



## wwPDB EM Validation Summary Report ⓘ

May 20, 2026 – 10:25 PM JST

PDB ID : 9UZM / pdb\_00009uzm  
EMDB ID : EMD-64646  
Title : 40S ribosome without initiation factors  
Authors : Das, D.; Hussain, T.  
Deposited on : 2025-05-16  
Resolution : 4.50 Å(reported)  
Based on initial models : 8OZ0, 6YAN, .

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

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

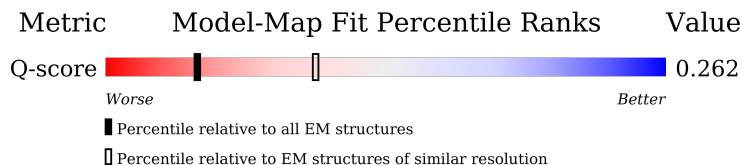
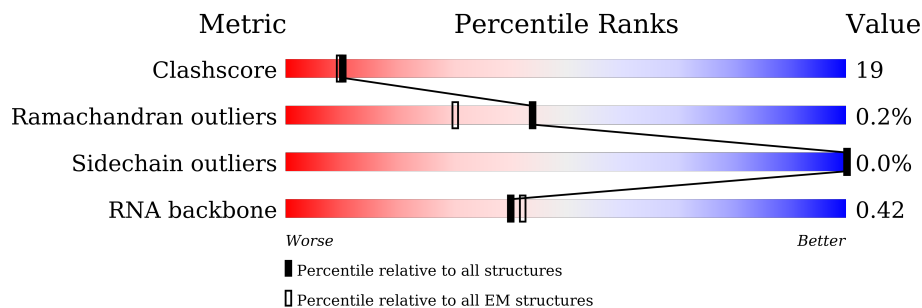
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.50 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.













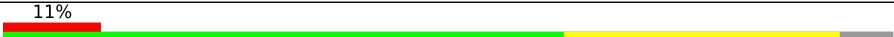


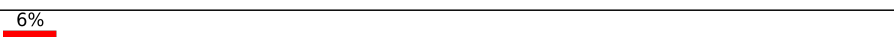
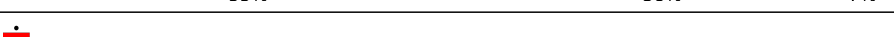
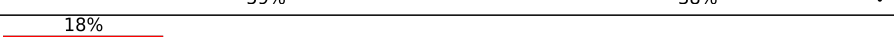



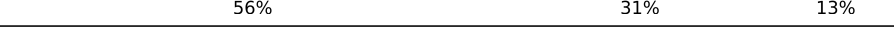





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 ( 4.00 - 5.00 )

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  $\geq 3$ , 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	2	1863	
2	C	295	
3	D	264	



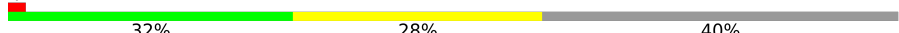

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Mol	Chain	Length	Quality of chain
4	E	226	
5	F	243	
6	G	263	
7	H	204	
8	I	249	
9	J	194	
10	K	208	
11	L	194	
12	M	225	
13	N	158	
14	O	132	
15	P	151	
16	Q	168	
17	R	145	
18	S	146	
19	T	135	
20	U	152	
21	V	141	
22	W	119	
23	X	83	
24	Y	130	
25	Z	143	
26	a	126	
27	b	115	
28	c	84	

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Mol	Chain	Length	Quality of chain
29	d	64	
30	e	56	
31	f	156	
32	g	317	
33	h	125	
34	i	59	
35	l	25	

## 2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 76441 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1744	Total	C	N	O	P	0	0
			37194	16608	6662	12184	1740		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	220	Total	C	N	O	S	0	0
			1704	1104	292	299	9		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	206	Total	C	N	O	S	0	0
			1679	1054	329	291	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	182	Total	C	N	O	S	0	0
			1498	952	300	244	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-30	THR	ALA	conflict	UNP A0AAG1W9A6

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 16 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	135	Total	C	N	O	S	0	0
			1111	704	211	189	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	141	Total	C	N	O	S	0	0
			1123	715	212	193	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	142	Total	C	N	O	S	0	0
			1172	733	239	199	1		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	82	Total	C	N	O	S	0	0
			619	378	117	119	5		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	3	SER	ASN	conflict	UNP G1TM82
X	4	ASN	ASP	conflict	UNP G1TM82
X	33	PRO	GLN	conflict	UNP G1TM82
X	50	SER	PHE	conflict	UNP G1TM82
X	76	HIS	ASP	conflict	UNP G1TM82

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		



- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	126	Total	C	N	O	S	0	0
			1022	645	198	174	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 28 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 29 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	64	Total	C	N	O	S	0	0
			507	308	102	95	2		

- Molecule 30 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 31 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 32 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 33 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 34 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

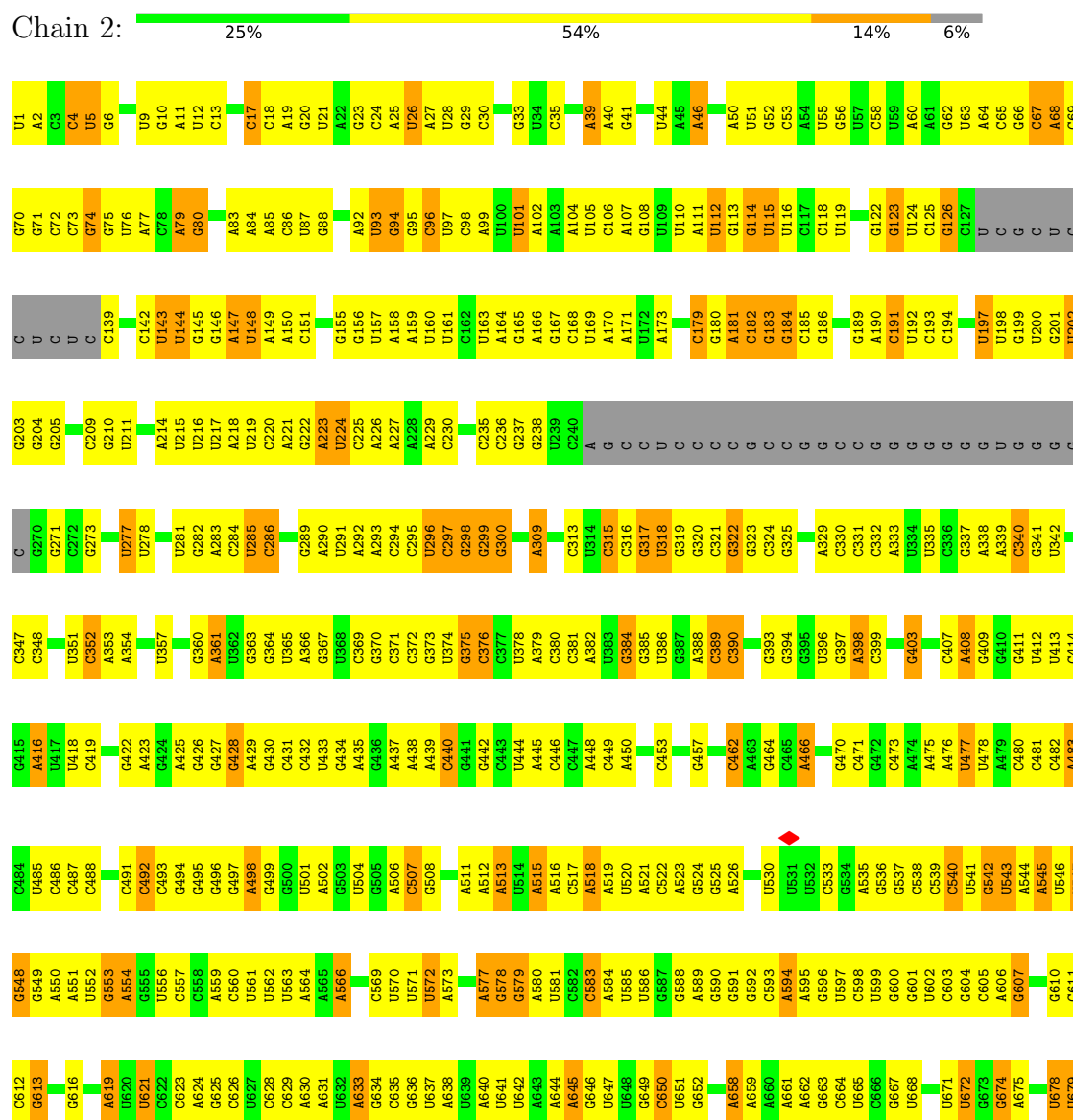
- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

