



wwPDB EM Validation Summary Report ⓘ

Oct 1, 2025 – 02:17 PM JST

PDB ID : 9V27 / pdb_00009v27
EMDB ID : EMD-64719
Title : Cryo- EM structure of small subunit (body) of 75S ribosome with A/P- & P/E- tRNAs from *Entamoeba histolytica*
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.21 Å(reported)
Based on initial model : .

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

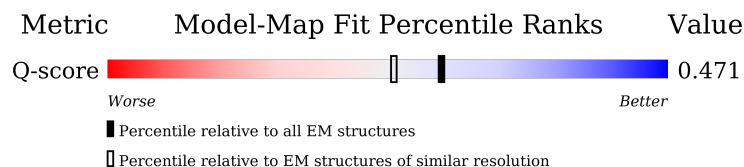
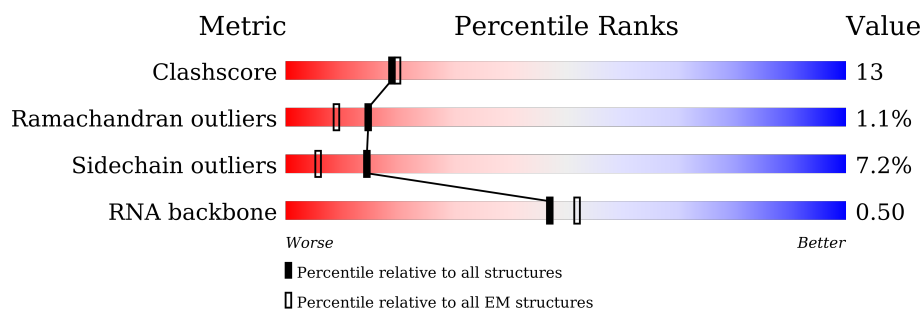
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.21 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.





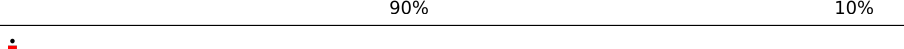
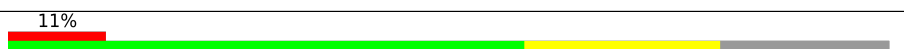


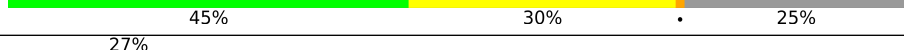
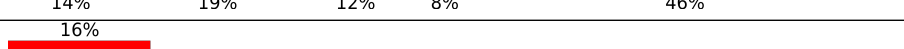
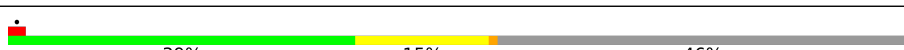


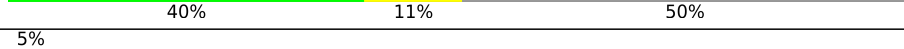

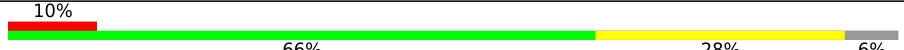





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14613 (2.71 - 3.71)

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	6	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	sI	76	
5	sJ	77	
6	sK	10	
7	sa	1947	
8	sb	254	
9	sc	255	
10	se	256	
11	sf	326	
12	sh	266	
13	si	201	
14	sj	237	
15	sk	185	
16	sm	156	
17	so	151	
18	sp	146	
19	sr	130	
20	sx	86	
21	sy	141	
22	sz	140	

2 Entry composition [i](#)

There are 22 unique types of molecules in this entry. The entry contains 41199 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	31	Total	C	N	O	S	0	0
			238	152	41	44	1		

- Molecule 3 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	sH	2	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 4 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sI	73	Total	C	N	O	P	0	0
			1556	695	283	506	72		

- Molecule 5 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sJ	72	Total	C	N	O	P	0	0
			1530	683	269	506	72		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sK	10	Total	C	N	O	P	0	0
			215	97	41	67	10		

- Molecule 7 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sa	975	Total	C	N	O	P	0	0
			20871	9343	3807	6746	975		

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sb	205	Total	C	N	O	S	0	0
			1626	1029	286	296	15		

- Molecule 9 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 10 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	se	129	Total	C	N	O	S	0	0
			1042	669	186	181	6		

- Molecule 11 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	sf	246	Total	C	N	O	S	0	0
			1949	1245	364	329	11		

- Molecule 12 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	sh	143	Total	C	N	O	S	0	0
			1132	709	233	185	5		

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	si	72	Total	C	N	O	S	0	0
			568	367	105	95	1		

- Molecule 14 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sj	129	Total	C	N	O	S	0	0
			1012	628	201	179	4		

- Molecule 15 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sk	157	Total	C	N	O	S	0	0
			1288	825	245	212	6		

- Molecule 16 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sm	141	Total	C	N	O	S	0	0
			1161	735	224	196	6		

- Molecule 17 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	so	76	Total	C	N	O	S	0	0
			644	410	123	108	3		

- Molecule 18 is a protein called Ribosomal protein S14, putative.

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

- Molecule 19 is a protein called 40S ribosomal protein S15a, putative.

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

- Molecule 20 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	sx	81	Total	C	N	O	S	0	0
			634	402	113	116	3		

- Molecule 21 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	sy	106	Total	C	N	O	S	0	0
			836	522	169	142	3		

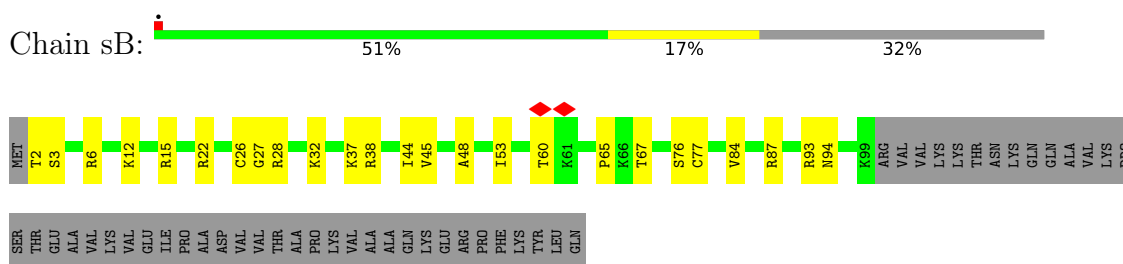
- Molecule 22 is a protein called 40S ribosomal protein S24, putative.

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

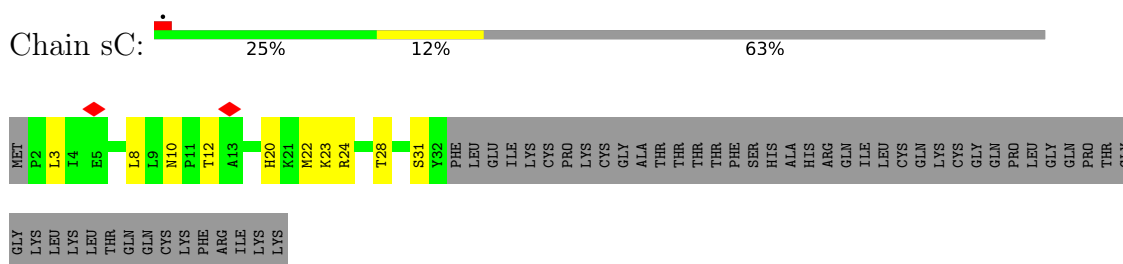
3 Residue-property plots [i](#)

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.

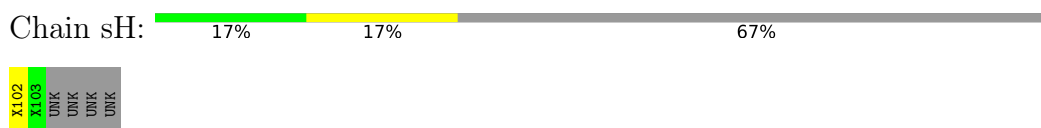
- Molecule 1: 40S ribosomal protein S26



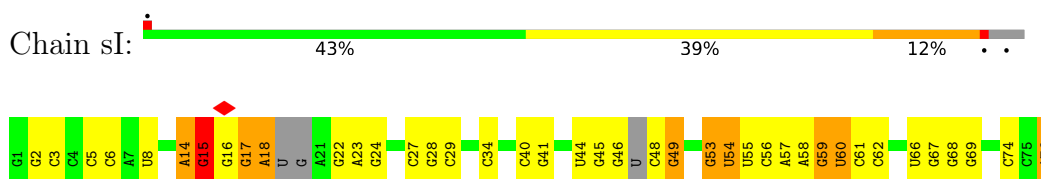
- Molecule 2: Small ribosomal subunit protein eS27



