



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 04:03 PM UTC

PDB ID : 9QJC / pdb_00009qjc
EMDB ID : EMD-53201
Title : Yeast pre-60S Domain II intermediate
Authors : Grundmann, L.; Gerhalter, M.; Prattes, M.; Grishkovskaya, I.; Kotisch, H.;
Haselbach, D.; Bergler, H.
Deposited on : 2025-03-19
Resolution : 3.20 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

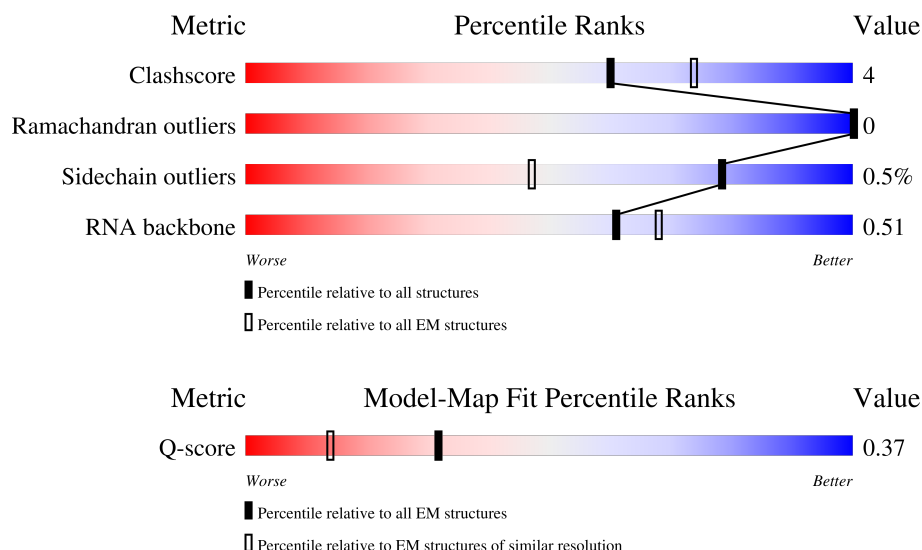
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



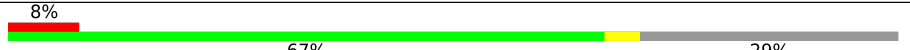
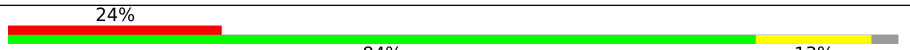
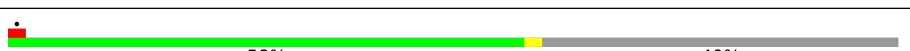
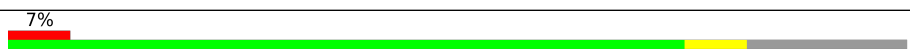
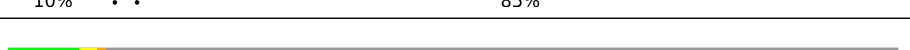
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	5	1025	
2	6	710	
3	C	362	

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Mol	Chain	Length	Quality of chain
4	D	306	
5	E	176	
6	F	244	
7	M	138	
8	O	199	
9	Q	186	
10	S	172	
11	e	130	
12	f	107	
13	z	278	
14	1	3396	
15	2	159	
16	B	685	

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 64675 atoms, of which 29858 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 Ribosome biogenesis protein MAK21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	5	530	Total	C	H	N	O	S	0	0
			8728	2806	4396	716	803	7		

- Molecule 2 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	6	514	Total	C	H	N	O	S	0	0
			8460	2678	4304	704	759	15		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	283	Total	C	H	N	O		
			4461	1371	2295	404	391	0	0

- Molecule 4 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	130	Total	C	H	N	O	S	0	0
			2179	685	1093	202	191	8		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	143	Total	C	H	N	O	S	0	0
			2356	738	1219	202	196	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	242	Total	C	H	N	O	S	0	0
			3980	1249	2038	352	340	1		

- Molecule 7 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	M	115	Total	C	H	N	O	S	0	0
			1859	573	967	169	148	2		

- Molecule 8 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	O	183	Total	C	H	N	O	S	0	0
			2984	930	1543	264	246	1		

- Molecule 9 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Q	132	Total	C	H	N	O	S	0	0
			2112	648	1097	191	175	1		

- Molecule 10 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	S	166	Total	C	H	N	O	S	0	0
			2833	895	1439	261	235	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	e	78	Total	C	H	N	O	S	0	0
			1244	382	646	110	105	1		

- Molecule 12 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	f	88	Total	C	H	N	O	S	0	0
			1437	454	730	134	118	1		

- Molecule 13 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	z	243	Total	C	H	N	O	S	0	0
			4155	1334	2097	353	366	5		

- Molecule 14 is a RNA chain called 25S ribosomal RNA.

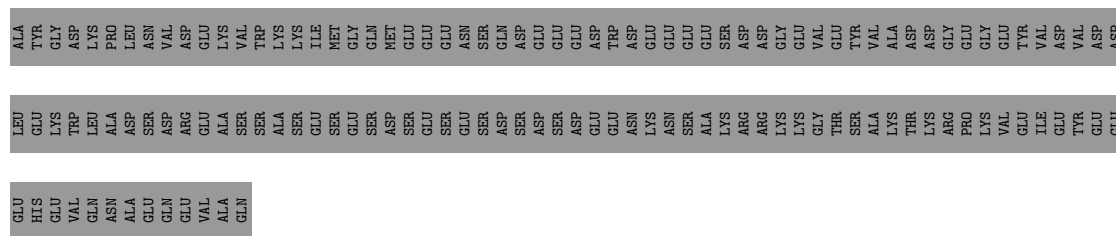
Mol	Chain	Residues	Atoms						AltConf	Trace
14	1	509	Total	C	H	N	O	P	0	0
			16395	4869	5480	1984	3553	509		

- Molecule 15 is a RNA chain called 5.8S ribosomal RNA.

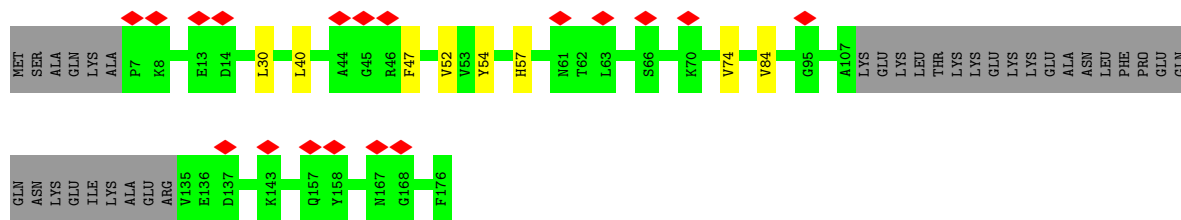
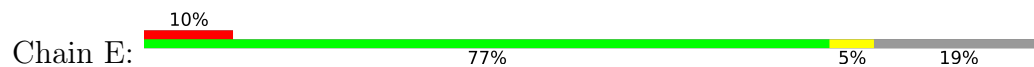
Mol	Chain	Residues	Atoms						AltConf	Trace
15	2	17	Total	C	H	N	O	P	0	0
			544	163	185	68	112	16		

- Molecule 16 is a protein called Nucleolar protein 4.

