



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:56 AM UTC

PDB ID : 8WIF / pdb_00008wif
EMDB ID : EMD-37565
Title : Cryo- EM structure of Mycobacterium smegmatis 30S ribosomal subunit (body 2) of 70S ribosome and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 2.90 Å(reported)
Based on initial model : 8WHX

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

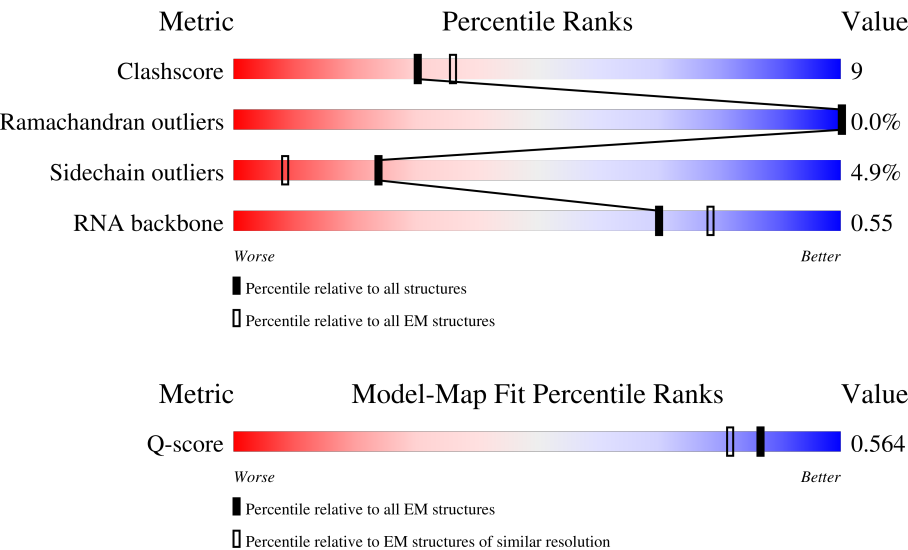
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



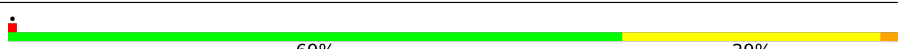
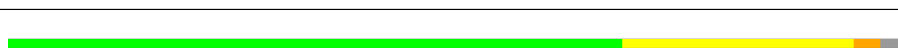
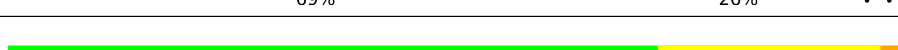
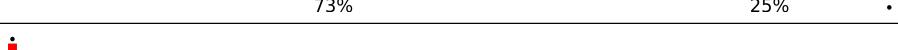
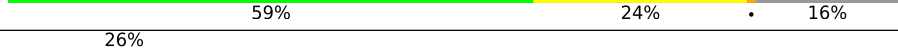
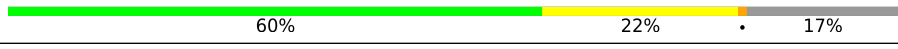
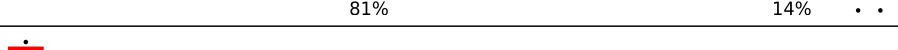
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	a	1528	58%34%8%
2	v	33	76%18%6%
3	d	275	9% 56%19%25%

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Mol	Chain	Length	Quality of chain
4	e	201	
5	f	214	
6	g	96	
7	h	156	
8	i	132	
9	j	150	
10	k	101	
11	l	138	
12	m	124	
13	n	124	
14	o	101	
15	p	89	
16	q	156	
17	r	98	
18	s	84	
19	t	93	
20	u	86	
21	c	277	
22	x	75	
23	w	264	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 52783 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1517	Total	C	N	O	P	0	0
			32561	14503	5949	10592	1517		

- Molecule 2 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	170	Total	C	N	O	S	0	0
			1236	778	232	222	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	j	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	98	Total	C	N	O	S	0	0
			784	493	145	143	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 18 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 22 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	x	11	Total	C	N	O	0	0
			94	59	21	14		

- Molecule 23 is a protein called Ribosome hibernation promotion factor RaffH.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	126	Total	C	N	O	S	0	0
			1004	609	214	180	1		

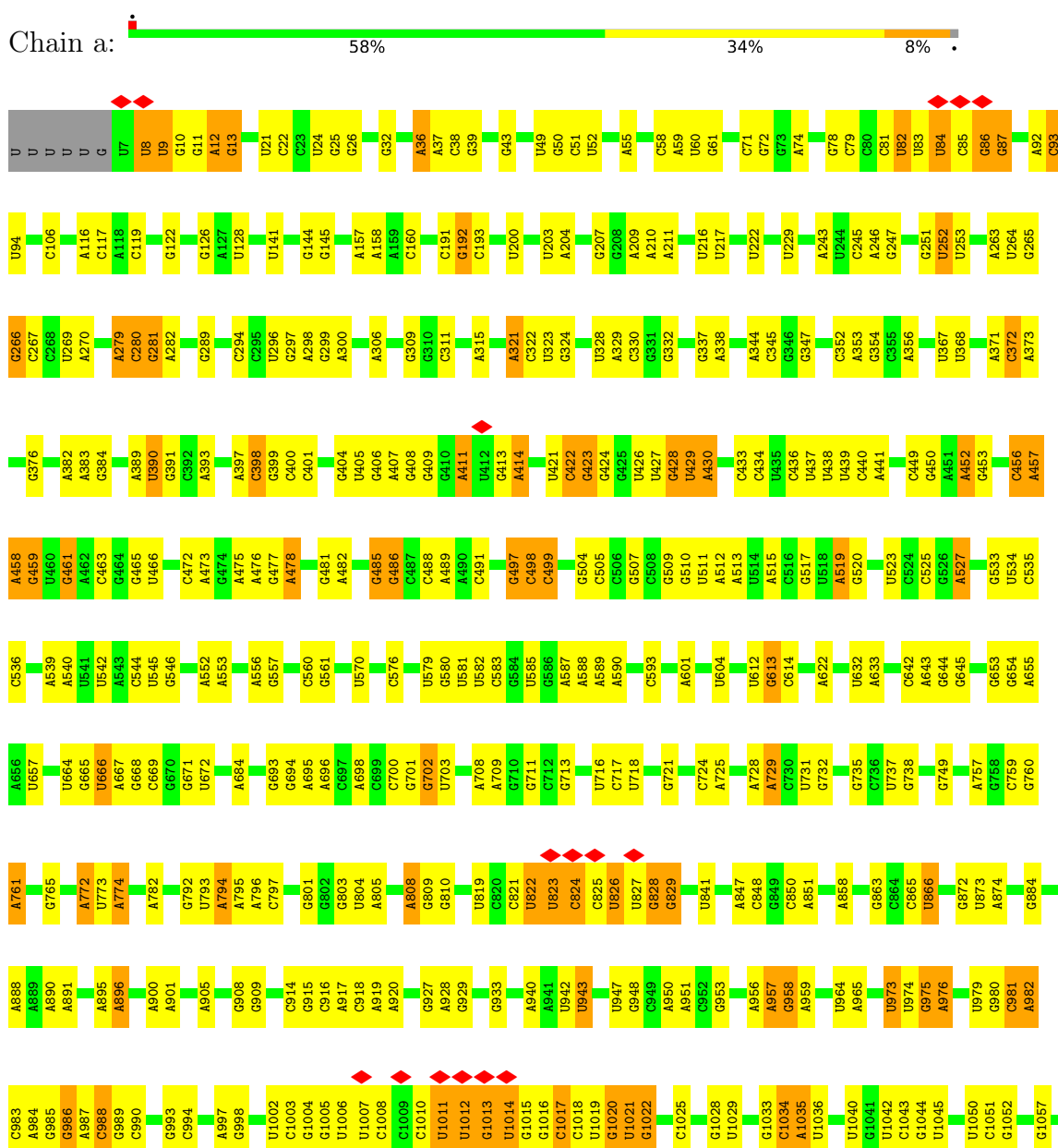
There are 6 discrepancies between the modelled and reference sequences:

