



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:34 PM UTC

PDB ID : 7ZOD / pdb_00007zod
EMDB ID : EMD-14846
Title : 70S E. coli ribosome with an extended uL23 loop from Candidatus marinimicrobia
Authors : Mitropoulou, A.; Plessa, E.; Wlodarski, T.; Ahn, M.; Sidhu, H.; Becker, T.A.; Beckmann, R.; Cabrita, L.D.; Christodoulou, J.
Deposited on : 2022-04-25
Resolution : 2.56 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:

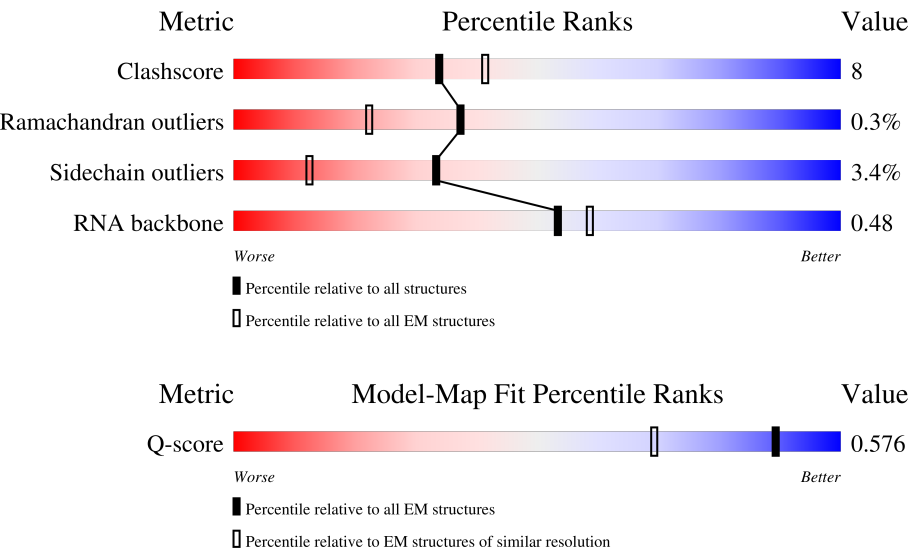
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.56 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	7558 (2.06 - 3.06)

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	78	
2	1	63	
3	2	59	

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Mol	Chain	Length	Quality of chain
4	3	57	
5	4	55	
6	6	46	
7	7	65	
8	8	50	
9	a	120	
10	b	2904	
11	c	273	
12	d	209	
13	e	201	
14	f	179	
15	g	177	
16	h	149	
17	j	142	
18	k	123	
19	l	144	
20	m	136	
21	n	127	
22	o	117	
23	p	115	
24	q	118	
25	r	103	
26	s	110	
27	t	108	
28	u	104	

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Mol	Chain	Length	Quality of chain
29	v	77	 82% 34% 47% 19%
30	w	94	 12% 76% 23%
31	y	85	 68% 18% 12%

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 90702 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	102	Total	C	N	O	S	0	0
			810	513	152	143	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	101	Total	C	N	O	S	0	0
			793	497	150	143	3		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	68	ARG	-	insertion	UNP P0ADZ0
t	69	GLN	-	insertion	UNP P0ADZ0
t	70	MET	-	insertion	UNP P0ADZ0
t	71	THR	-	insertion	UNP P0ADZ0
t	72	VAL	LYS	conflict	UNP P0ADZ0
t	74	SER	HIS	conflict	UNP P0ADZ0
t	76	GLY	GLN	conflict	UNP P0ADZ0
t	78	VAL	-	insertion	UNP P0ADZ0
t	80	ARG	-	insertion	UNP P0ADZ0
t	81	THR	-	insertion	UNP P0ADZ0
t	82	SER	-	insertion	UNP P0ADZ0

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

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

- Molecule 29 is a RNA chain called Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 30 is a protein called 50S ribosomal protein L25.

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

- Molecule 31 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	75	Total	C	N	O	S	0	0
			572	355	116	100	1		

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L28

Chain 0: 



- Molecule 2: 50S ribosomal protein L29

Chain 1: 



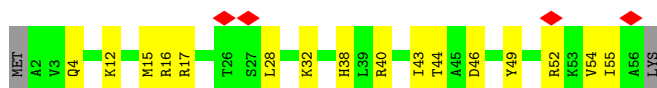
- Molecule 3: 50S ribosomal protein L30

Chain 2: 



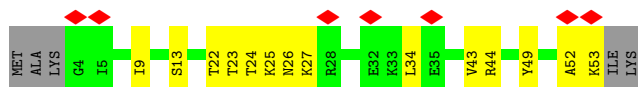
- Molecule 4: 50S ribosomal protein L32

Chain 3: 

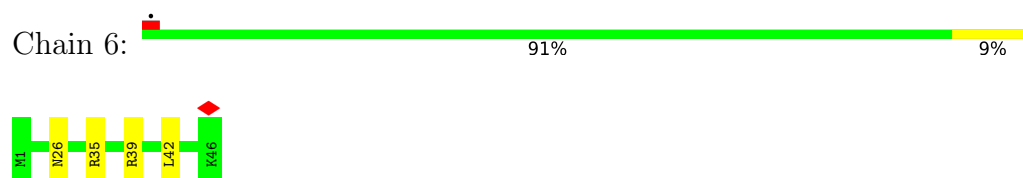


- Molecule 5: 50S ribosomal protein L33

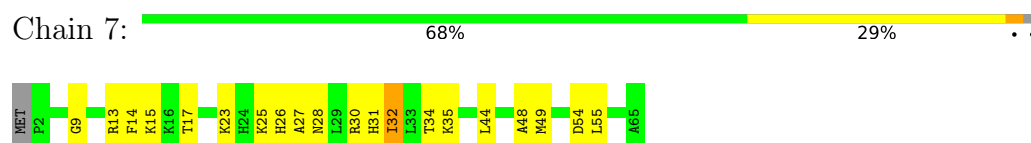
Chain 4: 