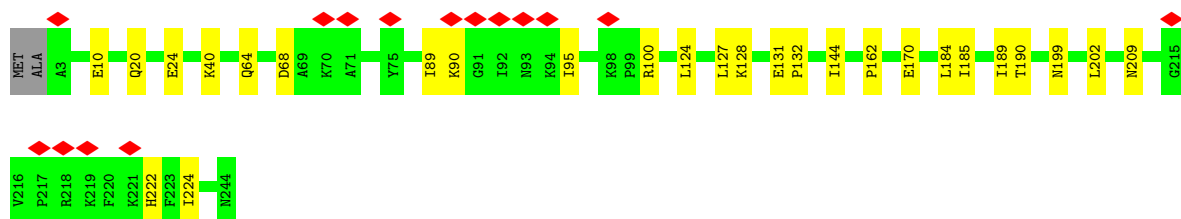
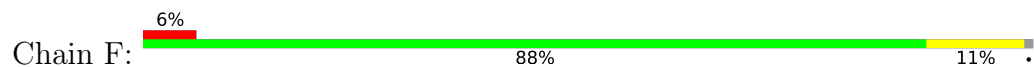
Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	123	Total	C	H	N	O	0	0
			948	373	329	123	123		



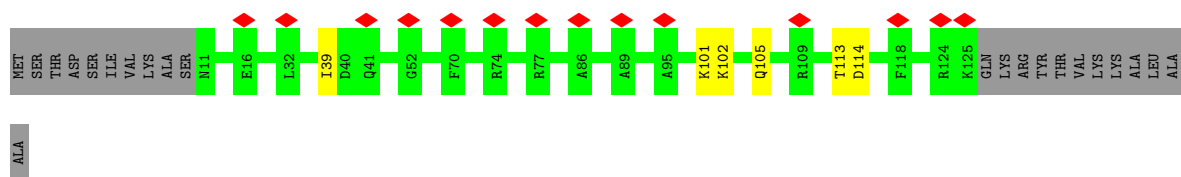
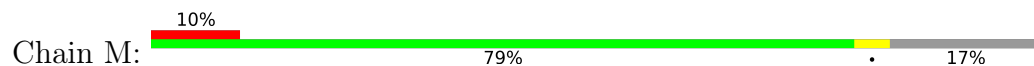
- Molecule 5: 60S ribosomal protein L6-A



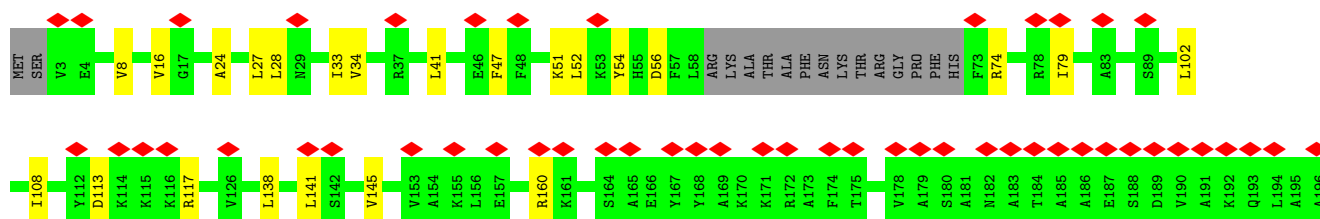
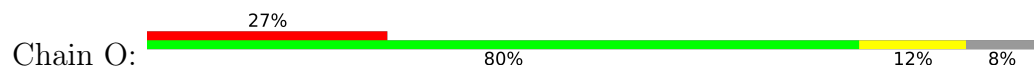
- Molecule 6: 60S ribosomal protein L7-A

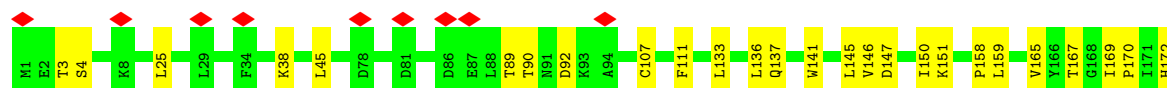


- Molecule 7: 60S ribosomal protein L14-A



- Molecule 8: 60S ribosomal protein L16-A

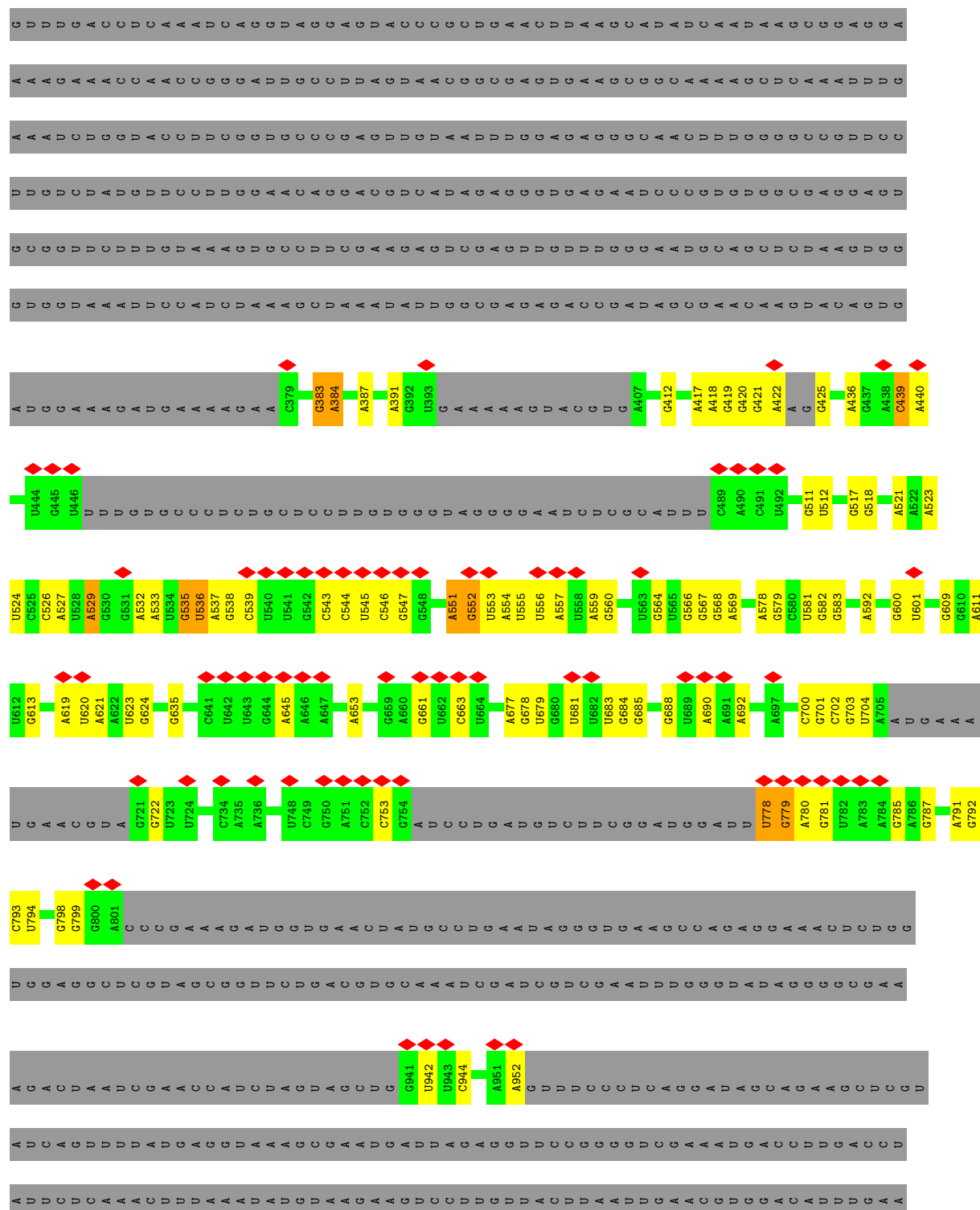






• Molecule 14: 25S ribosomal RNA

Chain 1: 10% . . . 85%



G	U	U	U	C	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U</
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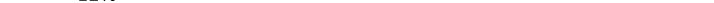
[illegible]

