



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 11:58 PM UTC

PDB ID : 9F67 / pdb_00009f67
EMDB ID : EMD-50217
Title : Trypanosoma brucei nuclear cap-binding complex (CBC) bound to cap4
Authors : Bernhard, H.; Warminski, M.; Dolce, L.G.; Kowalinski, E.
Deposited on : 2024-04-30
Resolution : 2.80 Å(reported)

This is a Full wwPDB EM Validation 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : **FAILED**
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

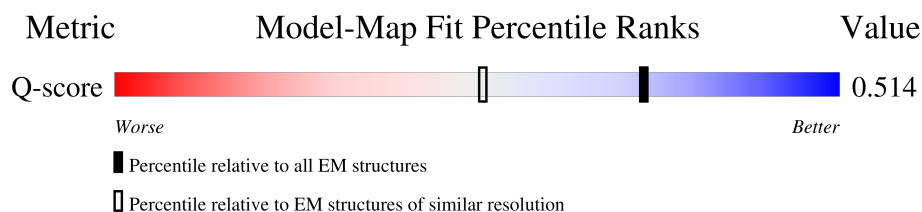
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	11806 (2.30 - 3.30)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7938 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Nuclear cap binding complex subunit CBP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	59	Total	C	N	O	S	0	0
			480	305	87	85	3		

- Molecule 2 is a protein called Nuclear cap binding complex subunit CBP110.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	747	Total	C	N	O	S	0	0
			5912	3782	1032	1066	32		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-14	HIS	-	expression tag	UNP Q38BU6
1	-13	HIS	-	expression tag	UNP Q38BU6
1	-12	HIS	-	expression tag	UNP Q38BU6
1	-11	HIS	-	expression tag	UNP Q38BU6
1	-10	HIS	-	expression tag	UNP Q38BU6
1	-9	HIS	-	expression tag	UNP Q38BU6
1	-8	HIS	-	expression tag	UNP Q38BU6
1	-7	HIS	-	expression tag	UNP Q38BU6
1	-6	PRO	-	expression tag	UNP Q38BU6
1	-5	PRO	-	expression tag	UNP Q38BU6
1	-4	SER	-	expression tag	UNP Q38BU6
1	-3	GLY	-	expression tag	UNP Q38BU6
1	-2	ALA	-	expression tag	UNP Q38BU6
1	-1	ASP	-	expression tag	UNP Q38BU6
1	0	PRO	-	expression tag	UNP Q38BU6

- Molecule 3 is a protein called Nuclear cap-binding protein subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	175	Total	C	N	O	S	0	0
			1404	877	256	263	8		

- Molecule 4 is a RNA chain called cap4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	6	Total	C	N	O	P	0	0
			142	66	25	44	7		

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3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.360	Depositor
Minimum map value	-0.557	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	294.0, 294.0, 294.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	A1IC1	A	5	4	20,23,24	1.49	4 (20%)	26,33,36	2.16	8 (30%)
4	OMC	A	4	4	19,22,23	1.89	2 (10%)	25,31,34	2.09	8 (32%)
4	A2M	A	3	4	22,25,26	1.85	7 (31%)	30,36,39	2.81	13 (43%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1IC1	A	5	4	-	6/9/27/28	0/2/2/2
4	OMC	A	4	4	-	0/9/27/28	0/2/2/2
4	A2M	A	3	4	-	6/9/27/28	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4	OMC	O2-C2	6.62	1.36	1.23
4	A	5	A1IC1	C2-N1	-3.73	1.33	1.38
4	A	3	A2M	C2-N3	3.54	1.40	1.33
4	A	3	A2M	C5-C4	-3.53	1.32	1.39
4	A	5	A1IC1	C4-N3	-3.48	1.33	1.40
4	A	3	A2M	C5-N7	-3.47	1.32	1.39
4	A	3	A2M	C2-N1	3.41	1.40	1.33
4	A	4	OMC	C2-N1	-3.23	1.33	1.40
4	A	3	A2M	C8-N9	-3.01	1.32	1.37
4	A	5	A1IC1	C2-N3	-2.75	1.33	1.39
4	A	3	A2M	C5-C6	-2.70	1.33	1.41
4	A	3	A2M	C4-N9	-2.43	1.32	1.37
4	A	5	A1IC1	C5-C4	-2.13	1.38	1.43

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	3	A2M	N3-C2-N1	-7.01	117.97	128.58
4	A	3	A2M	C4'-O4'-C1'	-5.28	97.81	109.47
4	A	4	OMC	O4'-C1'-N1	5.23	120.22	108.36
4	A	4	OMC	O4'-C1'-C2'	-4.94	98.09	106.59
4	A	3	A2M	N9-C8-N7	-4.83	107.08	113.94
4	A	3	A2M	O4'-C1'-C2'	-4.72	98.45	106.59
4	A	5	A1IC1	O4'-C1'-C2'	-4.27	99.24	106.59
4	A	3	A2M	C5-C4-N3	-4.17	120.97	126.72
4	A	5	A1IC1	C5-C4-N3	4.01	120.32	115.04
4	A	5	A1IC1	C4'-O4'-C1'	-3.94	100.78	109.47
4	A	5	A1IC1	O4'-C1'-N1	3.86	117.10	108.36
4	A	5	A1IC1	C4-N3-C2	-3.82	121.50	124.58
4	A	4	OMC	C3'-C2'-C1'	-3.41	96.28	102.81
4	A	3	A2M	C5-N7-C8	3.41	108.81	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	3	A2M	C2-N3-C4	3.20	119.65	111.83
4	A	3	A2M	C4-N9-C8	3.18	109.08	105.74
4	A	4	OMC	CM2-O2'-C2'	-2.96	106.87	114.47
4	A	3	A2M	C1'-N9-C8	-2.92	120.61	127.09
4	A	3	A2M	C5-C6-N6	-2.79	116.39	123.29
4	A	4	OMC	C4'-O4'-C1'	-2.77	103.36	109.47
4	A	3	A2M	N3-C4-N9	2.72	131.79	127.17
4	A	3	A2M	C6-C5-C4	2.66	120.81	117.18
4	A	5	A1IC1	C1'-N1-C2	2.57	121.25	117.04
4	A	3	A2M	C4-C5-N7	-2.44	107.80	110.58
4	A	4	OMC	C5-C6-N1	-2.43	117.89	121.84
4	A	5	A1IC1	C6-N1-C2	-2.27	119.95	121.80
4	A	5	A1IC1	C50-O2'-C2'	-2.24	108.71	114.47
4	A	4	OMC	C5'-C4'-C3'	-2.15	107.48	115.21
4	A	4	OMC	C2'-C1'-N1	-2.03	110.40	114.24

