



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:49 PM UTC

PDB ID : 8TID / pdb_00008tid
EMDB ID : EMD-41284
Title : Combined linker domain of N-DRC and associated proteins Tetrahymena
Authors : Ghanaeian, A.G.; Majhi, S.M.; McCaffrey, C.M.; Nami, B.N.; Black, C.B.;
Yang, S.K.; Legal, T.L.; Papoulas, O.P.; Janowska, M.J.; Valente-Paterno,
M.V.; Marcotte, E.M.; Wloga, D.W.; Bui, K.H.
Deposited on : 2023-07-19
Resolution : 3.60 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 : **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

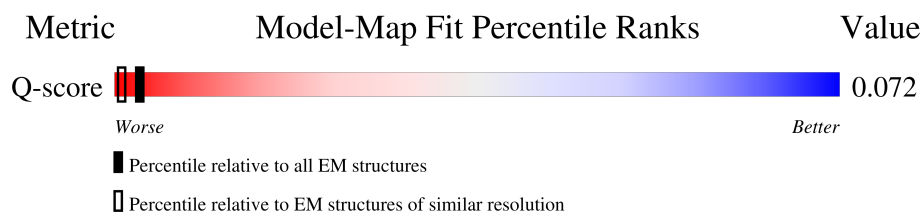
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 123416 atoms, of which 12979 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 Dynein regulatory complex protein 1/2 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	458	Total	C	N	O	S	0	0
			3929	2479	695	734	21		

- Molecule 2 is a protein called Coiled-coil protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	460	Total	C	N	O	S	0	0
			3873	2427	697	733	16		

- Molecule 3 is a protein called LRRC48 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	533	Total	C	N	O	S	0	0
			4433	2771	760	890	12		

- Molecule 4 is a protein called Growth-arrest-specific microtubule-binding protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	461	Total	C	H	N	O	S	0	0
			6572	2431	2704	672	756	9		

- Molecule 5 is a protein called Growth-arrest-specific microtubule-binding protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	464	Total	C	H	N	O	S	0	0
			6424	2418	2565	678	754	9		

- Molecule 6 is a protein called Flagellar associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	461	Total	C	N	O	S	0	0
			3714	2351	632	714	17		

- Molecule 7 is a protein called Kinase domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	345	Total	C	N	O	S	0	0
			2780	1763	474	527	16		

- Molecule 8 is a protein called Coiled-coil lobo-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	820	Total	C	N	O	S	0	0
			6857	4318	1192	1314	33		

- Molecule 9 is a protein called EF-hand calcium-binding domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	185	Total	C	N	O	S	0	0
			1553	1002	244	301	6		
9	i	185	Total	C	N	O	S	0	0
			1553	1002	244	301	6		

- Molecule 10 is a protein called Dynein regulatory complex protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	372	Total	C	N	O	S	0	0
			3151	1949	574	620	8		

- Molecule 11 is a protein called Dynein regulatory complex protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	434	Total	C	N	O	S	0	0
			3588	2229	647	699	13		

- Molecule 12 is a protein called AAA family ATPase CDC48 subfamily protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	862	Total	C	N	O	S	0	0
			7102	4513	1213	1345	31		

- Molecule 13 is a protein called Cilia- and flagella-associated protein 91.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	164	Total	C	N	O	S	0	0
			1373	851	259	260	3		

- Molecule 14 is a protein called Flagella associated protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	434	Total	C	H	N	O	S	0	0
			5707	2237	2099	650	709	12		
14	n	208	Total	C	H	N	O	S	0	0
			3483	1076	1740	312	352	3		

- Molecule 15 is a protein called Coiled-coil protein, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	430	Total	C	H	N	O	S	0	0
			5711	2223	2107	653	721	7		
15	o	205	Total	C	H	N	O	S	0	0
			3470	1063	1764	302	334	7		

- Molecule 16 is a protein called DUF4201 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	631	Total	C	N	O	S		0	0
			5310	3305	956	1034	15			

- Molecule 17 is a protein called Calmodulin 7-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	202	Total	C	N	O	S		0	0
			1679	1061	276	338	4			
17	R	202	Total	C	N	O	S		0	0
			1679	1061	276	338	4			

- Molecule 18 is a protein called Coiled-coil domain-containing protein 153.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	187	Total	C	N	O	S		0	0
			1542	943	274	314	11			
18	s	187	Total	C	N	O	S		0	0
			1542	943	274	314	11			

- Molecule 19 is a protein called Flagellar associated protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	335	Total	C	N	O	S		0	0
			2782	1740	489	548	5			

- Molecule 20 is a protein called L-shape (Unknown-protein).

Mol	Chain	Residues	Atoms				AltConf	Trace
20	U	597	Total	C	N	O	0	0
			2985	1791	597	597		
20	V	594	Total	C	N	O	0	0
			2970	1782	594	594		

- Molecule 21 is a protein called WD40 domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	1171	Total	C	N	O	S	0	0
			9536	5994	1665	1830	47		

- Molecule 22 is a protein called EF hand protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	830	Total	C	N	O	S	0	0
			6730	4277	1134	1286	33		

- Molecule 23 is a protein called CFAP20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	187	Total	C	N	O	S	0	0
			1556	1003	269	277	7		

- Molecule 24 is a protein called WD40 domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	w	1192	Total	C	N	O	S	0	0
			9832	6196	1691	1893	52		

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

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211502	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.497	Depositor
Minimum map value	-1.582	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.240	Depositor
Recommended contour level	0.545	Depositor
Map size ($\text{\AA}$)	1293.28, 1293.28, 1293.28	wwPDB
Map dimensions	472, 472, 472	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.74, 2.74, 2.74	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

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 ⓘ

There are no chain breaks in this entry.

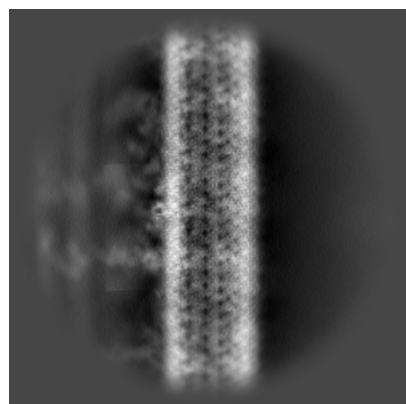
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41284. These allow visual inspection of the internal detail of the map and identification of artifacts.

