



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 03:58 AM UTC

PDB ID : 8G4L / pdb_00008g4l
EMDB ID : EMD-29722
Title : Cryo-EM structure of the human cardiac myosin filament
Authors : Dutta, D.; Nguyen, V.; Padron, R.; Craig, R.
Deposited on : 2023-02-10
Resolution : 6.40 Å(reported)
Based on initial models : ., 5N69, 2FXO

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

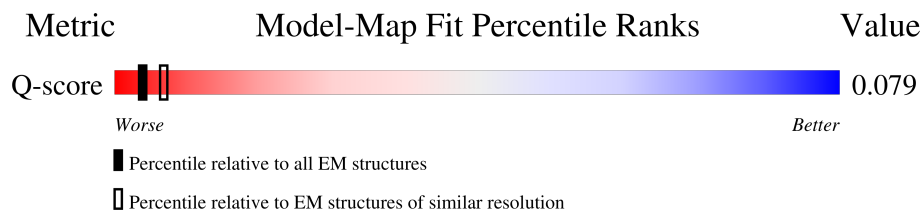
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.40 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	544 (5.90 - 6.90)

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

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 828952 atoms, of which 415168 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 Myosin-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	BB	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	BA	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	BG	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	BH	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	BI	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	BJ	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	BK	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	BL	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	BM	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	BN	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	BO	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	BP	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	BQ	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	BR	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	BS	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	BT	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	BU	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	BV	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	BW	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	BX	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	BY	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	BZ	1005	Total	C	H	N	O	S	0	0
			16317	5163	8185	1391	1535	43		
1	be	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	bf	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	bk	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	bl	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	AA	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	AB	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	AG	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	AH	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	AI	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	AJ	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	AK	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	AL	350	Total	C	H	N	O	S	0	0
			5683	1723	2843	521	587	9		
1	AM	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	AN	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	AO	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	AP	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	AQ	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	AR	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	AS	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	AT	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	AU	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	AV	325	Total	C	H	N	O	S	0	0
			5317	1592	2682	493	540	10		
1	AW	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	AX	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	AY	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	AZ	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	ae	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	af	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	ak	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	al	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	A	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	B	1133	Total	C	H	N	O	S	0	0
			18432	5800	9251	1582	1753	46		
1	G	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	H	355	Total	C	H	N	O	S	0	0
			5809	1751	2928	515	603	12		
1	I	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	J	357	Total	C	H	N	O	S	0	0
			5820	1753	2926	528	604	9		
1	K	350	Total	C	H	N	O	S	0	0
			5682	1723	2842	521	587	9		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	L	350	Total	C	H	N	O	S	0	0
			5682	1723	2842	521	587	9		
1	M	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	N	359	Total	C	H	N	O	S	0	0
			5823	1776	2906	522	611	8		
1	O	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	P	358	Total	C	H	N	O	S	0	0
			5809	1773	2902	523	603	8		
1	Q	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	R	357	Total	C	H	N	O	S	0	0
			5757	1748	2877	519	604	9		
1	S	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	T	359	Total	C	H	N	O	S	0	0
			5863	1760	2957	538	596	12		
1	U	325	Total	C	H	N	O	S	0	0
			5316	1592	2681	493	540	10		
1	V	325	Total	C	H	N	O	S	0	0
			5316	1592	2681	493	540	10		
1	W	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	X	224	Total	C	H	N	O	S	0	0
			3689	1107	1857	341	377	7		
1	Y	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	Z	1005	Total	C	H	N	O	S	0	0
			16316	5163	8184	1391	1535	43		
1	e	908	Total	C	H	N	O	S	0	0
			14751	4688	7390	1261	1370	42		
1	f	908	Total	C	H	N	O	S	0	0
			14752	4688	7391	1261	1370	42		
1	k	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		
1	l	132	Total	C	H	N	O	S	0	0
			2205	664	1111	207	221	2		

- Molecule 2 is a protein called Myosin light chain 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	BE	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	BF	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ba	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bb	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bg	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	bh	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	AE	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	AF	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	aa	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ab	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ag	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	ah	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	E	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	F	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	a	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	b	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	g	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		
2	h	161	Total	C	H	N	O	S	0	0
			2544	806	1260	213	254	11		

