



wwPDB EM Validation Summary Report ⓘ

Oct 1, 2025 – 02:17 PM JST

PDB ID : 9V1J / pdb_00009v1j
EMDB ID : EMD-64695
Title : Cryo- EM structure of small subunit (body) of 75S ribosome with P- tRNA from *Entamoeba histolytica*
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.10 Å (reported)
Based on initial models : 4UG0, 5XXB

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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

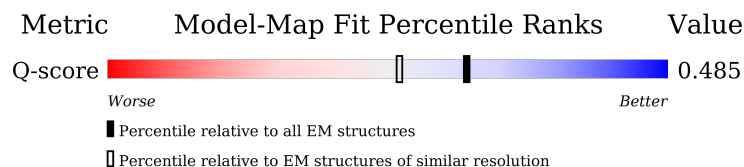
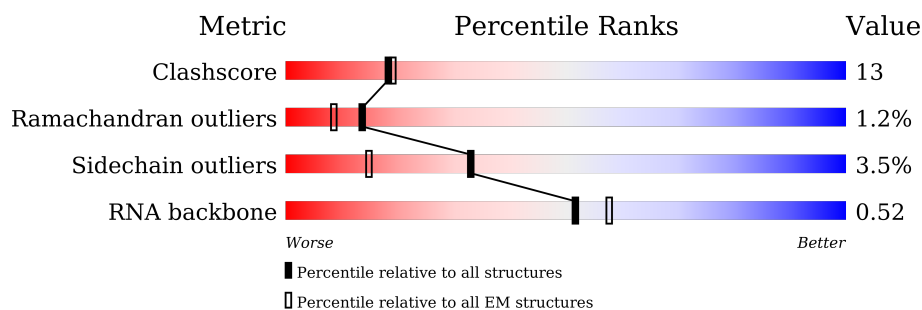
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY




The reported resolution of this entry is 3.10 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	sB	144	
2	sC	84	
3	sH	76	

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Mol	Chain	Length	Quality of chain
4	sK	6	100%
5	sa	1947	27% 19% . 50%
6	sb	254	53% 13% 34%
7	sc	255	64% 20% 16%
8	se	256	64% 18% 17%
9	sf	326	54% 23% . 21%
10	sh	266	12% 30% 21% 7% 6% 36%
11	si	201	9% 22% 10% . . 61%
12	sj	237	53% 18% 30%
13	sk	185	70% 15% 15%
14	sm	156	83% 15% .
15	so	151	77% 21% ..
16	sp	146	67% 23% . 9%
17	sr	130	78% 21% ..
18	sx	86	7% 71% 12% 17%
19	sy	141	60% 16% 10% 7% 8%
20	sz	140	8% 21% 19% 60%

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 41917 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 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 2 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	sC	83	Total	C	N	O	S	0	0
			641	407	117	111	6		

- Molecule 3 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	sH	75	Total	C	N	O	P	0	0
			1593	712	278	528	75		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sK	6	Total	C	N	O	P	0	0
			126	57	21	42	6		

- Molecule 5 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sa	981	Total	C	N	O	P	0	0
			20995	9399	3828	6787	981		

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sb	168	Total	C	N	O	S	0	0
			1327	840	236	240	11		

- Molecule 7 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sc	215	Total	C	N	O	S	0	0
			1642	1052	291	291	8		

- Molecule 8 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	se	212	Total	C	N	O	S	0	0
			1717	1097	305	306	9		

- Molecule 9 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	sf	256	Total	C	N	O	S	0	0
			2031	1297	378	345	11		

- Molecule 10 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	sh	169	Total	C	N	O	S	0	0
			1345	846	269	224	6		

- Molecule 11 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	si	79	Total	C	N	O	S	0	0
			615	394	114	106	1		

- Molecule 12 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	sj	167	Total	C	N	O	S	0	0
			1329	837	252	236	4		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	sk	158	Total	C	N	O	S	0	0
			1293	828	246	213	6		

- Molecule 14 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sm	154	Total	C	N	O	S	0	0
			1263	796	243	217	7		

- Molecule 15 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	so	150	Total	C	N	O	S	0	0
			1184	756	218	204	6		

- Molecule 16 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sp	133	Total	C	N	O	S	0	0
			999	615	192	186	6		

- Molecule 17 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 18 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	sx	71	Total	C	N	O	S	0	0
			560	356	101	100	3		

- Molecule 19 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sy	130	Total	C	N	O	S	0	0
			1010	637	200	169	4		

- Molecule 20 is a protein called 40S ribosomal protein S24, putative.

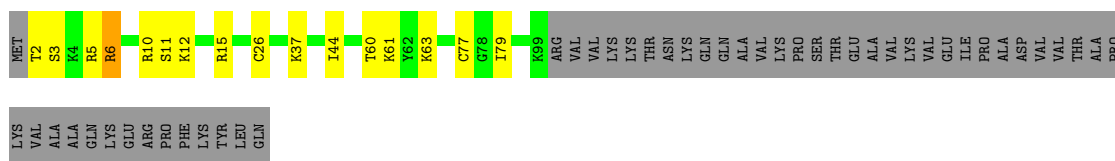
Mol	Chain	Residues	Atoms					AltConf	Trace
20	sz	56	Total	C	N	O	S	0	0
			438	288	74	75	1		

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.

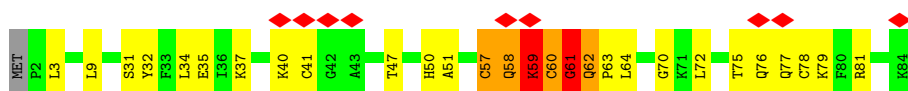
- Molecule 1: 40S ribosomal protein S26

Chain sB: 



- Molecule 2: Small ribosomal subunit protein eS27

Chain sC: 



- Molecule 3: P-tRNA

Chain sH: 



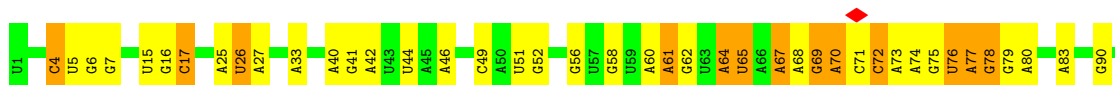
- Molecule 4: mRNA

Chain sK: 

There are no outlier residues recorded for this chain.

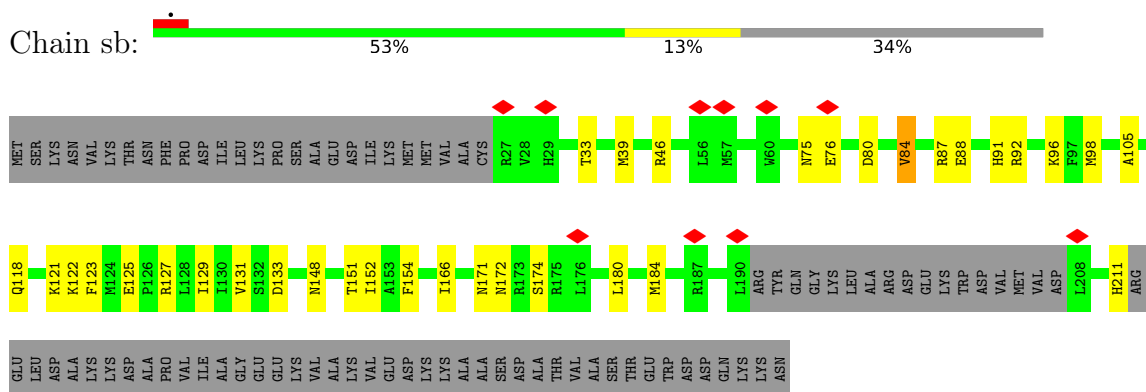
- Molecule 5: 17S rRNA

Chain sa: 