- Molecule 3: Unknown peptide



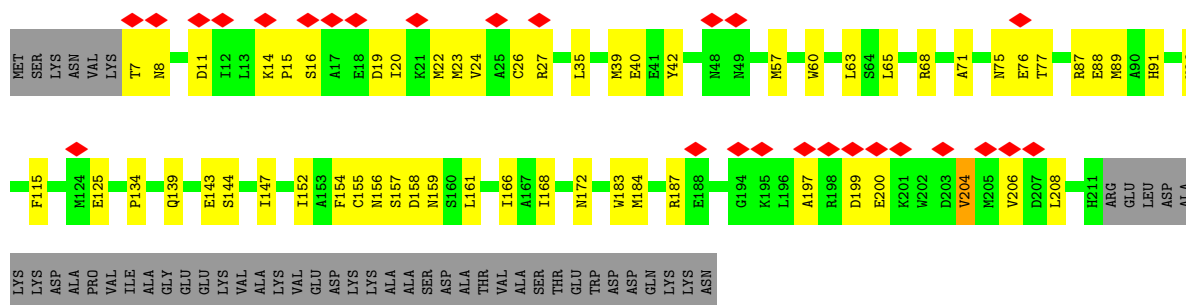
- Molecule 4: A/P-tRNA



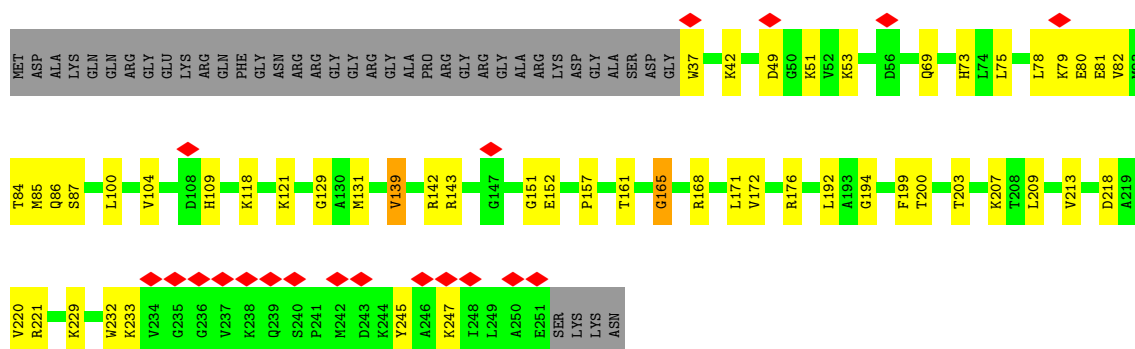
- Molecule 5: P/E-tRNA



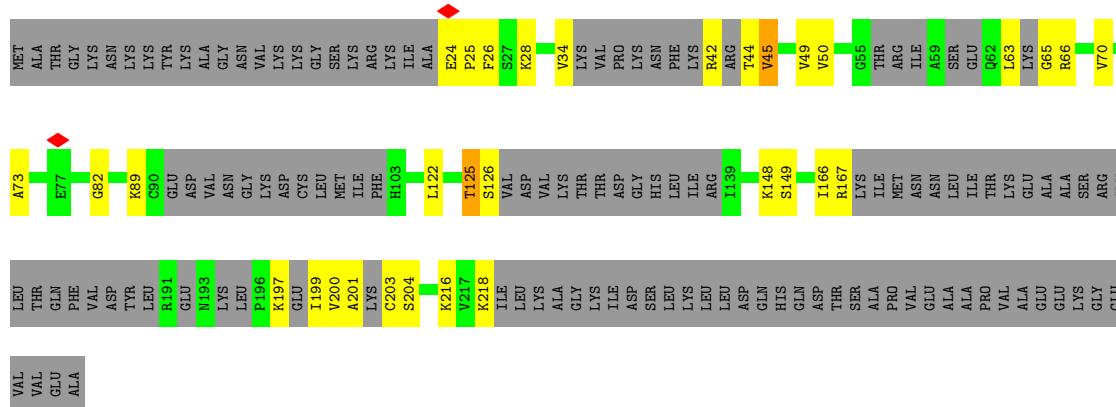
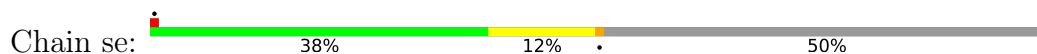




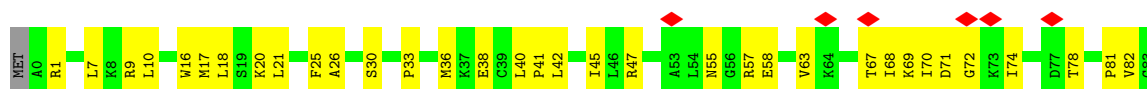
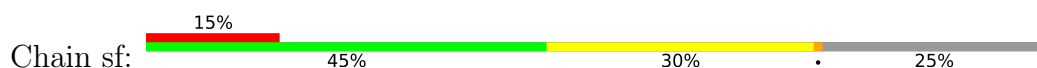
• Molecule 9: Small ribosomal subunit protein uS5

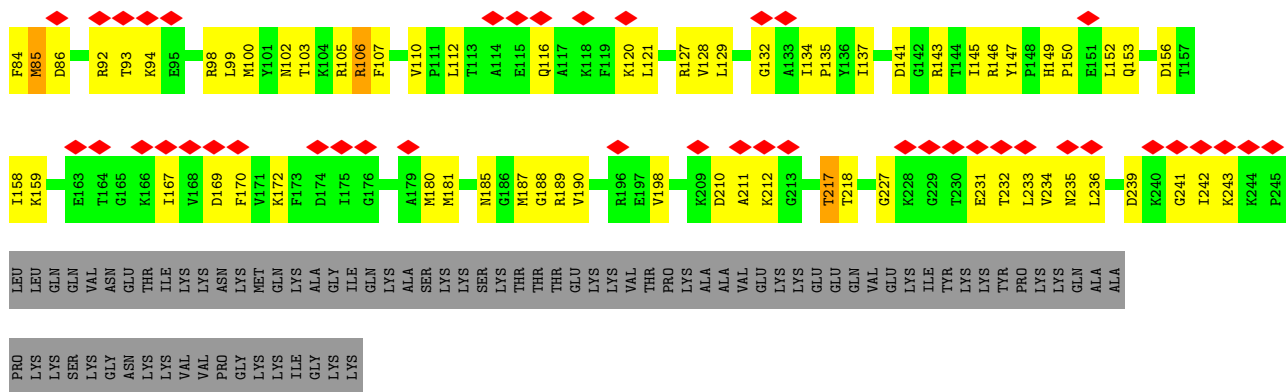


• Molecule 10: Small ribosomal subunit protein eS1

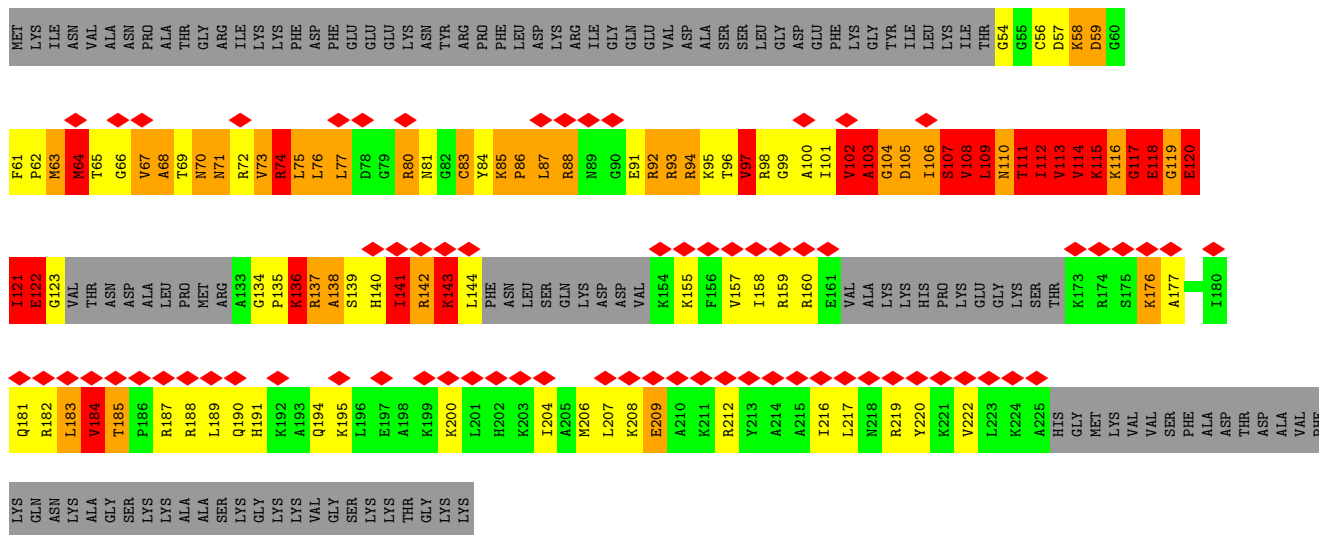
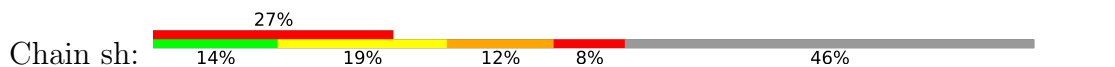


