



wwPDB EM Validation Summary Report ⓘ

Jul 2, 2026 – 05:46 PM JST

PDB ID : 9L9J / pdb_0000919j
EMDB ID : EMD-62907
Title : State H of archaeal pre-50S ribosome
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2024-12-30
Resolution : 3.26 Å (reported)

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:

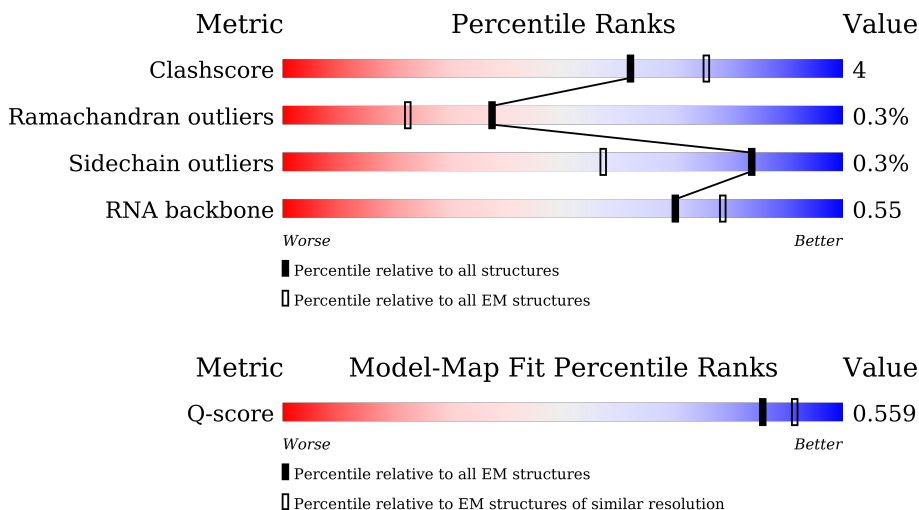
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.26 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	14557 (2.76 - 3.76)

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	2916	
2	1	122	
3	A	50	

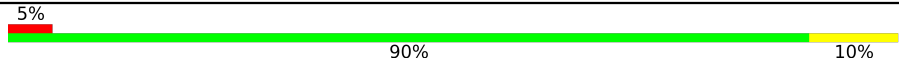



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Mol	Chain	Length	Quality of chain
4	B	221	57% 80% 20%
5	E	120	78% 22%
6	F	176	80% 14% 7%
7	G	196	80% 16% ...
8	H	116	91% 9%
9	I	184	83% 17%
10	J	151	82% 15% ..
11	K	96	85% 14%
12	L	153	86% 12%
13	M	67	78% 9% 13%
14	N	118	82% 14%
15	O	154	85% 15%
16	P	92	79% 17%
17	Q	234	52% 9% 39%
18	R	89	75% 15% 10%
19	S	58	93% 5%
20	T	93	80% 20%
21	U	241	80% 14% 5%
22	V	338	88% 10% ..
23	W	248	86% 14%
24	X	172	6% 73% 25%
25	Y	178	87% 11%
26	b	145	79% 20%
27	c	83	90% 10%
28	d	70	6% 84% 13%

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Mol	Chain	Length	Quality of chain
29	e	58	 <p>5% 90% 10%</p>
30	f	132	 <p>81% 18%</p>
31	i	168	 <p>74% 14% 11%</p>
32	j	48	 <p>10% 75% 12% 12%</p>

2 Entry composition [i](#)

There are 34 unique types of molecules in this entry. The entry contains 90337 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 RNA chain called 23S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	2624	56266	25113	10375	18154	2624	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	120	2551	1138	453	840	120	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	49	414	252	89	71	2	0	0

- Molecule 4 is a protein called Translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	220	1562	968	259	332	3	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	119	880	546	141	192	1	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	164	1304	814	237	245	8	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	192	1564	955	333	274	2	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	H	115	887	544	167	176	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	183	1417	880	258	278	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	147	1179	712	243	223	1	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	95	736	451	150	133	2	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	151	1174	730	214	226	4	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	58	466	287	83	94	2	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	114	Total	C	N	O	0	0
			903	545	171	187		

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	154	Total	C	N	O	S	0	0
			1200	731	220	245	4		

- Molecule 16 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	89	Total	C	N	O	S	0	0
			722	446	138	137	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	142	Total	C	N	O	S	0	0
			1128	689	228	210	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	80	Total	C	N	O	S	0	0
			617	374	125	117	1		

- Molecule 19 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	57	Total	C	N	O	S	0	0
			439	265	90	80	4		

- Molecule 20 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			746	457	152	129	8		

- Molecule 21 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	230	Total	C	N	O	S	0	0
			1717	1062	337	313	5		

- Molecule 22 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	337	Total	C	N	O	S	0	0
			2619	1623	484	502	10		

- Molecule 23 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	248	Total	C	N	O	S	0	0
			1898	1164	354	377	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	169	Total	C	N	O	S	0	0
			1206	742	222	239	3		

- Molecule 25 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	174	Total	C	N	O	S	0	0
			1346	832	228	283	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	143	Total	C	N	O	S	0	0
			1121	698	200	218	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	83	Total	C	N	O	S	0	0
			651	404	113	130	4		

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	68	Total	C	N	O	S	0	0
			519	319	88	111	1		

- Molecule 29 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	58	Total	C	N	O	S	0	0
			439	272	77	89	1		

- Molecule 30 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	132	Total	C	N	O	S	0	0
			981	604	188	185	4		

- Molecule 31 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	i	150	Total	C	N	O	0	0
			1138	683	227	228		

- Molecule 32 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	42	Total	C	N	O	S	0	0
			342	206	77	54	5		

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
33	0	187	Total	Mg	0
			187	187	
33	1	3	Total	Mg	0
			3	3	
33	G	1	Total	Mg	0
			1	1	
33	I	2	Total	Mg	0
			2	2	
33	O	2	Total	Mg	0
			2	2	
33	T	1	Total	Mg	0
			1	1	

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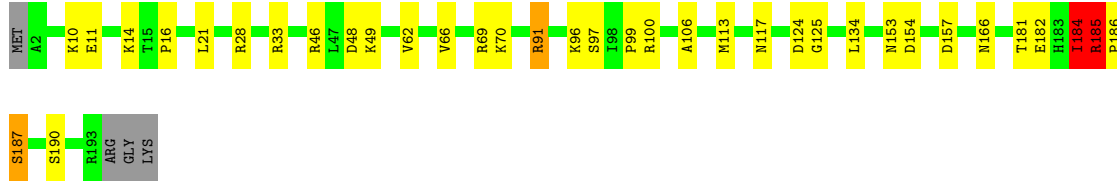
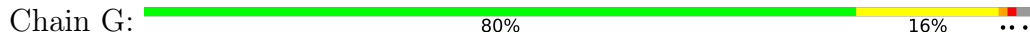
Mol	Chain	Residues	Atoms		AltConf
33	U	1	Total 1	Mg 1	0
33	W	1	Total 1	Mg 1	0
33	b	1	Total 1	Mg 1	0
33	f	2	Total 2	Mg 2	0
33	i	2	Total 2	Mg 2	0

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

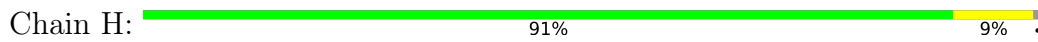
Mol	Chain	Residues	Atoms		AltConf
34	S	1	Total 1	Zn 1	0
34	T	1	Total 1	Zn 1	0

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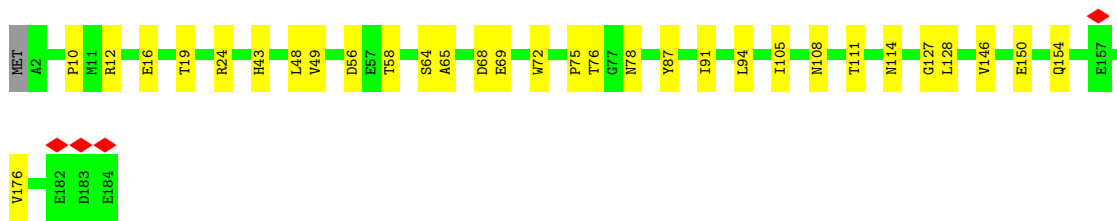
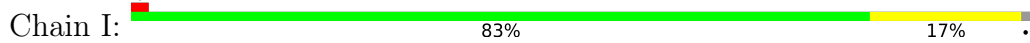
- Molecule 7: Large ribosomal subunit protein eL15



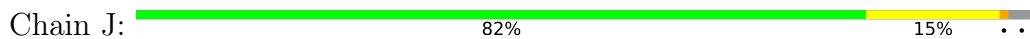
- Molecule 8: Large ribosomal subunit protein eL18