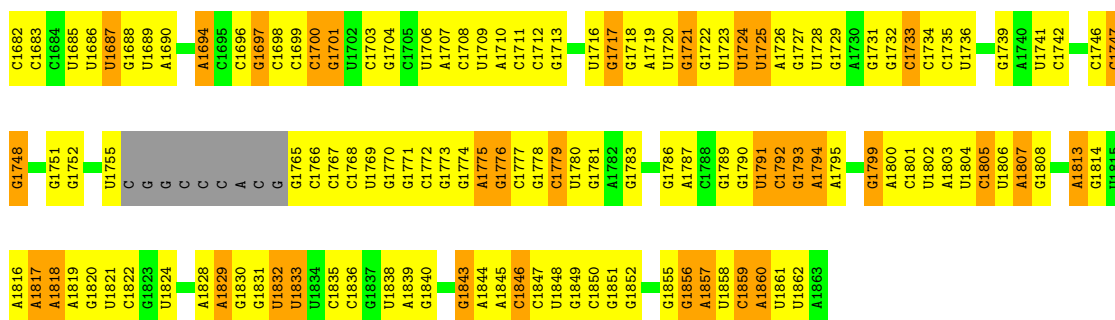
### 3 Residue-property plots

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

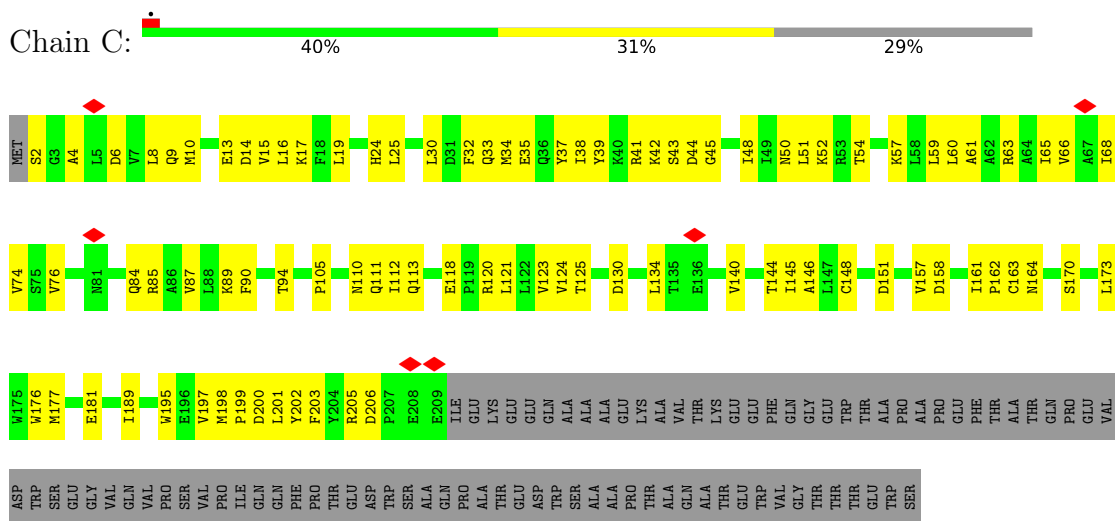
#### • Molecule 1: 18S ribosomal RNA



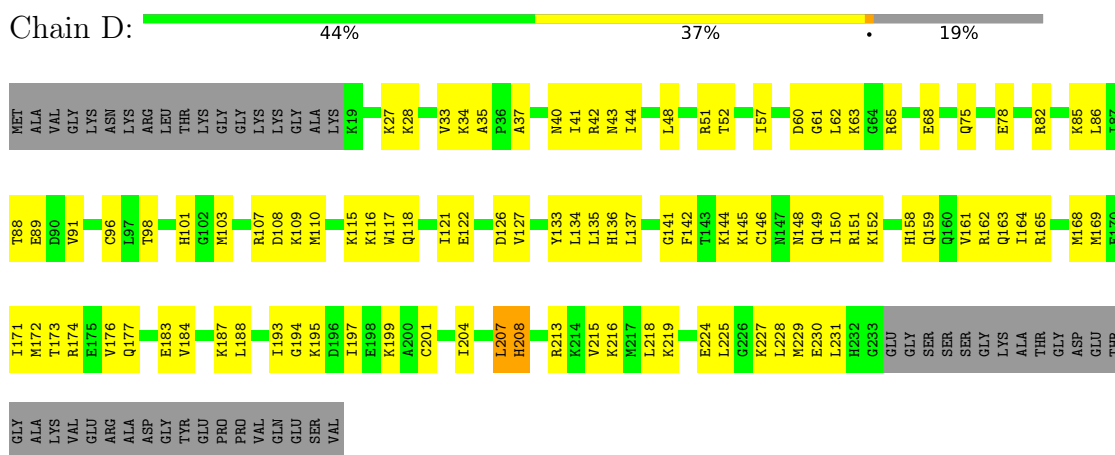




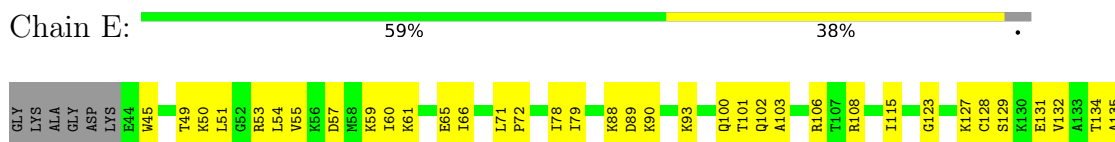
• Molecule 2: Small ribosomal subunit protein uS2

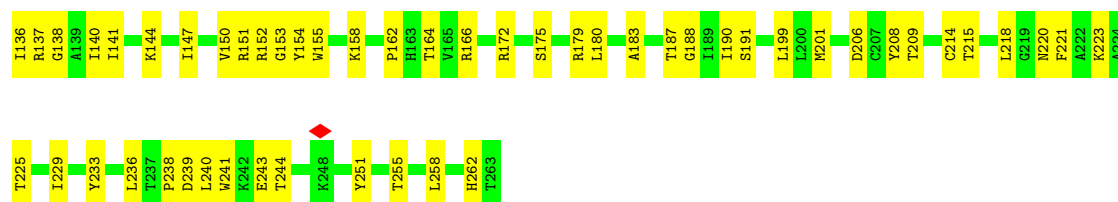


• Molecule 3: Small ribosomal subunit protein eS1

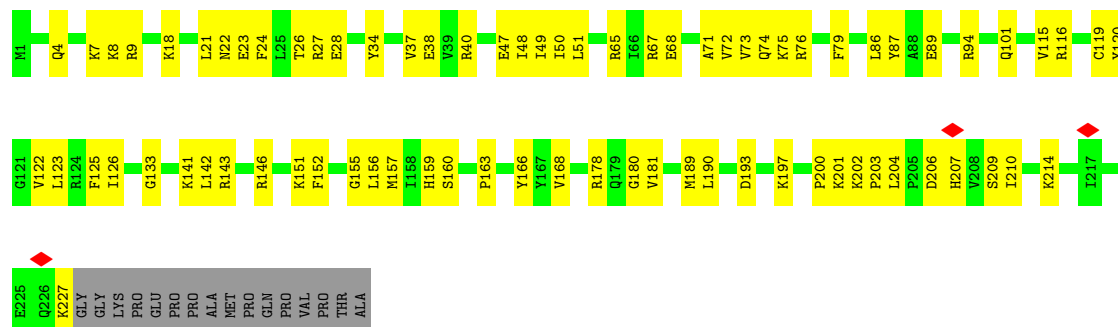


• Molecule 4: Small ribosomal subunit protein uS5

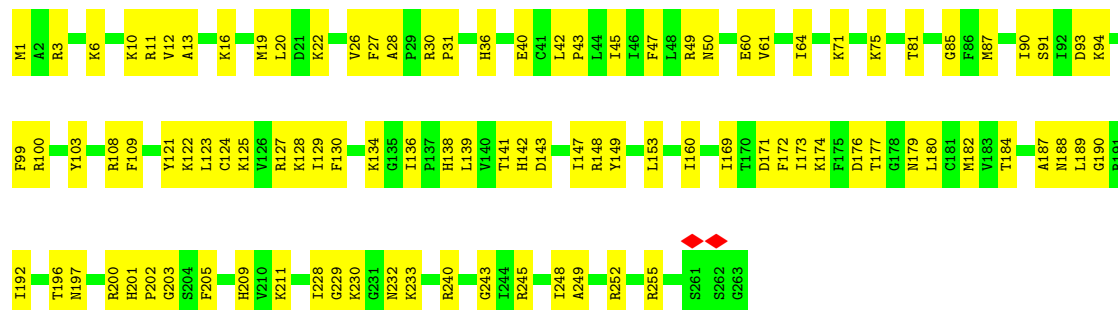




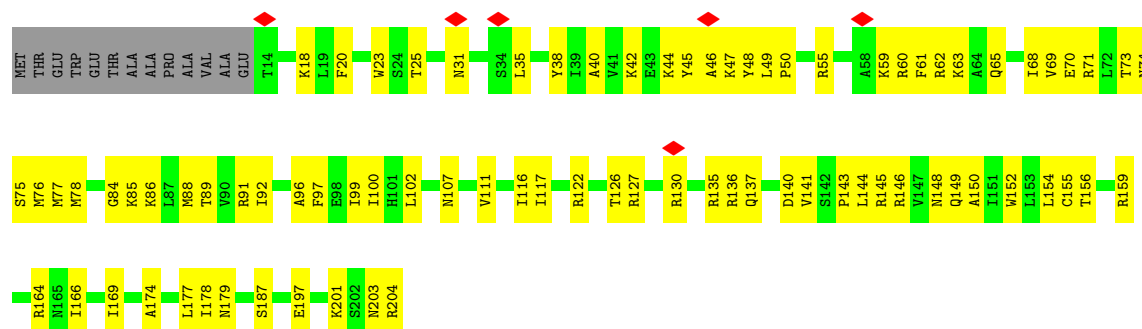
• Molecule 5: Small ribosomal subunit protein uS3



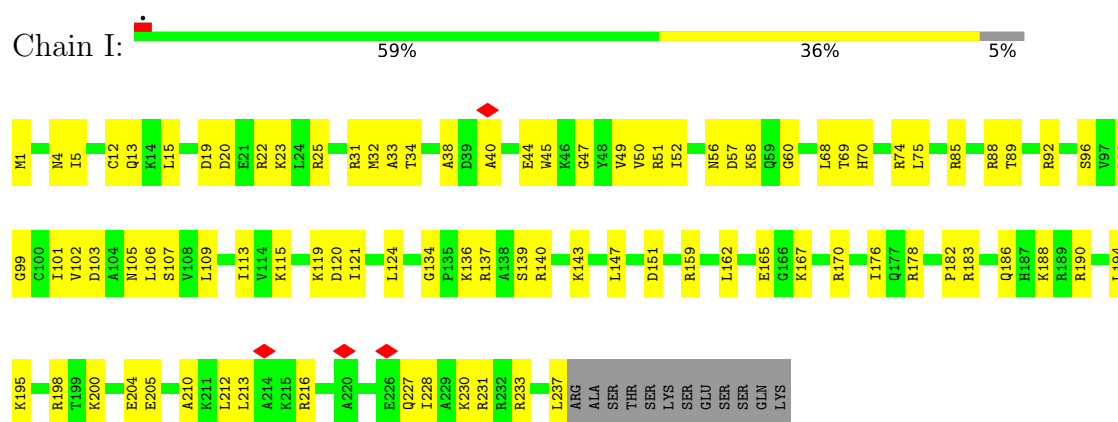
• Molecule 6: Small ribosomal subunit protein eS4



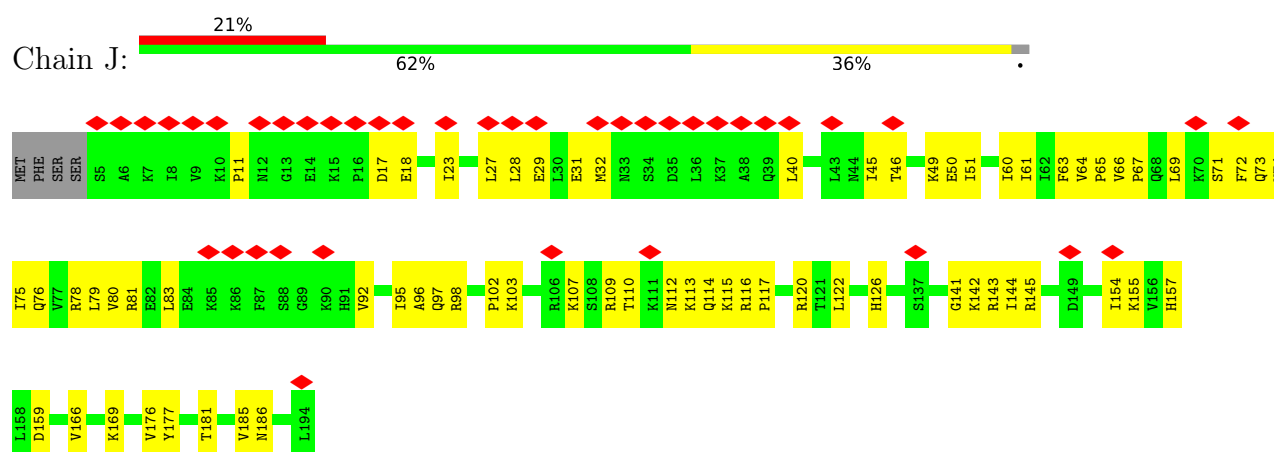
• Molecule 7: Small ribosomal subunit protein uS7