• Molecule 11: 40S ribosomal protein S4, putative

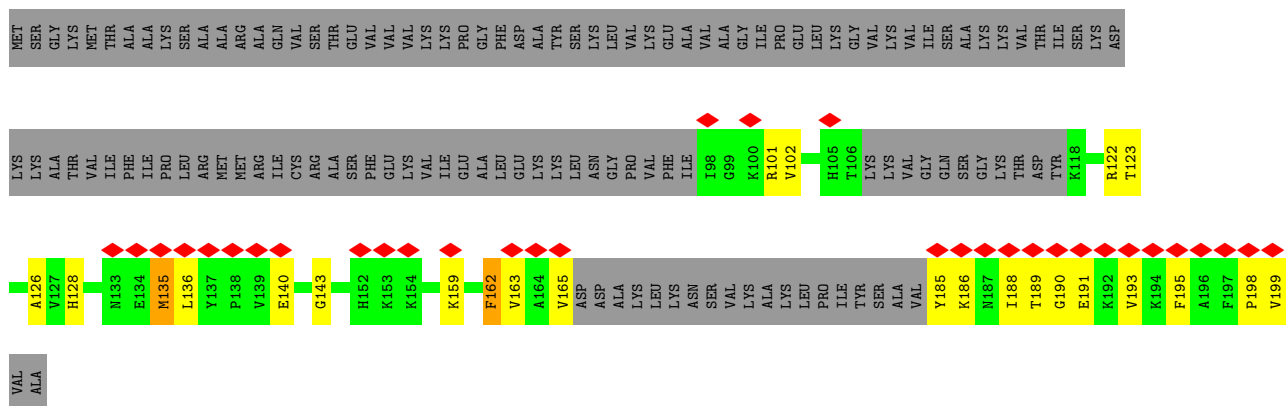




- Molecule 12: 40S ribosomal protein S6



- Molecule 13: 40S ribosomal protein S7



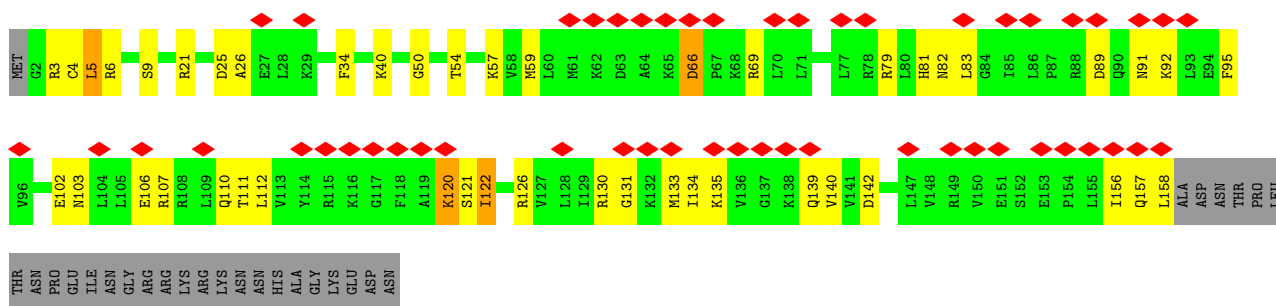
- Molecule 14: 40S ribosomal protein S8

Chain sj: 



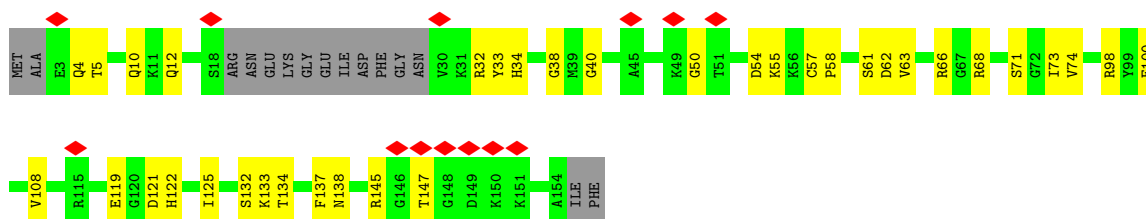
• Molecule 15: Small ribosomal subunit protein uS4

Chain sk: 



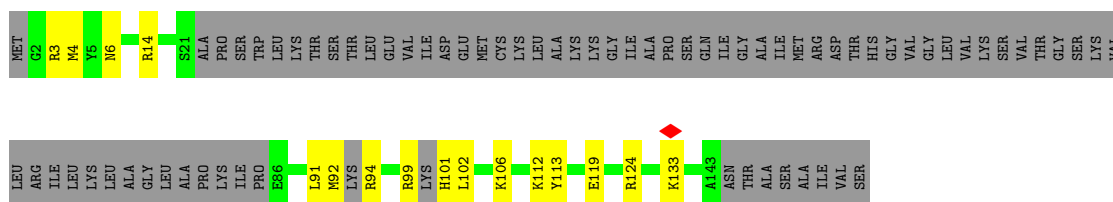
• Molecule 16: 40S ribosomal protein S11, putative

Chain sm: 




• Molecule 17: 40S ribosomal protein S13, putative

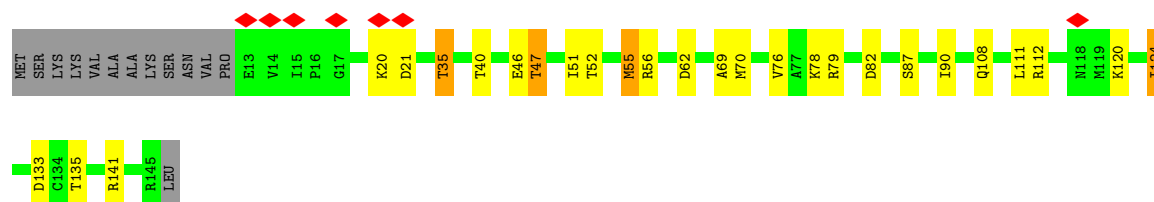
Chain so: 



• Molecule 18: Ribosomal protein S14, putative

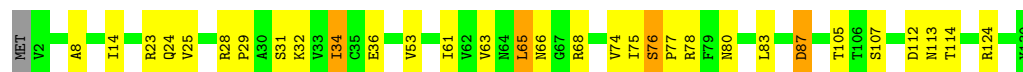
Chain sp: 





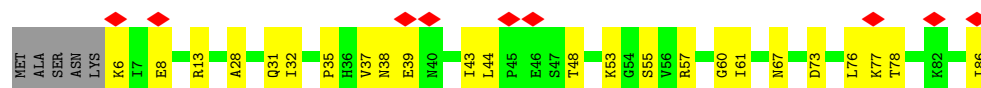
- Molecule 19: 40S ribosomal protein S15a, putative

Chain sr: 75% 21% . .



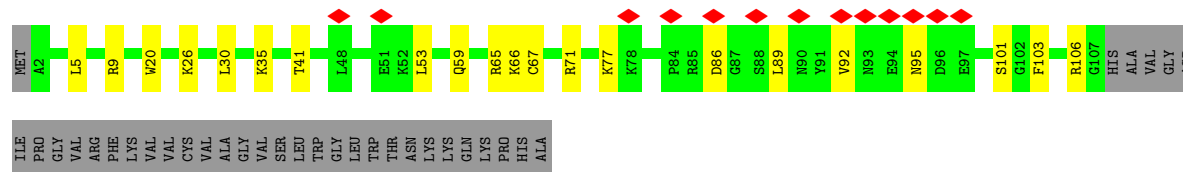
- Molecule 20: 40S ribosomal protein S21

Chain sx: 10% 66% 28% 6%



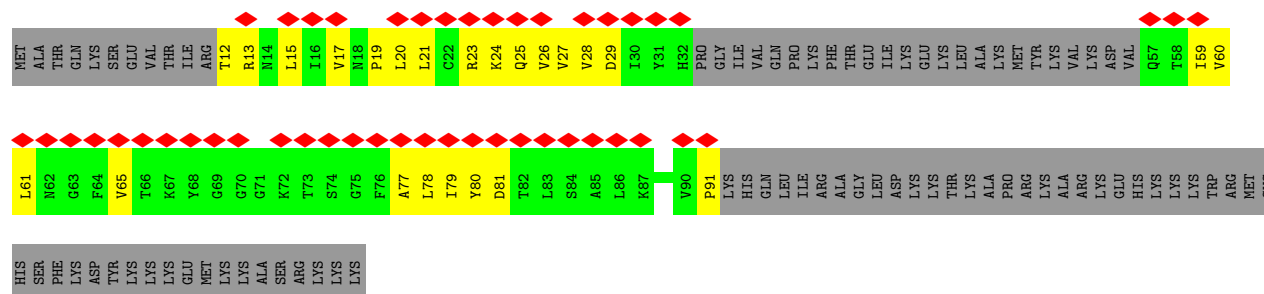
- Molecule 21: 40S ribosomal protein S23, putative

Chain sy: 9% 60% 15% 25%



- Molecule 22: 40S ribosomal protein S24, putative

Chain sz: 34% 23% 17% 60%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39958	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	15.101	Depositor
Minimum map value	-5.678	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.2	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	0.22	0/797	0.27	0/1062
2	sC	0.16	0/243	0.28	0/330
4	sI	0.18	0/1737	0.39	1/2702 (0.0%)
5	sJ	0.16	0/1706	0.27	0/2649
6	sK	0.19	0/241	0.24	0/373
7	sa	0.25	5/23375 (0.0%)	0.33	3/36404 (0.0%)
8	sb	0.17	0/1659	0.26	0/2243
9	sc	0.20	0/1673	0.31	0/2257
10	se	0.18	0/1047	0.25	0/1380
11	sf	0.16	0/1990	0.30	0/2681
12	sh	1.65	36/1141 (3.2%)	1.46	24/1510 (1.6%)
13	si	0.15	0/578	0.29	0/777
14	sj	0.17	0/1025	0.26	0/1372
15	sk	0.14	0/1308	0.25	0/1749
16	sm	0.18	0/1187	0.27	0/1586
17	so	0.18	0/654	0.22	0/866
18	sp	0.19	0/1013	0.28	0/1361
19	sr	0.21	0/1040	0.33	0/1404
20	sx	0.20	0/646	0.30	0/876
21	sy	0.15	0/848	0.28	0/1131
22	sz	0.13	0/445	0.25	0/601
All	All	0.34	41/44353 (0.1%)	0.38	28/65314 (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
12	sh	0	2
19	sr	0	1
All	All	0	3

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	sh	106	ILE	CA-C	-16.05	1.31	1.52
12	sh	121	ILE	CA-C	-11.29	1.38	1.52
12	sh	106	ILE	C-O	-11.23	1.11	1.24
12	sh	106	ILE	CA-CB	-10.89	1.39	1.53
12	sh	142	ARG	N-CA	-10.24	1.34	1.46

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	sh	102	VAL	O-C-N	-18.00	103.31	122.57
12	sh	139	SER	N-CA-C	-14.95	94.33	113.17
12	sh	113	VAL	CB-CA-C	12.21	131.32	111.29
12	sh	111	THR	CB-CA-C	-9.87	90.78	110.42
12	sh	137	ARG	N-CA-C	-9.79	95.48	109.29

