



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 02:42 AM UTC

PDB ID : 9OY8 / pdb_00009oy8
EMDB ID : EMD-71002
Title : Flavobacterium johnsoniae 30S ribosomal subunit.
Authors : Ortega, J.; Arpin, D.
Deposited on : 2025-06-04
Resolution : 2.70 Å(reported)

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:

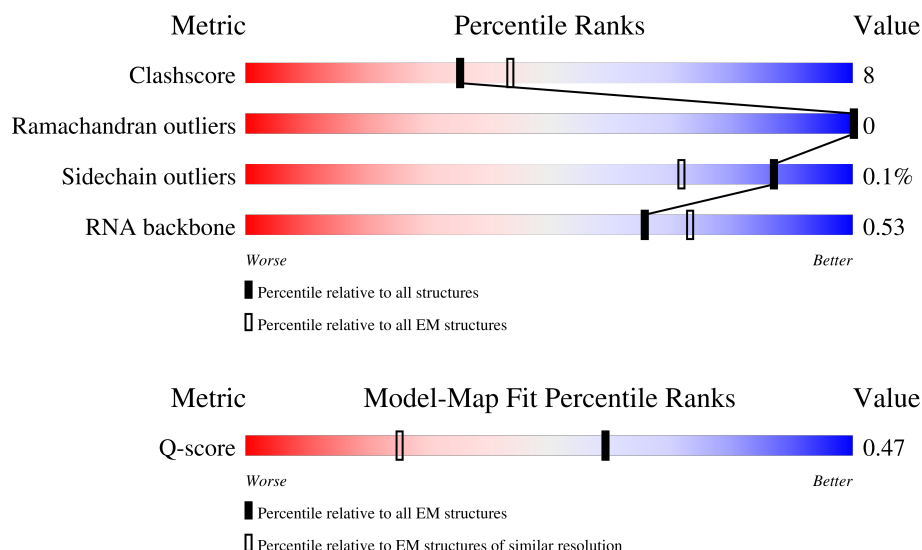
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	2	1520	
2	H	254	
3	h	252	

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Mol	Chain	Length	Quality of chain
4	i	201	
5	j	173	
6	k	113	
7	l	158	
8	m	132	
9	n	128	
10	o	101	
11	p	127	
12	q	127	
13	r	124	
14	s	89	
15	t	88	
16	u	188	
17	v	86	
18	w	98	
19	x	92	
20	y	83	
21	z	64	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 49671 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 16 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1481	Total	C	N	O	P	0	0
			31728	14167	5801	10279	1481		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	219	Total	C	N	O	S	0	0
			1666	1058	293	307	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	215	Total	C	N	O	S	0	0
			1600	1015	290	289	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	i	200	Total	C	N	O	S	0	0
			1561	988	289	281	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	169	Total	C	N	O	S	0	0
			1160	732	226	201	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	k	107	Total	C	N	O	S	0	0
			815	534	149	130	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	l	132	Total	C	N	O	S	0	0
			1040	657	203	175	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	m	131	Total	C	N	O	S	0	0
			961	623	167	169	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	125	Total	C	N	O	S	0	0
			972	612	188	168	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	o	98	Total	C	N	O	S	0	0
			701	450	123	126	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	p	117	Total	C	N	O	S	0	0
			819	512	159	143	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	q	121	Total	C	N	O	S	0	0
			918	564	194	157	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	r	91	Total	C	N	O	S	0	0
			673	416	132	123	2		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	s	88	Total	C	N	O	S	0	0
			665	416	136	110	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	t	87	Total	C	N	O		0	0
			685	437	134	114			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	71	ARG	LYS	conflict	UNP A0A1M6QTP8

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	109	Total	C	N	O		0	0
			779	490	151	138			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	56	ILE	ALA	conflict	UNP A0A1M6QGN9
u	62	GLN	ASN	conflict	UNP A0A1M6QGN9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	80	Total	C	N	O	S	0	0
			638	404	124	107	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	65	Total	C	N	O	S	0	0
			521	342	96	81	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	83	Total	C	N	O	S	0	0
			632	404	118	108	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	y	79	Total	C	N	O	S	0	0
			615	381	129	104	1		

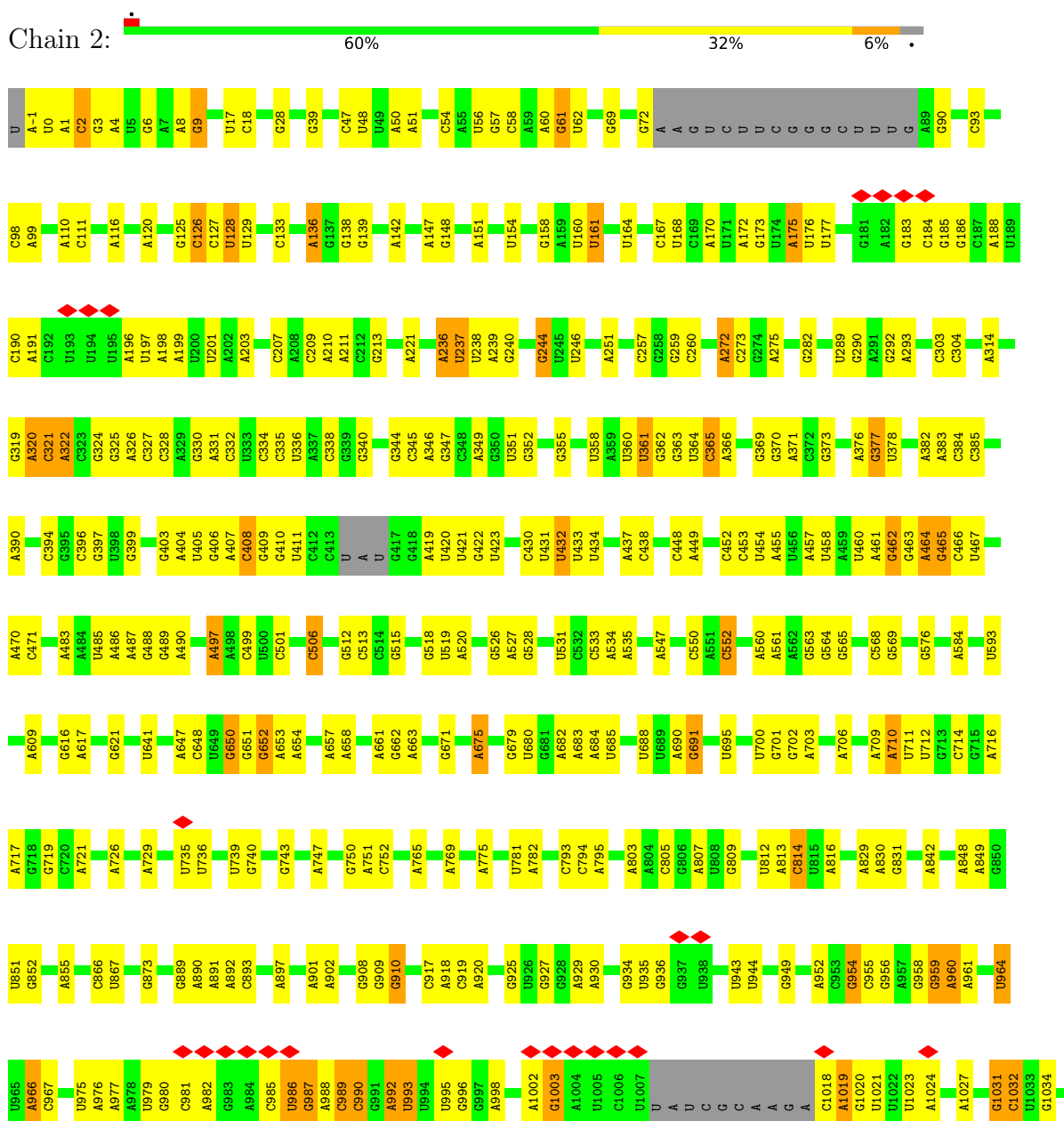
- Molecule 21 is a protein called 30S ribosomal protein S21.