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3	A2M	C4'-C5'-O5'-P
4	A	3	A2M	C2'-C1'-N9-C8
4	A	3	A2M	C2'-C1'-N9-C4
4	A	5	A1IC1	O4'-C1'-N1-C6
4	A	5	A1IC1	O4'-C1'-N1-C2
4	A	3	A2M	O4'-C4'-C5'-O5'
4	A	3	A2M	C3'-C4'-C5'-O5'
4	A	5	A1IC1	C2'-C1'-N1-C6
4	A	5	A1IC1	C2'-C1'-N1-C2
4	A	3	A2M	C3'-C2'-O2'-CM'
4	A	5	A1IC1	C4'-C5'-O5'-P
4	A	5	A1IC1	C3'-C2'-O2'-C50

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

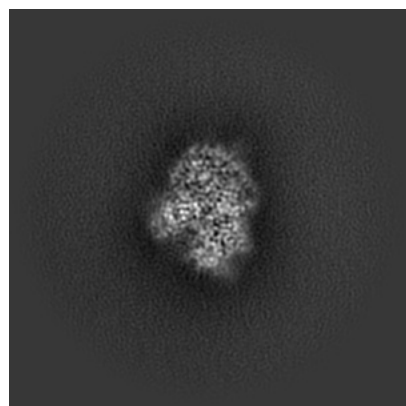
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50217. These allow visual inspection of the internal detail of the map and identification of artifacts.

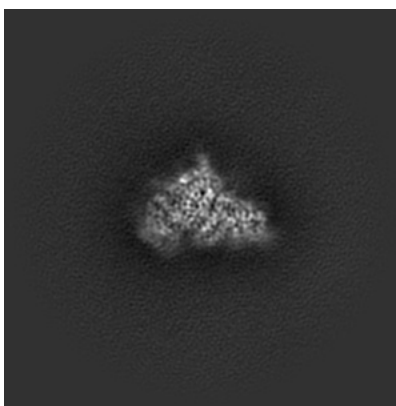
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

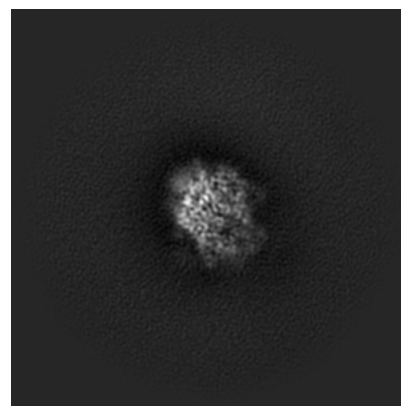
5.1.1 Primary map



X

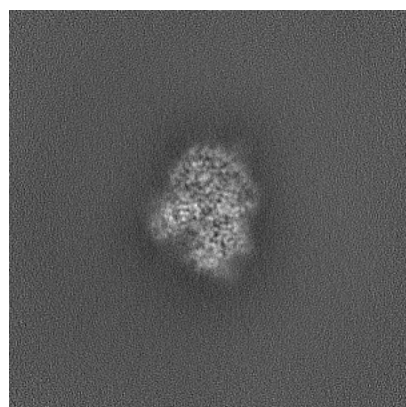


Y

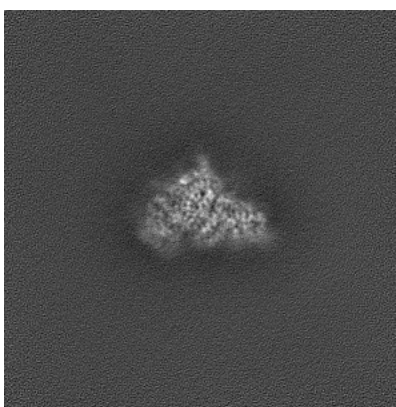


Z

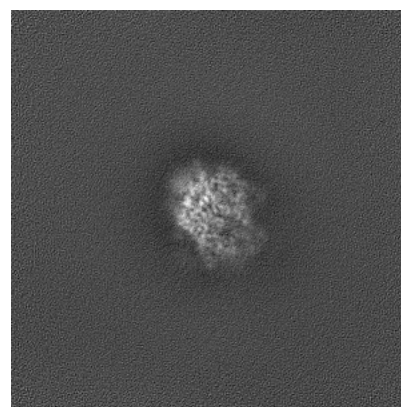
5.1.2 Raw map



X



Y

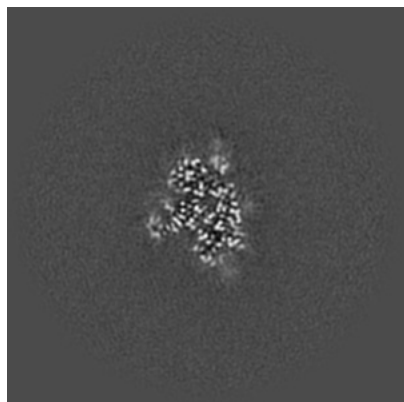


Z

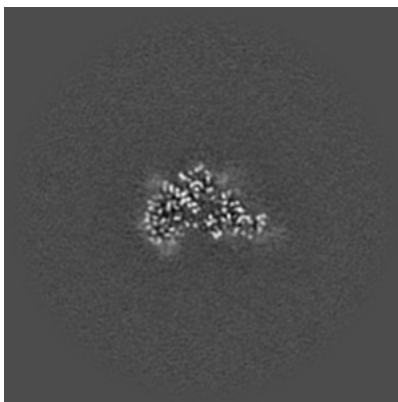
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