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	sh	102	VAL	Mainchain
12	sh	183	LEU	Peptide
19	sr	76	SER	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	sB	787	0	833	17	0
2	sC	238	0	250	5	0
3	sH	9	0	4	1	0
4	sI	1556	0	795	41	0
5	sJ	1530	0	778	27	0
6	sK	215	0	108	2	0
7	sa	20871	0	10485	335	0
8	sb	1626	0	1627	37	0
9	sc	1642	0	1721	32	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	se	1042	0	1094	21	0
11	sf	1949	0	2055	81	0
12	sh	1132	0	1245	211	0
13	si	568	0	599	14	0
14	sj	1012	0	1051	27	0
15	sk	1288	0	1391	30	0
16	sm	1161	0	1181	22	0
17	so	644	0	664	14	0
18	sp	999	0	1024	19	0
19	sr	1022	0	1051	24	0
20	sx	634	0	649	14	0
21	sy	836	0	885	12	0
22	sz	438	0	465	18	0
All	All	41199	0	29955	877	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 877 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)
12:sh:80:ARG:HH12	12:sh:81:ASN:ND2	1.31	1.26
12:sh:58:LYS:HG2	12:sh:105:ASP:HB2	1.43	1.01
7:sa:69:G:N2	7:sa:80:A:H62	1.58	1.00
12:sh:80:ARG:NH1	12:sh:81:ASN:ND2	2.13	0.96
7:sa:69:G:H21	7:sa:80:A:N6	1.64	0.95

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	91 (95%)	5 (5%)	0	100	100
2	sC	29/84 (34%)	29 (100%)	0	0	100	100
8	sb	203/254 (80%)	195 (96%)	8 (4%)	0	100	100
9	sc	213/255 (84%)	199 (93%)	13 (6%)	1 (0%)	25	59
10	se	107/256 (42%)	101 (94%)	6 (6%)	0	100	100
11	sf	244/326 (75%)	223 (91%)	21 (9%)	0	100	100
12	sh	135/266 (51%)	84 (62%)	30 (22%)	21 (16%)	0	1
13	si	66/201 (33%)	62 (94%)	4 (6%)	0	100	100
14	sj	123/237 (52%)	117 (95%)	6 (5%)	0	100	100
15	sk	155/185 (84%)	149 (96%)	6 (4%)	0	100	100
16	sm	137/156 (88%)	127 (93%)	10 (7%)	0	100	100
17	so	68/151 (45%)	66 (97%)	2 (3%)	0	100	100
18	sp	131/146 (90%)	121 (92%)	10 (8%)	0	100	100
19	sr	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
20	sx	79/86 (92%)	77 (98%)	2 (2%)	0	100	100
21	sy	104/141 (74%)	96 (92%)	8 (8%)	0	100	100
22	sz	52/140 (37%)	47 (90%)	4 (8%)	1 (2%)	6	32
All	All	2069/3158 (66%)	1898 (92%)	148 (7%)	23 (1%)	15	43

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	sh	108	VAL
12	sh	111	THR
12	sh	114	VAL
12	sh	120	GLU
12	sh	184	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	sB	87/127 (68%)	83 (95%)	4 (5%)	23	54
2	sC	27/73 (37%)	24 (89%)	3 (11%)	5	21
8	sb	178/218 (82%)	173 (97%)	5 (3%)	38	66
9	sc	172/199 (86%)	165 (96%)	7 (4%)	26	57
10	se	116/225 (52%)	107 (92%)	9 (8%)	10	37
11	sf	213/283 (75%)	203 (95%)	10 (5%)	22	53
12	sh	117/220 (53%)	81 (69%)	36 (31%)	0	1
13	si	61/167 (36%)	57 (93%)	4 (7%)	14	43
14	sj	108/205 (53%)	102 (94%)	6 (6%)	17	49
15	sk	140/164 (85%)	130 (93%)	10 (7%)	12	40
16	sm	126/138 (91%)	119 (94%)	7 (6%)	17	49
17	so	68/129 (53%)	68 (100%)	0	100	100
18	sp	103/114 (90%)	95 (92%)	8 (8%)	10	37
19	sr	112/113 (99%)	104 (93%)	8 (7%)	12	40
20	sx	73/77 (95%)	67 (92%)	6 (8%)	9	34
21	sy	86/114 (75%)	79 (92%)	7 (8%)	9	35
22	sz	49/125 (39%)	46 (94%)	3 (6%)	15	46
All	All	1836/2691 (68%)	1703 (93%)	133 (7%)	14	40

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	sr	87	ASP
20	sx	43	ILE
22	sz	20	LEU
12	sh	80	ARG
12	sh	77	LEU

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

Mol	Chain	Res	Type
15	sk	43	GLN
20	sx	31	GLN
22	sz	32	HIS
22	sz	14	ASN
22	sz	25	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	sI	70/76 (92%)	15 (21%)	0
5	sJ	69/77 (89%)	19 (27%)	0
6	sK	9/10 (90%)	0	0
7	sa	961/1947 (49%)	207 (21%)	0
All	All	1109/2110 (52%)	241 (21%)	0

5 of 241 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	sI	14	A
4	sI	15	G
4	sI	16	G
4	sI	17	G
4	sI	18	A

There are no RNA pucker outliers to report.

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

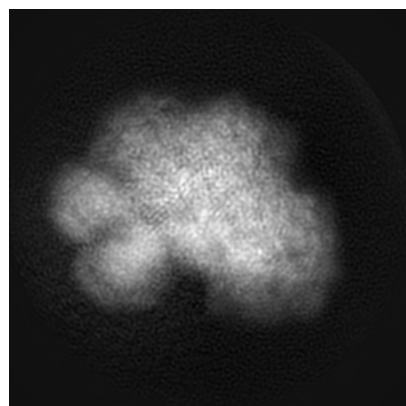
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64719. These allow visual inspection of the internal detail of the map and identification of artifacts.

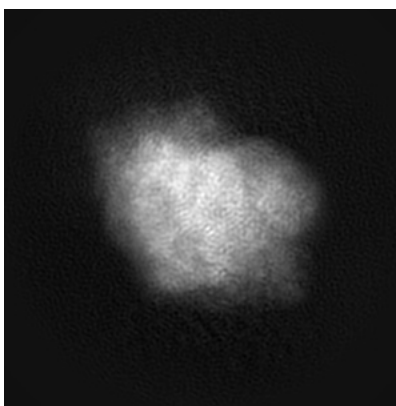
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

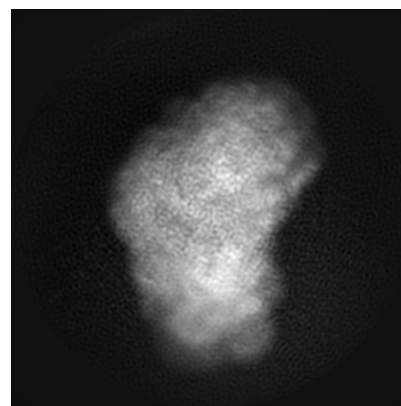
6.1.1 Primary map



X

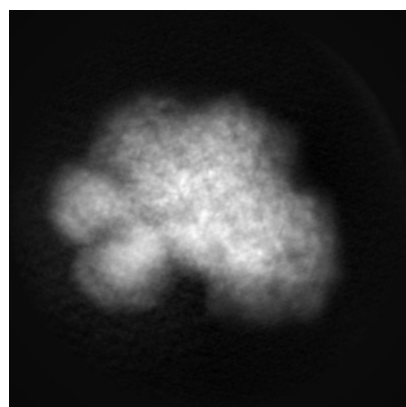


Y

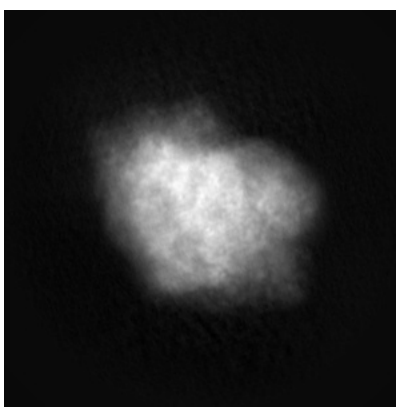


Z

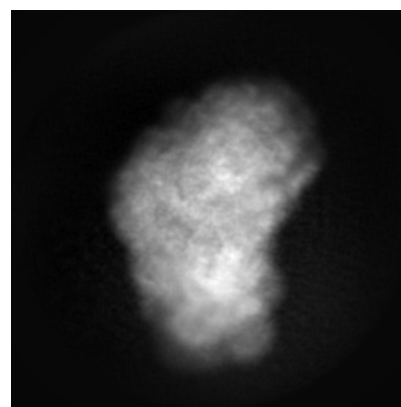
6.1.2 Raw map



X



Y

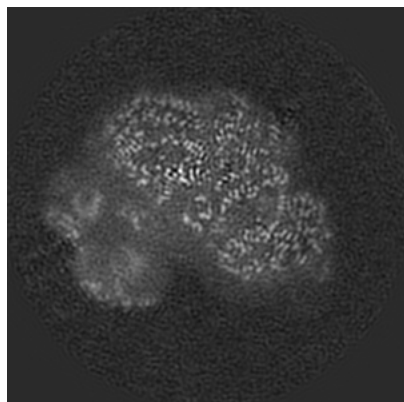


Z

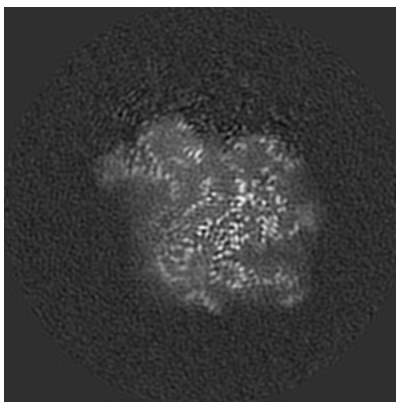
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