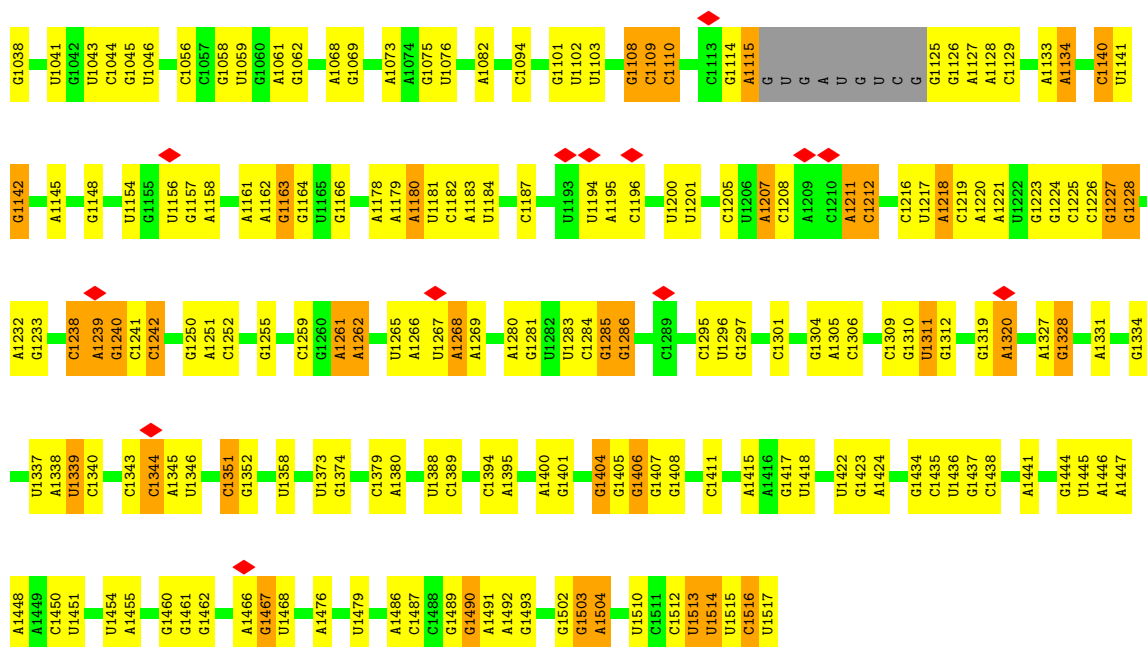
Mol	Chain	Residues	Atoms					AltConf	Trace
21	z	64	Total	C	N	O	S	0	0
			522	331	99	91	1		

3 Residue-property plots

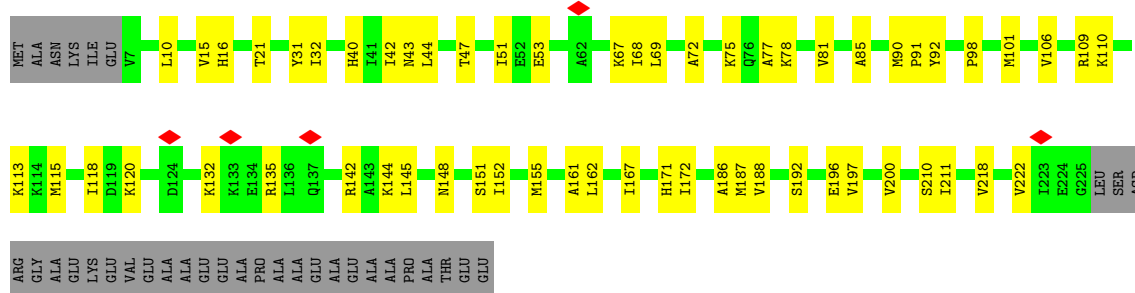
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16 rRNA

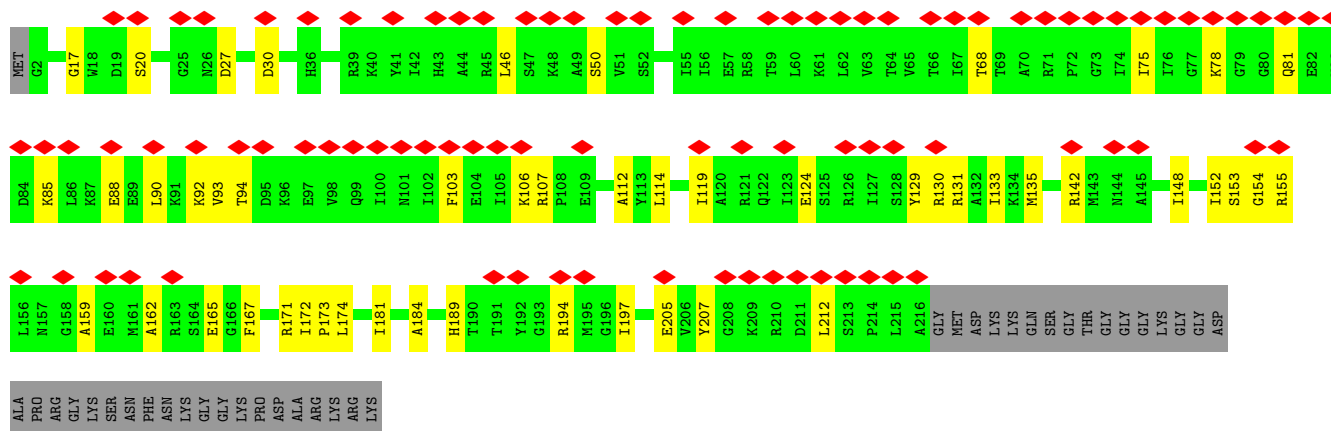





• Molecule 2: Small ribosomal subunit protein uS2

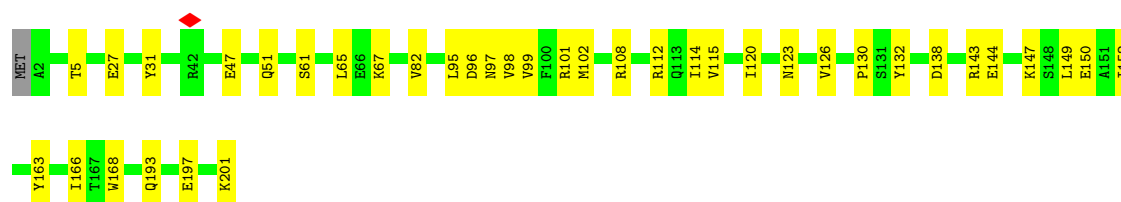


• Molecule 3: 30S ribosomal protein S3




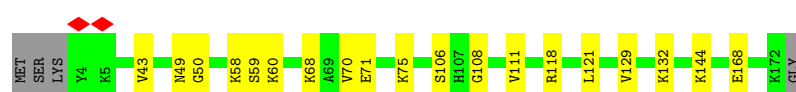
- Molecule 4: 30S ribosomal protein S4

Chain i:  81% 19%



- Molecule 5: 30S ribosomal protein S5

Chain j:  87% 11% .



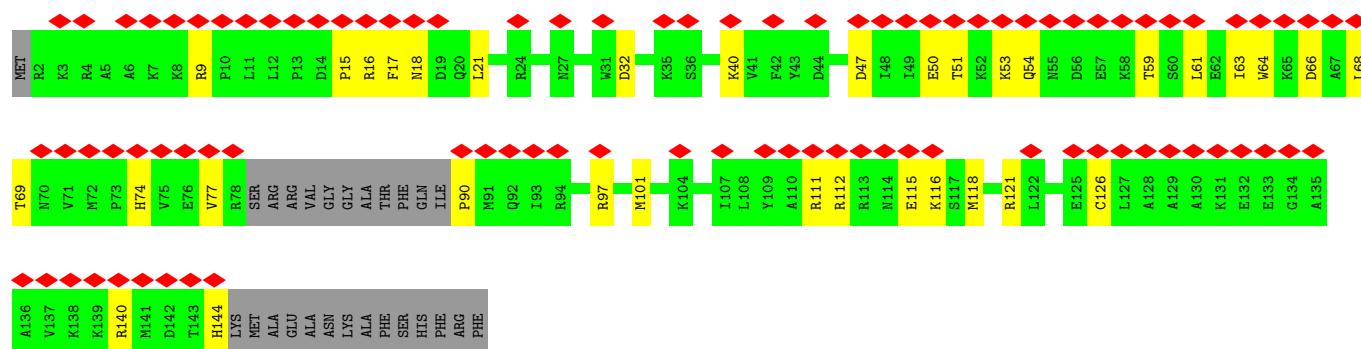
- Molecule 6: 30S ribosomal protein S6

Chain k:  68% 27% 5%



- Molecule 7: 30S ribosomal protein S7

Chain l:  58% 62% 22% 16%




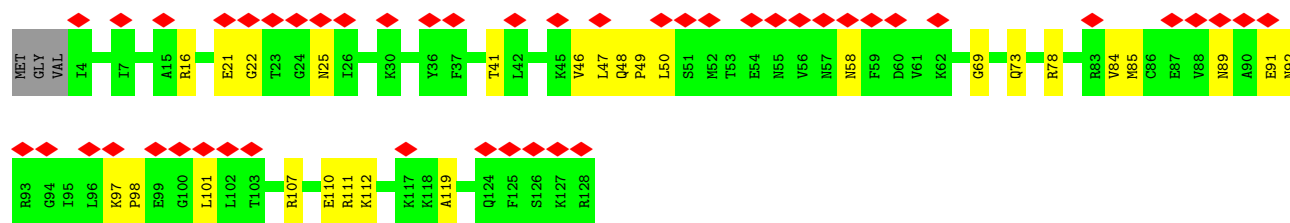
- Molecule 8: 30S ribosomal protein S8

Chain m:  88% 11% .

