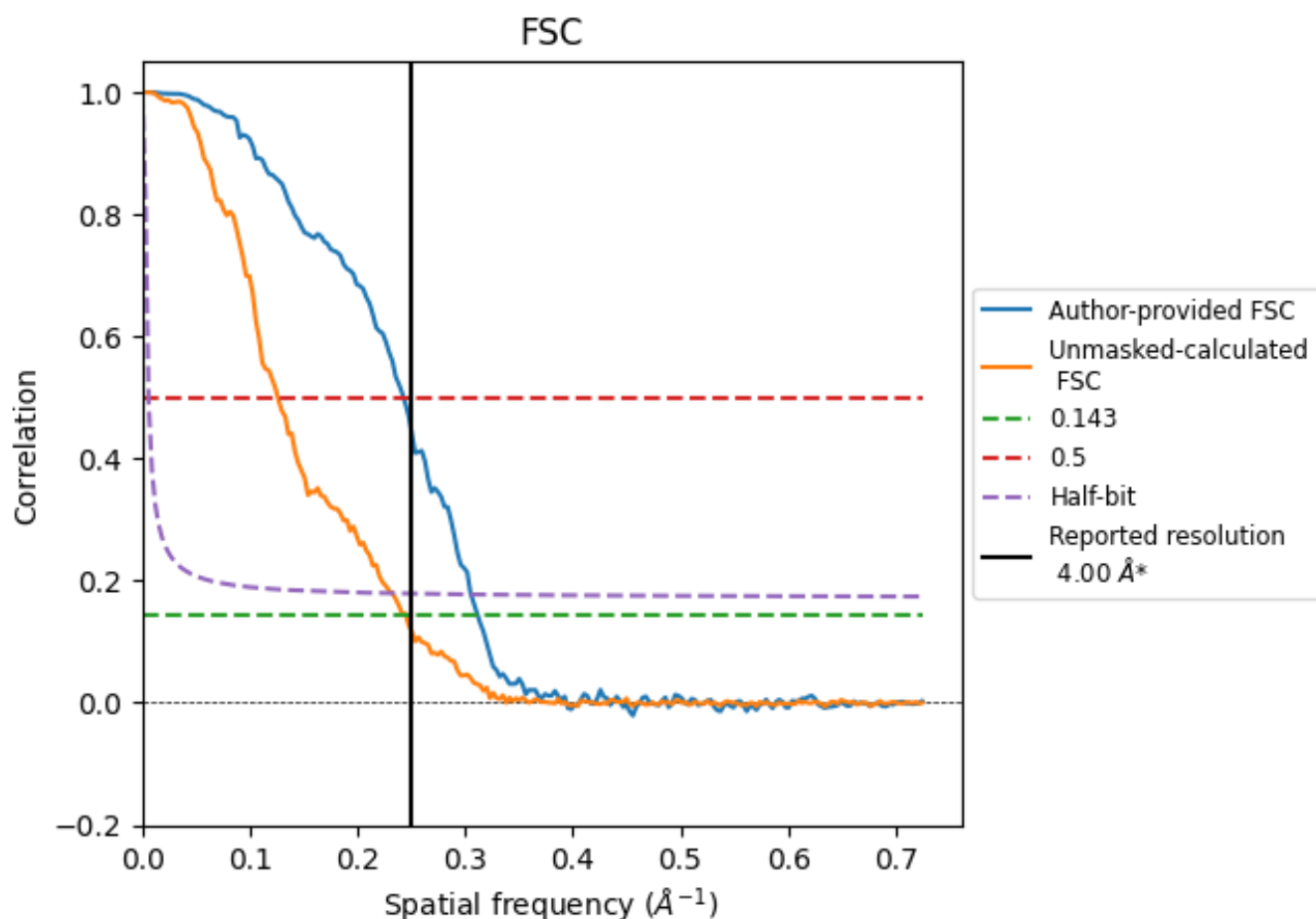


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

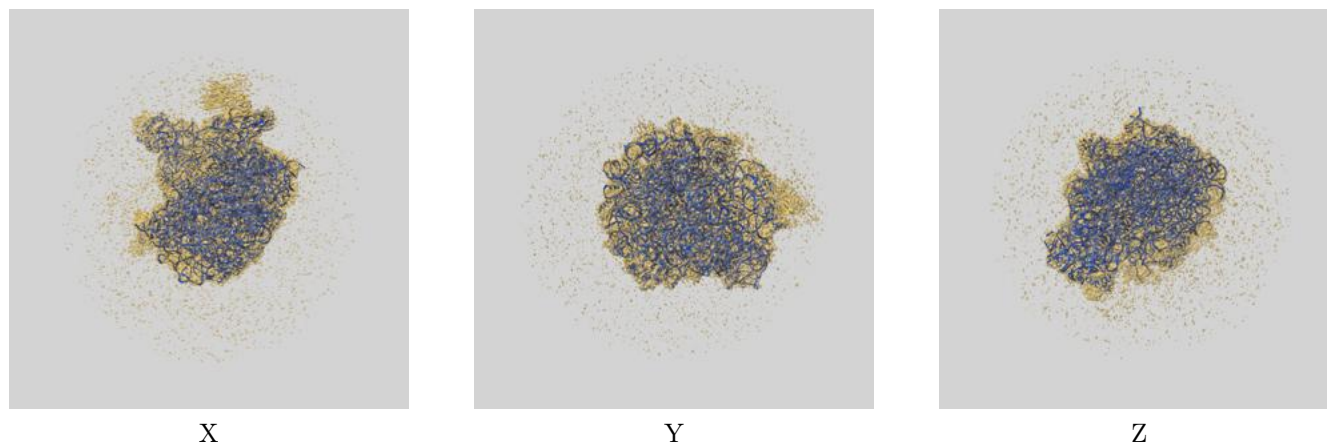
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.21	4.12	3.27
Unmasked-calculated*	4.08	7.94	4.30

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.21 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