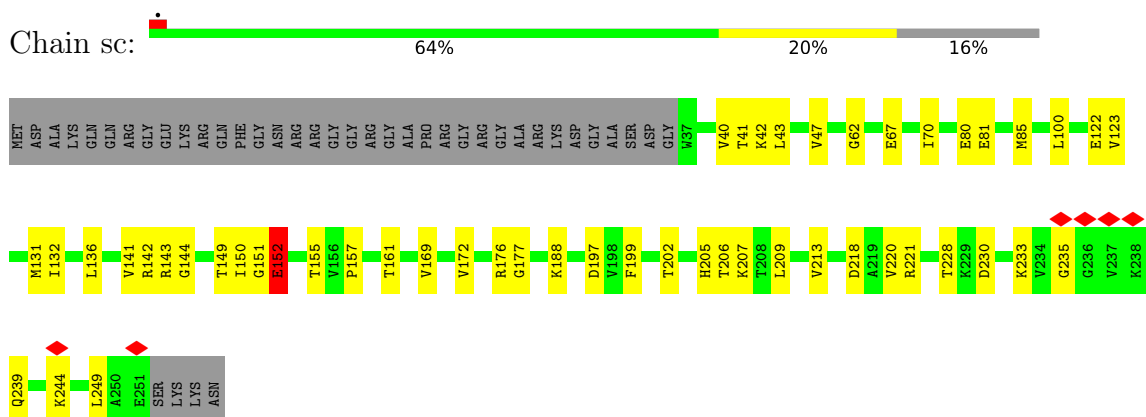




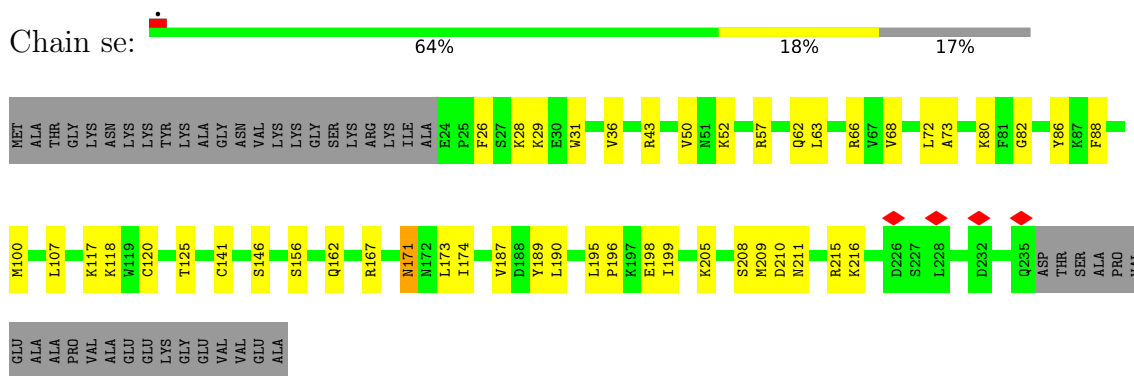
- Molecule 6: Small ribosomal subunit protein uS2



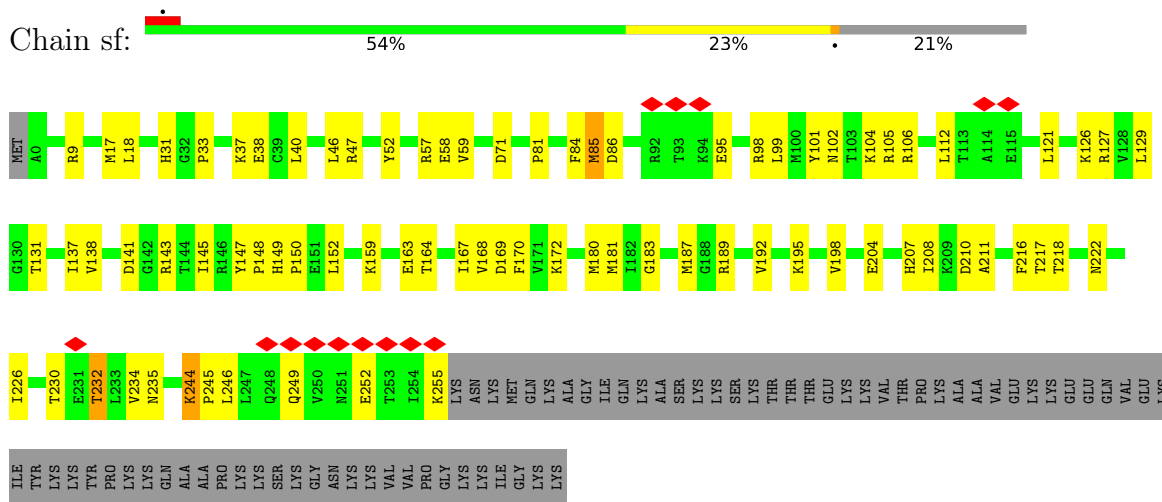
- Molecule 7: Small ribosomal subunit protein uS5



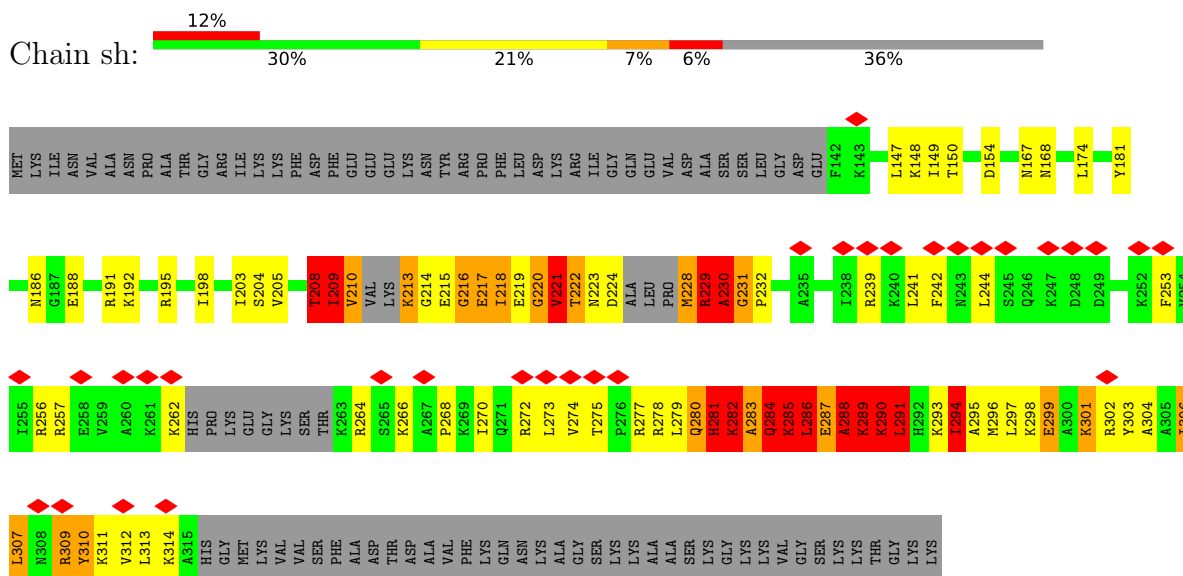
- Molecule 8: Small ribosomal subunit protein eS1



- Molecule 9: 40S ribosomal protein S4, putative



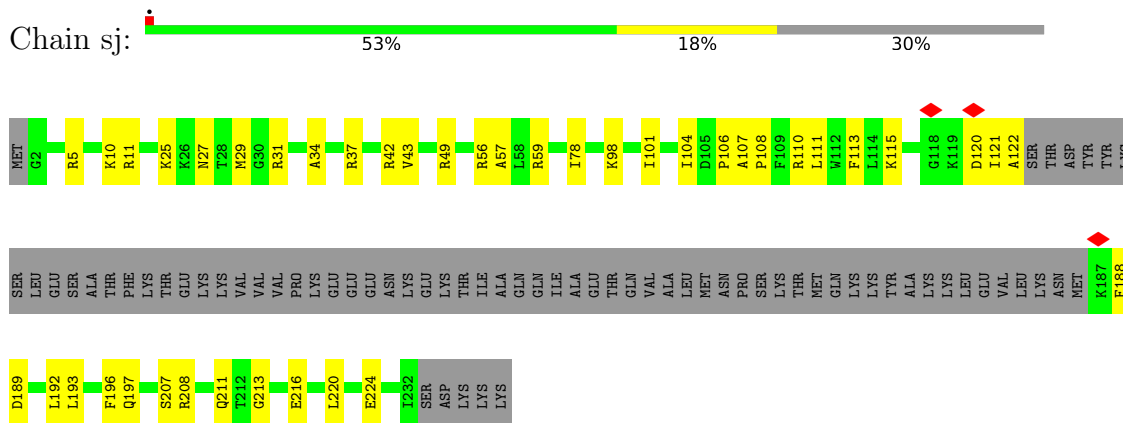
- Molecule 10: 40S ribosomal protein S6



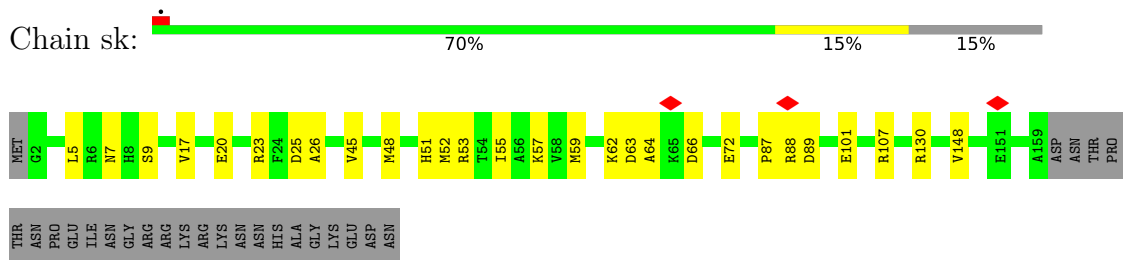
- Molecule 11: 40S ribosomal protein S7



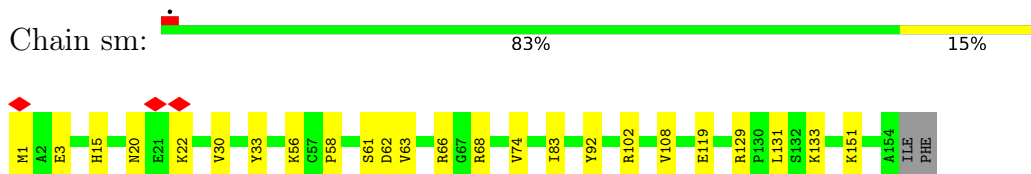
- Molecule 12: 40S ribosomal protein S8



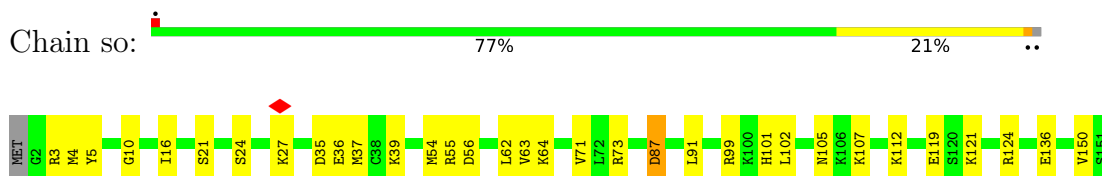
- Molecule 13: Small ribosomal subunit protein uS4