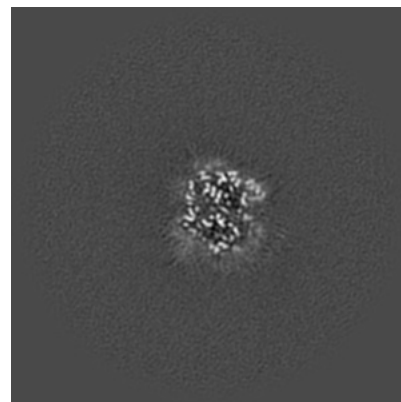
5.2.1 Primary map



X Index: 175

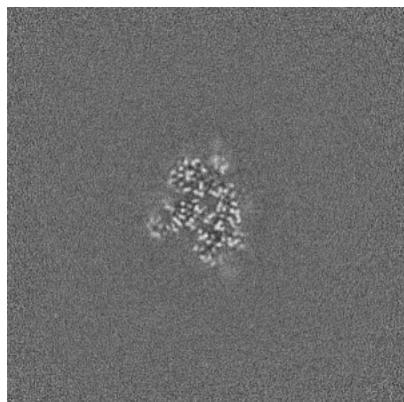


Y Index: 175

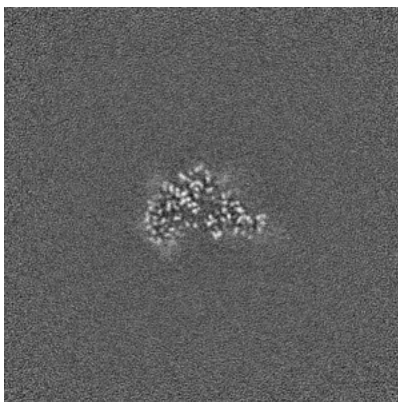


Z Index: 175

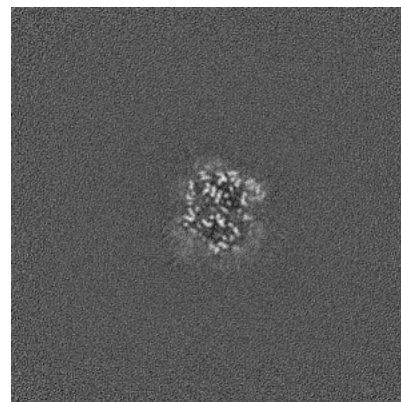
5.2.2 Raw map



X Index: 175



Y Index: 175

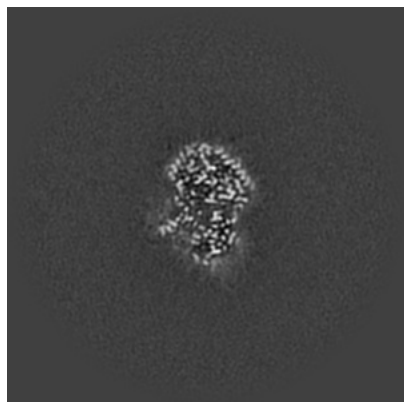


Z Index: 175

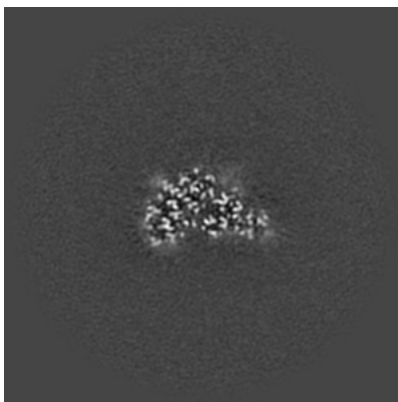
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

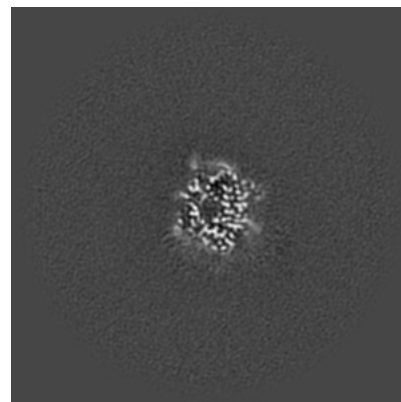
5.3.1 Primary map



X Index: 166

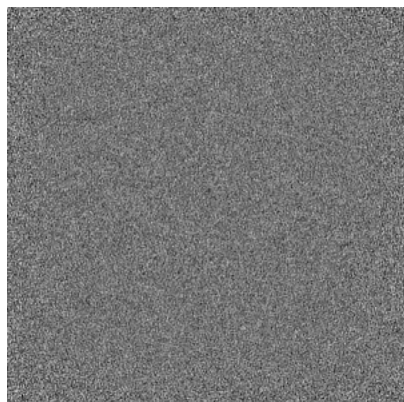


Y Index: 173

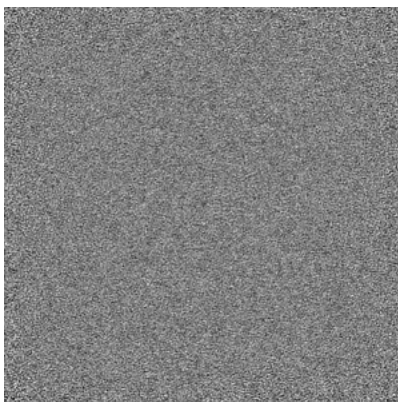


Z Index: 178

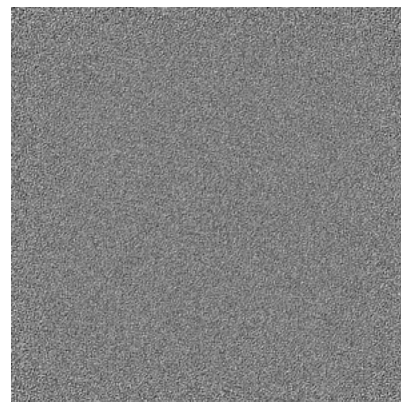
5.3.2 Raw map



X Index: 0



Y Index: 0

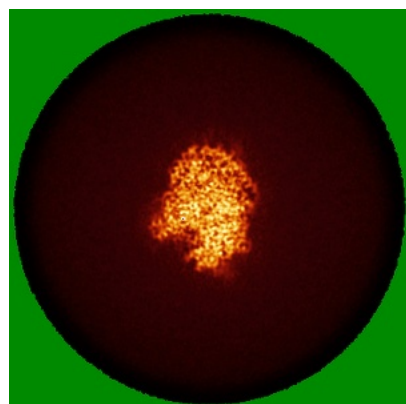


Z Index: 349

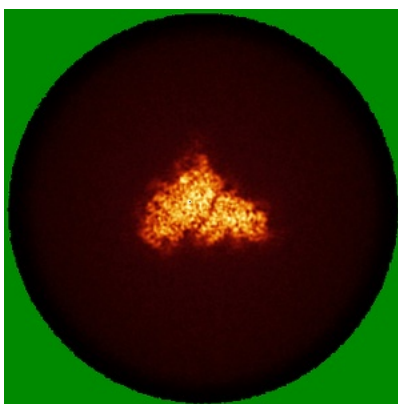
The images above show the largest variance slices of the map in three orthogonal directions.