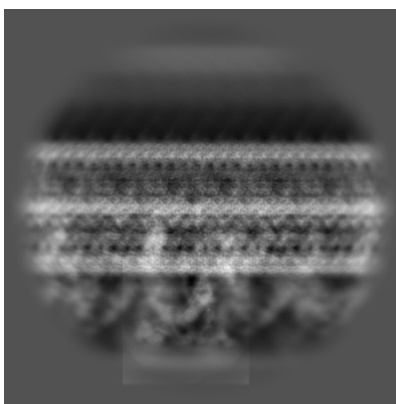
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

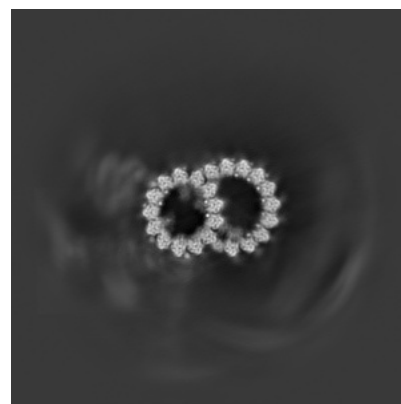
5.1.1 Primary map



X

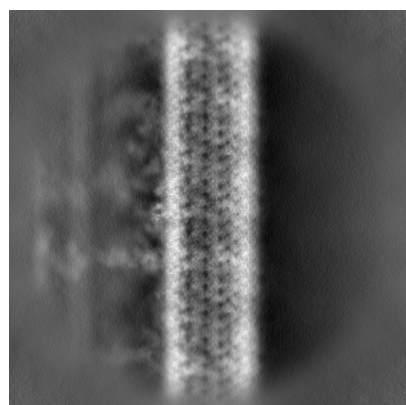


Y

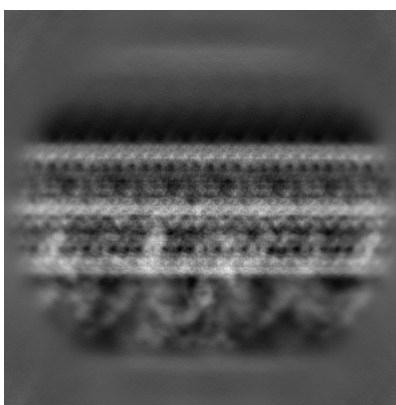


Z

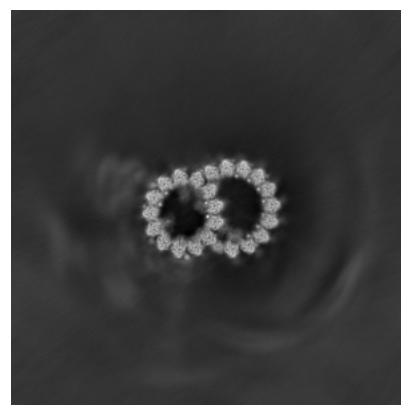
5.1.2 Raw map



X



Y

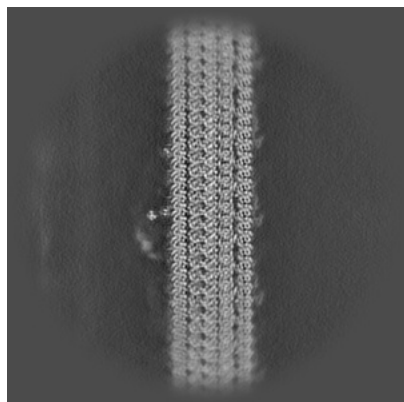


Z

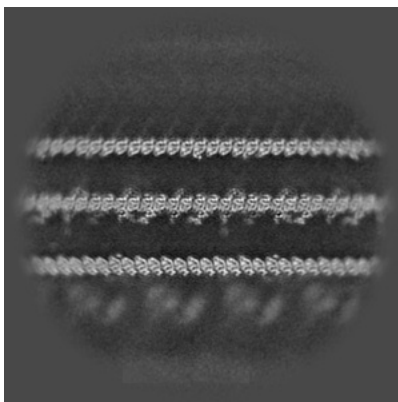
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