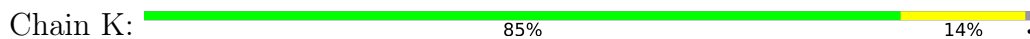
- Molecule 9: Large ribosomal subunit protein uL18



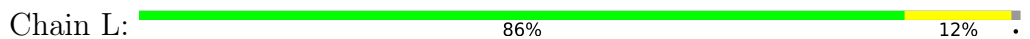
- Molecule 10: Large ribosomal subunit protein eL19



- Molecule 11: Large ribosomal subunit protein eL21

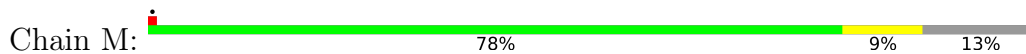


- Molecule 12: Large ribosomal subunit protein uL22

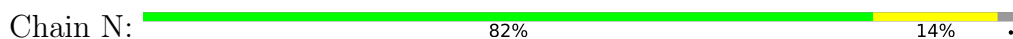




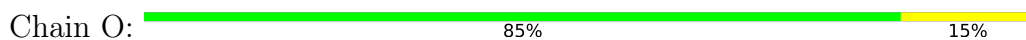
- Molecule 13: Large ribosomal subunit protein eL24



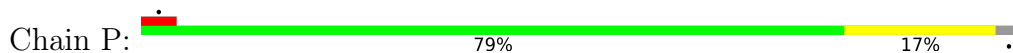
- Molecule 14: Large ribosomal subunit protein uL24



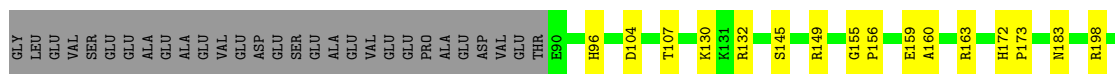
- Molecule 15: Large ribosomal subunit protein uL30



- Molecule 16: Large ribosomal subunit protein eL31

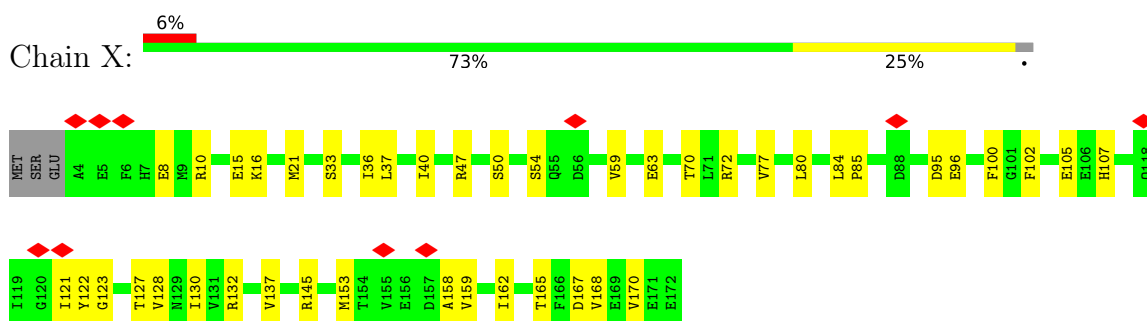


- Molecule 17: Large ribosomal subunit protein eL32

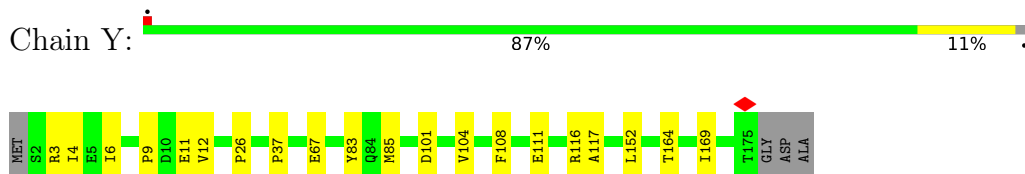


- Molecule 18: Large ribosomal subunit protein eL43

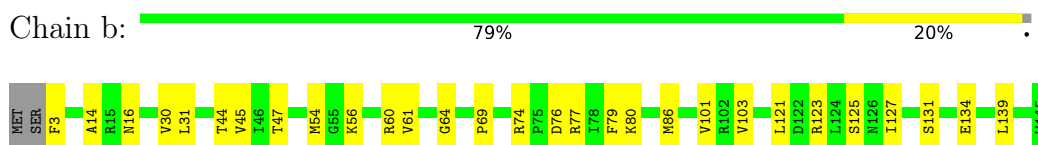




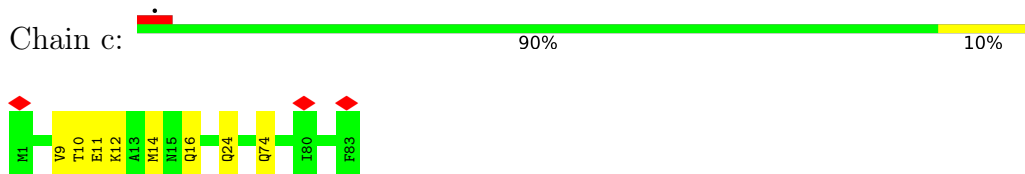
- Molecule 25: Large ribosomal subunit protein uL6



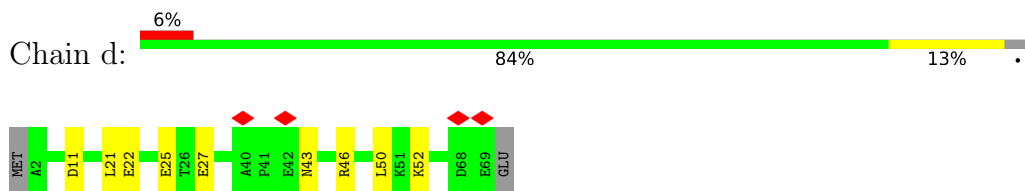
- Molecule 26: Large ribosomal subunit protein uL13



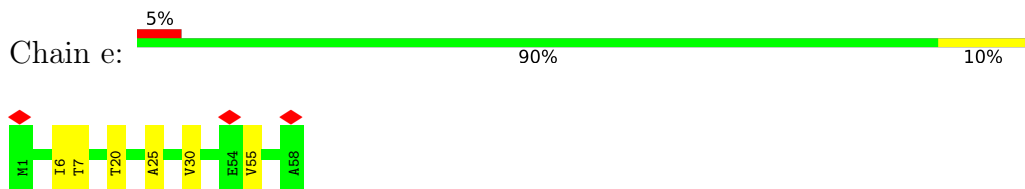
- Molecule 27: Large ribosomal subunit protein uL23



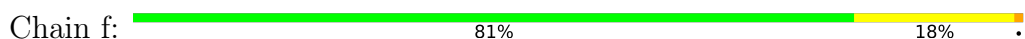
- Molecule 28: Large ribosomal subunit protein uL29

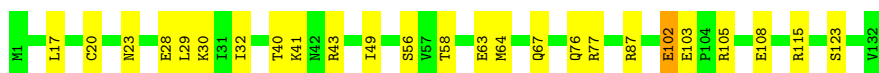


- Molecule 29: Large ribosomal subunit protein eL20

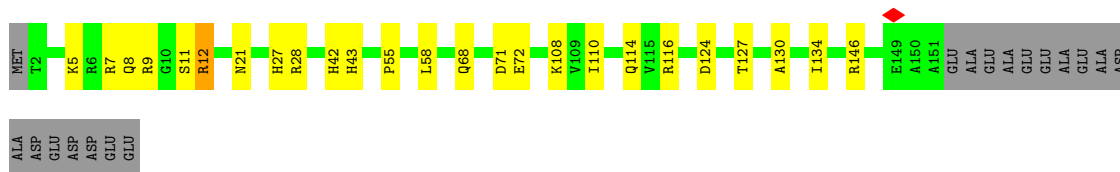


- Molecule 30: Large ribosomal subunit protein uL14

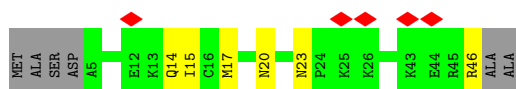
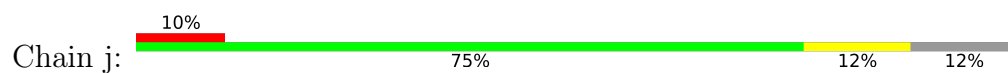