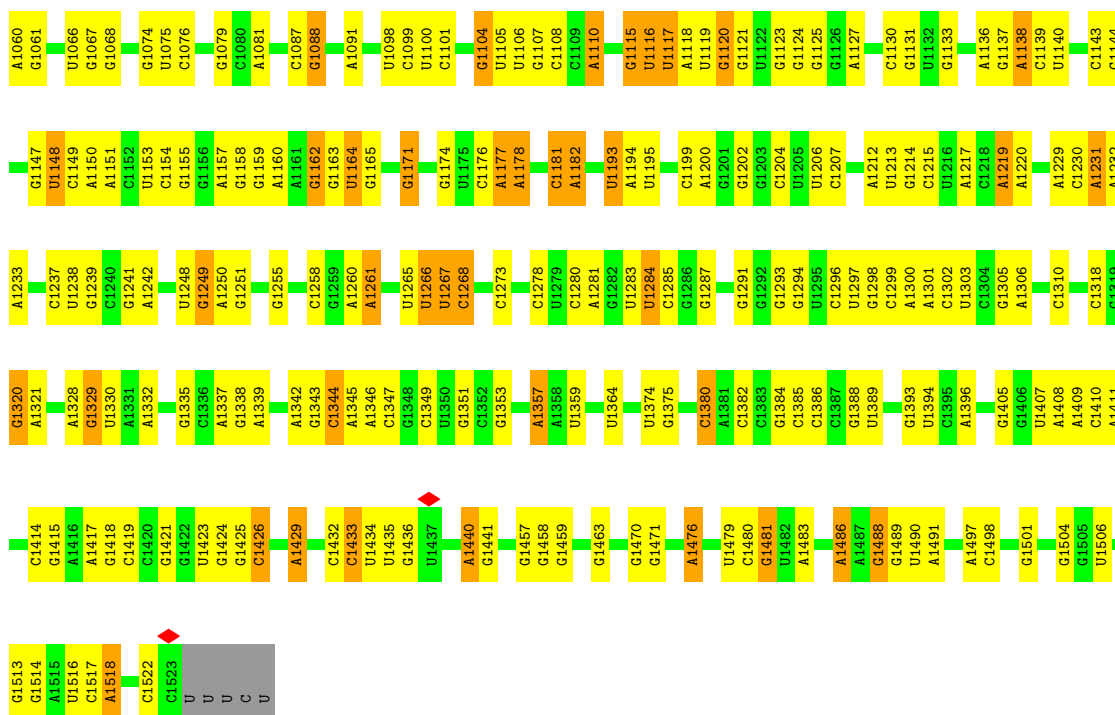
Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

3 Residue-property plots

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

• Molecule 1: 16S rRNA





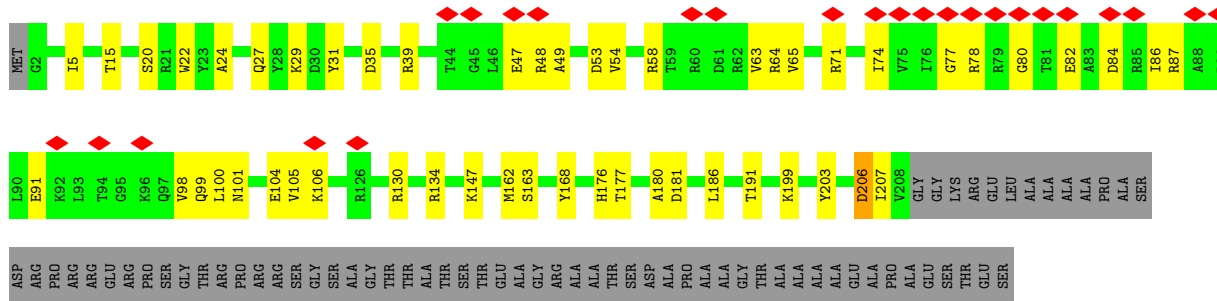
• Molecule 2: 30S ribosomal protein S22

Chain v: 76% 18% 6%



• Molecule 3: 30S ribosomal protein S3

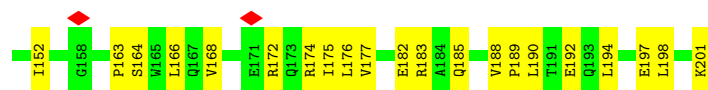
Chain d: 9% 56% 19% 25%



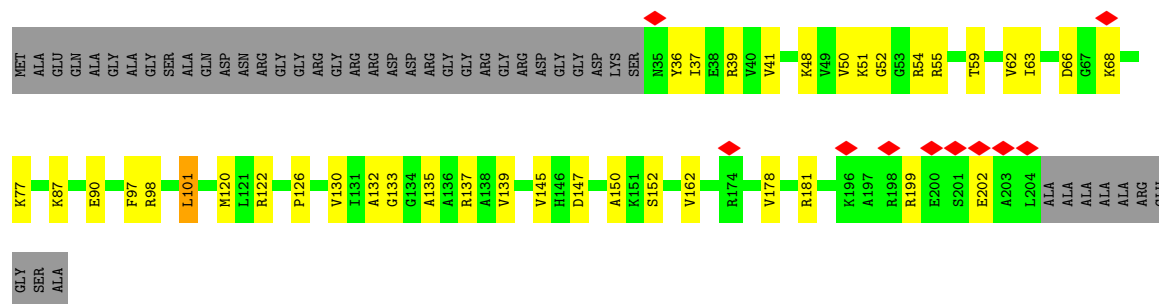
• Molecule 4: 30S ribosomal protein S4

Chain e: 73% 25%





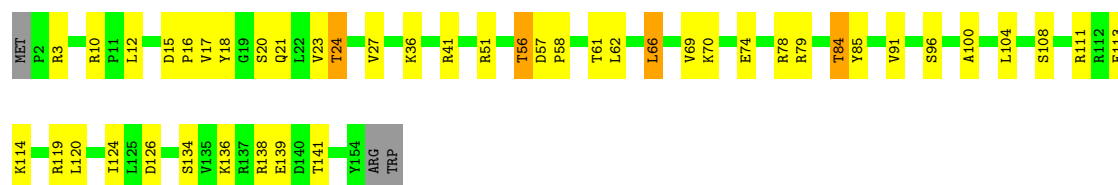
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8

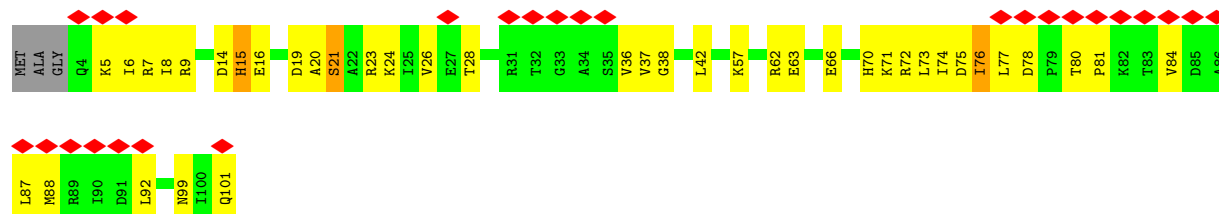


• Molecule 9: 30S ribosomal protein S9

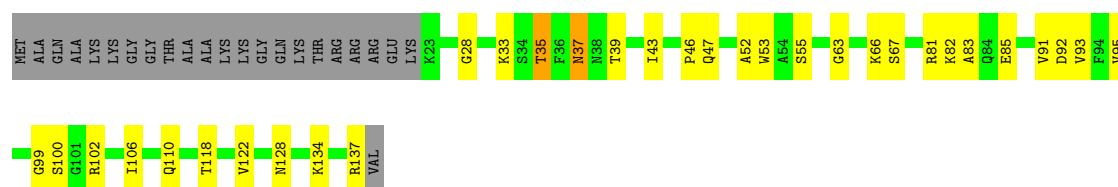




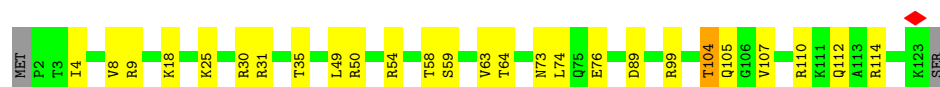
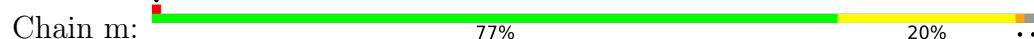
• Molecule 10: 30S ribosomal protein S10



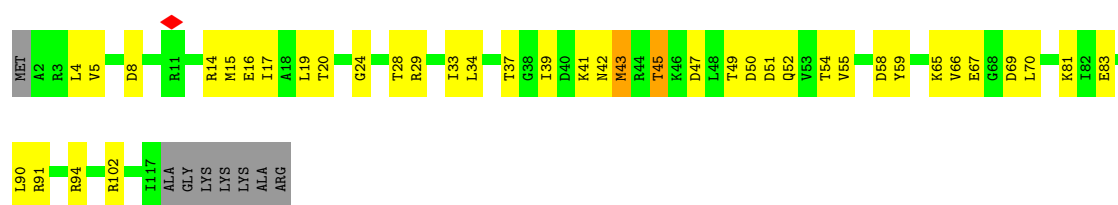
• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12