- Molecule 15: 5.8S ribosomal RNA

Chain 2: 8% .. 89%

Sequence logo for the 5' region of the 16S rRNA gene. The y-axis represents information content in bits, with a scale from 0 to 2. The x-axis shows nucleotide positions from 1 to 16. The logo is divided into three main sections: positions 1-4 (A, G, A, A), positions 5-10 (U, G, C, C, G, G), and positions 11-16 (U, U, U, U, U, U). The most conserved positions are 1, 2, and 3, all showing a strong preference for Adenine (A). Position 4 shows a strong preference for Guanine (G). Positions 5-10 show a mix of conserved nucleotides, with U and G being prominent. Positions 11-16 show a strong preference for Uracil (U).

- Molecule 16: Nucleolar protein 4

Chain B: 

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54106	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.420	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.0981	Depositor
Map size (Å)	402.03, 402.03, 402.03	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9137045, 0.9137045, 0.9137045	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	5	0.19	0/4423	0.34	0/5985
2	6	0.22	0/4236	0.37	0/5720
3	C	0.20	0/2202	0.33	0/2985
4	D	0.26	0/1110	0.36	0/1493
5	E	0.15	0/1158	0.29	0/1558
6	F	0.21	0/1980	0.34	0/2661
7	M	0.14	0/906	0.31	0/1222
8	O	0.15	0/1466	0.30	0/1966
9	Q	0.22	0/1030	0.31	0/1393
10	S	0.14	0/1427	0.33	0/1916
11	e	0.24	0/607	0.31	0/816
12	f	0.22	0/722	0.32	0/971
13	z	0.20	0/2104	0.33	0/2832
14	1	0.19	0/12212	0.29	0/19028
15	2	0.26	0/402	0.35	0/624
16	B	0.15	0/624	0.34	0/872
All	All	0.20	0/36609	0.32	0/52042

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	5	4332	4396	4392	48	0
2	6	4156	4304	4302	57	0
3	C	2166	2295	2291	25	0
4	D	1086	1093	1092	7	0
5	E	1137	1219	1218	5	0
6	F	1942	2038	2037	17	0
7	M	892	967	966	5	0
8	O	1441	1543	1541	20	0
9	Q	1015	1097	1096	6	0
10	S	1394	1439	1438	17	0
11	e	598	646	645	1	0
12	f	707	730	727	6	0
13	z	2058	2097	2096	22	0
14	1	10915	5480	5489	61	0
15	2	359	185	186	3	0
16	B	619	329	328	0	0
All	All	34817	29858	29844	289	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 4.

The worst 5 of 289 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S:77:VAL:HG13	10:S:126:VAL:HG22	1.59	0.85
8:O:24:ALA:O	8:O:28:LEU:HD12	1.80	0.82
2:6:492:PHE:CD1	2:6:522:ILE:HD11	2.18	0.79
8:O:54:TYR:HD2	8:O:141:LEU:HD21	1.52	0.75
10:S:31:ALA:HB1	10:S:36:ILE:HG23	1.67	0.75

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	5	522/1025 (51%)	504 (97%)	18 (3%)	0	100	100
2	6	510/710 (72%)	494 (97%)	16 (3%)	0	100	100
3	C	279/362 (77%)	265 (95%)	14 (5%)	0	100	100
4	D	128/306 (42%)	118 (92%)	10 (8%)	0	100	100
5	E	139/176 (79%)	131 (94%)	8 (6%)	0	100	100
6	F	240/244 (98%)	230 (96%)	10 (4%)	0	100	100
7	M	113/138 (82%)	109 (96%)	4 (4%)	0	100	100
8	O	179/199 (90%)	176 (98%)	3 (2%)	0	100	100
9	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
10	S	164/172 (95%)	158 (96%)	6 (4%)	0	100	100
11	e	76/130 (58%)	73 (96%)	3 (4%)	0	100	100
12	f	82/107 (77%)	81 (99%)	1 (1%)	0	100	100
13	z	239/278 (86%)	229 (96%)	10 (4%)	0	100	100
16	B	121/685 (18%)	116 (96%)	5 (4%)	0	100	100
All	All	2922/4718 (62%)	2812 (96%)	110 (4%)	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	
1	5	489/932 (52%)	487 (100%)	2 (0%)	84	86
2	6	469/647 (72%)	466 (99%)	3 (1%)	78	84
3	C	234/289 (81%)	232 (99%)	2 (1%)	70	81
4	D	120/274 (44%)	119 (99%)	1 (1%)	73	82
5	E	124/153 (81%)	124 (100%)	0	100	100
6	F	204/205 (100%)	204 (100%)	0	100	100
7	M	90/109 (83%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	O	149/162 (92%)	149 (100%)	0	100	100
9	Q	108/151 (72%)	108 (100%)	0	100	100
10	S	150/156 (96%)	149 (99%)	1 (1%)	76	83
11	e	64/111 (58%)	64 (100%)	0	100	100
12	f	75/91 (82%)	74 (99%)	1 (1%)	61	78
13	z	225/257 (88%)	222 (99%)	3 (1%)	61	78
16	B	6/597 (1%)	6 (100%)	0	100	100
All	All	2507/4134 (61%)	2494 (100%)	13 (0%)	78	85

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	127	LEU
10	S	8	GLN
13	z	236	GLU
13	z	167	THR
13	z	218	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
12	f	42	GLN
12	f	39	GLN
3	C	322	GLN
10	S	68	HIS
3	C	291	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	1	501/3396 (14%)	88 (17%)	5 (0%)
15	2	16/159 (10%)	1 (6%)	0
All	All	517/3555 (14%)	89 (17%)	5 (0%)

5 of 89 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	1	383	G
14	1	384	A
14	1	387	A
14	1	391	A
14	1	421	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	1	535	G
14	1	551	A
14	1	778	U
14	1	1189	C
14	1	1431	G

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.

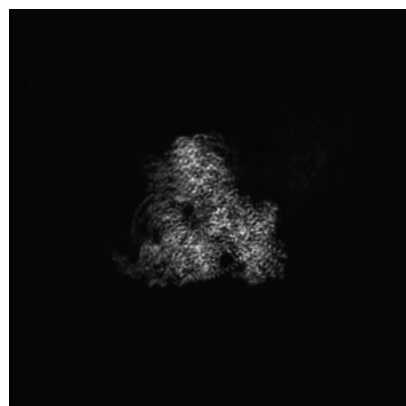
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53201. These allow visual inspection of the internal detail of the map and identification of artifacts.