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

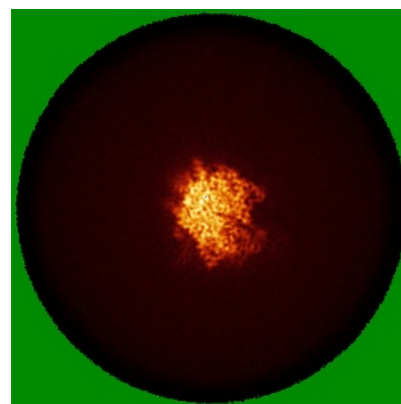
5.4.1 Primary map



X

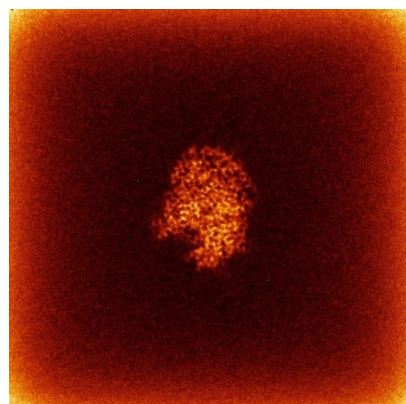


Y

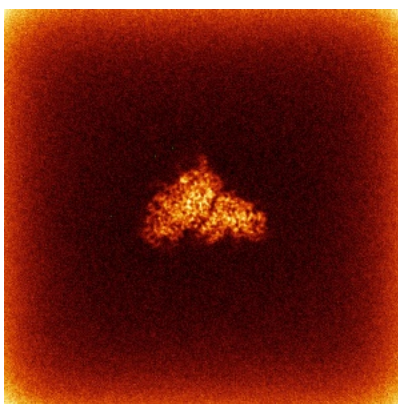


Z

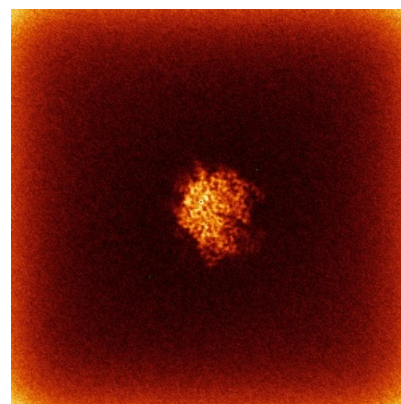
5.4.2 Raw map



X



Y

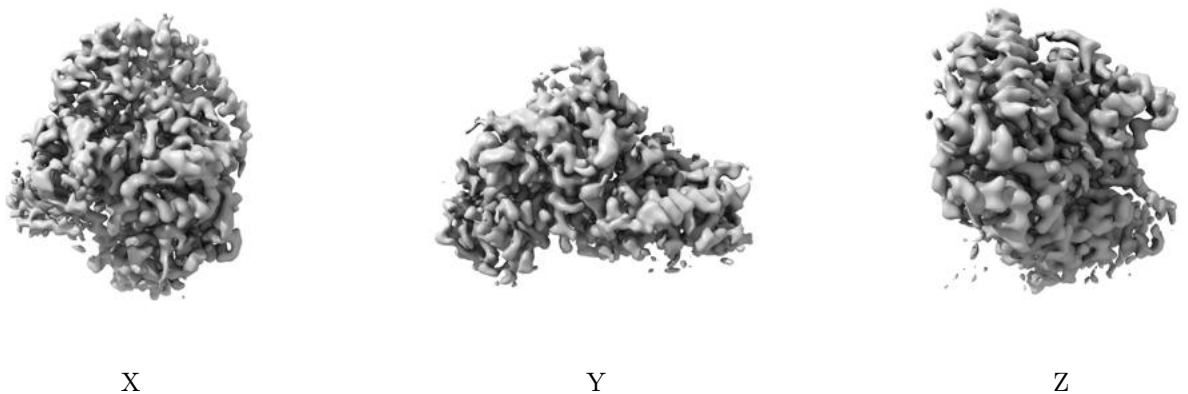


Z

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.

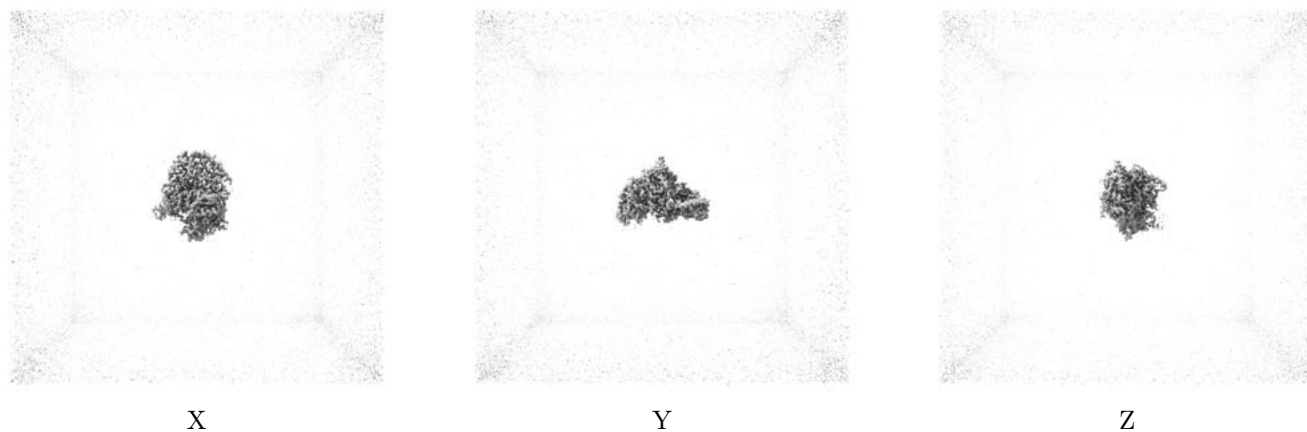
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 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.