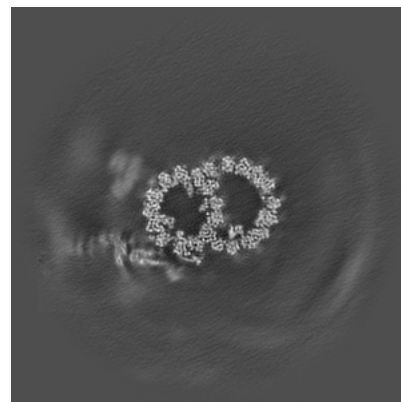
5.2.1 Primary map



X Index: 236

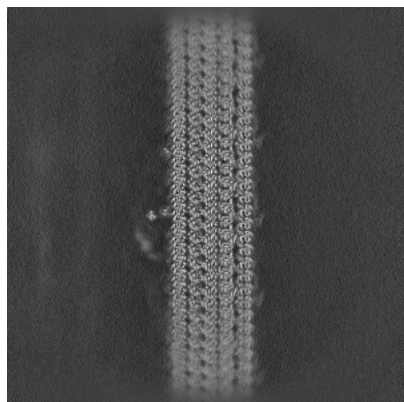


Y Index: 236

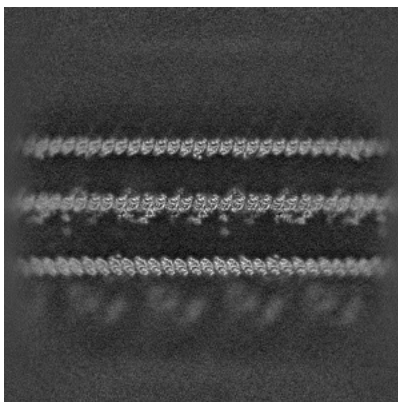


Z Index: 236

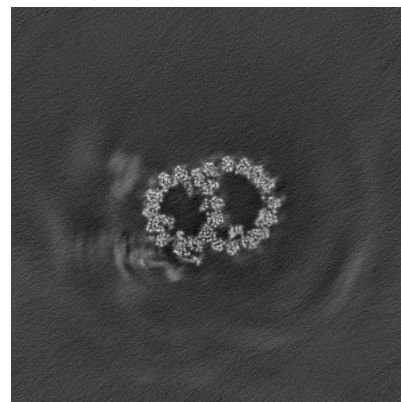
5.2.2 Raw map



X Index: 235



Y Index: 235

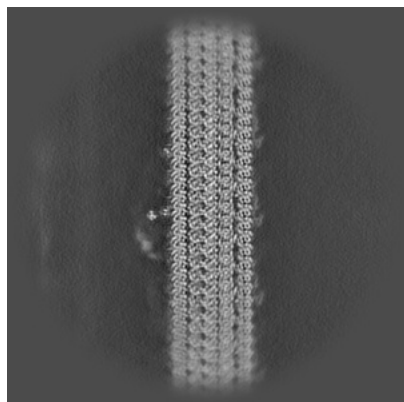


Z Index: 235

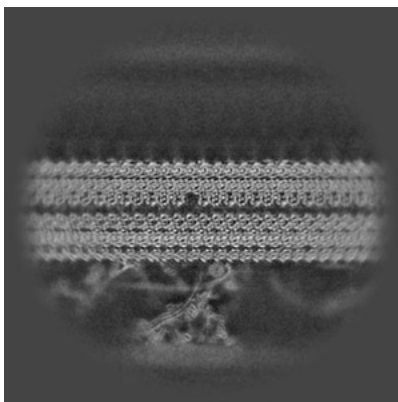
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

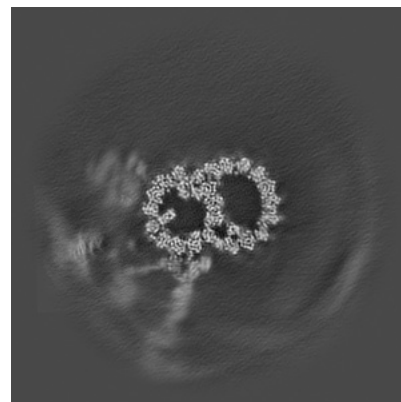
5.3.1 Primary map



X Index: 236

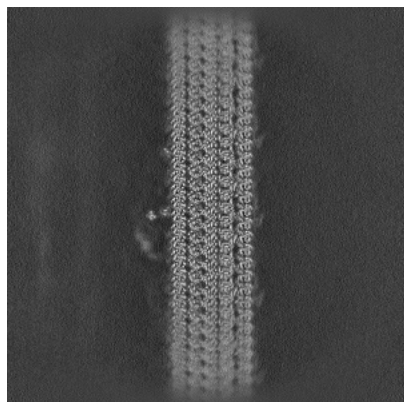


Y Index: 192

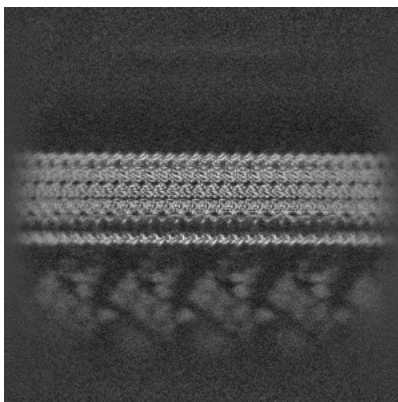


Z Index: 180

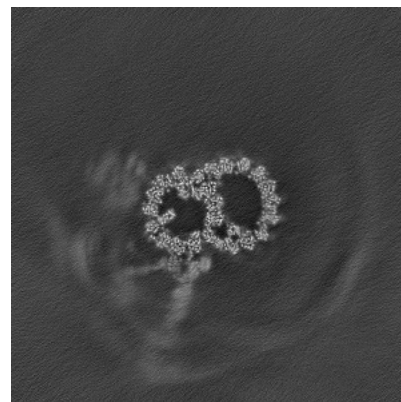
5.3.2 Raw map



X Index: 235



Y Index: 280

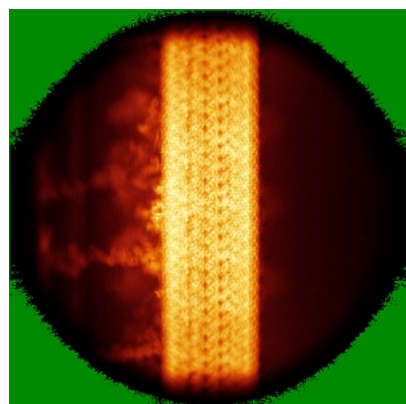


Z Index: 179

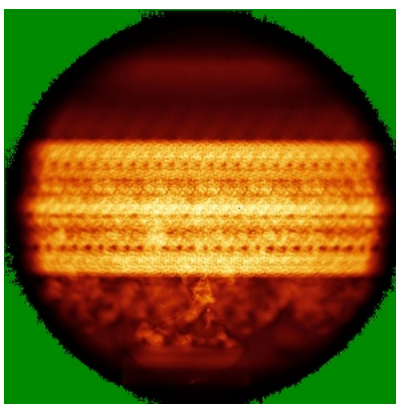
The images above show the largest variance slices of the map in three orthogonal directions.