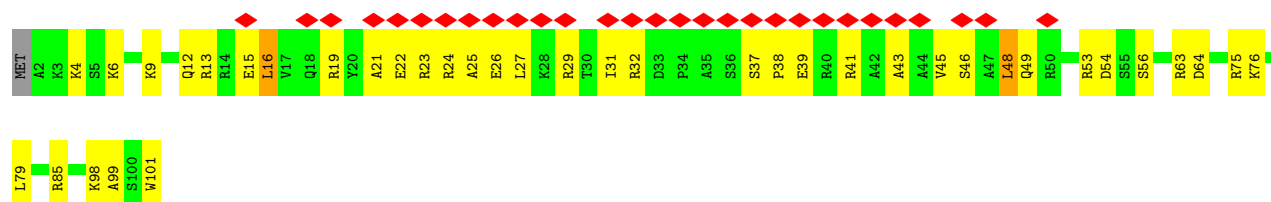


• Molecule 13: 30S ribosomal protein S13

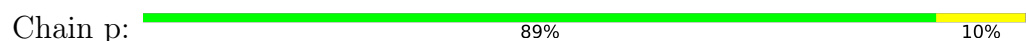


• Molecule 14: 30S ribosomal protein S14A

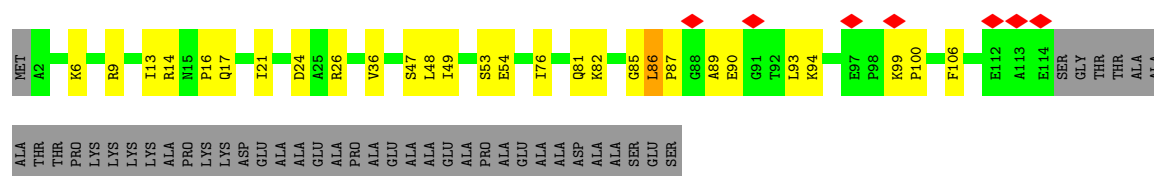




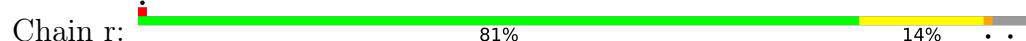
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



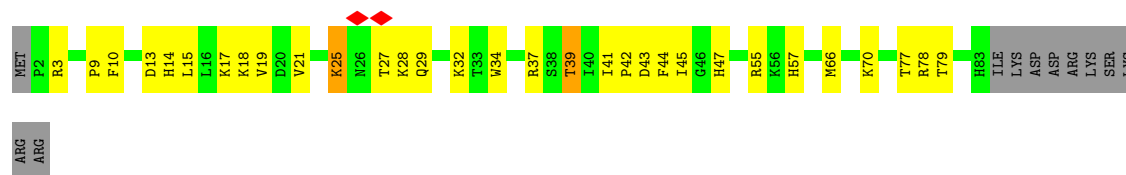
- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S ribosomal protein S18B

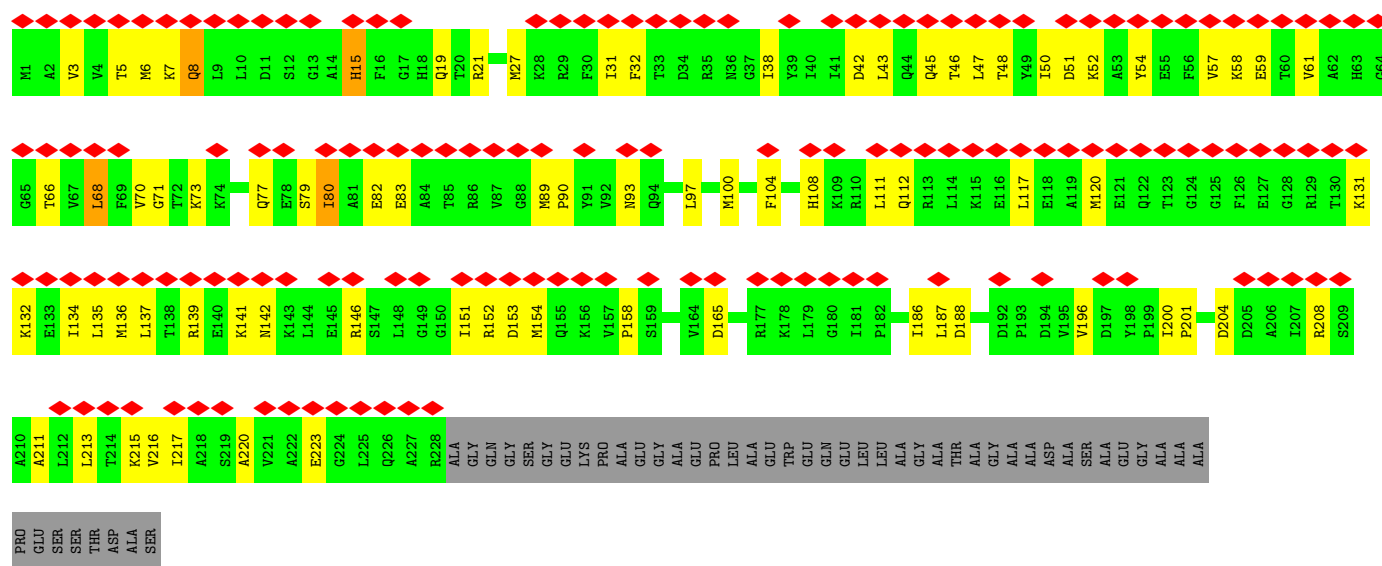


- Molecule 19: 30S ribosomal protein S19

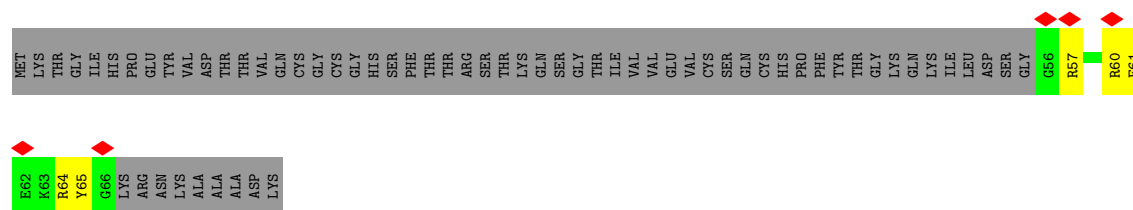


- Molecule 20: 30S ribosomal protein S20

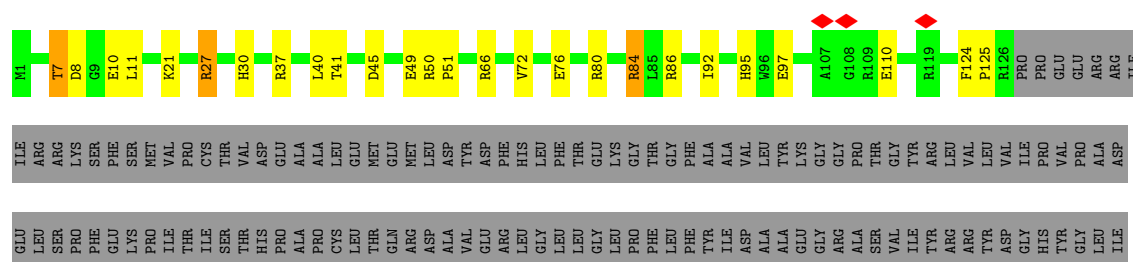
Chain c: 55% 54% 27% 18%



Chain x: 7% 8% 7% 85%



Chain w:



THR
PRO
ALA
ASP
GLY
HIS
HIS
HIS
HIS
HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.236	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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	a	0.34	0/36444	0.31	0/56866
2	v	0.19	0/271	0.33	0/348
3	d	0.22	0/1680	0.32	0/2256
4	e	0.26	0/1672	0.36	0/2251
5	f	0.19	0/1252	0.28	0/1691
6	g	0.28	0/782	0.38	0/1059
7	h	0.24	0/1225	0.37	0/1653
8	i	0.32	0/1025	0.36	0/1385
9	j	0.25	0/1012	0.42	0/1362
10	k	0.21	0/798	0.41	0/1081
11	l	0.28	0/873	0.43	0/1180
12	m	0.29	0/969	0.33	0/1294
13	n	0.25	0/942	0.45	0/1260
14	o	0.26	0/830	0.45	0/1106
15	p	0.29	0/729	0.36	0/977
16	q	0.30	0/908	0.39	0/1226
17	r	0.30	0/759	0.40	0/1016
18	s	0.28	0/518	0.35	0/693
19	t	0.27	0/680	0.44	0/915
20	u	0.30	0/663	0.41	0/882
21	c	0.16	0/1822	0.34	0/2457
22	x	0.16	0/95	0.32	0/123
23	w	0.23	0/1023	0.31	0/1381
All	All	0.31	0/56972	0.33	0/84462

There are no bond length outliers.

There are no bond angle outliers.