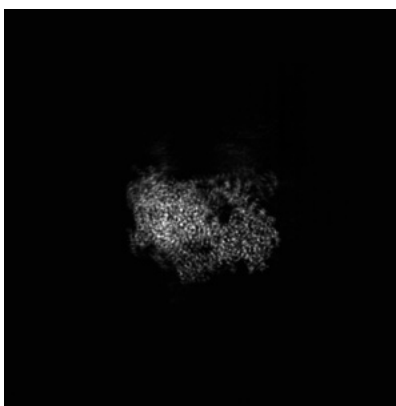
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

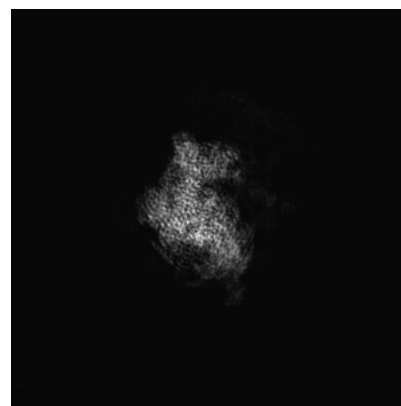
6.1.1 Primary map



X

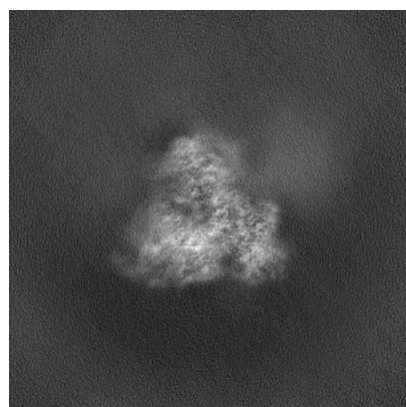


Y

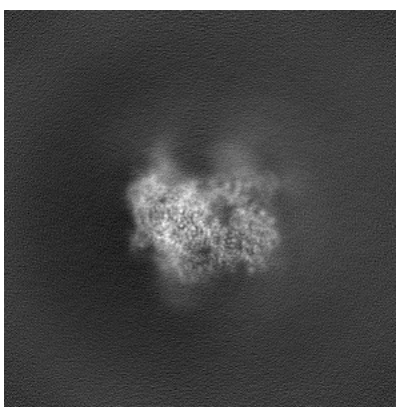


Z

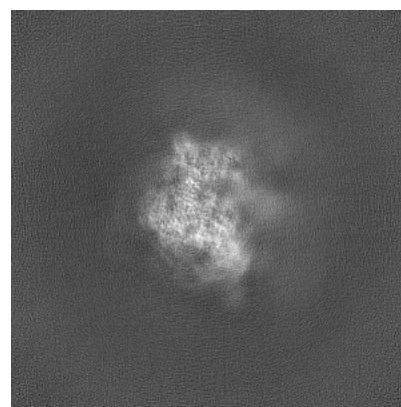
6.1.2 Raw map



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: 220

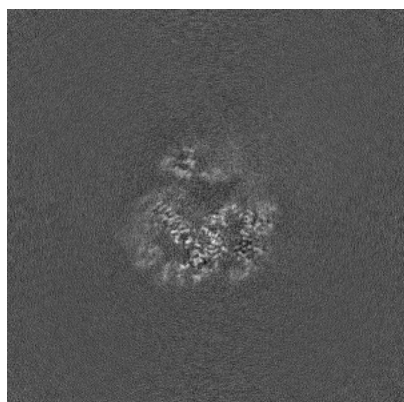


Y Index: 220

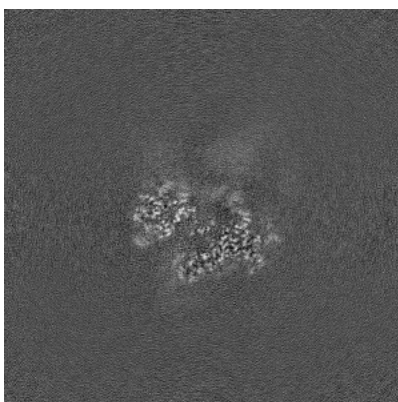


Z Index: 220

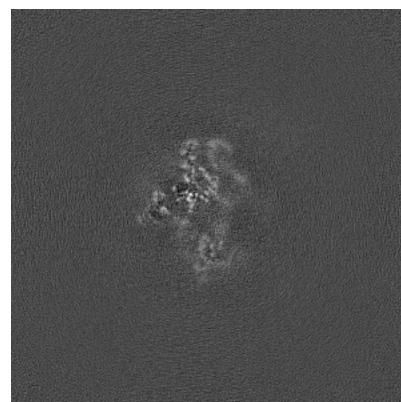
6.2.2 Raw map



X Index: 220



Y Index: 220



Z Index: 220

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: 203

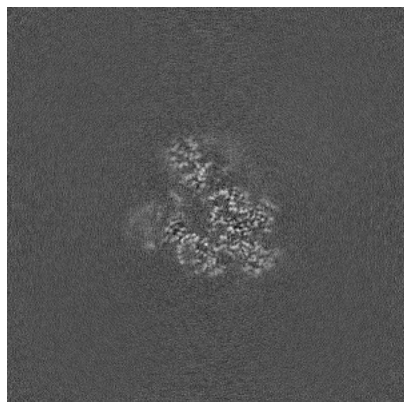


Y Index: 199

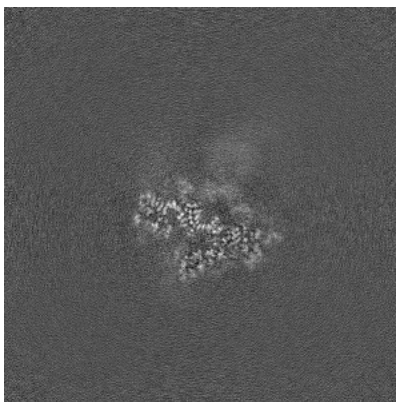


Z Index: 178

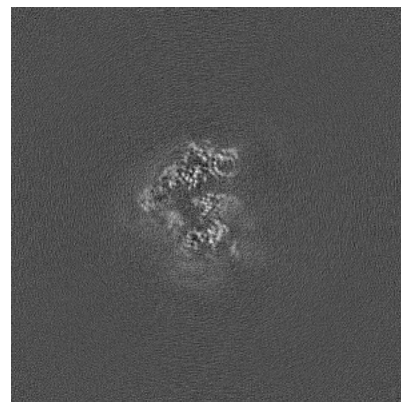
6.3.2 Raw map



X Index: 202



Y Index: 225

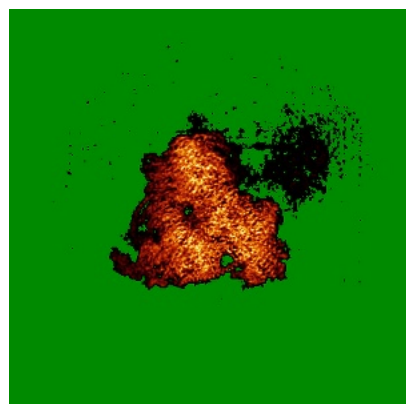


Z Index: 194

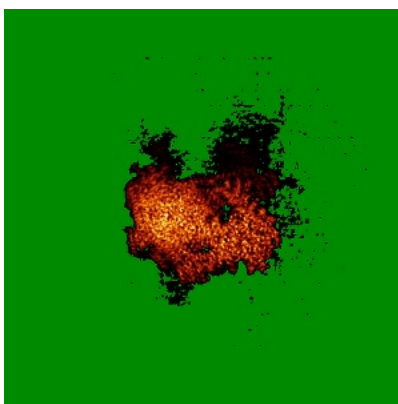
The images above show the largest variance slices of the map in three orthogonal directions.