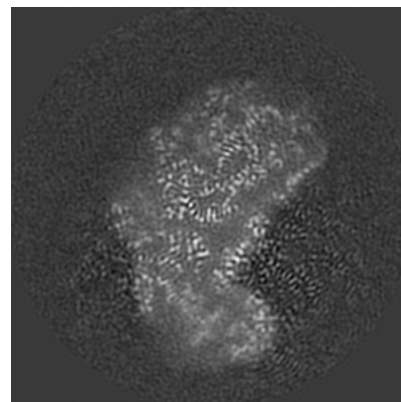
6.2.1 Primary map



X Index: 135

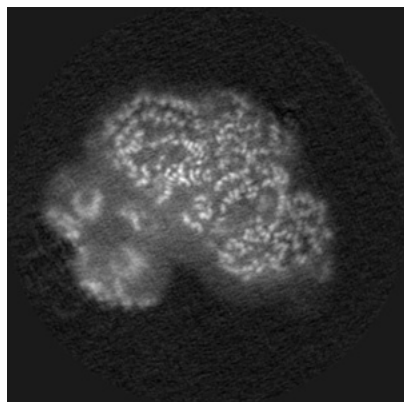


Y Index: 135

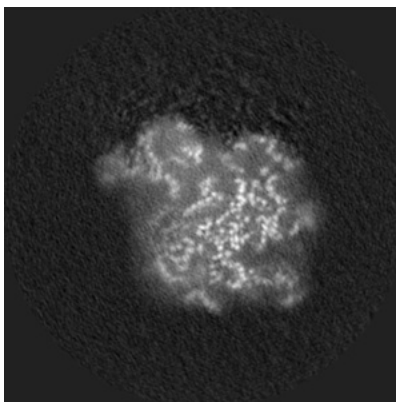


Z Index: 135

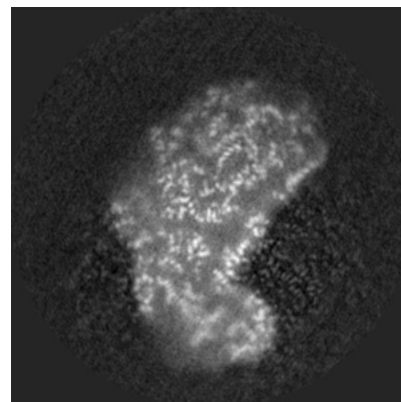
6.2.2 Raw map



X Index: 135



Y Index: 135

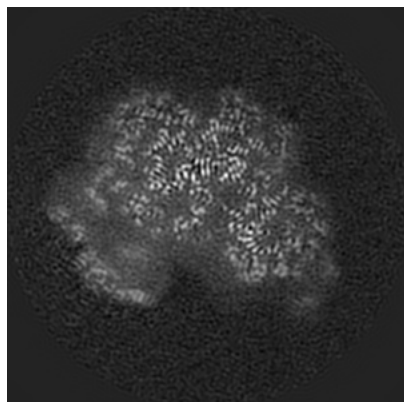


Z Index: 135

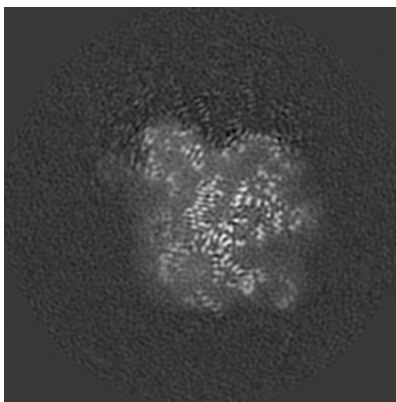
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

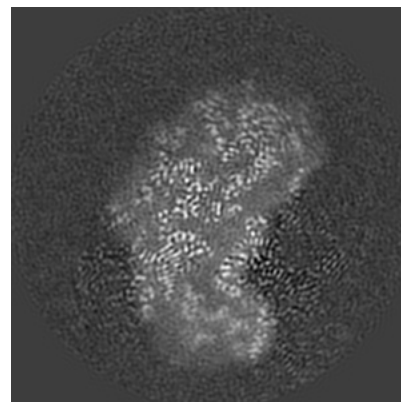
6.3.1 Primary map



X Index: 141

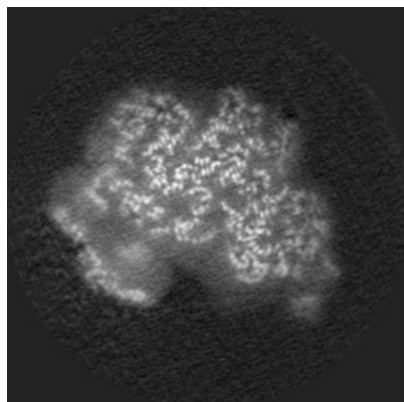


Y Index: 132

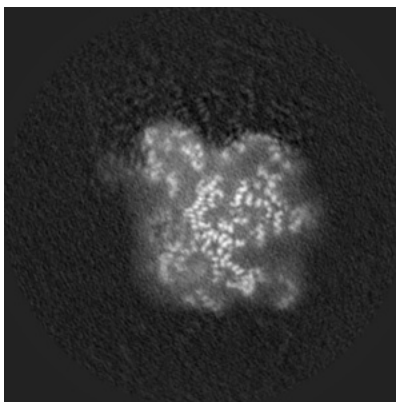


Z Index: 138

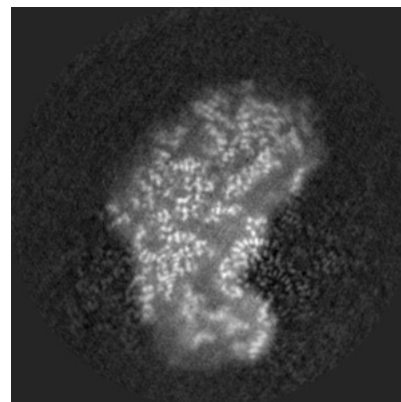
6.3.2 Raw map



X Index: 142



Y Index: 132

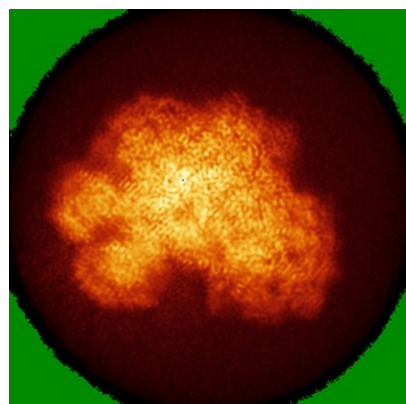


Z Index: 139

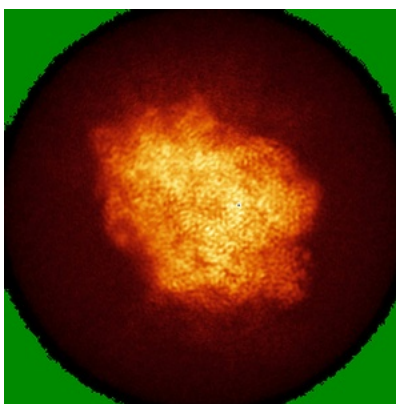
The images above show the largest variance slices of the map in three orthogonal directions.