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	a	32561	0	16386	396	0
2	v	271	0	329	5	0
3	d	1656	0	1704	35	0
4	e	1641	0	1668	45	0
5	f	1236	0	1303	24	0
6	g	771	0	797	22	0
7	h	1207	0	1259	29	0
8	i	1010	0	1046	27	0
9	j	994	0	1050	29	0
10	k	784	0	816	33	0
11	l	855	0	863	19	0
12	m	958	0	1045	19	0
13	n	935	0	986	29	0
14	o	819	0	866	38	0
15	p	720	0	760	4	0
16	q	891	0	935	20	0
17	r	748	0	795	10	0
18	s	513	0	540	13	0
19	t	662	0	677	21	0
20	u	660	0	712	7	0
21	c	1793	0	1839	58	0
22	x	94	0	95	6	0
23	w	1004	0	991	20	0
All	All	52783	0	37462	794	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 9.

The worst 5 of 794 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1010:C:H42	1:a:1014:U:H3	1.05	0.97
1:a:1232:A:H62	1:a:1268:C:H42	1.11	0.93
1:a:1010:C:N4	1:a:1014:U:H3	1.68	0.90
21:c:27:MET:HE1	21:c:187:LEU:HD13	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:772:A:O2'	1:a:774:A:N7	2.08	0.86

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	v	29/33 (88%)	29 (100%)	0	0	100	100
3	d	205/275 (74%)	196 (96%)	9 (4%)	0	100	100
4	e	198/201 (98%)	184 (93%)	14 (7%)	0	100	100
5	f	168/214 (78%)	160 (95%)	8 (5%)	0	100	100
6	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
7	h	151/156 (97%)	147 (97%)	4 (3%)	0	100	100
8	i	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
9	j	124/150 (83%)	117 (94%)	7 (6%)	0	100	100
10	k	96/101 (95%)	92 (96%)	3 (3%)	1 (1%)	12	39
11	l	113/138 (82%)	106 (94%)	7 (6%)	0	100	100
12	m	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
13	n	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
14	o	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
15	p	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	q	111/156 (71%)	106 (96%)	5 (4%)	0	100	100
17	r	92/98 (94%)	88 (96%)	4 (4%)	0	100	100
18	s	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
19	t	80/93 (86%)	76 (95%)	4 (5%)	0	100	100
20	u	83/86 (96%)	83 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	c	226/277 (82%)	210 (93%)	16 (7%)	0	100	100
22	x	9/75 (12%)	9 (100%)	0	0	100	100
23	w	124/264 (47%)	120 (97%)	4 (3%)	0	100	100
All	All	2513/3067 (82%)	2398 (95%)	114 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	k	57	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	v	29/31 (94%)	29 (100%)	0	100	100
3	d	170/212 (80%)	164 (96%)	6 (4%)	32	66
4	e	175/176 (99%)	170 (97%)	5 (3%)	37	71
5	f	124/147 (84%)	116 (94%)	8 (6%)	15	44
6	g	85/85 (100%)	82 (96%)	3 (4%)	32	66
7	h	129/132 (98%)	121 (94%)	8 (6%)	16	46
8	i	107/108 (99%)	100 (94%)	7 (6%)	15	44
9	j	102/125 (82%)	99 (97%)	3 (3%)	37	71
10	k	89/90 (99%)	83 (93%)	6 (7%)	15	43
11	l	89/105 (85%)	81 (91%)	8 (9%)	9	28
12	m	103/105 (98%)	99 (96%)	4 (4%)	28	63
13	n	99/104 (95%)	92 (93%)	7 (7%)	13	40
14	o	85/86 (99%)	83 (98%)	2 (2%)	43	75
15	p	76/77 (99%)	73 (96%)	3 (4%)	28	63
16	q	92/118 (78%)	88 (96%)	4 (4%)	26	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	r	80/83 (96%)	77 (96%)	3 (4%)	29	64
18	s	55/72 (76%)	53 (96%)	2 (4%)	31	65
19	t	73/84 (87%)	68 (93%)	5 (7%)	14	42
20	u	69/70 (99%)	66 (96%)	3 (4%)	26	60
21	c	191/218 (88%)	181 (95%)	10 (5%)	21	52
22	x	8/63 (13%)	8 (100%)	0	100	100
23	w	98/215 (46%)	91 (93%)	7 (7%)	13	40
All	All	2128/2506 (85%)	2024 (95%)	104 (5%)	24	54

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	m	104	THR
16	q	48	LEU
23	w	41	THR
13	n	5	VAL
14	o	16	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
19	t	22	GLN
23	w	95	HIS
20	u	84	ASN
10	k	56	HIS
16	q	57	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1516/1528 (99%)	271 (17%)	0

5 of 271 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	U
1	a	9	U

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Mol	Chain	Res	Type
1	a	12	A
1	a	13	G
1	a	36	A

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.

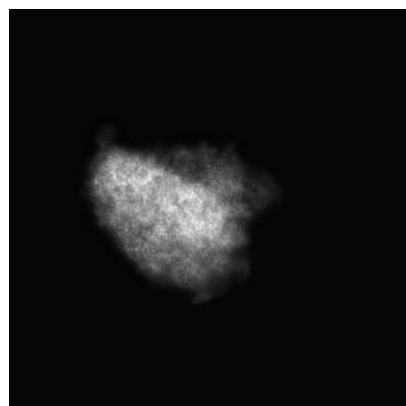
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37565. These allow visual inspection of the internal detail of the map and identification of artifacts.

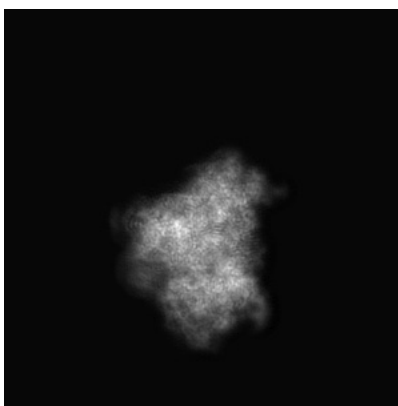
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

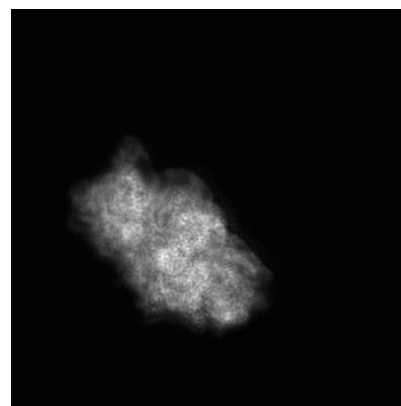
6.1.1 Primary map



X

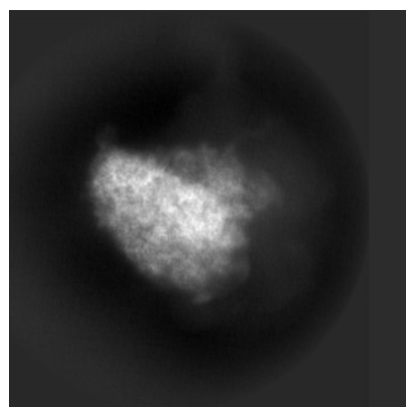


Y

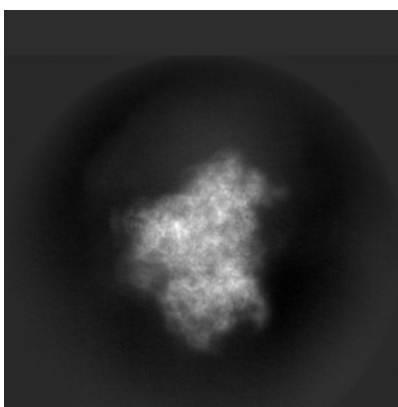


Z

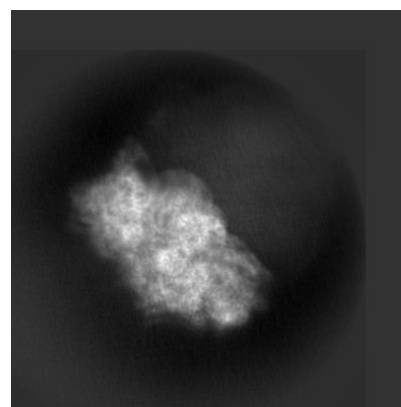
6.1.2 Raw map



X



Y

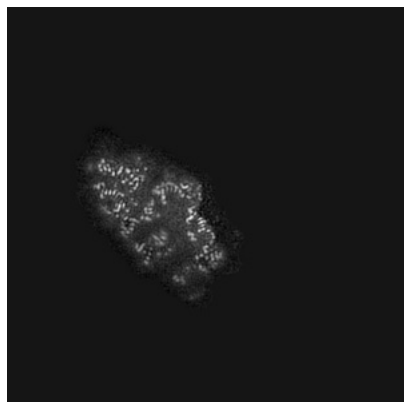


Z

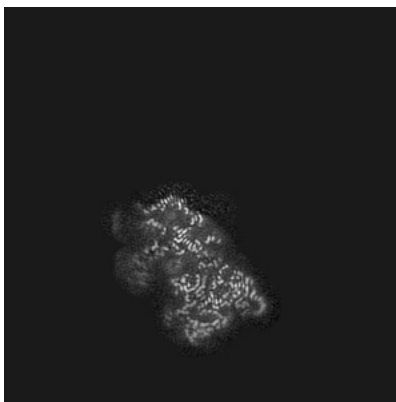
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