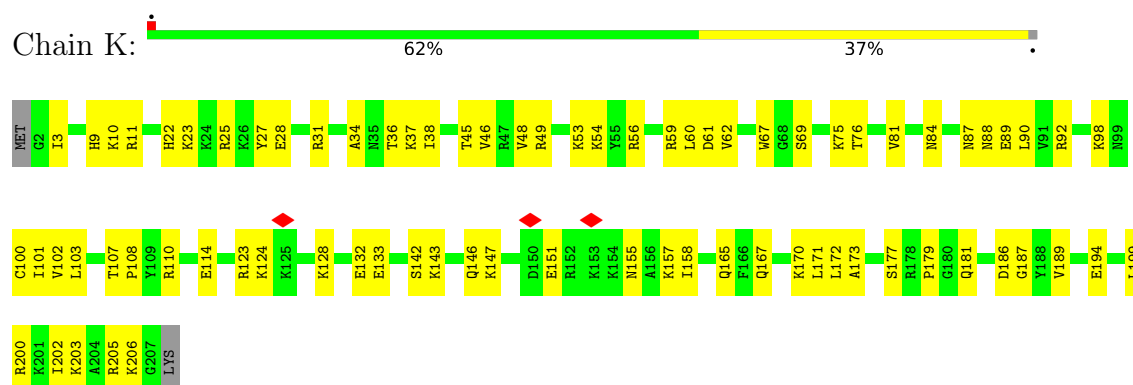
• Molecule 8: Small ribosomal subunit protein eS6



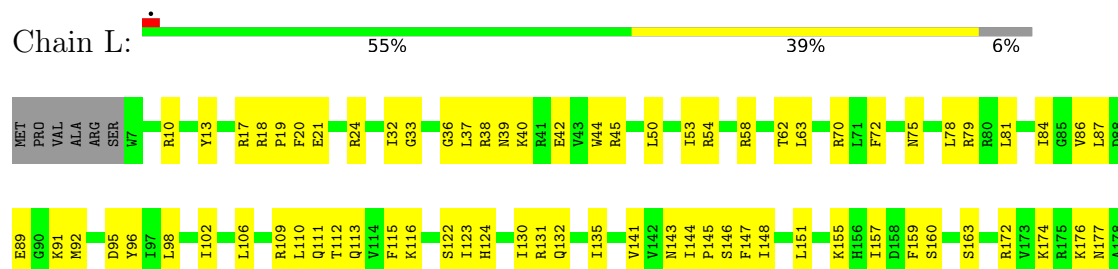
• Molecule 9: Small ribosomal subunit protein eS7



• Molecule 10: Small ribosomal subunit protein eS8

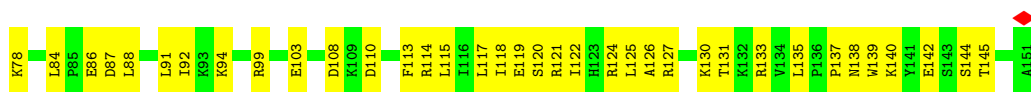


• Molecule 11: Small ribosomal subunit protein uS4

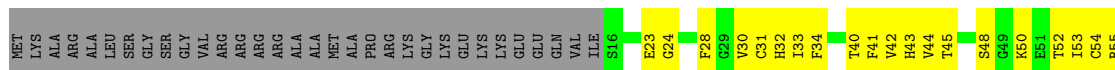




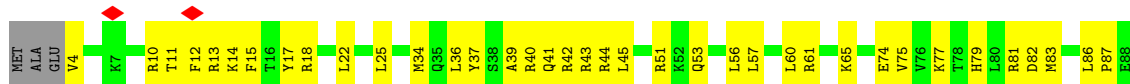




• Molecule 16: Ribosomal protein S14



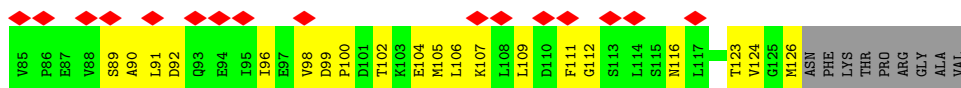
• Molecule 17: Small ribosomal subunit protein uS19



• Molecule 18: Small ribosomal subunit protein uS9

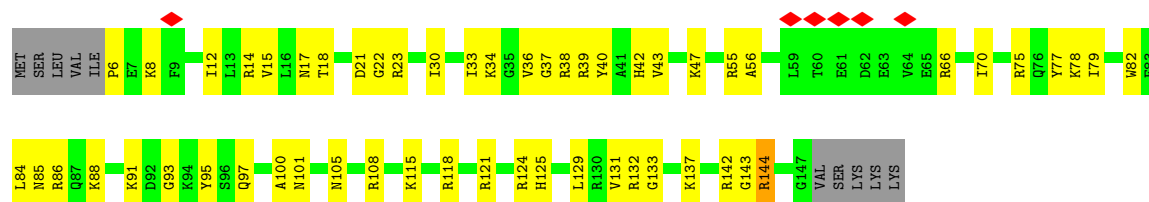


• Molecule 19: Small ribosomal subunit protein eS17



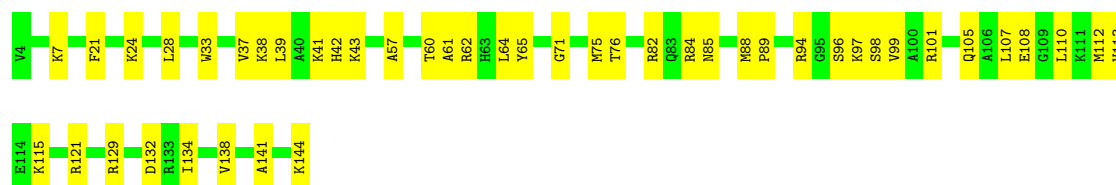
• Molecule 20: Small ribosomal subunit protein uS13

Chain U:  57% 36% 7%



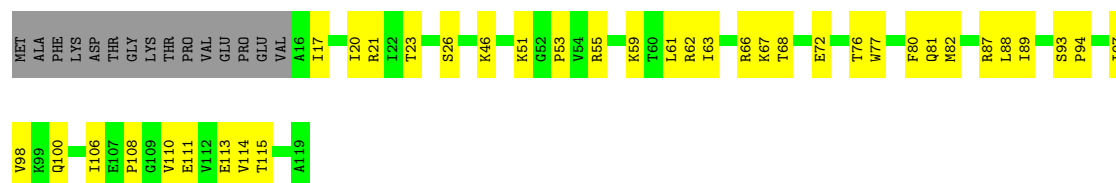
- Molecule 21: Small ribosomal subunit protein eS19

Chain V:  68% 32%



- Molecule 22: Small ribosomal subunit protein uS10

Chain W:  56% 31% 13%



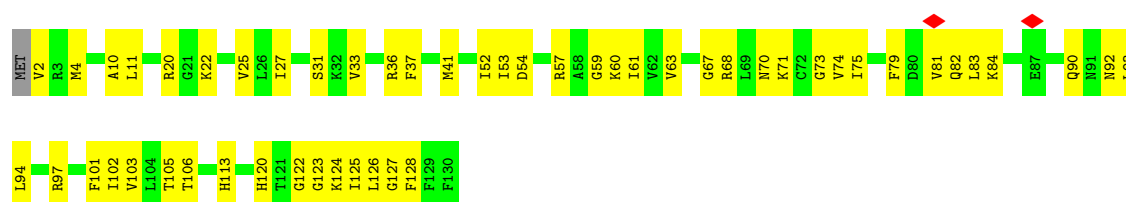
- Molecule 23: Small ribosomal subunit protein eS21

Chain X:  65% 33% 2%

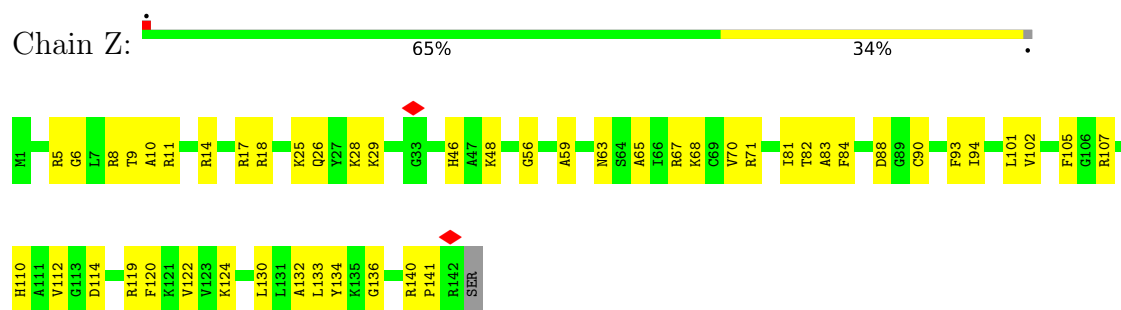


- Molecule 24: Small ribosomal subunit protein uS8

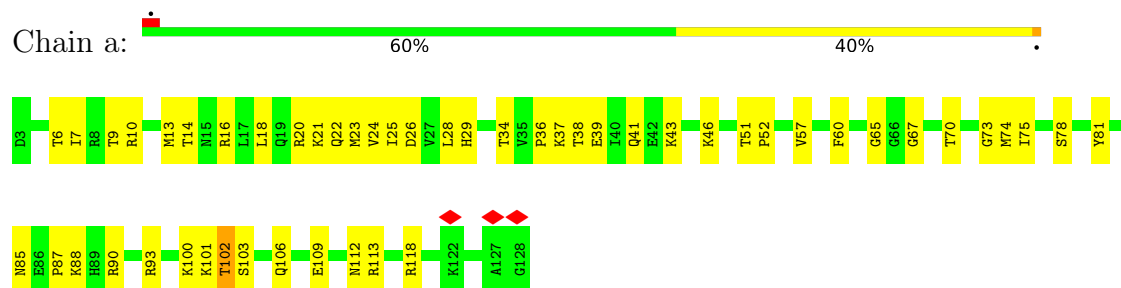
Chain Y:  59% 40% 1%



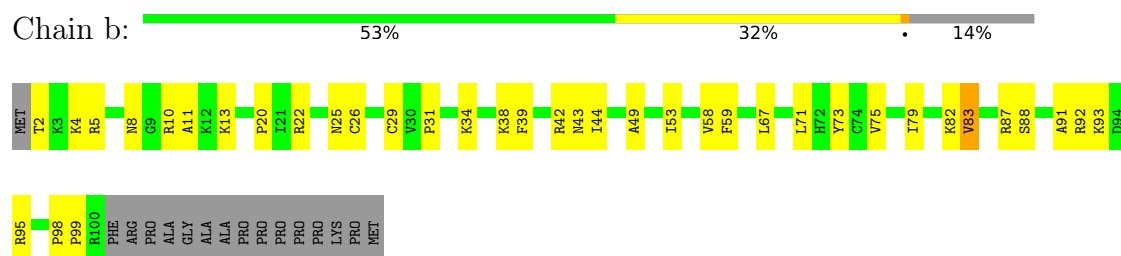
- Molecule 25: Small ribosomal subunit protein uS12



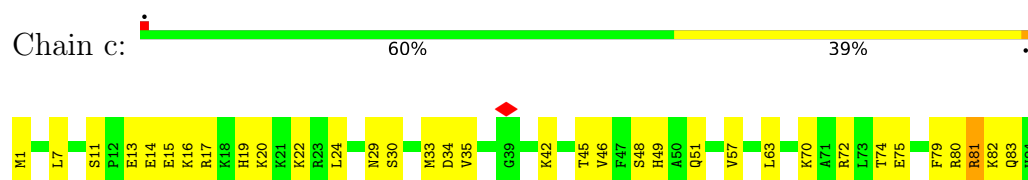
- Molecule 26: 40S ribosomal protein S24