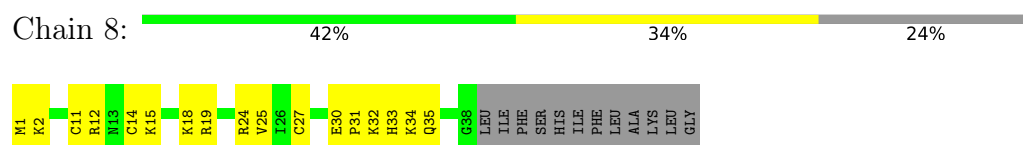
- Molecule 6: 50S ribosomal protein L34



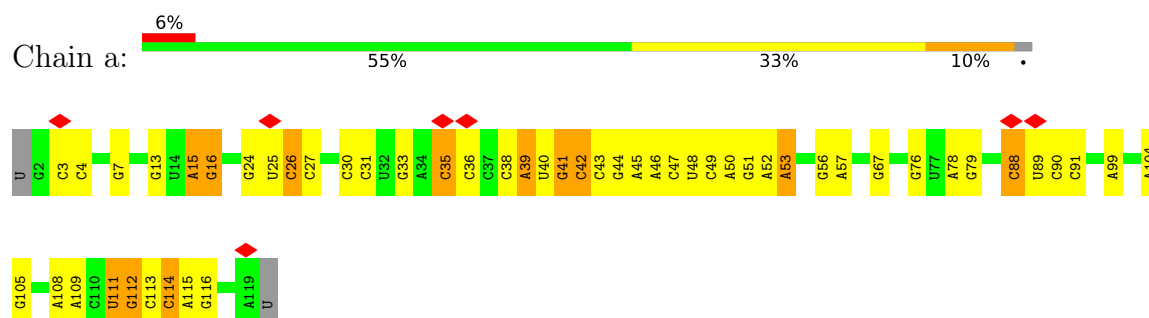
- Molecule 7: 50S ribosomal protein L35



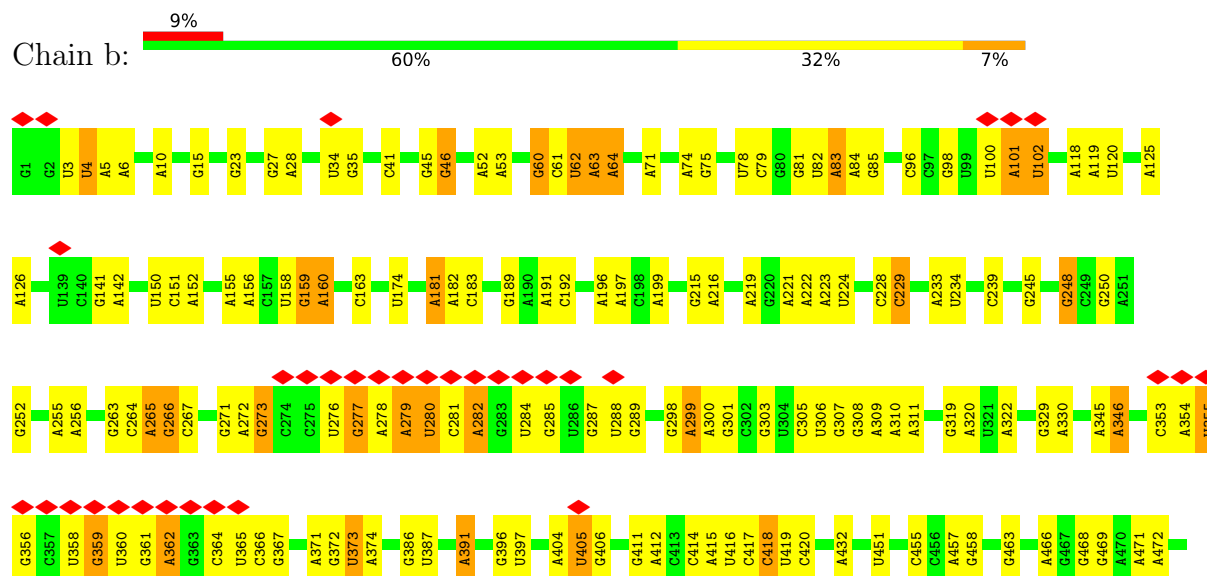
- Molecule 8: 50S ribosomal protein L36



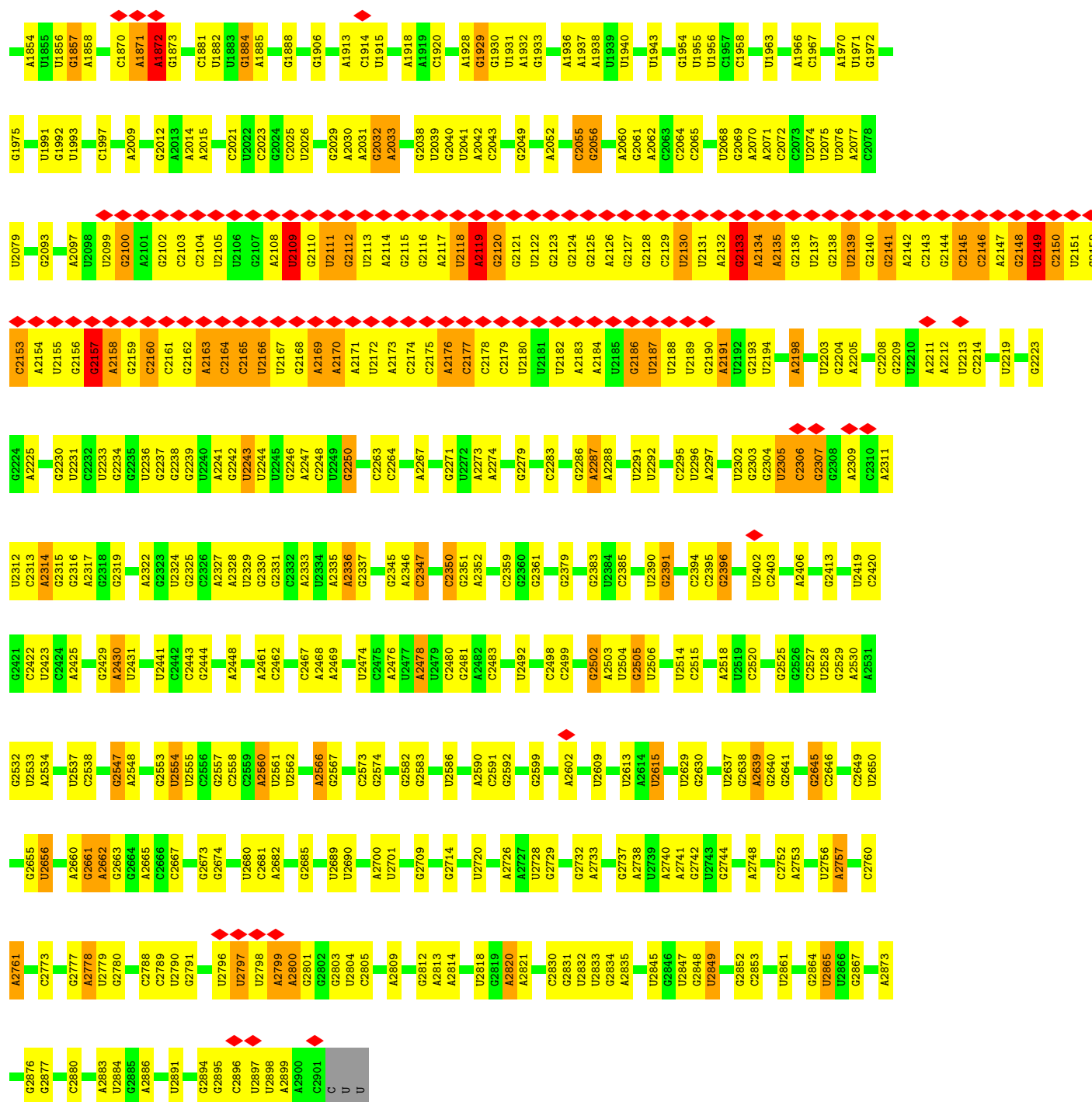
- Molecule 9: 5S rRNA



- Molecule 10: 23S rRNA



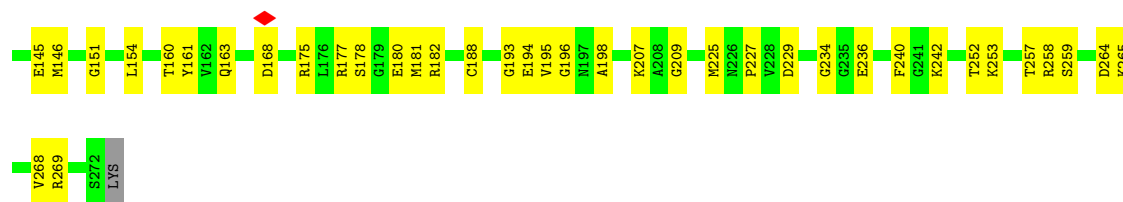




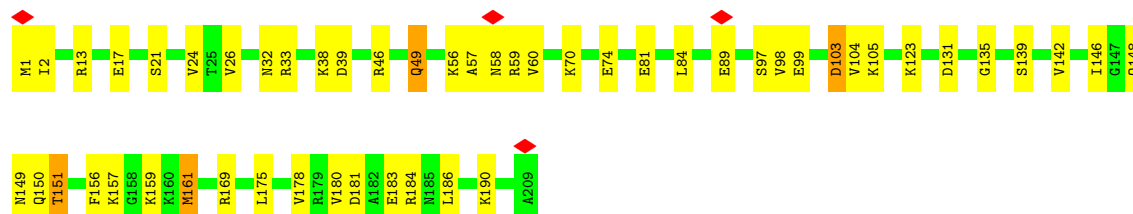
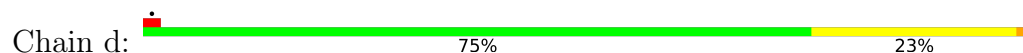
• Molecule 11: 50S ribosomal protein L2

Chain c: 74% 26%

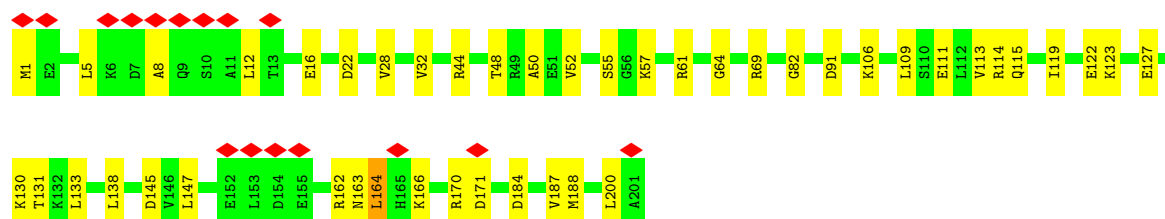
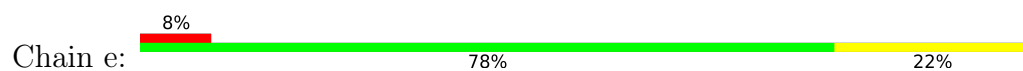




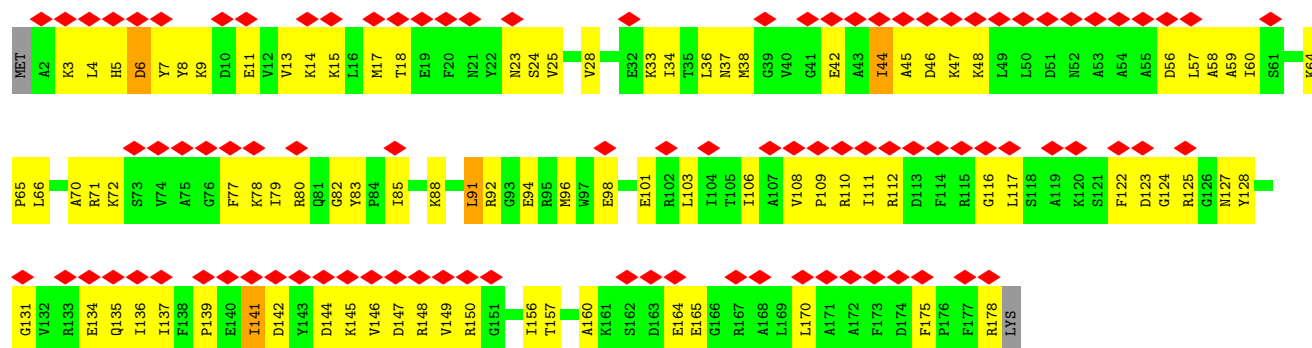
• Molecule 12: 50S ribosomal protein L3



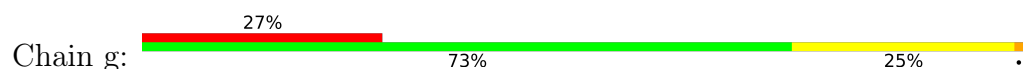
• Molecule 13: 50S ribosomal protein L4

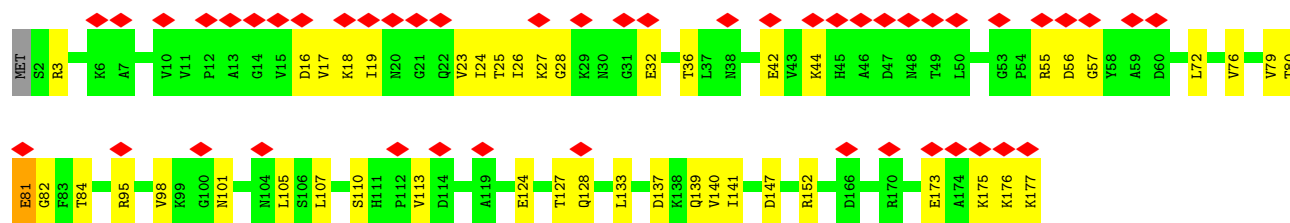


• Molecule 14: 50S ribosomal protein L5

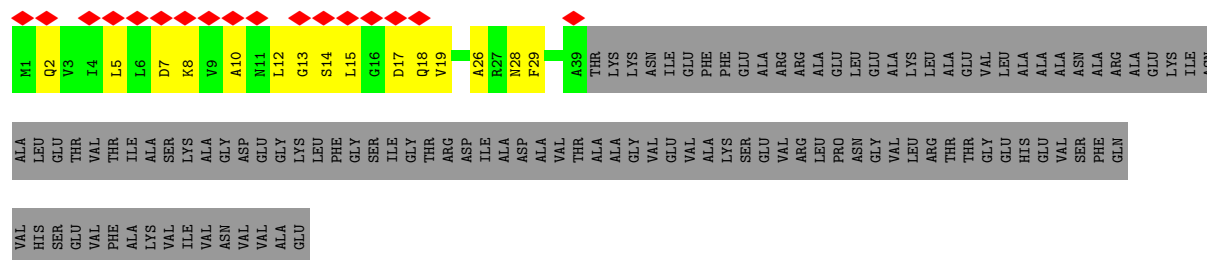


• Molecule 15: 50S ribosomal protein L6

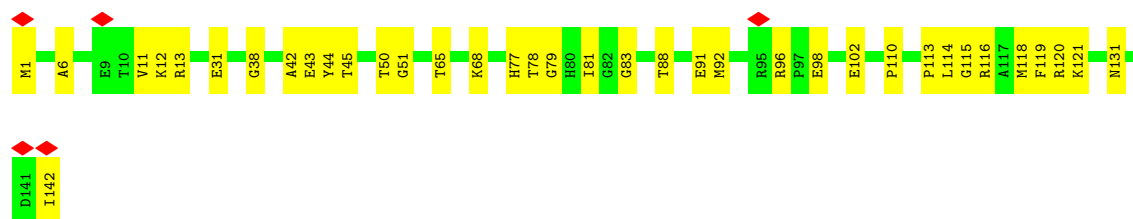




• Molecule 16: 50S ribosomal protein L9



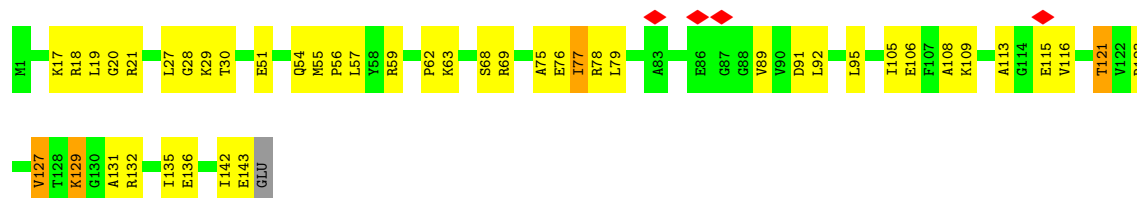
• Molecule 17: 50S ribosomal protein L13