- Molecule 14: 40S ribosomal protein S11, putative

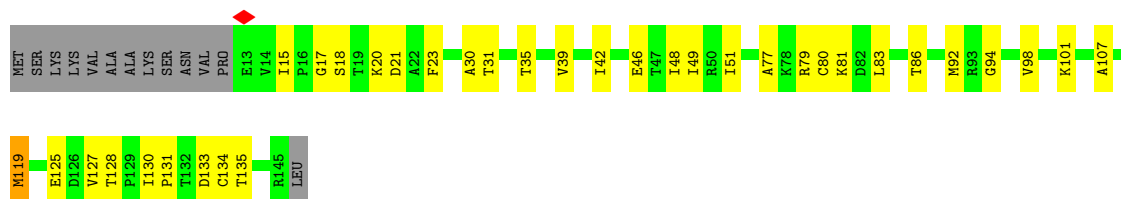


- Molecule 15: 40S ribosomal protein S13, putative




- Molecule 16: Ribosomal protein S14, putative

Chain sp:  67% 23% 9%



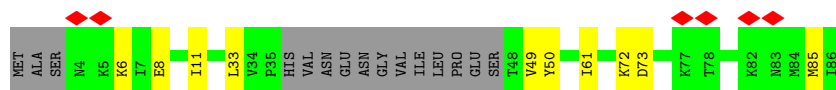
- Molecule 17: 40S ribosomal protein S15a, putative

Chain sr:  78% 21% 1%



- Molecule 18: 40S ribosomal protein S21

Chain sx:  7% 71% 12% 17%



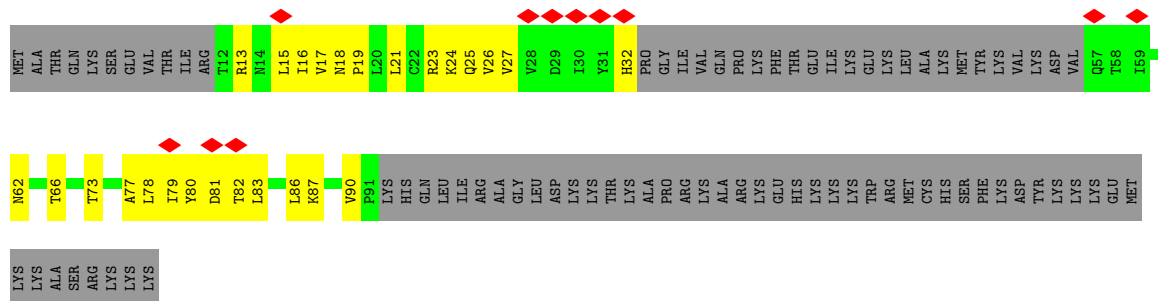
- Molecule 19: 40S ribosomal protein S23, putative

Chain sy:  60% 16% 10% 7% 8%



- Molecule 20: 40S ribosomal protein S24, putative

Chain sz:  8% 21% 19% 60%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.439	Depositor
Minimum map value	-4.365	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	288.90002, 288.90002, 288.90002	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	sB	0.15	0/797	0.28	0/1062
2	sC	1.06	11/654 (1.7%)	0.84	10/879 (1.1%)
3	sH	0.12	0/1778	0.29	0/2765
4	sK	0.11	0/140	0.22	0/215
5	sa	0.21	2/23516 (0.0%)	0.32	5/36630 (0.0%)
6	sb	0.15	0/1353	0.32	0/1829
7	sc	0.60	9/1673 (0.5%)	0.48	3/2257 (0.1%)
8	se	0.12	0/1741	0.25	0/2328
9	sf	0.15	0/2072	0.32	0/2792
10	sh	1.56	36/1357 (2.7%)	1.82	30/1799 (1.7%)
11	si	1.67	16/626 (2.6%)	1.47	18/842 (2.1%)
12	sj	0.13	0/1350	0.27	0/1804
13	sk	0.12	0/1313	0.23	0/1756
14	sm	0.14	0/1291	0.28	0/1725
15	so	0.13	0/1204	0.29	0/1613
16	sp	0.14	0/1013	0.30	0/1361
17	sr	0.15	0/1040	0.31	0/1404
18	sx	0.14	0/569	0.26	0/767
19	sy	1.58	34/1027 (3.3%)	1.54	32/1376 (2.3%)
20	sz	0.17	0/445	0.51	0/601
All	All	0.48	108/44959 (0.2%)	0.52	98/65805 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	sh	0	2
17	sr	0	1
19	sy	0	1
All	All	0	4

The worst 5 of 108 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	si	118	LYS	CA-C	-15.53	1.34	1.52
10	sh	283	ALA	CA-C	-14.94	1.34	1.52
10	sh	282	LYS	CA-C	-13.64	1.34	1.52
10	sh	284	GLN	N-CA	-13.17	1.29	1.46
10	sh	218	ILE	CA-C	-12.76	1.36	1.52

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	sh	210	VAL	CB-CA-C	-23.66	66.45	111.40
10	sh	289	LYS	N-CA-C	-22.44	85.24	113.97
10	sh	209	ILE	N-CA-C	22.19	135.28	110.21
10	sh	283	ALA	N-CA-C	-20.04	89.13	110.97
10	sh	231	GLY	CA-C-N	-18.77	99.09	120.11

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	sh	208	THR	Mainchain
10	sh	284	GLN	Mainchain
17	sr	76	SER	Peptide
19	sy	103	PHE	Mainchain

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	sB	787	0	833	15	0
2	sC	641	0	681	33	0
3	sH	1593	0	806	22	0
4	sK	126	0	64	0	0
5	sa	20995	0	10547	337	0
6	sb	1327	0	1327	21	0
7	sc	1642	0	1721	36	0
8	se	1717	0	1824	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	sf	2031	0	2145	63	0
10	sh	1345	0	1467	189	0
11	si	615	0	648	64	0
12	sj	1329	0	1370	28	0
13	sk	1293	0	1396	22	0
14	sm	1263	0	1279	20	0
15	so	1184	0	1272	26	0
16	sp	999	0	1024	25	0
17	sr	1022	0	1051	21	0
18	sx	560	0	581	6	0
19	sy	1010	0	1067	84	0
20	sz	438	0	465	18	0
All	All	41917	0	31568	940	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 13.

The worst 5 of 940 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:sh:220:GLY:O	10:sh:221:VAL:HG23	1.32	1.22
10:sh:215:GLU:HG2	10:sh:220:GLY:CA	1.73	1.17
10:sh:215:GLU:HG2	10:sh:220:GLY:HA2	1.27	1.14
11:si:104:ALA:HB2	11:si:118:LYS:HE3	1.37	1.03
10:sh:280:GLN:HA	10:sh:283:ALA:HB2	1.41	1.02

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	sB	96/144 (67%)	93 (97%)	3 (3%)	0	100	100
2	sC	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	11	38
6	sb	164/254 (65%)	157 (96%)	7 (4%)	0	100	100
7	sc	213/255 (84%)	201 (94%)	12 (6%)	0	100	100
8	se	210/256 (82%)	204 (97%)	6 (3%)	0	100	100
9	sf	254/326 (78%)	237 (93%)	15 (6%)	2 (1%)	16	48
10	sh	161/266 (60%)	133 (83%)	17 (11%)	11 (7%)	1	6
11	si	75/201 (37%)	64 (85%)	7 (9%)	4 (5%)	1	10
12	sj	163/237 (69%)	159 (98%)	4 (2%)	0	100	100
13	sk	156/185 (84%)	154 (99%)	2 (1%)	0	100	100
14	sm	152/156 (97%)	145 (95%)	7 (5%)	0	100	100
15	so	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
16	sp	131/146 (90%)	125 (95%)	6 (5%)	0	100	100
17	sr	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
18	sx	67/86 (78%)	67 (100%)	0	0	100	100
19	sy	128/141 (91%)	109 (85%)	10 (8%)	9 (7%)	1	5
20	sz	52/140 (37%)	45 (86%)	6 (12%)	1 (2%)	6	27
All	All	2378/3158 (75%)	2228 (94%)	122 (5%)	28 (1%)	14	38