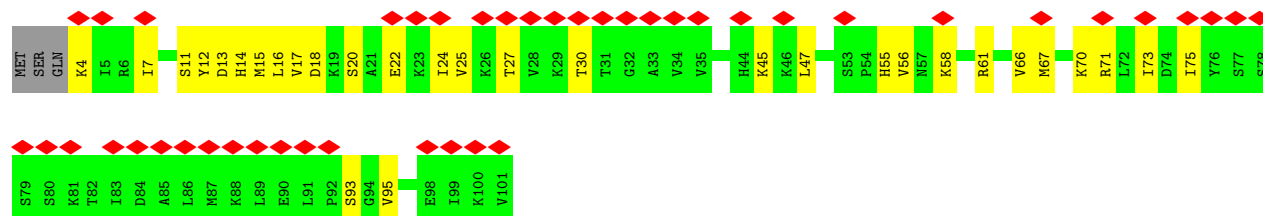
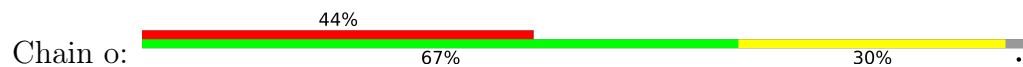


- Molecule 9: 30S ribosomal protein S9

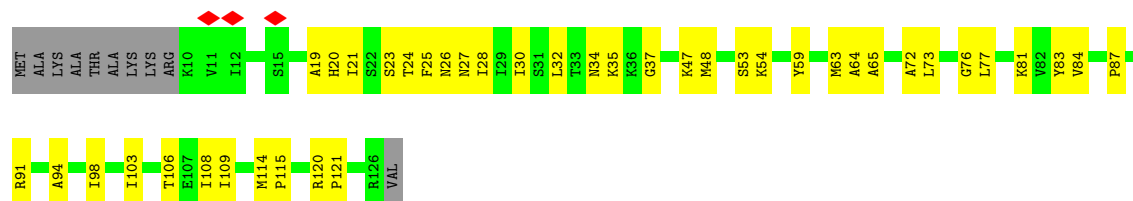
Chain n:  37% 77% 21% .



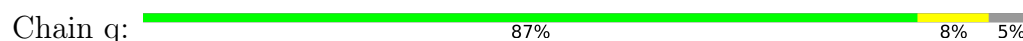
• Molecule 10: 30S ribosomal protein S10



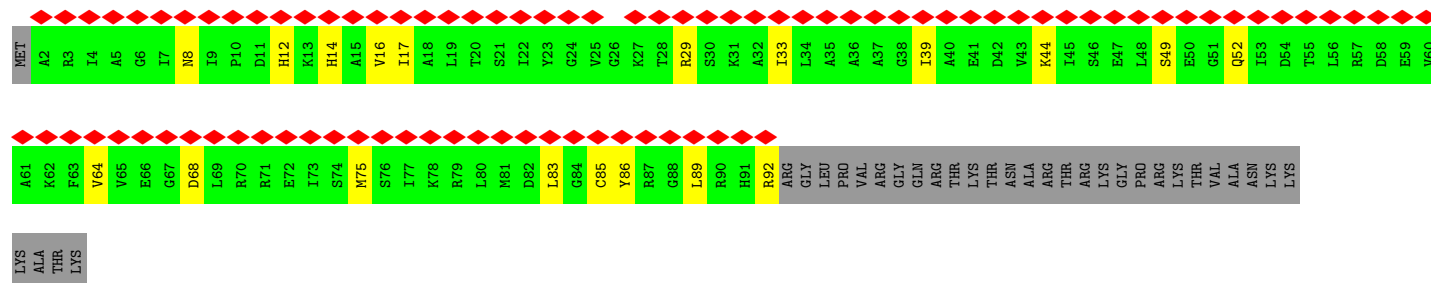
• Molecule 11: 30S ribosomal protein S11



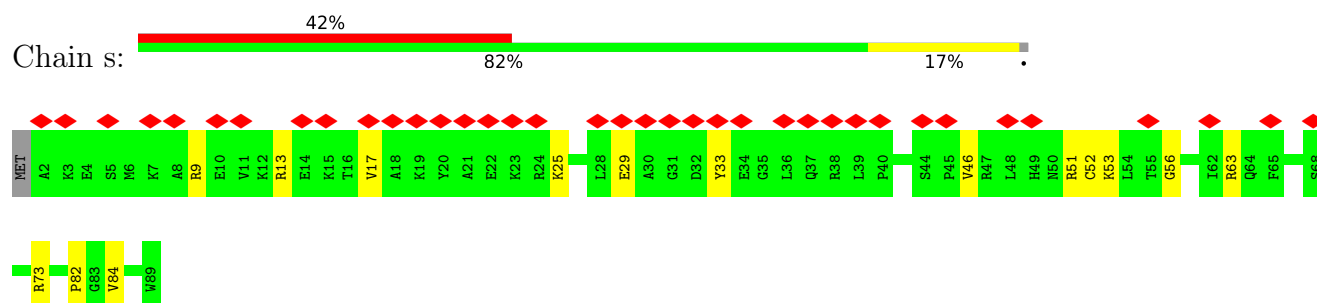
• Molecule 12: 30S ribosomal protein S12



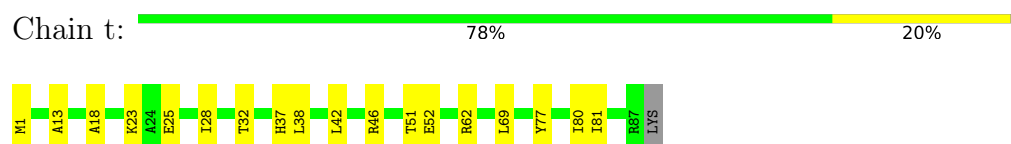
• Molecule 13: 30S ribosomal protein S13



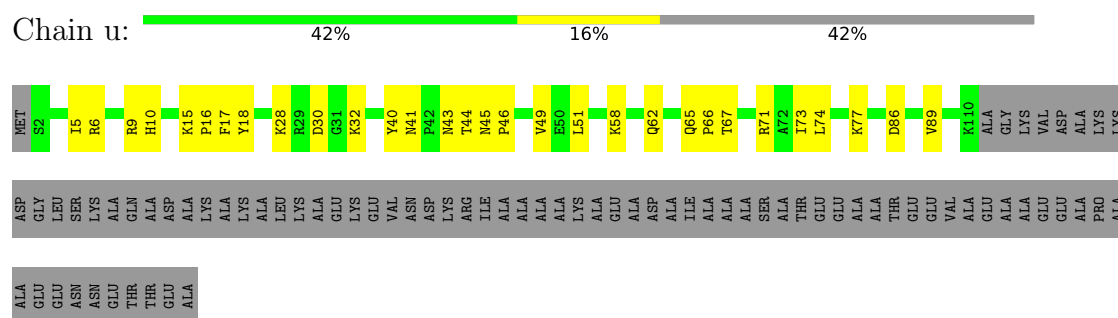
- Molecule 14: 30S ribosomal protein S14



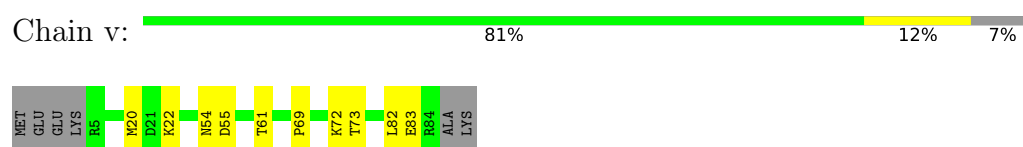
- Molecule 15: 30S ribosomal protein S15



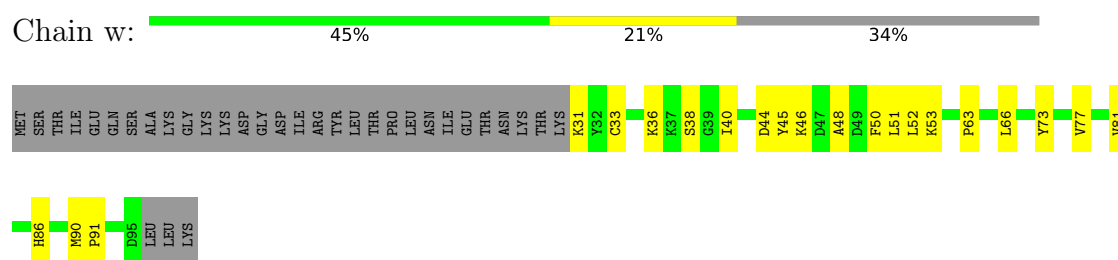
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

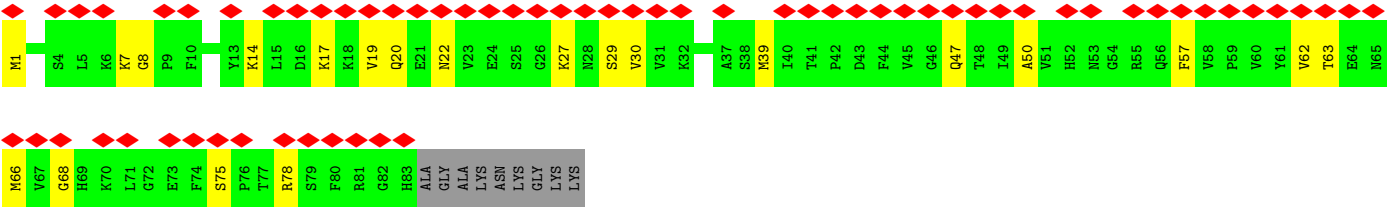


- Molecule 18: 30S ribosomal protein S18

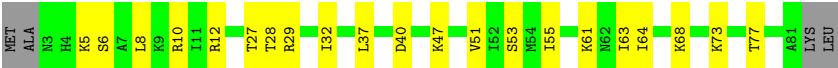


- Molecule 19: 30S ribosomal protein S19





● Molecule 20: 30S ribosomal protein S20



● Molecule 21: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	431185	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.240	Depositor
Minimum map value	-0.111	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	342.0, 342.0, 342.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	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	2	0.23	0/35523	0.30	0/55388
2	H	0.19	0/1692	0.44	0/2288
3	h	0.25	0/1623	0.40	0/2190
4	i	0.18	0/1591	0.31	0/2139
5	j	0.20	0/1175	0.32	0/1589
6	k	0.18	0/834	0.41	0/1129
7	l	0.22	0/1058	0.43	0/1421
8	m	0.20	0/976	0.28	0/1324
9	n	0.25	0/986	0.44	0/1322
10	o	0.25	0/712	0.41	0/973
11	p	0.18	0/833	0.39	0/1130
12	q	0.18	0/931	0.29	0/1254
13	r	0.14	0/679	0.42	0/910
14	s	0.25	0/676	0.35	0/906
15	t	0.22	0/695	0.35	0/935
16	u	0.21	0/795	0.42	0/1081
17	v	0.18	0/646	0.34	0/866
18	w	0.20	0/531	0.36	0/710
19	x	0.21	0/648	0.45	0/876
20	y	0.20	0/619	0.44	0/825
21	z	0.18	0/527	0.42	0/701
All	All	0.22	0/53750	0.33	0/79957