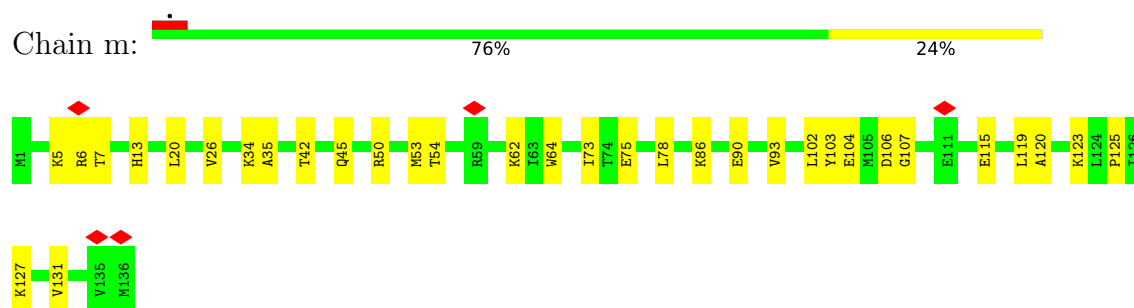
• Molecule 18: 50S ribosomal protein L14



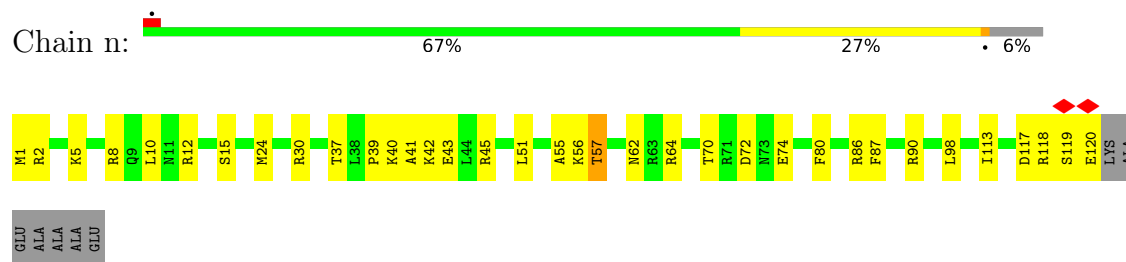
• Molecule 19: 50S ribosomal protein L15



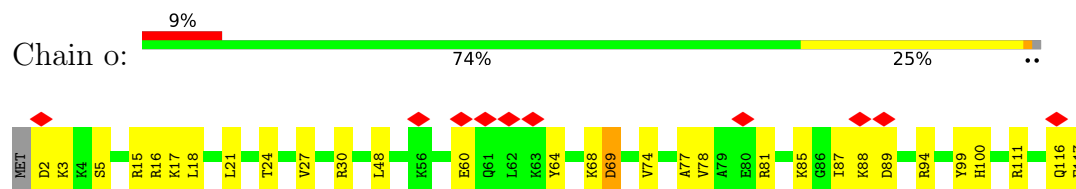
• Molecule 20: 50S ribosomal protein L16



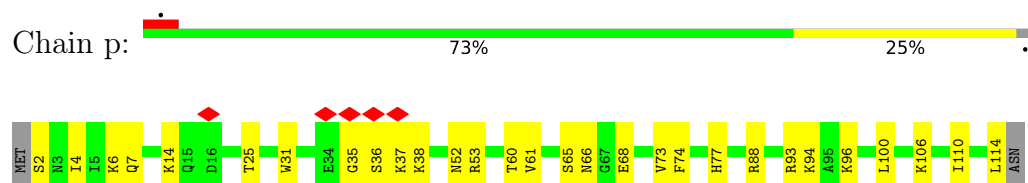
- Molecule 21: 50S ribosomal protein L17



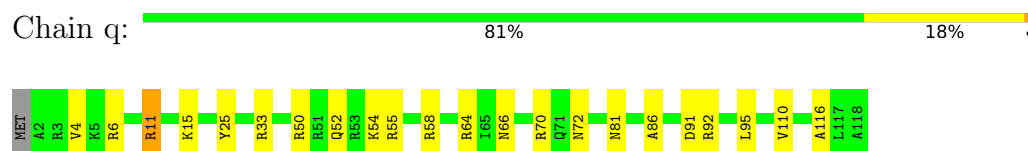
- Molecule 22: 50S ribosomal protein L18



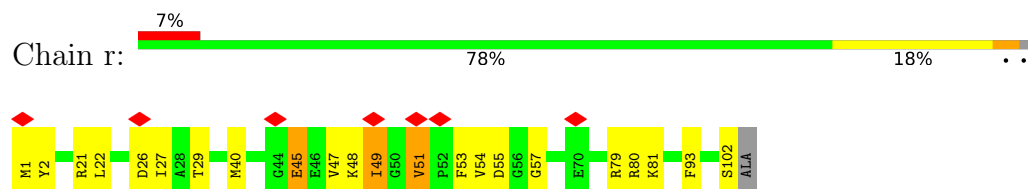
- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20

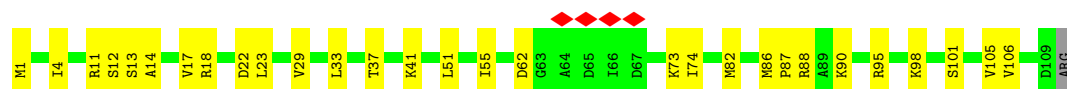


- Molecule 25: 50S ribosomal protein L21



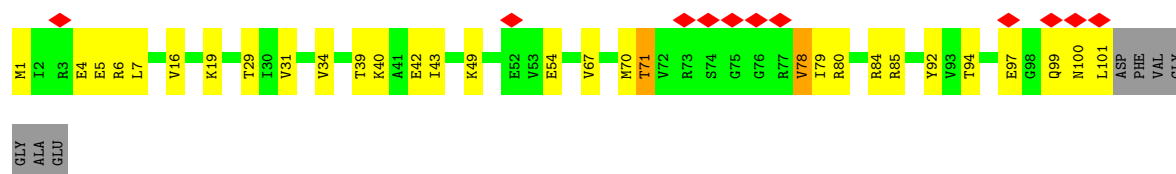
- Molecule 26: 50S ribosomal protein L22

Chain s: 



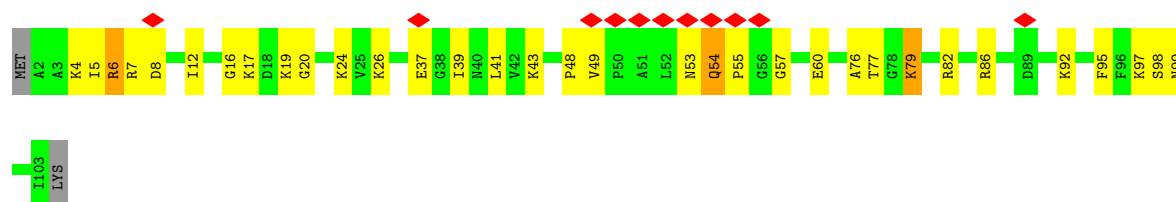
- Molecule 27: 50S ribosomal protein L23

Chain t: 



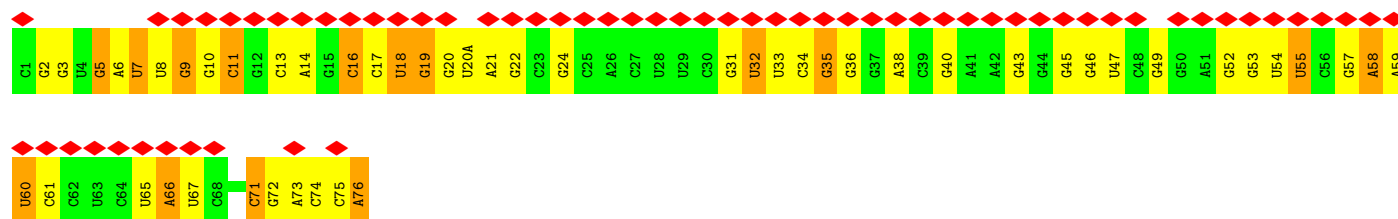
- Molecule 28: 50S ribosomal protein L24

Chain u: 



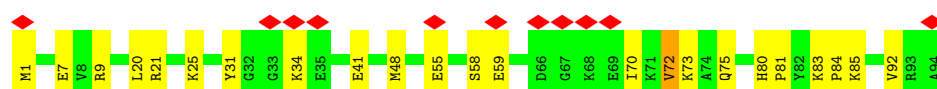
- Molecule 29: Pro-tRNA

Chain v: 



- Molecule 30: 50S ribosomal protein L25

Chain w: 