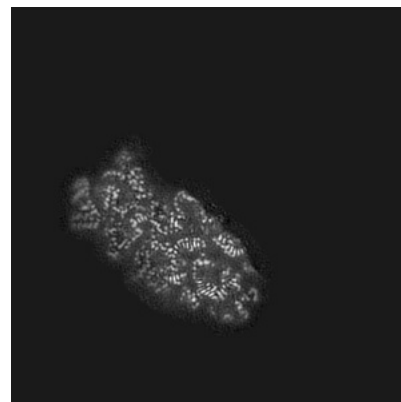
6.2.1 Primary map



X Index: 190

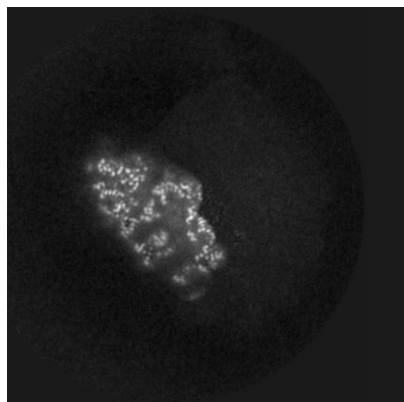


Y Index: 190

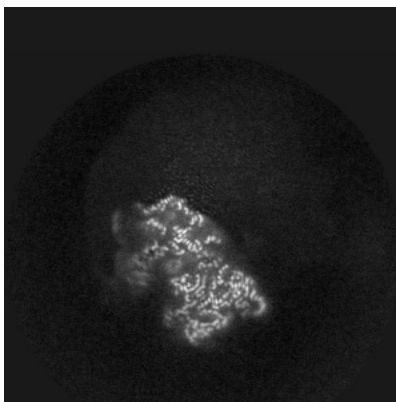


Z Index: 190

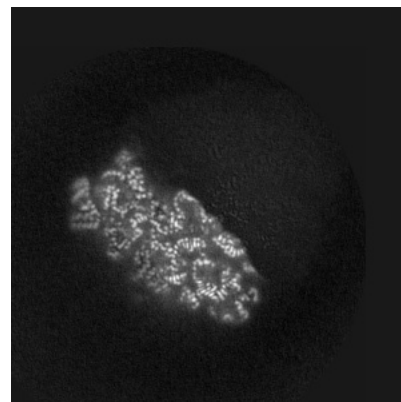
6.2.2 Raw map



X Index: 190



Y Index: 190

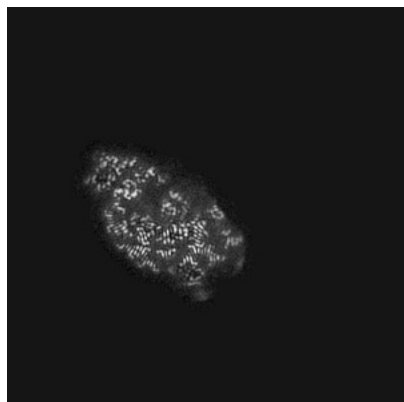


Z Index: 190

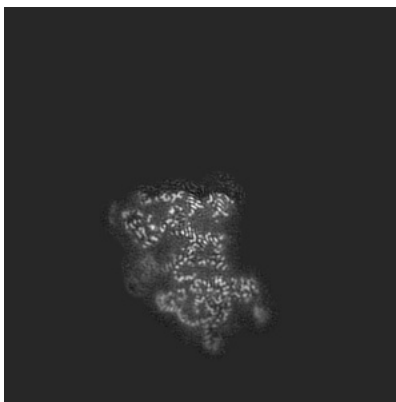
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

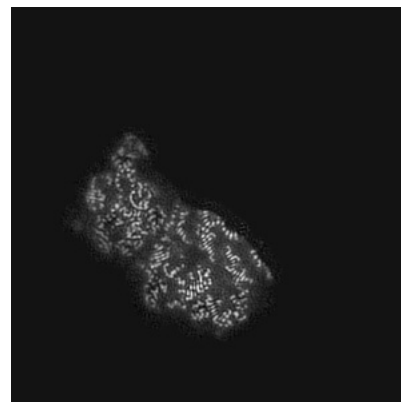
6.3.1 Primary map



X Index: 171

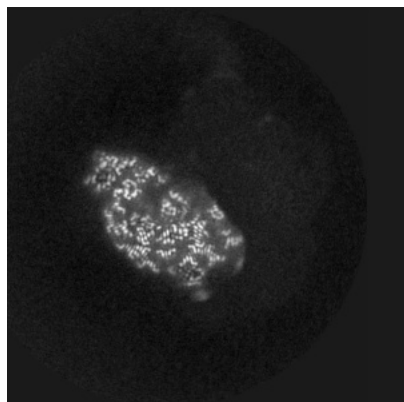


Y Index: 174

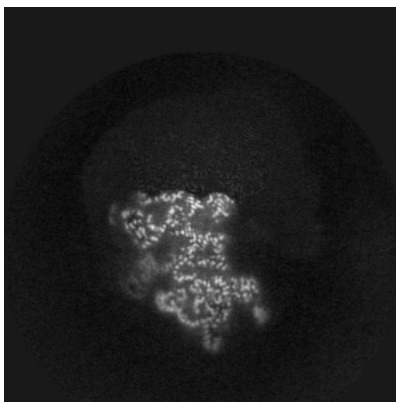


Z Index: 205

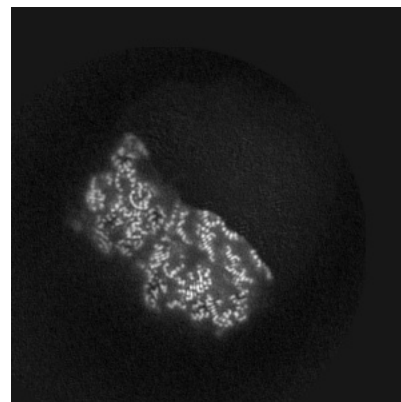
6.3.2 Raw map



X Index: 171



Y Index: 174

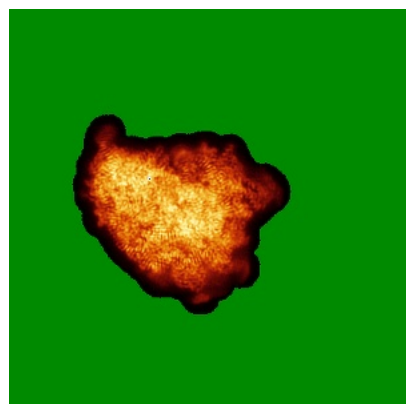


Z Index: 205

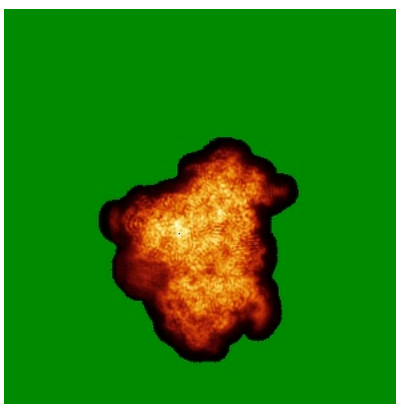
The images above show the largest variance slices of the map in three orthogonal directions.

