



## wwPDB EM Validation Summary Report ⓘ

Jan 7, 2025 – 07:00 pm GMT

PDB ID : 9FO0  
EMDB ID : EMD-50613  
Title : PF30S ribosomal subunit - control  
Authors : Hassan, A.H.; Demo, G.  
Deposited on : 2024-06-11  
Resolution : 3.40 Å(reported)  
Based on initial models : 7ZHG, 4V6U, .

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.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

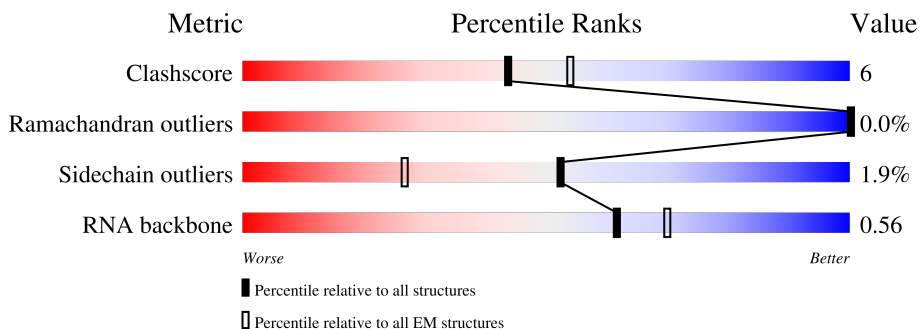
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




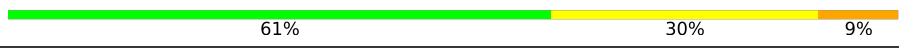



The reported resolution of this entry is 3.40 Å.

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.






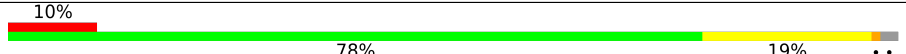
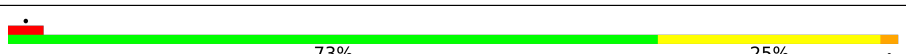
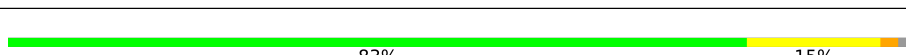
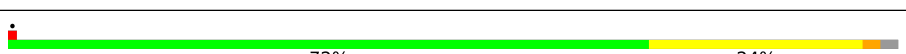
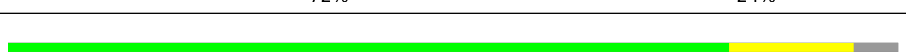

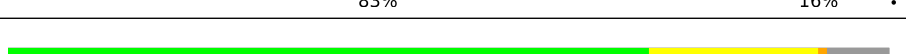
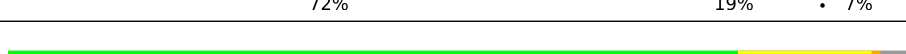
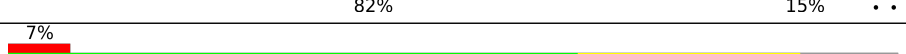
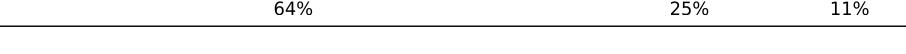
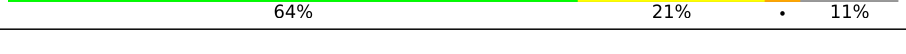




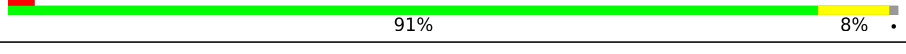
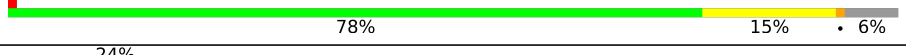

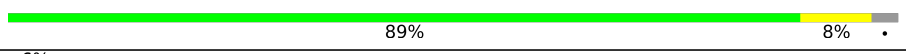
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	A1	60	
2	A2	37	
3	A5	123	
4	AA	1495	
5	AB	202	
6	AC	210	
7	AD	198	

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Mol	Chain	Length	Quality of chain
8	AE	180	
9	AF	243	
10	AG	236	
11	AH	125	
12	AI	215	
13	AJ	130	
14	AK	127	
15	AL	135	
16	AM	102	
17	AN	137	
18	AO	147	
19	AP	148	
20	AQ	56	
21	AR	158	
22	AS	113	
23	AT	67	
24	AU	132	
25	AV	150	
26	AW	99	
27	AX	50	
28	AY	63	
29	AZ	71	

## 2 Entry composition [i](#)

There are 29 unique types of molecules in this entry. The entry contains 60801 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 RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	60	Total	C	N	O	S	0	0
			471	295	83	83	10		

- Molecule 2 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	35	Total	C	N	O	S	0	0
			335	212	83	38	2		

- Molecule 3 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A5	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 4 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	1495	Total	C	N	O	P	0	0
			32135	14297	5954	10389	1495		

- Molecule 5 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	197	Total	C	N	O	S	0	0
			1579	1022	271	282	4		

- Molecule 6 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	195	Total	C	N	O	S	0	0
			1532	980	283	266	3		

- Molecule 7 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	184	Total	C	N	O	S	0	0
			1511	978	263	265	5		

- Molecule 8 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	173	Total	C	N	O	S	0	0
			1455	915	282	254	4		

- Molecule 9 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	242	Total	C	N	O	S	0	0
			1981	1280	356	340	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	227	Total	C	N	O	S	0	0
			1794	1134	335	318	7		

- Molecule 11 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AH	123	Total	C	N	O	S	0	0
			971	615	178	177	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	214	Total	C	N	O	S	0	0
			1728	1095	325	301	7		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 14 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AK	124	Total	C	N	O		
			977	607	204	166	0	0

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AL	128	Total	C	N	O	S	
			1006	630	191	180	5	0

- Molecule 16 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AM	102	Total	C	N	O	S	
			822	507	159	152	4	0

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AN	127	Total	C	N	O	S	
			954	591	190	171	2	0

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AO	143	Total	C	N	O	S	
			1118	710	215	190	3	0

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	AP	131	Total	C	N	O	S	
			1052	663	206	178	5	0

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AQ	50	Total	C	N	O	S	
			417	266	88	58	5	0

- Molecule 21 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AR	155	Total	C	N	O	S	0	0
			1283	818	244	217	4		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AS	110	Total	C	N	O	S	0	0
			903	575	168	156	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AT	63	Total	C	N	O	S	0	0
			522	330	100	90	2		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AU	115	Total	C	N	O	S	0	0
			948	609	177	156	6		

- Molecule 25 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AV	148	Total	C	N	O		0	0
			1209	781	218	210			

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AW	93	Total	C	N	O	S	0	0
			774	503	126	143	2		

- Molecule 27 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AX	45	Total	C	N	O	S	0	0
			369	238	67	59	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AY	61	Total 465	C 298	N 83	O 79	S 5	0	0

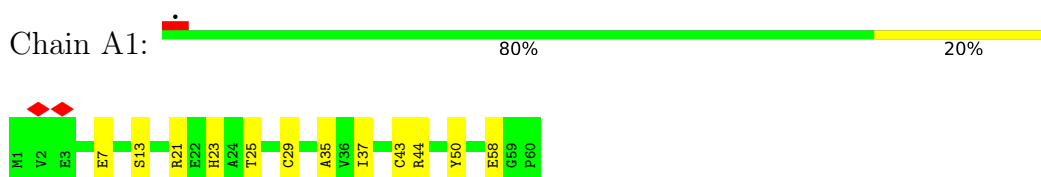
- Molecule 29 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AZ	66	Total 523	C 320	N 104	O 99		0	0

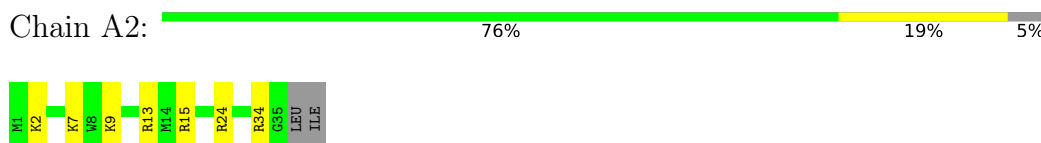
### 3 Residue-property plots [i](#)

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.