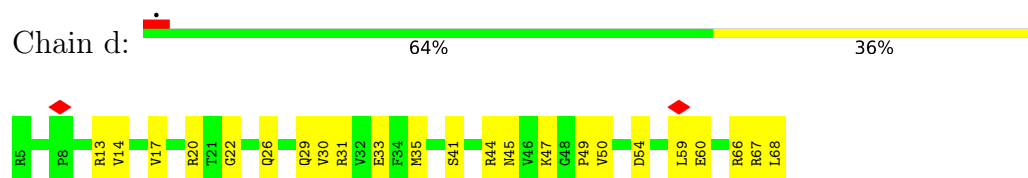
- Molecule 27: Small ribosomal subunit protein eS26



- Molecule 28: Small ribosomal subunit protein eS27



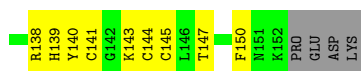
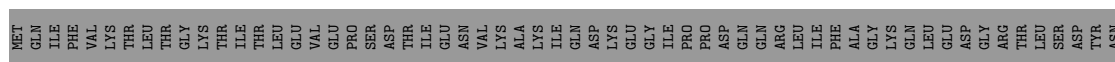
- Molecule 29: Small ribosomal subunit protein eS28



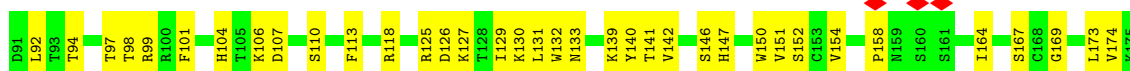
- Molecule 30: Small ribosomal subunit protein uS14



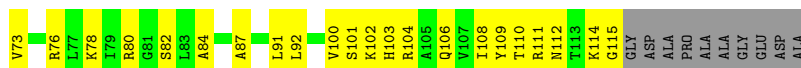
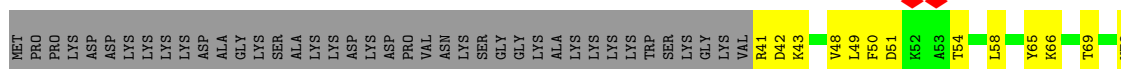
- Molecule 31: Ubiquitin-ribosomal protein eS31 fusion protein



- Molecule 32: Small ribosomal subunit protein RACK1



- Molecule 33: Small ribosomal subunit protein eS25



- Molecule 34: Small ribosomal subunit protein eS30





• Molecule 35: Small ribosomal subunit protein eS32



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	125503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.783	Depositor
Minimum map value	-0.396	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.07	Depositor
Map size ( $\text{\AA}$ )	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.17, 1.17, 1.17	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	2	0.12	0/41585	0.29	0/64808
2	C	0.19	0/1679	0.49	0/2283
3	D	0.16	0/1769	0.45	0/2367
4	E	0.14	0/1740	0.39	0/2349
5	F	0.13	0/1792	0.44	2/2412 (0.1%)
6	G	0.18	0/2125	0.43	0/2856
7	H	0.12	0/1531	0.35	0/2059
8	I	0.12	0/1945	0.35	0/2587
9	J	0.14	0/1553	0.42	0/2079
10	K	0.15	0/1708	0.60	2/2278 (0.1%)
11	L	0.17	0/1522	0.44	0/2031
12	M	0.15	0/851	0.49	2/1147 (0.2%)
13	N	0.14	0/1319	0.41	0/1761
14	O	0.10	0/968	0.32	0/1296
15	P	0.15	0/1232	0.39	0/1656
16	Q	0.14	0/1029	0.43	0/1380
17	R	0.13	0/1132	0.44	0/1510
18	S	0.12	0/1141	0.39	0/1528
19	T	0.14	0/1031	0.44	0/1383
20	U	0.10	0/1190	0.35	0/1592
21	V	0.11	0/1133	0.32	0/1517
22	W	0.10	0/832	0.34	0/1117
23	X	0.15	0/626	0.48	0/839
24	Y	0.15	0/1051	0.44	0/1406
25	Z	0.13	0/1124	0.38	0/1500
26	a	0.14	0/1039	0.51	2/1380 (0.1%)
27	b	0.15	0/802	0.45	1/1076 (0.1%)
28	c	0.16	0/673	0.58	2/902 (0.2%)
29	d	0.11	0/509	0.30	0/680
30	e	0.14	0/455	0.40	0/603
31	f	0.10	0/593	0.34	0/786
32	g	0.10	0/2493	0.31	0/3394
33	h	0.10	0/604	0.26	0/810
34	i	0.26	0/478	0.63	2/628 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.16	0/241	0.48	0/305
All	All	0.13	0/81495	0.36	13/118305 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	D	0	1
9	J	0	1
18	S	0	1
All	All	0	3

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	K	142	SER	CA-C-N	12.30	143.83	121.70
10	K	142	SER	C-N-CA	12.30	143.83	121.70
5	F	197	LYS	CA-C-N	7.68	135.53	121.70
5	F	197	LYS	C-N-CA	7.68	135.53	121.70
28	c	81	ARG	CA-C-N	7.31	134.85	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	208	HIS	Peptide
9	J	66	VAL	Peptide
18	S	43	GLU	Peptide

## 5.2 Too-close contacts

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37194	0	18794	1288	0
2	C	1642	0	1646	100	0
3	D	1741	0	1815	79	0
4	E	1704	0	1795	73	0
5	F	1764	0	1863	72	0
6	G	2083	0	2189	83	0
7	H	1509	0	1563	71	0
8	I	1923	0	2088	66	0
9	J	1530	0	1627	62	0
10	K	1679	0	1760	61	0
11	L	1498	0	1608	70	0
12	M	827	0	854	44	0
13	N	1296	0	1374	59	0
14	O	958	0	993	30	0
15	P	1208	0	1294	63	0
16	Q	1016	0	1039	62	0
17	R	1111	0	1168	55	0
18	S	1123	0	1193	49	0
19	T	1019	0	1075	59	0
20	U	1172	0	1226	50	0
21	V	1113	0	1149	38	0
22	W	822	0	887	30	0
23	X	619	0	622	31	0
24	Y	1034	0	1080	55	0
25	Z	1106	0	1179	51	0
26	a	1022	0	1085	44	0
27	b	789	0	839	36	0
28	c	659	0	683	26	0
29	d	507	0	536	16	0
30	e	445	0	442	35	0
31	f	581	0	599	32	0
32	g	2436	0	2393	96	0
33	h	598	0	656	26	0
34	i	473	0	524	28	0
35	l	240	0	289	17	0
All	All	76441	0	59927	2568	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 19.

The worst 5 of 2568 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)
1:2:1284:U:H3	1:2:1307:C:N4	1.43	1.16
1:2:1328:A:H62	1:2:1489:C:N4	1.59	1.00
1:2:1331:G:H1	1:2:1488:U:H3	1.02	0.99
1:2:1328:A:N6	1:2:1489:C:H42	1.64	0.95
1:2:930:G:H1	1:2:1004:A:H2	1.11	0.94

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	
2	C	206/295 (70%)	183 (89%)	22 (11%)	1 (0%)	24	63
3	D	213/264 (81%)	189 (89%)	23 (11%)	1 (0%)	24	63
4	E	218/226 (96%)	202 (93%)	15 (7%)	1 (0%)	24	63
5	F	225/243 (93%)	211 (94%)	13 (6%)	1 (0%)	30	67
6	G	261/263 (99%)	235 (90%)	26 (10%)	0	100	100
7	H	189/204 (93%)	174 (92%)	15 (8%)	0	100	100
8	I	233/249 (94%)	216 (93%)	17 (7%)	0	100	100
9	J	188/194 (97%)	173 (92%)	15 (8%)	0	100	100
10	K	204/208 (98%)	181 (89%)	22 (11%)	1 (0%)	24	63
11	L	180/194 (93%)	162 (90%)	17 (9%)	1 (1%)	21	58
12	M	96/225 (43%)	79 (82%)	16 (17%)	1 (1%)	12	47
13	N	156/158 (99%)	145 (93%)	11 (7%)	0	100	100
14	O	122/132 (92%)	109 (89%)	13 (11%)	0	100	100
15	P	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
16	Q	134/168 (80%)	114 (85%)	20 (15%)	0	100	100
17	R	133/145 (92%)	116 (87%)	17 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	S	139/146 (95%)	125 (90%)	14 (10%)	0	100	100
19	T	124/135 (92%)	117 (94%)	7 (6%)	0	100	100
20	U	140/152 (92%)	123 (88%)	16 (11%)	1 (1%)	18	55
21	V	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
22	W	102/119 (86%)	94 (92%)	8 (8%)	0	100	100
23	X	80/83 (96%)	73 (91%)	6 (8%)	1 (1%)	9	41
24	Y	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
25	Z	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
26	a	124/126 (98%)	117 (94%)	7 (6%)	0	100	100
27	b	97/115 (84%)	88 (91%)	9 (9%)	0	100	100
28	c	82/84 (98%)	71 (87%)	10 (12%)	1 (1%)	10	43
29	d	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
30	e	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
31	f	69/156 (44%)	60 (87%)	9 (13%)	0	100	100
32	g	311/317 (98%)	282 (91%)	29 (9%)	0	100	100
33	h	73/125 (58%)	70 (96%)	3 (4%)	0	100	100
34	i	57/59 (97%)	51 (90%)	6 (10%)	0	100	100
35	l	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
All	All	4846/5495 (88%)	4406 (91%)	430 (9%)	10 (0%)	44	77

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	U	144	ARG
10	K	158	ILE
12	M	34	GLU
3	D	207	LEU
5	F	193	ASP

### 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	
2	C	174/244 (71%)	174 (100%)	0	100	100
3	D	196/231 (85%)	196 (100%)	0	100	100
4	E	184/187 (98%)	184 (100%)	0	100	100
5	F	190/202 (94%)	190 (100%)	0	100	100
6	G	225/225 (100%)	225 (100%)	0	100	100
7	H	161/170 (95%)	161 (100%)	0	100	100
8	I	207/218 (95%)	207 (100%)	0	100	100
9	J	170/174 (98%)	170 (100%)	0	100	100
10	K	177/180 (98%)	177 (100%)	0	100	100
11	L	157/168 (94%)	157 (100%)	0	100	100
12	M	89/173 (51%)	89 (100%)	0	100	100
13	N	142/142 (100%)	141 (99%)	1 (1%)	76	79
14	O	104/108 (96%)	104 (100%)	0	100	100
15	P	130/131 (99%)	130 (100%)	0	100	100
16	Q	106/130 (82%)	106 (100%)	0	100	100
17	R	121/130 (93%)	121 (100%)	0	100	100
18	S	117/121 (97%)	117 (100%)	0	100	100
19	T	114/121 (94%)	114 (100%)	0	100	100
20	U	122/132 (92%)	122 (100%)	0	100	100
21	V	113/113 (100%)	113 (100%)	0	100	100
22	W	94/107 (88%)	94 (100%)	0	100	100
23	X	67/68 (98%)	67 (100%)	0	100	100
24	Y	112/113 (99%)	112 (100%)	0	100	100
25	Z	114/115 (99%)	114 (100%)	0	100	100
26	a	108/108 (100%)	108 (100%)	0	100	100
27	b	87/99 (88%)	87 (100%)	0	100	100
28	c	76/76 (100%)	76 (100%)	0	100	100
29	d	57/57 (100%)	57 (100%)	0	100	100
30	e	47/49 (96%)	47 (100%)	0	100	100
31	f	64/140 (46%)	64 (100%)	0	100	100
32	g	272/275 (99%)	272 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	66/103 (64%)	66 (100%)	0	100	100
34	i	49/49 (100%)	49 (100%)	0	100	100
35	l	24/24 (100%)	24 (100%)	0	100	100
All	All	4236/4683 (90%)	4235 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	N	13	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
20	U	85	ASN
32	g	181	ASN
20	U	97	GLN
24	Y	113	HIS
33	h	112	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1733/1863 (93%)	433 (24%)	3 (0%)