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	sh	219	GLU
10	sh	285	LYS
10	sh	288	ALA
11	si	112	SER
11	si	137	TYR

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	sB	87/127 (68%)	85 (98%)	2 (2%)	45	70
2	sC	72/73 (99%)	70 (97%)	2 (3%)	38	66
6	sb	145/218 (66%)	142 (98%)	3 (2%)	48	72
7	sc	172/199 (86%)	167 (97%)	5 (3%)	37	65
8	se	193/225 (86%)	191 (99%)	2 (1%)	73	86
9	sf	223/283 (79%)	219 (98%)	4 (2%)	54	76
10	sh	141/220 (64%)	122 (86%)	19 (14%)	3	13
11	si	66/167 (40%)	55 (83%)	11 (17%)	2	7
12	sj	140/205 (68%)	138 (99%)	2 (1%)	62	81
13	sk	140/164 (85%)	140 (100%)	0	100	100
14	sm	136/138 (99%)	135 (99%)	1 (1%)	81	90
15	so	128/129 (99%)	126 (98%)	2 (2%)	58	79
16	sp	103/114 (90%)	101 (98%)	2 (2%)	52	75
17	sr	112/113 (99%)	110 (98%)	2 (2%)	54	76
18	sx	64/77 (83%)	63 (98%)	1 (2%)	58	79
19	sy	104/114 (91%)	92 (88%)	12 (12%)	4	19
20	sz	49/125 (39%)	47 (96%)	2 (4%)	26	57
All	All	2075/2691 (77%)	2003 (96%)	72 (4%)	33	61

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	sx	11	ILE
20	sz	83	LEU
19	sy	105	ARG
19	sy	121	VAL
10	sh	282	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
10	sh	186	ASN
10	sh	281	HIS
19	sy	6	HIS
14	sm	10	GLN
15	so	105	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	sH	73/76 (96%)	20 (27%)	0
4	sK	5/6 (83%)	0	0
5	sa	970/1947 (49%)	197 (20%)	0
All	All	1048/2029 (51%)	217 (20%)	0

5 of 217 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	sH	10	G
3	sH	12	U
3	sH	13	C
3	sH	16	U
3	sH	20	U

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.

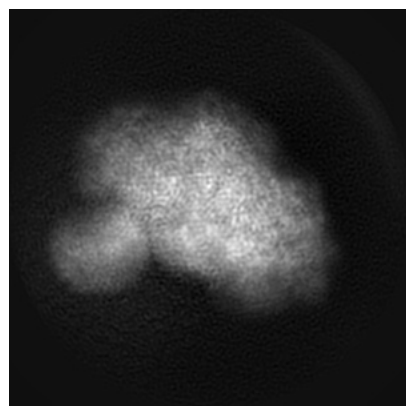
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64695. These allow visual inspection of the internal detail of the map and identification of artifacts.

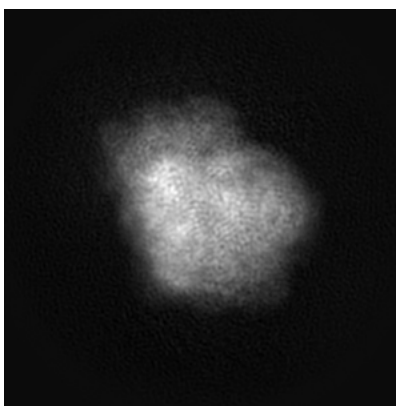
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

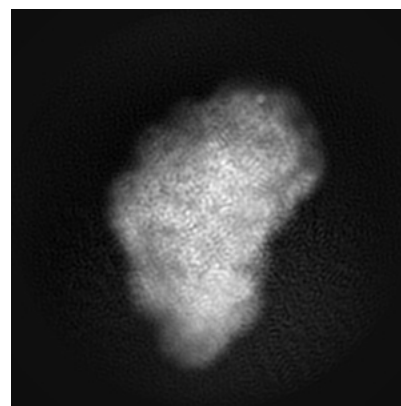
6.1.1 Primary map



X

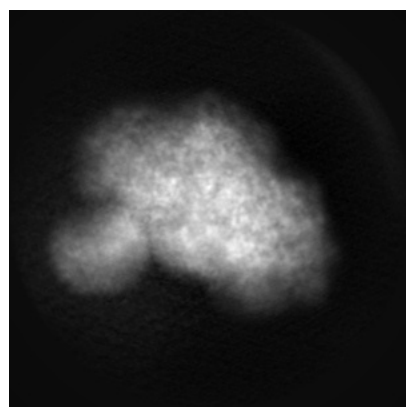


Y

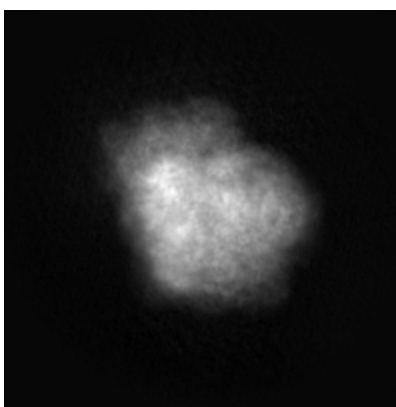


Z

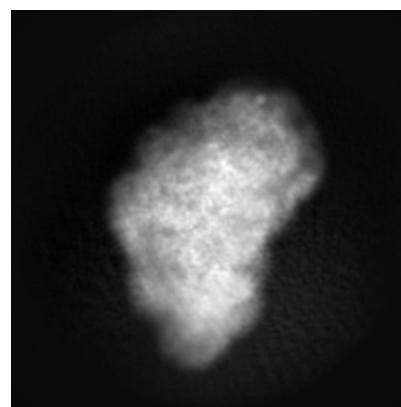
6.1.2 Raw map



X



Y

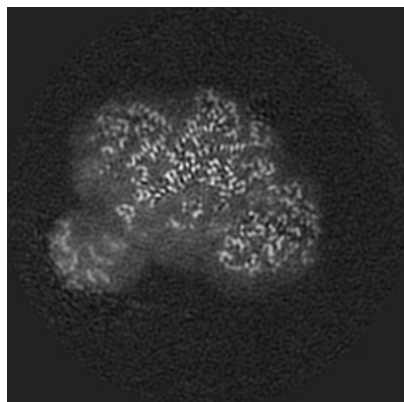


Z

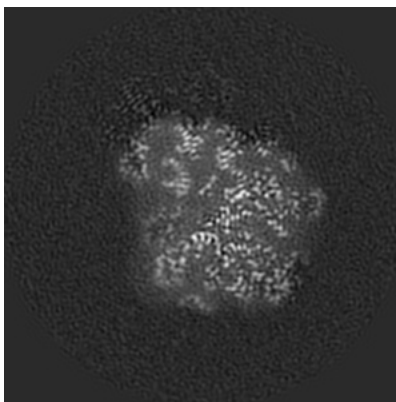
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