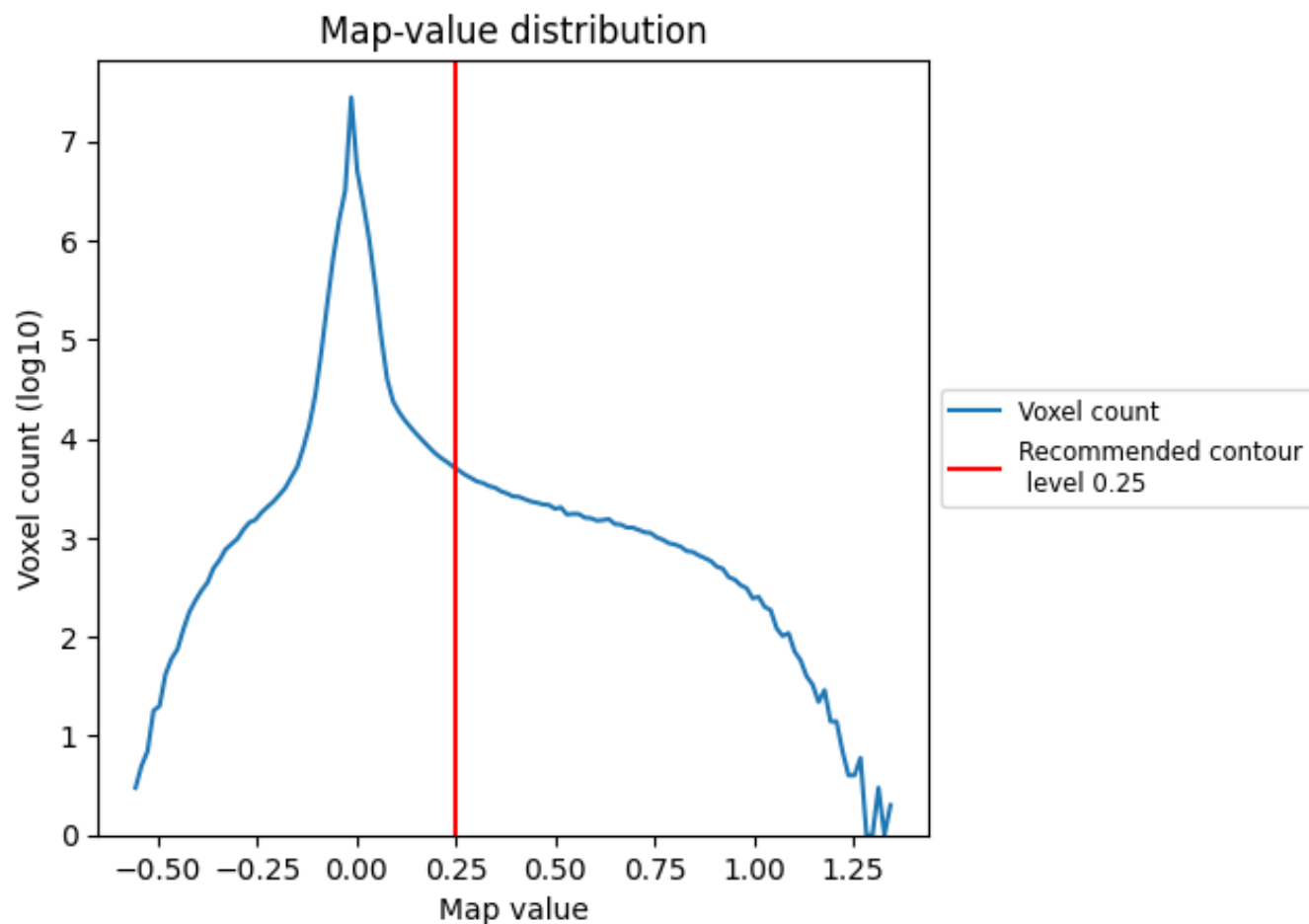
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

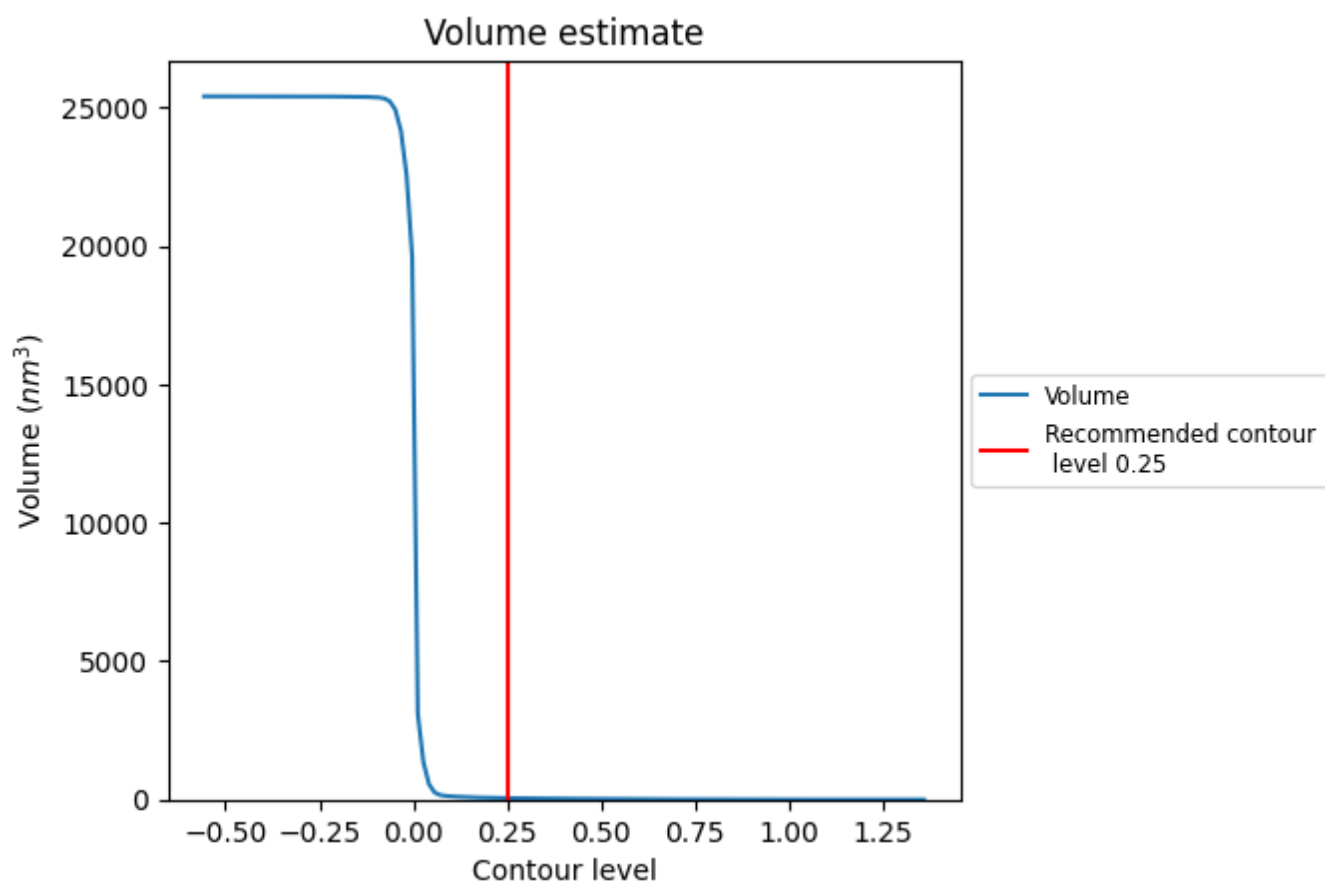
This section contains the results of statistical analysis of the map.