- Molecule 31: 50S ribosomal protein L27

Chain y: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	159764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.509	Depositor
Minimum map value	-0.279	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0441	Depositor
Map size ($\text{\AA}$)	409.72803, 409.72803, 409.72803	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.067, 1.067, 1.067	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.50	0/635	0.53	0/848
2	1	0.48	0/496	0.71	1/660 (0.2%)
3	2	0.47	0/443	0.52	0/593
4	3	0.51	0/440	0.56	0/588
5	4	0.49	0/416	0.64	0/554
6	6	0.54	0/380	0.53	0/498
7	7	0.56	0/513	0.59	0/676
8	8	0.55	0/302	0.73	0/397
9	a	0.47	0/2828	0.43	0/4410
10	b	0.56	0/69757	0.45	20/108827 (0.0%)
11	c	0.54	0/2121	0.57	0/2852
12	d	0.52	0/1586	0.55	0/2134
13	e	0.46	0/1571	0.56	0/2113
14	f	0.41	0/1434	0.74	0/1926
15	g	0.40	0/1343	0.64	0/1816
16	h	0.33	0/290	0.67	0/392
17	j	0.52	0/1152	0.53	0/1551
18	k	0.54	0/947	0.67	0/1268
19	l	0.58	0/1052	0.66	0/1401
20	m	0.48	0/1093	0.55	0/1460
21	n	0.54	0/973	0.60	0/1301
22	o	0.45	0/902	0.63	0/1209
23	p	0.51	0/920	0.56	0/1231
24	q	0.57	0/960	0.58	1/1278 (0.1%)
25	r	0.61	0/823	0.79	1/1100 (0.1%)
26	s	0.51	0/852	0.52	0/1142
27	t	0.61	0/798	0.77	0/1067
28	u	0.56	0/787	0.75	2/1051 (0.2%)
29	v	0.52	0/1839	0.76	1/2866 (0.0%)
30	w	0.43	0/766	0.54	0/1025
31	y	0.56	0/579	0.66	1/767 (0.1%)
All	All	0.55	0/98998	0.50	27/149001 (0.0%)

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2133	G	C2'-C3'-O3'	9.58	128.07	113.70
10	b	895	U	C2'-C3'-O3'	8.57	122.36	109.50
10	b	2157	G	C4'-C3'-O3'	7.76	121.04	109.40
10	b	2139	U	C2'-C3'-O3'	6.96	119.95	109.50
10	b	2118	U	C2'-C3'-O3'	6.82	119.73	109.50

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	625	0	652	9	0
2	1	495	0	526	14	0
3	2	439	0	482	13	0
4	3	434	0	445	12	0
5	4	409	0	440	14	0
6	6	377	0	418	3	0
7	7	504	0	572	18	0
8	8	301	0	341	15	0
9	a	2529	0	1281	31	0
10	b	62281	0	31323	620	0
11	c	2082	0	2154	55	0
12	d	1565	0	1616	45	0
13	e	1552	0	1619	38	0
14	f	1410	0	1444	95	0
15	g	1323	0	1371	34	0
16	h	287	0	307	11	0
17	j	1129	0	1162	30	0
18	k	938	0	1012	25	0
19	l	1043	0	1123	35	0
20	m	1074	0	1157	21	0
21	n	960	0	1000	28	0
22	o	892	0	923	26	0
23	p	908	0	956	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	q	947	0	1019	23	0
25	r	810	0	834	9	0
26	s	845	0	909	20	0
27	t	793	0	867	19	0
28	u	779	0	831	22	0
29	v	1646	0	832	12	0
30	w	753	0	780	18	0
31	y	572	0	593	12	0
All	All	90702	0	58989	1204	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 8.

The worst 5 of 1204 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)
10:b:62:U:C4	10:b:63:A:N6	2.10	1.18
10:b:62:U:O4	10:b:63:A:N6	1.83	1.09
10:b:2145:C:C5'	10:b:2146:C:H5'	1.90	1.00
10:b:2135:A:H5'	10:b:2157:G:H1'	1.48	0.96
10:b:2145:C:H5''	10:b:2146:C:H5'	1.48	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
2	1	59/63 (94%)	55 (93%)	3 (5%)	1 (2%)	7	8
3	2	55/59 (93%)	52 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	3	53/57 (93%)	51 (96%)	2 (4%)	0	100	100
5	4	48/55 (87%)	43 (90%)	5 (10%)	0	100	100
6	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
7	7	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	9
8	8	36/50 (72%)	36 (100%)	0	0	100	100
11	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
12	d	207/209 (99%)	201 (97%)	6 (3%)	0	100	100
13	e	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
14	f	175/179 (98%)	156 (89%)	19 (11%)	0	100	100
15	g	174/177 (98%)	164 (94%)	9 (5%)	1 (1%)	21	28
16	h	37/149 (25%)	29 (78%)	8 (22%)	0	100	100
17	j	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
18	k	120/123 (98%)	108 (90%)	11 (9%)	1 (1%)	16	22
19	l	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
20	m	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
21	n	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	o	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
23	p	111/115 (96%)	103 (93%)	8 (7%)	0	100	100
24	q	115/118 (98%)	115 (100%)	0	0	100	100
25	r	100/103 (97%)	89 (89%)	7 (7%)	4 (4%)	2	1
26	s	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
27	t	99/108 (92%)	94 (95%)	5 (5%)	0	100	100
28	u	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
30	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
31	y	73/85 (86%)	69 (94%)	3 (4%)	1 (1%)	9	11
All	All	3057/3287 (93%)	2862 (94%)	186 (6%)	9 (0%)	37	44

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	r	51	VAL
7	7	32	ILE
15	g	81	GLU

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Mol	Chain	Res	Type
31	y	44	LYS
25	r	54	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	67/68 (98%)	64 (96%)	3 (4%)	24	36
2	1	54/55 (98%)	51 (94%)	3 (6%)	19	28
3	2	47/49 (96%)	46 (98%)	1 (2%)	47	63
4	3	46/48 (96%)	44 (96%)	2 (4%)	26	38
5	4	45/49 (92%)	45 (100%)	0	100	100
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/44 (77%)	32 (94%)	2 (6%)	18	26
11	c	216/218 (99%)	213 (99%)	3 (1%)	59	73
12	d	164/164 (100%)	157 (96%)	7 (4%)	26	38
13	e	165/165 (100%)	164 (99%)	1 (1%)	78	85
14	f	148/150 (99%)	140 (95%)	8 (5%)	20	30
15	g	137/138 (99%)	134 (98%)	3 (2%)	45	61
16	h	30/114 (26%)	29 (97%)	1 (3%)	33	48
17	j	116/116 (100%)	111 (96%)	5 (4%)	26	38
18	k	103/104 (99%)	102 (99%)	1 (1%)	68	78
19	l	102/103 (99%)	97 (95%)	5 (5%)	22	33
20	m	109/109 (100%)	105 (96%)	4 (4%)	30	43
21	n	100/103 (97%)	96 (96%)	4 (4%)	28	40
22	o	86/87 (99%)	81 (94%)	5 (6%)	18	27
23	p	98/100 (98%)	97 (99%)	1 (1%)	68	78
24	q	89/90 (99%)	88 (99%)	1 (1%)	65	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	r	84/84 (100%)	76 (90%)	8 (10%)	8	10
26	s	92/93 (99%)	91 (99%)	1 (1%)	65	77
27	t	87/91 (96%)	81 (93%)	6 (7%)	14	20
28	u	83/85 (98%)	77 (93%)	6 (7%)	13	18
30	w	78/78 (100%)	77 (99%)	1 (1%)	61	74
31	y	57/63 (90%)	53 (93%)	4 (7%)	14	19
All	All	2526/2658 (95%)	2440 (97%)	86 (3%)	33	47

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	o	94	ARG
27	t	71	THR
24	q	11	ARG
25	r	49	ILE
28	u	6	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
26	s	7	HIS
31	y	40	GLN
15	g	115	HIS
14	f	63	GLN
31	y	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2900/2904 (99%)	618 (21%)	0
29	v	76/77 (98%)	45 (59%)	0
9	a	117/120 (97%)	32 (27%)	0
All	All	3093/3101 (99%)	695 (22%)	0

5 of 695 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	7	G

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Mol	Chain	Res	Type
9	a	13	G
9	a	15	A
9	a	16	G
9	a	24	G

There are no RNA pucker outliers to report.

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.

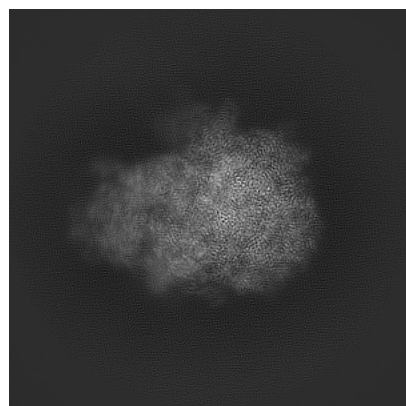
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14846. These allow visual inspection of the internal detail of the map and identification of artifacts.

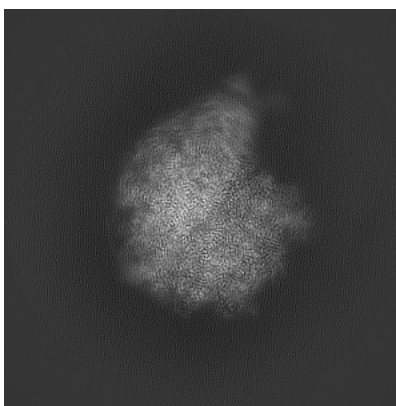
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