5 of 433 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	5	U
1	2	9	U
1	2	17	C
1	2	26	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	740	G
1	2	1338	U

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Mol	Chain	Res	Type
1	2	1492	U

## 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	1
8	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	730:C	O3'	731:C	P	8.60
1	I	217:MET	C	218:LYS	N	3.55

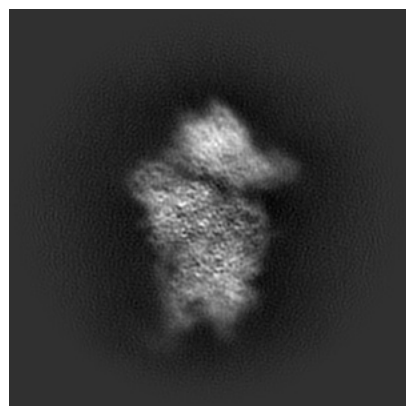
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64646. These allow visual inspection of the internal detail of the map and identification of artifacts.

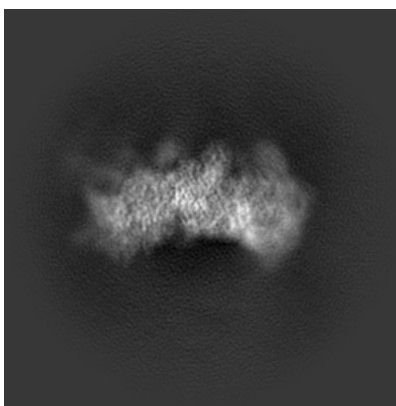
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

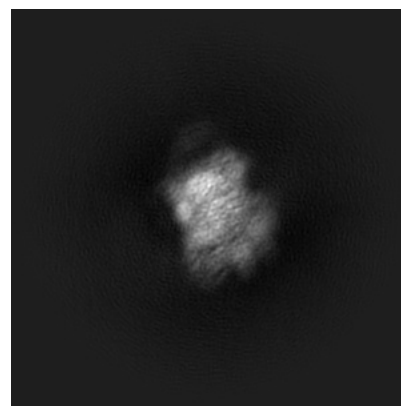
#### 6.1.1 Primary map



X

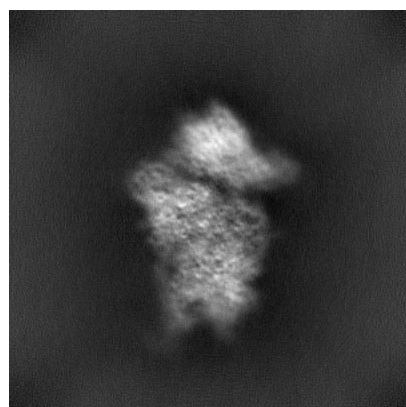


Y

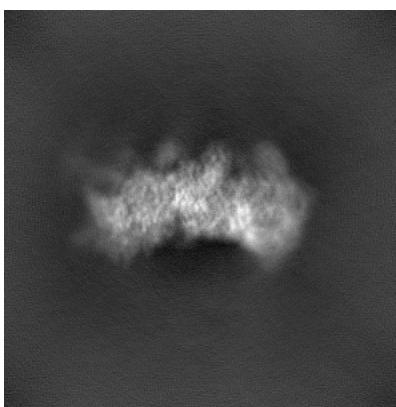


Z

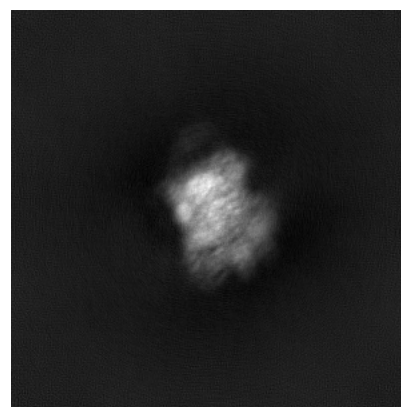
#### 6.1.2 Raw map



X



Y

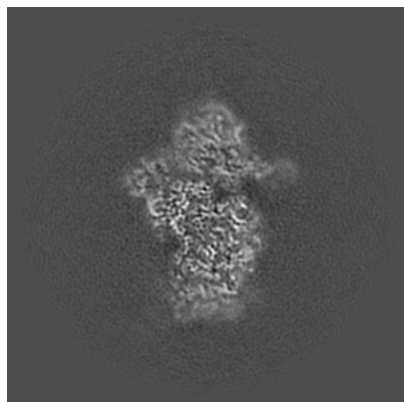


Z

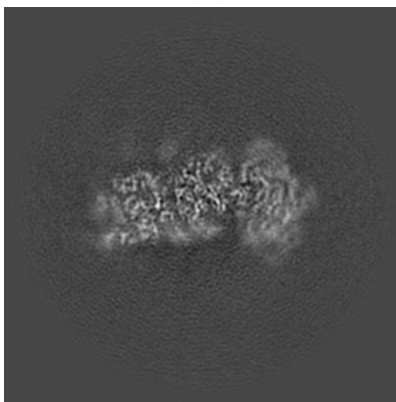
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