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

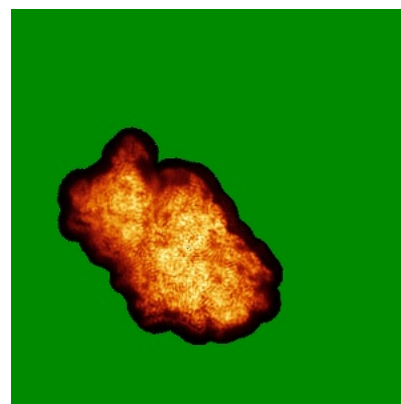
6.4.1 Primary map



X

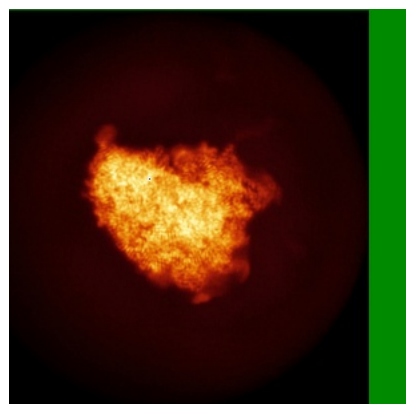


Y

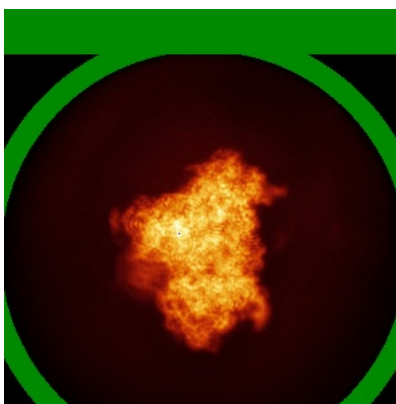


Z

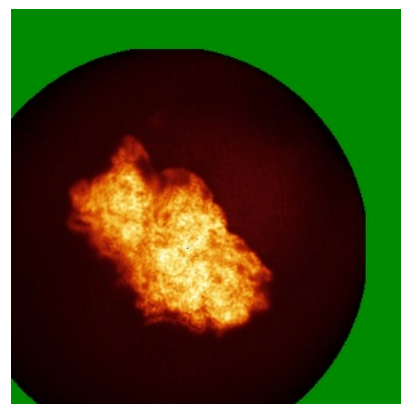
6.4.2 Raw map



X



Y

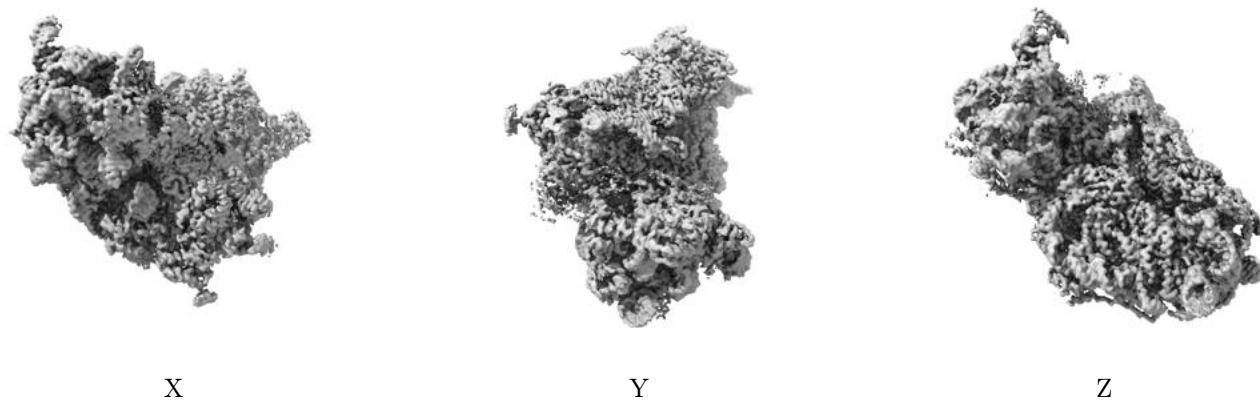


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. 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.

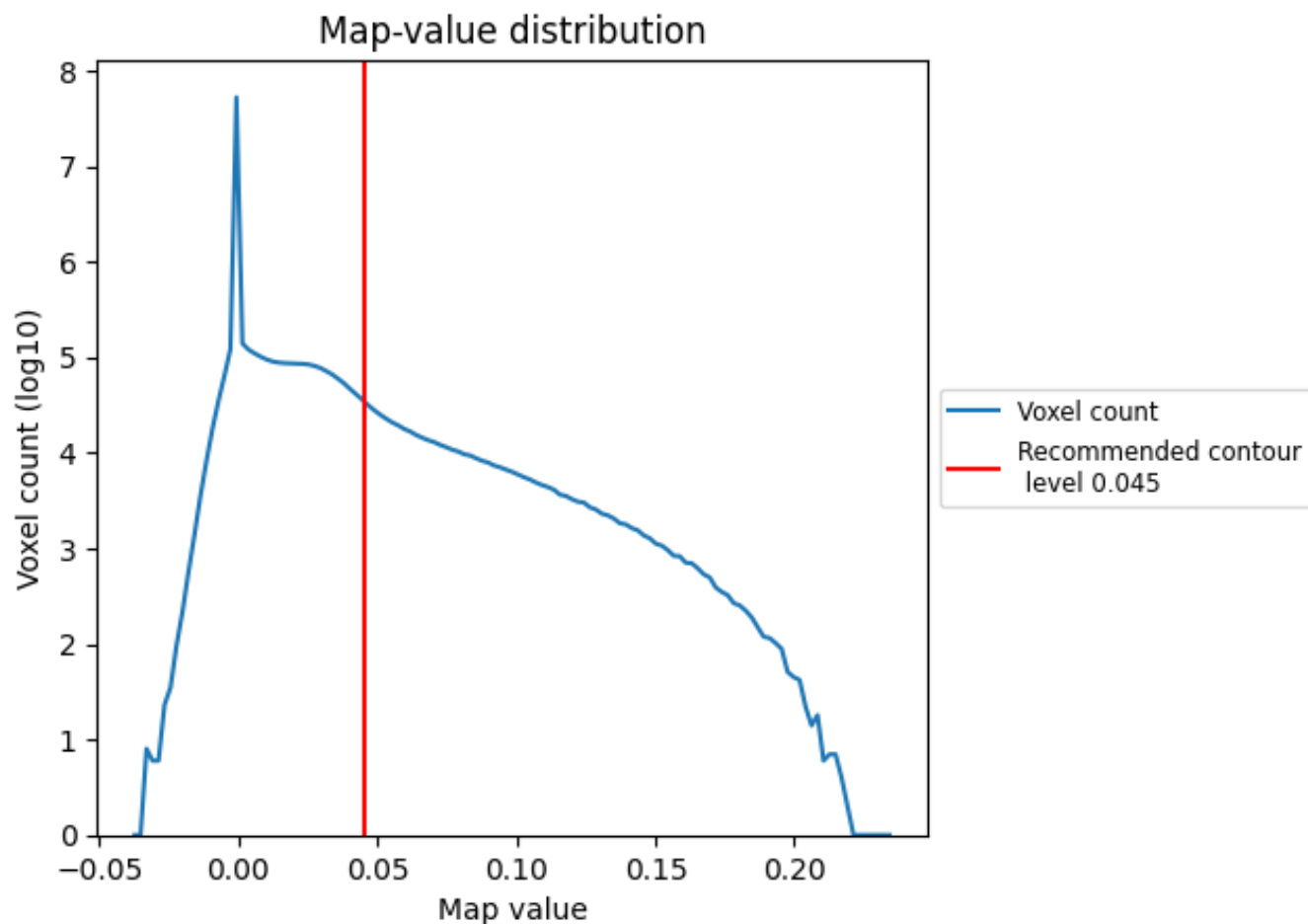
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

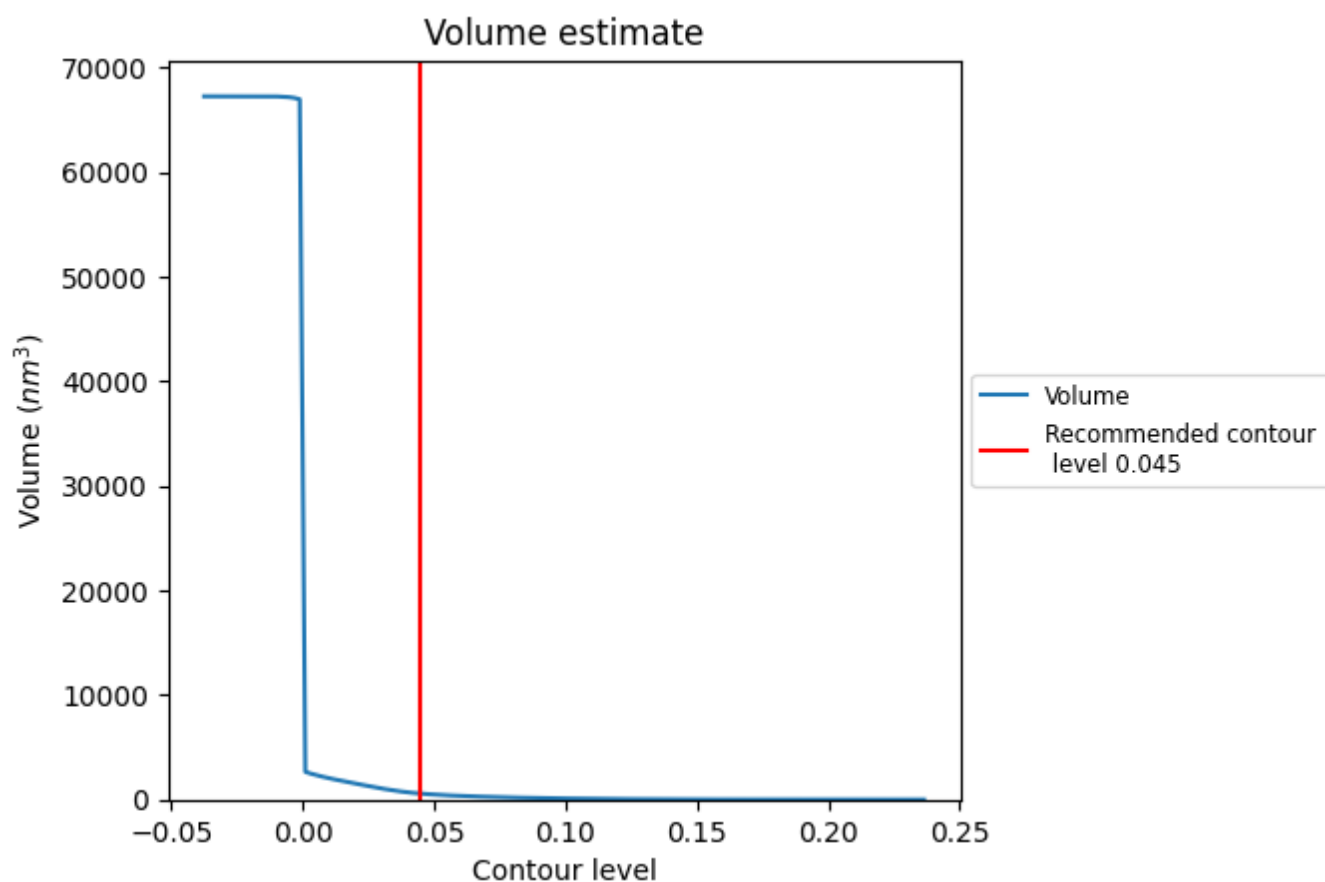
This section contains the results of statistical analysis of the map.