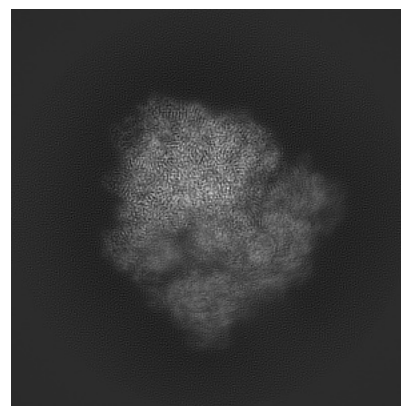
6.1.1 Primary map



X

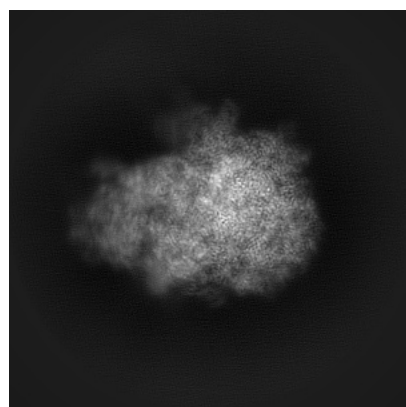


Y

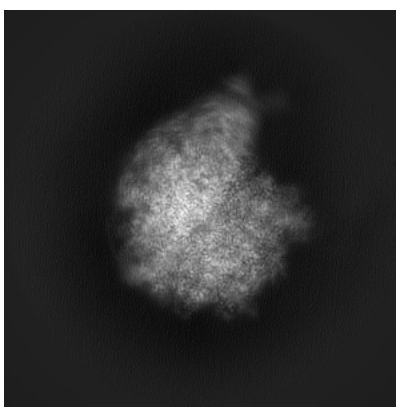


Z

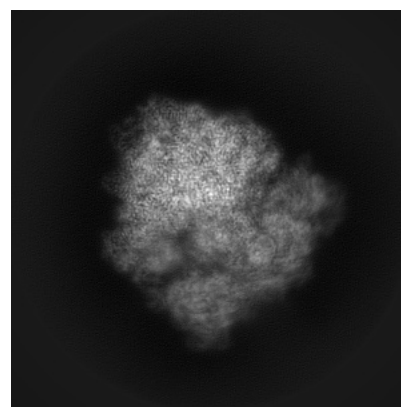
6.1.2 Raw map



X



Y

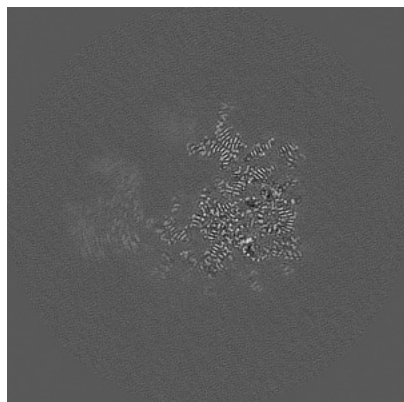


Z

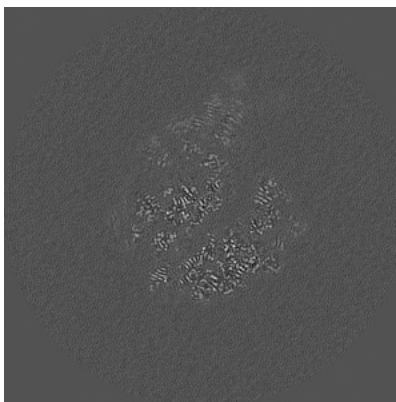
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

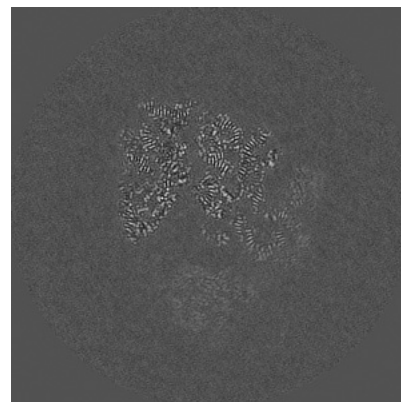
6.2.1 Primary map



X Index: 192

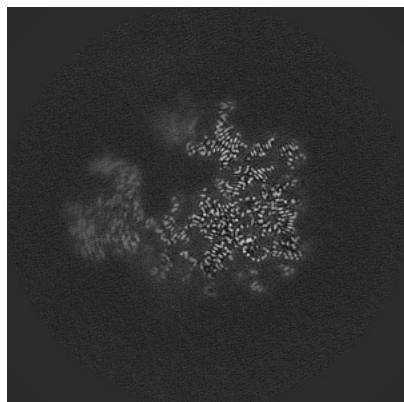


Y Index: 192

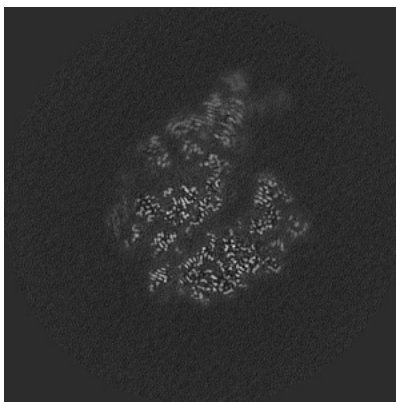


Z Index: 192

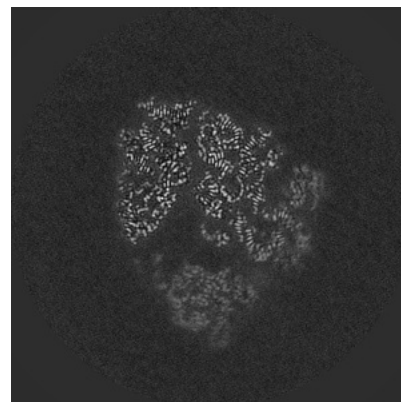
6.2.2 Raw map



X Index: 192



Y Index: 192

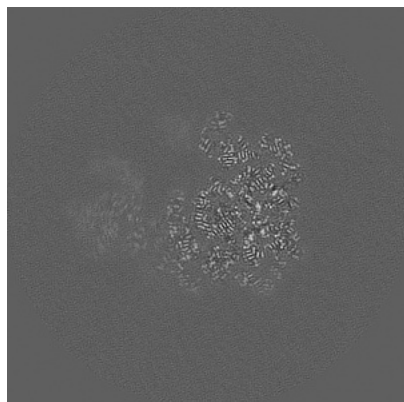


Z Index: 192

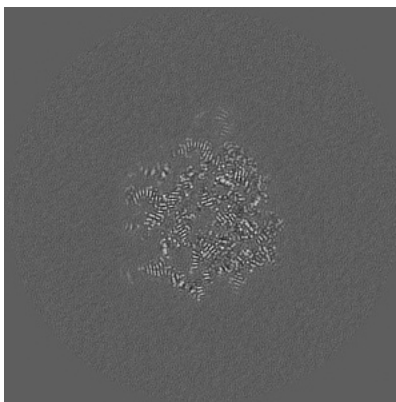
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

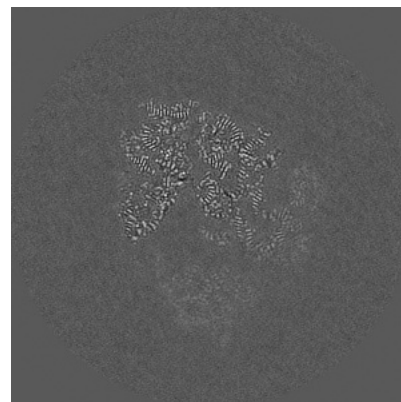
6.3.1 Primary map



X Index: 199

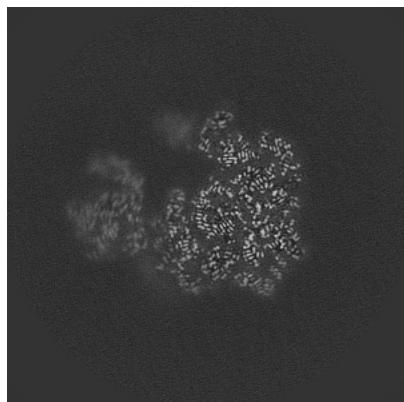


Y Index: 232

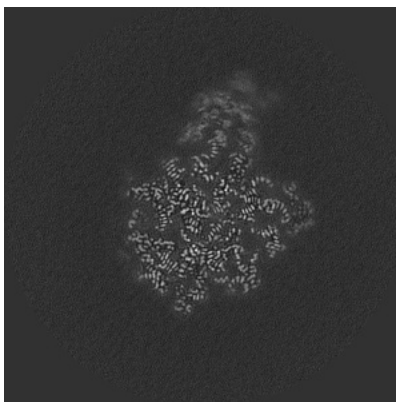


Z Index: 193

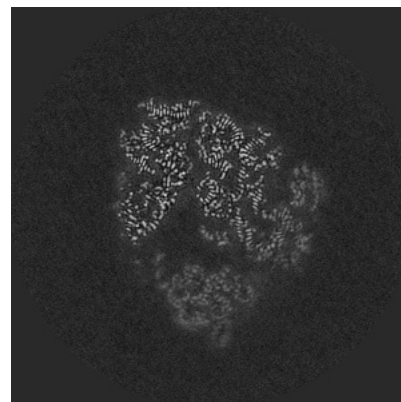
6.3.2 Raw map



X Index: 199



Y Index: 212

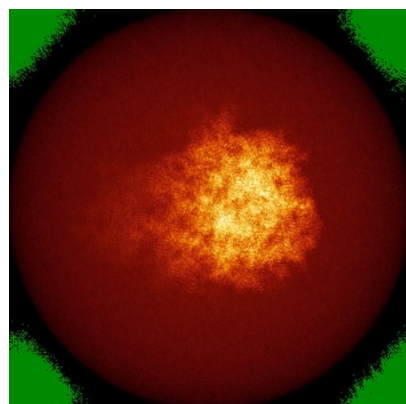


Z Index: 193

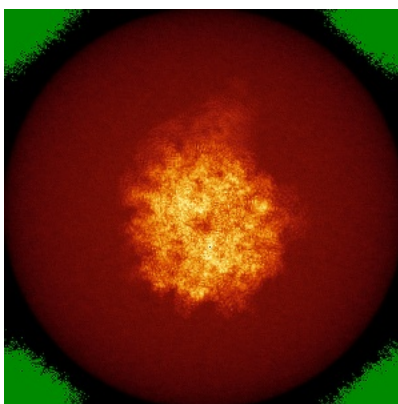
The images above show the largest variance slices of the map in three orthogonal directions.