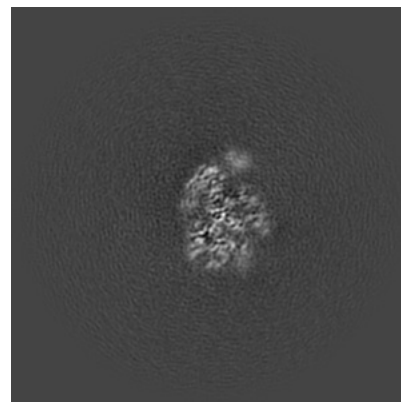
### 6.2.1 Primary map



X Index: 200

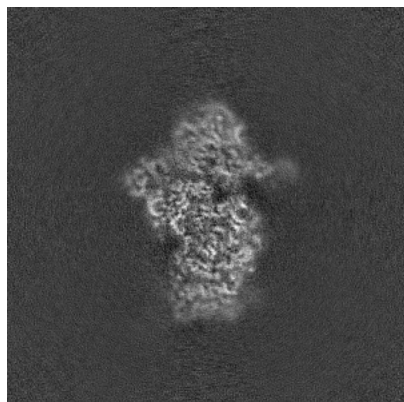


Y Index: 200

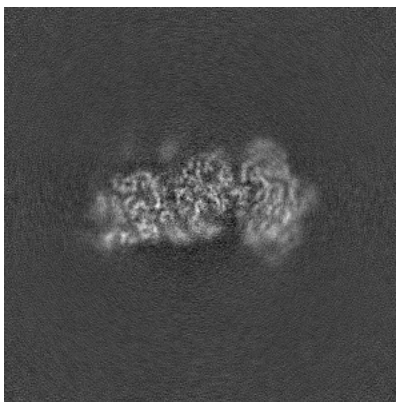


Z Index: 200

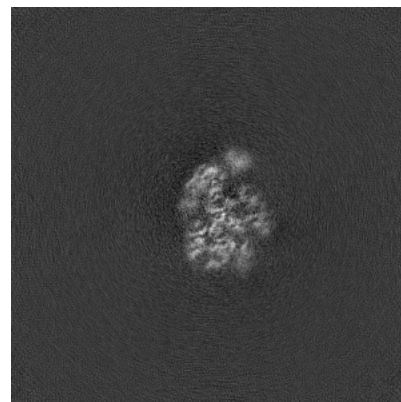
### 6.2.2 Raw map



X Index: 200



Y Index: 200



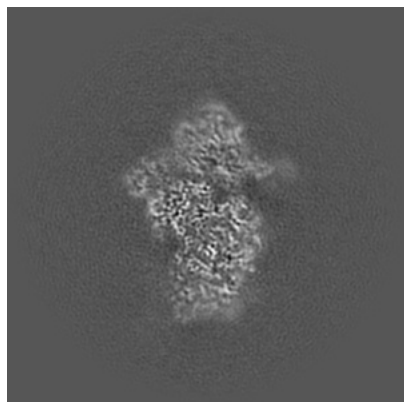
Z Index: 200

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

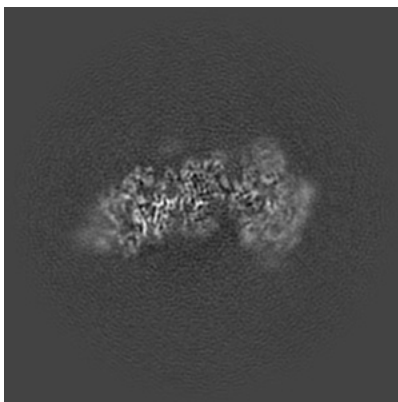


## 6.3 Largest variance slices [i](#)

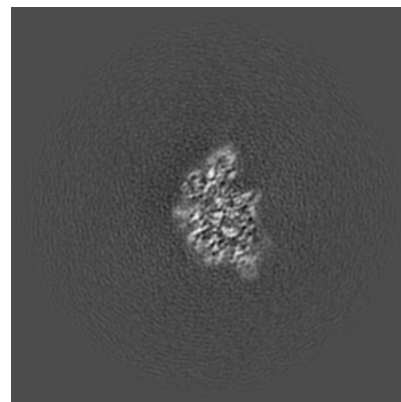
### 6.3.1 Primary map



X Index: 201

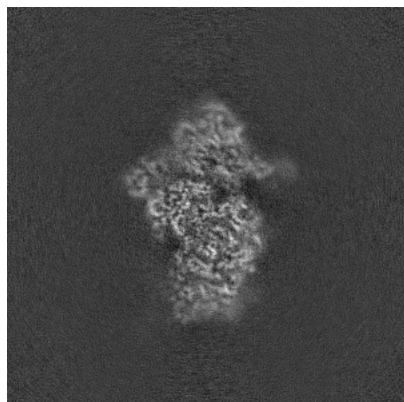


Y Index: 207

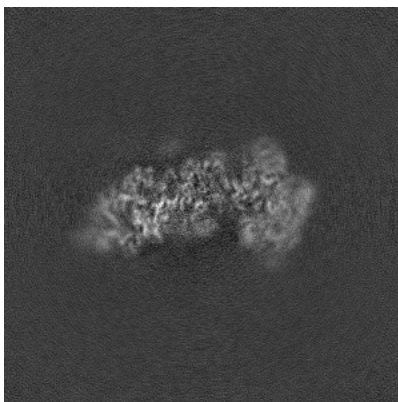


Z Index: 185

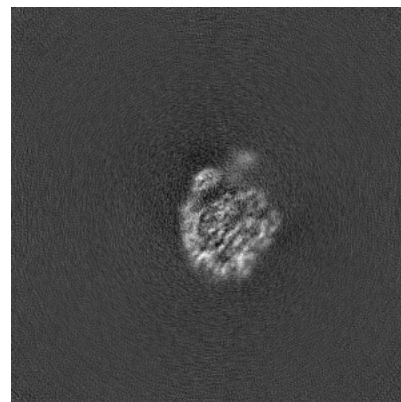
### 6.3.2 Raw map



X Index: 201



Y Index: 206

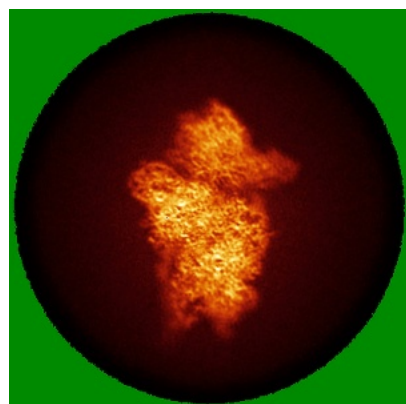


Z Index: 208

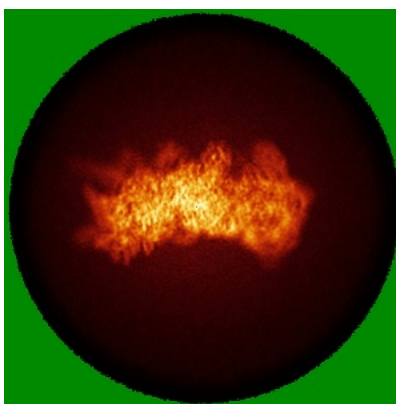
The images above show the largest variance slices of the map in three orthogonal directions.

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

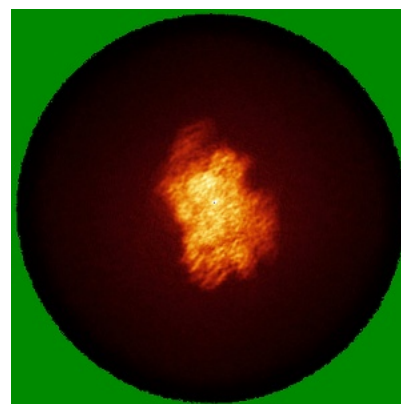
### 6.4.1 Primary map



X

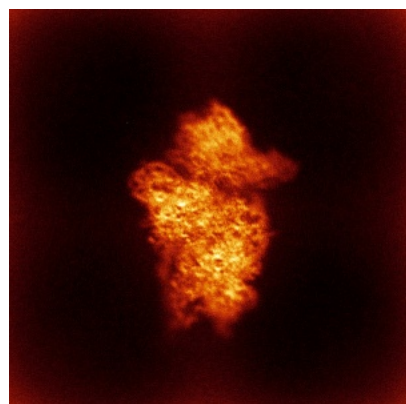


Y

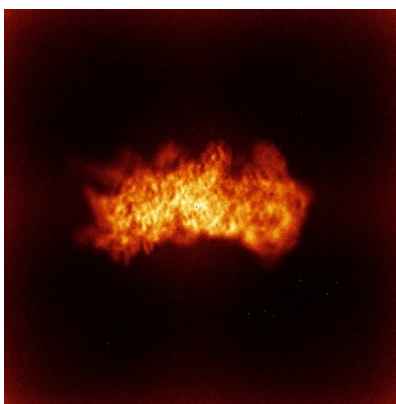


Z

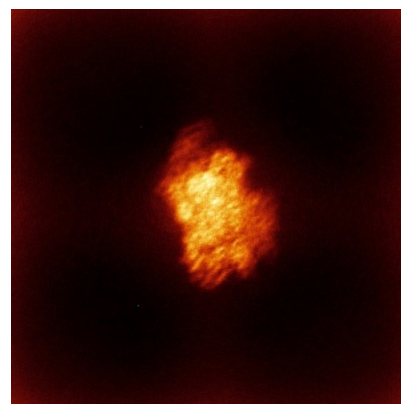
### 6.4.2 Raw map



X



Y

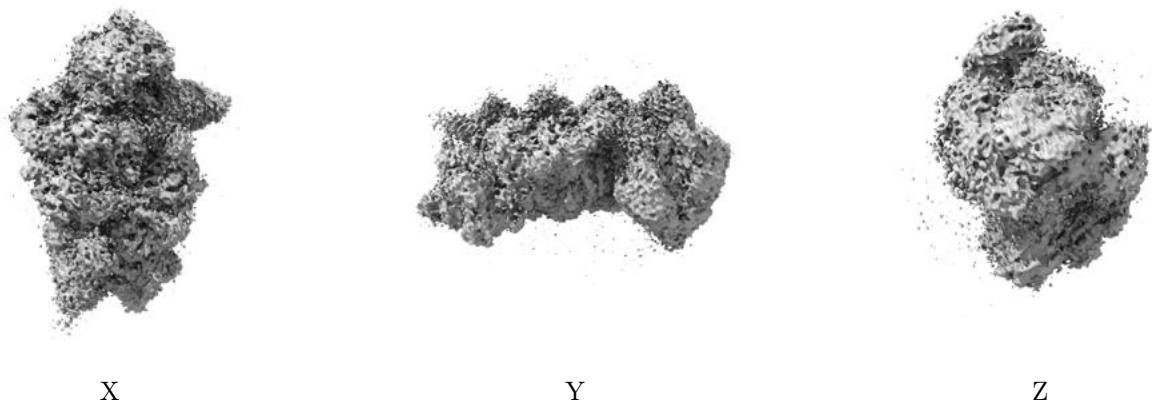


Z

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.

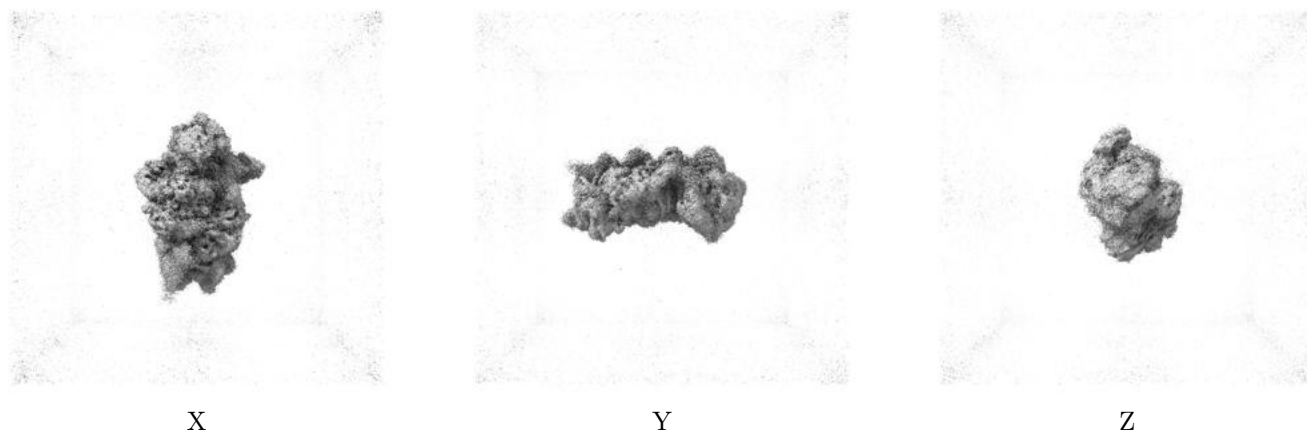
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

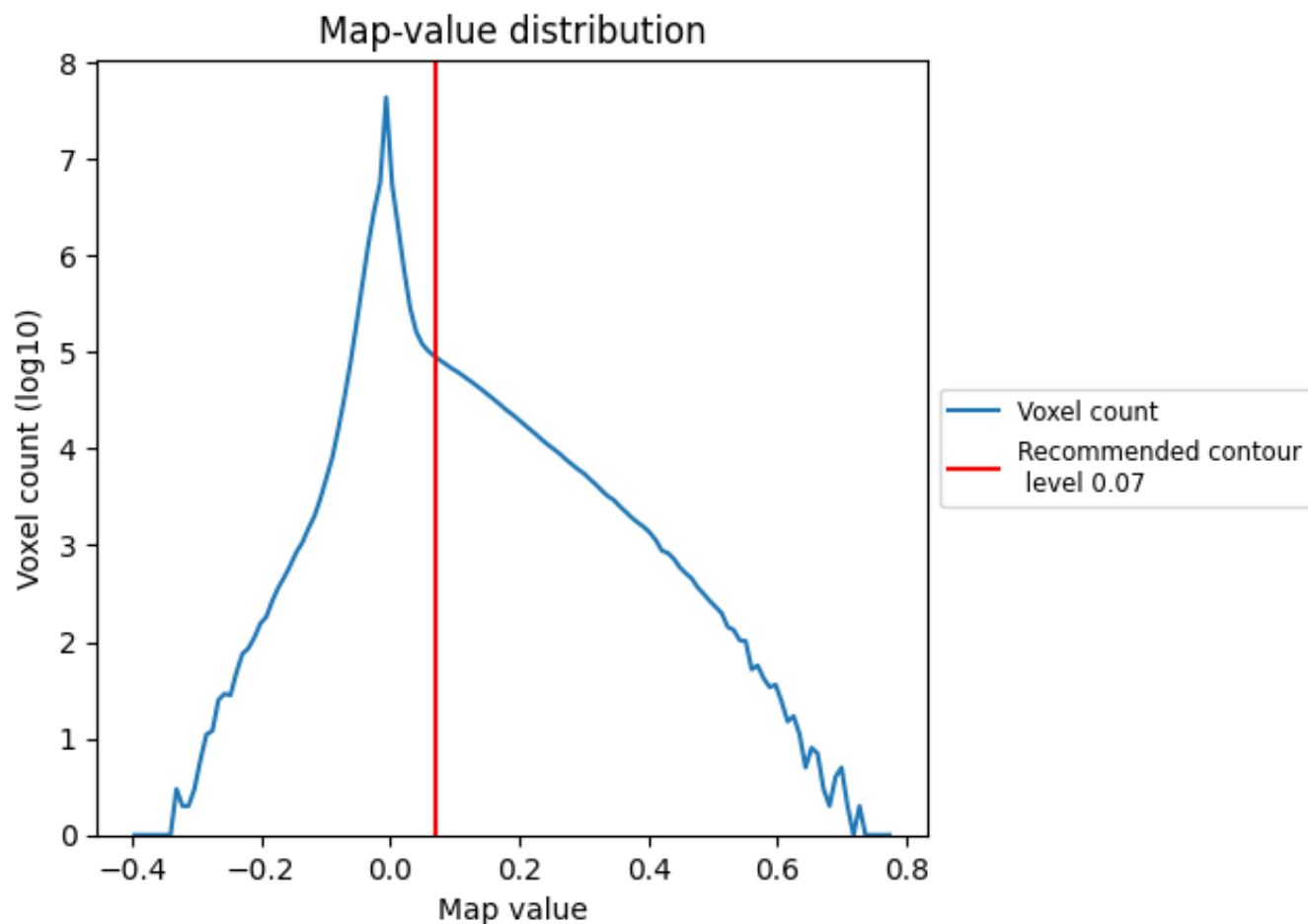
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