6.1 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.

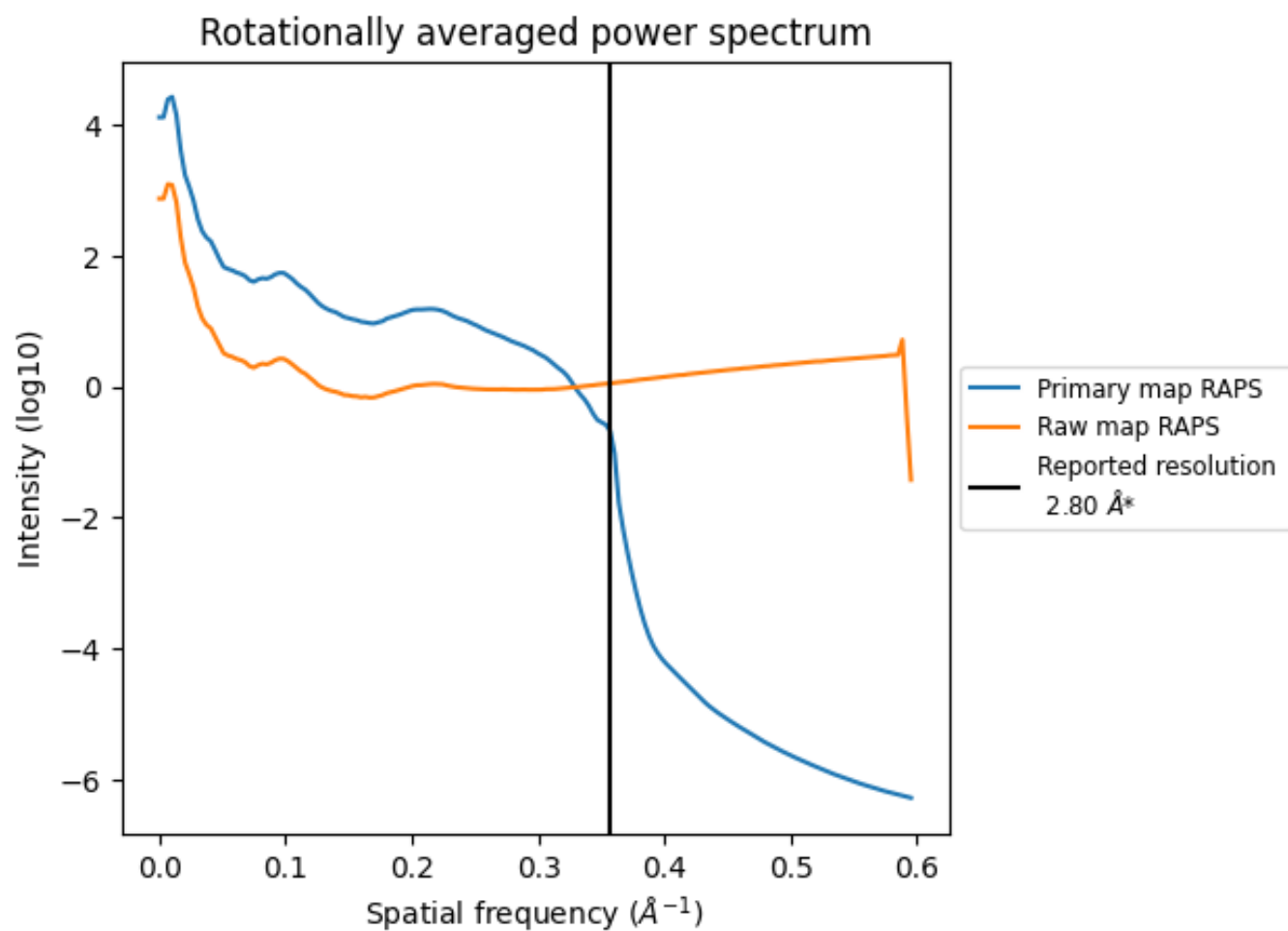
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 53 nm³; this corresponds to an approximate mass of 48 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.