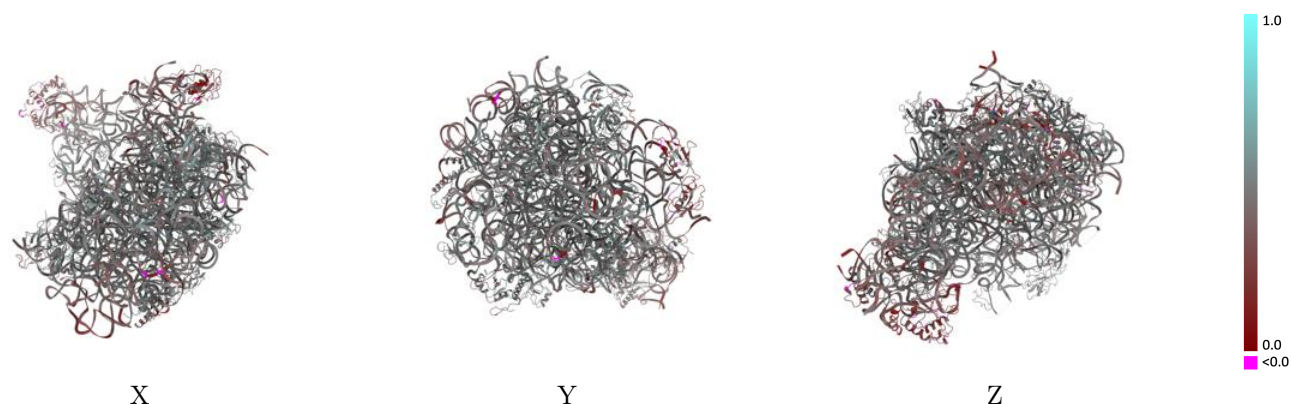
This section contains information regarding the fit between EMDB map EMD-61605 and PDB model 9JMK. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



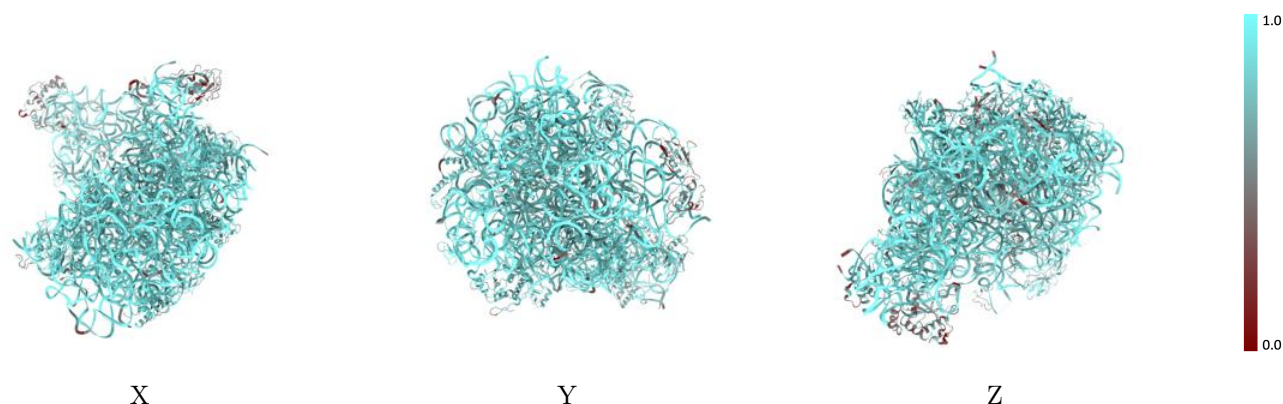
The images above show the 3D surface view of the map at the recommended contour level 0.0033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



