



wwPDB EM Validation Summary Report ⓘ

Dec 31, 2024 – 06:15 AM EST

PDB ID : 8HKV
EMDB ID : EMD-34861
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 4.94 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:

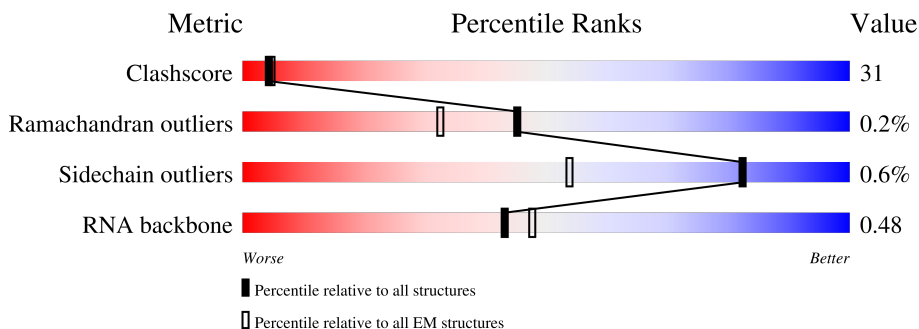
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 4.94 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A23S	3022	
2	A5S	122	
3	AL2P	234	
4	AL3P	339	
5	AL4P	251	
6	AL5P	168	
7	AL6P	181	

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Mol	Chain	Length	Quality of chain
8	ALX0	76	14% 99%
9	L10E	164	15% 99%
10	L13P	140	10% 99%
11	L141	86	9% 100%
11	L142	86	14% 99%
12	L14P	134	6% 100%
13	L15E	169	12% 100%
14	L18E	112	• 99%
15	L18P	193	11% 99%
16	L19E	144	• 100%
17	L22P	150	• 97%
18	L23P	81	6% 98%
19	L24E	54	• 100%
20	L24P	122	6% 99%
21	L29P	63	13% 98%
22	L30E	94	6% 99%
23	L30P	155	14% 99%
24	L31E	75	7% 99%
25	L32E	123	13% 100%
26	L34E	77	18% 95%
27	L37A	65	5% 100%
28	L37E	54	• 100%
29	L39E	49	14% 98%
30	L40E	55	36% 100%
31	L44E	92	15% 100%

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Mol	Chain	Length	Quality of chain
32	L7A1	123	<p>7% 100%</p>
32	L7A2	123	<p>25% 98%</p>
33	L15P	144	<p>8% 65% 35%</p>
34	L21E	97	<p>6% 100%</p>
35	L45A	101	<p>5% 95% 5%</p>
36	L46A	70	<p>6% 97%</p>
37	L47A	80	<p>26% 100%</p>

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 102540 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 rRNA (2996-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A23S	2989	64210	28607	11884	20730	2989	0	0

- Molecule 2 is a RNA chain called 5s rRNA (122-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A5S	122	2609	1163	476	849	121	0	0

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AL2P	234	1754	1101	344	307	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AL3P	339	2695	1730	484	477	4	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AL4P	251	1926	1223	356	345	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AL5P	168	1343	854	253	232	4	0	0

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AL6P	181	1431	920	246	264	1	0	0

- Molecule 8 is a protein called 50S ribosomal protein L18Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	ALX0	76	629	403	110	115	1	0	0

- Molecule 9 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L10E	164	1310	837	239	227	7	0	0

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L13P	140	1109	707	208	190	4	0	0

- Molecule 11 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L141	86	669	417	123	127	2	0	0
11	L142	86	669	417	123	127	2	0	0

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L14P	134	1034	655	194	181	4	0	0

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L15E	169	1423	899	283	236	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	L18E	112	895	576	163	153	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	L18P	193	1539	990	274	274	1	0	0

- Molecule 16 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	L19E	144	1206	753	247	206	0	0

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	L22P	150	1223	782	225	213	3	0	0

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L23P	81	650	419	109	121	1	0	0

- Molecule 19 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	L24E	54	441	282	80	73	6	0	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L24P	122	989	620	189	176	4	0	0

- Molecule 21 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L29P	63	Total	C	N	O	S	0	0
			513	319	95	96	3		

- Molecule 22 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L30E	94	Total	C	N	O	S	0	0
			729	474	116	136	3		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L30P	155	Total	C	N	O	S	0	0
			1254	804	222	223	5		

- Molecule 24 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L31E	75	Total	C	N	O	S	0	0
			625	398	126	97	4		

- Molecule 25 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L32E	123	Total	C	N	O	S	0	0
			1010	650	193	166	1		

- Molecule 26 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L34E	77	Total	C	N	O	S	0	0
			629	395	119	110	5		

- Molecule 27 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L37A	65	Total	C	N	O	S	0	0
			527	335	99	87	6		

- Molecule 28 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	L37E	54	436	267	94	69	6	0	0

- Molecule 29 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L39E	49	414	265	88	61		0	0

- Molecule 30 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	L40E	55	439	273	89	72	5	0	0

- Molecule 31 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	L44E	92	753	474	144	129	6	0	0

- Molecule 32 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	L7A1	123	935	593	155	184	3	0	0
32	L7A2	123	935	593	155	184	3	0	0

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	L15P	94	752	487	131	133	1	0	0

- Molecule 34 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	L21E	97	785	502	152	129	2	0	0

- Molecule 35 is a protein called DUF2280 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	L45A	101	816	515	141	156	4	0	0

- Molecule 36 is a protein called Conserved protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	L46A	70	586	382	101	102	1	0	0

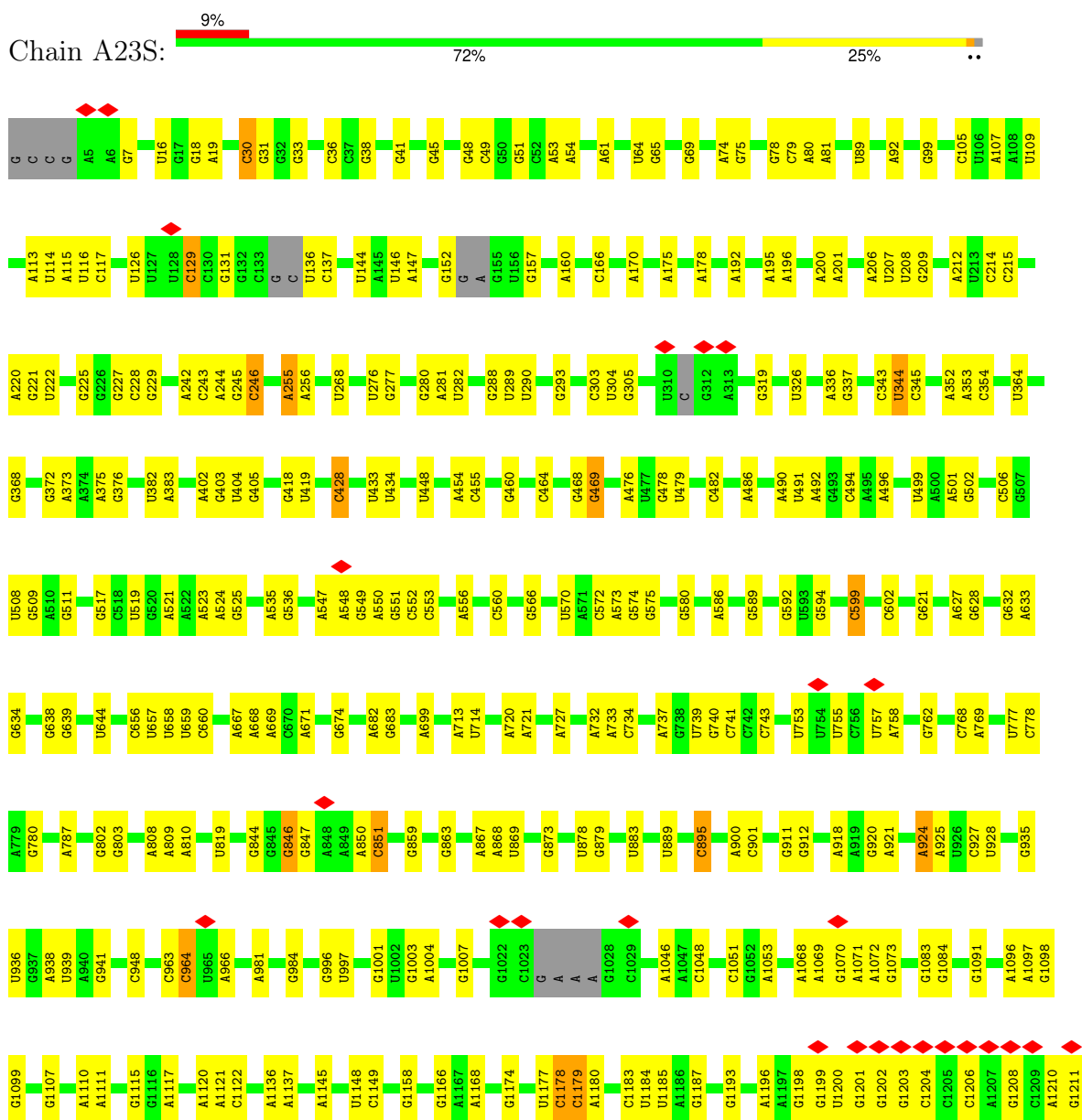
- Molecule 37 is a protein called 50S ribosomal protein L47A.