6.3 Rotationally averaged power spectrum ⓘ

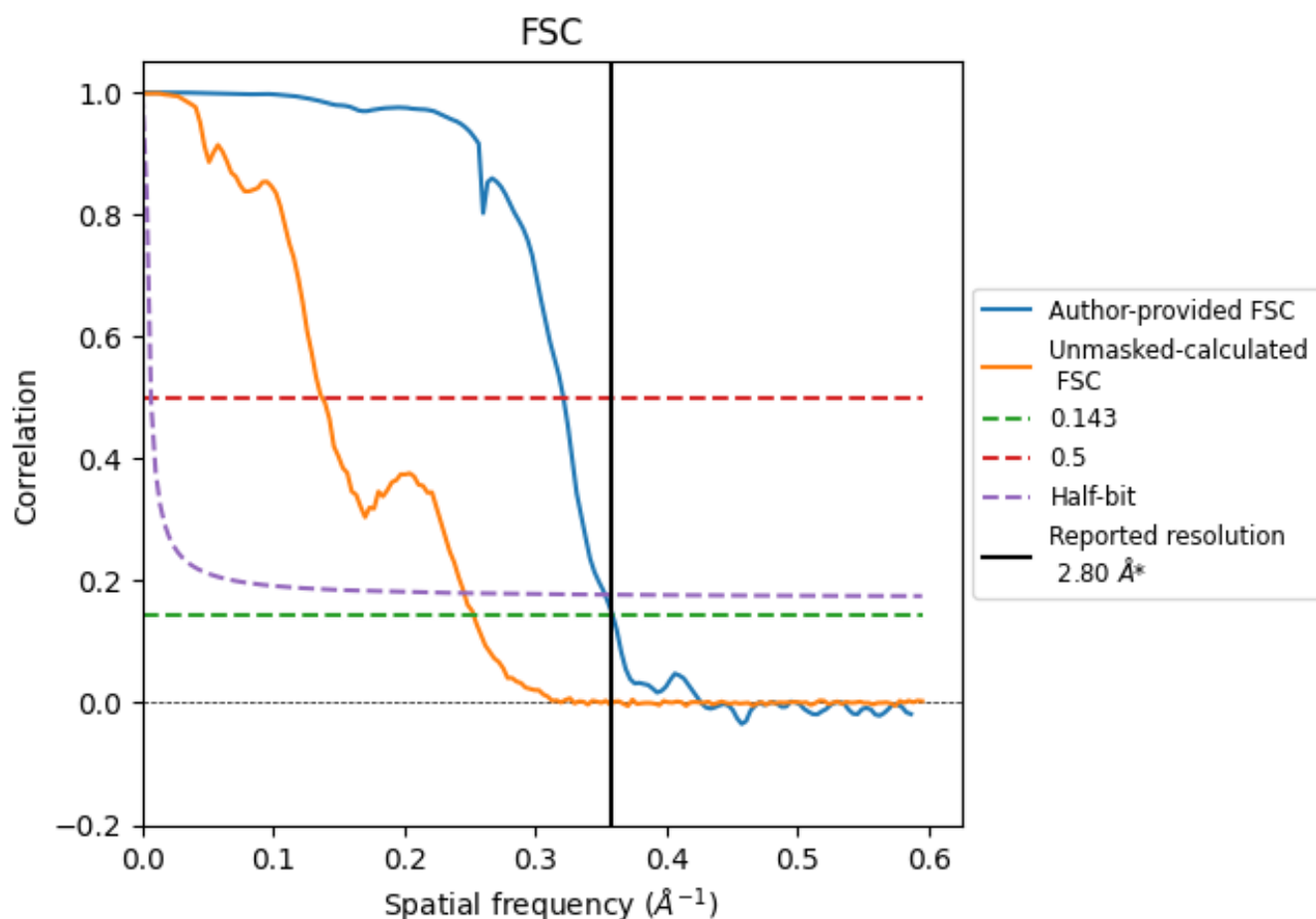


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

7.2 Resolution estimates [i](#)

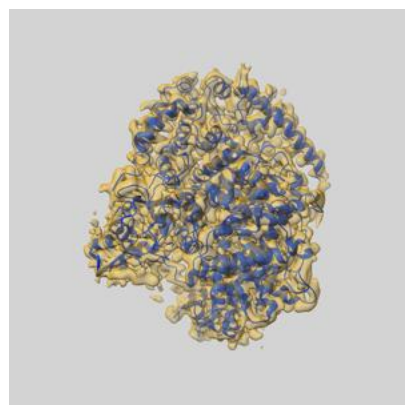
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.78	3.11	2.83
Unmasked-calculated*	3.95	7.29	4.07

*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 3.95 differs from the reported value 2.8 by more than 10 %

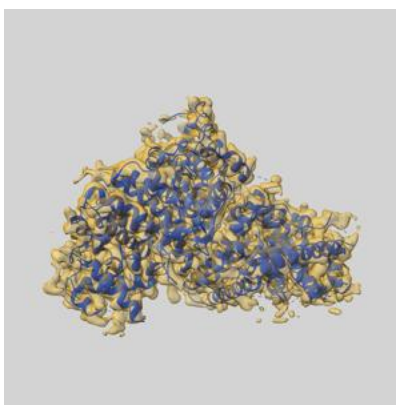
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50217 and PDB model 9F67. Per-residue inclusion information can be found in section ?? on page ??.

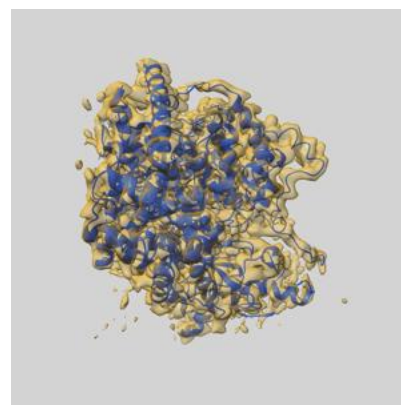
8.1 Map-model overlay [i](#)