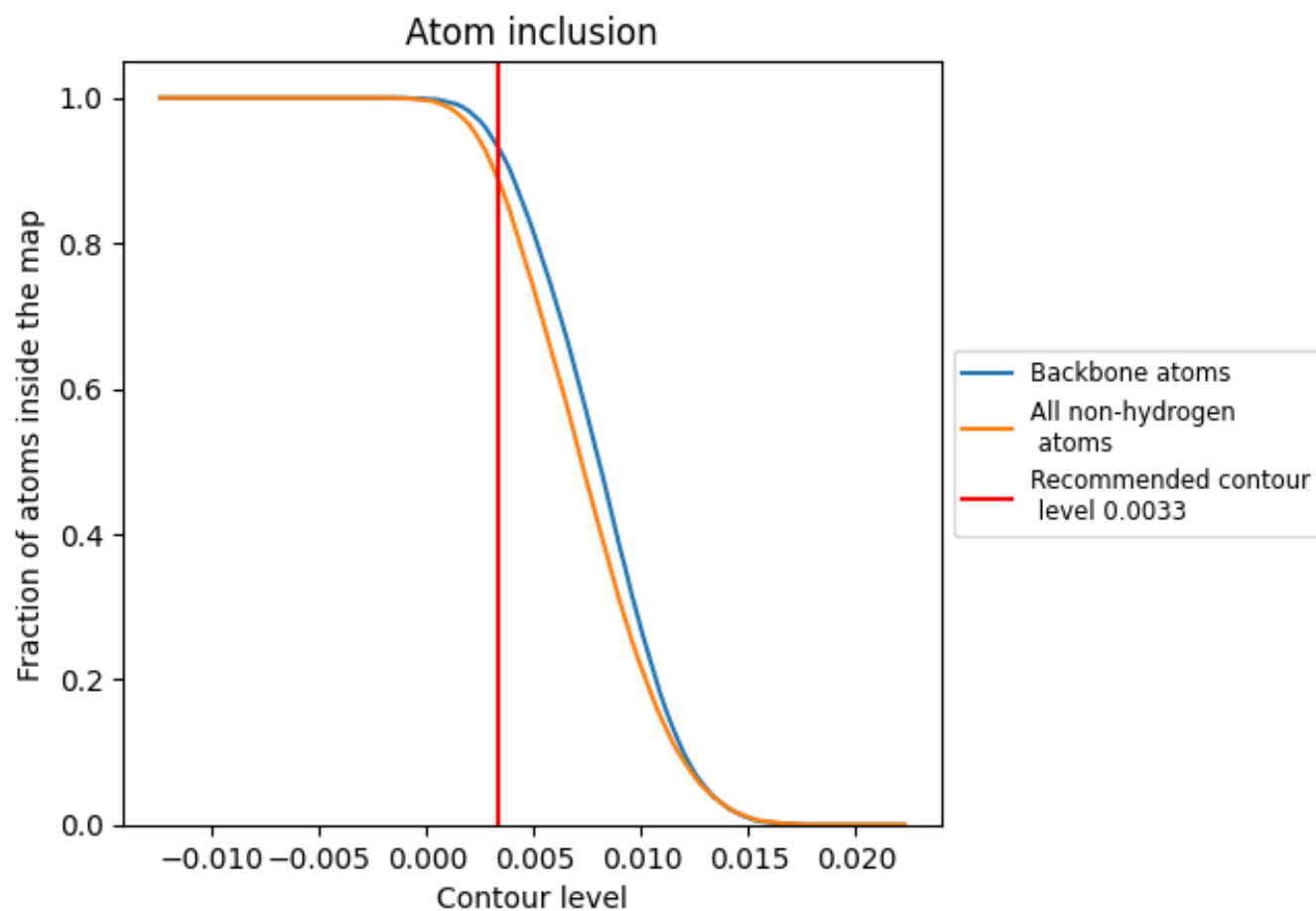
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0033).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 89% 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 (0.0033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.4510
0	 0.8600	 0.4830
1	 0.8760	 0.4920
2	 0.8420	 0.5050
3	 0.8660	 0.5120
A	 0.9310	 0.4520
B	 0.8850	 0.3900
C	 0.7960	 0.4690
D	 0.8510	 0.4900
E	 0.8290	 0.4870
F	 0.5200	 0.2800
G	 0.5240	 0.2900
H	 0.5670	 0.3460
J	 0.8640	 0.5080
K	 0.8000	 0.4580
L	 0.8420	 0.4690
N	 0.8860	 0.5010
O	 0.7550	 0.4030
P	 0.8410	 0.4760
Q	 0.8930	 0.5010
R	 0.8850	 0.5070
S	 0.8290	 0.4970
T	 0.8170	 0.4570
U	 0.8920	 0.4810
V	 0.7260	 0.4220
W	 0.8370	 0.5060
X	 0.8450	 0.4930
Y	 0.8210	 0.4450
Z	 0.8540	 0.4960