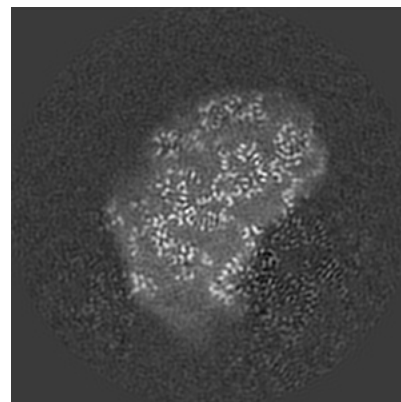
6.2.1 Primary map



X Index: 135

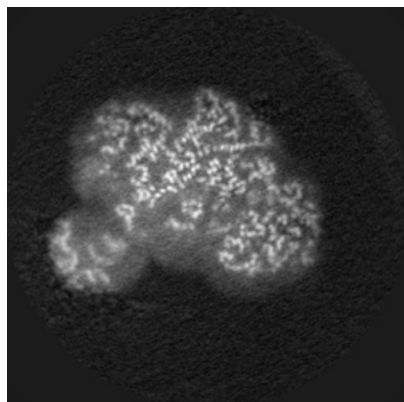


Y Index: 135

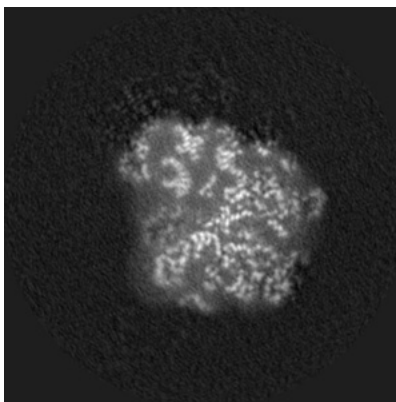


Z Index: 135

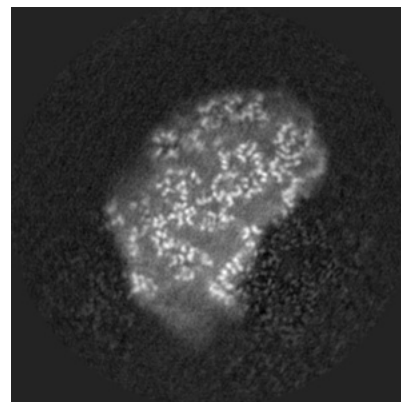
6.2.2 Raw map



X Index: 135



Y Index: 135

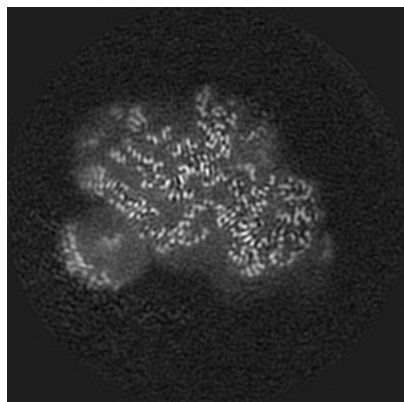


Z Index: 135

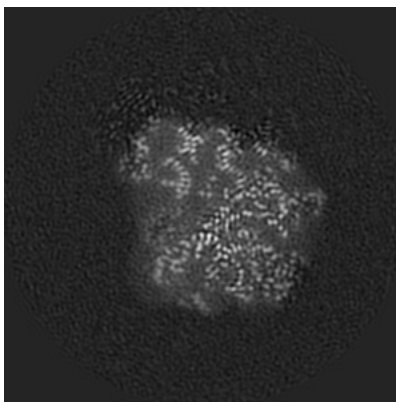
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

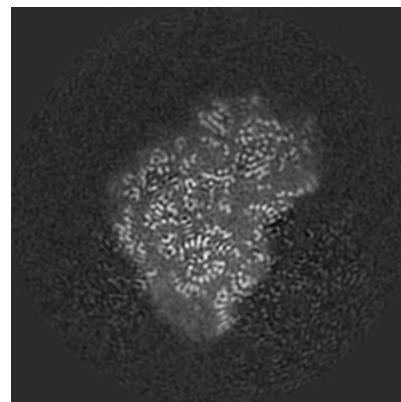
6.3.1 Primary map



X Index: 142

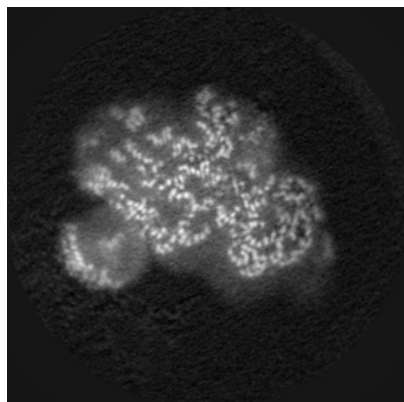


Y Index: 134

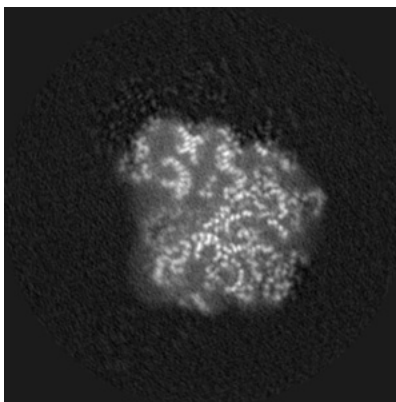


Z Index: 149

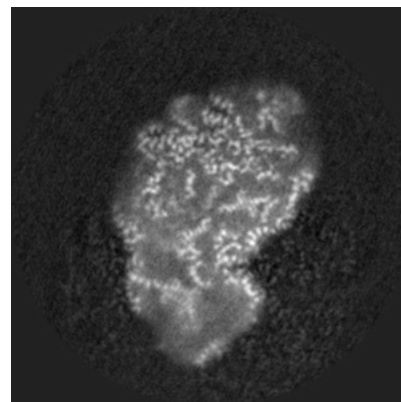
6.3.2 Raw map



X Index: 143



Y Index: 134

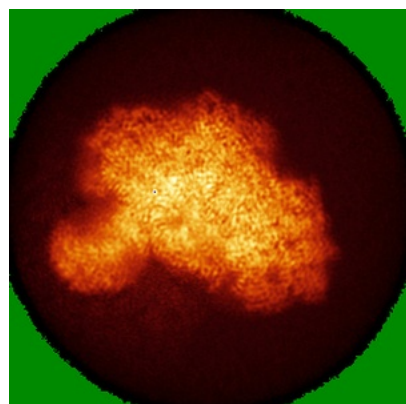


Z Index: 118

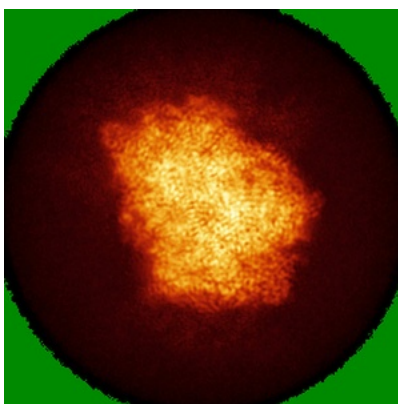
The images above show the largest variance slices of the map in three orthogonal directions.

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

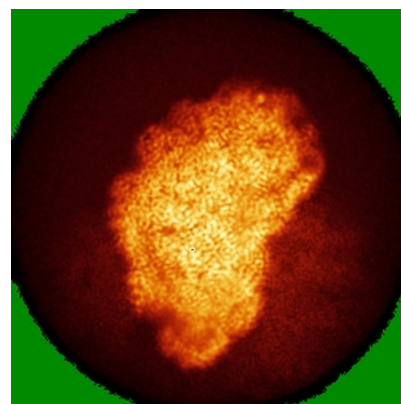
6.4.1 Primary map



X

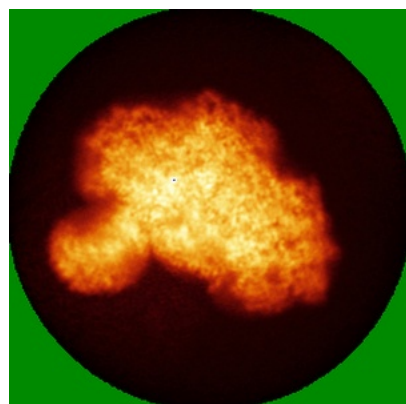


Y

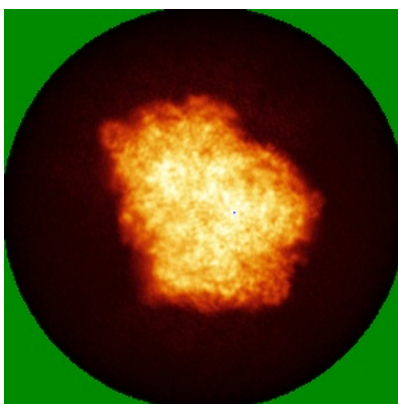


Z

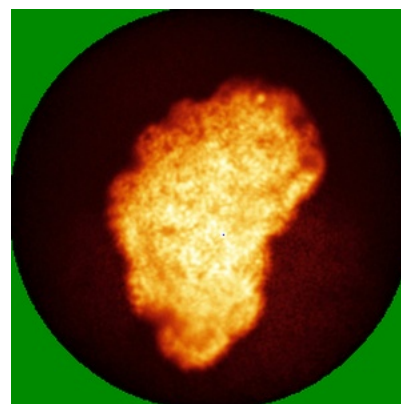
6.4.2 Raw map



X



Y

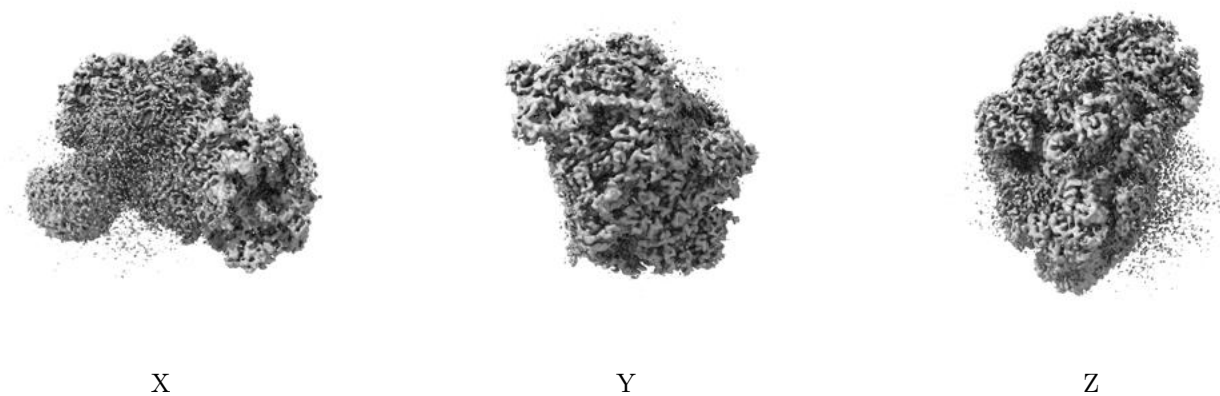


Z

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.