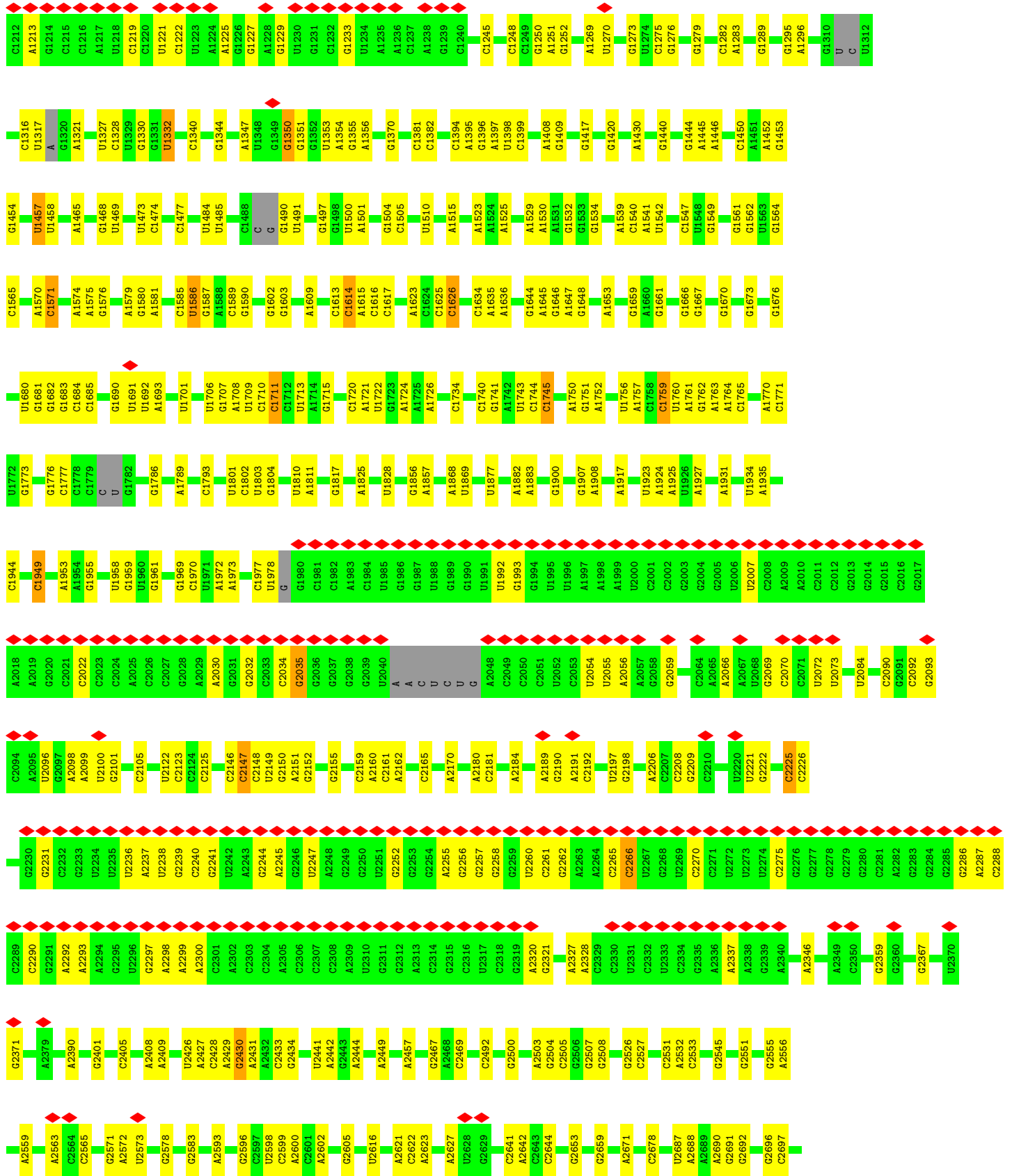
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	L47A	80	648	405	113	128	2	0	0

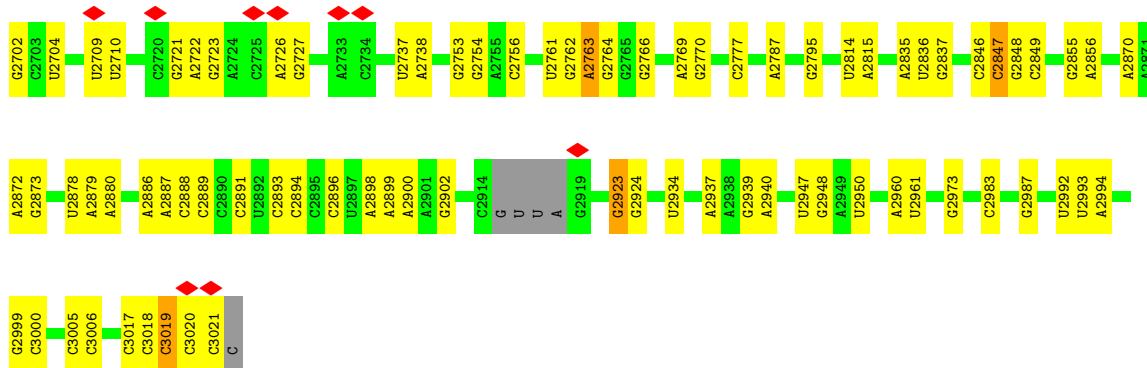
3 Residue-property plots i

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

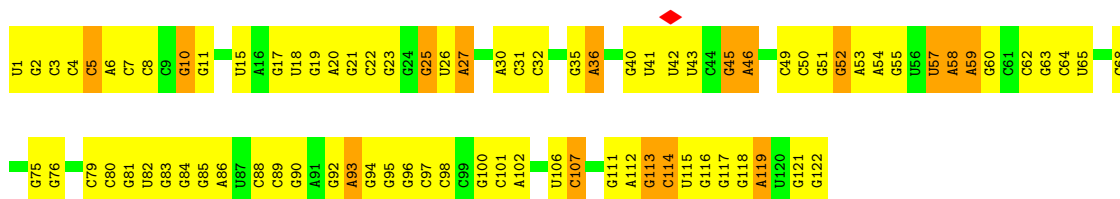
• Molecule 1: 23s rRNA (2996-MER)



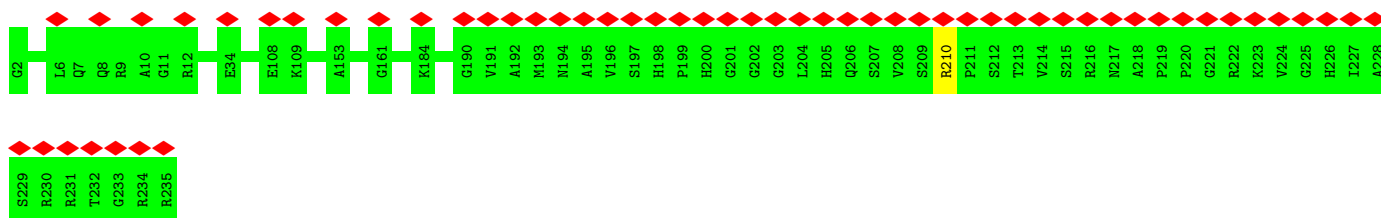




• Molecule 2: 5s rRNA (122-MER)



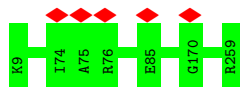
• Molecule 3: 50S ribosomal protein L2



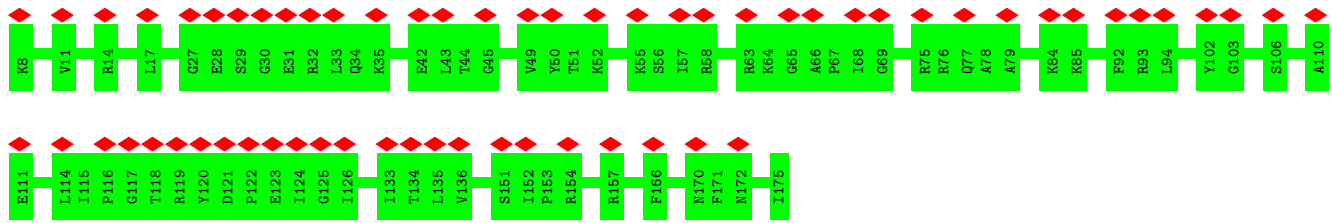
• Molecule 4: 50S ribosomal protein L3



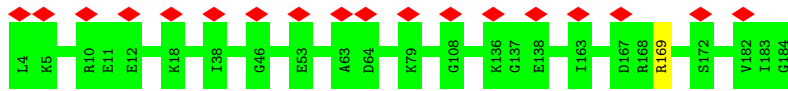
• Molecule 5: 50S ribosomal protein L4



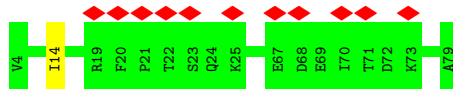
• Molecule 6: 50S ribosomal protein L5



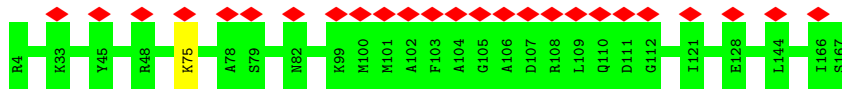
- Molecule 7: 50S ribosomal protein L6



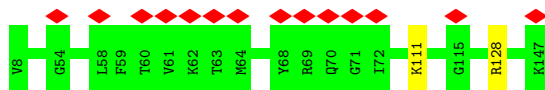
- Molecule 8: 50S ribosomal protein L18Ae



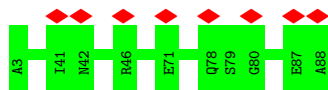
- Molecule 9: 50S ribosomal protein L10e



- Molecule 10: 50S ribosomal protein L13

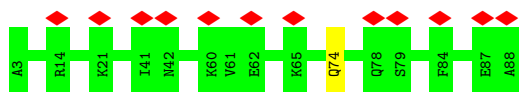


- Molecule 11: 50S ribosomal protein L14e

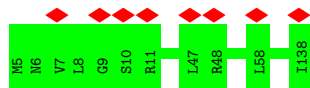


- Molecule 11: 50S ribosomal protein L14e

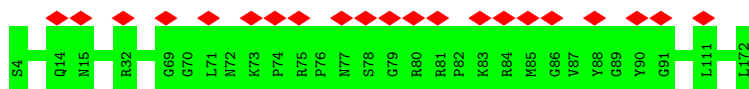




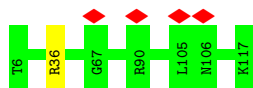
- Molecule 12: 50S ribosomal protein L14



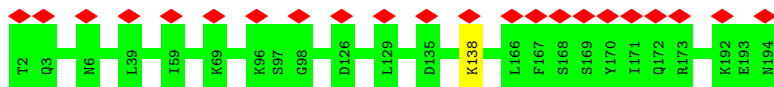
- Molecule 13: 50S ribosomal protein L15e



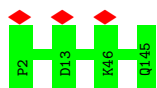
- Molecule 14: 50S ribosomal protein L18e



- Molecule 15: 50S ribosomal protein L18



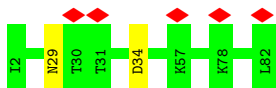
- Molecule 16: 50S ribosomal protein L19e



- Molecule 17: 50S ribosomal protein L22



- Molecule 18: 50S ribosomal protein L23

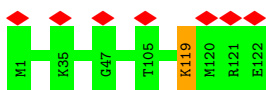


- Molecule 19: 50S ribosomal protein L24e

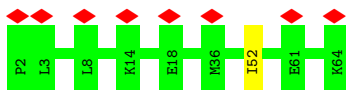


There are no outlier residues recorded for this chain.