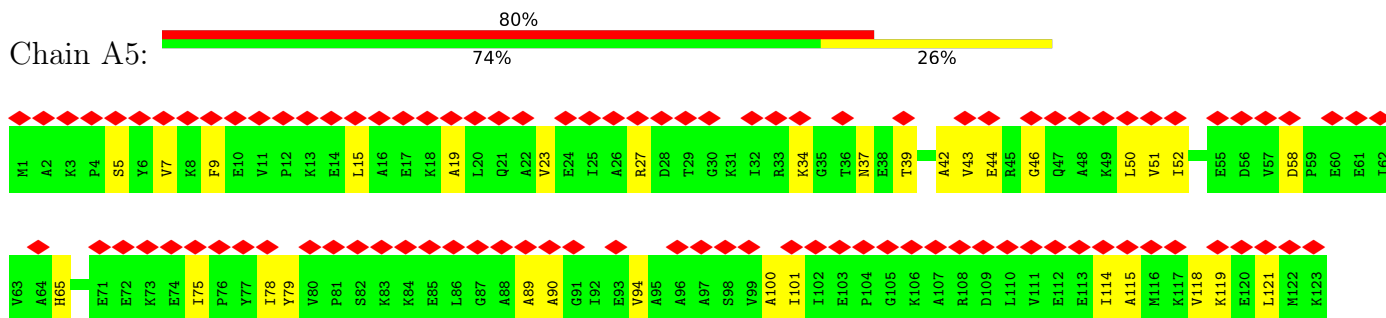
- Molecule 1: RNA-binding protein



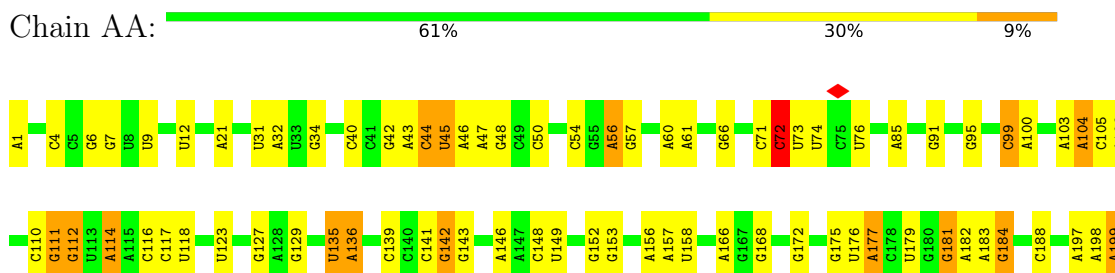
- Molecule 2: Small ribosomal subunit protein eS32

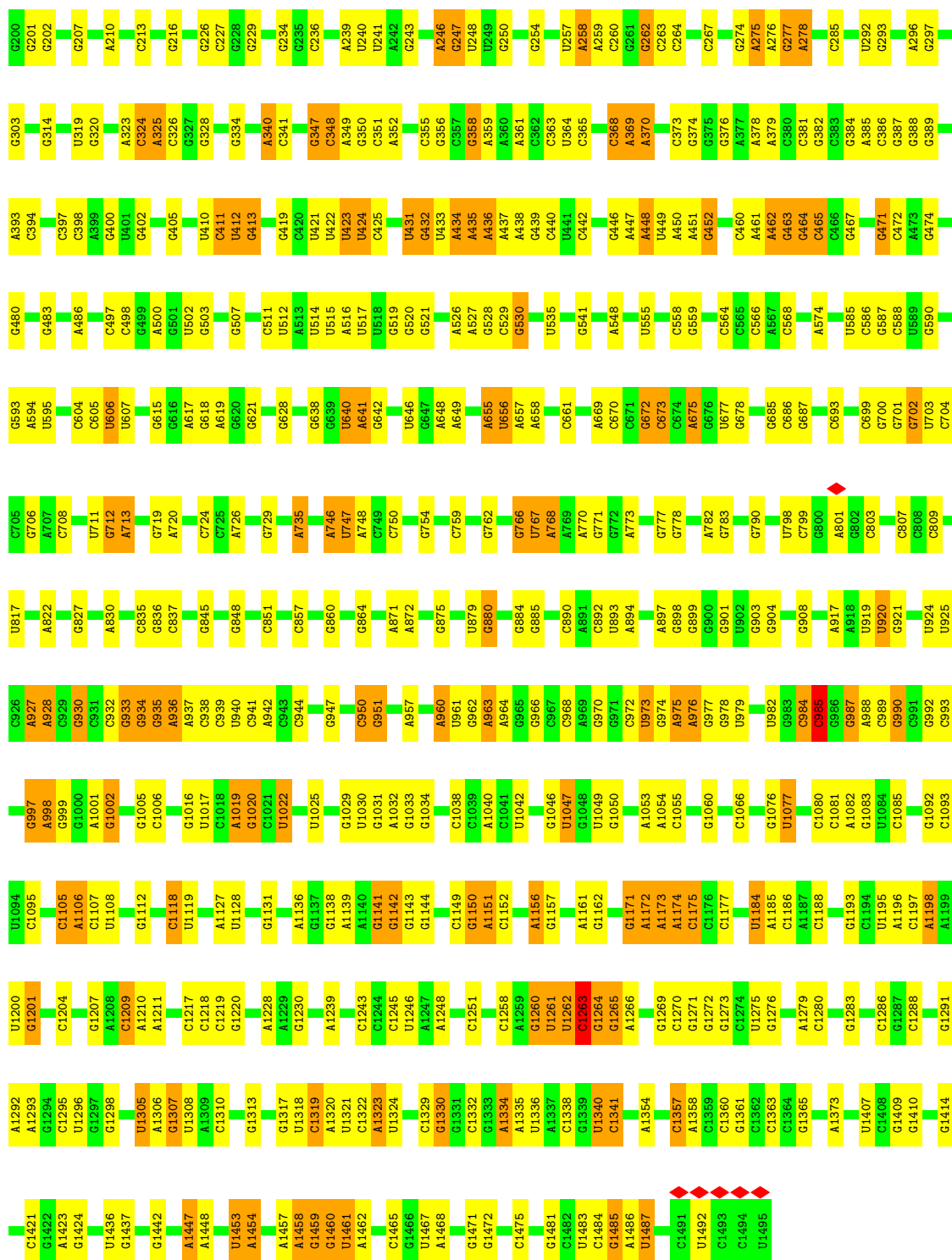


- Molecule 3: Large ribosomal subunit protein eL8



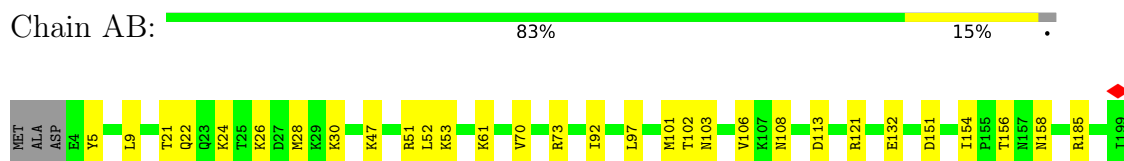
- Molecule 4: 16S rRNA





• Molecule 5: Small ribosomal subunit protein uS2

Chain AB:





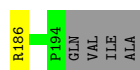
- Molecule 6: Small ribosomal subunit protein uS3

Chain AC: 87% 6% 7%



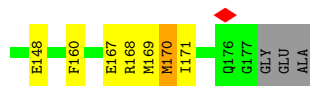
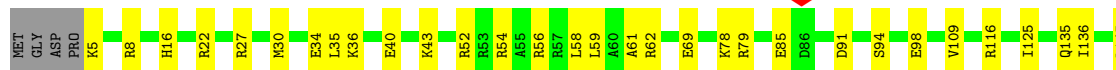
- Molecule 7: Small ribosomal subunit protein eS1

Chain AD: 79% 14% 7%



- Molecule 8: Small ribosomal subunit protein uS4

Chain AE: 75% 21% 4%



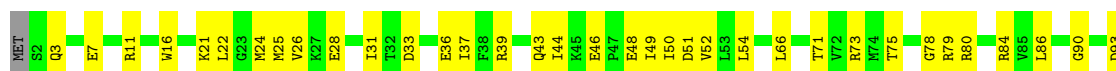
- Molecule 9: Small ribosomal subunit protein eS4

Chain AF: 84% 15% 1%



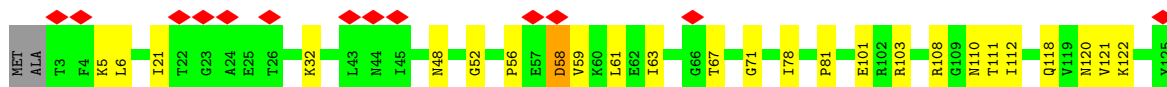
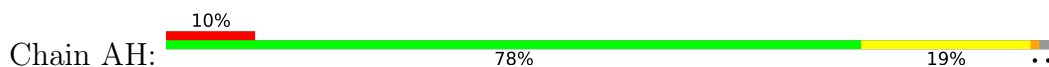
- Molecule 10: Small ribosomal subunit protein uS5

Chain AG: 72% 24% 4%

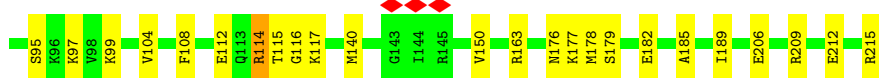
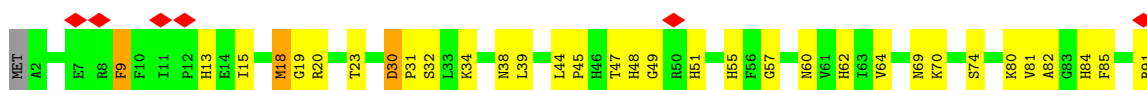




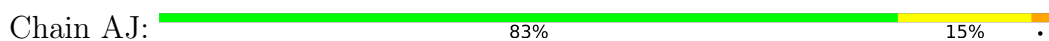
- Molecule 11: Small ribosomal subunit protein eS6



- Molecule 12: Small ribosomal subunit protein uS7



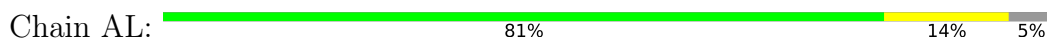
- Molecule 13: Small ribosomal subunit protein uS8



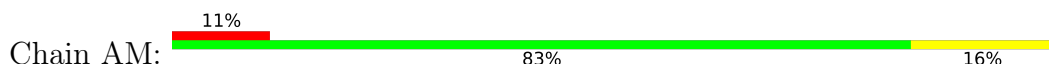
- Molecule 14: Small ribosomal subunit protein eS8