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

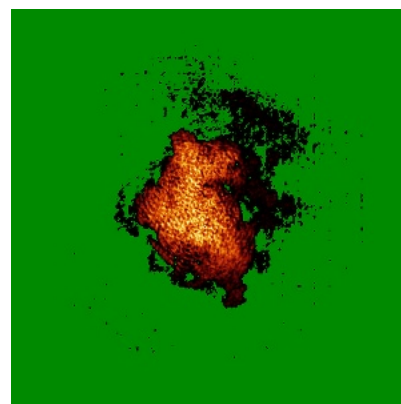
6.4.1 Primary map



X

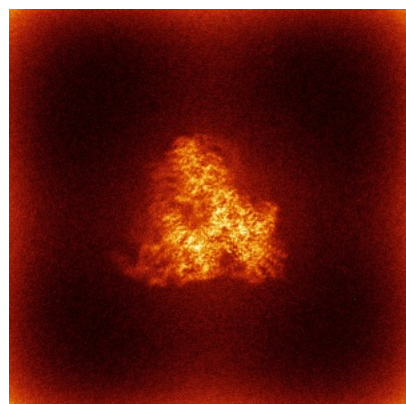


Y

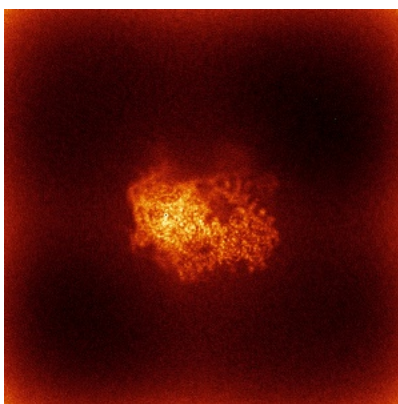


Z

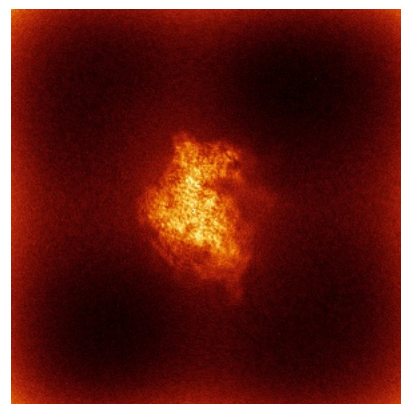
6.4.2 Raw map



X



Y

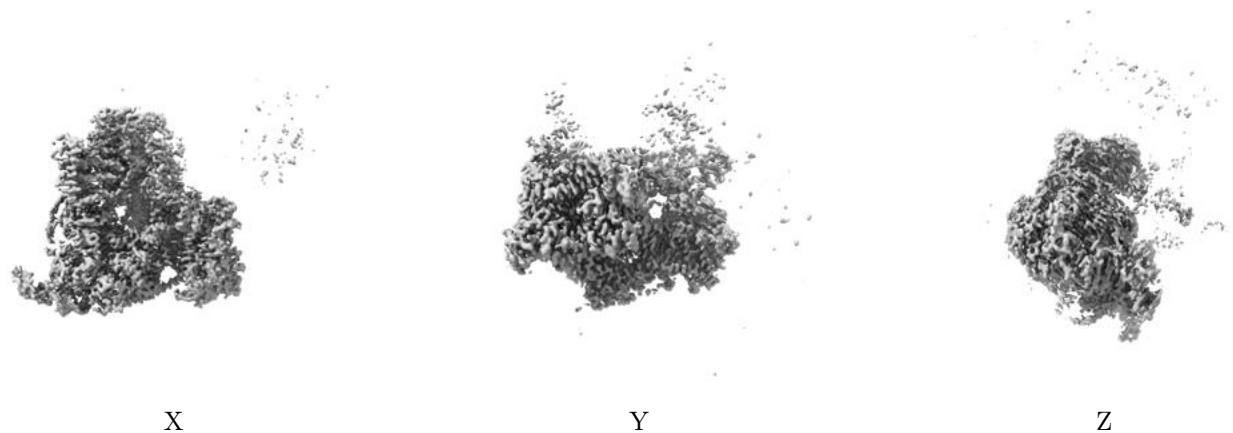


Z

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.

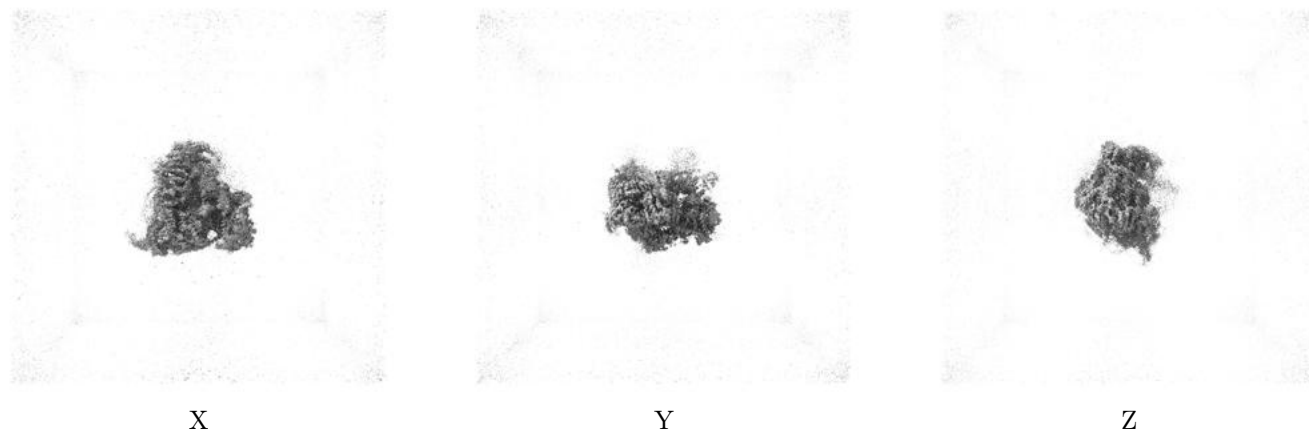
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0981. 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.