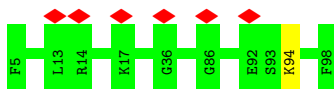
- Molecule 20: 50S ribosomal protein L24



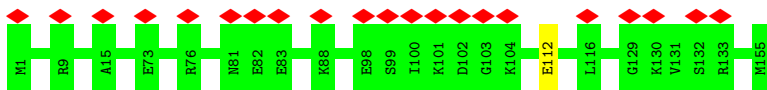
- Molecule 21: 50S ribosomal protein L29



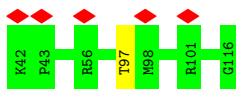
- Molecule 22: 50S ribosomal protein L30e



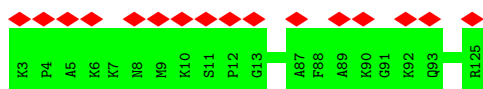
- Molecule 23: 50S ribosomal protein L30



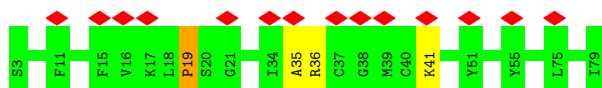
- Molecule 24: 50S ribosomal protein L31e



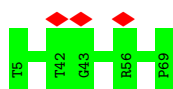
- Molecule 25: 50S ribosomal protein L32e



- Molecule 26: 50S ribosomal protein L34e



- Molecule 27: 50S ribosomal protein L37Ae



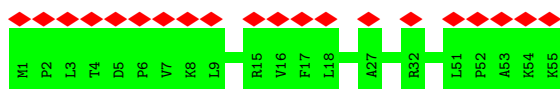
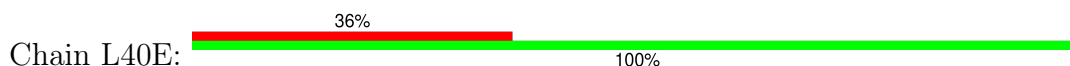
- Molecule 28: 50S ribosomal protein L37e



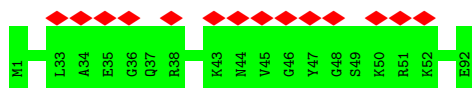
- Molecule 29: 50S ribosomal protein L39e



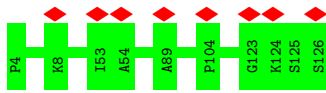
- Molecule 30: 50S ribosomal protein L40E



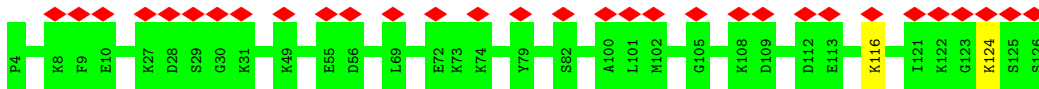
- Molecule 31: 50S ribosomal protein L44e



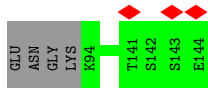
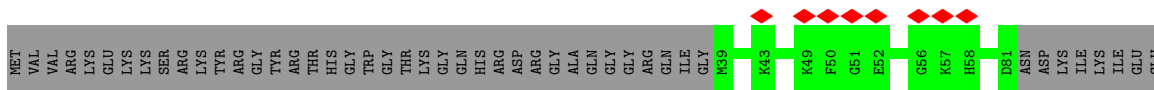
- Molecule 32: 50S ribosomal protein L7Ae



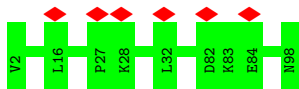
- Molecule 32: 50S ribosomal protein L7Ae



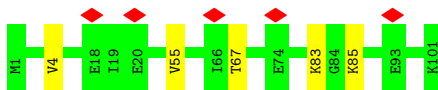
- Molecule 33: 50S ribosomal protein L15



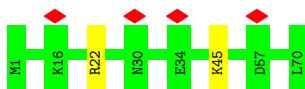
- Molecule 34: 50S ribosomal protein L21e



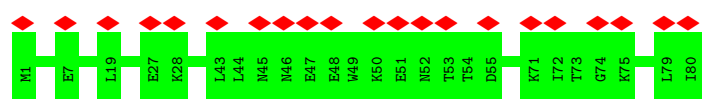
- Molecule 35: DUF2280 domain-containing protein



- Molecule 36: Conserved protein



- Molecule 37: 50S ribosomal protein L47A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	617754	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.481	Depositor
Minimum map value	-2.589	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.178	Depositor
Recommended contour level	0.69	Depositor
Map size (\AA)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.4, 2.4, 2.4	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	A23S	0.63	3/71882 (0.0%)	0.99	152/112144 (0.1%)
2	A5S	0.39	0/2917	0.73	0/4549
3	AL2P	0.35	0/1787	0.57	0/2409
4	AL3P	0.38	0/2758	0.59	0/3727
5	AL4P	0.38	0/1956	0.59	0/2635
6	AL5P	0.27	0/1364	0.55	0/1827
7	AL6P	0.31	0/1450	0.52	0/1949
8	ALX0	0.34	0/638	0.64	0/851
9	L10E	0.30	0/1334	0.56	0/1787
10	L13P	0.34	0/1123	0.60	0/1502
11	L141	0.35	0/673	0.58	0/900
11	L142	0.30	0/673	0.55	0/900
12	L14P	0.34	0/1054	0.59	0/1425
13	L15E	0.37	0/1458	0.63	0/1956
14	L18E	0.35	0/907	0.56	0/1214
15	L18P	0.30	0/1570	0.49	0/2115
16	L19E	0.35	0/1223	0.60	0/1622
17	L22P	0.39	0/1246	0.60	0/1671
18	L23P	0.35	0/655	0.55	0/874
19	L24E	0.36	0/451	0.55	0/599
20	L24P	0.34	0/1000	0.61	0/1329
21	L29P	0.30	0/513	0.60	0/678
22	L30E	0.33	0/738	0.51	0/985
23	L30P	0.38	0/1278	0.60	0/1713
24	L31E	0.39	0/632	0.65	0/837
25	L32E	0.39	0/1027	0.59	0/1366
26	L34E	0.42	0/642	0.78	1/854 (0.1%)
27	L37A	0.36	0/542	0.59	0/726
28	L37E	0.42	0/445	0.69	0/585
29	L39E	0.38	0/422	0.71	0/562
30	L40E	0.30	0/443	0.58	0/587
31	L44E	0.29	0/763	0.52	0/1008
32	L7A1	0.29	0/946	0.43	0/1272
32	L7A2	0.29	0/946	0.47	0/1272

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L15P	0.32	0/766	0.55	0/1023
34	L21E	0.31	0/800	0.53	0/1067
35	L45A	0.34	0/824	0.56	0/1094
36	L46A	0.35	0/595	0.53	0/793
37	L47A	0.31	0/652	0.56	0/870
All	All	0.55	3/111093 (0.0%)	0.88	153/165277 (0.1%)

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	AL3P	0	1
8	ALX0	0	1
17	L22P	0	1
18	L23P	0	1
20	L24P	0	1
23	L30P	0	1
24	L31E	0	1
26	L34E	0	1
29	L39E	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A23S	1179	C	N1-C6	-6.93	1.32	1.37
1	A23S	1179	C	C4-C5	-5.82	1.38	1.43
1	A23S	924	A	N9-C4	-5.05	1.34	1.37

The worst 5 of 153 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A23S	2433	C	N3-C4-N4	-21.43	103.00	118.00
1	A23S	2430	G	N1-C6-O6	-16.75	109.85	119.90
1	A23S	2433	C	C5-C4-N4	15.94	131.36	120.20
1	A23S	2430	G	C5-C6-O6	13.65	136.79	128.60
1	A23S	469	G	N3-C4-N9	12.72	133.63	126.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AL3P	252	PRO	Peptide
8	ALX0	14	ILE	Peptide
17	L22P	6	TYR	Peptide
18	L23P	34	ASP	Peptide
20	L24P	119	LYS	Peptide

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	A23S	64210	0	0	0	0
2	A5S	2609	0	1324	78	0
3	AL2P	1754	0	0	0	0
4	AL3P	2695	0	0	0	0
5	AL4P	1926	0	0	0	0
6	AL5P	1343	0	0	0	0
7	AL6P	1431	0	0	0	0
8	ALX0	629	0	0	0	0
9	L10E	1310	0	0	0	0
10	L13P	1109	0	0	0	0
11	L141	669	0	0	0	0
11	L142	669	0	0	0	0
12	L14P	1034	0	0	0	0
13	L15E	1423	0	0	0	0
14	L18E	895	0	0	0	0
15	L18P	1539	0	0	0	0
16	L19E	1206	0	0	0	0
17	L22P	1223	0	0	0	0
18	L23P	650	0	0	0	0
19	L24E	441	0	0	0	0
20	L24P	989	0	0	0	0
21	L29P	513	0	0	0	0
22	L30E	729	0	0	0	0
23	L30P	1254	0	0	0	0
24	L31E	625	0	0	0	0
25	L32E	1010	0	0	0	0
26	L34E	629	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	L37A	527	0	0	0	0
28	L37E	436	0	0	0	0
29	L39E	414	0	0	0	0
30	L40E	439	0	0	0	0
31	L44E	753	0	0	0	0
32	L7A1	935	0	0	0	0
32	L7A2	935	0	0	0	0
33	L15P	752	0	0	0	0
34	L21E	785	0	0	0	0
35	L45A	816	0	0	0	0
36	L46A	586	0	0	0	0
37	L47A	648	0	0	0	0
All	All	102540	0	1324	78	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 31.