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

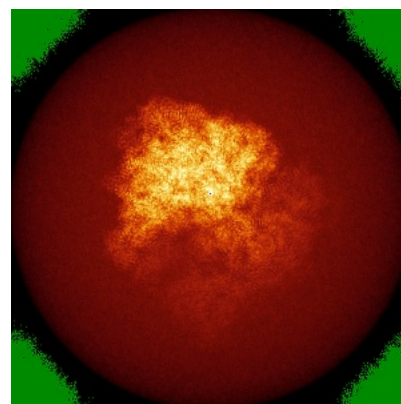
6.4.1 Primary map



X

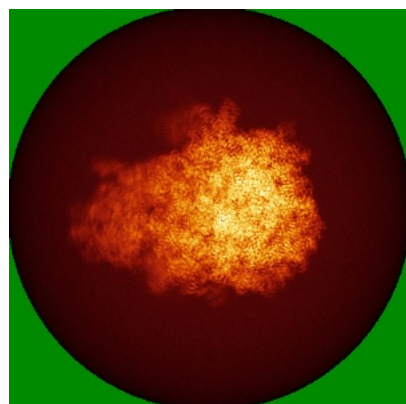


Y

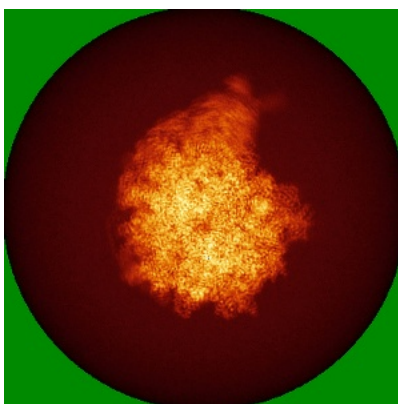


Z

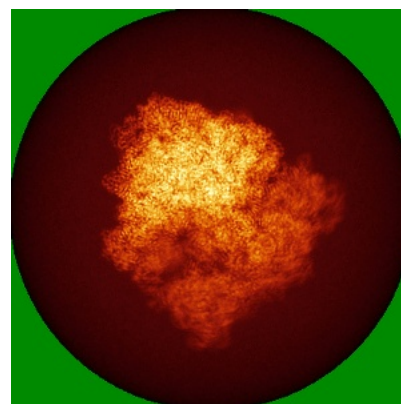
6.4.2 Raw map



X



Y

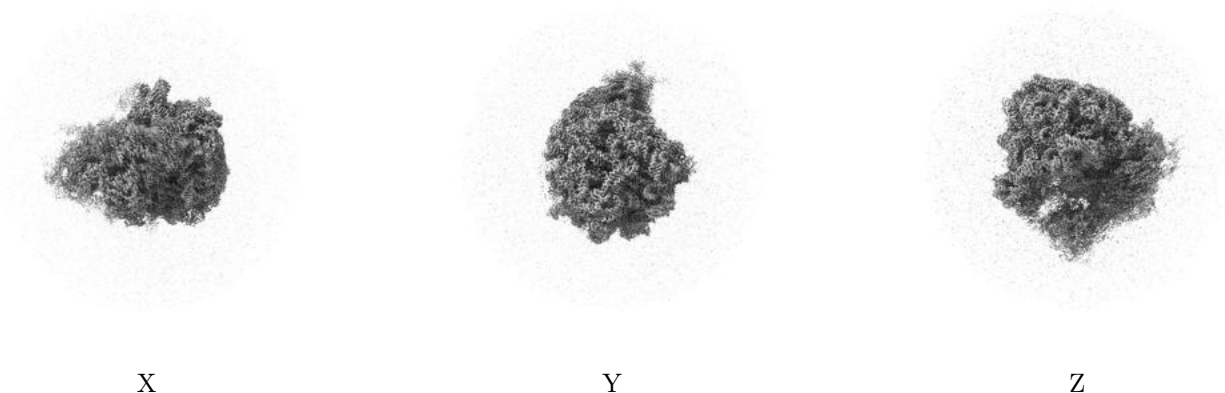


Z

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.

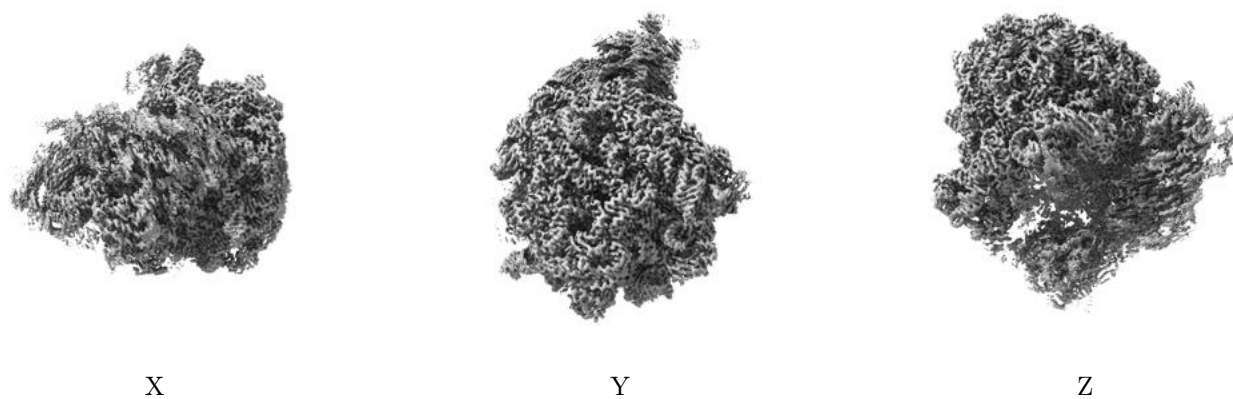
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0441. 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.

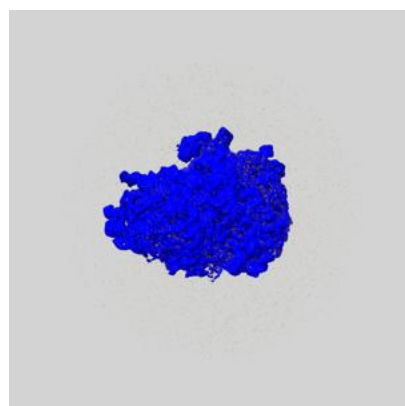
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

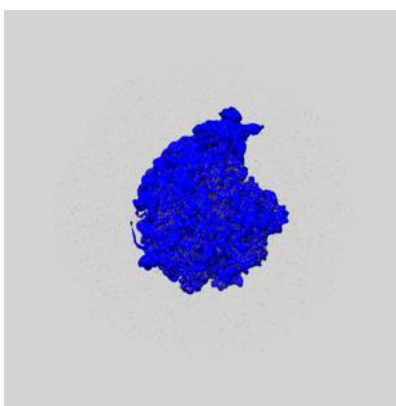
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

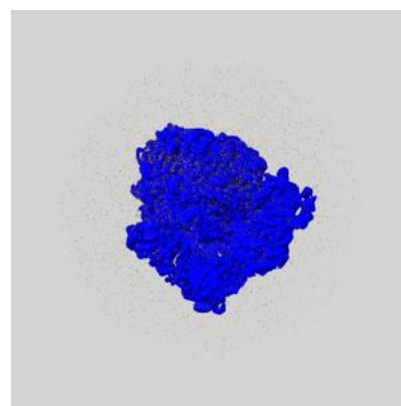
6.6.1 emd_14846_msk_1.map [i](#)