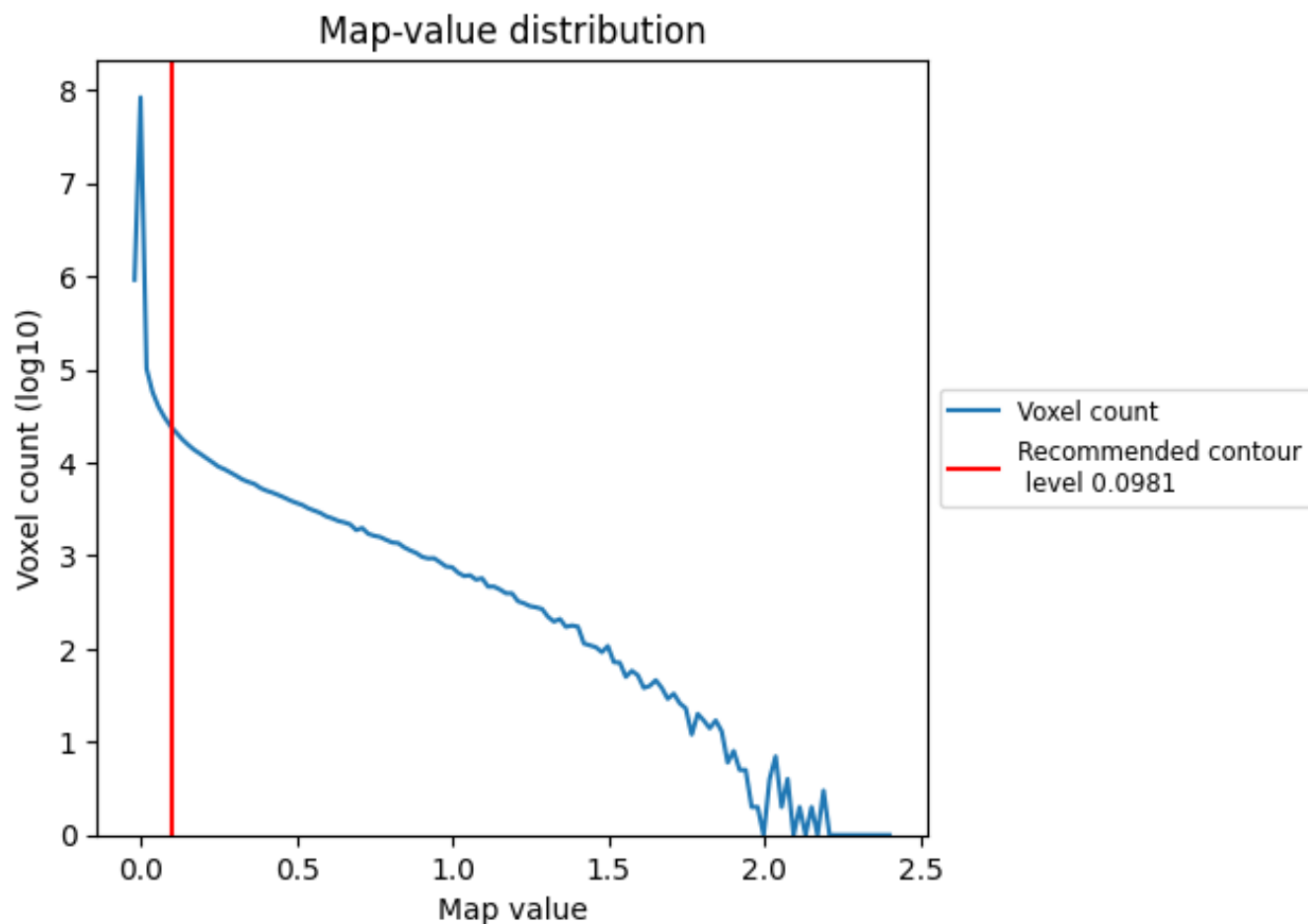
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

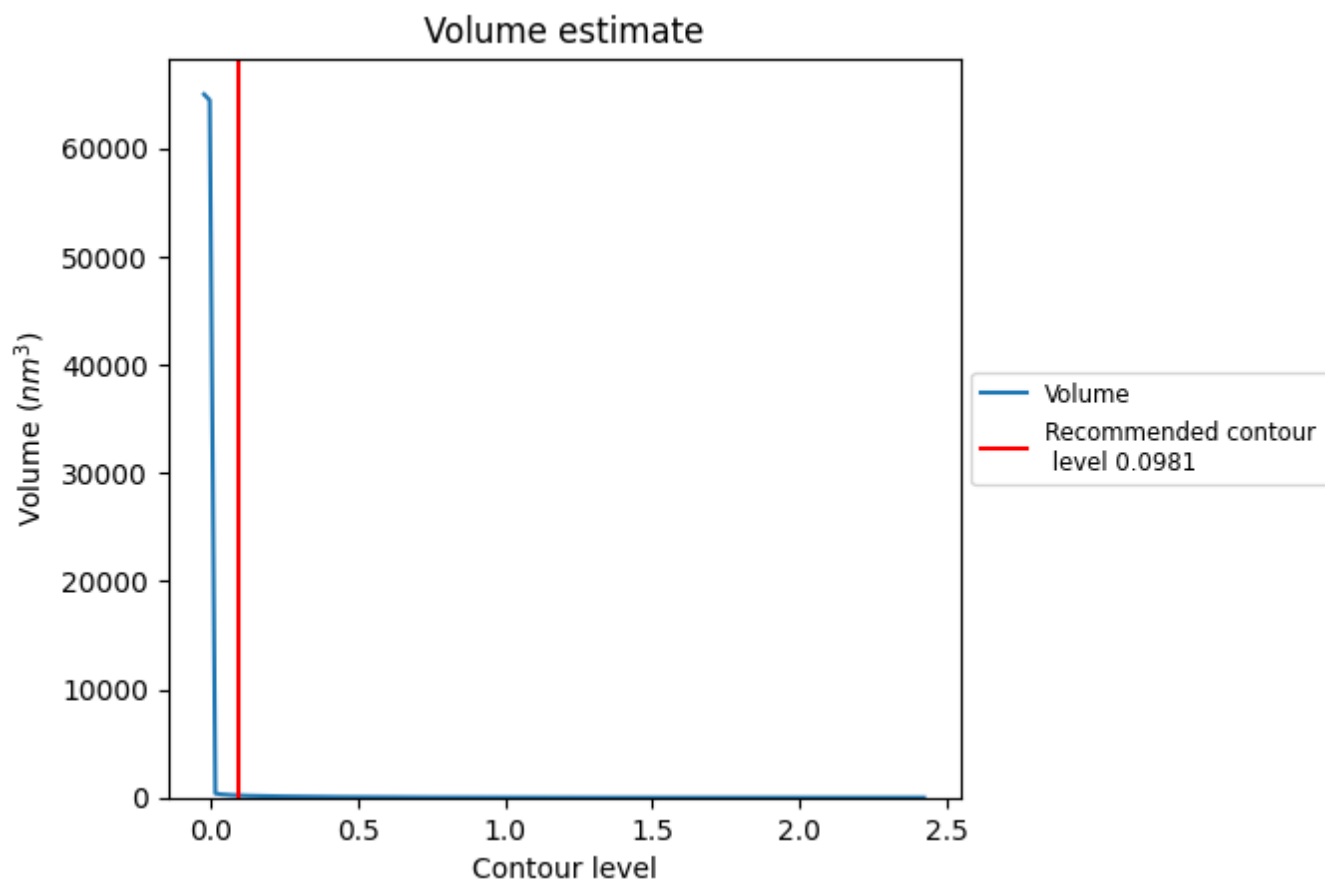
This section contains the results of statistical analysis of the map.

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.