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.

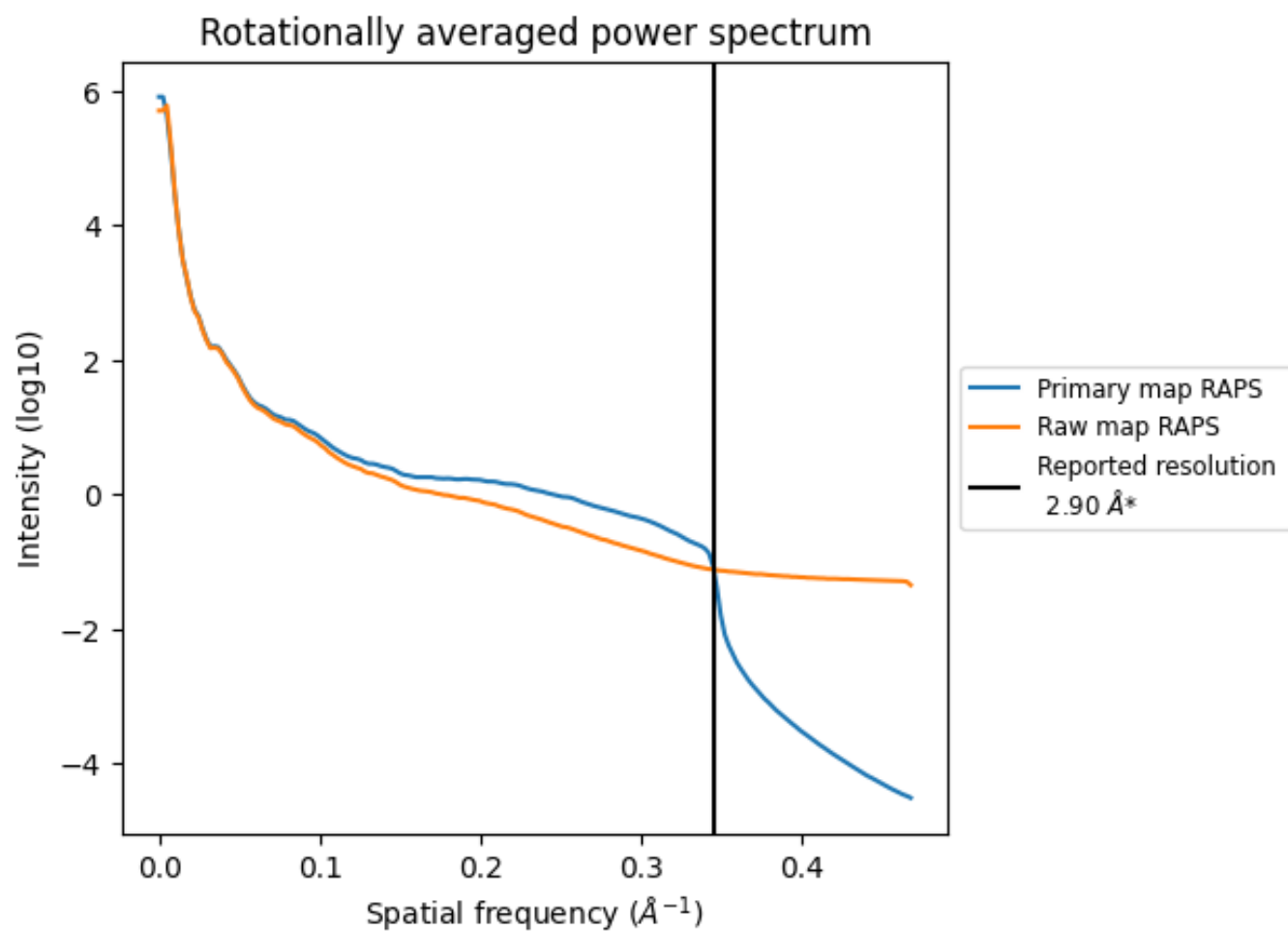
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 570 nm^3 ; this corresponds to an approximate mass of 515 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 ⓘ