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

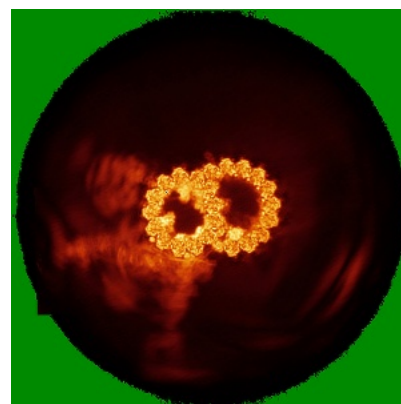
5.4.1 Primary map



X

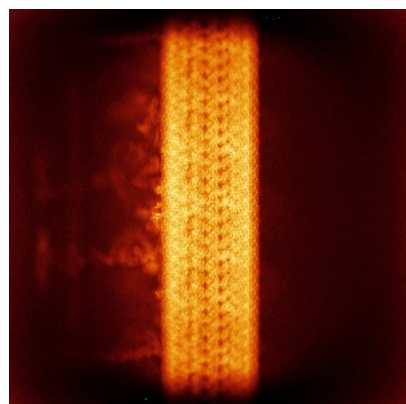


Y

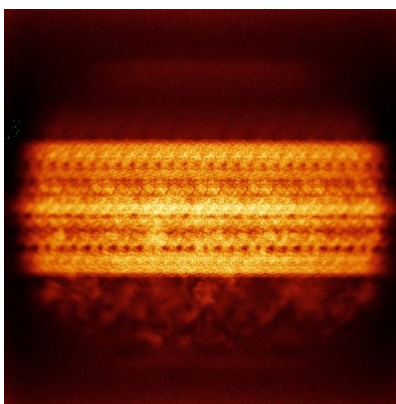


Z

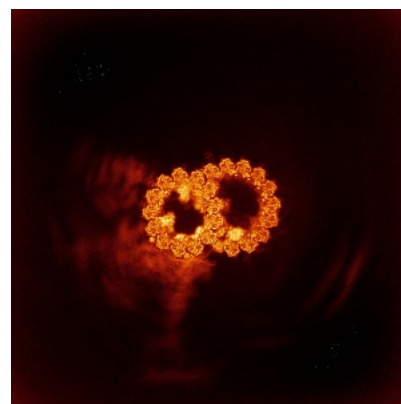
5.4.2 Raw map



X



Y

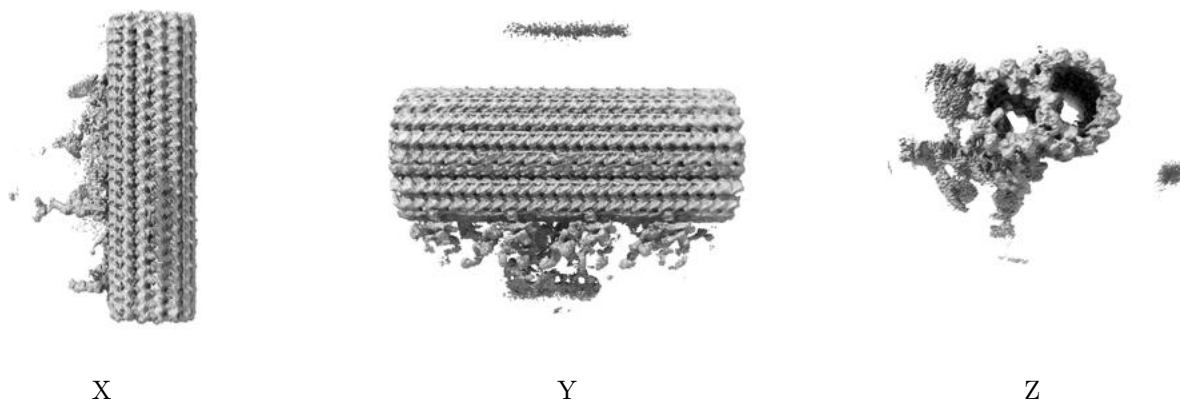


Z

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.

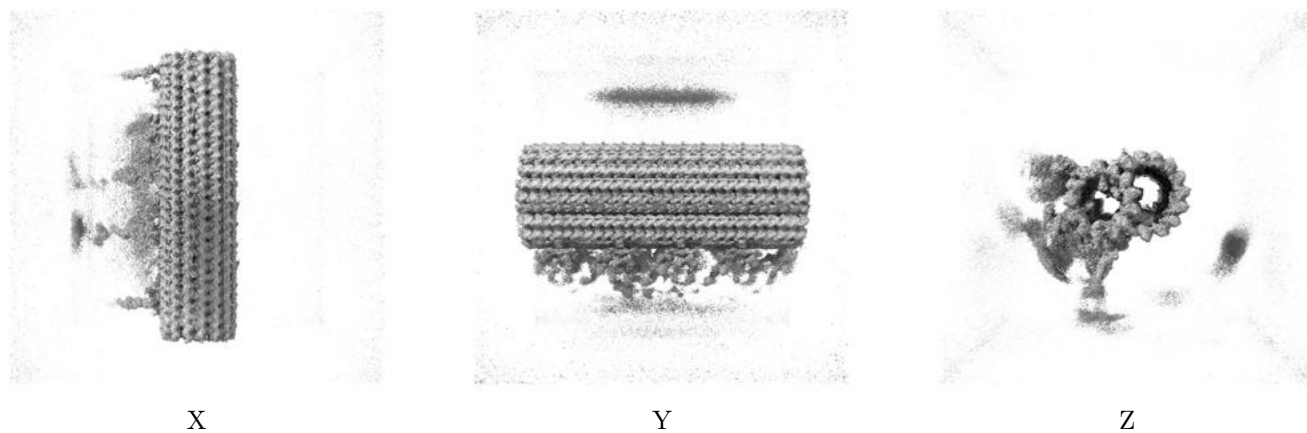
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.545. 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.

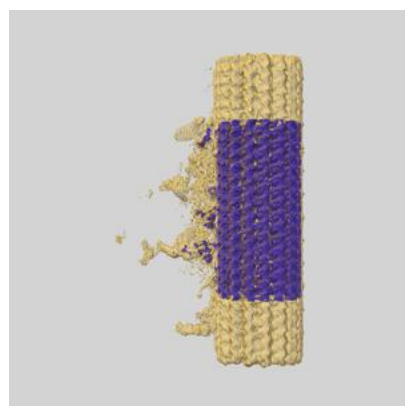
5.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

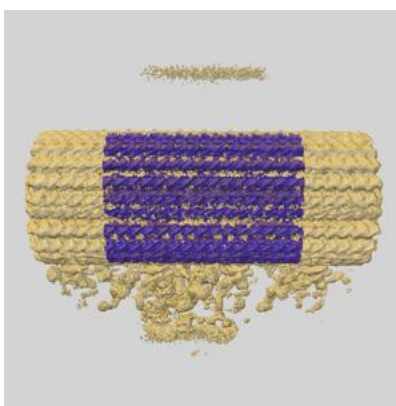
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

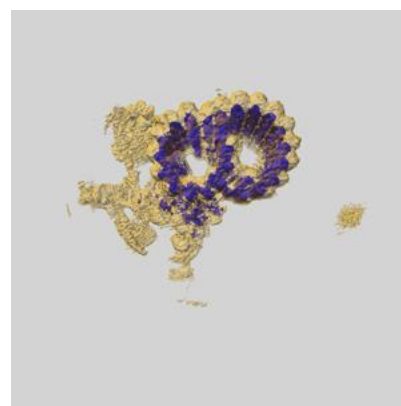
5.6.1 emd_41284_msk_1.map [i](#)