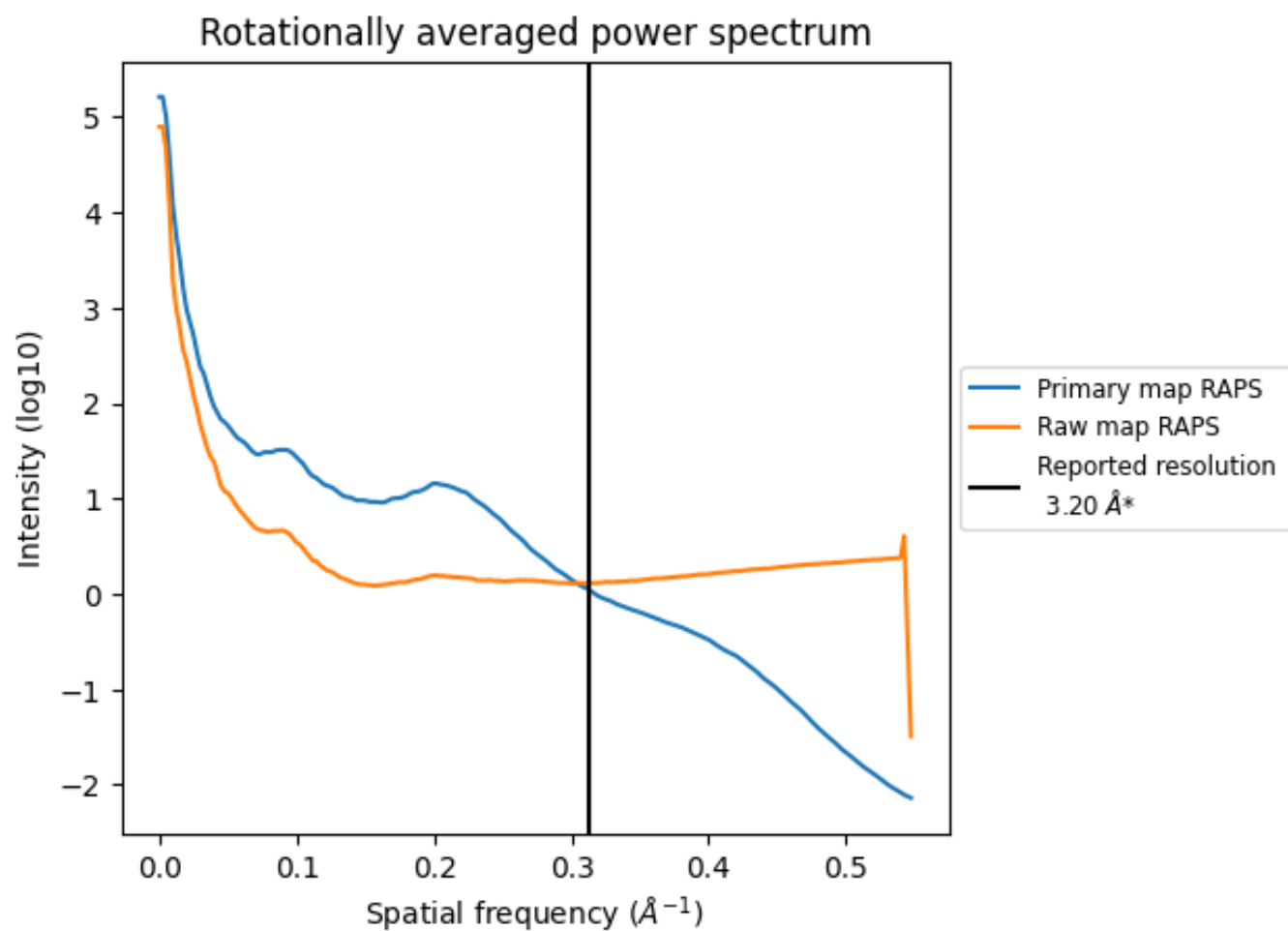
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 199 nm³; this corresponds to an approximate mass of 180 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 ⓘ