- Molecule 31: Large ribosomal subunit protein uL15



- Molecule 32: Large ribosomal subunit protein eL40



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	918876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.473	Depositor
Minimum map value	-2.204	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.668, 0.668, 0.668	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.16	0/63006	0.28	0/98265
2	1	0.13	0/2848	0.27	0/4436
3	A	0.16	0/419	0.29	0/553
4	B	0.11	0/1581	0.32	0/2165
5	E	0.16	0/889	0.33	0/1209
6	F	0.17	0/1326	0.33	0/1780
7	G	0.36	1/1591 (0.1%)	0.46	3/2126 (0.1%)
8	H	0.16	0/895	0.32	0/1210
9	I	0.14	0/1447	0.30	0/1969
10	J	0.17	0/1191	0.35	0/1587
11	K	0.17	0/750	0.29	0/1001
12	L	0.17	0/1199	0.34	0/1619
13	M	0.16	0/474	0.33	0/634
14	N	0.16	0/911	0.34	0/1232
15	O	0.17	0/1218	0.36	0/1651
16	P	0.15	0/737	0.31	0/993
17	Q	0.17	0/1147	0.29	0/1539
18	R	0.16	0/624	0.33	0/835
19	S	0.18	0/446	0.31	0/586
20	T	0.17	0/764	0.32	0/1015
21	U	0.18	0/1751	0.36	0/2358
22	V	0.40	2/2677 (0.1%)	0.58	8/3617 (0.2%)
23	W	0.16	0/1925	0.33	0/2598
24	X	0.14	0/1223	0.41	0/1659
25	Y	0.14	0/1368	0.32	0/1859
26	b	0.17	0/1138	0.33	0/1533
27	c	0.14	0/657	0.29	0/881
28	d	0.12	0/522	0.29	0/704
29	e	0.12	0/445	0.24	0/599
30	f	0.16	0/989	0.39	2/1329 (0.2%)
31	i	0.17	0/1153	0.34	0/1546
32	j	0.10	0/345	0.25	0/453

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.17	3/97656 (0.0%)	0.31	13/145541 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	V	16	PRO	CA-CB	-6.42	1.44	1.53
22	V	245	PRO	CA-CB	-6.17	1.45	1.53
7	G	187	SER	CA-CB	-5.56	1.44	1.53

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	245	PRO	N-CA-C	-11.00	89.81	112.47
22	V	244	ASN	CA-C-N	10.32	132.75	119.84
22	V	244	ASN	C-N-CA	10.32	132.75	119.84
22	V	244	ASN	C-N-CD	-9.05	87.88	125.00
7	G	184	ILE	CB-CA-C	-6.52	100.60	111.29

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	0	56266	0	28377	278	0
2	1	2551	0	1298	16	0
3	A	414	0	442	4	0
4	B	1562	0	1484	27	0
5	E	880	0	852	15	0
6	F	1304	0	1306	18	0
7	G	1564	0	1590	25	0
8	H	887	0	907	6	0
9	I	1417	0	1365	17	0
10	J	1179	0	1183	17	0
11	K	736	0	745	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1174	0	1146	15	0
13	M	466	0	443	4	0
14	N	903	0	886	11	0
15	O	1200	0	1159	16	0
16	P	722	0	699	11	0
17	Q	1128	0	1123	15	0
18	R	617	0	618	8	0
19	S	439	0	445	2	0
20	T	746	0	736	11	0
21	U	1717	0	1741	26	0
22	V	2619	0	2572	33	0
23	W	1898	0	1895	21	0
24	X	1206	0	1112	31	0
25	Y	1346	0	1292	10	0
26	b	1121	0	1113	22	0
27	c	651	0	656	5	0
28	d	519	0	519	6	0
29	e	439	0	434	3	0
30	f	981	0	1027	19	0
31	i	1138	0	1091	17	0
32	j	342	0	370	5	0
33	0	187	0	0	0	0
33	1	3	0	0	0	0
33	G	1	0	0	0	0
33	I	2	0	0	0	0
33	O	2	0	0	0	0
33	T	1	0	0	0	0
33	U	1	0	0	0	0
33	W	1	0	0	0	0
33	b	1	0	0	0	0
33	f	2	0	0	0	0
33	i	2	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
All	All	90337	0	60626	634	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 4.

The worst 5 of 634 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)
1:0:319:G:N2	1:0:342:A:H61	1.57	1.03
1:0:319:G:H21	1:0:342:A:N6	1.62	0.97
22:V:15:SER:HB3	22:V:16:PRO:HD2	1.56	0.88
1:0:1514:U:N3	1:0:1662:A:N6	2.25	0.84
1:0:319:G:H21	1:0:342:A:H61	0.83	0.82

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	
3	A	47/50 (94%)	42 (89%)	5 (11%)	0	100	100
4	B	218/221 (99%)	204 (94%)	14 (6%)	0	100	100
5	E	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
6	F	160/176 (91%)	157 (98%)	3 (2%)	0	100	100
7	G	190/196 (97%)	176 (93%)	13 (7%)	1 (0%)	24	55
8	H	113/116 (97%)	110 (97%)	3 (3%)	0	100	100
9	I	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
10	J	145/151 (96%)	138 (95%)	6 (4%)	1 (1%)	18	48
11	K	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
12	L	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
13	M	56/67 (84%)	52 (93%)	4 (7%)	0	100	100
14	N	112/118 (95%)	103 (92%)	9 (8%)	0	100	100
15	O	152/154 (99%)	147 (97%)	5 (3%)	0	100	100
16	P	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
17	Q	140/234 (60%)	137 (98%)	3 (2%)	0	100	100
18	R	78/89 (88%)	74 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
20	T	91/93 (98%)	91 (100%)	0	0	100	100
21	U	228/241 (95%)	211 (92%)	15 (7%)	2 (1%)	14	42
22	V	335/338 (99%)	318 (95%)	12 (4%)	5 (2%)	8	32
23	W	246/248 (99%)	240 (98%)	6 (2%)	0	100	100
24	X	167/172 (97%)	155 (93%)	12 (7%)	0	100	100
25	Y	172/178 (97%)	163 (95%)	9 (5%)	0	100	100
26	b	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
27	c	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
28	d	66/70 (94%)	66 (100%)	0	0	100	100
29	e	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	f	130/132 (98%)	122 (94%)	8 (6%)	0	100	100
31	i	148/168 (88%)	144 (97%)	3 (2%)	1 (1%)	18	48
32	j	40/48 (83%)	36 (90%)	4 (10%)	0	100	100
All	All	3994/4249 (94%)	3823 (96%)	161 (4%)	10 (0%)	37	66

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	U	170	VAL
22	V	16	PRO
22	V	245	PRO
22	V	15	SER
31	i	12	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	45/46 (98%)	45 (100%)	0	100	100
4	B	158/171 (92%)	158 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	93/94 (99%)	93 (100%)	0	100	100
6	F	139/147 (95%)	139 (100%)	0	100	100
7	G	160/163 (98%)	157 (98%)	3 (2%)	50	67
8	H	98/99 (99%)	98 (100%)	0	100	100
9	I	144/145 (99%)	142 (99%)	2 (1%)	59	72
10	J	117/121 (97%)	117 (100%)	0	100	100
11	K	77/78 (99%)	77 (100%)	0	100	100
12	L	122/124 (98%)	122 (100%)	0	100	100
13	M	48/55 (87%)	48 (100%)	0	100	100
14	N	98/102 (96%)	98 (100%)	0	100	100
15	O	132/132 (100%)	132 (100%)	0	100	100
16	P	77/80 (96%)	77 (100%)	0	100	100
17	Q	116/191 (61%)	116 (100%)	0	100	100
18	R	61/68 (90%)	61 (100%)	0	100	100
19	S	48/49 (98%)	48 (100%)	0	100	100
20	T	77/77 (100%)	77 (100%)	0	100	100
21	U	177/186 (95%)	177 (100%)	0	100	100
22	V	277/278 (100%)	274 (99%)	3 (1%)	65	75
23	W	198/198 (100%)	197 (100%)	1 (0%)	81	82
24	X	116/147 (79%)	116 (100%)	0	100	100
25	Y	149/151 (99%)	147 (99%)	2 (1%)	61	73
26	b	121/123 (98%)	121 (100%)	0	100	100
27	c	74/76 (97%)	74 (100%)	0	100	100
28	d	54/56 (96%)	54 (100%)	0	100	100
29	e	48/49 (98%)	48 (100%)	0	100	100
30	f	102/106 (96%)	102 (100%)	0	100	100
31	i	110/123 (89%)	110 (100%)	0	100	100
32	j	36/40 (90%)	36 (100%)	0	100	100
All	All	3272/3475 (94%)	3261 (100%)	11 (0%)	84	86

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	V	245	PRO
23	W	67	MET
25	Y	101	ASP
25	Y	85	MET
9	I	154	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
25	Y	151	GLN
31	i	8	GLN
32	j	29	GLN
31	i	19	HIS
17	Q	113	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2619/2916 (89%)	392 (14%)	13 (0%)
2	1	119/122 (97%)	21 (17%)	0
All	All	2738/3038 (90%)	413 (15%)	13 (0%)

5 of 413 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	15	A
1	0	18	G
1	0	38	C
1	0	49	C
1	0	66	A

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1375	A
1	0	1499	A
1	0	2534	U
1	0	1659	A
1	0	2337	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](#)

Of 205 ligands modelled in this entry, 205 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

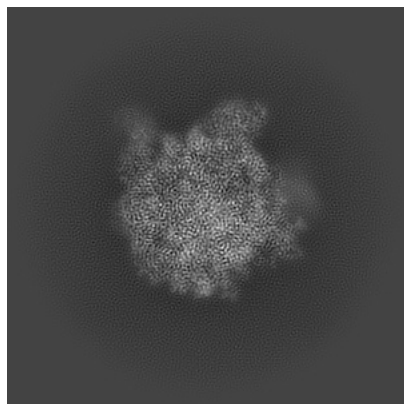
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62907. These allow visual inspection of the internal detail of the map and identification of artifacts.