- Molecule 15: Small ribosomal subunit protein uS9



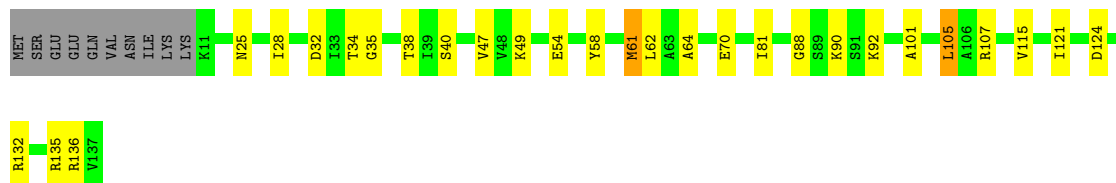
- Molecule 16: Small ribosomal subunit protein uS10





- Molecule 17: Small ribosomal subunit protein uS11

Chain AN: 72% 19% 7%



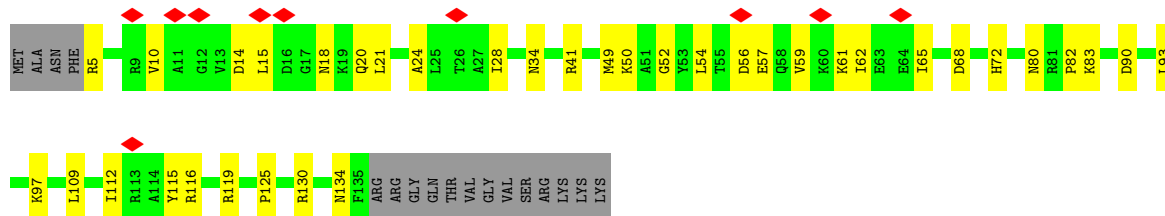
- Molecule 18: Small ribosomal subunit protein uS12

Chain AO: 82% 15% 3%



- Molecule 19: Small ribosomal subunit protein uS13

Chain AP: 7% 64% 25% 11%



- Molecule 20: Small ribosomal subunit protein uS14

Chain AQ: 64% 21% 11% 4%



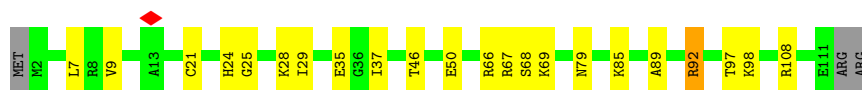
- Molecule 21: Small ribosomal subunit protein uS15

Chain AR: 84% 14% 2%



- Molecule 22: Small ribosomal subunit protein uS17

Chain AS: 78% 19% 3% 2%



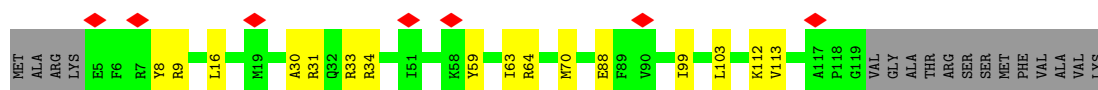
- Molecule 23: Small ribosomal subunit protein eS17

Chain AT: 78% 16% 6%



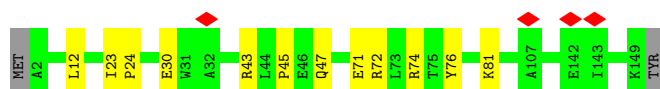
- Molecule 24: Small ribosomal subunit protein uS19

Chain AU: 5% 75% 12% 13%



- Molecule 25: Small ribosomal subunit protein eS19

Chain AV: 91% 8% .



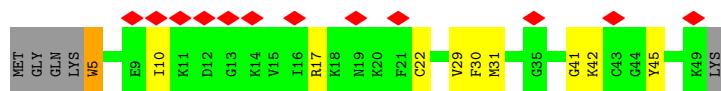
- Molecule 26: Small ribosomal subunit protein eS24

Chain AW: 78% 15% 6%



- Molecule 27: Small ribosomal subunit protein eS31

Chain AX: 24% 70% 18% 10%

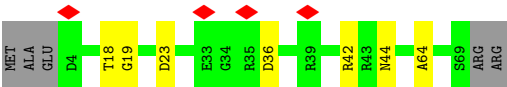
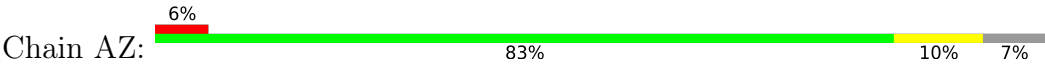


- Molecule 28: Small ribosomal subunit protein eS27

Chain AY: 89% 8% .



- Molecule 29: Small ribosomal subunit protein eS28



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25356	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	13.465	Depositor
Minimum map value	-3.095	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.731	Depositor
Recommended contour level	3	Depositor
Map size (Å)	400.896, 400.896, 400.896	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.783, 0.783, 0.783	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	A1	0.32	0/485	0.57	0/656
2	A2	0.29	0/341	0.72	0/440
3	A5	0.27	0/951	0.51	0/1281
4	AA	0.45	0/35966	0.87	12/56138 (0.0%)
5	AB	0.29	0/1610	0.55	0/2177
6	AC	0.28	0/1554	0.63	1/2087 (0.0%)
7	AD	0.29	0/1537	0.58	0/2060
8	AE	0.28	0/1478	0.59	0/1980
9	AF	0.29	0/2030	0.59	0/2739
10	AG	0.29	0/1824	0.60	0/2457
11	AH	0.27	0/986	0.58	0/1320
12	AI	0.29	0/1765	0.62	0/2371
13	AJ	0.31	0/1049	0.58	0/1408
14	AK	0.27	0/986	0.64	0/1315
15	AL	0.27	0/1021	0.67	0/1369
16	AM	0.28	0/830	0.70	0/1113
17	AN	0.28	0/972	0.65	0/1309
18	AO	0.29	0/1134	0.60	0/1508
19	AP	0.26	0/1070	0.63	0/1440
20	AQ	0.29	0/426	0.72	0/562
21	AR	0.27	0/1311	0.58	0/1763
22	AS	0.30	0/925	0.60	0/1249
23	AT	0.29	0/528	0.61	0/701
24	AU	0.28	0/968	0.60	0/1293
25	AV	0.27	0/1238	0.55	0/1668
26	AW	0.30	0/790	0.59	0/1061
27	AX	0.30	0/381	0.60	0/509
28	AY	0.30	0/472	0.60	0/634
29	AZ	0.27	0/525	0.66	0/703
All	All	0.38	0/65153	0.77	13/95311 (0.0%)

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(°)
6	AC	39	PRO	CA-N-CD	-7.76	100.64	111.50
4	AA	72	C	N3-C2-O2	-6.58	117.29	121.90
4	AA	1263	C	N1-C2-O2	6.48	122.79	118.90
4	AA	139	C	N1-C2-O2	6.24	122.64	118.90
4	AA	213	C	N3-C2-O2	-6.21	117.56	121.90

There are no chirality outliers.

There are no planarity outliers.

## 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	A1	471	0	457	11	0
2	A2	335	0	396	8	0
3	A5	939	0	994	21	0
4	AA	32135	0	16231	345	0
5	AB	1579	0	1638	19	0
6	AC	1532	0	1622	6	0
7	AD	1511	0	1595	20	0
8	AE	1455	0	1531	27	0
9	AF	1981	0	2051	25	0
10	AG	1794	0	1850	42	0
11	AH	971	0	1027	17	0
12	AI	1728	0	1775	48	0
13	AJ	1028	0	1065	15	0
14	AK	977	0	1064	22	0
15	AL	1006	0	1052	16	0
16	AM	822	0	870	11	0
17	AN	954	0	981	19	0
18	AO	1118	0	1214	18	0
19	AP	1052	0	1094	25	0
20	AQ	417	0	445	10	0
21	AR	1283	0	1358	18	0
22	AS	903	0	922	16	0
23	AT	522	0	557	5	0
24	AU	948	0	1007	13	0
25	AV	1209	0	1254	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	AW	774	0	794	10	0
27	AX	369	0	361	8	0
28	AY	465	0	507	3	0
29	AZ	523	0	551	4	0
All	All	60801	0	46263	644	0

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

The worst 5 of 644 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)
4:AA:937:A:C2	4:AA:1276:G:N2	2.32	0.97
12:AI:212:GLU:HA	12:AI:215:ARG:NH1	1.84	0.93
4:AA:962:G:C2	4:AA:988:A:C5	2.58	0.91
4:AA:1141:G:O2'	4:AA:1142:G:O4'	1.90	0.88
4:AA:962:G:N2	4:AA:988:A:C5	2.43	0.87