- Molecule 3 is a protein called Myosin regulatory light chain 2, ventricular/cardiac muscle isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	bc	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	bd	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	bi	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	bj	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	bq	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	br	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ac	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	ad	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ai	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	aj	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	aq	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	ar	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	c	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	d	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	i	153	Total	C	H	N	O	S	0	0
			2418	780	1187	200	245	6		
3	j	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	q	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		
3	r	166	Total	C	H	N	O	S	0	0
			2617	836	1296	220	258	7		

- Molecule 4 is a protein called Titin.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	bm	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	bn	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		

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Mol	Chain	Residues	Atoms						AltConf	Trace
4	am	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	an	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	m	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		
4	n	1084	Total	C	H	N	O	S	0	0
			16881	5325	8458	1439	1632	27		

- Molecule 5 is a protein called Myosin-binding protein C, cardiac-type.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	bo	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		
5	ao	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		
5	o	598	Total	C	H	N	O	S	0	0
			9440	2992	4728	825	873	22		

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, C3	Depositor
Number of particles used	102581	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 ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.360	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	869.83997, 869.83997, 869.83997	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0873, 1.0873, 1.0873	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.

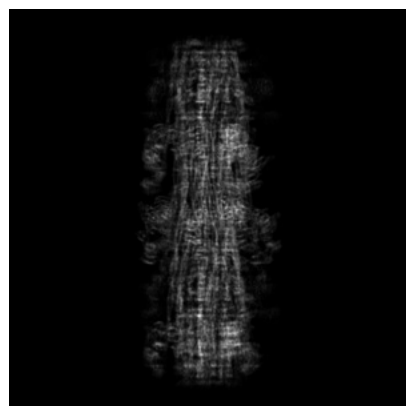
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29722. These allow visual inspection of the internal detail of the map and identification of artifacts.

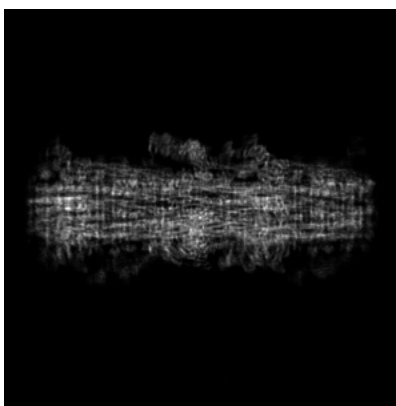
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