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

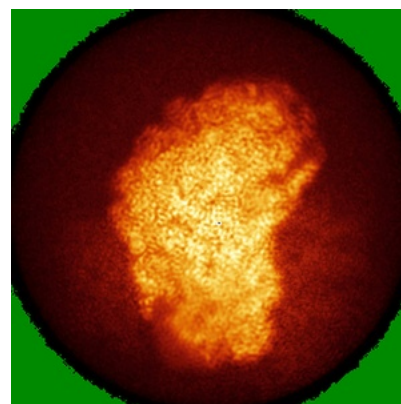
6.4.1 Primary map



X

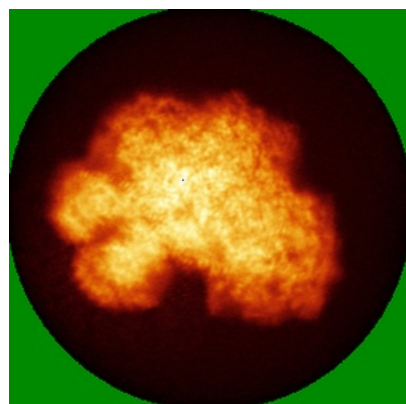


Y

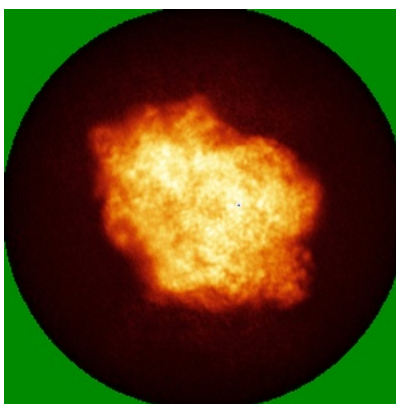


Z

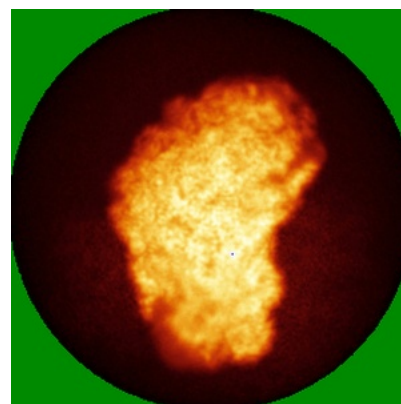
6.4.2 Raw map



X



Y

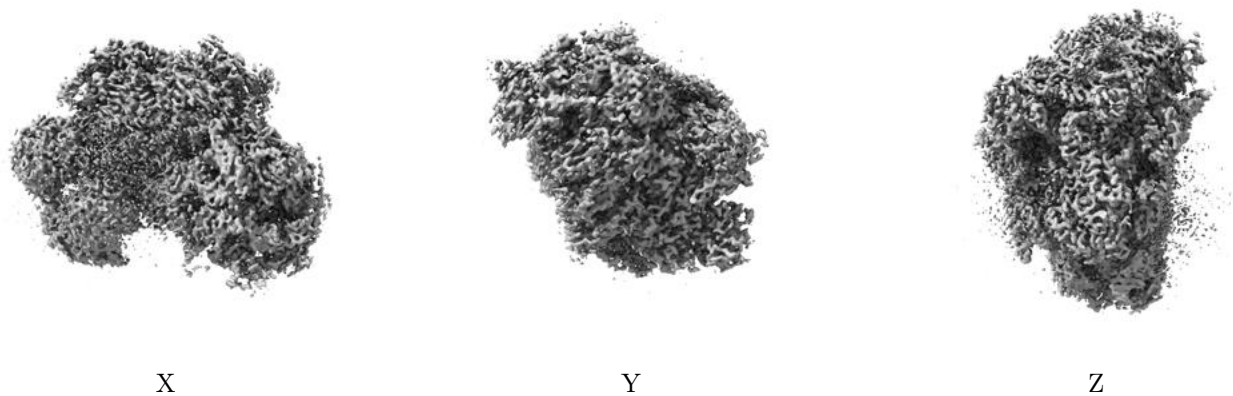


Z

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.

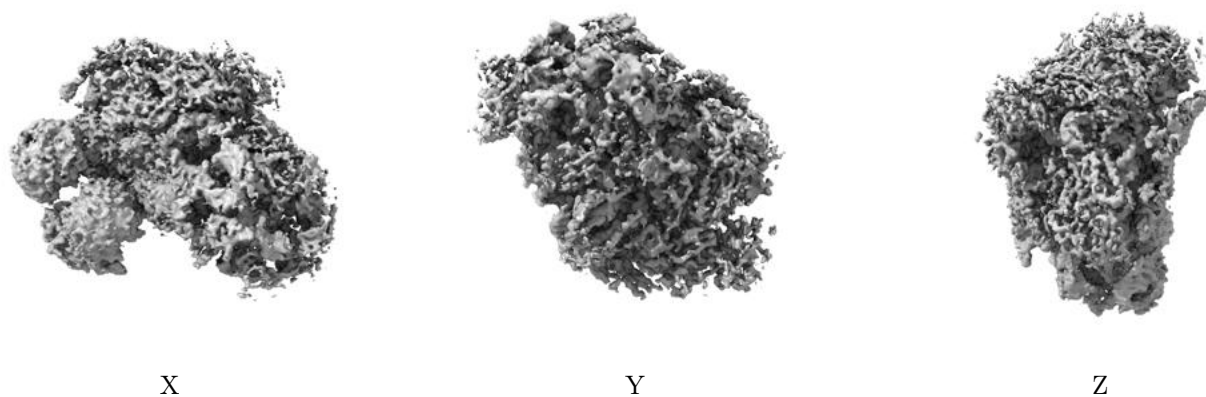
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.2. 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.

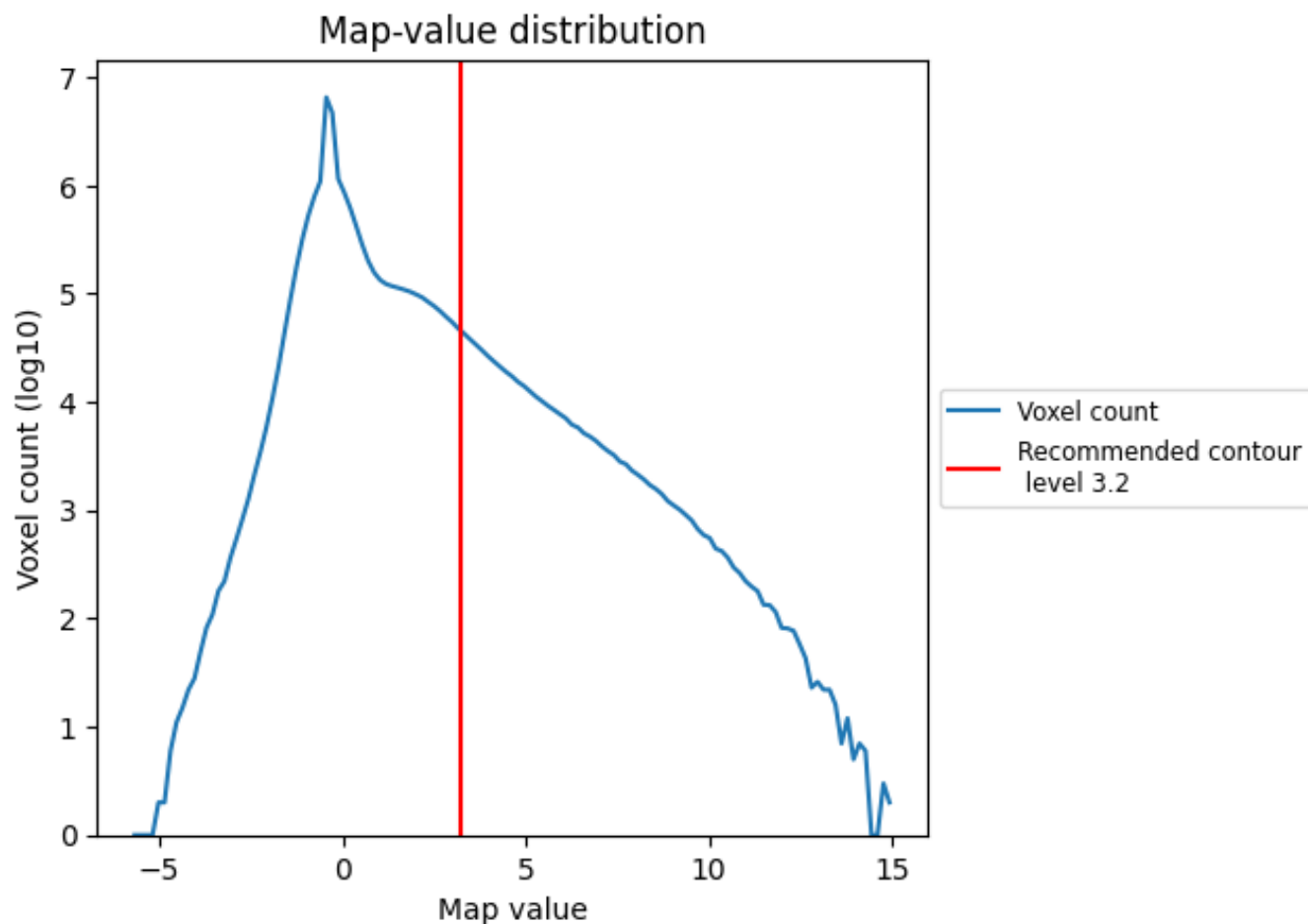
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

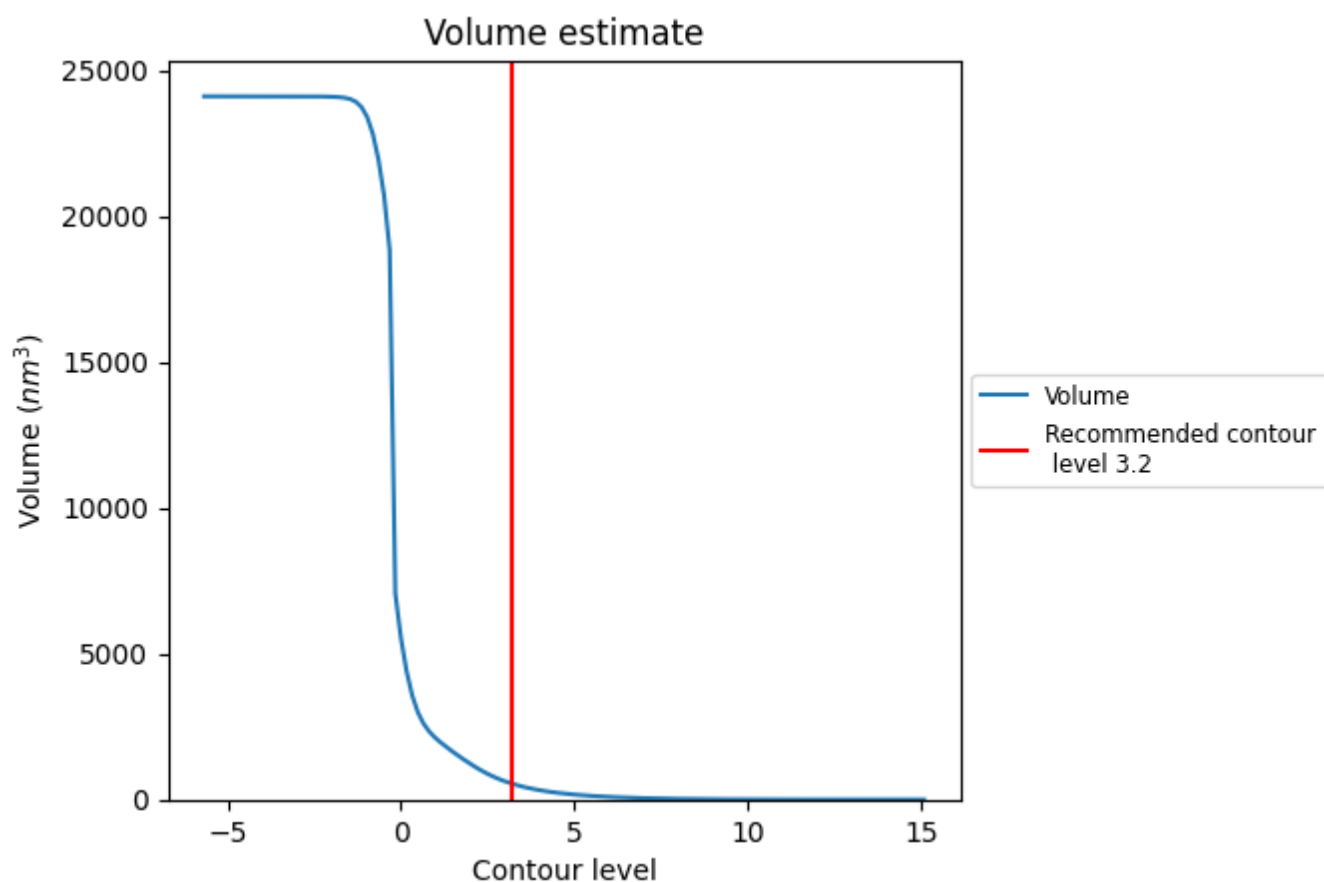
This section contains the results of statistical analysis of the map.