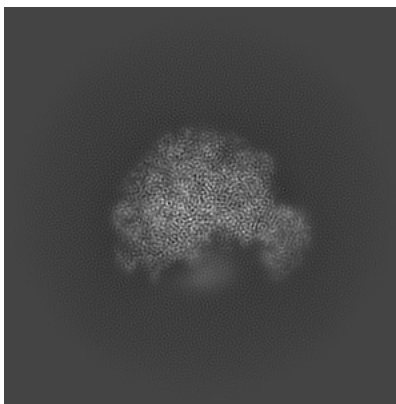
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

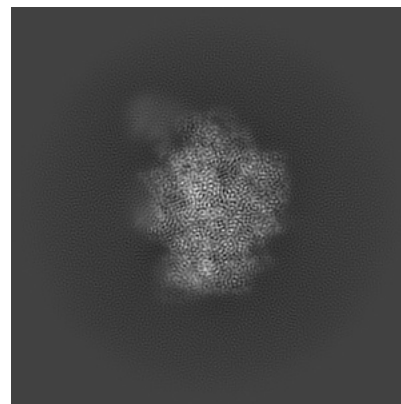
6.1.1 Primary map



X

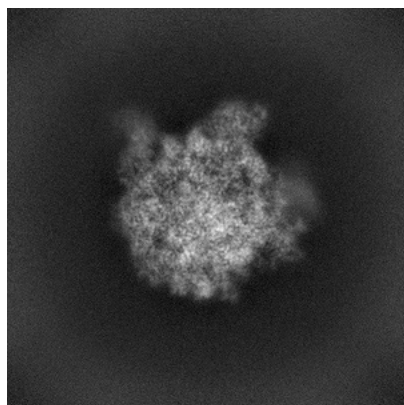


Y

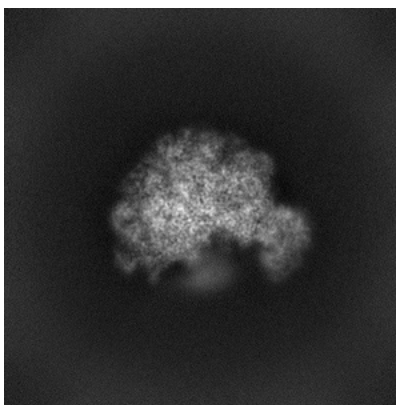


Z

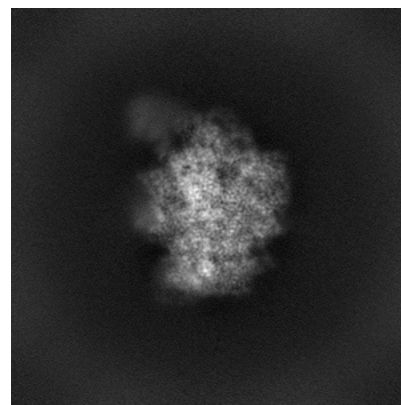
6.1.2 Raw map



X



Y

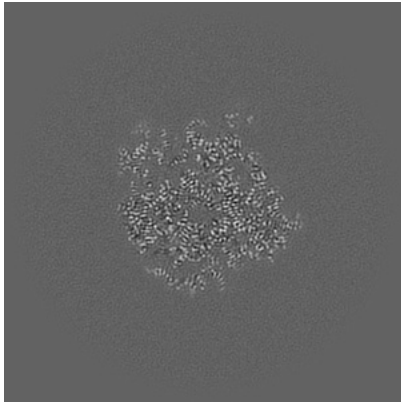


Z

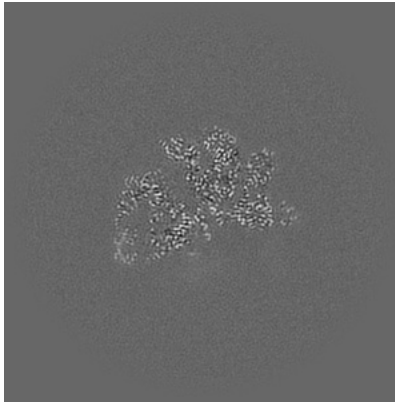
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

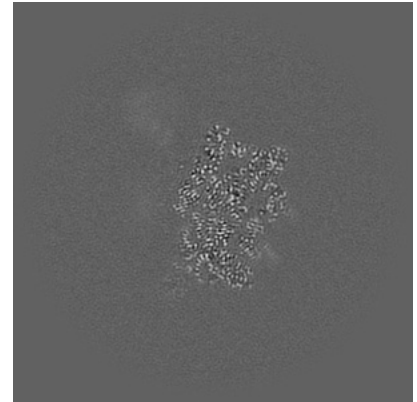
6.2.1 Primary map



X Index: 320

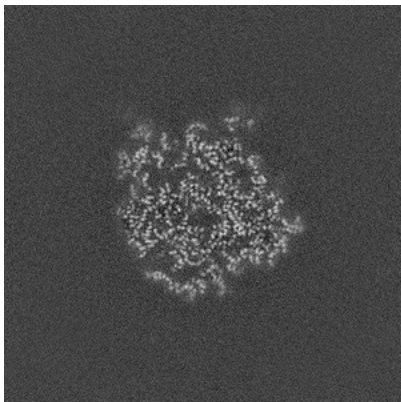


Y Index: 320

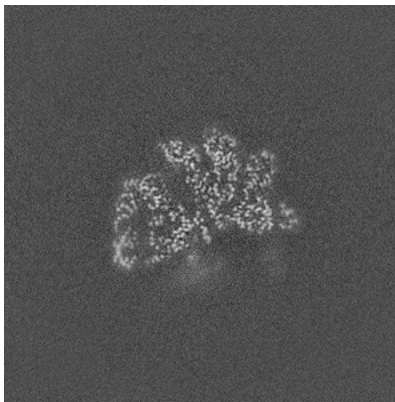


Z Index: 320

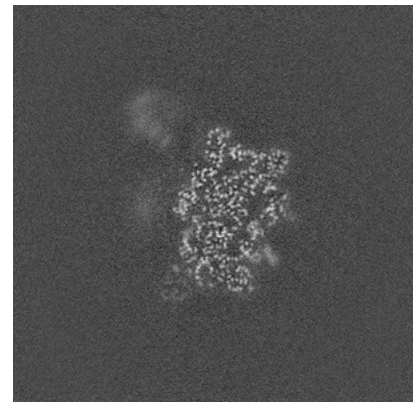
6.2.2 Raw map



X Index: 320



Y Index: 320

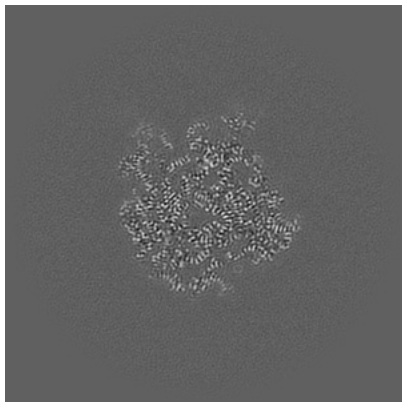


Z Index: 320

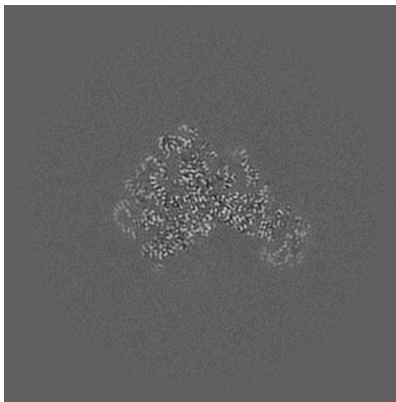
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