X



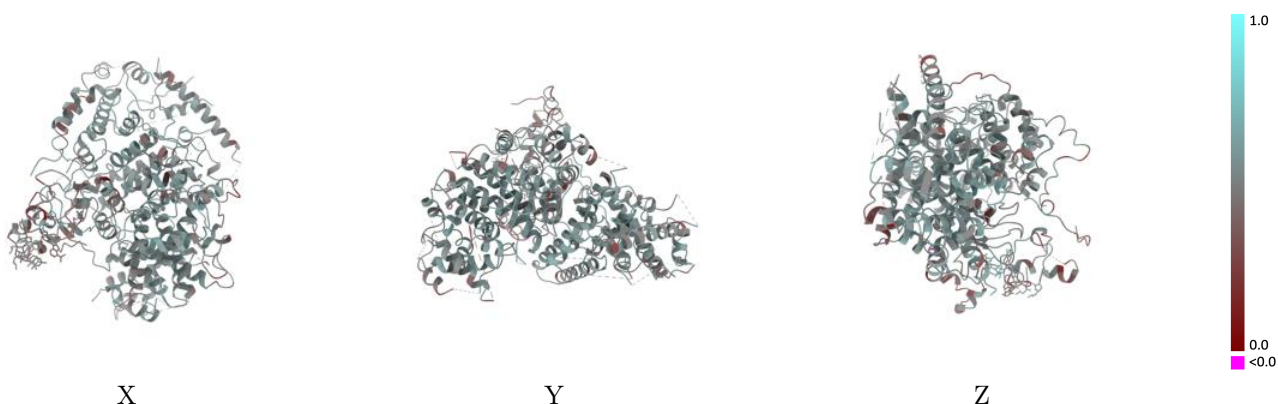
Y



Z

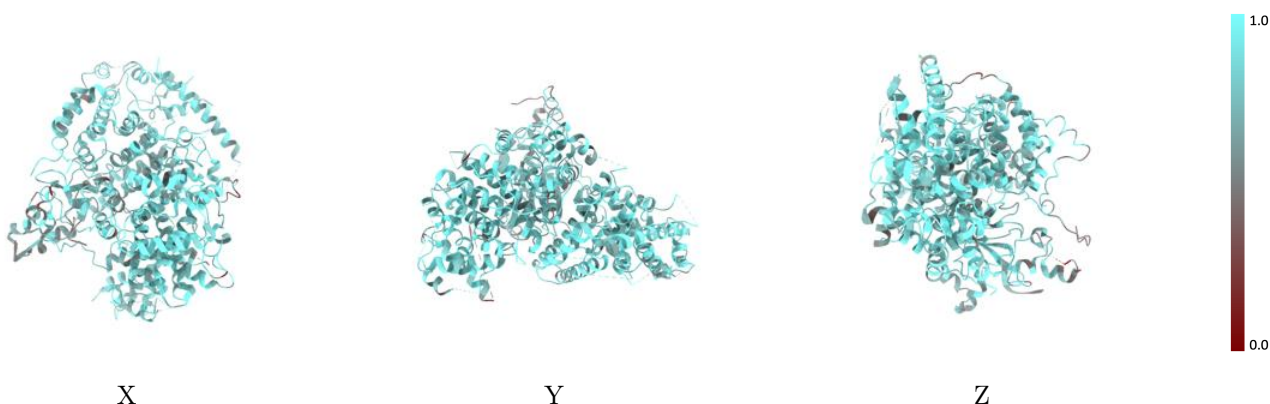
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



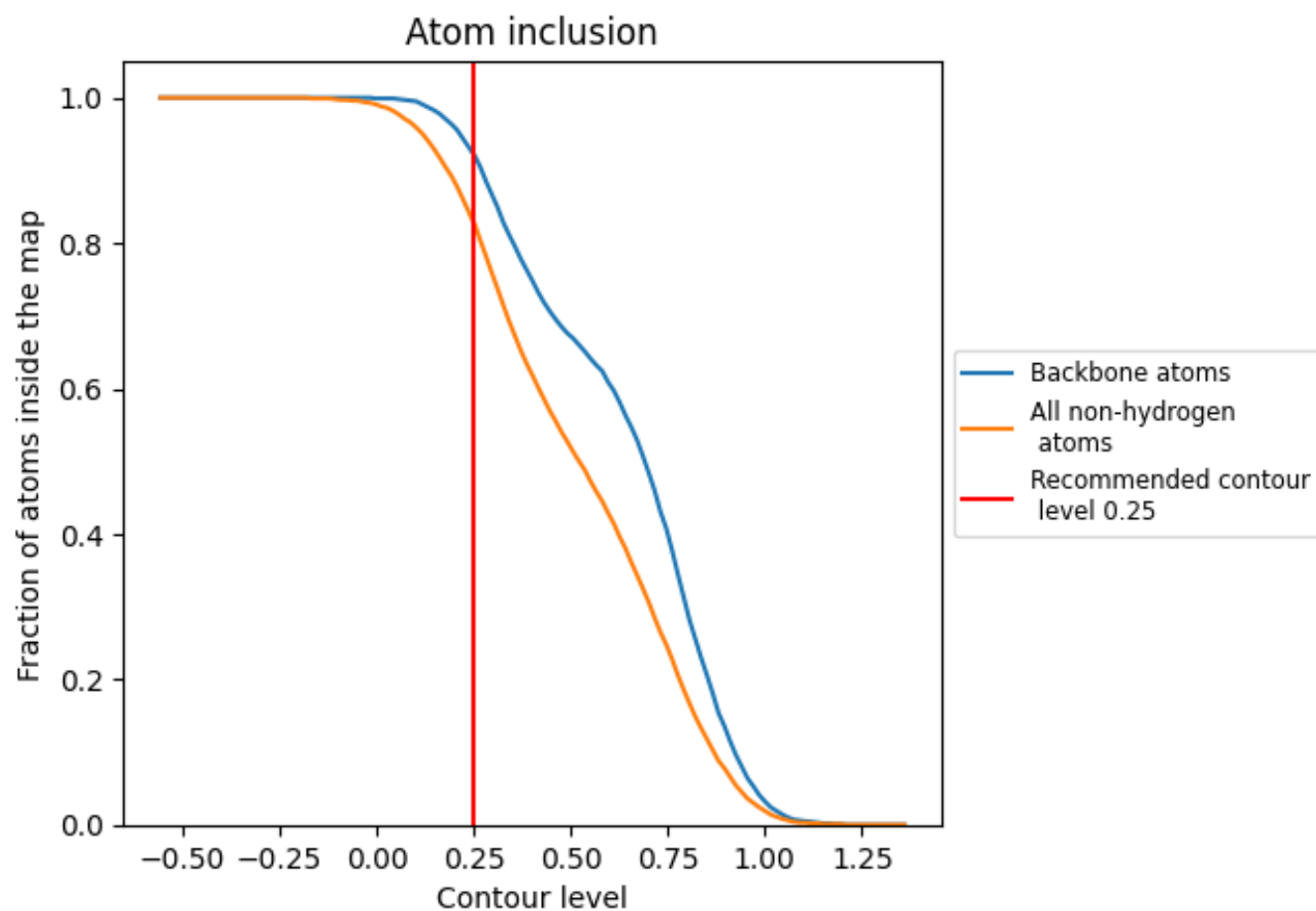
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 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 (0.25).

8.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8280	0.5140
1	0.8490	0.5280
2	0.7710	0.4660
3	0.7880	0.4850
A	0.6480	0.4920