X



Y

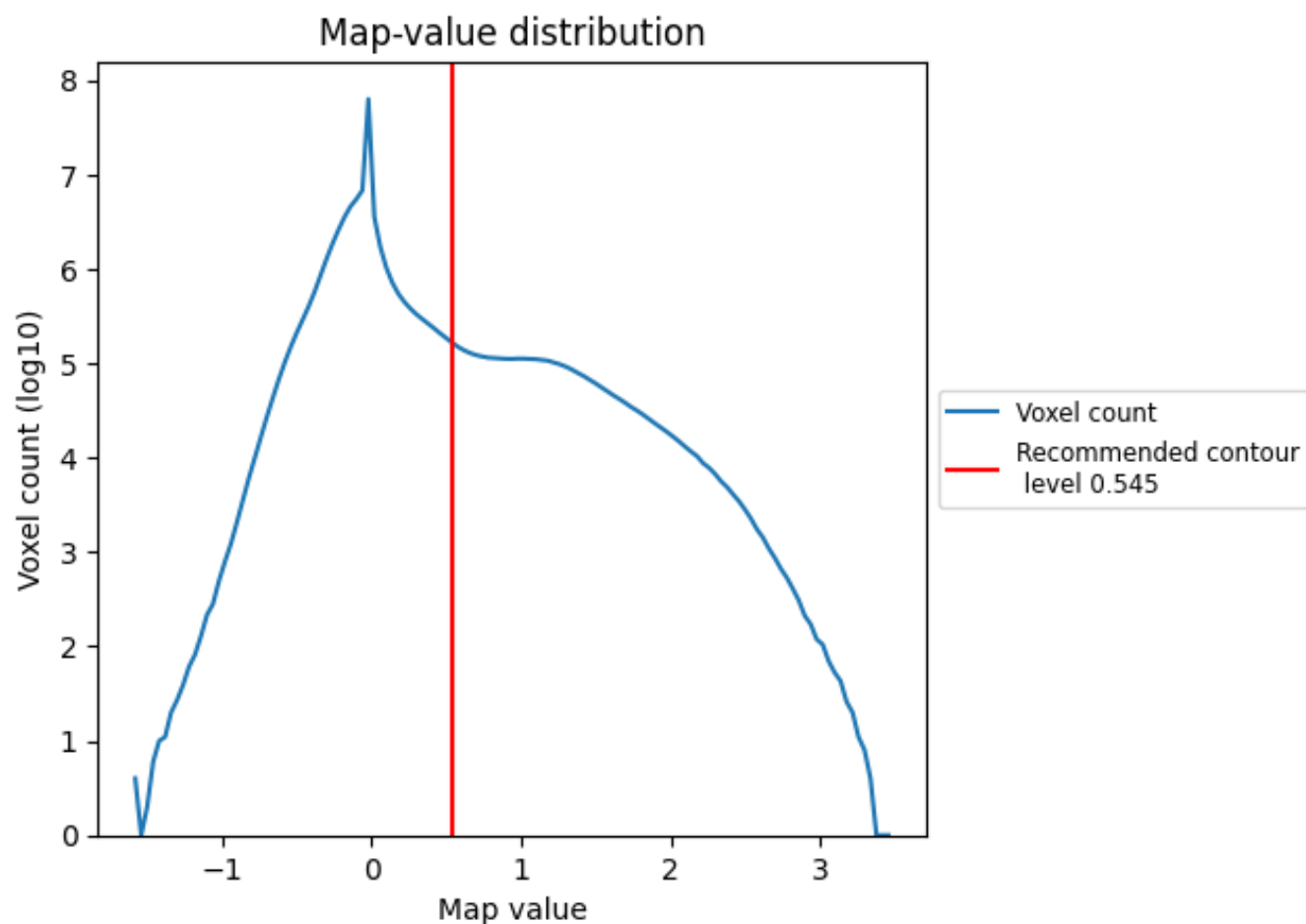


Z

6 Map analysis [i](#)

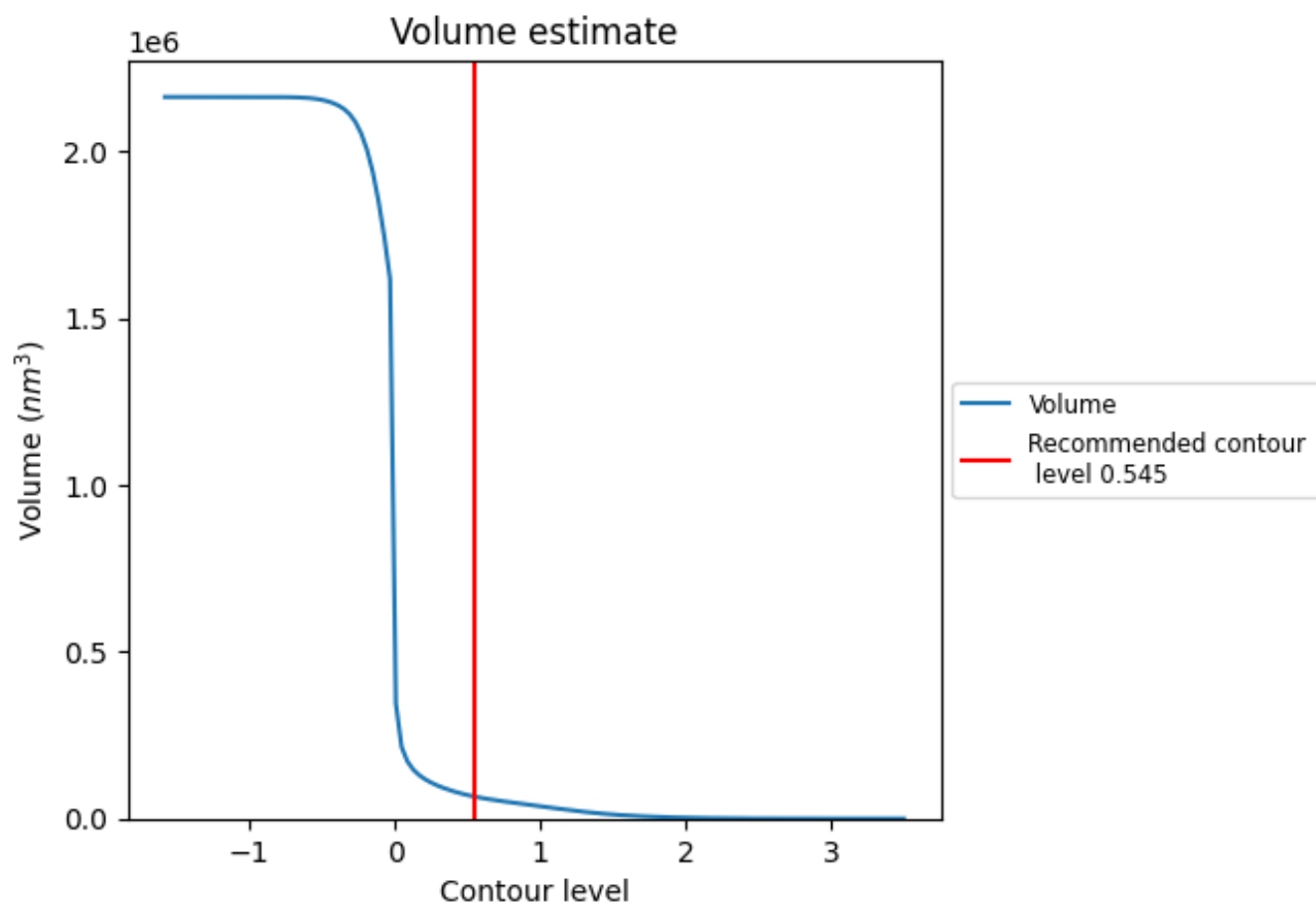
This section contains the results of statistical analysis of the map.