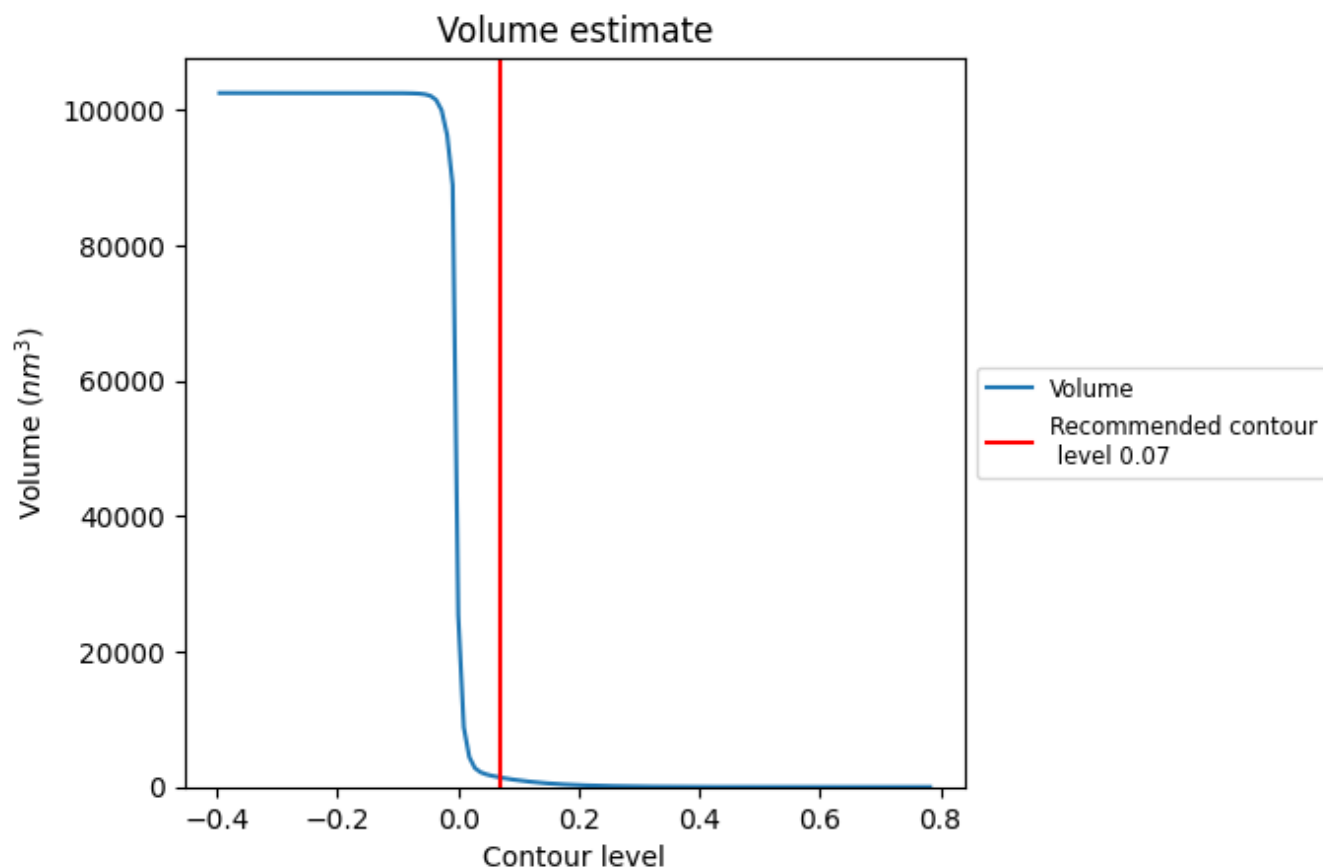
This section contains the results of statistical analysis of the map.

### 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.

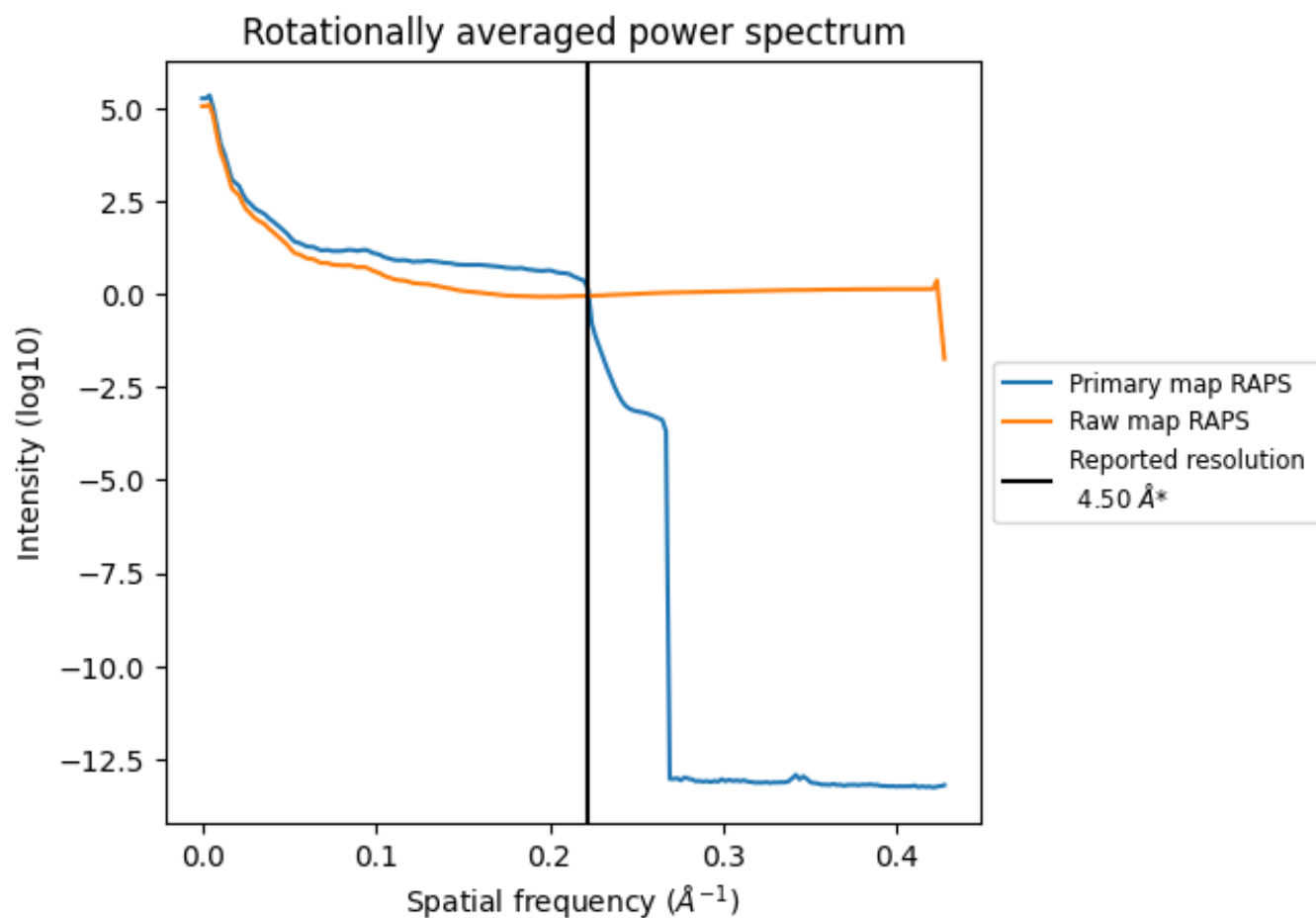
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1397 nm<sup>3</sup>; this corresponds to an approximate mass of 1262 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 ⓘ

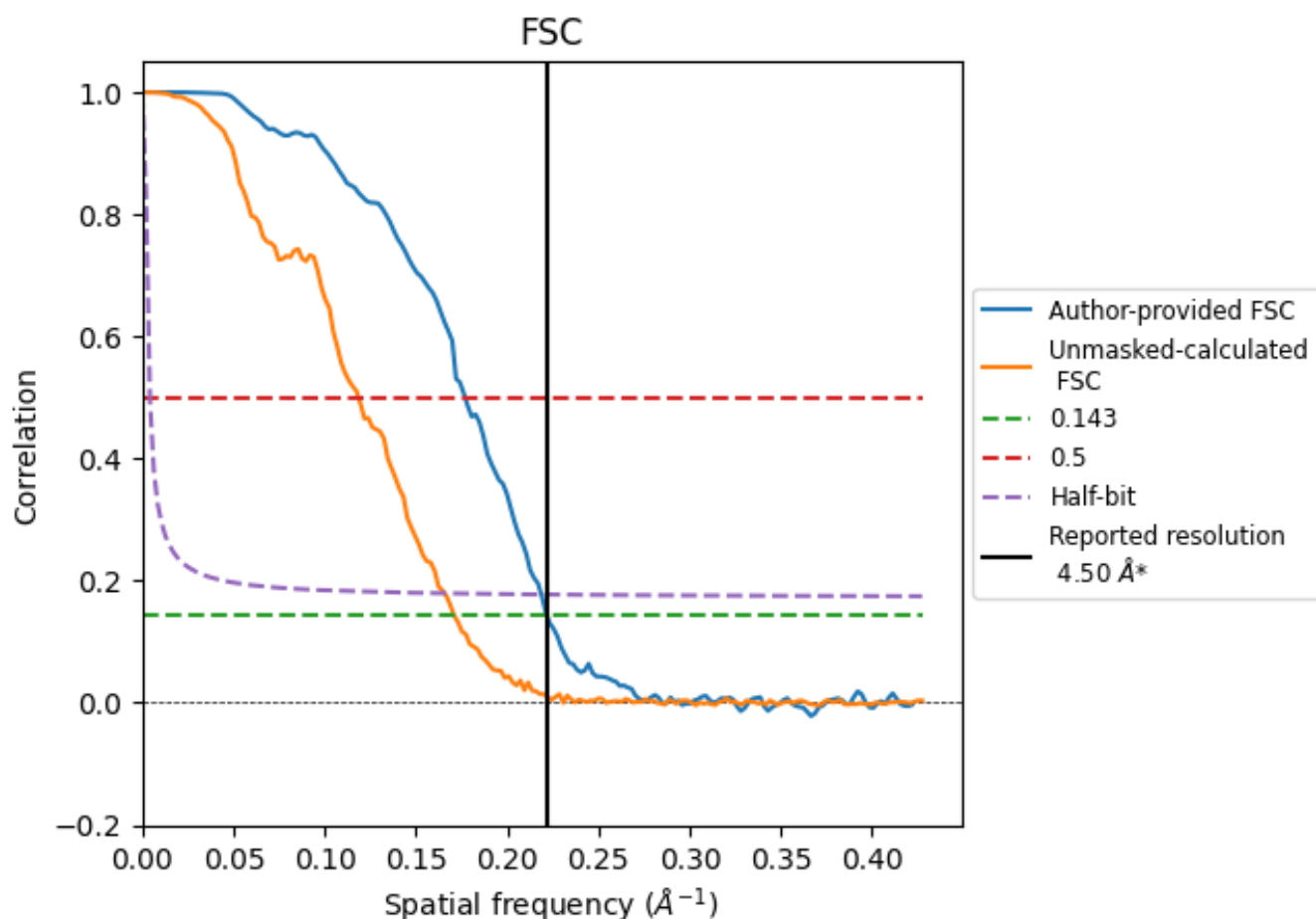


\*Reported resolution corresponds to spatial frequency of 0.222  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.51	5.65	4.57
Unmasked-calculated*	5.85	8.44	6.04