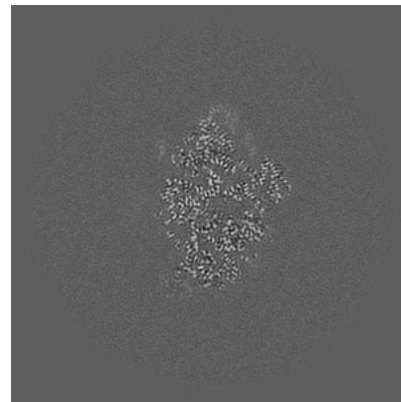
6.3.1 Primary map



X Index: 316

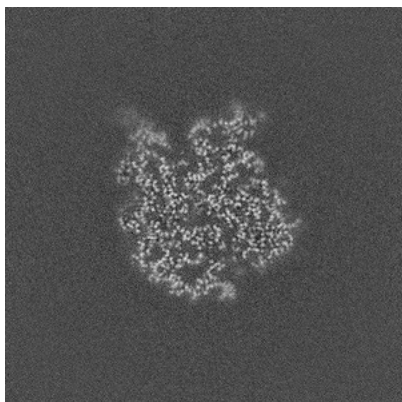


Y Index: 350

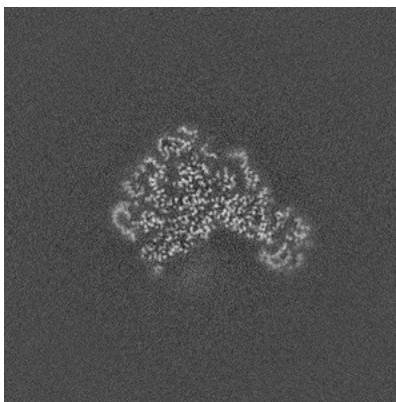


Z Index: 287

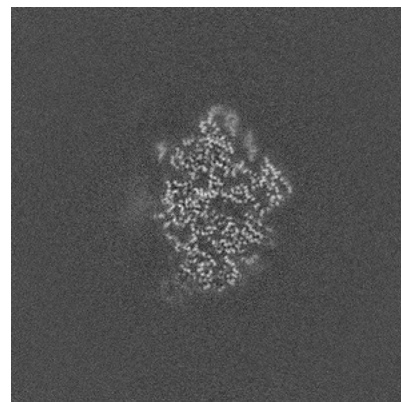
6.3.2 Raw map



X Index: 312



Y Index: 350

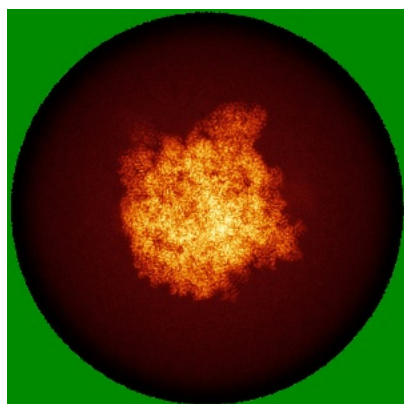


Z Index: 285

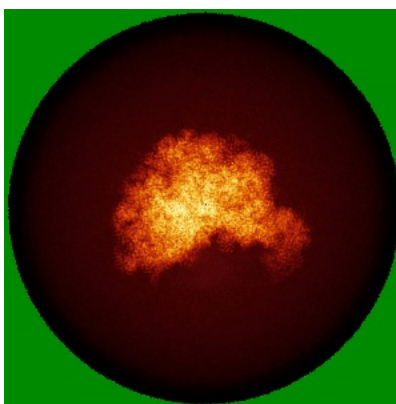
The images above show the largest variance slices of the map in three orthogonal directions.

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

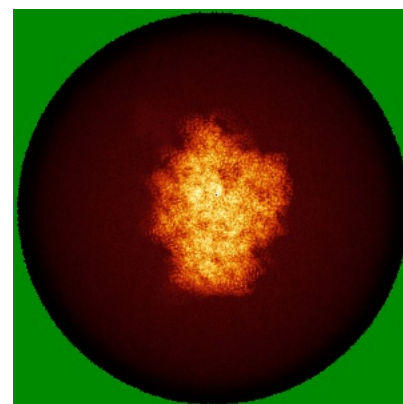
6.4.1 Primary map



X

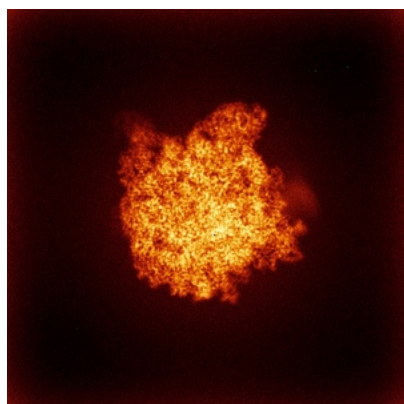


Y

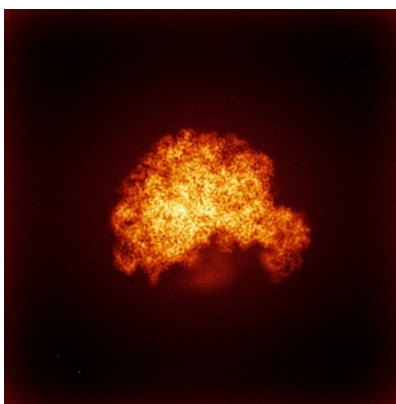


Z

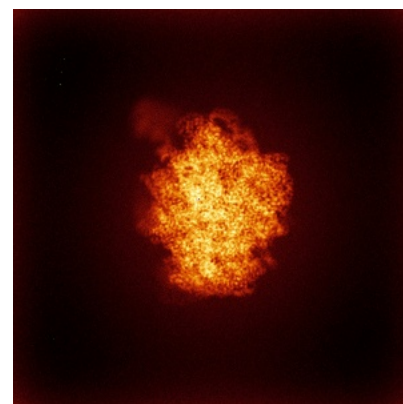
6.4.2 Raw map



X



Y

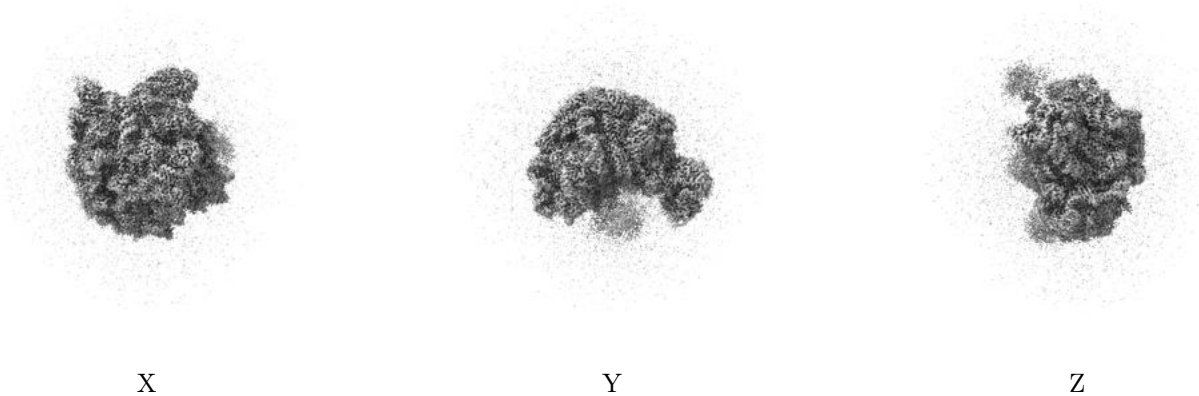


Z

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.

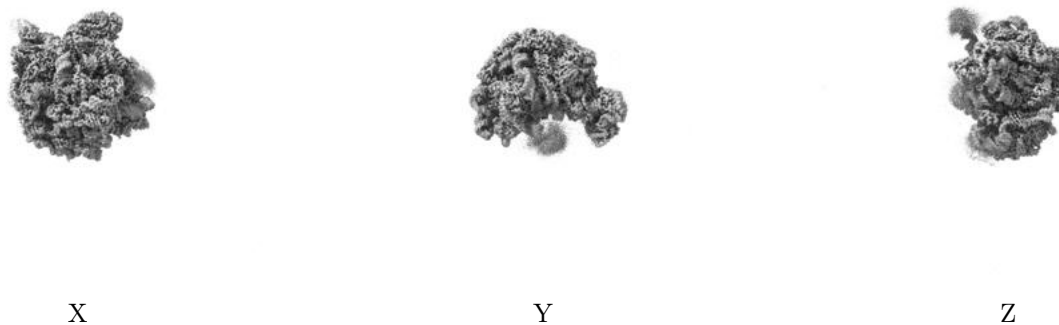
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.24. 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.