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.

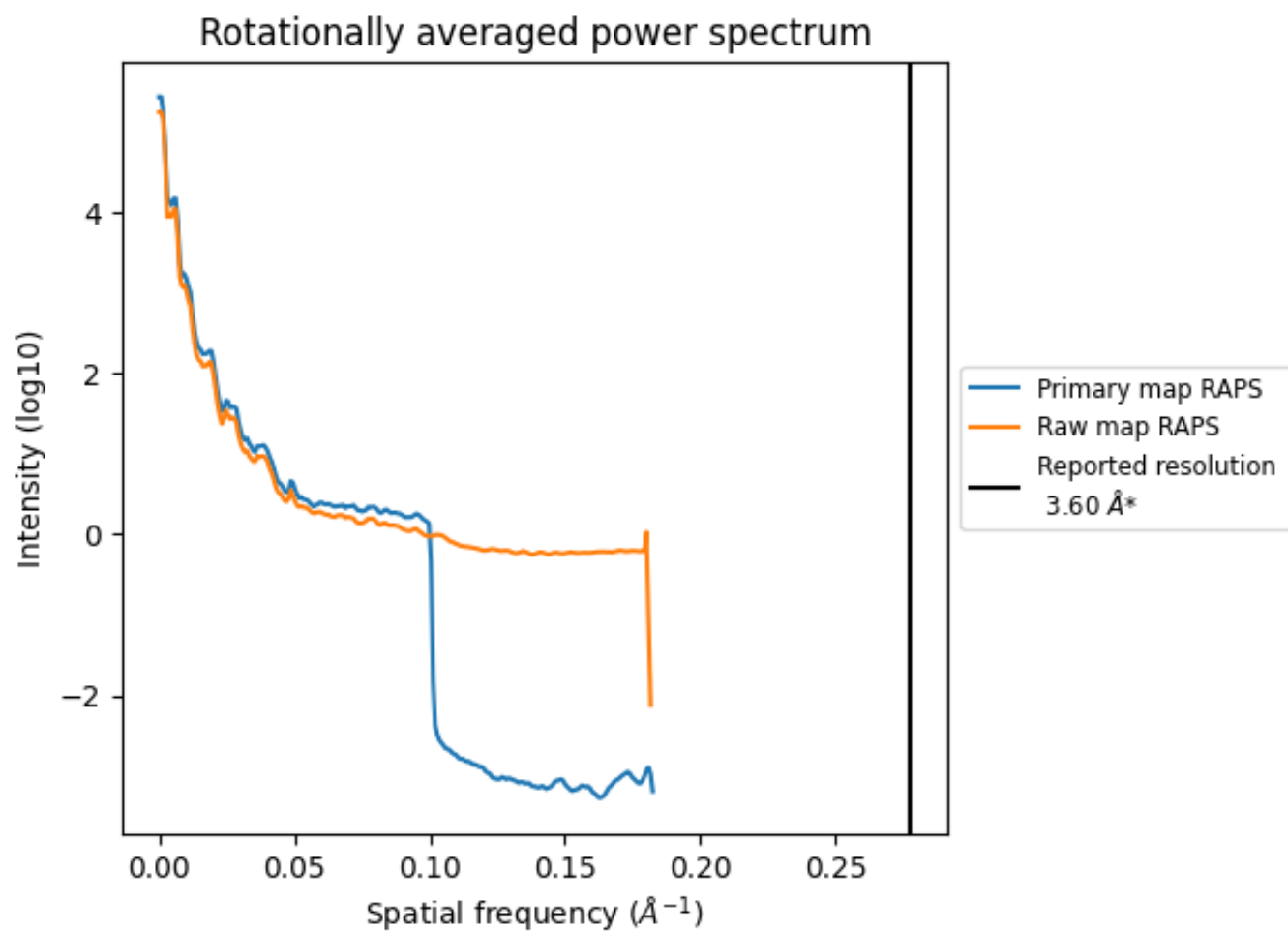
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 66091 nm^3 ; this corresponds to an approximate mass of 59702 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 [i](#)