The worst 5 of 78 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)
2:A5S:8:C:H42	2:A5S:117:G:H1	1.30	0.77
2:A5S:95:G:H2'	2:A5S:96:G:H8	1.51	0.75
2:A5S:41:U:O2'	2:A5S:46:A:N6	2.25	0.69
2:A5S:95:G:H2'	2:A5S:96:G:C8	2.28	0.68
2:A5S:5:C:H2'	2:A5S:6:A:C8	2.32	0.65

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	AL2P	232/234 (99%)	218 (94%)	14 (6%)	0	100	100
4	AL3P	337/339 (99%)	287 (85%)	49 (14%)	1 (0%)	37	72
5	AL4P	249/251 (99%)	213 (86%)	36 (14%)	0	100	100
6	AL5P	166/168 (99%)	154 (93%)	12 (7%)	0	100	100
7	AL6P	179/181 (99%)	166 (93%)	13 (7%)	0	100	100
8	ALX0	74/76 (97%)	63 (85%)	11 (15%)	0	100	100
9	L10E	162/164 (99%)	146 (90%)	16 (10%)	0	100	100
10	L13P	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
11	L141	84/86 (98%)	70 (83%)	14 (17%)	0	100	100
11	L142	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
12	L14P	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
13	L15E	167/169 (99%)	153 (92%)	14 (8%)	0	100	100
14	L18E	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
15	L18P	191/193 (99%)	178 (93%)	13 (7%)	0	100	100
16	L19E	142/144 (99%)	130 (92%)	12 (8%)	0	100	100
17	L22P	148/150 (99%)	126 (85%)	21 (14%)	1 (1%)	19	56
18	L23P	79/81 (98%)	70 (89%)	8 (10%)	1 (1%)	10	42
19	L24E	52/54 (96%)	46 (88%)	6 (12%)	0	100	100
20	L24P	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
21	L29P	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
22	L30E	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
23	L30P	153/155 (99%)	129 (84%)	24 (16%)	0	100	100
24	L31E	73/75 (97%)	59 (81%)	14 (19%)	0	100	100
25	L32E	121/123 (98%)	102 (84%)	19 (16%)	0	100	100
26	L34E	75/77 (97%)	51 (68%)	22 (29%)	2 (3%)	4	25
27	L37A	63/65 (97%)	51 (81%)	12 (19%)	0	100	100
28	L37E	52/54 (96%)	39 (75%)	13 (25%)	0	100	100
29	L39E	47/49 (96%)	37 (79%)	10 (21%)	0	100	100
30	L40E	53/55 (96%)	35 (66%)	18 (34%)	0	100	100
31	L44E	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
32	L7A1	121/123 (98%)	113 (93%)	8 (7%)	0	100	100
32	L7A2	121/123 (98%)	113 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	L15P	90/144 (62%)	81 (90%)	9 (10%)	0	100	100
34	L21E	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
35	L45A	99/101 (98%)	77 (78%)	18 (18%)	4 (4%)	2	18
36	L46A	68/70 (97%)	57 (84%)	11 (16%)	0	100	100
37	L47A	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
All	All	4398/4524 (97%)	3878 (88%)	511 (12%)	9 (0%)	45	78

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AL3P	231	ARG
35	L45A	4	VAL
35	L45A	55	VAL
35	L45A	67	THR
26	L34E	35	ALA

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	AL2P	181/181 (100%)	180 (99%)	1 (1%)	84	88
4	AL3P	297/297 (100%)	294 (99%)	3 (1%)	73	82
5	AL4P	212/212 (100%)	212 (100%)	0	100	100
6	AL5P	144/144 (100%)	144 (100%)	0	100	100
7	AL6P	157/157 (100%)	156 (99%)	1 (1%)	84	88
8	ALX0	68/68 (100%)	68 (100%)	0	100	100
9	L10E	137/137 (100%)	136 (99%)	1 (1%)	81	87
10	L13P	121/121 (100%)	119 (98%)	2 (2%)	56	72
11	L141	74/74 (100%)	74 (100%)	0	100	100
11	L142	74/74 (100%)	73 (99%)	1 (1%)	62	76
12	L14P	110/110 (100%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	L15E	146/146 (100%)	146 (100%)	0	100	100
14	L18E	98/98 (100%)	97 (99%)	1 (1%)	73	82
15	L18P	162/162 (100%)	161 (99%)	1 (1%)	84	88
16	L19E	126/126 (100%)	126 (100%)	0	100	100
17	L22P	131/131 (100%)	129 (98%)	2 (2%)	60	75
18	L23P	74/74 (100%)	74 (100%)	0	100	100
19	L24E	50/50 (100%)	50 (100%)	0	100	100
20	L24P	108/108 (100%)	107 (99%)	1 (1%)	75	83
21	L29P	59/59 (100%)	58 (98%)	1 (2%)	56	72
22	L30E	83/83 (100%)	82 (99%)	1 (1%)	67	79
23	L30P	136/136 (100%)	136 (100%)	0	100	100
24	L31E	66/66 (100%)	66 (100%)	0	100	100
25	L32E	106/106 (100%)	106 (100%)	0	100	100
26	L34E	70/70 (100%)	69 (99%)	1 (1%)	62	76
27	L37A	53/53 (100%)	53 (100%)	0	100	100
28	L37E	45/45 (100%)	45 (100%)	0	100	100
29	L39E	44/44 (100%)	44 (100%)	0	100	100
30	L40E	50/50 (100%)	50 (100%)	0	100	100
31	L44E	84/84 (100%)	84 (100%)	0	100	100
32	L7A1	104/104 (100%)	104 (100%)	0	100	100
32	L7A2	104/104 (100%)	102 (98%)	2 (2%)	52	70
33	L15P	78/118 (66%)	78 (100%)	0	100	100
34	L21E	85/85 (100%)	85 (100%)	0	100	100
35	L45A	91/91 (100%)	90 (99%)	1 (1%)	70	80
36	L46A	66/66 (100%)	64 (97%)	2 (3%)	36	56
37	L47A	74/74 (100%)	74 (100%)	0	100	100
All	All	3868/3908 (99%)	3846 (99%)	22 (1%)	82	88

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	L29P	52	ILE
32	L7A2	116	LYS

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Mol	Chain	Res	Type
26	L34E	41	LYS
32	L7A2	124	LYS
10	L13P	111	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A23S	2979/3022 (98%)	739 (24%)	44 (1%)
2	A5S	121/122 (99%)	21 (17%)	1 (0%)
All	All	3100/3144 (98%)	760 (24%)	45 (1%)

5 of 760 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A23S	7	G
1	A23S	16	U
1	A23S	18	G
1	A23S	19	A
1	A23S	30	C

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A23S	1646	G
1	A23S	2098	A
1	A23S	1647	A
1	A23S	1751	G
1	A23S	2146	C

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.

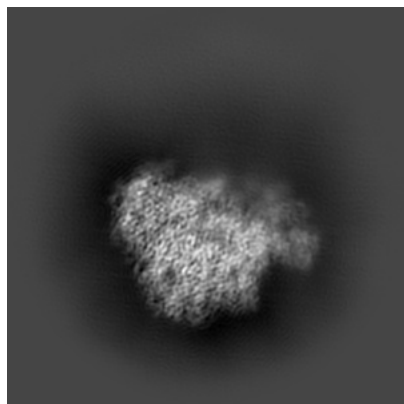
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34861. These allow visual inspection of the internal detail of the map and identification of artifacts.

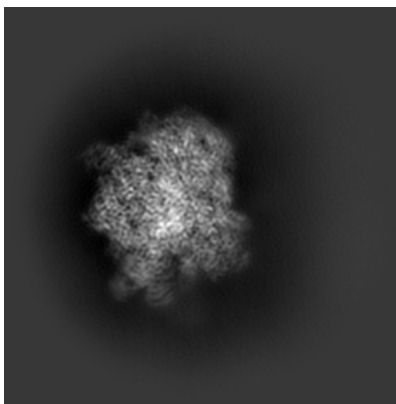
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