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	31728	0	15978	311	0
2	H	1666	0	1689	41	0
3	h	1600	0	1604	33	0
4	i	1561	0	1562	26	0
5	j	1160	0	1164	14	0
6	k	815	0	780	26	0
7	l	1040	0	1057	23	0
8	m	961	0	978	8	0
9	n	972	0	1005	21	0
10	o	701	0	694	25	0
11	p	819	0	809	29	0
12	q	918	0	962	8	0
13	r	673	0	673	13	0
14	s	665	0	669	12	0
15	t	685	0	690	16	0
16	u	779	0	735	23	0
17	v	638	0	684	7	0
18	w	521	0	553	17	0
19	x	632	0	624	16	0
20	y	615	0	672	21	0
21	z	522	0	573	19	0
All	All	49671	0	34155	639	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 8.

The worst 5 of 639 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)
18:w:38:SER:OG	18:w:40:ILE:CD1	1.75	1.32
18:w:38:SER:OG	18:w:40:ILE:HD12	1.22	1.21
2:H:118:ILE:HD11	2:H:142:ARG:HD3	1.43	1.00
1:2:710:A:H3'	21:z:48:GLN:NE2	1.78	0.99
1:2:955:C:O2'	10:o:56:VAL:HG23	1.76	0.86

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	
2	H	217/254 (85%)	208 (96%)	9 (4%)	0	100	100
3	h	213/252 (84%)	190 (89%)	23 (11%)	0	100	100
4	i	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
5	j	167/173 (96%)	156 (93%)	11 (7%)	0	100	100
6	k	105/113 (93%)	103 (98%)	2 (2%)	0	100	100
7	l	128/158 (81%)	122 (95%)	6 (5%)	0	100	100
8	m	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
9	n	123/128 (96%)	116 (94%)	7 (6%)	0	100	100
10	o	96/101 (95%)	88 (92%)	8 (8%)	0	100	100
11	p	115/127 (91%)	111 (96%)	4 (4%)	0	100	100
12	q	119/127 (94%)	111 (93%)	8 (7%)	0	100	100
13	r	89/124 (72%)	85 (96%)	4 (4%)	0	100	100
14	s	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
15	t	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
16	u	107/188 (57%)	101 (94%)	6 (6%)	0	100	100
17	v	78/86 (91%)	74 (95%)	4 (5%)	0	100	100
18	w	63/98 (64%)	62 (98%)	1 (2%)	0	100	100
19	x	81/92 (88%)	76 (94%)	5 (6%)	0	100	100
20	y	77/83 (93%)	73 (95%)	4 (5%)	0	100	100
21	z	62/64 (97%)	62 (100%)	0	0	100	100
All	All	2338/2678 (87%)	2216 (95%)	122 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	H	171/207 (83%)	171 (100%)	0	100	100
3	h	153/201 (76%)	153 (100%)	0	100	100
4	i	159/173 (92%)	158 (99%)	1 (1%)	78	91
5	j	109/138 (79%)	109 (100%)	0	100	100
6	k	74/101 (73%)	74 (100%)	0	100	100
7	l	103/136 (76%)	103 (100%)	0	100	100
8	m	93/111 (84%)	93 (100%)	0	100	100
9	n	99/107 (92%)	99 (100%)	0	100	100
10	o	72/94 (77%)	72 (100%)	0	100	100
11	p	79/102 (78%)	79 (100%)	0	100	100
12	q	96/107 (90%)	96 (100%)	0	100	100
13	r	64/100 (64%)	64 (100%)	0	100	100
14	s	61/73 (84%)	61 (100%)	0	100	100
15	t	65/79 (82%)	65 (100%)	0	100	100
16	u	67/136 (49%)	67 (100%)	0	100	100
17	v	71/81 (88%)	71 (100%)	0	100	100
18	w	52/87 (60%)	52 (100%)	0	100	100
19	x	66/78 (85%)	66 (100%)	0	100	100
20	y	65/72 (90%)	65 (100%)	0	100	100
21	z	56/56 (100%)	56 (100%)	0	100	100
All	All	1775/2239 (79%)	1774 (100%)	1 (0%)	87	96

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

Mol	Chain	Res	Type
4	i	31	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13

such sidechains are listed below:

Mol	Chain	Res	Type
11	p	99	HIS
11	p	116	HIS
21	z	48	GLN
18	w	74	GLN
19	x	52	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1476/1520 (97%)	257 (17%)	21 (1%)

5 of 257 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	G
1	2	4	A
1	2	9	G
1	2	39	G
1	2	47	C

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1225	C
1	2	1280	A
1	2	1379	C
1	2	1285	G
1	2	1238	C

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.

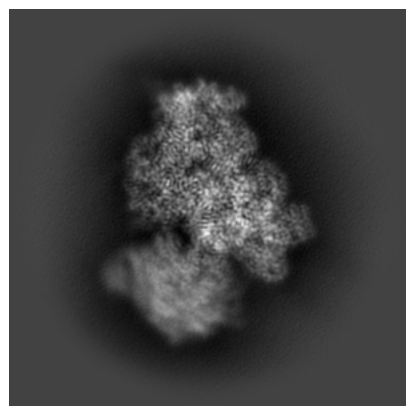
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71002. These allow visual inspection of the internal detail of the map and identification of artifacts.

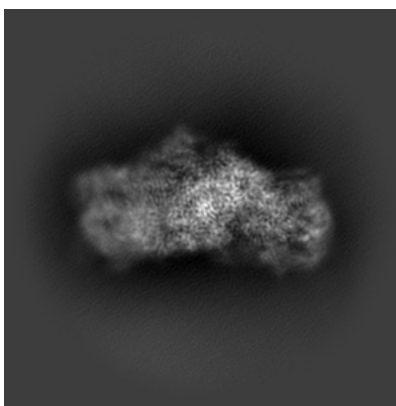
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

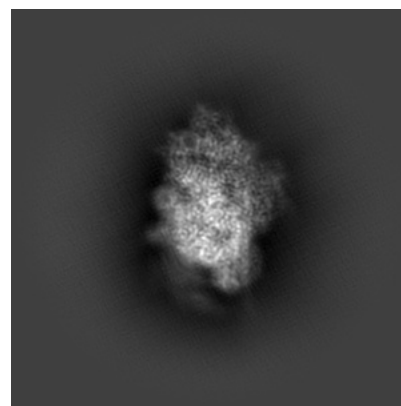
6.1.1 Primary map



X

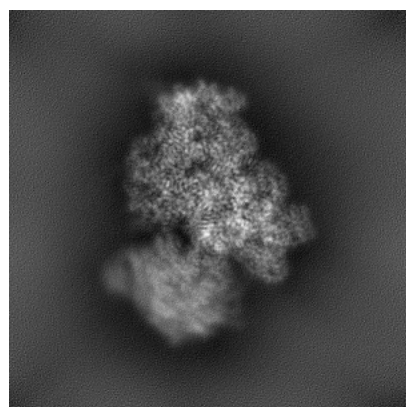


Y

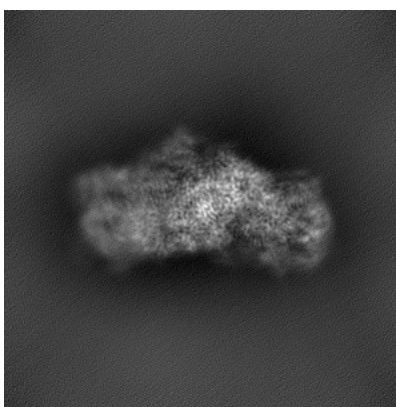


Z

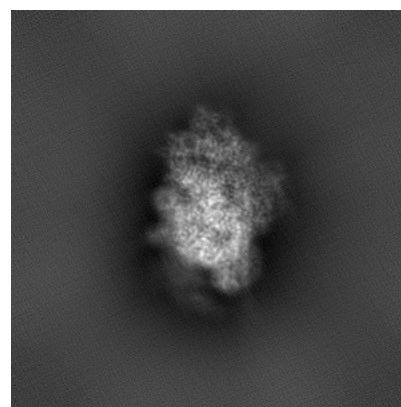
6.1.2 Raw map



X



Y

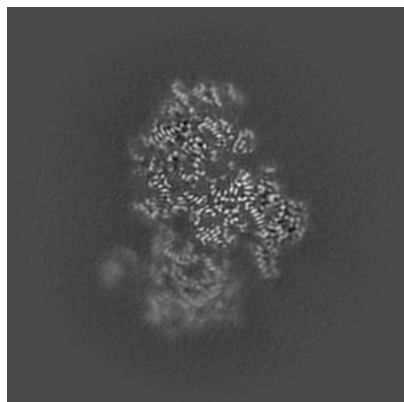


Z

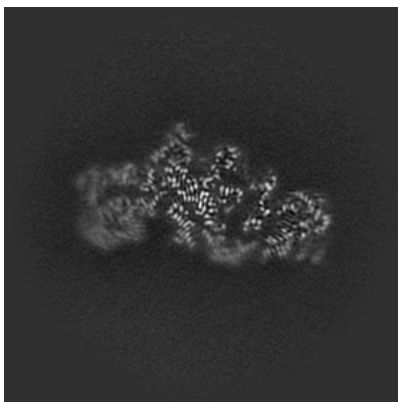
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