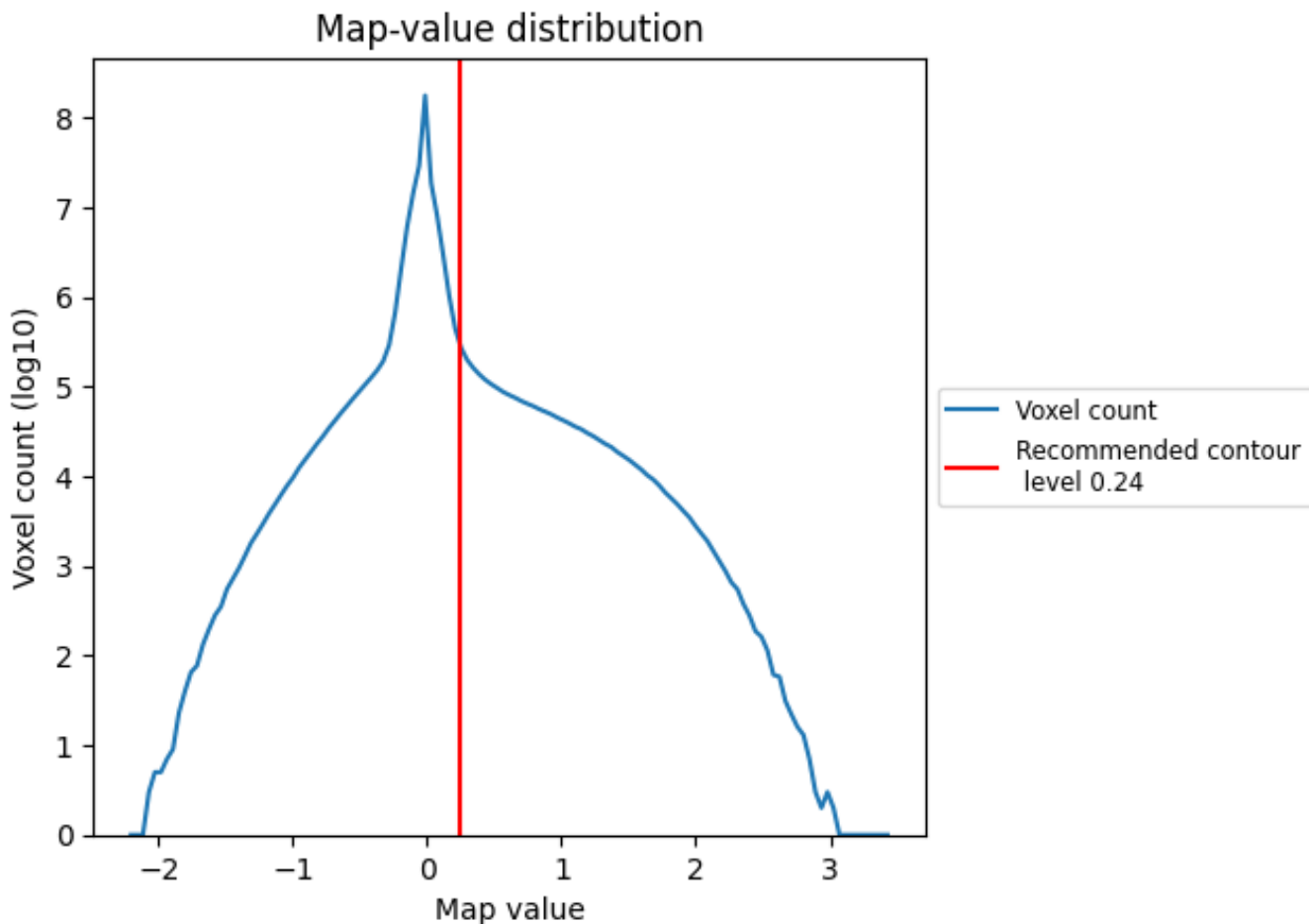
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

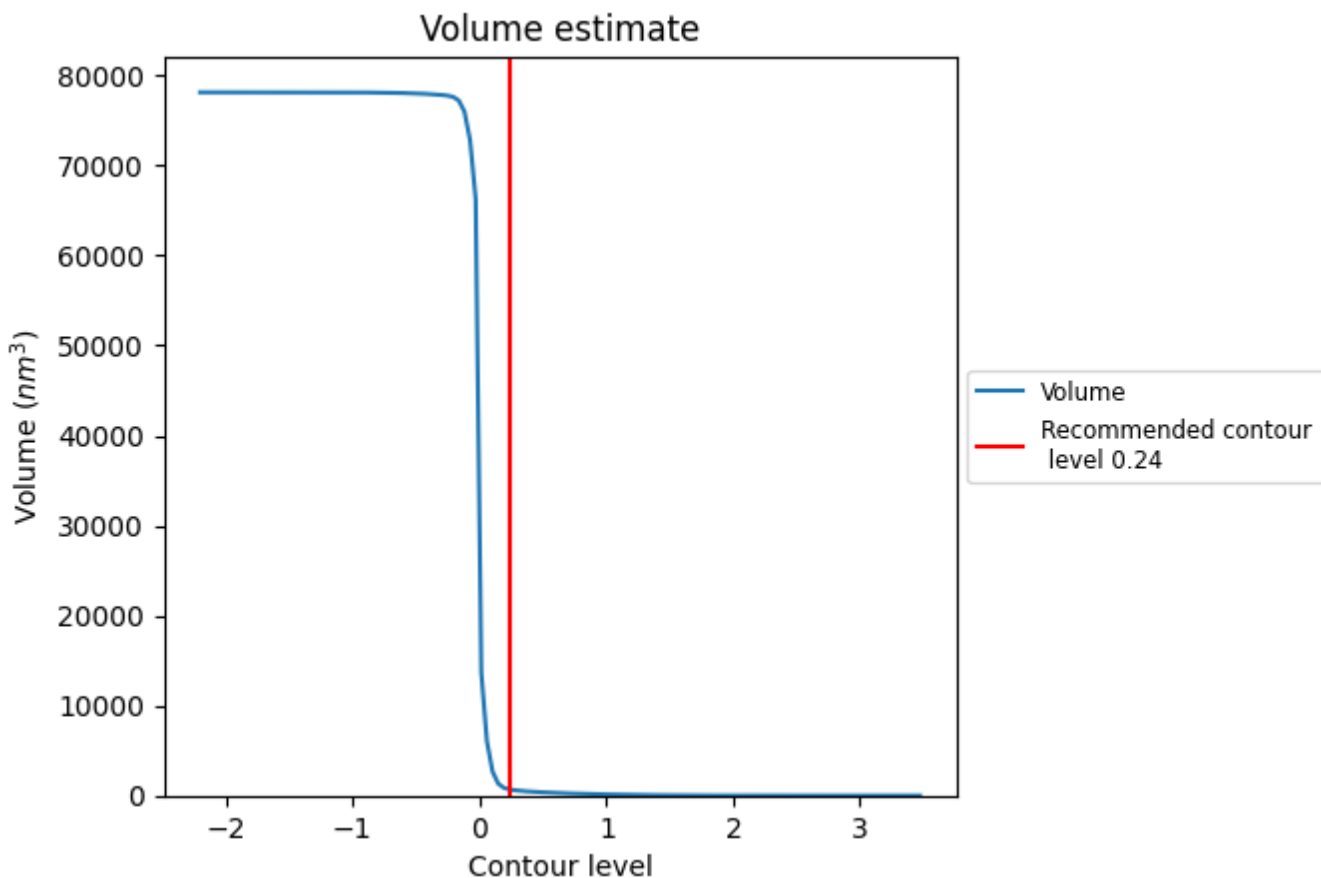
This section contains the results of statistical analysis of the map.

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.