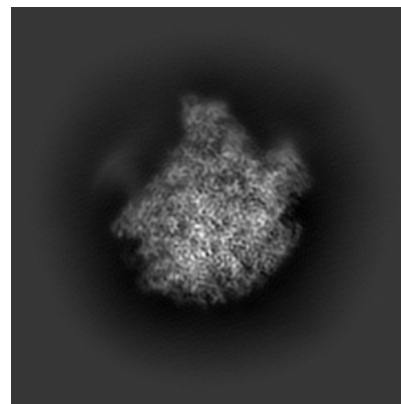
6.1.1 Primary map



X

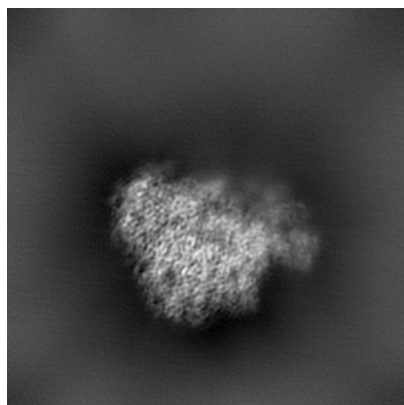


Y

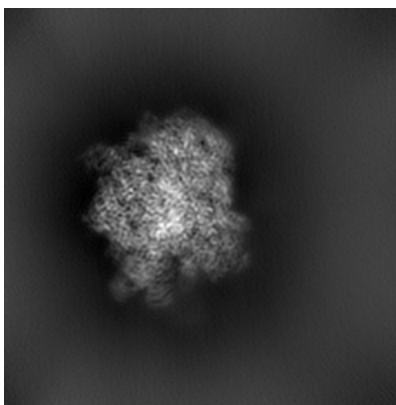


Z

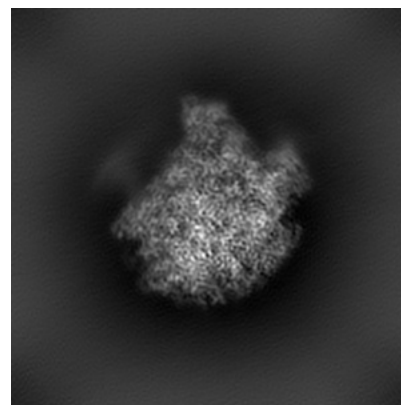
6.1.2 Raw map



X



Y

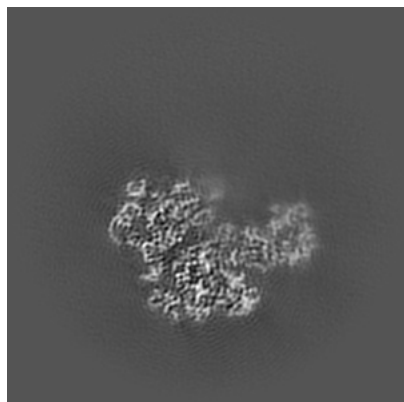


Z

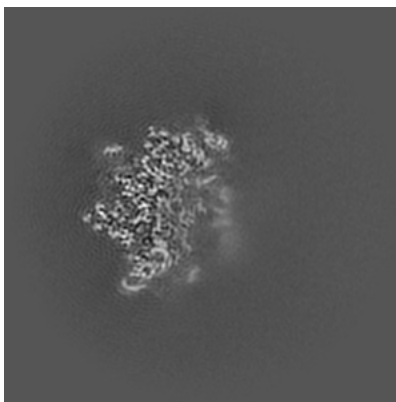
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

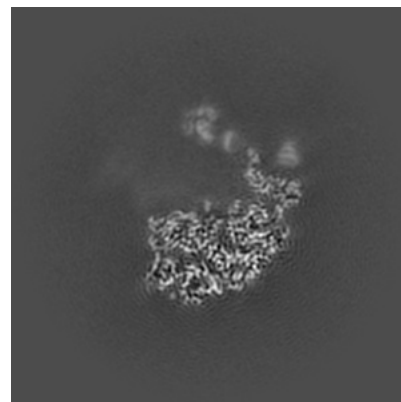
6.2.1 Primary map



X Index: 90

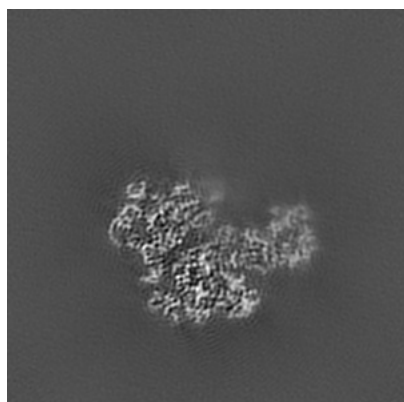


Y Index: 90

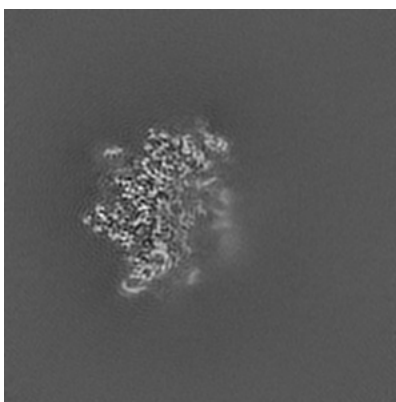


Z Index: 90

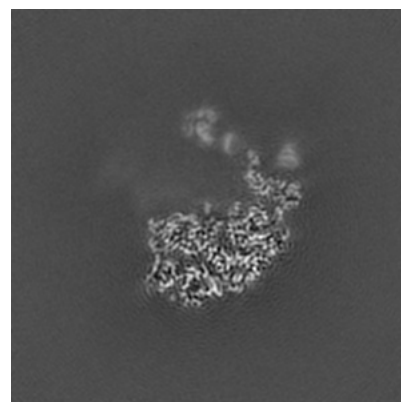
6.2.2 Raw map



X Index: 90



Y Index: 90

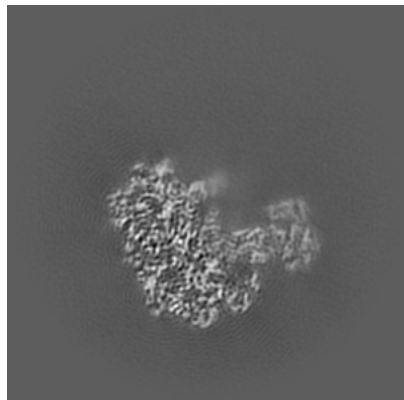


Z Index: 90

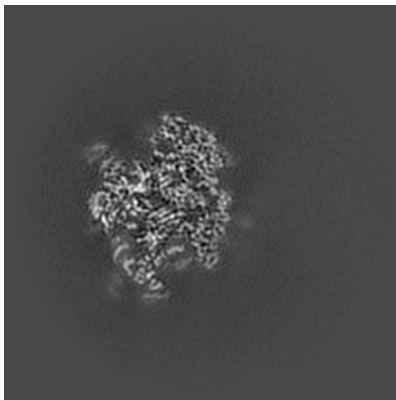
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