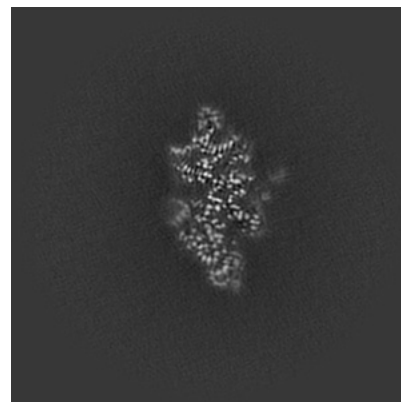
6.2.1 Primary map



X Index: 200

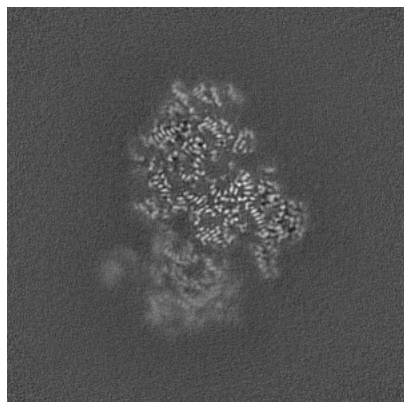


Y Index: 200

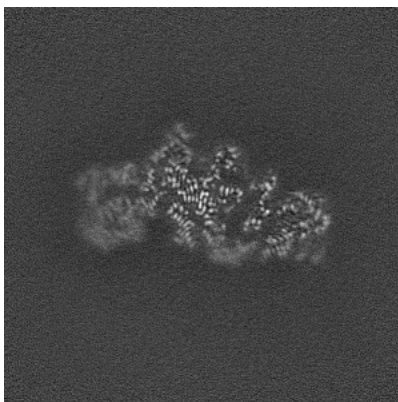


Z Index: 200

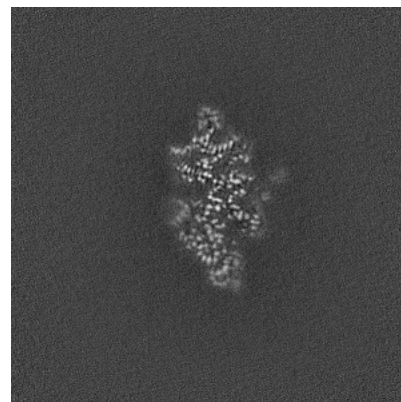
6.2.2 Raw map



X Index: 200



Y Index: 200

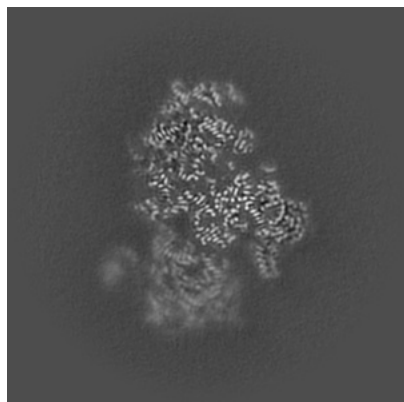


Z Index: 200

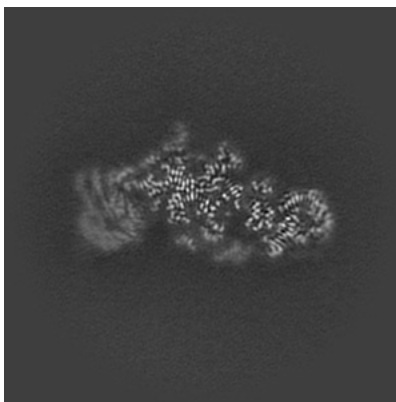
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

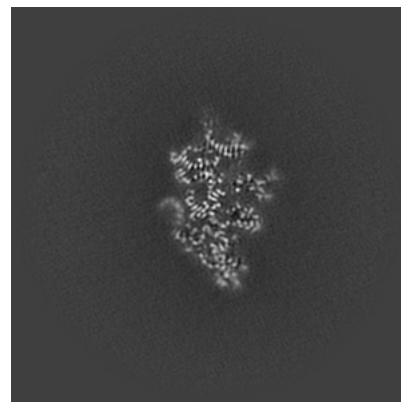
6.3.1 Primary map



X Index: 199

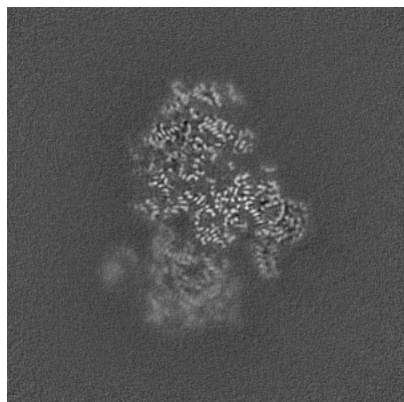


Y Index: 195

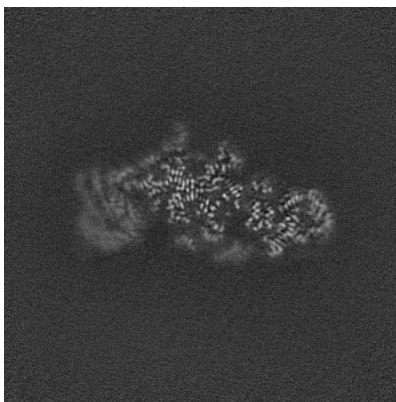


Z Index: 206

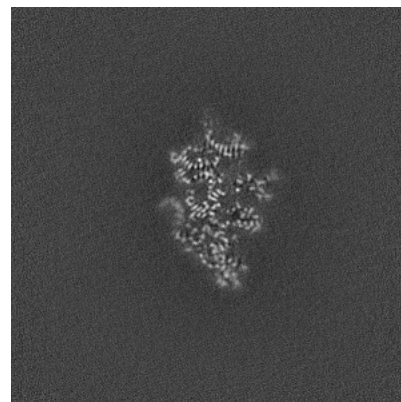
6.3.2 Raw map



X Index: 199



Y Index: 195

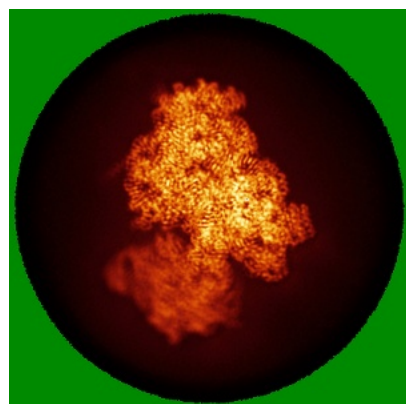


Z Index: 206

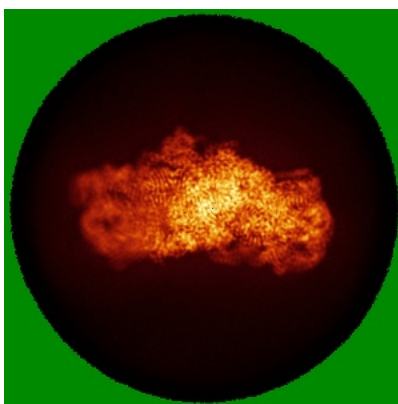
The images above show the largest variance slices of the map in three orthogonal directions.