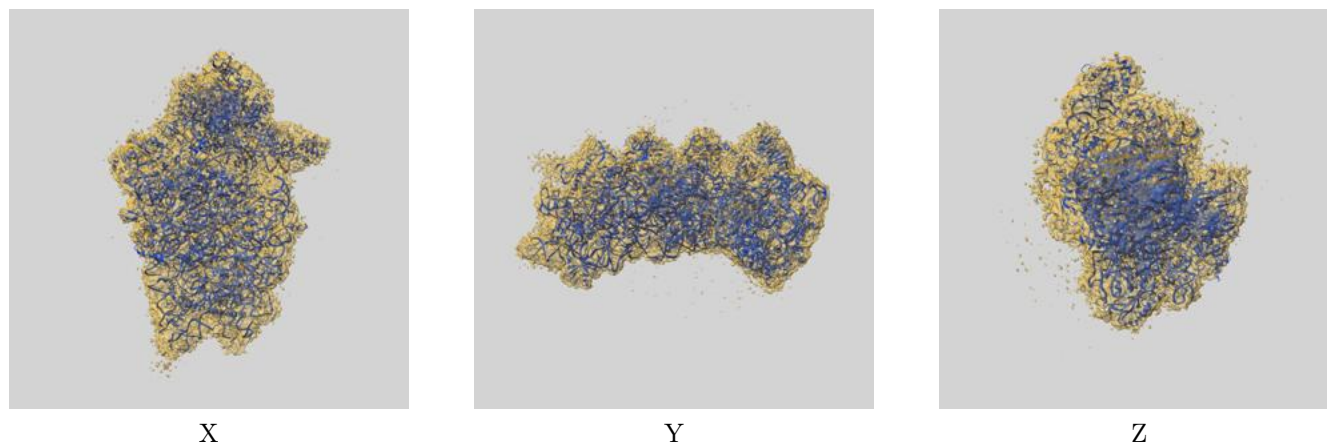
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.85 differs from the reported value 4.5 by more than 10 %



## 9 Map-model fit [i](#)

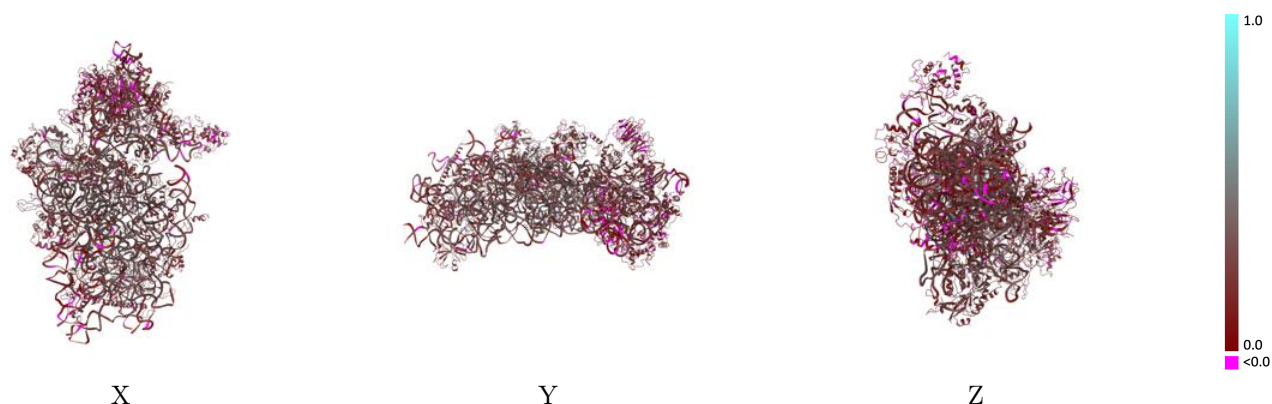
This section contains information regarding the fit between EMDB map EMD-64646 and PDB model 9UZM. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

### 9.1 Map-model overlay [i](#)



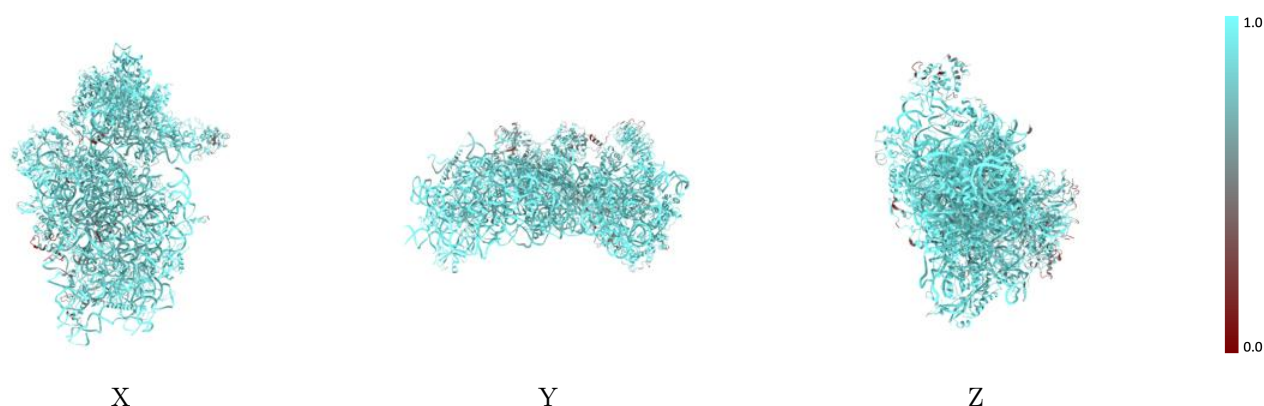
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



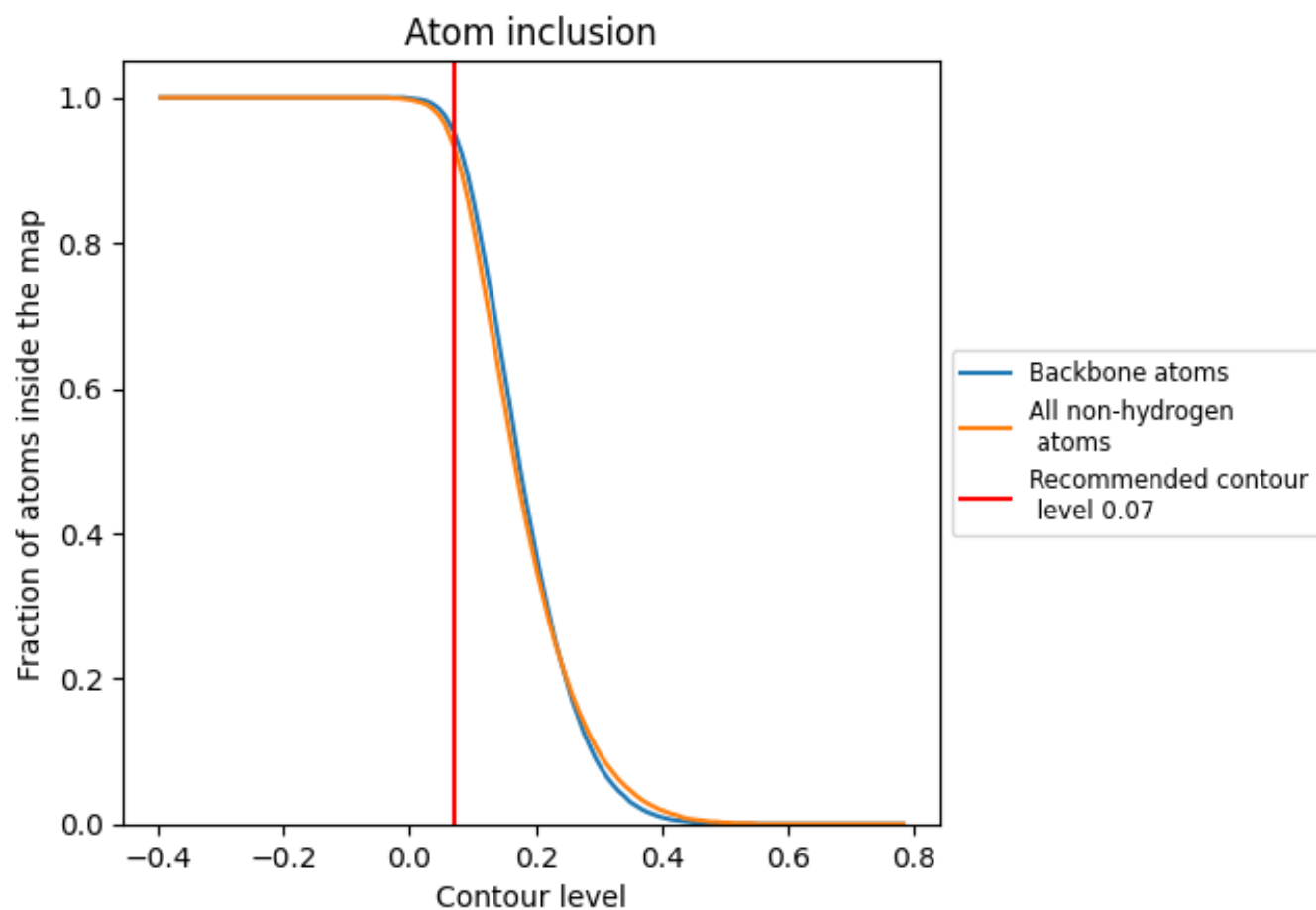
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.2620
2	 0.9720	 0.2700
C	 0.8690	 0.2900
D	 0.9410	 0.2750
E	 0.8860	 0.3090
F	 0.8880	 0.2470
G	 0.9220	 0.3020
H	 0.9300	 0.1780
I	 0.9450	 0.2670
J	 0.6680	 0.2250
K	 0.8960	 0.2720
L	 0.9160	 0.2970
M	 0.9490	 0.2200
N	 0.8430	 0.3210
O	 0.7820	 0.1460
P	 0.9150	 0.3020
Q	 0.9720	 0.2820
R	 0.8810	 0.1790
S	 0.9360	 0.2430
T	 0.7290	 0.2160
U	 0.9290	 0.1690
V	 0.9770	 0.1920
W	 0.9610	 0.2590
X	 0.9040	 0.2930
Y	 0.8570	 0.3430
Z	 0.9340	 0.3500
a	 0.9650	 0.2960
b	 0.9220	 0.3280
c	 0.9230	 0.3170
d	 0.8520	 0.2160
e	 0.9390	 0.2760
f	 0.8220	 0.1400
g	 0.8830	 0.1610
h	 0.9540	 0.1380
i	 0.9010	 0.2690
l	 0.8680	 0.2830