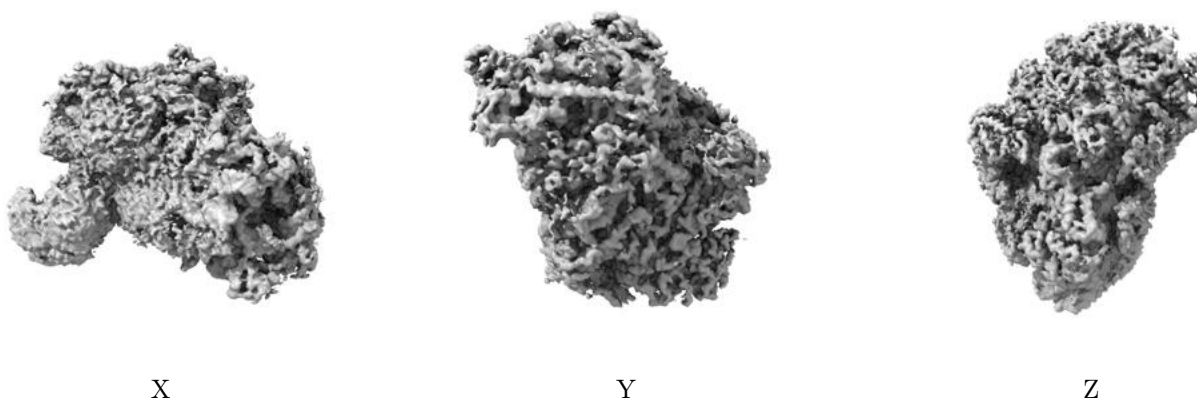
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. 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.

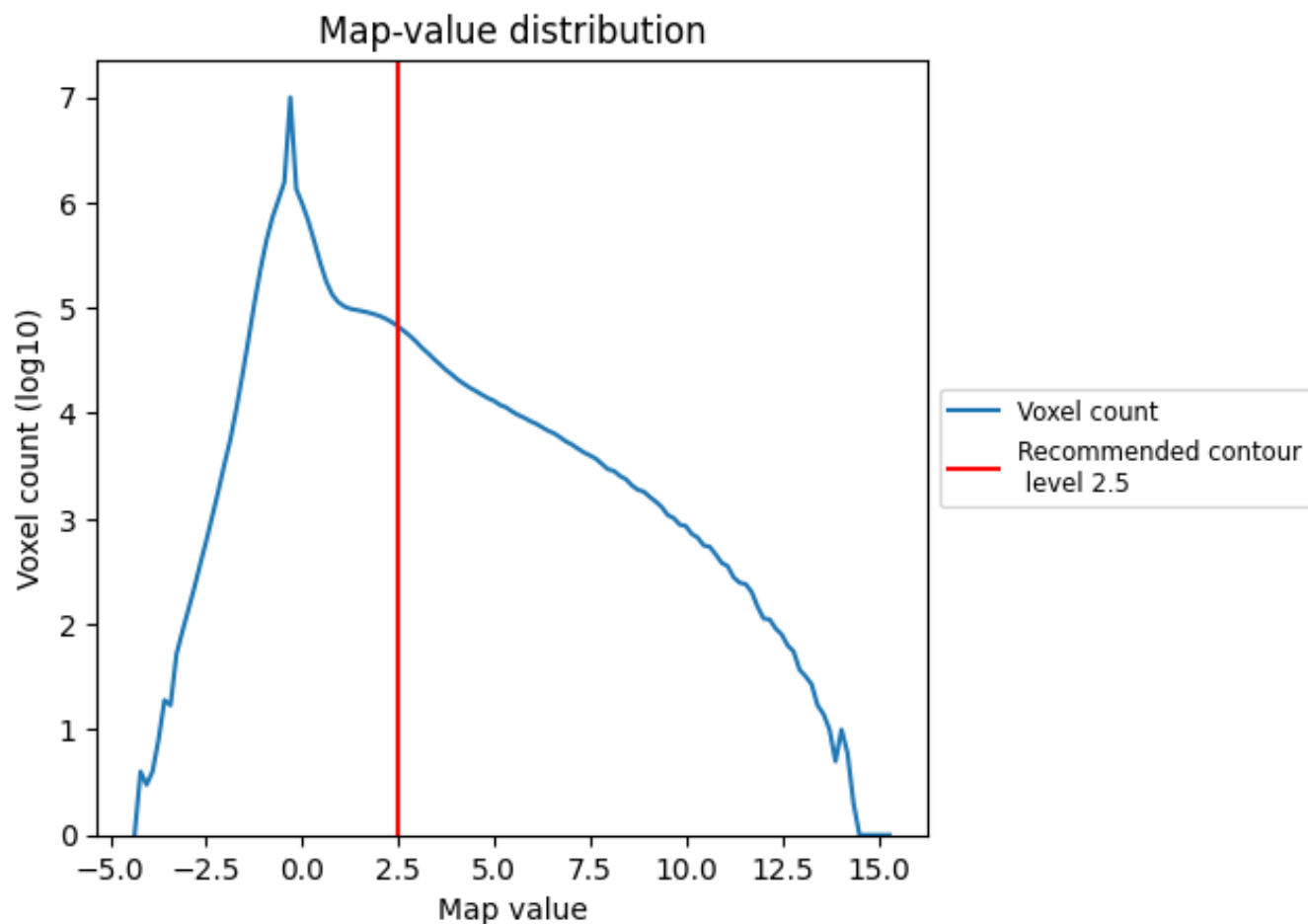
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

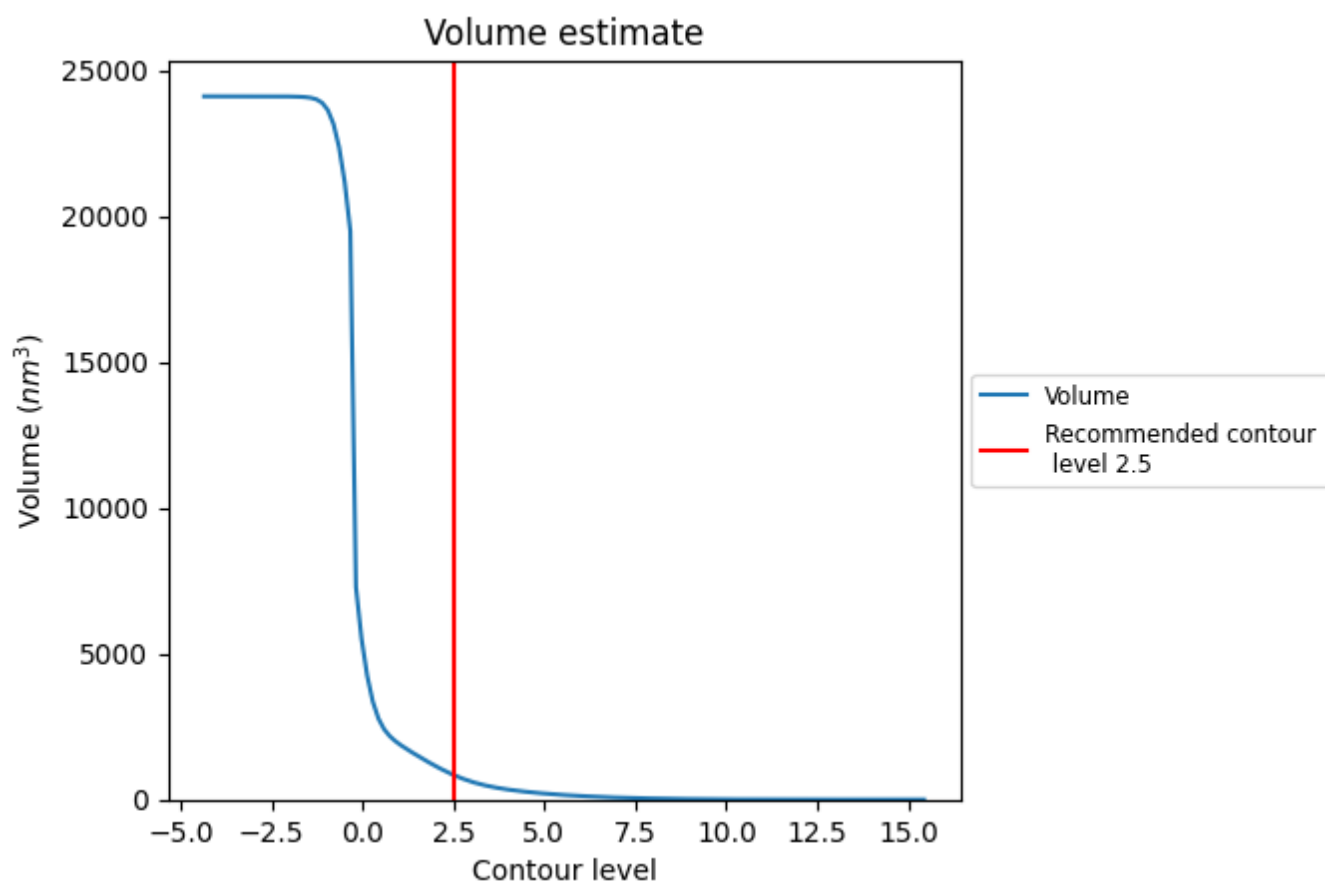
This section contains the results of statistical analysis of the map.