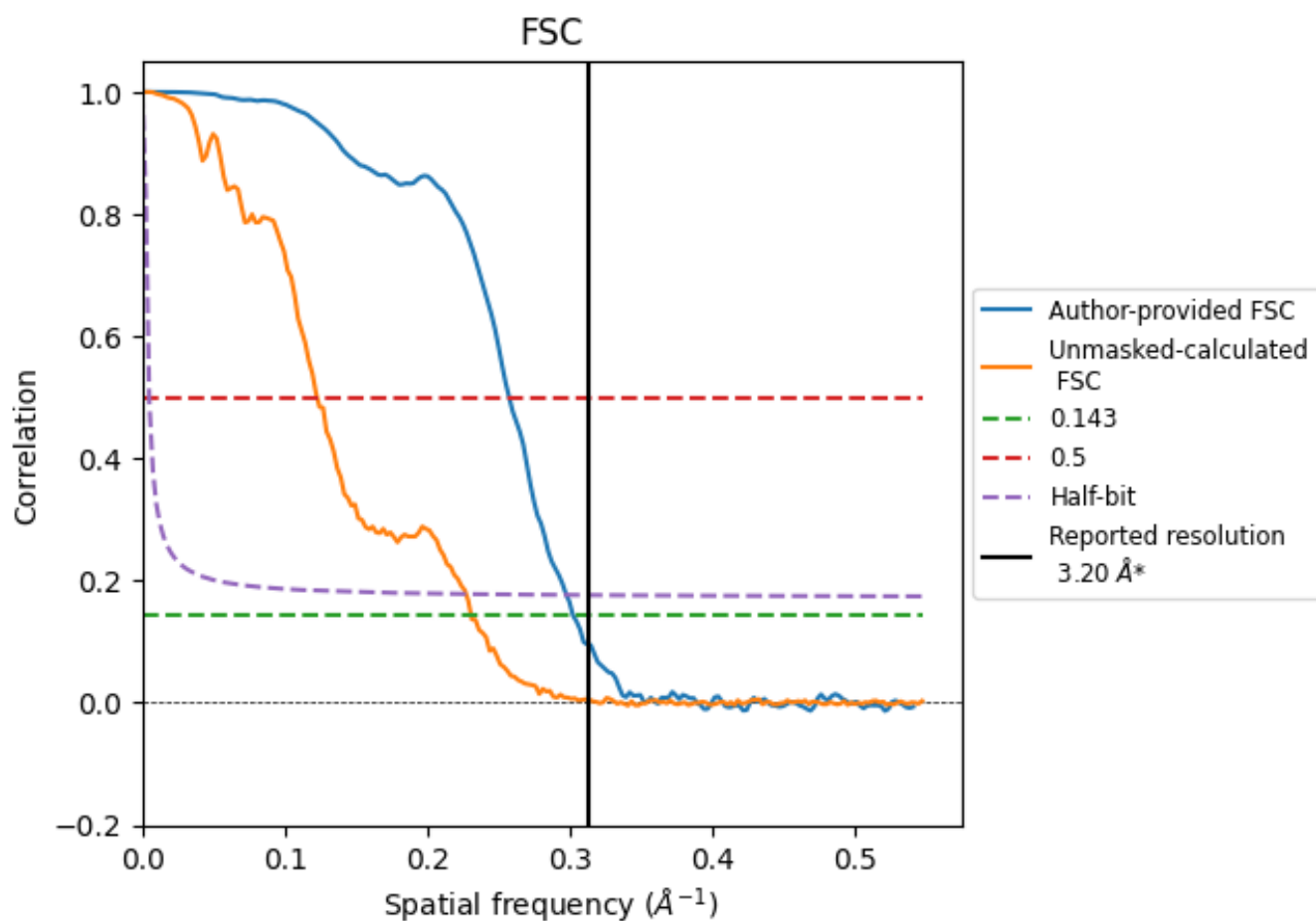


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

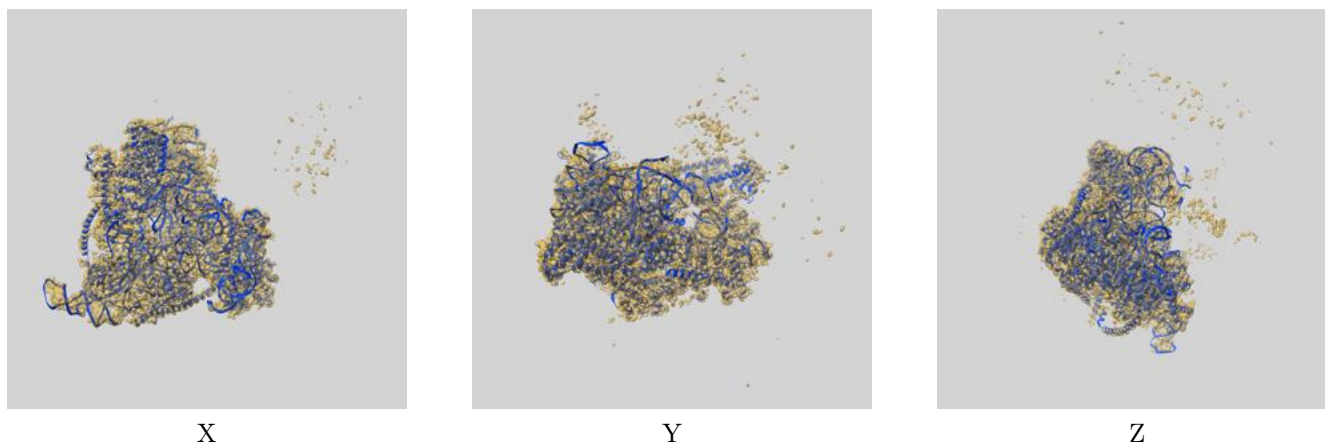
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.31	3.88	3.36
Unmasked-calculated*	4.33	8.15	4.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.33 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53201 and PDB model 9QJC. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



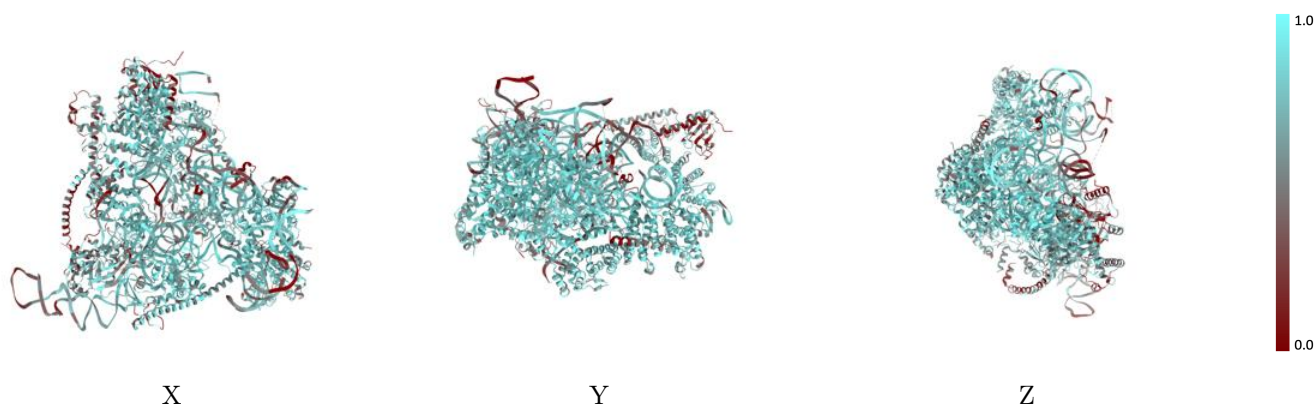
The images above show the 3D surface view of the map at the recommended contour level 0.0981 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



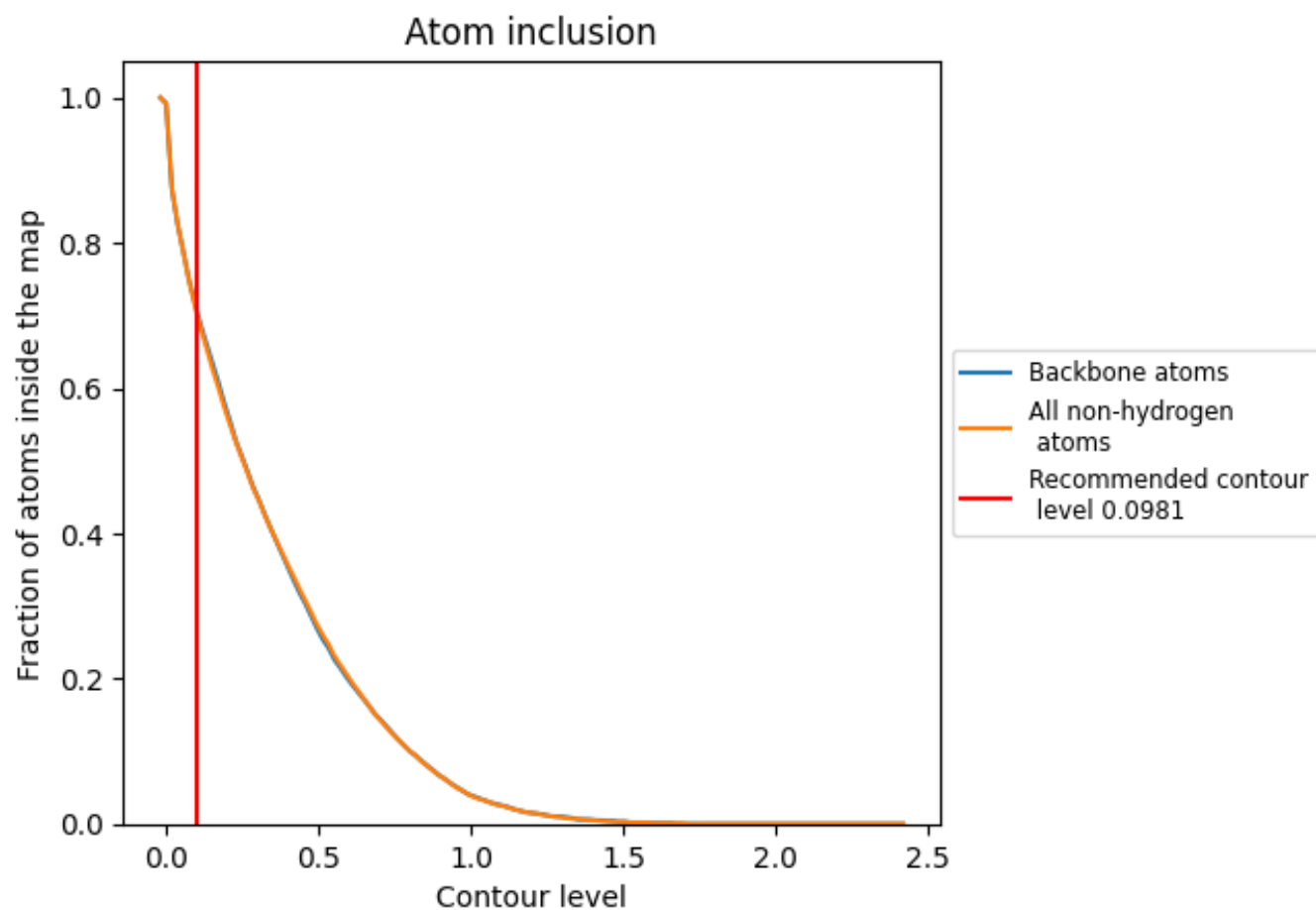
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0981).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 71% 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 (0.0981) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7060	 0.3700
1	 0.6900	 0.3310
2	 0.8270	 0.4210
5	 0.7310	 0.3790
6	 0.7490	 0.4040
B	 0.3650	 0.1660
C	 0.7770	 0.4430
D	 0.8470	 0.5050
E	 0.6570	 0.3360
F	 0.7650	 0.4320
M	 0.6260	 0.2950
O	 0.5580	 0.2690
Q	 0.7540	 0.4270
S	 0.5660	 0.2550
e	 0.8320	 0.5040
f	 0.7560	 0.4410
z	 0.7840	 0.4320