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	A1	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
2	A2	33/37 (89%)	33 (100%)	0	0	100	100
3	A5	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
5	AB	195/202 (96%)	187 (96%)	8 (4%)	0	100	100
6	AC	193/210 (92%)	186 (96%)	7 (4%)	0	100	100
7	AD	182/198 (92%)	178 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AE	171/180 (95%)	169 (99%)	2 (1%)	0	100	100
9	AF	240/243 (99%)	234 (98%)	6 (2%)	0	100	100
10	AG	225/236 (95%)	217 (96%)	8 (4%)	0	100	100
11	AH	121/125 (97%)	116 (96%)	5 (4%)	0	100	100
12	AI	212/215 (99%)	193 (91%)	18 (8%)	1 (0%)	25	54
13	AJ	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
14	AK	122/127 (96%)	115 (94%)	7 (6%)	0	100	100
15	AL	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
16	AM	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
17	AN	125/137 (91%)	120 (96%)	5 (4%)	0	100	100
18	AO	141/147 (96%)	138 (98%)	3 (2%)	0	100	100
19	AP	129/148 (87%)	124 (96%)	5 (4%)	0	100	100
20	AQ	48/56 (86%)	46 (96%)	2 (4%)	0	100	100
21	AR	153/158 (97%)	150 (98%)	3 (2%)	0	100	100
22	AS	108/113 (96%)	105 (97%)	3 (3%)	0	100	100
23	AT	61/67 (91%)	61 (100%)	0	0	100	100
24	AU	113/132 (86%)	111 (98%)	2 (2%)	0	100	100
25	AV	146/150 (97%)	142 (97%)	4 (3%)	0	100	100
26	AW	91/99 (92%)	89 (98%)	2 (2%)	0	100	100
27	AX	43/50 (86%)	41 (95%)	2 (5%)	0	100	100
28	AY	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
29	AZ	64/71 (90%)	63 (98%)	1 (2%)	0	100	100
All	All	3507/3714 (94%)	3376 (96%)	130 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AI	15	ILE

### 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	A1	53/53 (100%)	53 (100%)	0	100	100
2	A2	33/35 (94%)	33 (100%)	0	100	100
3	A5	99/99 (100%)	97 (98%)	2 (2%)	50	70
5	AB	169/173 (98%)	166 (98%)	3 (2%)	54	73
6	AC	153/167 (92%)	150 (98%)	3 (2%)	50	70
7	AD	161/171 (94%)	156 (97%)	5 (3%)	35	60
8	AE	156/160 (98%)	154 (99%)	2 (1%)	65	78
9	AF	212/213 (100%)	211 (100%)	1 (0%)	86	91
10	AG	188/197 (95%)	185 (98%)	3 (2%)	58	75
11	AH	107/108 (99%)	105 (98%)	2 (2%)	52	71
12	AI	183/184 (100%)	175 (96%)	8 (4%)	24	50
13	AJ	107/108 (99%)	105 (98%)	2 (2%)	52	71
14	AK	100/103 (97%)	98 (98%)	2 (2%)	50	70
15	AL	104/111 (94%)	104 (100%)	0	100	100
16	AM	91/91 (100%)	89 (98%)	2 (2%)	47	68
17	AN	94/104 (90%)	91 (97%)	3 (3%)	34	59
18	AO	117/121 (97%)	116 (99%)	1 (1%)	75	86
19	AP	108/122 (88%)	106 (98%)	2 (2%)	52	71
20	AQ	42/46 (91%)	39 (93%)	3 (7%)	12	37
21	AR	140/143 (98%)	140 (100%)	0	100	100
22	AS	99/102 (97%)	98 (99%)	1 (1%)	73	83
23	AT	57/61 (93%)	53 (93%)	4 (7%)	12	37
24	AU	101/114 (89%)	100 (99%)	1 (1%)	73	83
25	AV	125/127 (98%)	124 (99%)	1 (1%)	79	87
26	AW	84/89 (94%)	81 (96%)	3 (4%)	30	56
27	AX	37/41 (90%)	34 (92%)	3 (8%)	9	31
28	AY	53/54 (98%)	52 (98%)	1 (2%)	52	71
29	AZ	56/60 (93%)	55 (98%)	1 (2%)	54	73
All	All	3029/3157 (96%)	2970 (98%)	59 (2%)	52	71

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	AI	178	MET
27	AX	31	MET
17	AN	58	TYR
27	AX	5	TRP
24	AU	88	GLU

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

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	AA	1494/1495 (99%)	285 (19%)	54 (3%)

5 of 285 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	AA	4	C
4	AA	21	A
4	AA	34	G
4	AA	42	G
4	AA	43	A

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	AA	871	A
4	AA	1019	A
4	AA	1340	U
4	AA	919	U
4	AA	975	A

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

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.

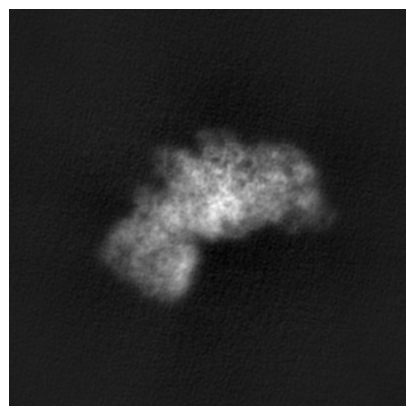
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50613. These allow visual inspection of the internal detail of the map and identification of artifacts.

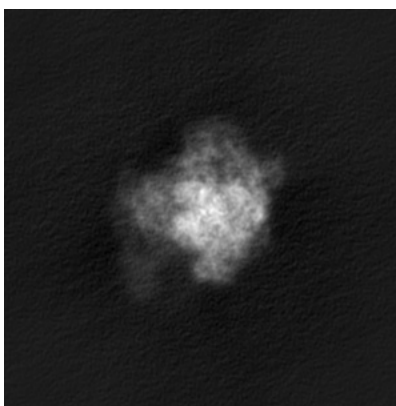
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

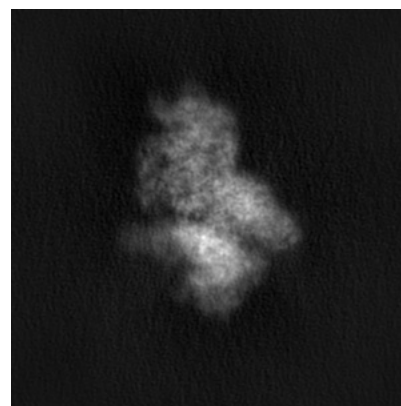
#### 6.1.1 Primary map



X

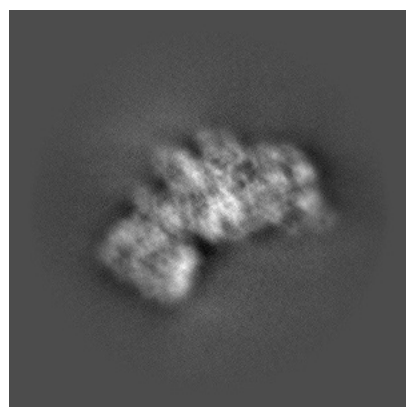


Y

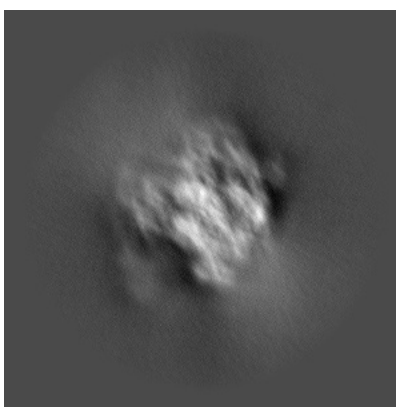


Z

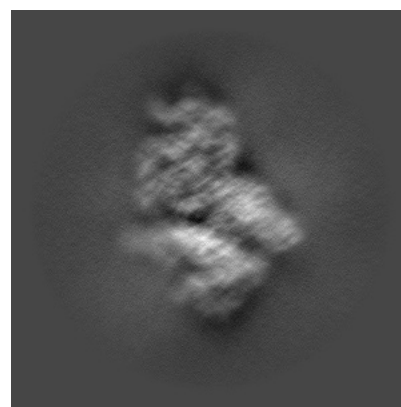
#### 6.1.2 Raw map



X



Y

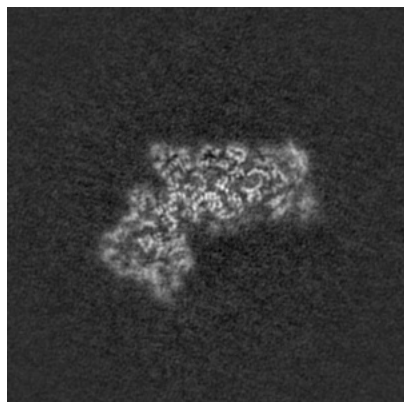


Z

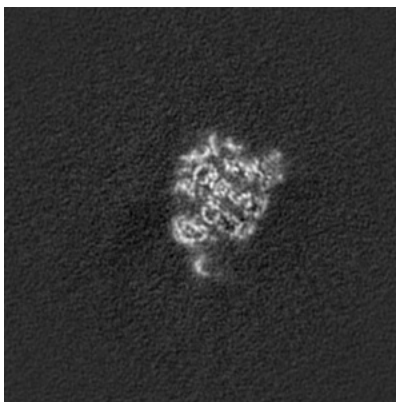
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