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.

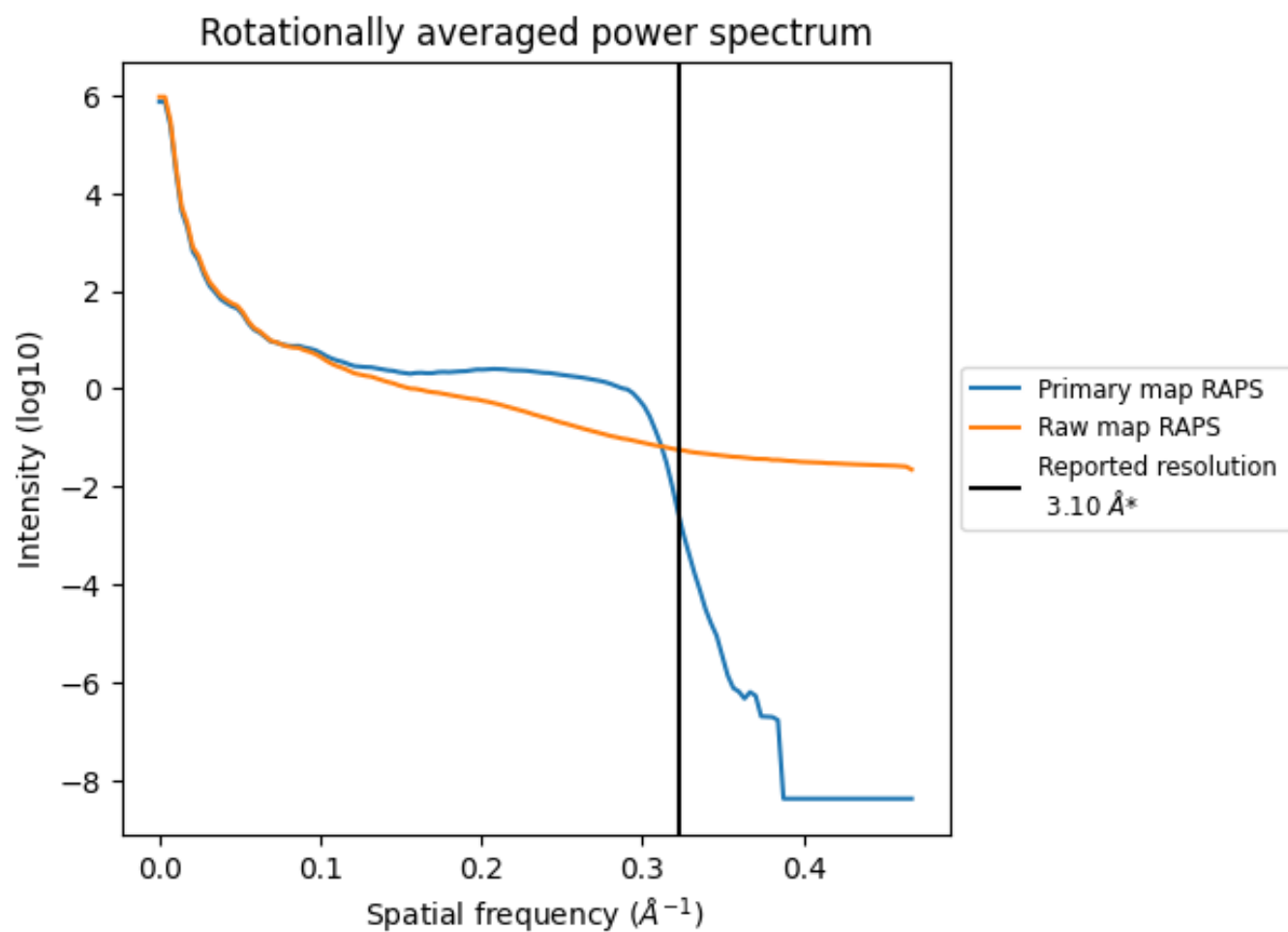
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 843 nm³; this corresponds to an approximate mass of 761 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 ⓘ

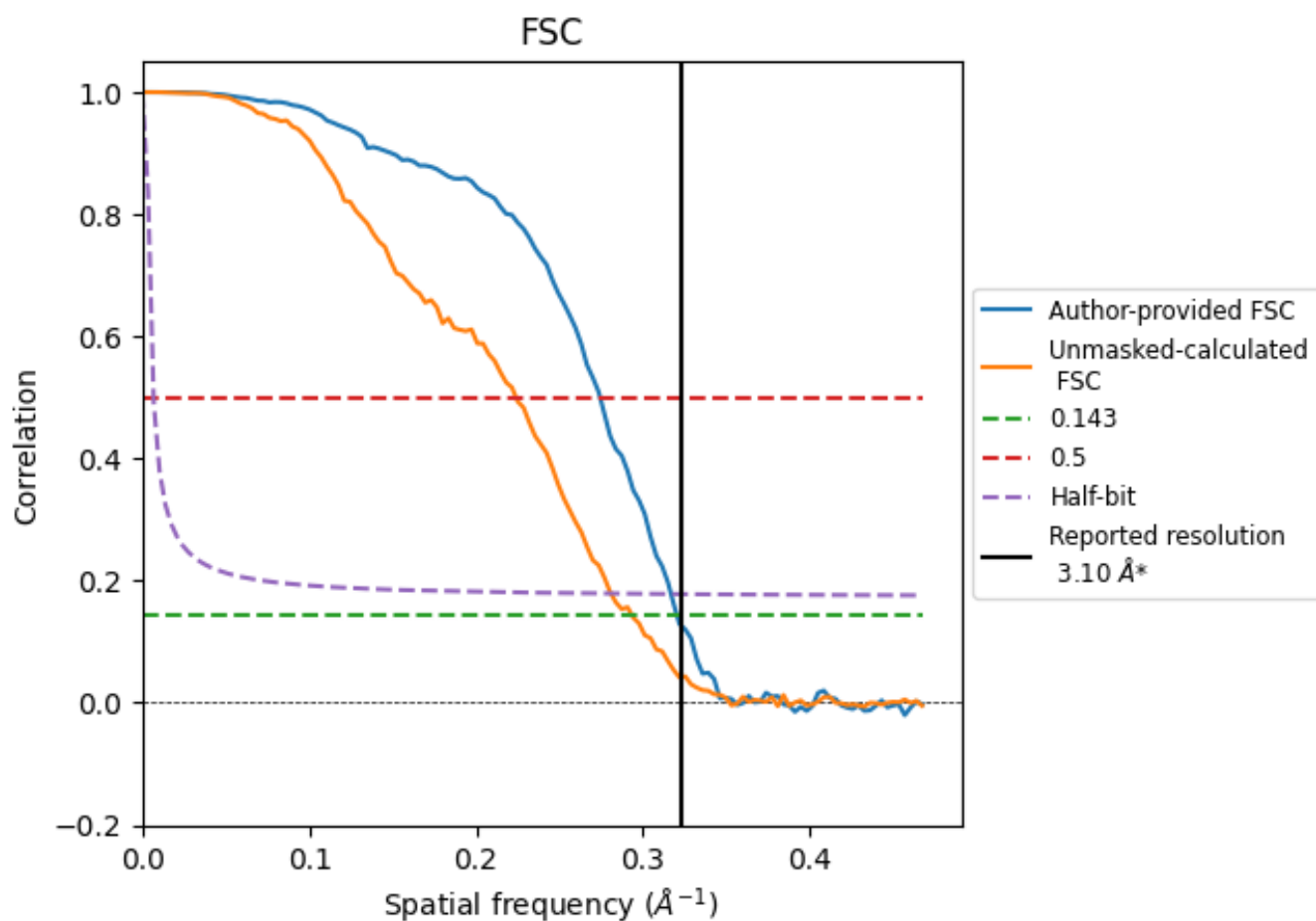


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

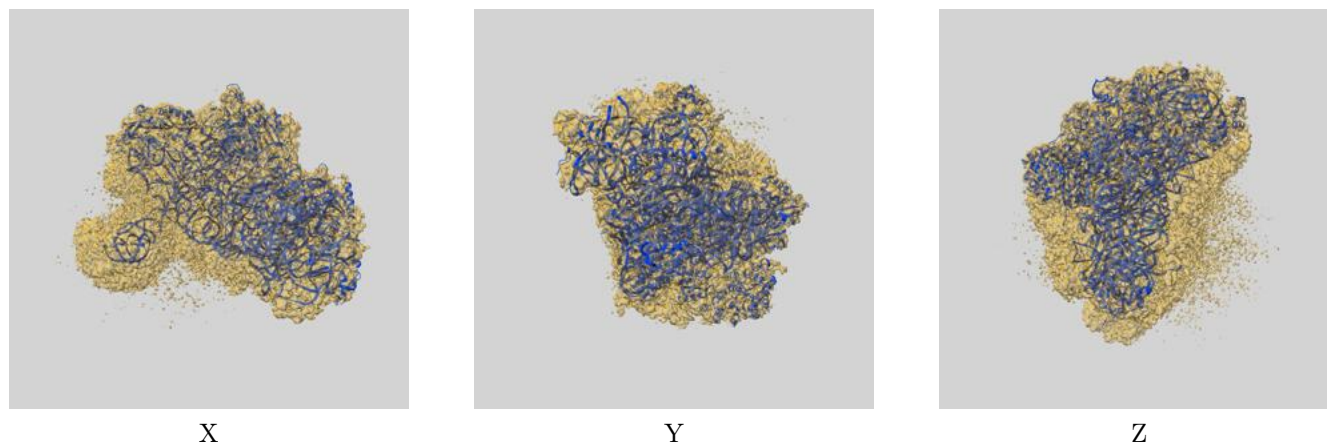
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.65	3.16
Unmasked-calculated*	3.41	4.46	3.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.41 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