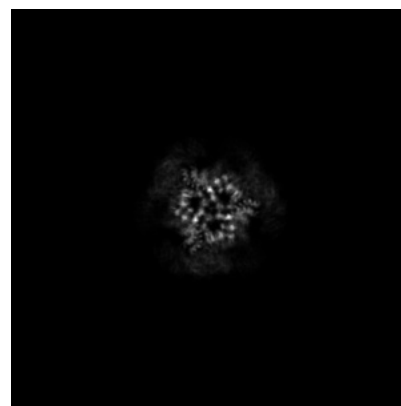
5.1.1 Primary map



X

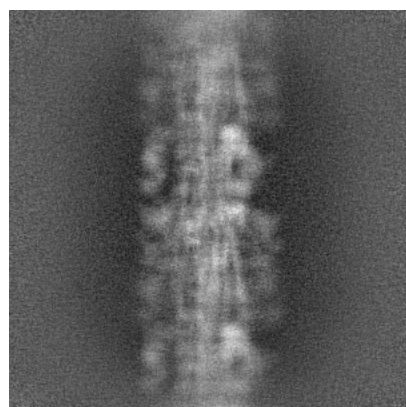


Y

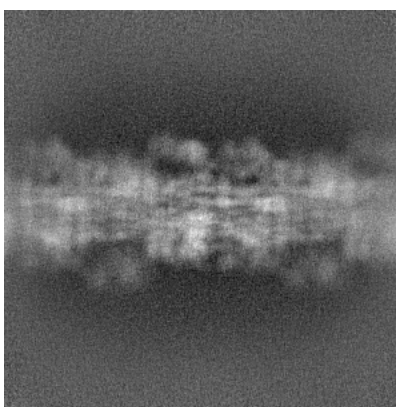


Z

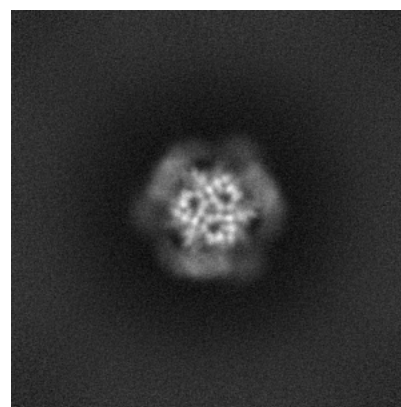
5.1.2 Raw map



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: 400

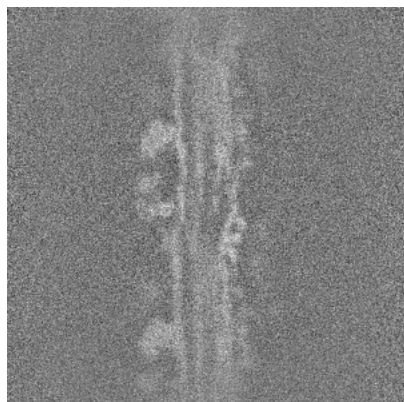


Y Index: 400

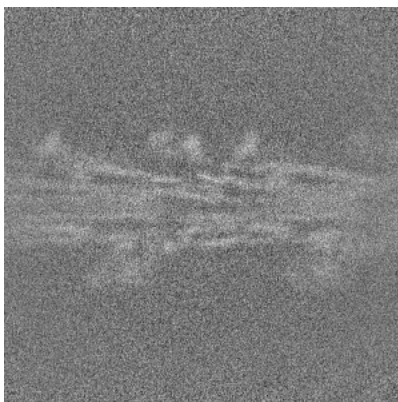


Z Index: 400

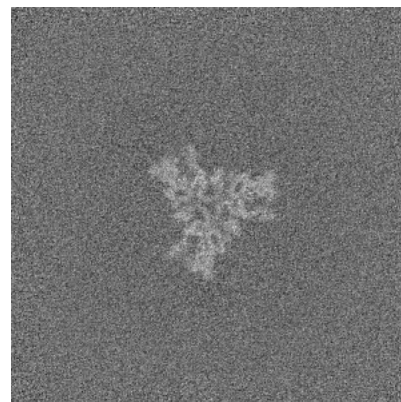
5.2.2 Raw map



X Index: 400



Y Index: 400



Z Index: 400

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: 368

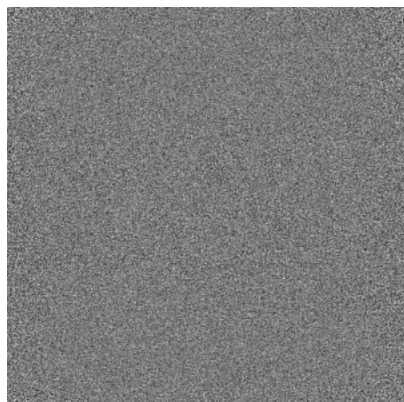


Y Index: 381

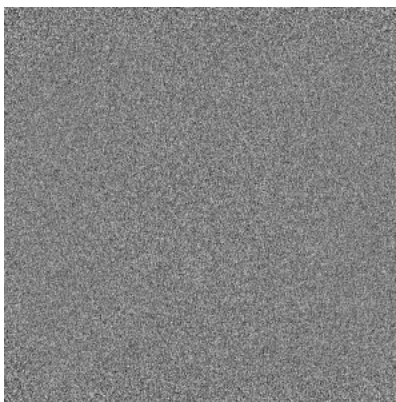


Z Index: 129

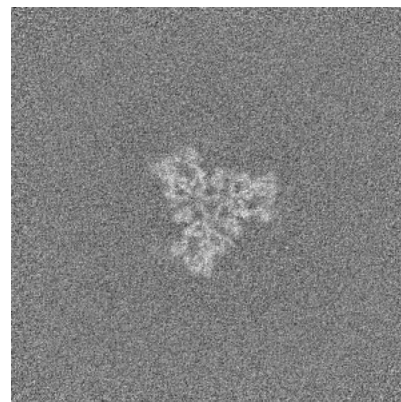
5.3.2 Raw map



X Index: 0



Y Index: 0

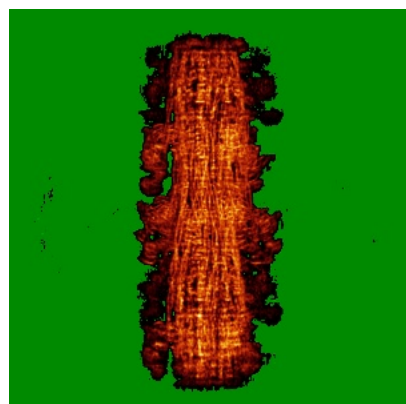