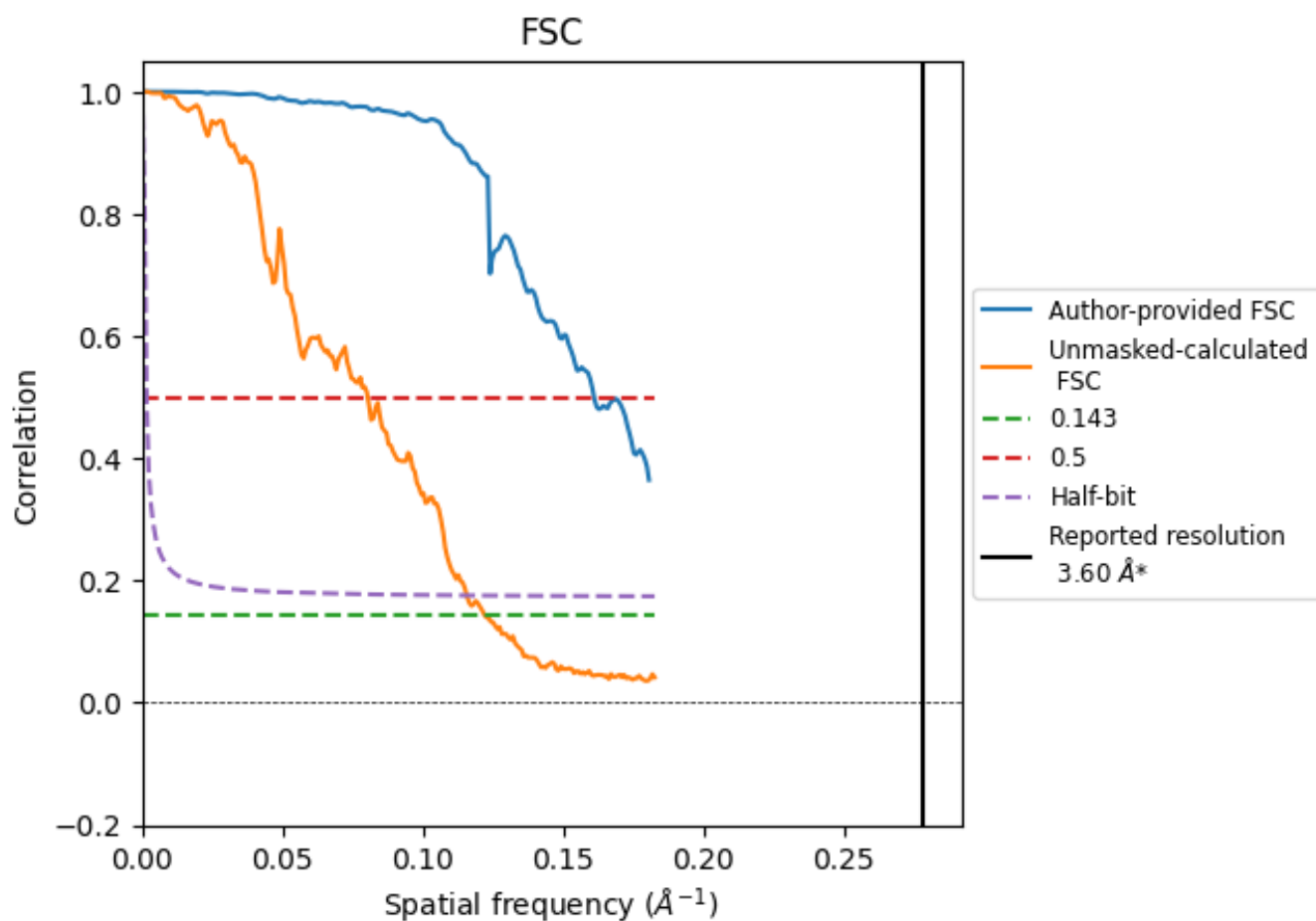


*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

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 0.278 Å⁻¹

7.2 Resolution estimates [i](#)

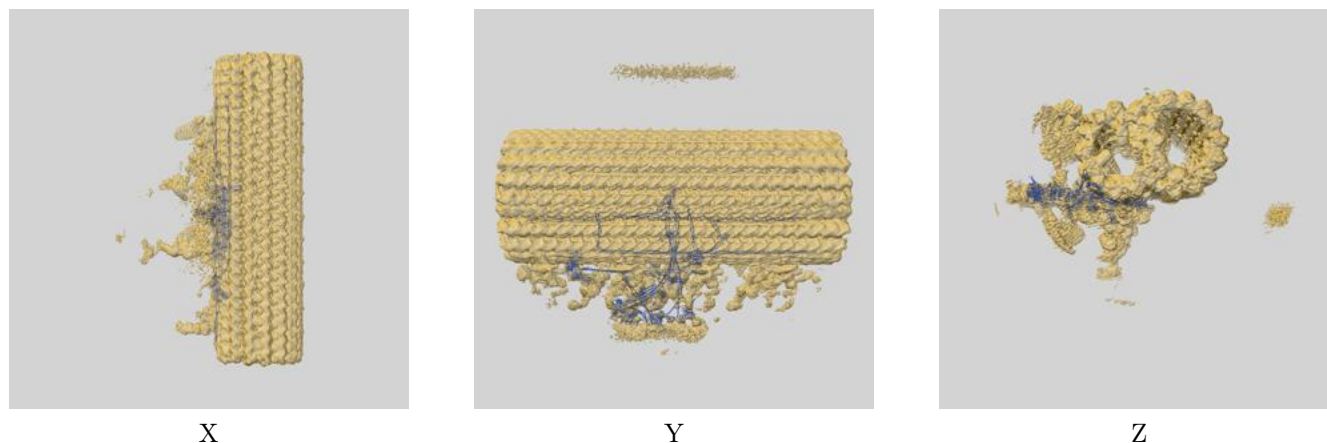
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.60
Author-provided FSC curve	-	6.22	-	-
Unmasked-calculated*	8.20	12.45	8.65	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

8 Map-model fit [i](#)

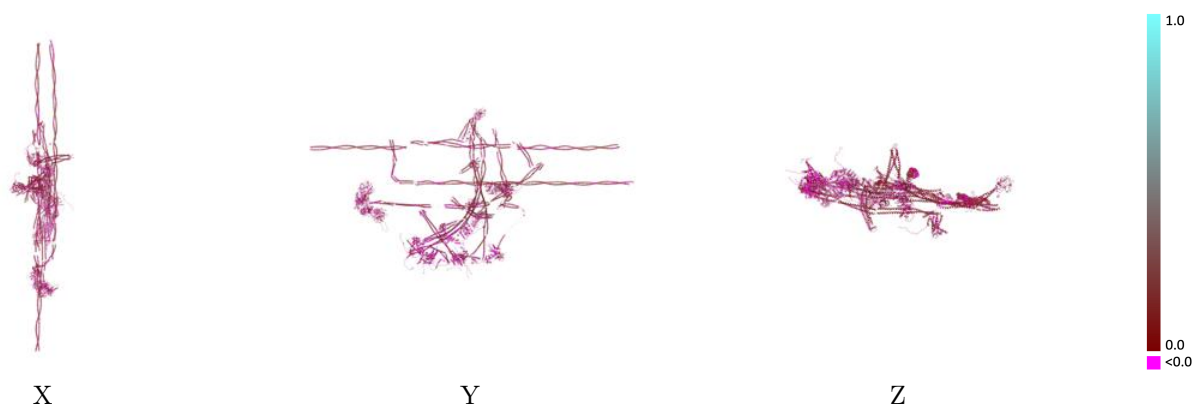
This section contains information regarding the fit between EMDB map EMD-41284 and PDB model 8TID. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