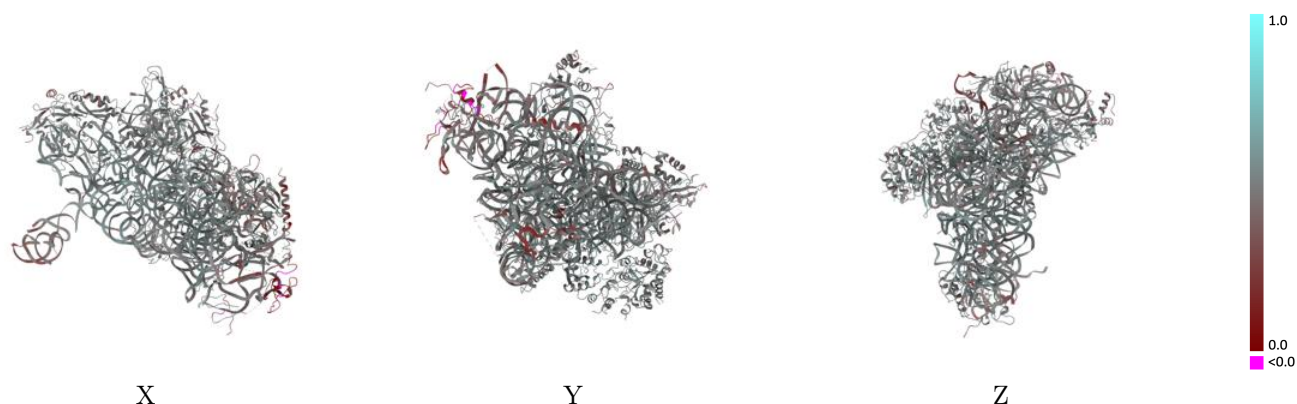
This section contains information regarding the fit between EMDB map EMD-64695 and PDB model 9V1J. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



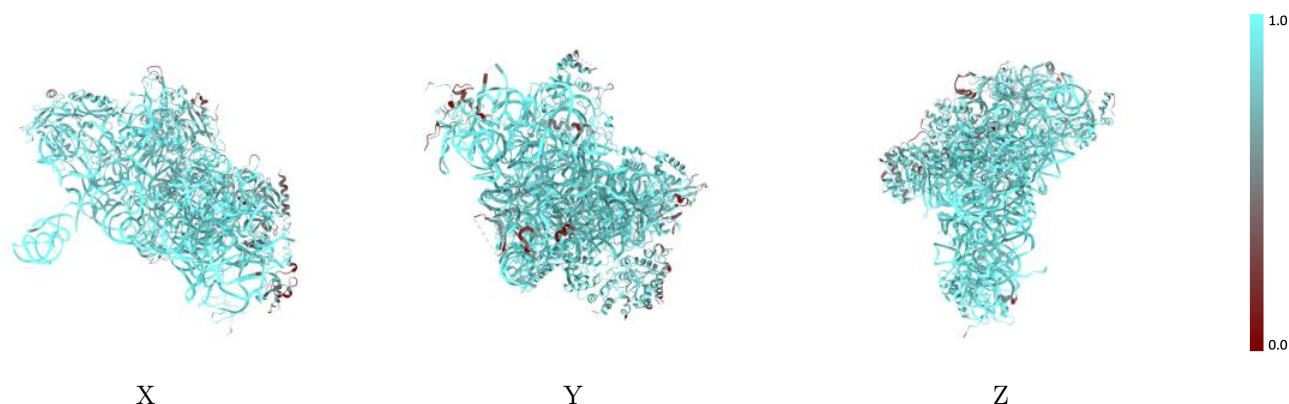
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



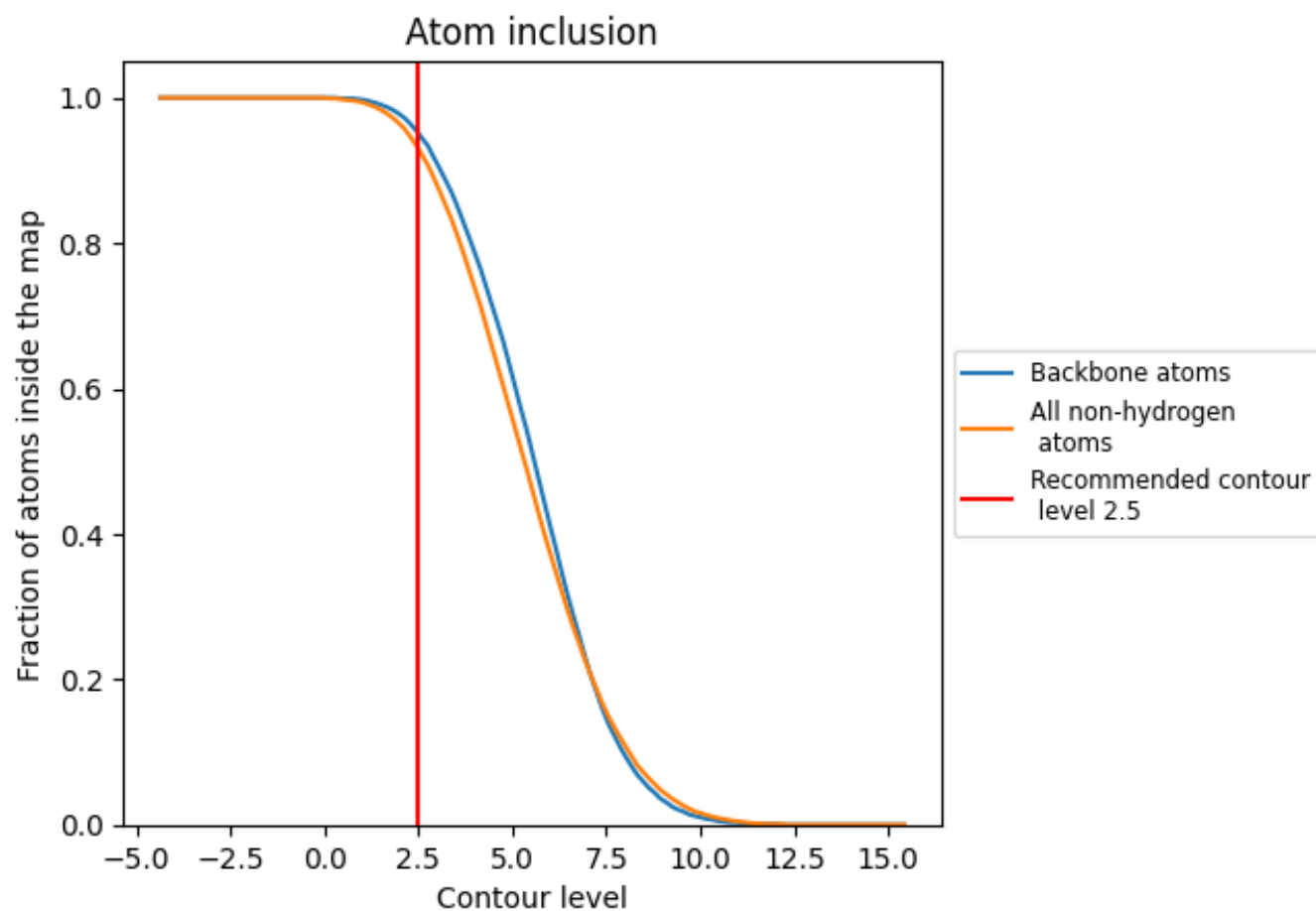
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).











































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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.4850
sB	 0.9640	 0.5220
sC	 0.8080	 0.4780
sH	 0.9900	 0.4240
sK	 1.0000	 0.5280
sa	 0.9830	 0.4930
sb	 0.8290	 0.4940
sc	 0.8970	 0.5150
se	 0.8990	 0.4820
sf	 0.8380	 0.4850
sh	 0.7020	 0.3390
si	 0.6390	 0.4510
sj	 0.9080	 0.4850
sk	 0.8720	 0.4950
sm	 0.9360	 0.4960
so	 0.9280	 0.4790
sp	 0.9580	 0.4980
sr	 0.9490	 0.5120
sx	 0.8150	 0.5000
sy	 0.9140	 0.4930
sz	 0.5850	 0.4450