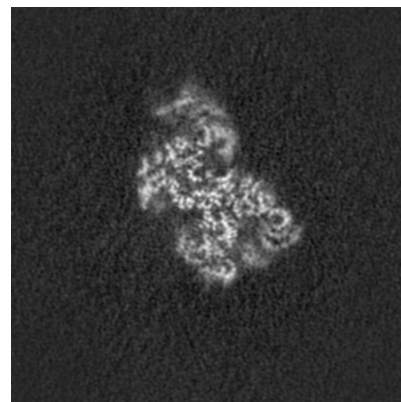
### 6.2.1 Primary map



X Index: 256

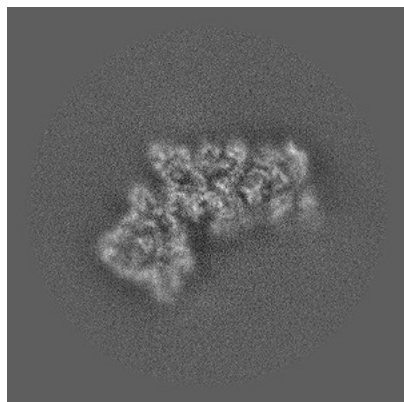


Y Index: 256

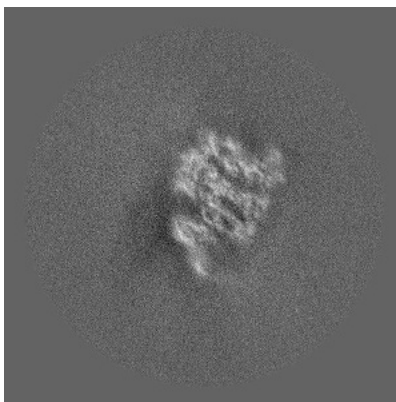


Z Index: 256

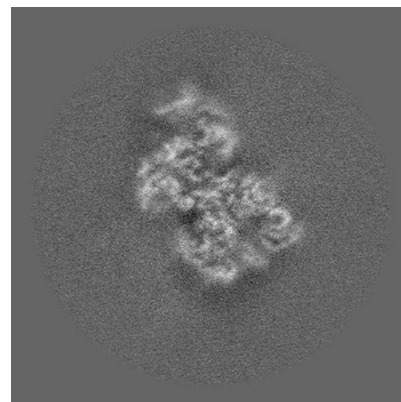
### 6.2.2 Raw map



X Index: 256



Y Index: 256

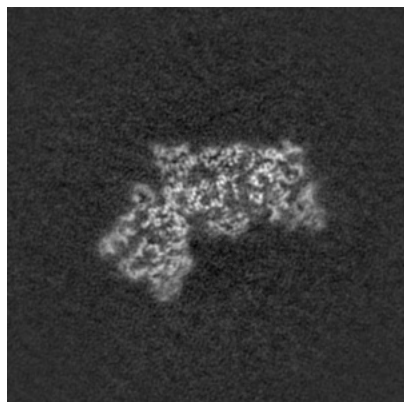


Z Index: 256

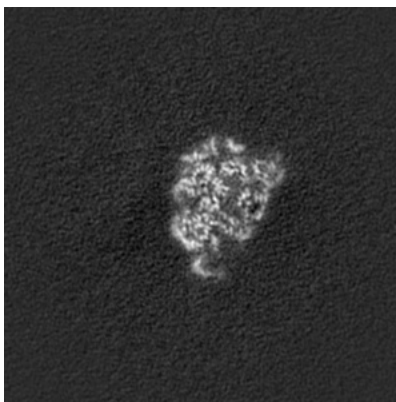
The images above show central slices of the map in three orthogonal directions.

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

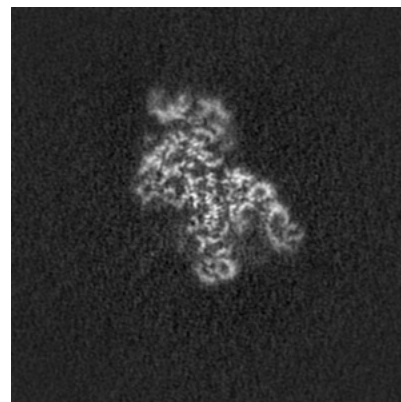
### 6.3.1 Primary map



X Index: 248

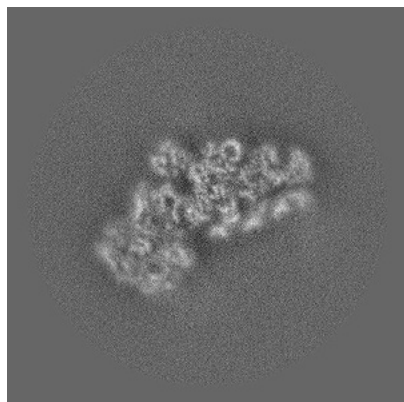


Y Index: 260

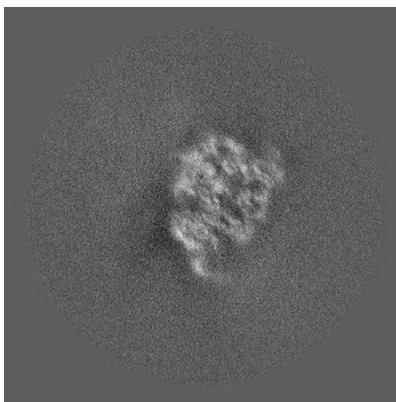


Z Index: 265

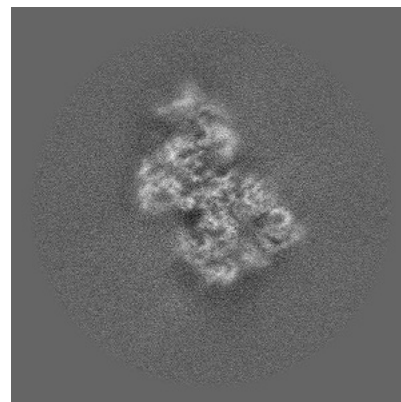
### 6.3.2 Raw map



X Index: 268



Y Index: 259

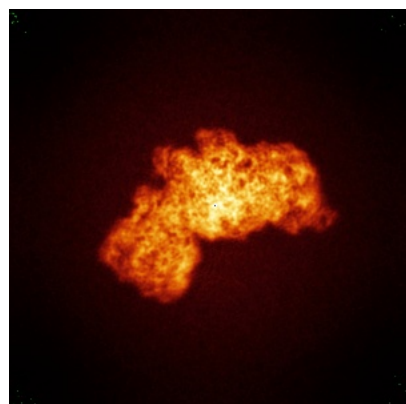


Z Index: 255

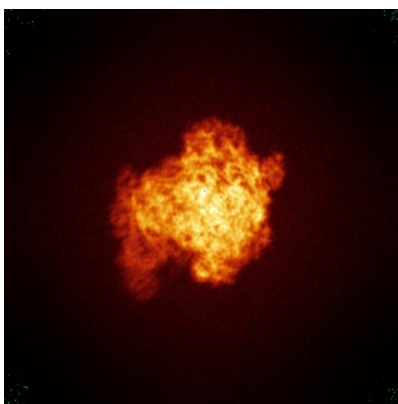
The images above show the largest variance slices of the map in three orthogonal directions.

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

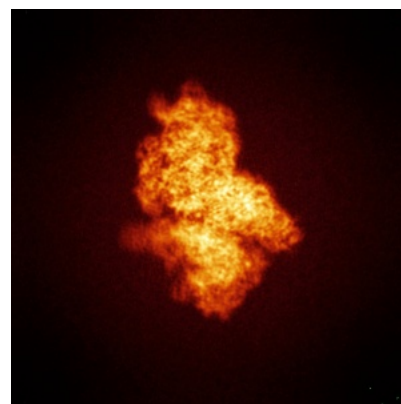
### 6.4.1 Primary map



X

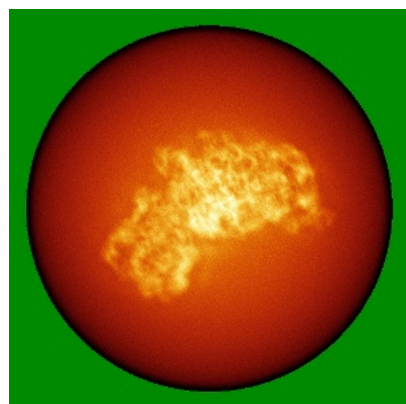


Y

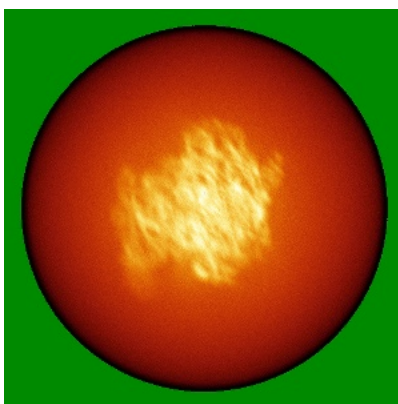


Z

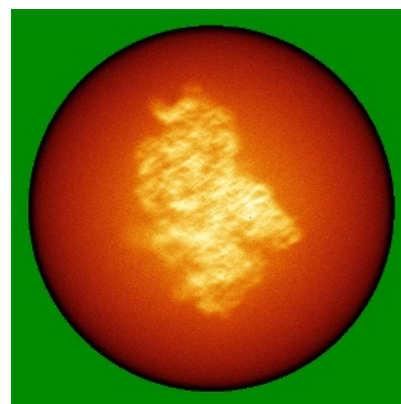
### 6.4.2 Raw map



X



Y

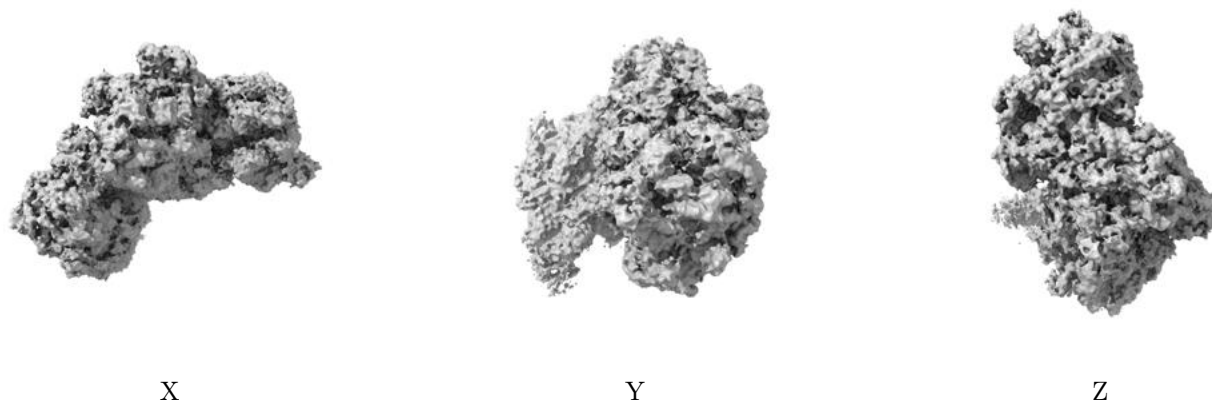


Z

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.