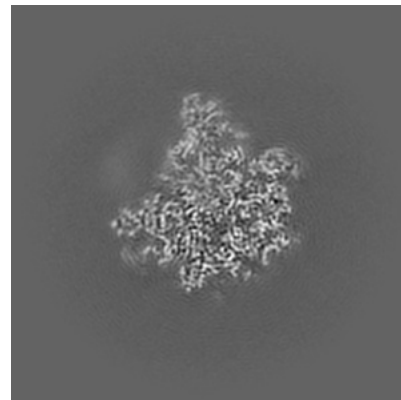
6.3.1 Primary map



X Index: 84

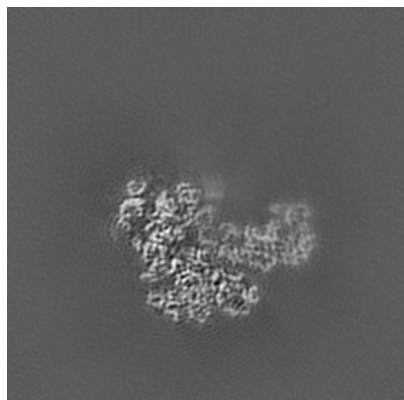


Y Index: 76

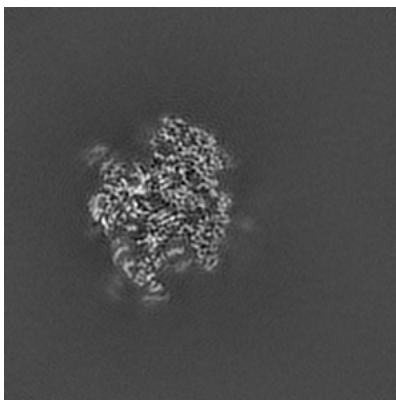


Z Index: 70

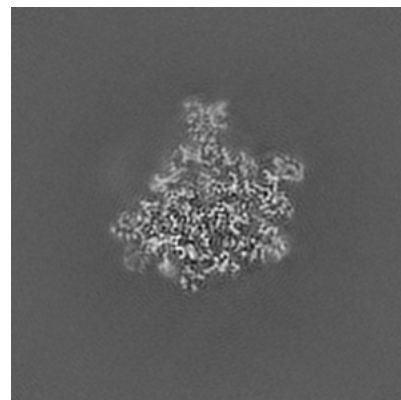
6.3.2 Raw map



X Index: 89



Y Index: 76

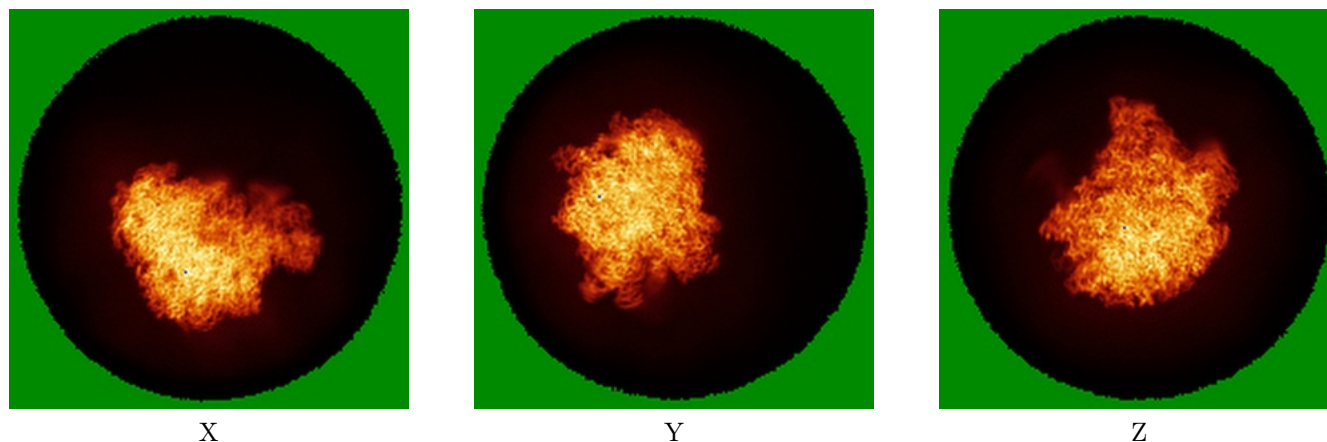


Z Index: 67

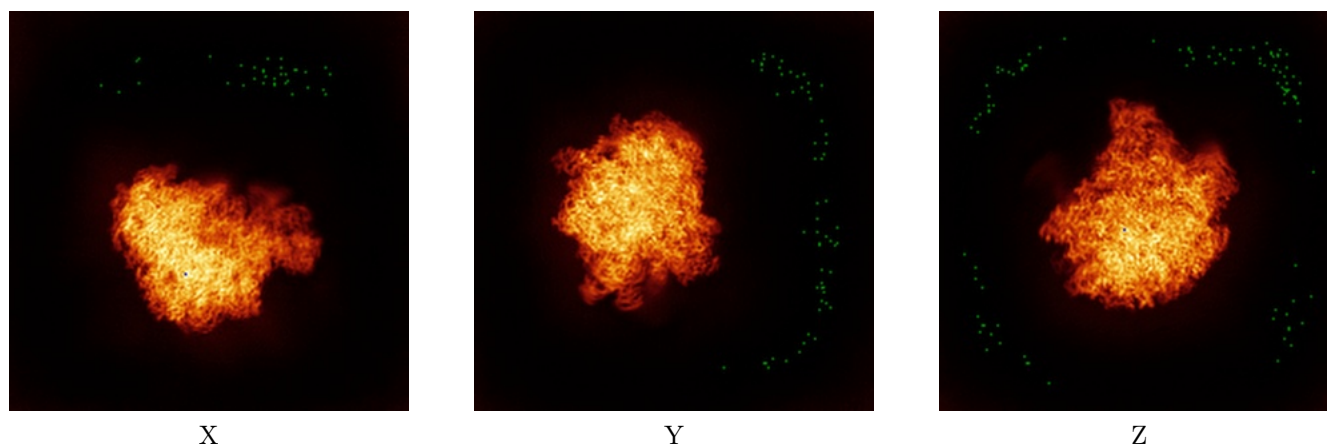
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



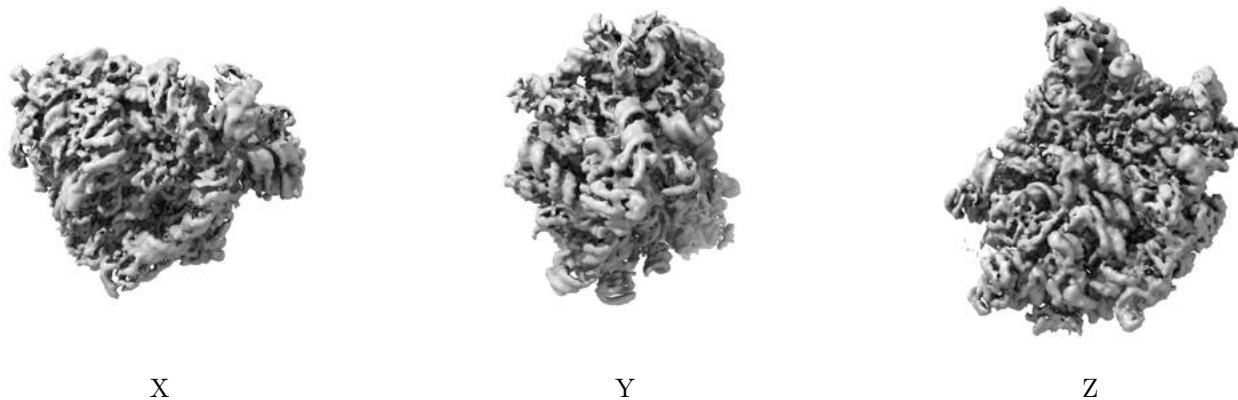
6.4.2 Raw map



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 0.69. 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.

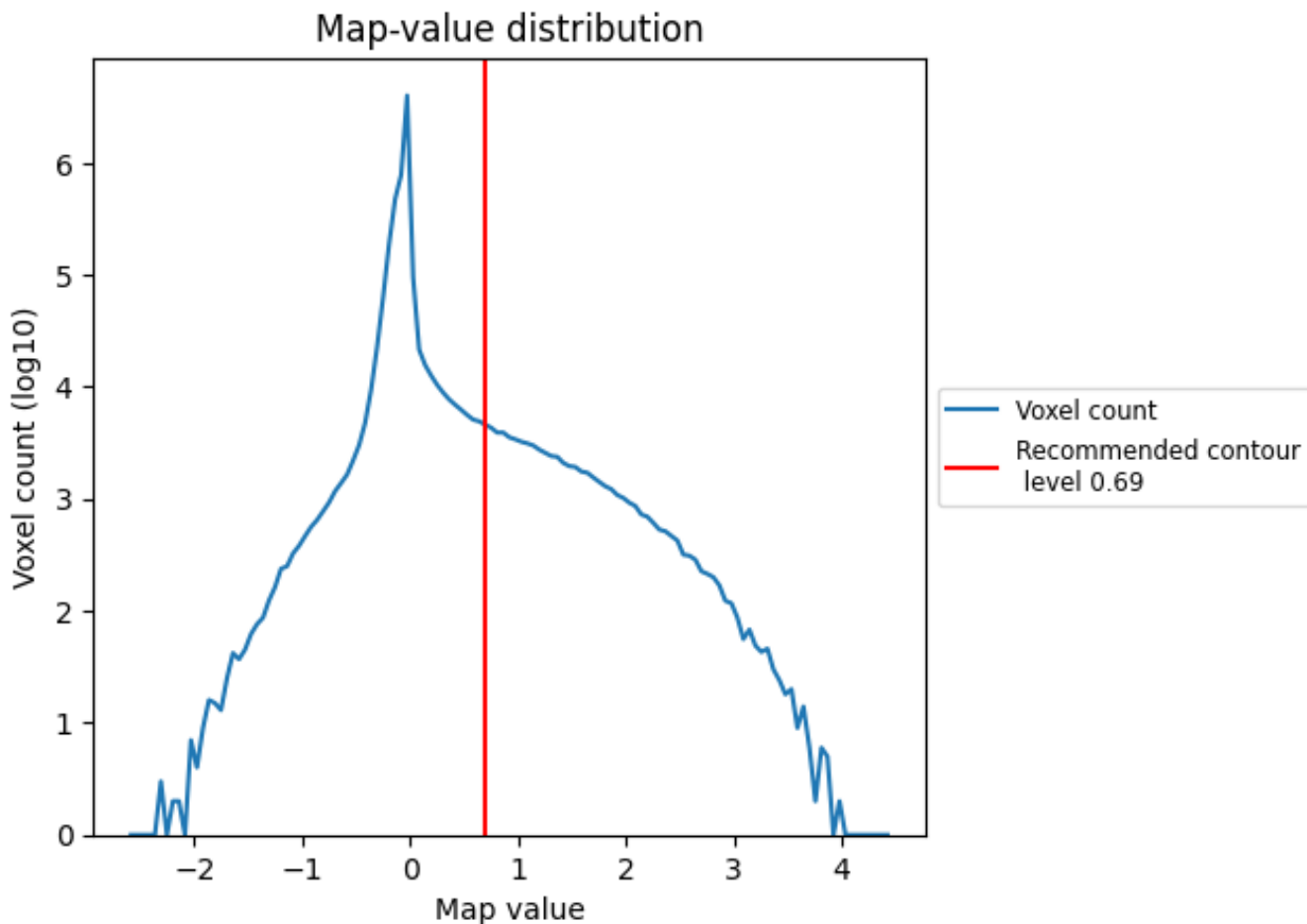
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

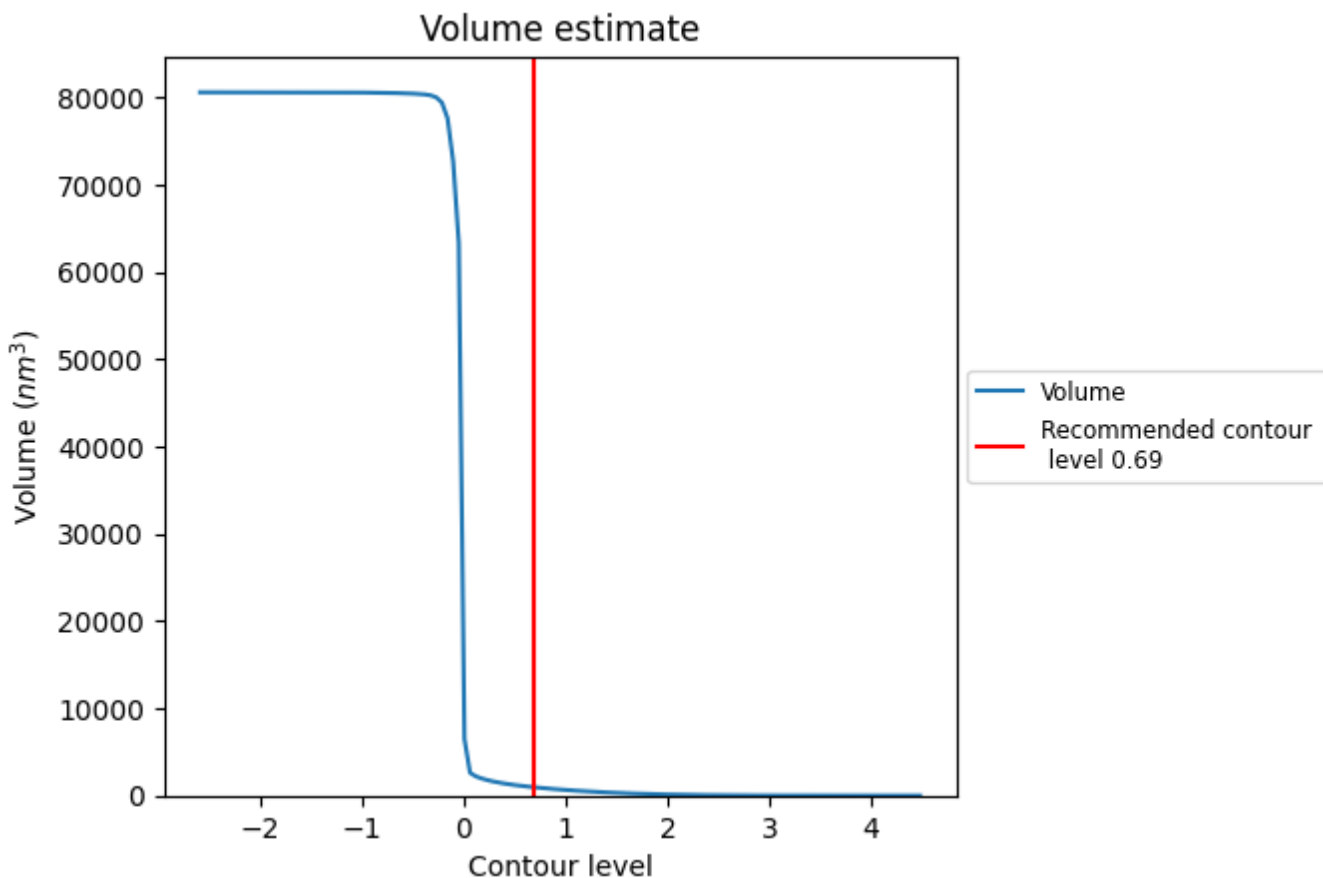
This section contains the results of statistical analysis of the map.