X



Y

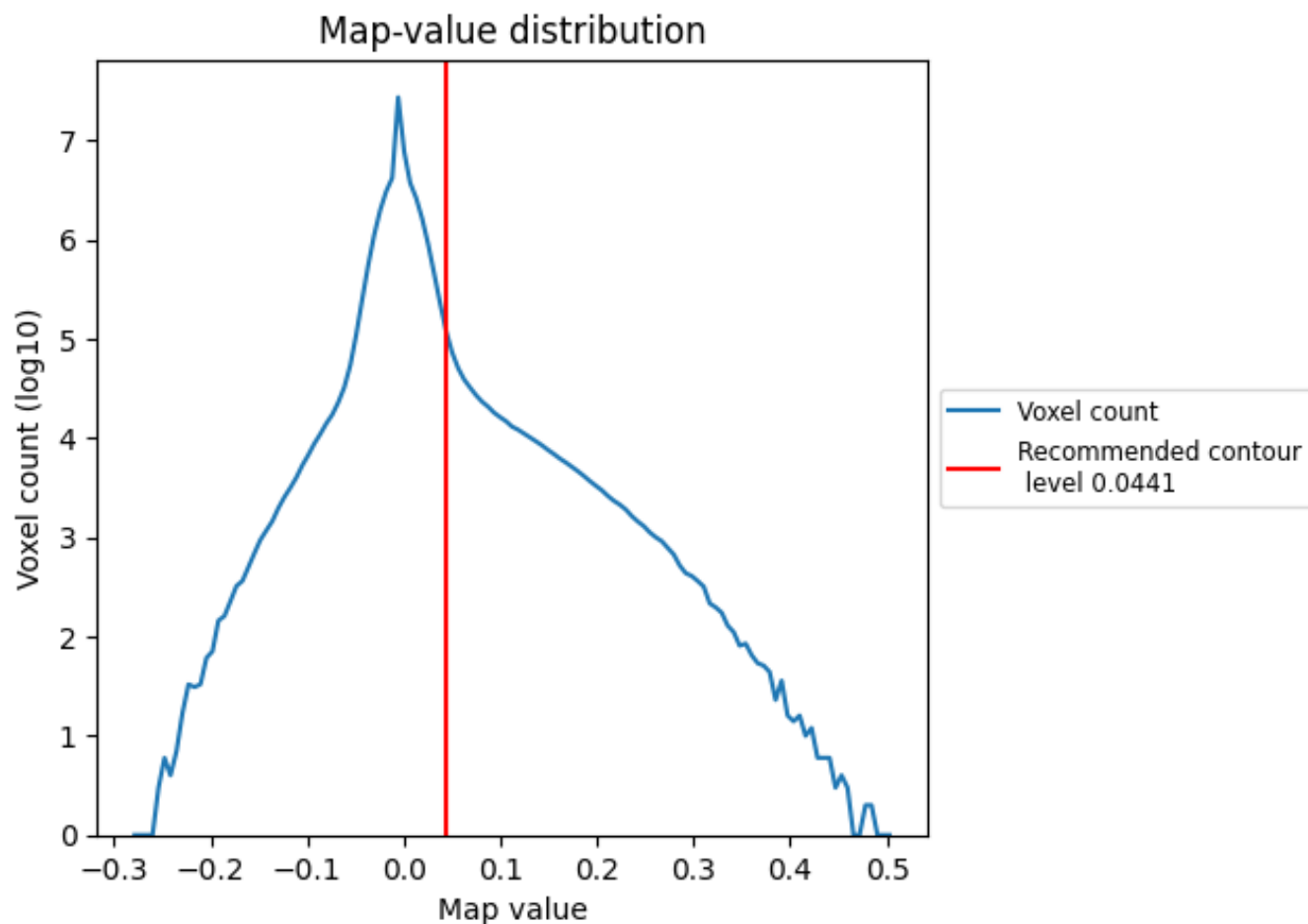


Z

7 Map analysis [i](#)

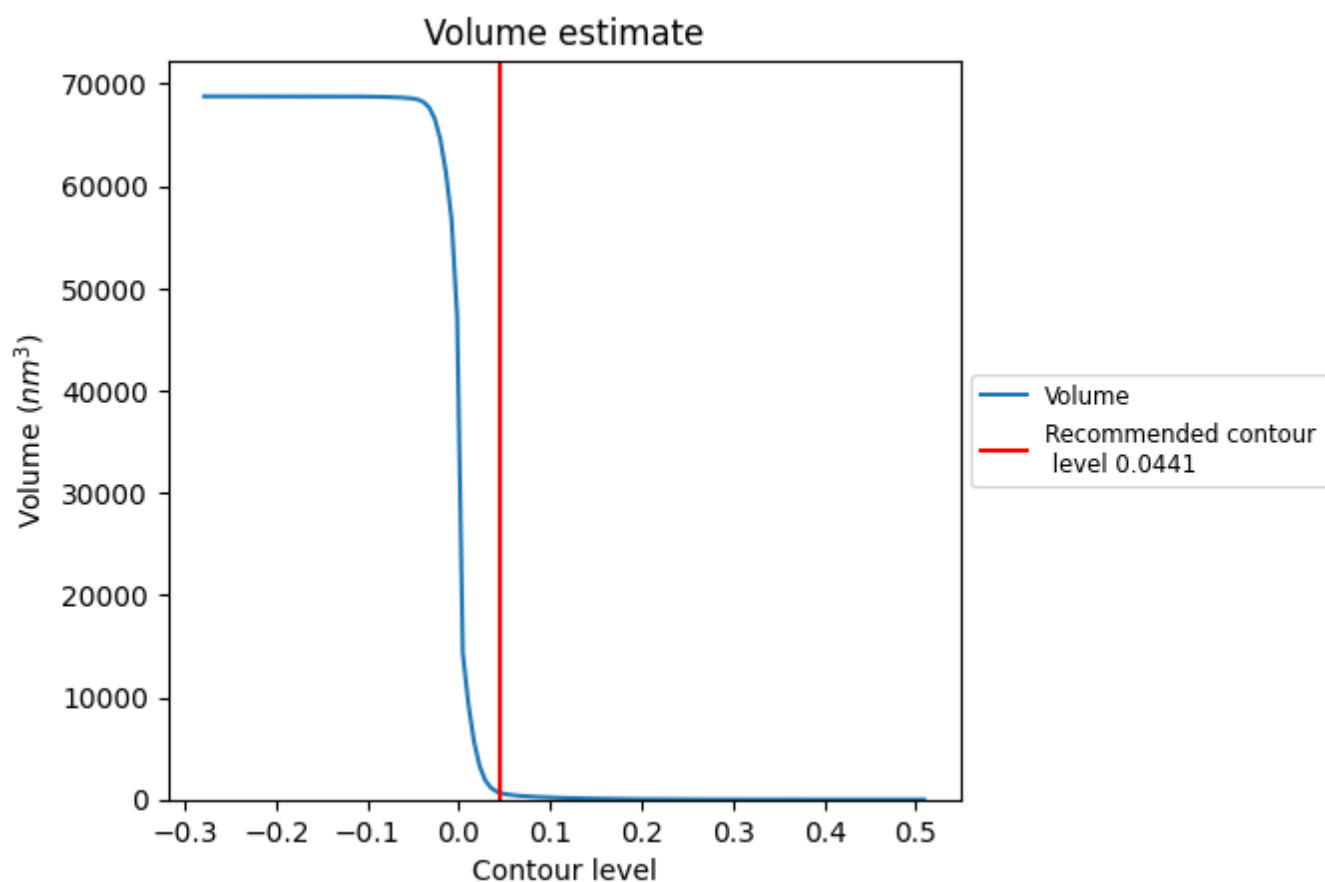
This section contains the results of statistical analysis of the map.

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.

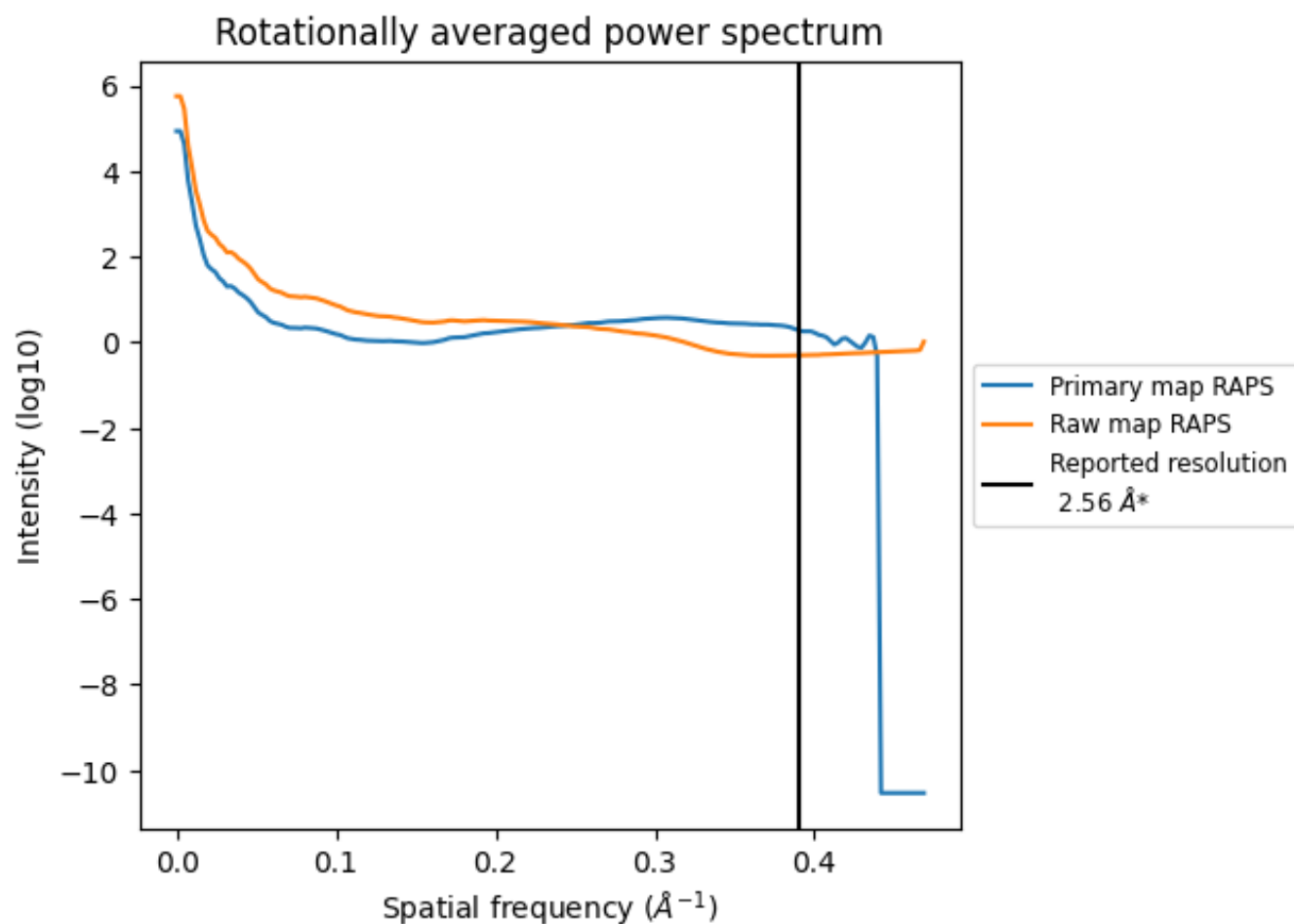
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 699 nm³; this corresponds to an approximate mass of 632 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 ⓘ