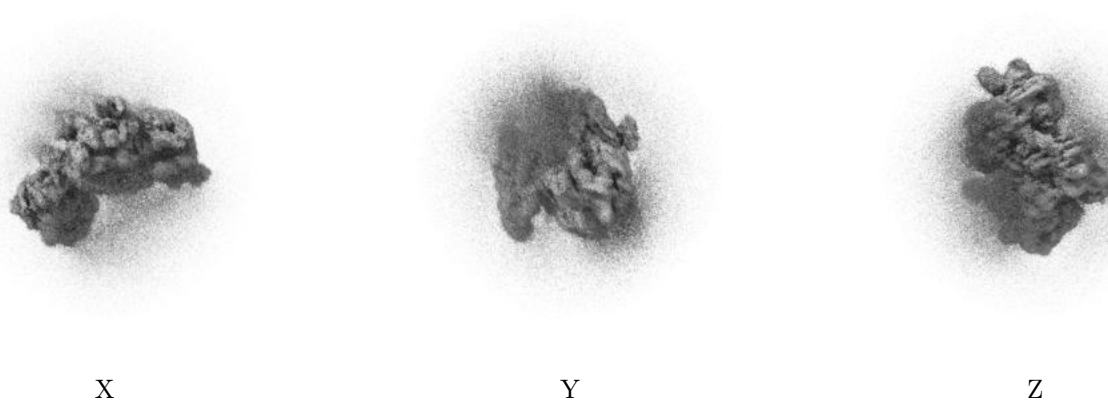
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

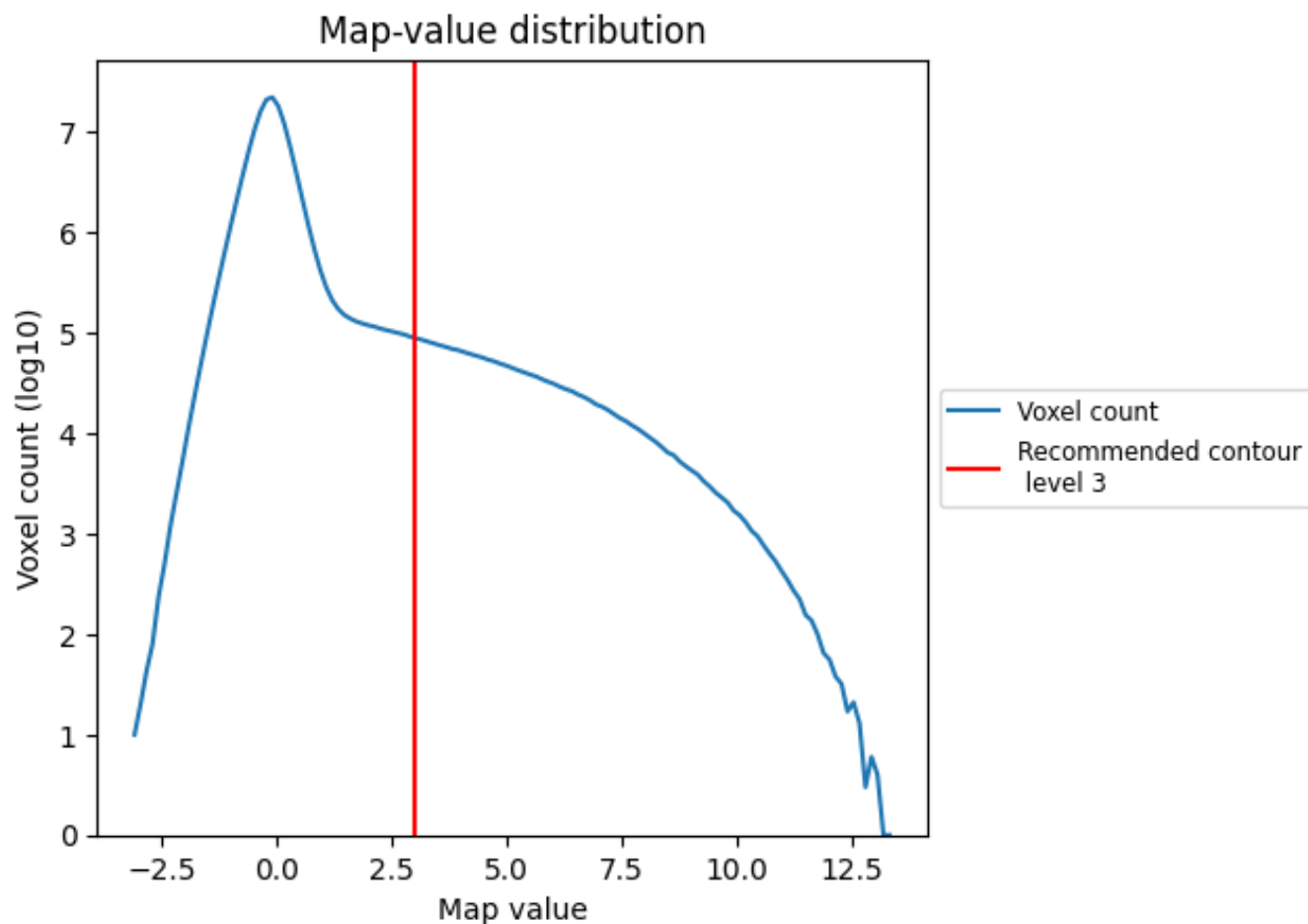
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

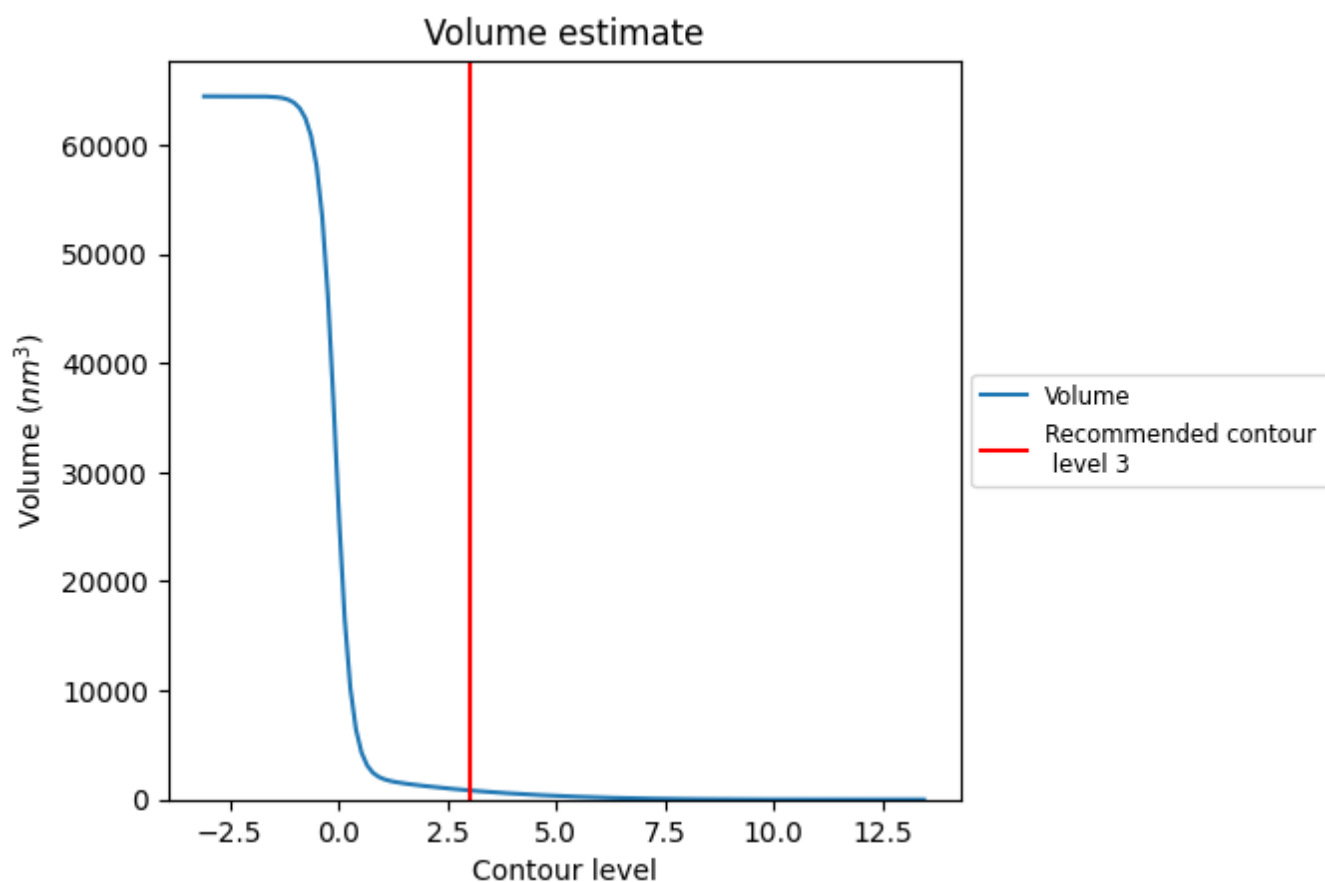
This section contains the results of statistical analysis of the map.