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.

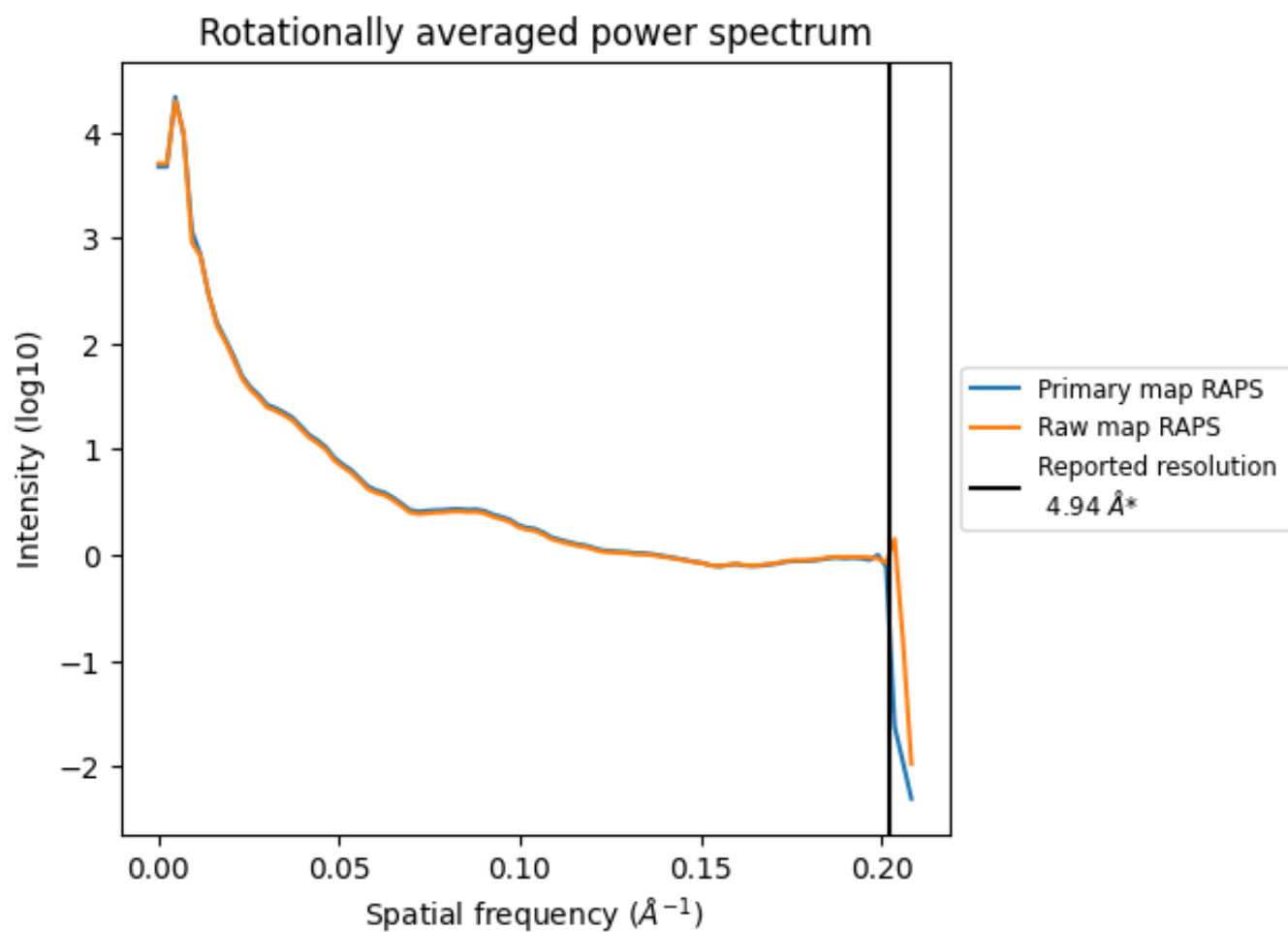
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 953 nm³; this corresponds to an approximate mass of 861 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

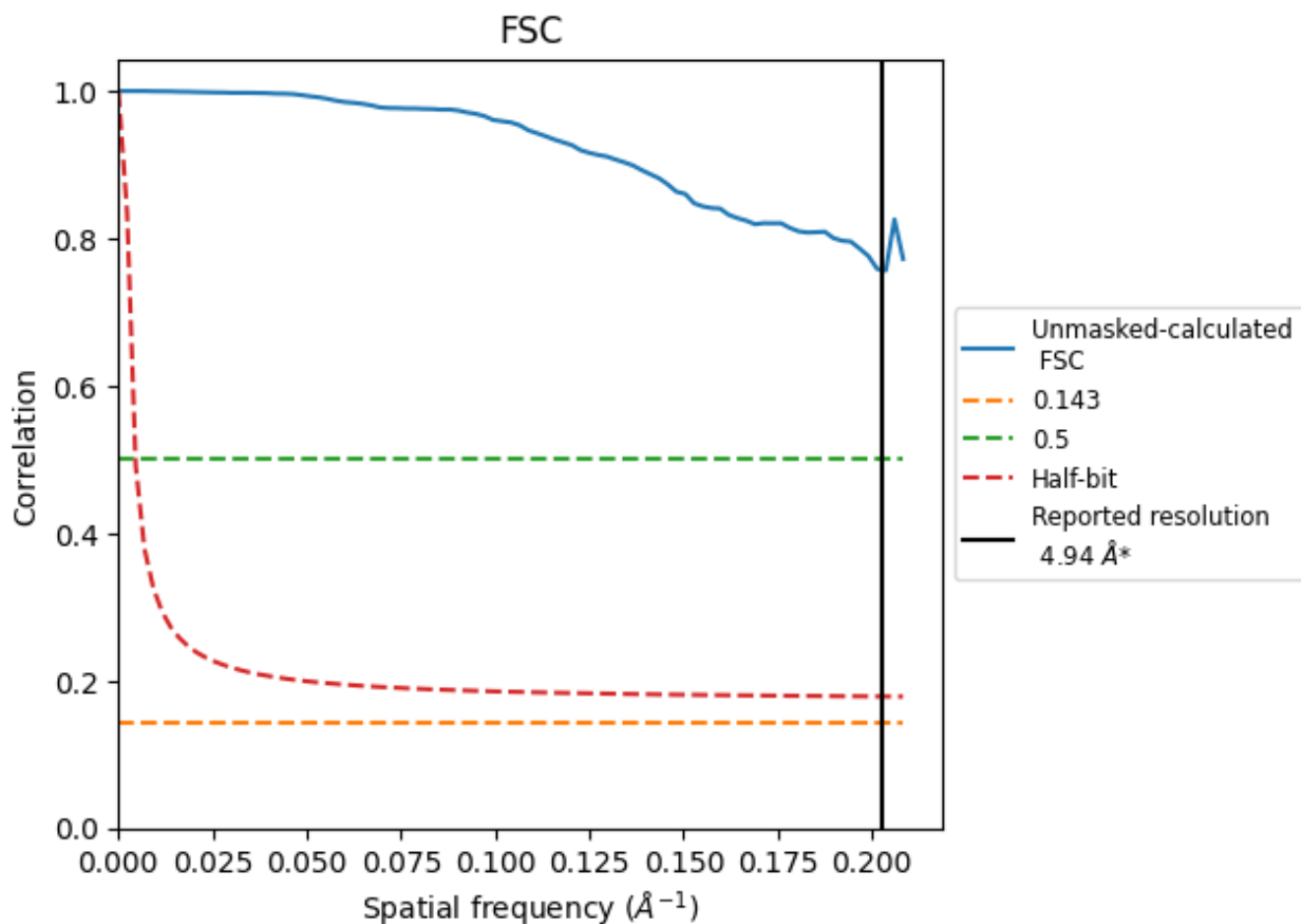


*Reported resolution corresponds to spatial frequency of 0.202 Å⁻¹

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 0.202 Å⁻¹

8.2 Resolution estimates [i](#)

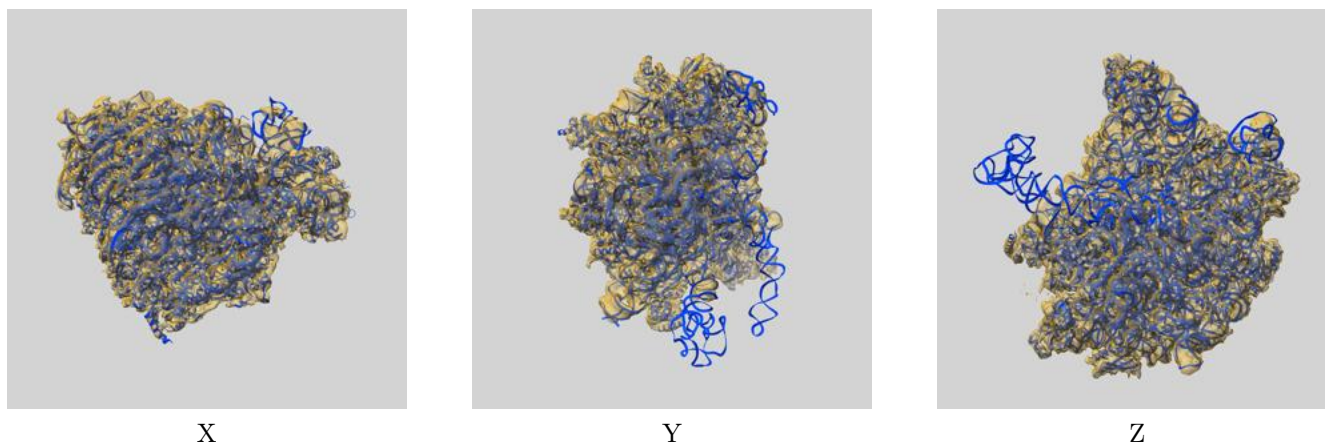
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