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

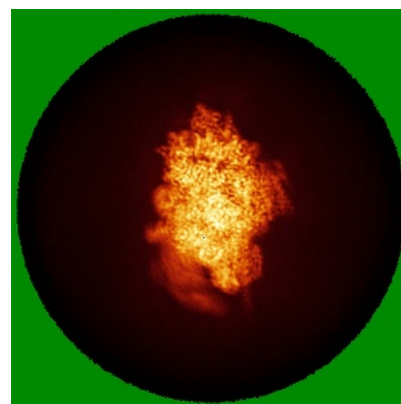
6.4.1 Primary map



X

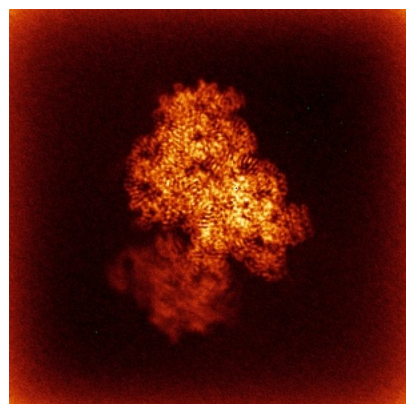


Y

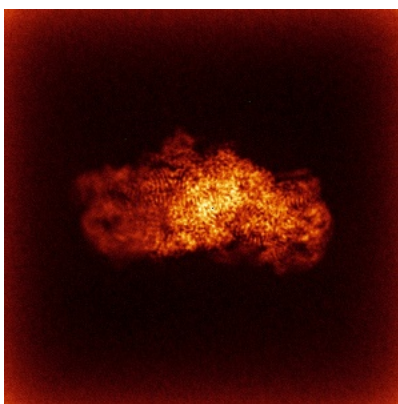


Z

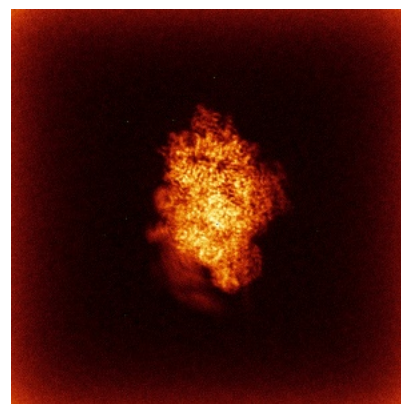
6.4.2 Raw map



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](#)

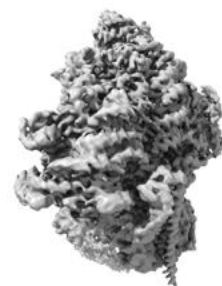
6.5.1 Primary map



X



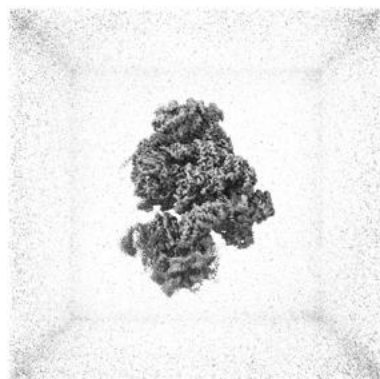
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

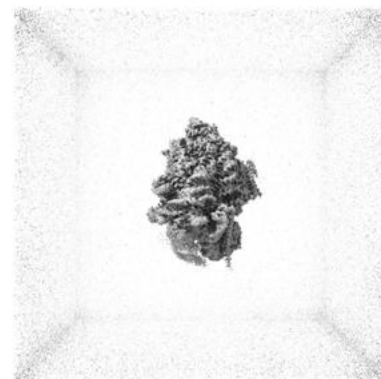
6.5.2 Raw map



X



Y



Z

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.

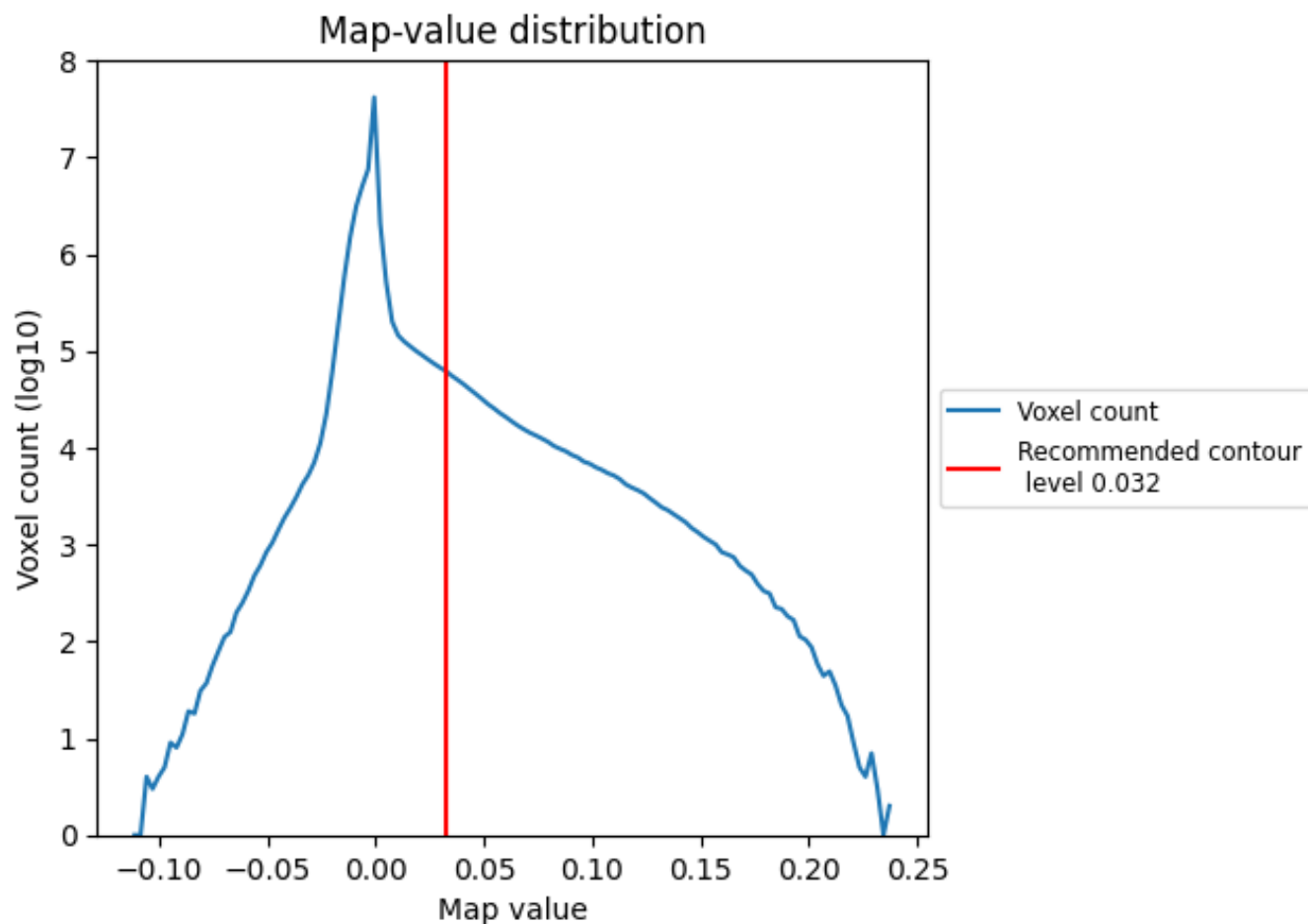
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

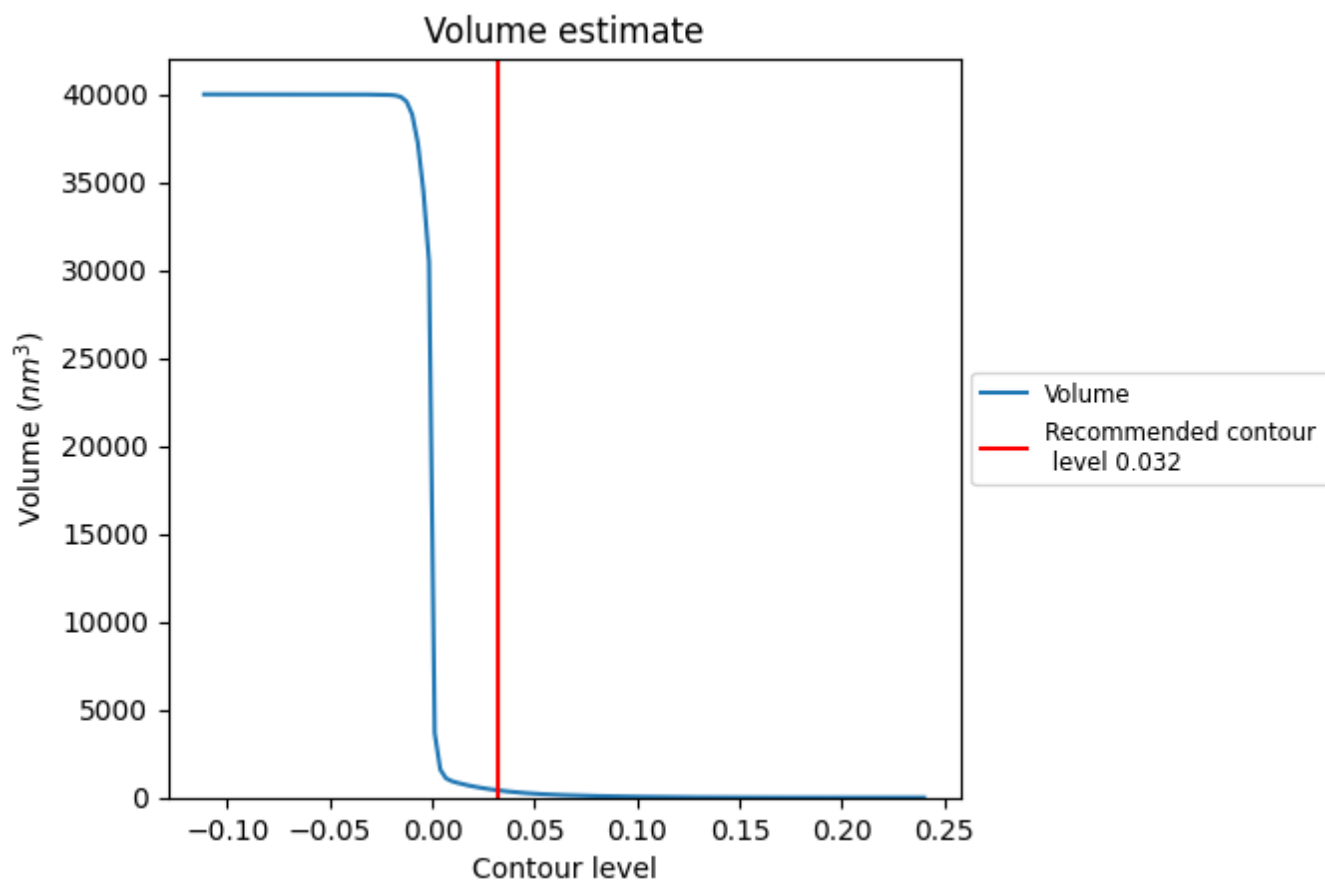
This section contains the results of statistical analysis of the map.