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.

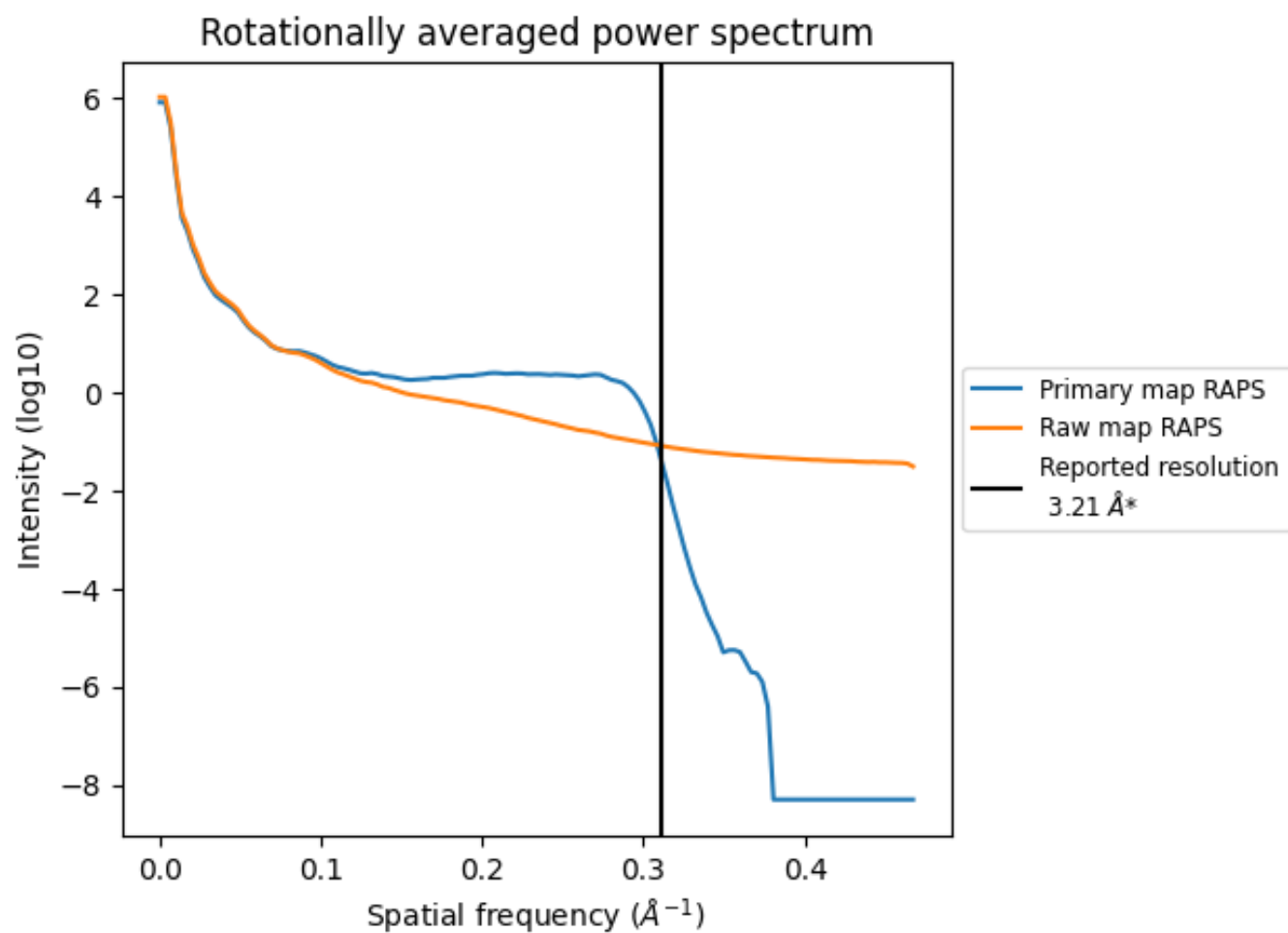
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 548 nm³; this corresponds to an approximate mass of 495 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 ⓘ

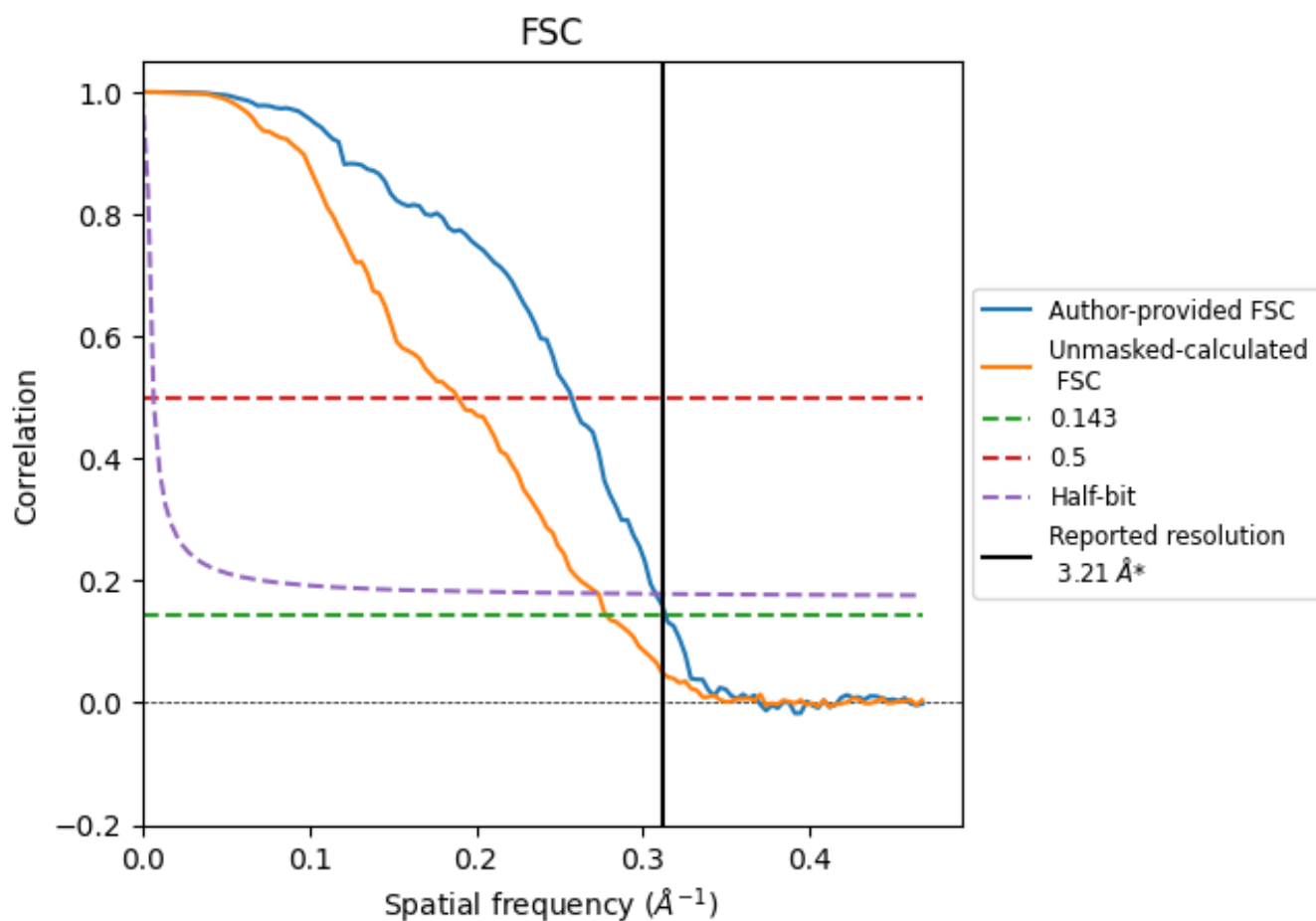


*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}

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 0.312 \AA^{-1}

8.2 Resolution estimates [i](#)

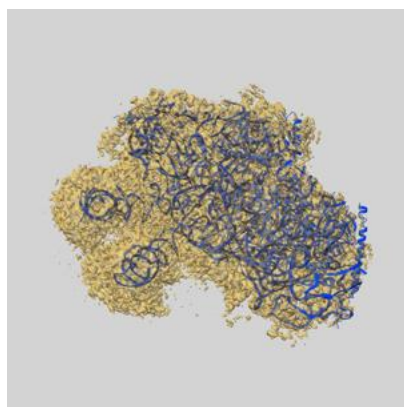
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.19	3.89	3.25
Unmasked-calculated*	3.59	5.29	3.66