### 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.

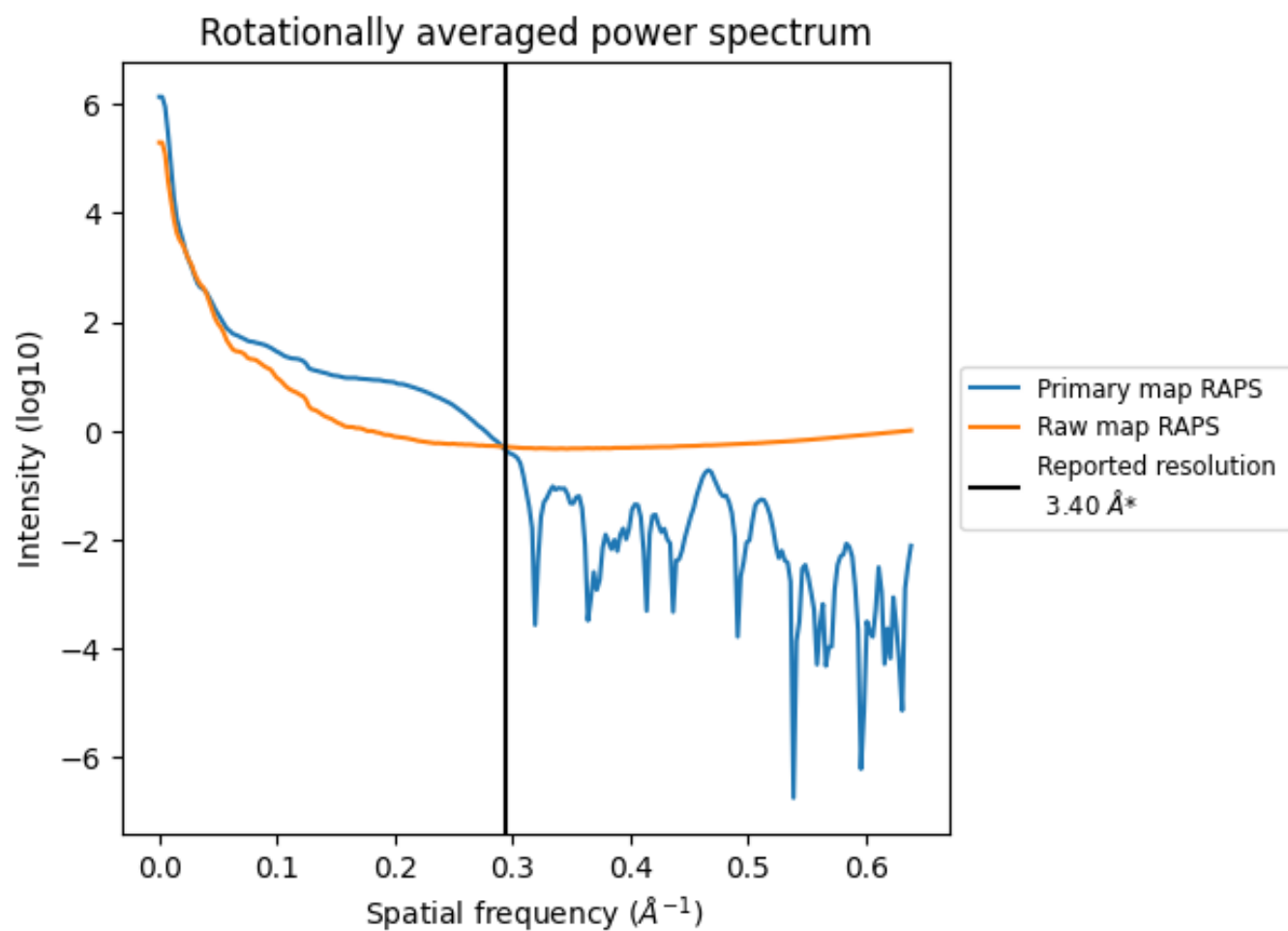
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 843 nm<sup>3</sup>; this corresponds to an approximate mass of 762 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 ⓘ

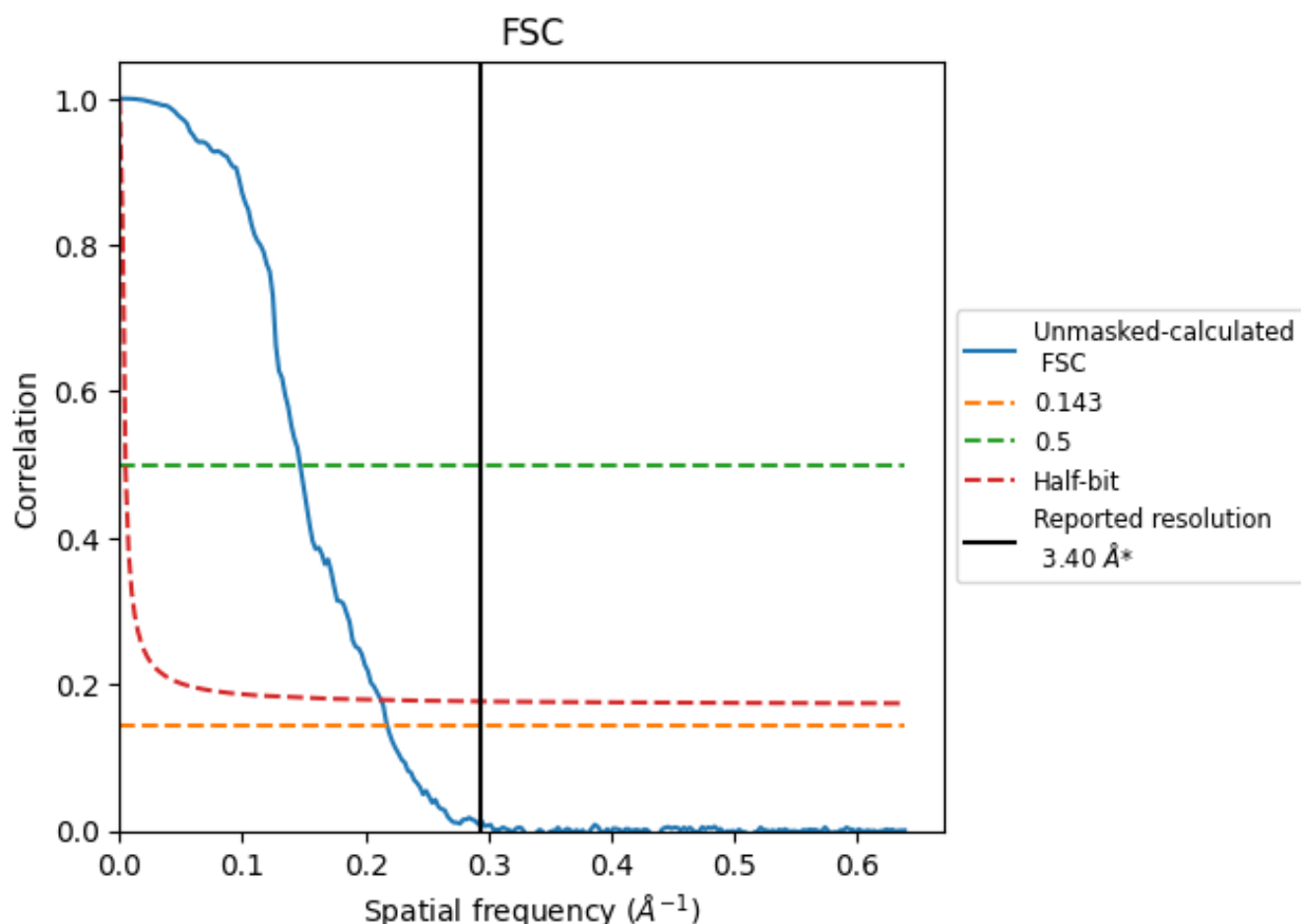


\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 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 0.294 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

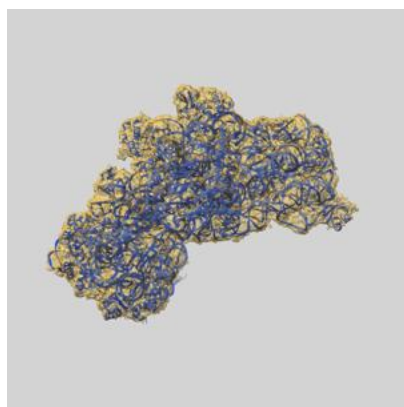
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.59	6.81	4.70

\*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 4.59 differs from the reported value 3.4 by more than 10 %

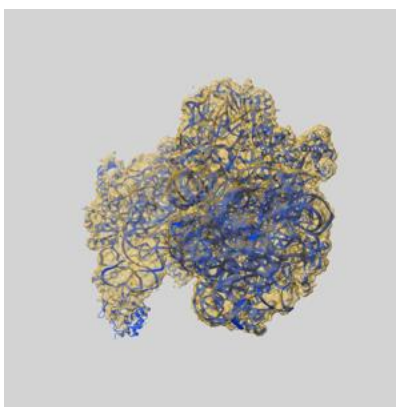
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50613 and PDB model 9FO0. Per-residue inclusion information can be found in section [3](#) on page [9](#).