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.

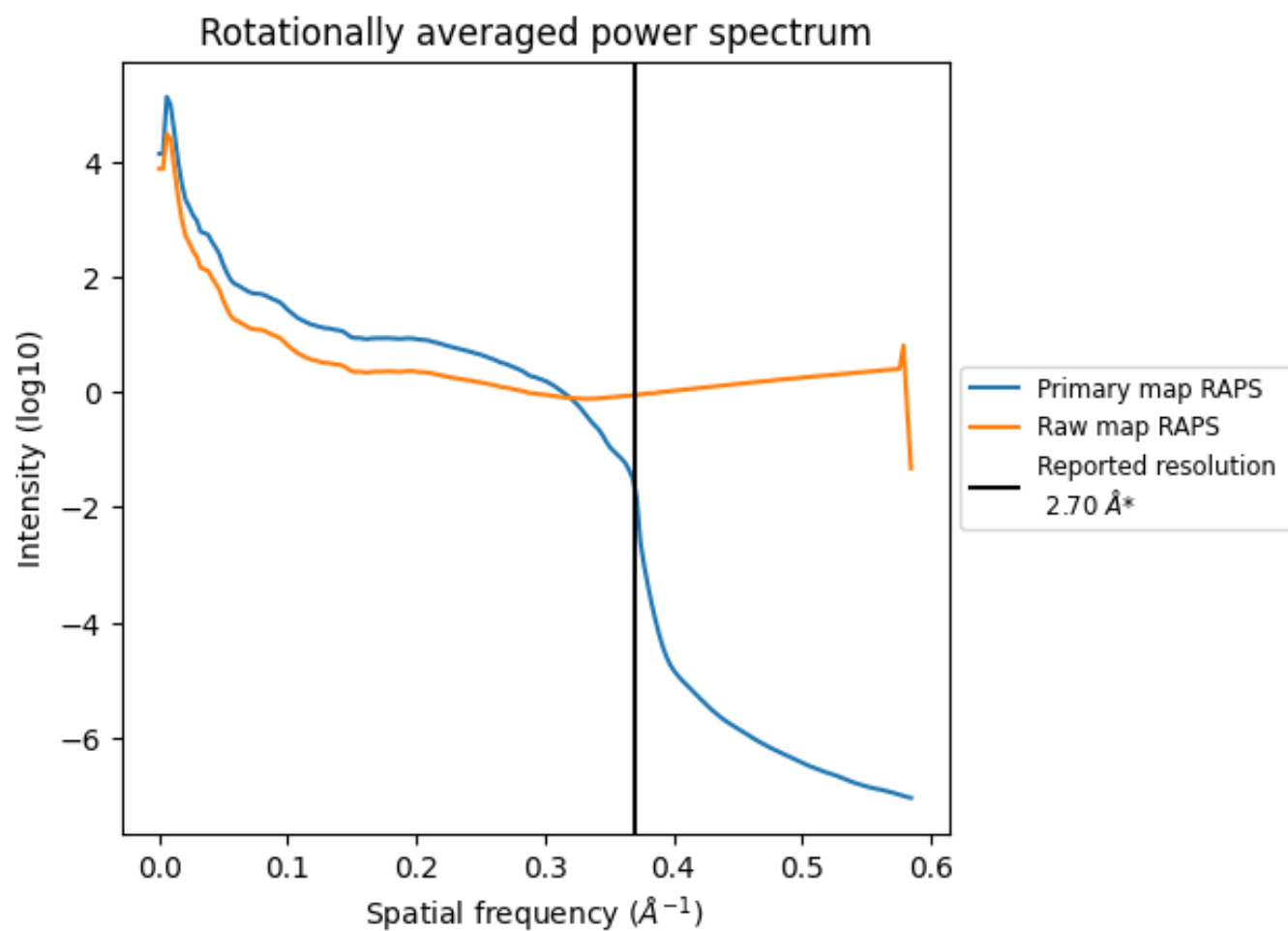
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 414 nm^3 ; this corresponds to an approximate mass of 374 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 ⓘ

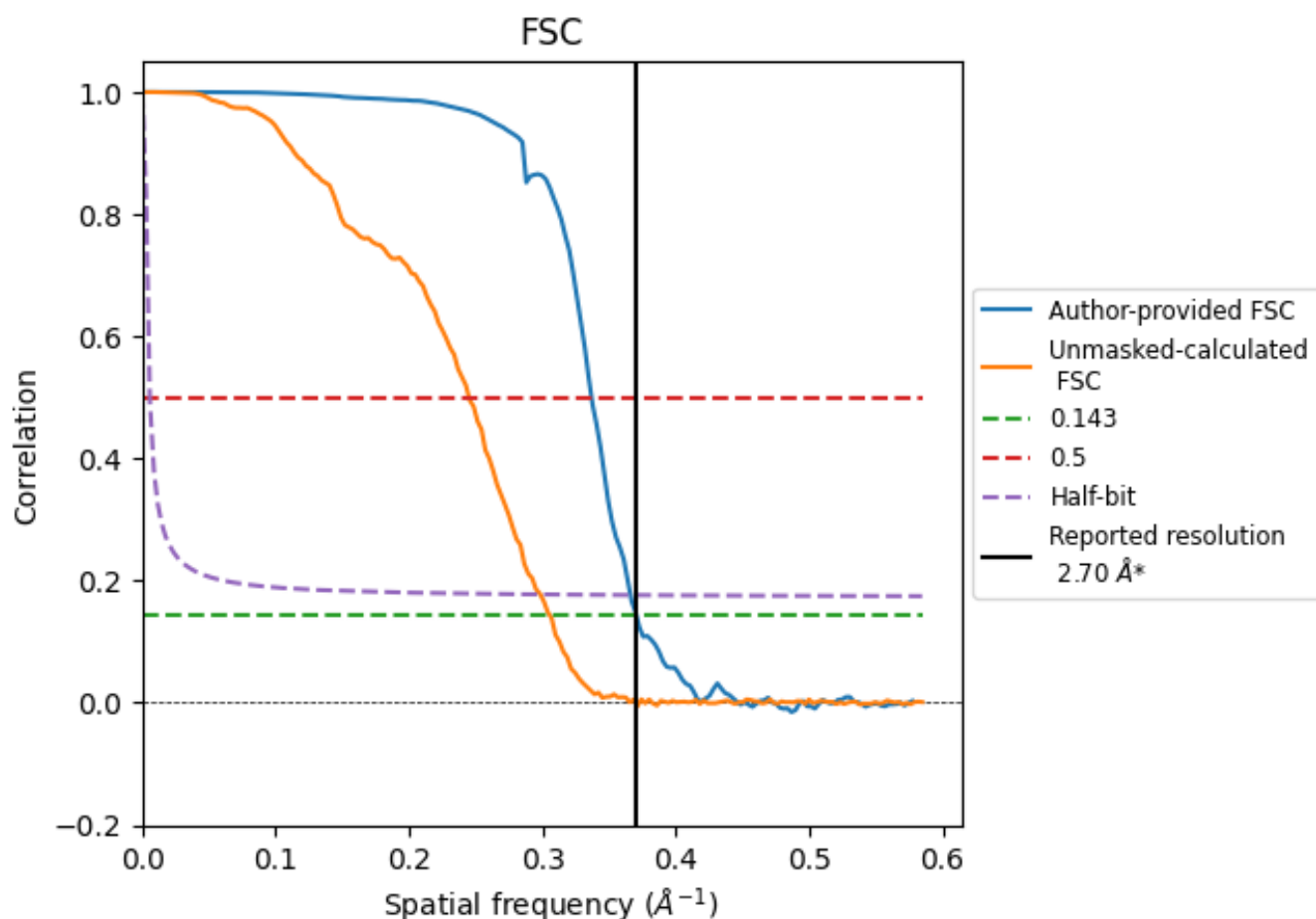


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

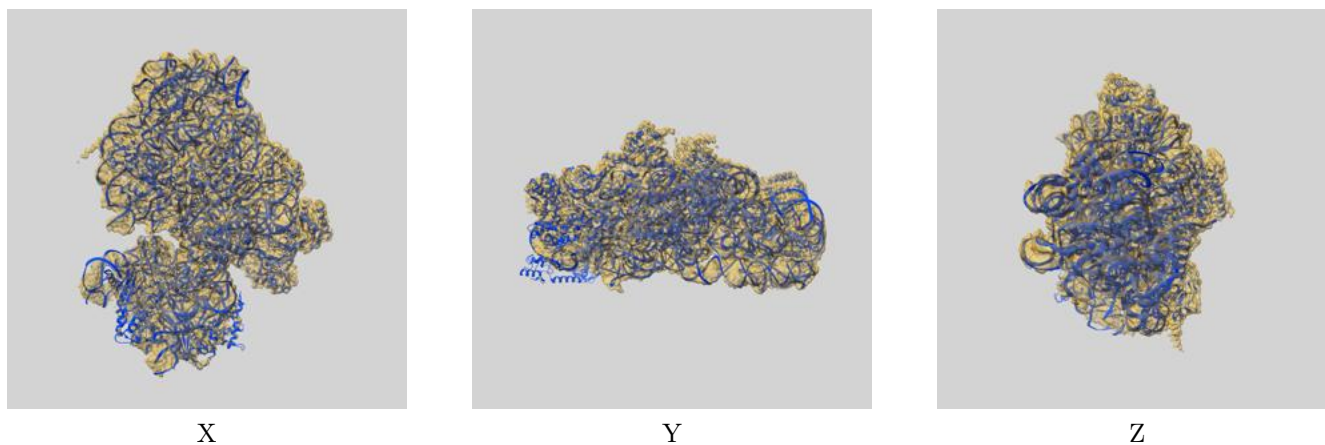
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	2.97	2.73
Unmasked-calculated*	3.27	4.08	3.35