Z Index: 396

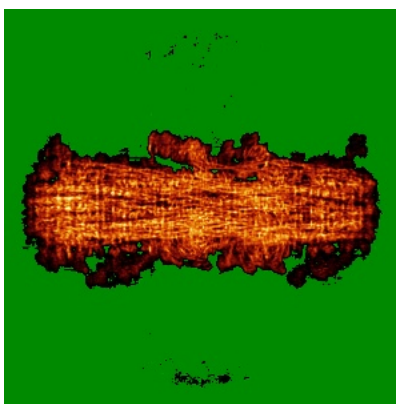
The images above show the largest variance slices of the map in three orthogonal directions.

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

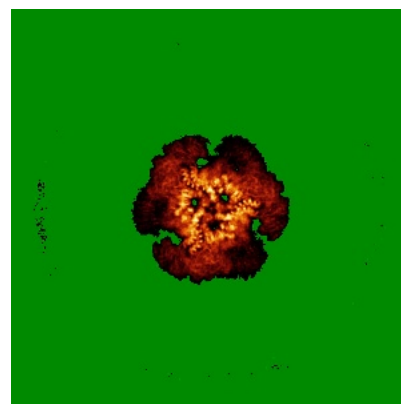
5.4.1 Primary map



X

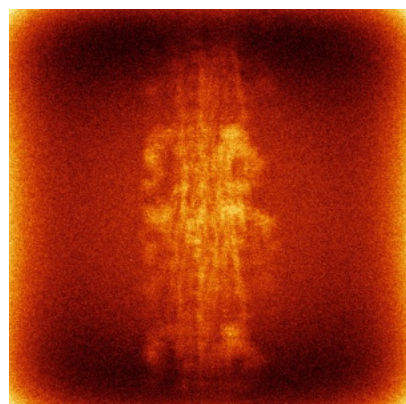


Y

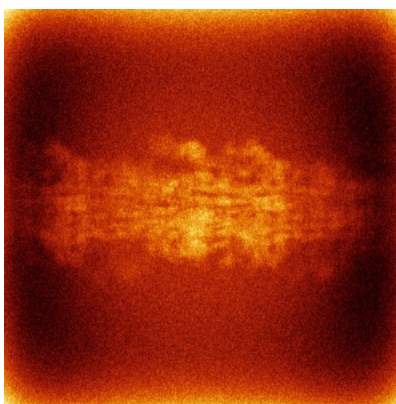


Z

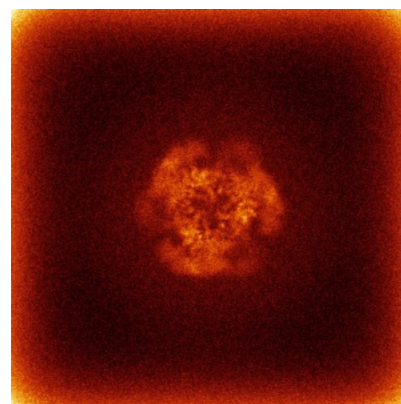
5.4.2 Raw map



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](#)

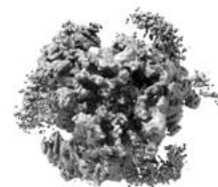
5.5.1 Primary map



X



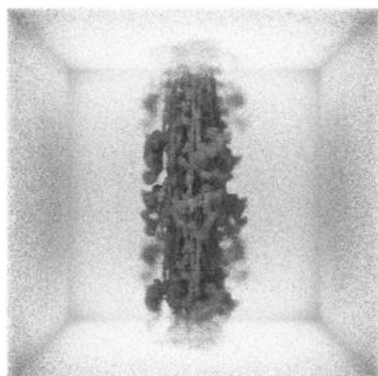
Y



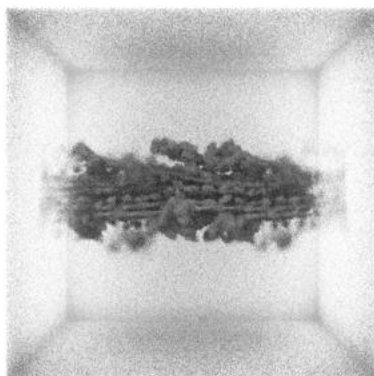
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

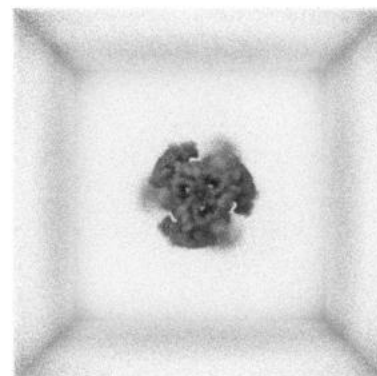
5.5.2 Raw map



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.