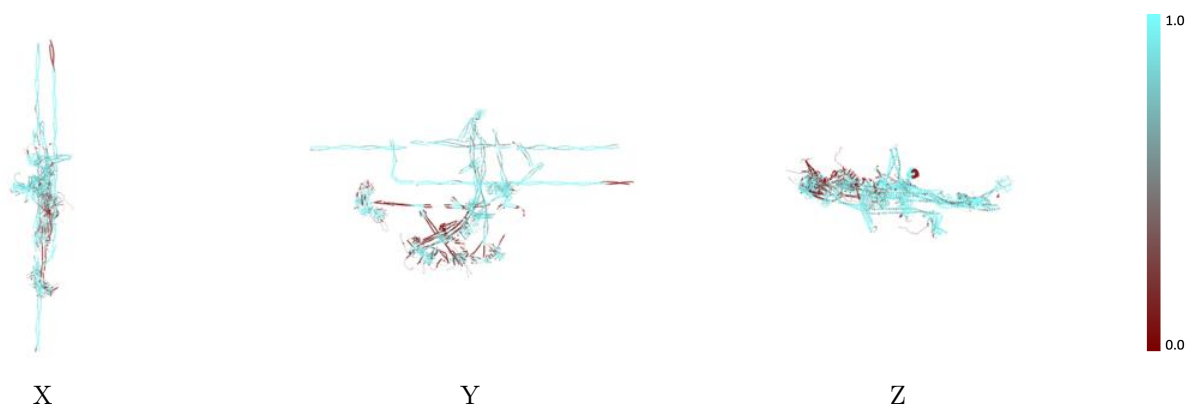
The images above show the 3D surface view of the map at the recommended contour level 0.545 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



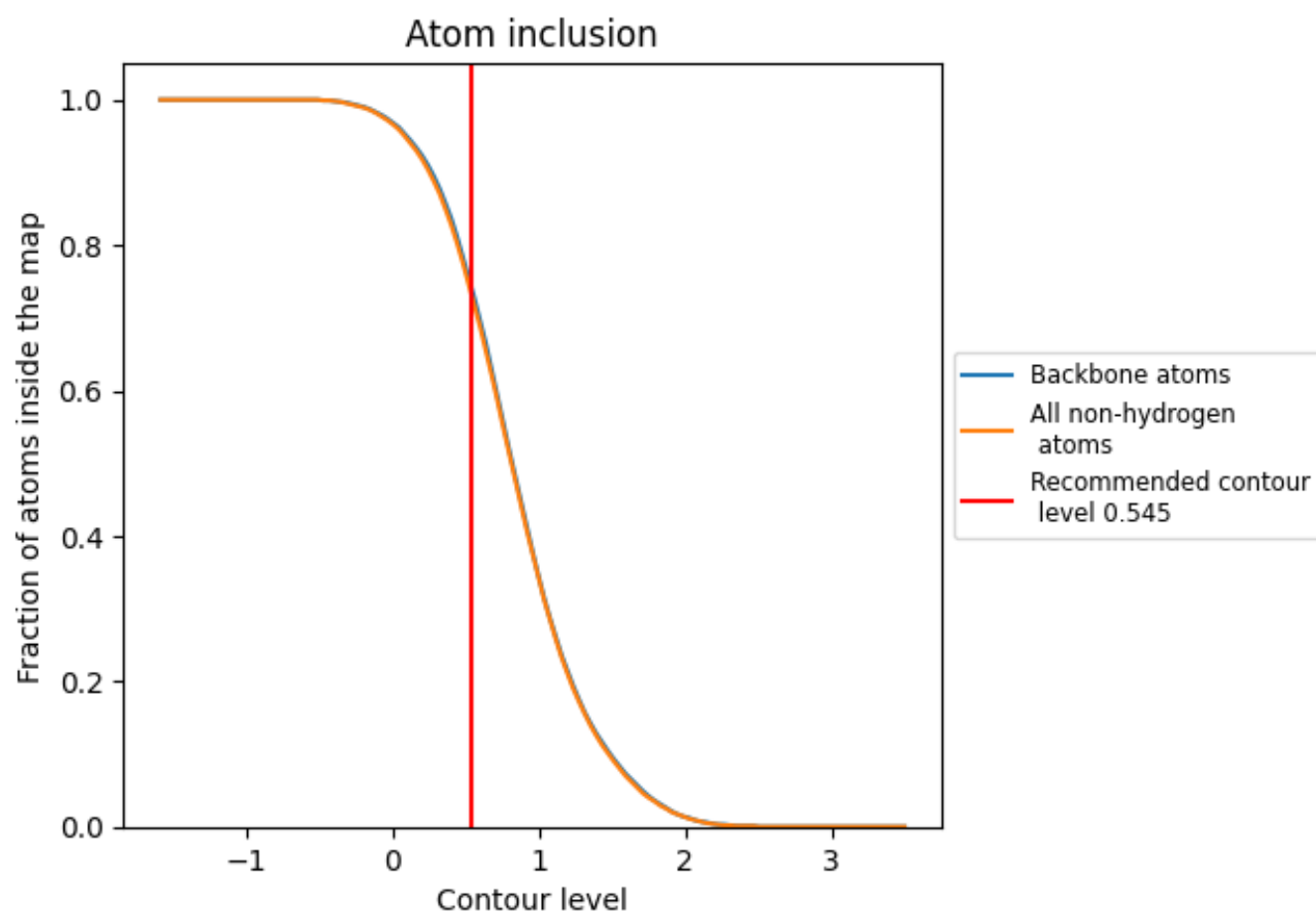
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.545).

8.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.545) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.0720
A	 0.6230	 0.0950
B	 0.5970	 0.0830
C	 0.9270	 0.0770
D	 0.7550	 0.0730
E	 0.8160	 0.0820
F	 0.2470	 0.0370
G	 0.7240	 0.0260
H	 0.7160	 0.0520
I	 0.9500	 0.0550
J	 0.7650	 0.0910
K	 0.7430	 0.0850
L	 0.6950	 0.0270
M	 0.8070	 0.1190
N	 0.8400	 0.0930
O	 0.8500	 0.1080
P	 0.7040	 0.0780
Q	 0.7370	 0.0350
R	 0.5740	 0.0500
S	 0.2970	 0.0610
T	 0.7580	 0.0850
U	 0.8690	 0.1310
V	 0.8790	 0.1240
W	 0.6990	 0.0670
Z	 0.8920	 0.0660
g	 0.8900	 0.0900
i	 0.5020	 0.0310
n	 0.8830	 0.0990
o	 0.9210	 0.1230
s	 0.2660	 0.0440
w	 0.6180	 0.0630