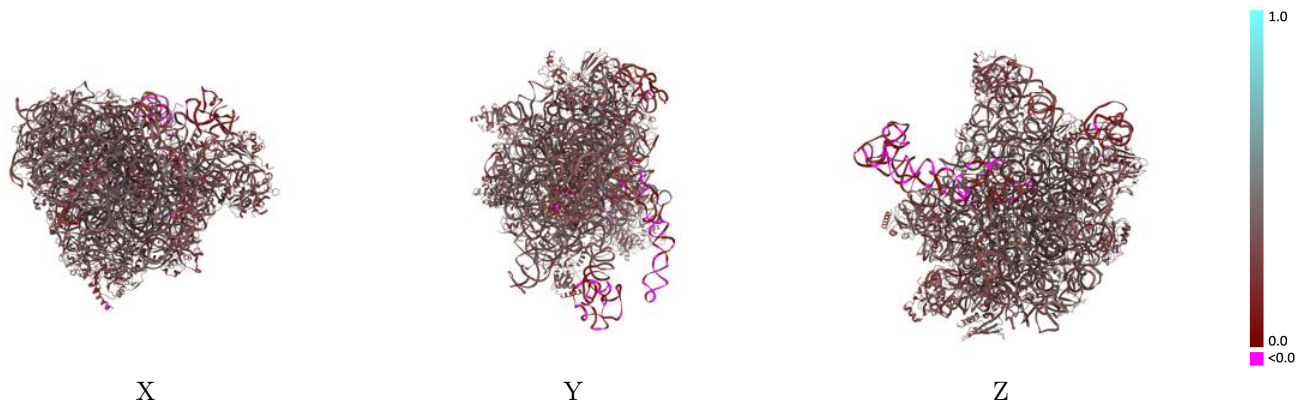
This section contains information regarding the fit between EMDB map EMD-34861 and PDB model 8HKV. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



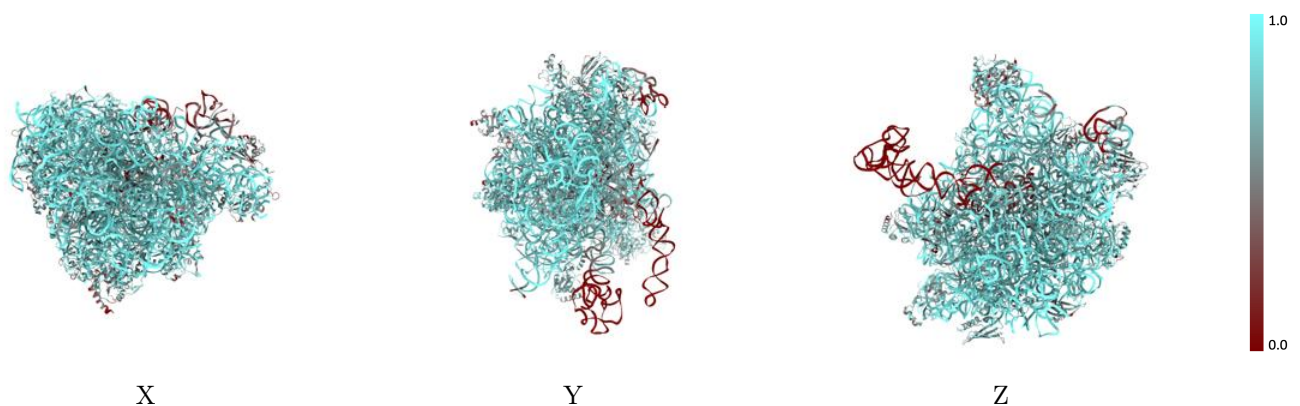
The images above show the 3D surface view of the map at the recommended contour level 0.69 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



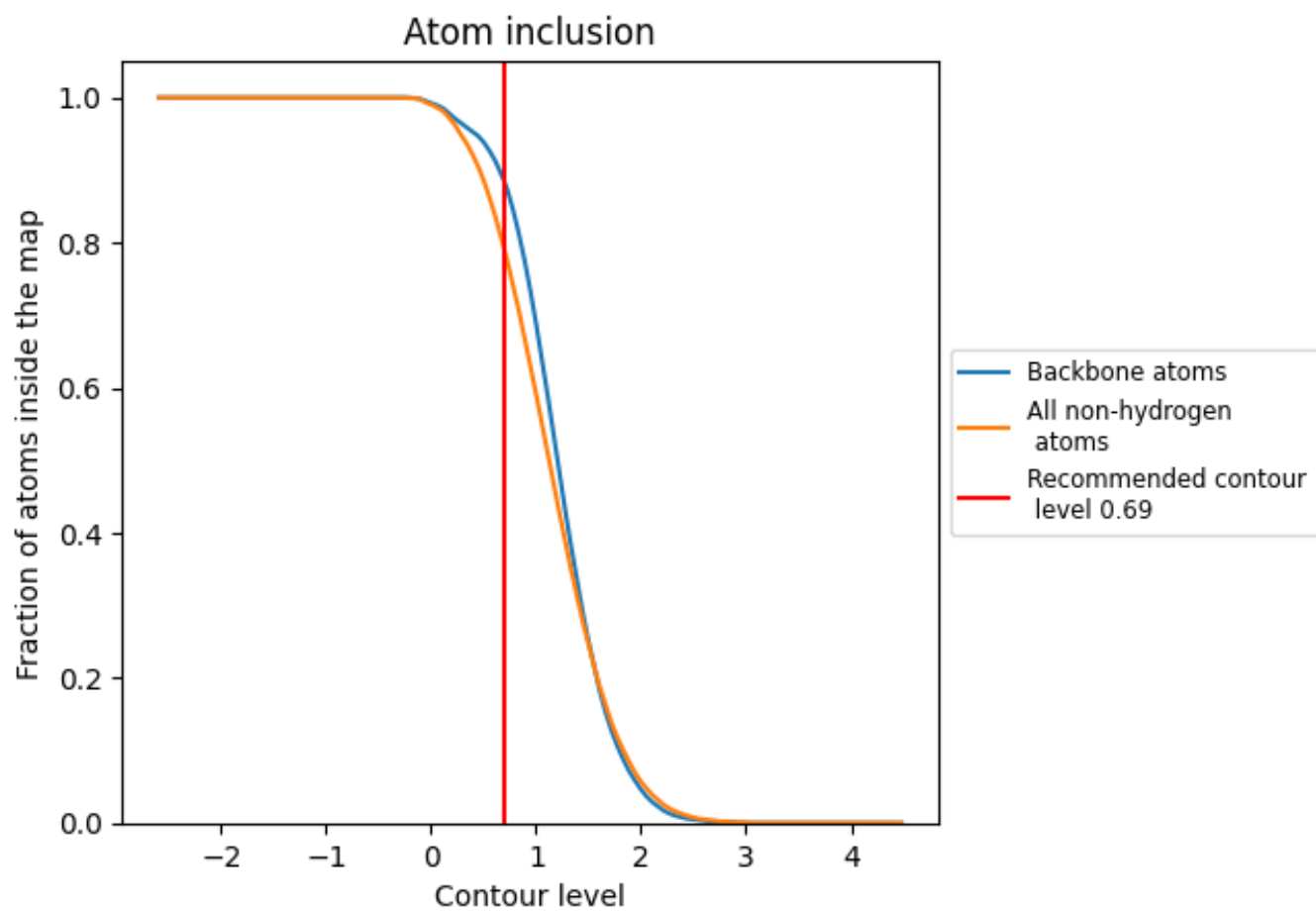
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.69).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 80% 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 (0.69) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7950	 0.3240
A23S	 0.8550	 0.3230
A5S	 0.9440	 0.3270
AL2P	 0.5930	 0.3040
AL3P	 0.7390	 0.3370
AL4P	 0.7680	 0.3660
AL5P	 0.4510	 0.2690
AL6P	 0.6410	 0.3270
ALX0	 0.6370	 0.2910
L10E	 0.6080	 0.3240
L13P	 0.7150	 0.3250
L141	 0.7020	 0.3140
L142	 0.6150	 0.2910
L14P	 0.7560	 0.3410
L15E	 0.6800	 0.3270
L15P	 0.6610	 0.3280
L18E	 0.7540	 0.3570
L18P	 0.6560	 0.2780
L19E	 0.7650	 0.3470
L21E	 0.6980	 0.3510
L22P	 0.7280	 0.3560
L23P	 0.6980	 0.3600
L24E	 0.8440	 0.3630
L24P	 0.6950	 0.3400
L29P	 0.6450	 0.3100
L30E	 0.6990	 0.3060
L30P	 0.6880	 0.2950
L31E	 0.7450	 0.3670
L32E	 0.6570	 0.3640
L34E	 0.6830	 0.2840
L37A	 0.7680	 0.3250
L37E	 0.7720	 0.3440
L39E	 0.7060	 0.3240
L40E	 0.4890	 0.2630
L44E	 0.6560	 0.3200



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Chain	Atom inclusion	Q-score
L45A	 0.6630	 0.3430
L46A	 0.6560	 0.3500
L47A	 0.5490	 0.3610
L7A1	 0.6780	 0.2980
L7A2	 0.5400	 0.2830