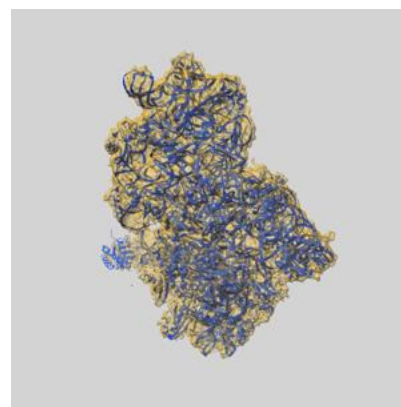
### 9.1 Map-model overlay [i](#)



X



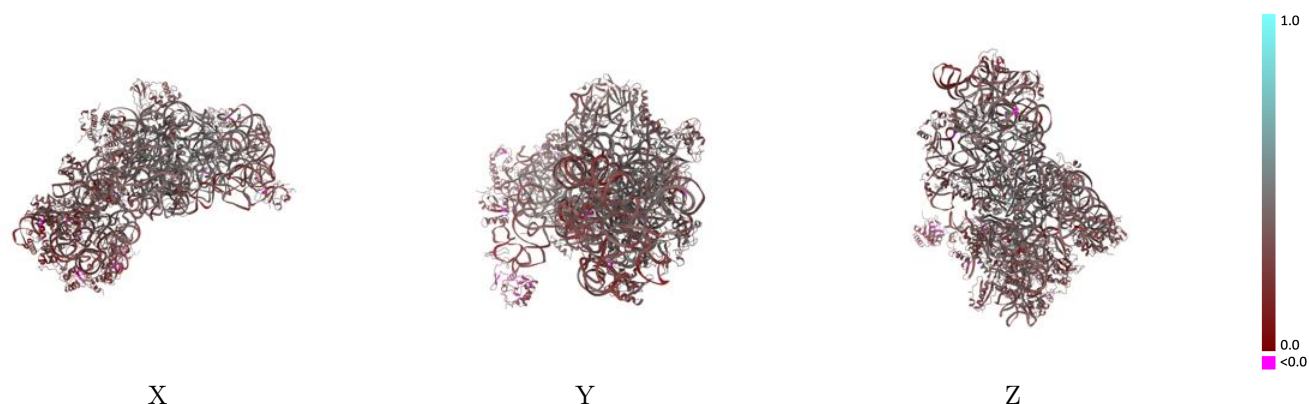
Y



Z

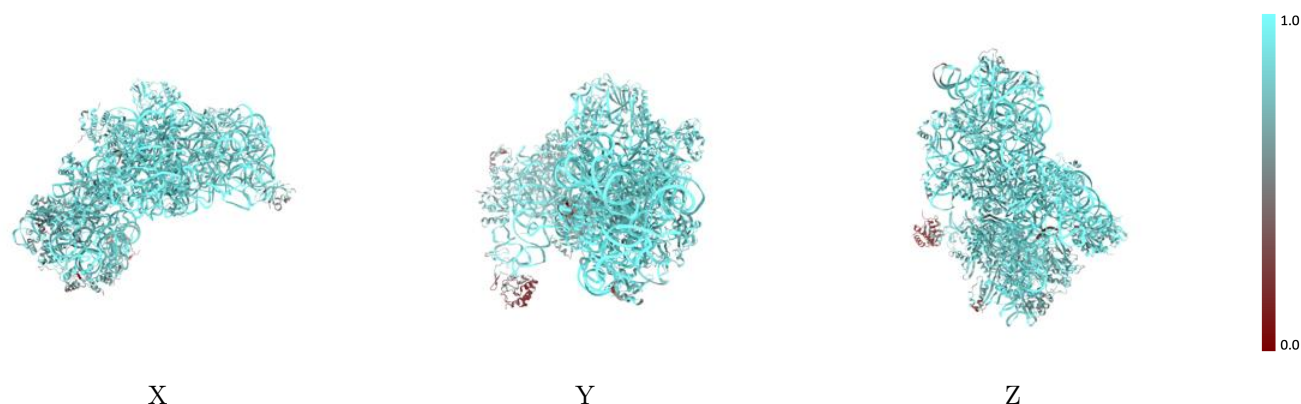
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



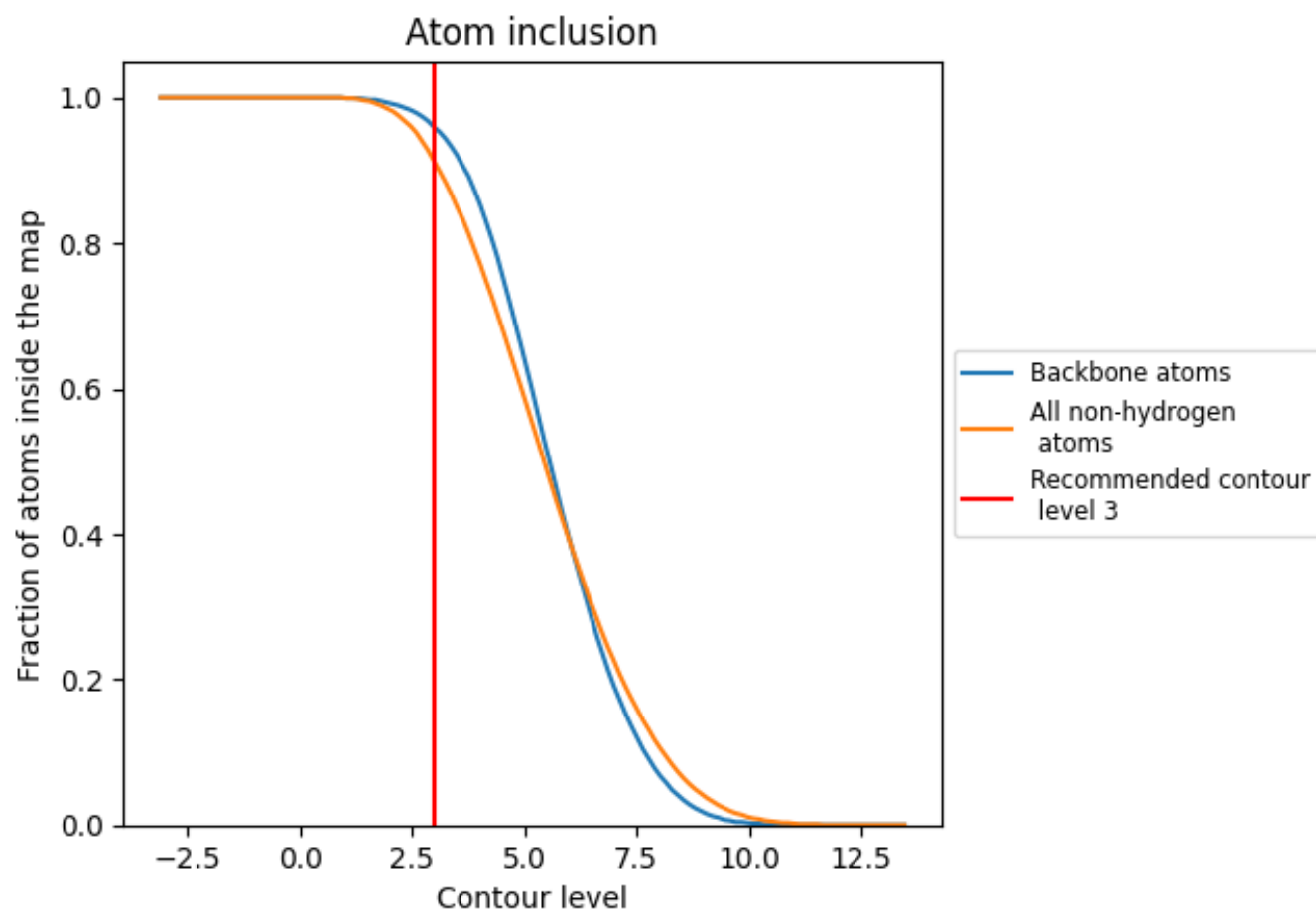
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).





























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 91% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.3480
A1	 0.9040	 0.3650
A2	 0.9610	 0.3880
A5	 0.2280	 0.1700
AA	 0.9780	 0.3580
AB	 0.8770	 0.3480
AC	 0.8270	 0.3160
AD	 0.8730	 0.3560
AE	 0.8940	 0.3810
AF	 0.8760	 0.3980
AG	 0.8900	 0.3900
AH	 0.7300	 0.2810
AI	 0.8000	 0.2610
AJ	 0.9160	 0.4130
AK	 0.8920	 0.3840
AL	 0.8230	 0.3280
AM	 0.7290	 0.3170
AN	 0.9210	 0.3380
AO	 0.9410	 0.4170
AP	 0.7520	 0.2510
AQ	 0.9240	 0.3600
AR	 0.9010	 0.3870
AS	 0.9280	 0.4070
AT	 0.9030	 0.3140
AU	 0.8150	 0.2320
AV	 0.7860	 0.2870
AW	 0.8730	 0.3560
AX	 0.6310	 0.1650
AY	 0.9100	 0.3640
AZ	 0.8320	 0.3270