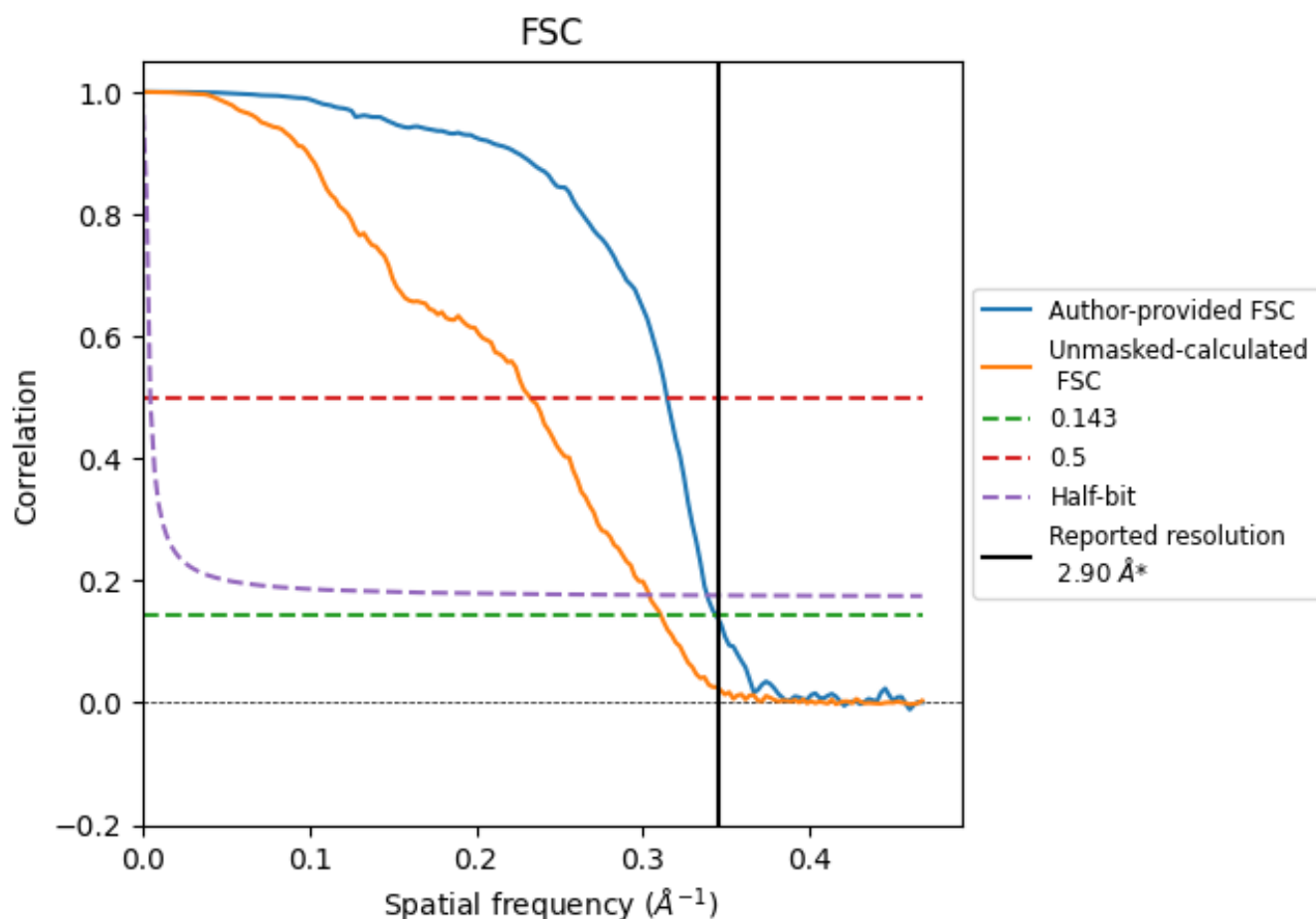


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

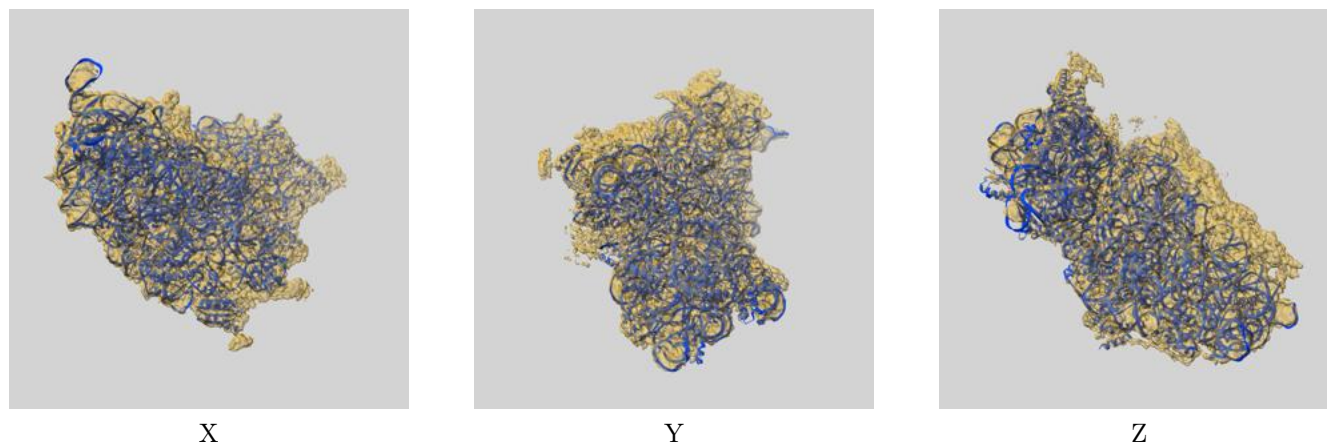
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.91	3.18	2.95
Unmasked-calculated*	3.22	4.30	3.29

*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 3.22 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

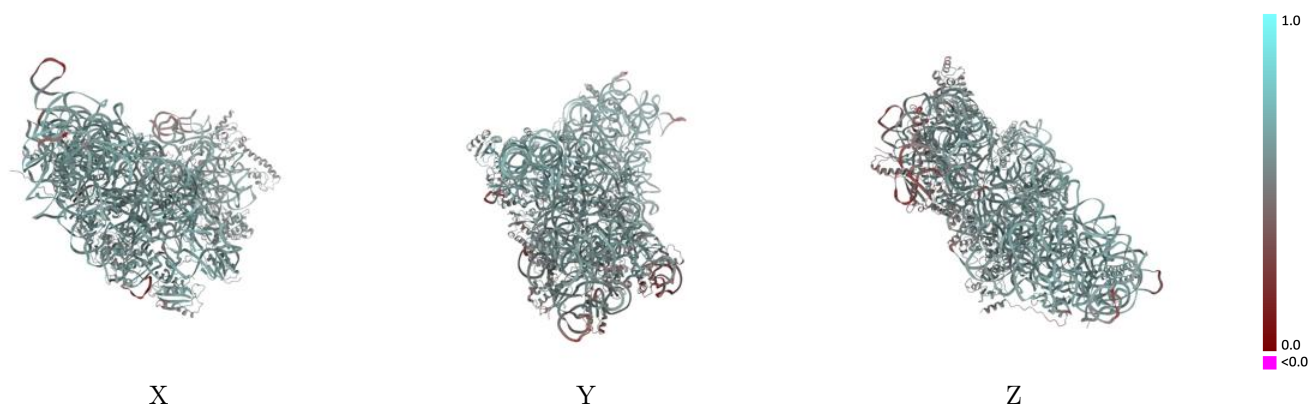
This section contains information regarding the fit between EMDB map EMD-37565 and PDB model 8WIF. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



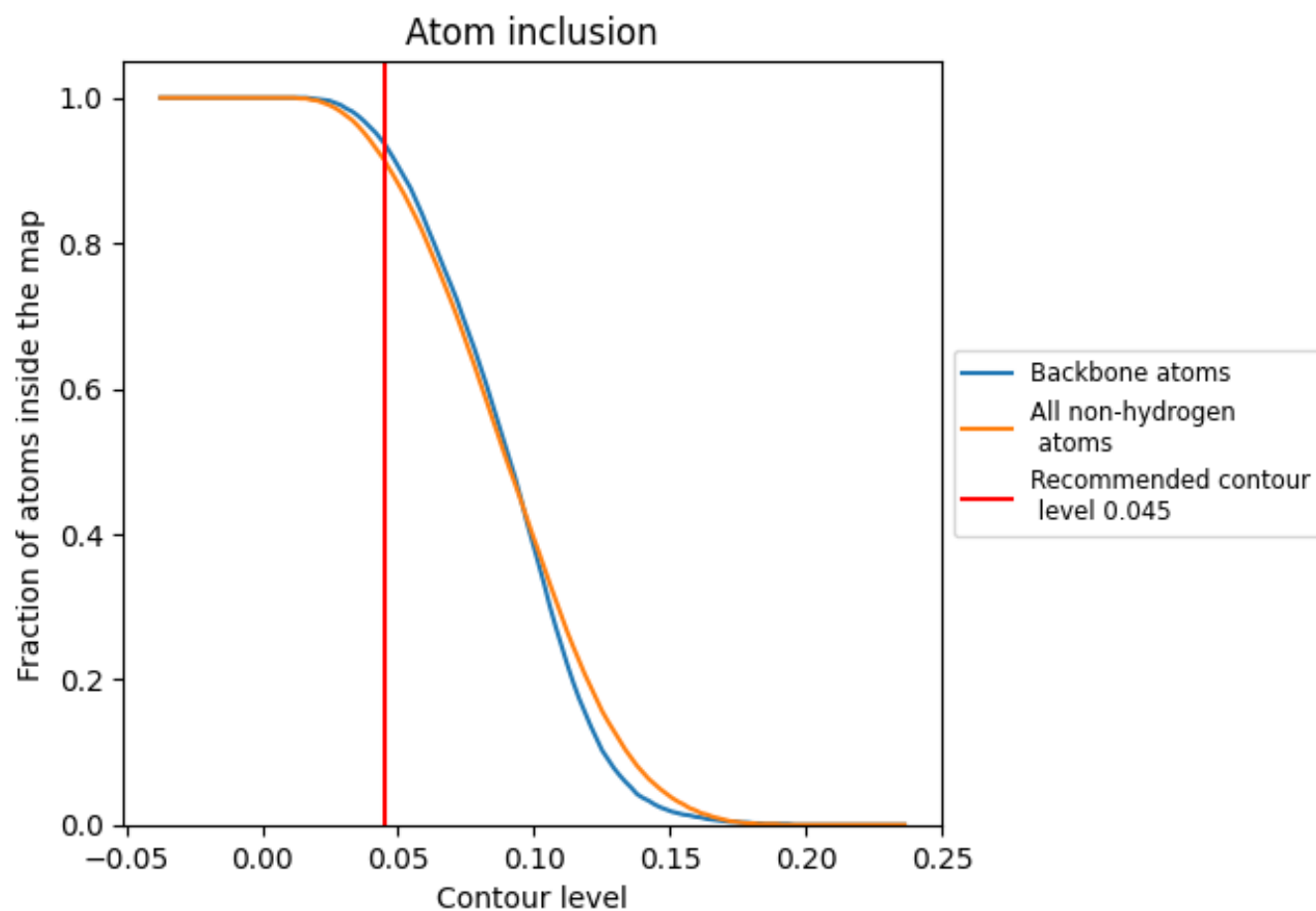
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.5640
a	 0.9750	 0.5780
c	 0.2960	 0.4670
d	 0.7340	 0.5040
e	 0.8800	 0.5530
f	 0.7940	 0.5600
g	 0.8800	 0.5530
h	 0.8990	 0.5370
i	 0.9560	 0.5860
j	 0.8690	 0.5190
k	 0.6410	 0.5020
l	 0.9300	 0.5670
m	 0.9420	 0.5900
n	 0.8870	 0.5210
o	 0.6550	 0.4790
p	 0.9410	 0.5760
q	 0.8970	 0.5670
r	 0.9310	 0.5850
s	 0.9070	 0.5490
t	 0.8880	 0.5410
u	 0.9630	 0.5810
v	 0.9880	 0.5840
w	 0.9170	 0.5640
x	 0.5060	 0.4720