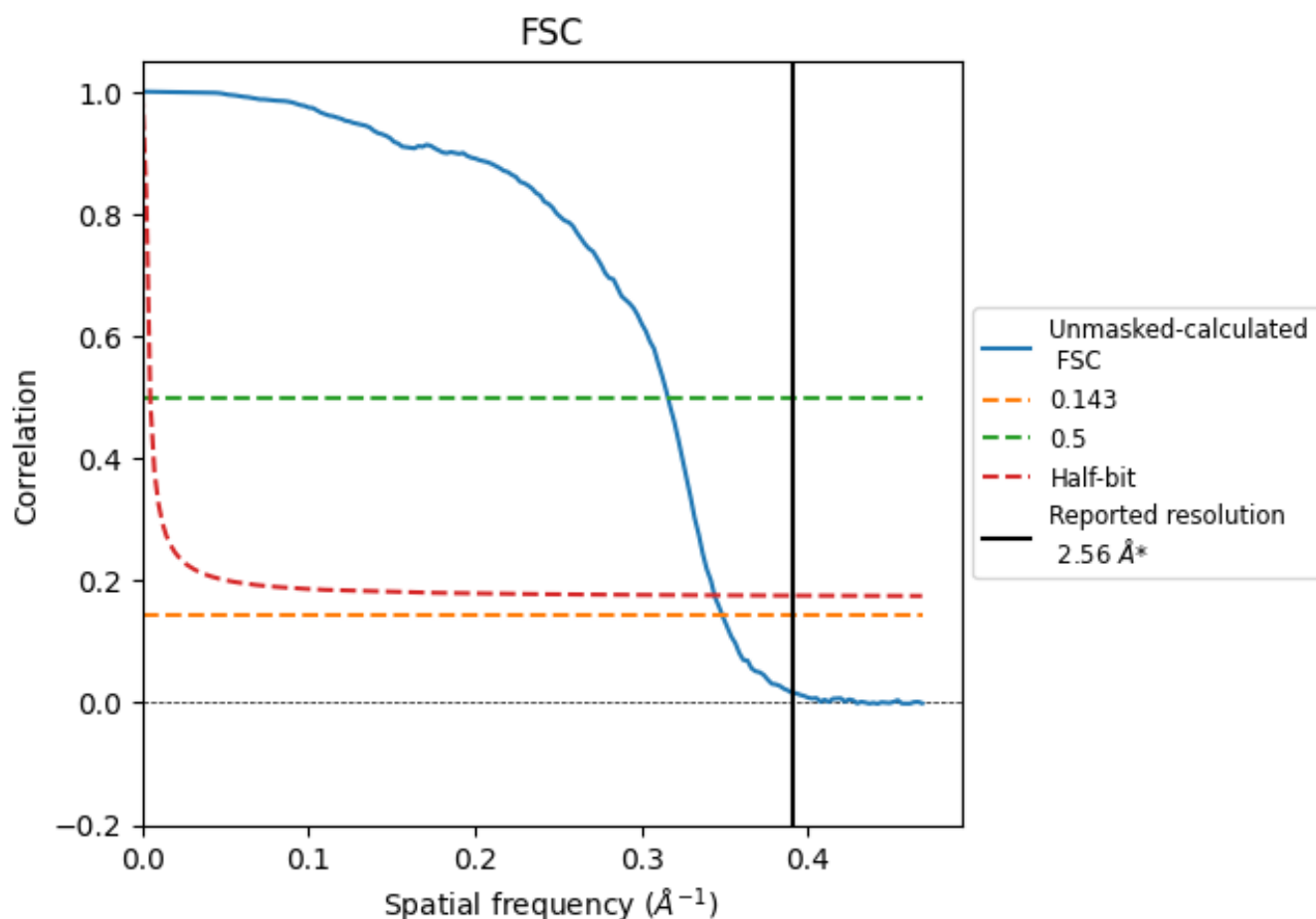


*Reported resolution corresponds to spatial frequency of 0.391 Å⁻¹

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 0.391 Å⁻¹

8.2 Resolution estimates [i](#)

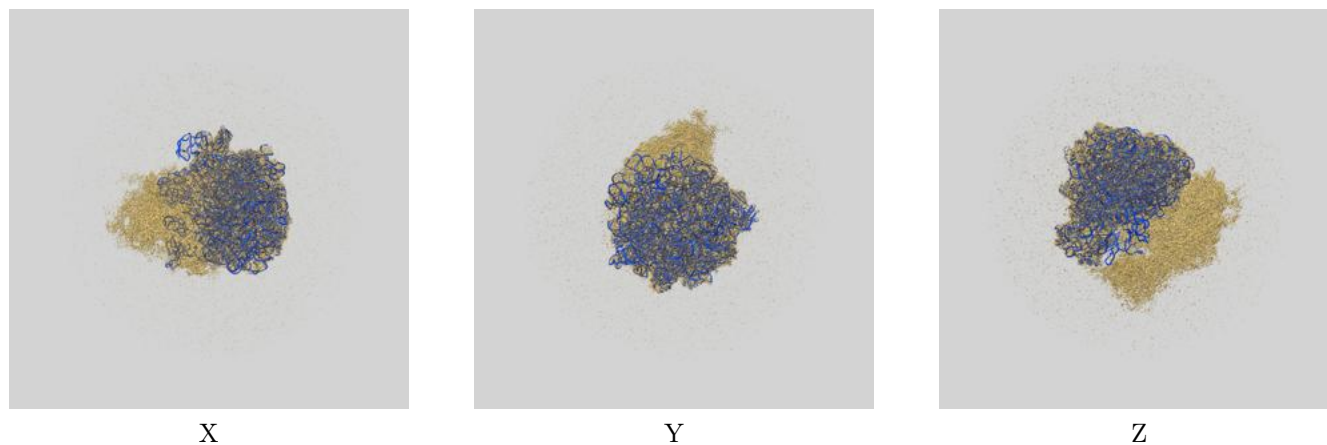
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.56	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.87	3.17	2.91

*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 2.87 differs from the reported value 2.56 by more than 10 %

9 Map-model fit [i](#)

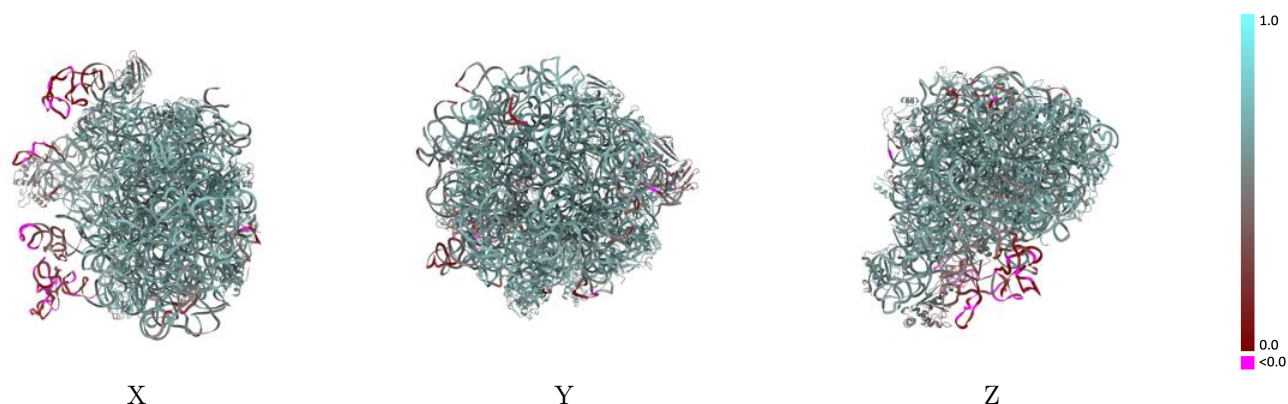
This section contains information regarding the fit between EMDB map EMD-14846 and PDB model 7ZOD. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



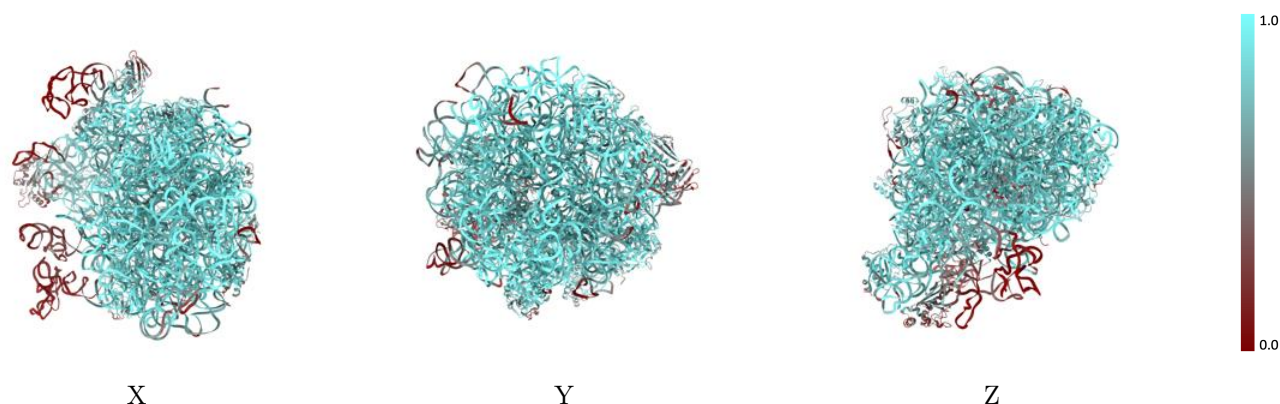
The images above show the 3D surface view of the map at the recommended contour level 0.0441 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



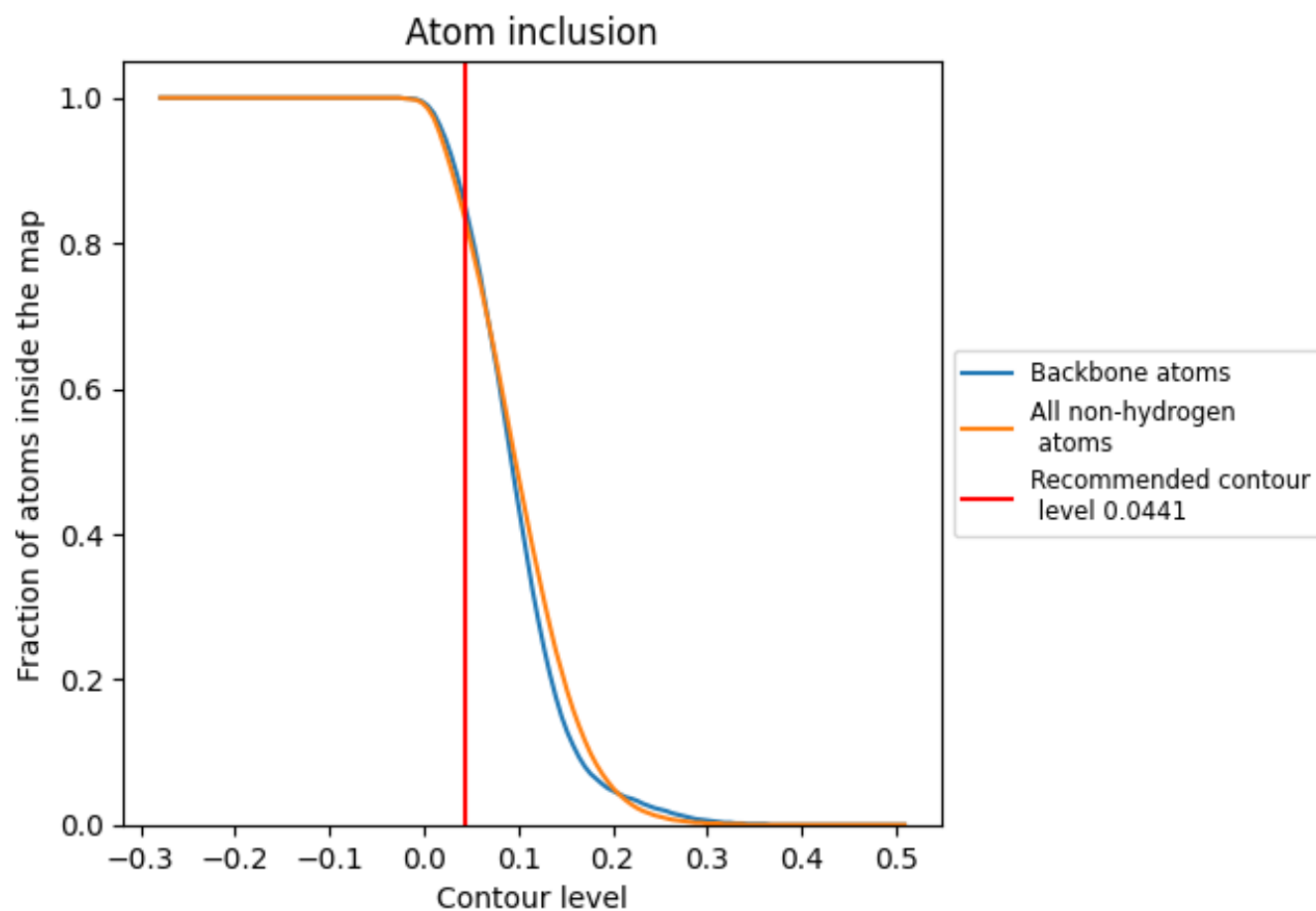
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0441).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 83% 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 (0.0441) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8310	 0.5760
0	 0.8880	 0.6240
1	 0.7430	 0.5720
2	 0.8550	 0.6020
3	 0.8590	 0.6160
4	 0.7760	 0.5830
6	 0.9610	 0.6500
7	 0.9450	 0.6490
8	 0.8450	 0.6040
a	 0.8240	 0.5700
b	 0.8550	 0.5800
c	 0.9180	 0.6360
d	 0.8840	 0.6160
e	 0.7910	 0.5900
f	 0.3910	 0.4290
g	 0.5710	 0.5090
h	 0.4820	 0.4780
j	 0.8860	 0.6170
k	 0.8610	 0.6070
l	 0.8760	 0.6170
m	 0.8670	 0.6160
n	 0.9190	 0.6300
o	 0.7590	 0.5700
p	 0.8490	 0.5980
q	 0.9290	 0.6330
r	 0.8170	 0.5910
s	 0.8840	 0.6260
t	 0.7810	 0.5720
u	 0.7310	 0.5530
v	 0.2450	 0.2240
w	 0.7560	 0.5850
y	 0.8780	 0.6230