*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 3.27 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

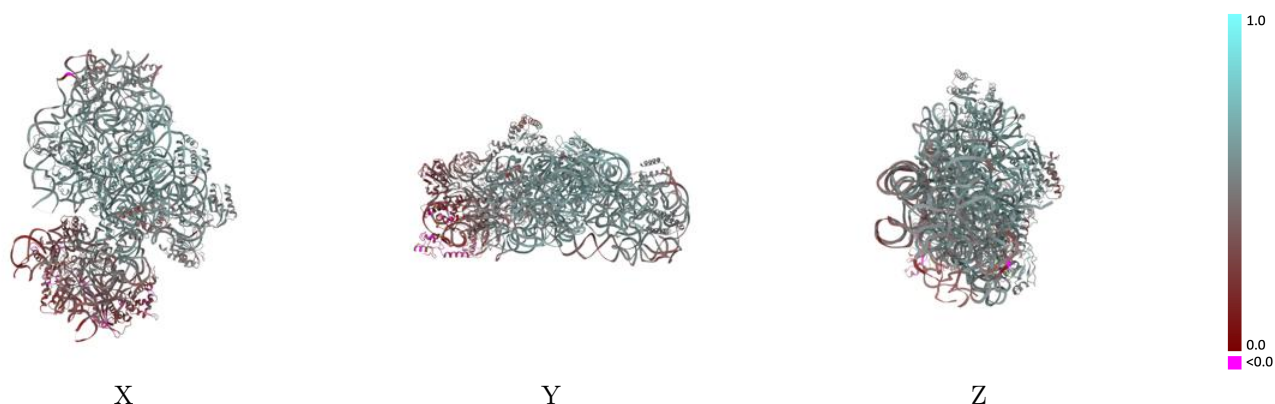
This section contains information regarding the fit between EMDB map EMD-71002 and PDB model 9OY8. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



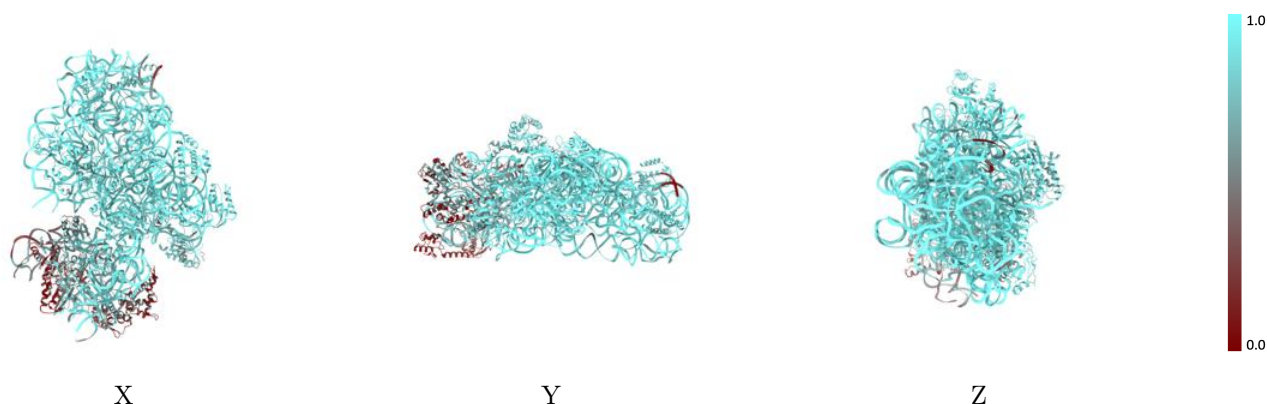
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



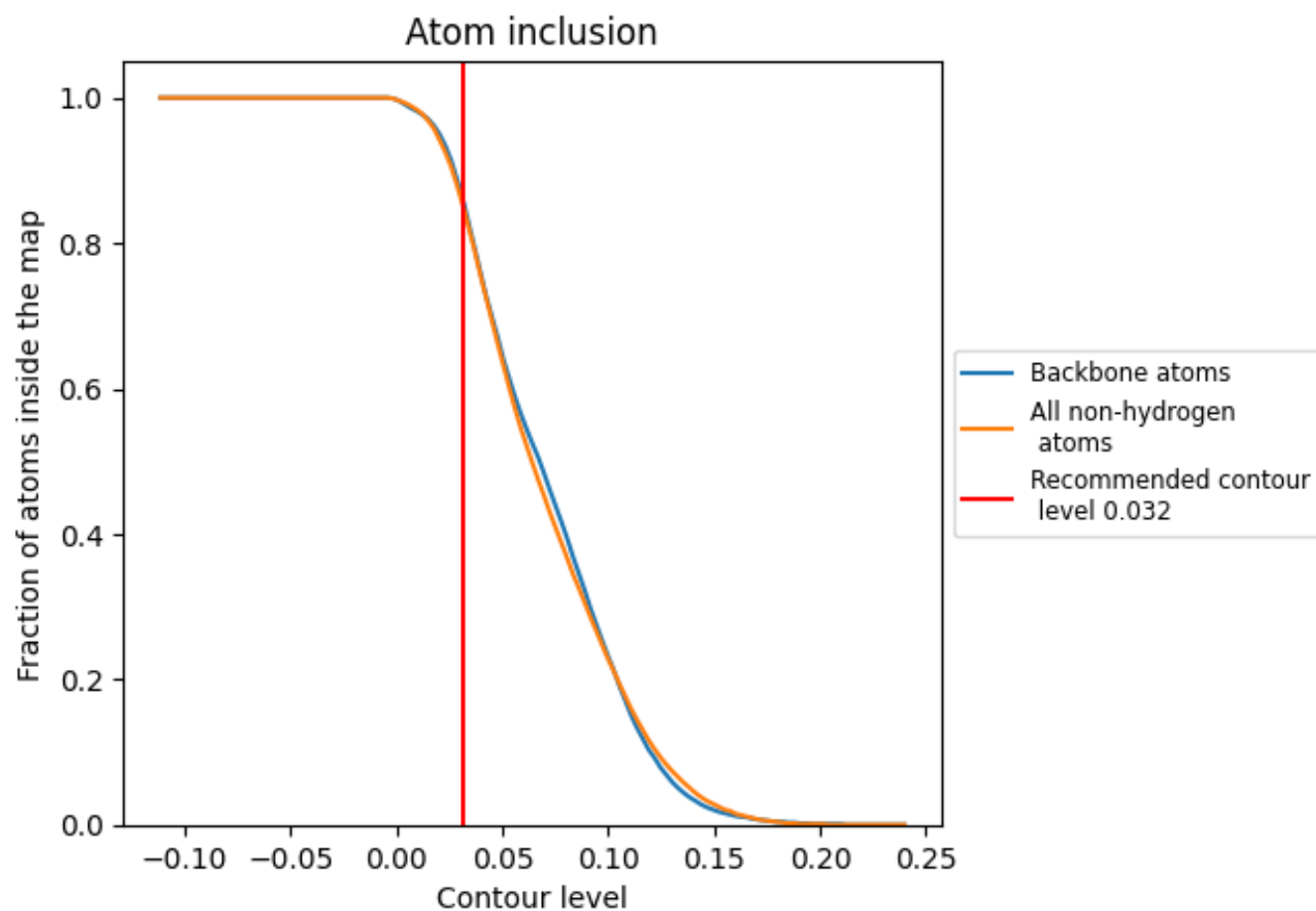
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.032).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4700
2	 0.9160	 0.4850
H	 0.8180	 0.4680
h	 0.4710	 0.3590
i	 0.9090	 0.5420
j	 0.9620	 0.5980
k	 0.9320	 0.5180
l	 0.2570	 0.2210
m	 0.9770	 0.6030
n	 0.4950	 0.3100
o	 0.4330	 0.3400
p	 0.8800	 0.4980
q	 0.9390	 0.5800
r	 0.0050	 0.0610
s	 0.4770	 0.2900
t	 0.9650	 0.5710
u	 0.9590	 0.5200
v	 0.9560	 0.5880
w	 0.9780	 0.5490
x	 0.2060	 0.1580
y	 0.9050	 0.4920
z	 0.7510	 0.5020