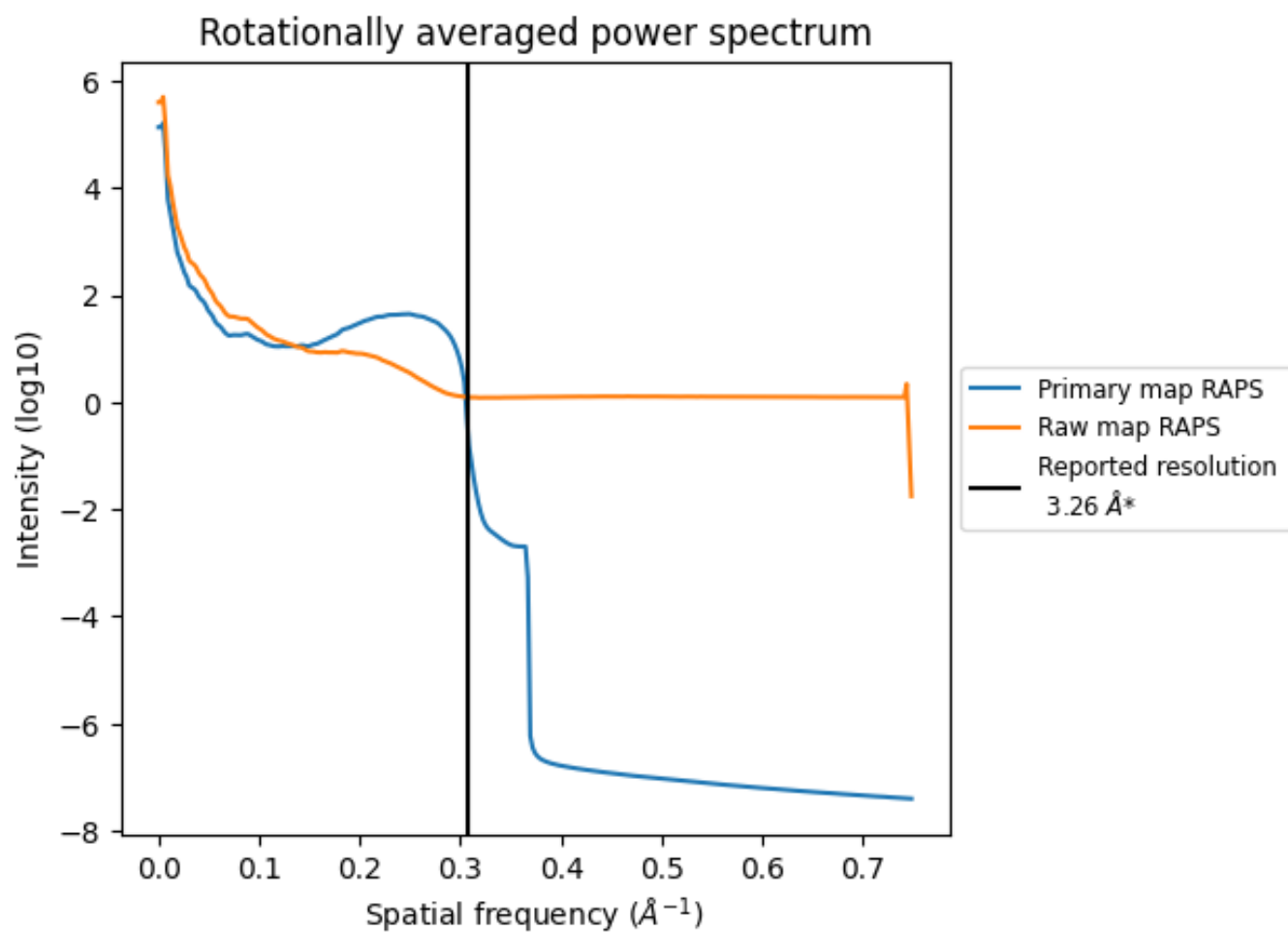
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 675 nm³; this corresponds to an approximate mass of 610 kDa.

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

7.3 Rotationally averaged power spectrum i

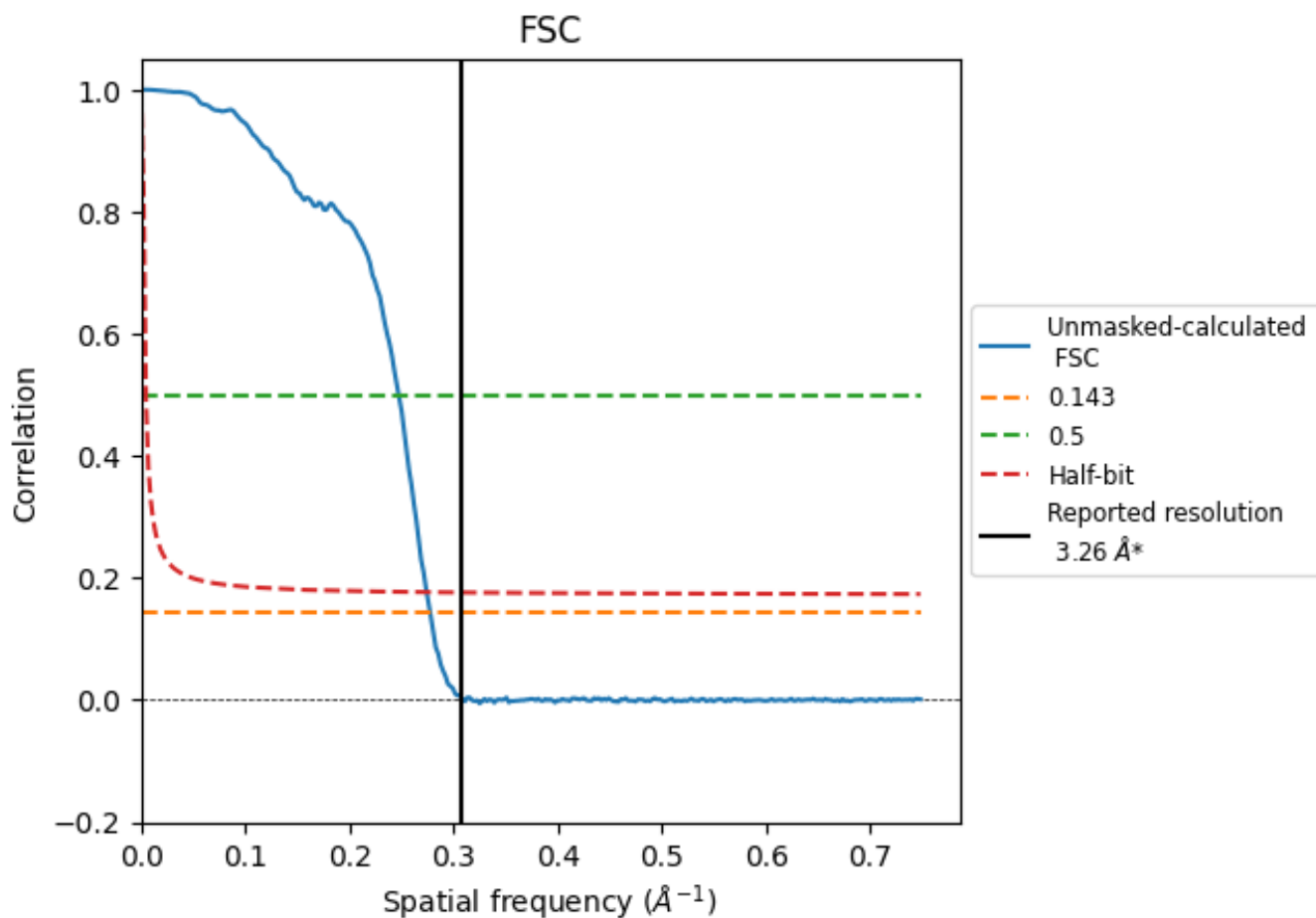


*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

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 0.307 Å⁻¹

8.2 Resolution estimates [i](#)

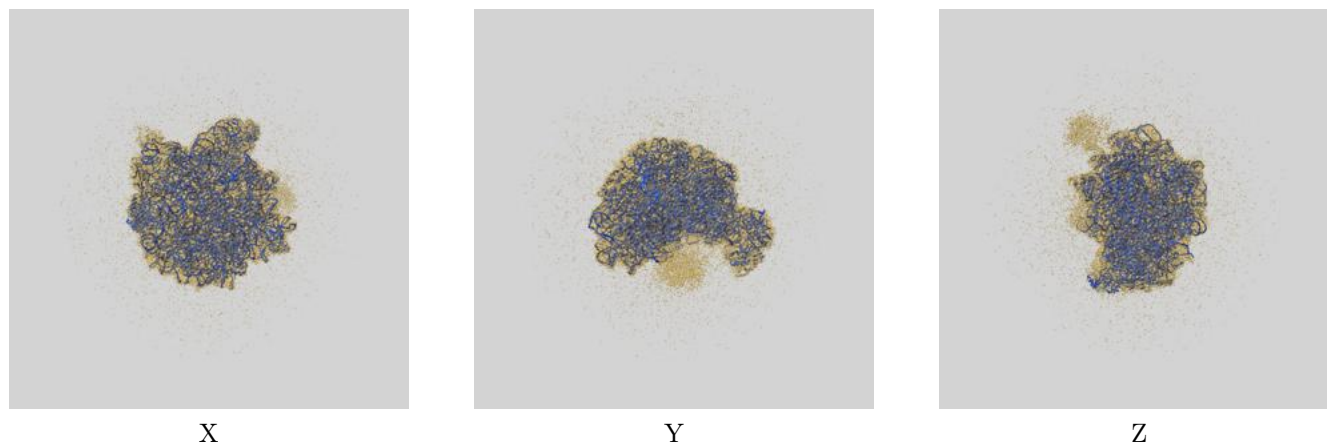
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.26	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	4.04	3.65