*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 3.59 differs from the reported value 3.21 by more than 10 %

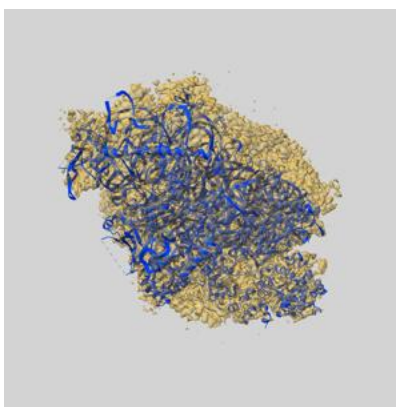
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64719 and PDB model 9V27. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

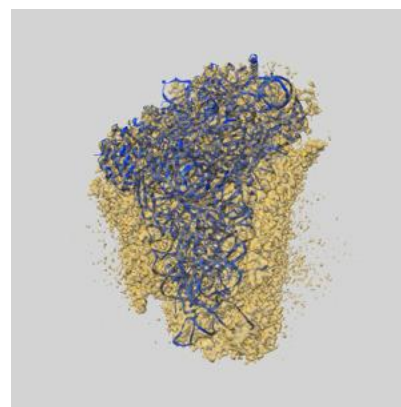
9.1 Map-model overlay [i](#)



X



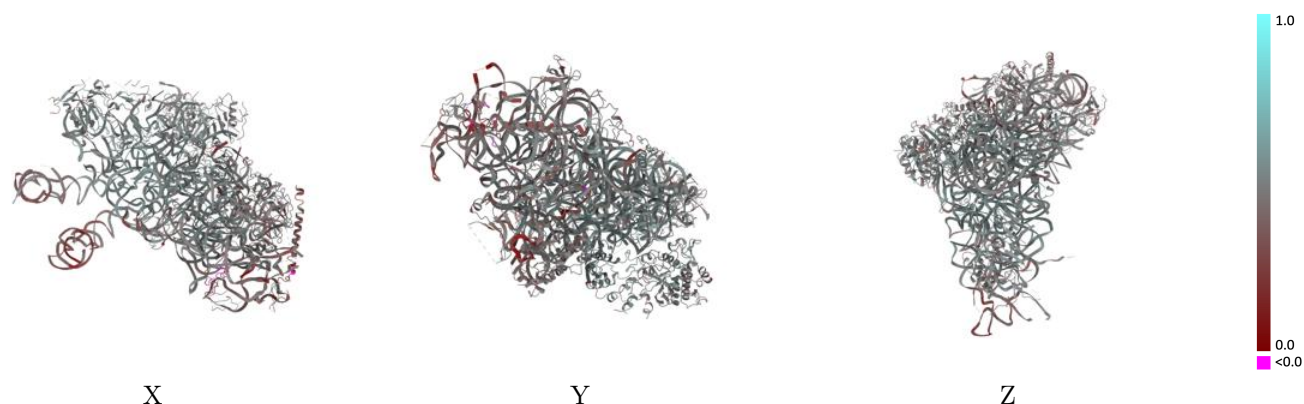
Y



Z

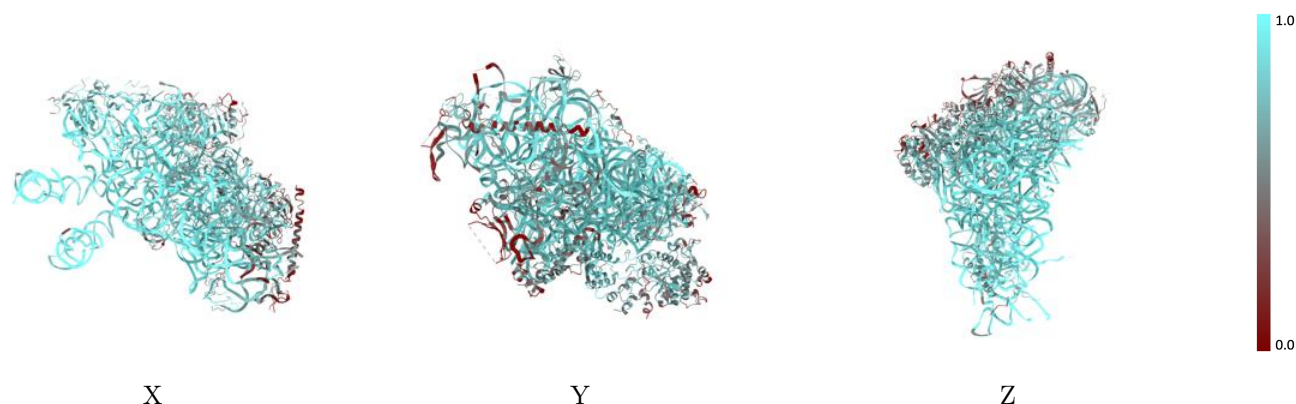
The images above show the 3D surface view of the map at the recommended contour level 3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



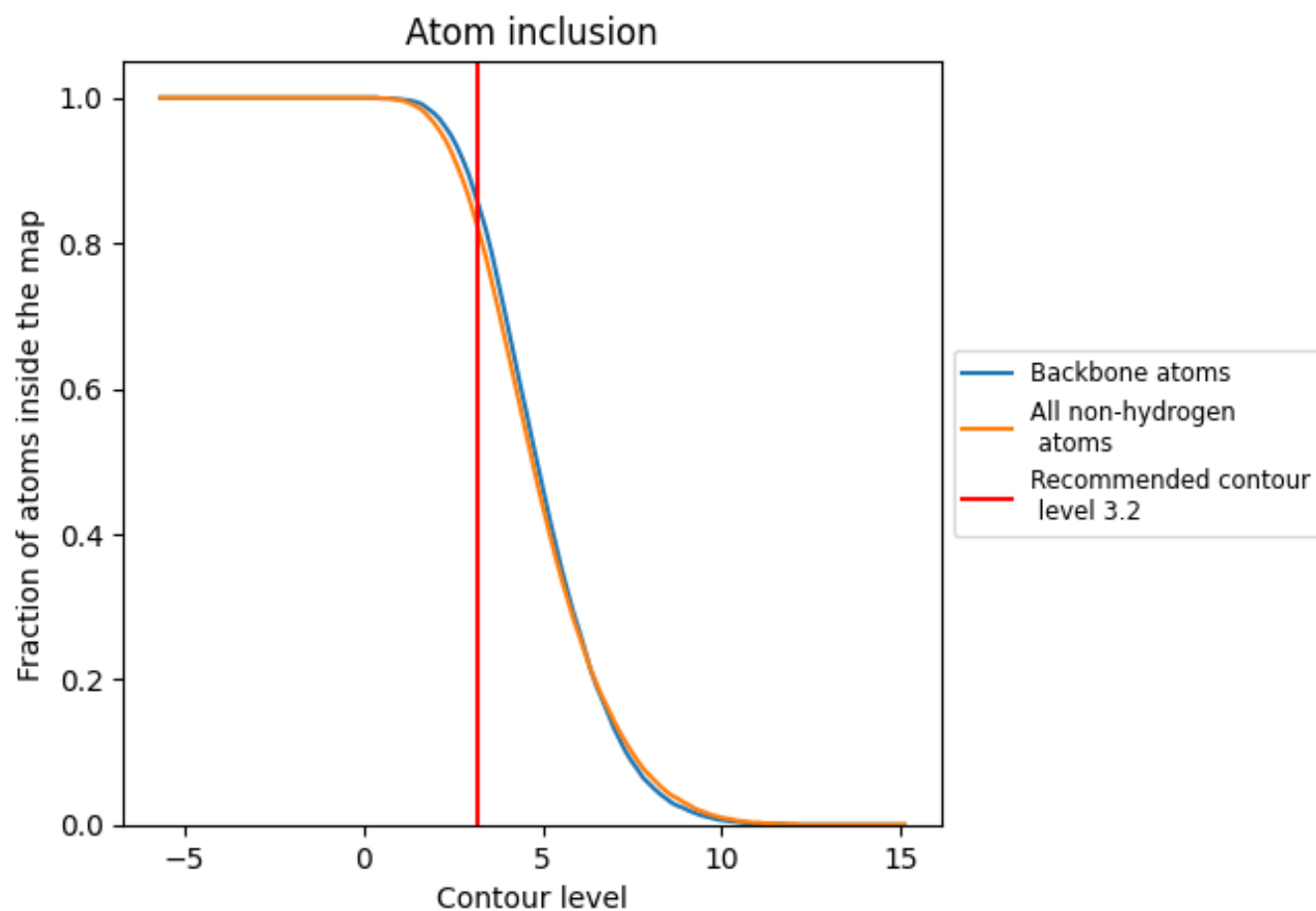
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4710
sB	 0.8780	 0.5250
sC	 0.6890	 0.5040
sH	 1.0000	 0.5540
sI	 0.9260	 0.3470
sJ	 0.9410	 0.4120
sK	 0.9950	 0.5330
sa	 0.9070	 0.4800
sb	 0.6640	 0.4850
sc	 0.7600	 0.5130
se	 0.7980	 0.5070
sf	 0.6130	 0.4640
sh	 0.4340	 0.3080
si	 0.4070	 0.4590
sj	 0.7680	 0.4810
sk	 0.5360	 0.4590
sm	 0.7590	 0.4780
so	 0.8560	 0.4980
sp	 0.8370	 0.5030
sr	 0.8360	 0.5140
sx	 0.6840	 0.5030
sy	 0.7170	 0.4770
sz	 0.1650	 0.4160