*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 3.60 differs from the reported value 3.26 by more than 10 %

9 Map-model fit [i](#)

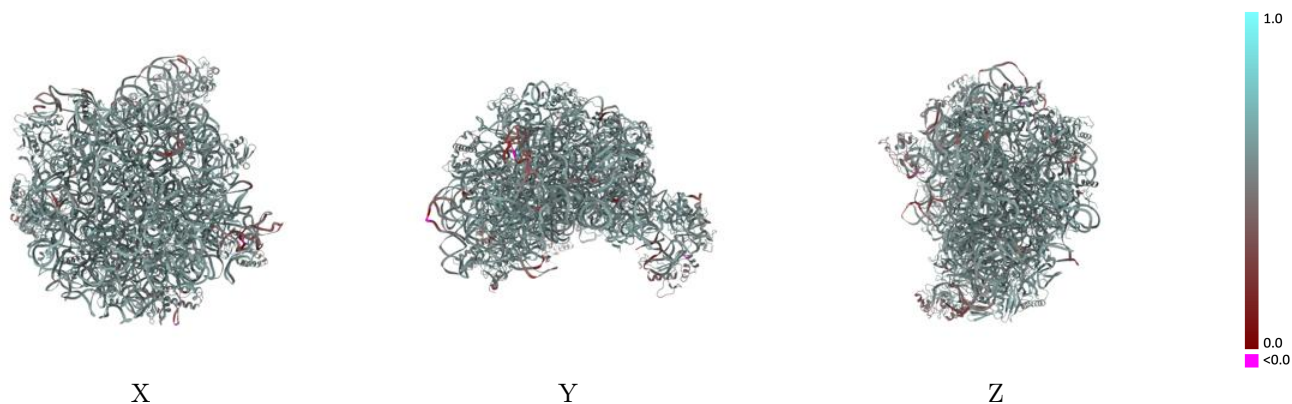
This section contains information regarding the fit between EMDB map EMD-62907 and PDB model 9L9J. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



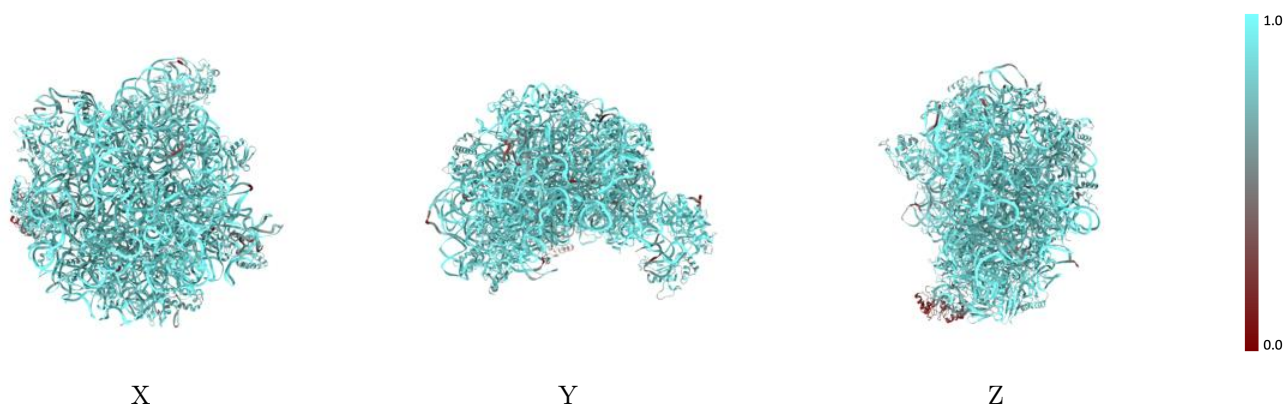
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



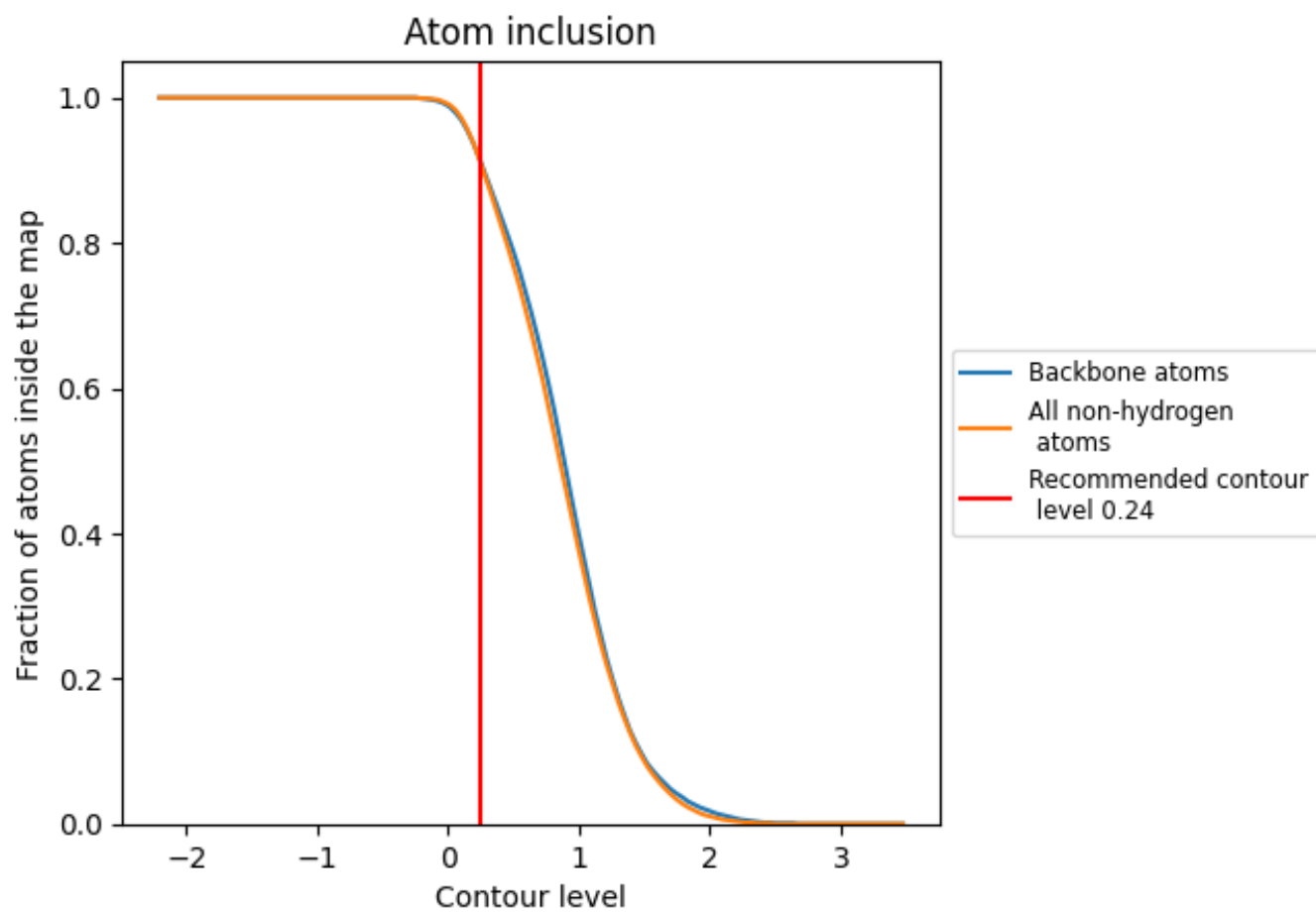
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.24).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9150	 0.5590
0	 0.9440	 0.5600
1	 0.9230	 0.5360
A	 0.8690	 0.5560
B	 0.3610	 0.4490
E	 0.8520	 0.5520
F	 0.9030	 0.5730
G	 0.9290	 0.5920
H	 0.8890	 0.5710
I	 0.8790	 0.5570
J	 0.8930	 0.5660
K	 0.9180	 0.5870
L	 0.9170	 0.5830
M	 0.8740	 0.5580
N	 0.8960	 0.5750
O	 0.9030	 0.5770
P	 0.8770	 0.5540
Q	 0.9050	 0.5800
R	 0.8810	 0.5530
S	 0.9510	 0.6000
T	 0.9210	 0.5900
U	 0.9050	 0.5730
V	 0.9200	 0.5870
W	 0.9050	 0.5810
X	 0.7770	 0.4790
Y	 0.8590	 0.5580
b	 0.9040	 0.5680
c	 0.8280	 0.5470
d	 0.7780	 0.5020
e	 0.7410	 0.5150
f	 0.9050	 0.5670
i	 0.8800	 0.5690
j	 0.7370	 0.5340