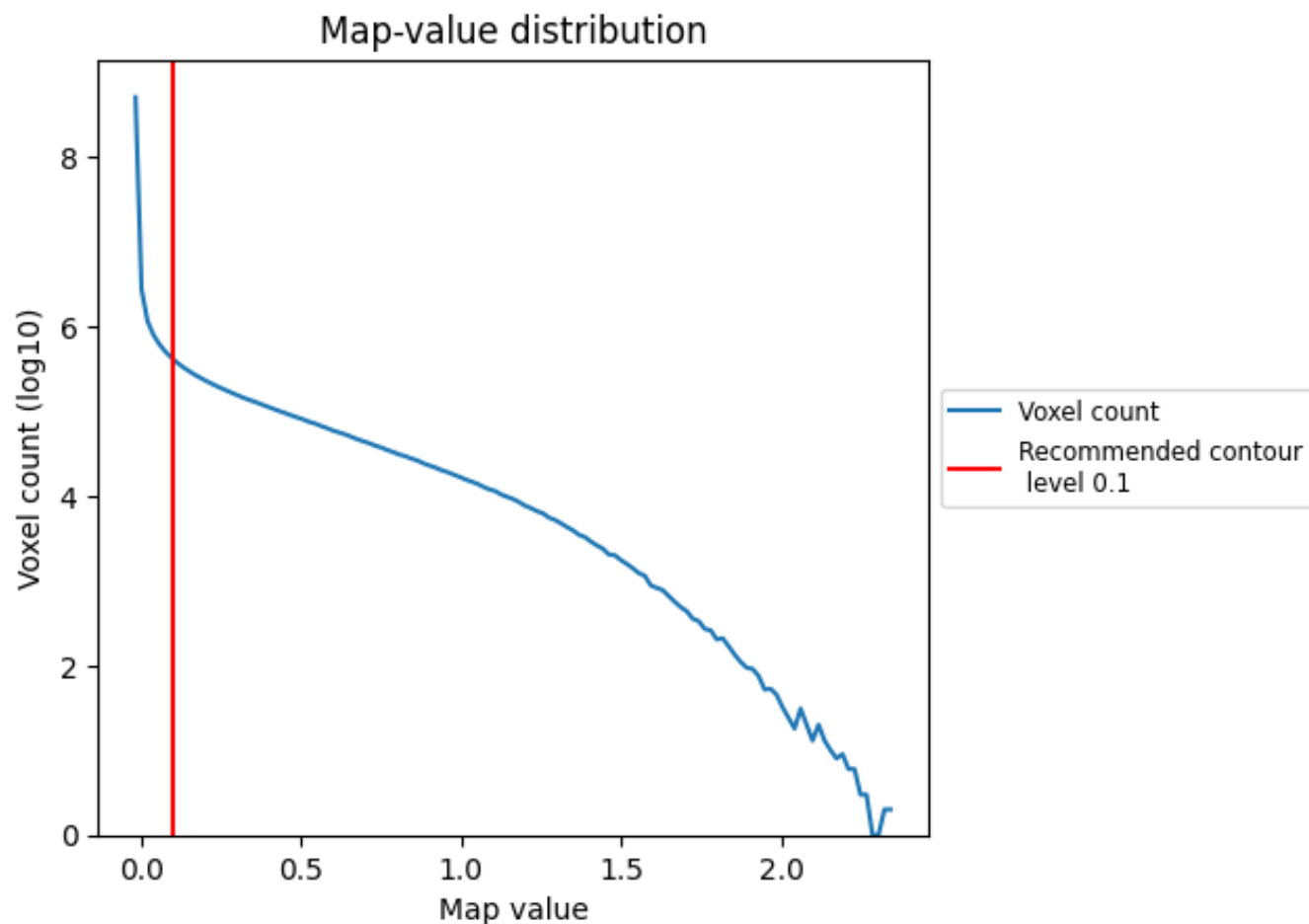
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

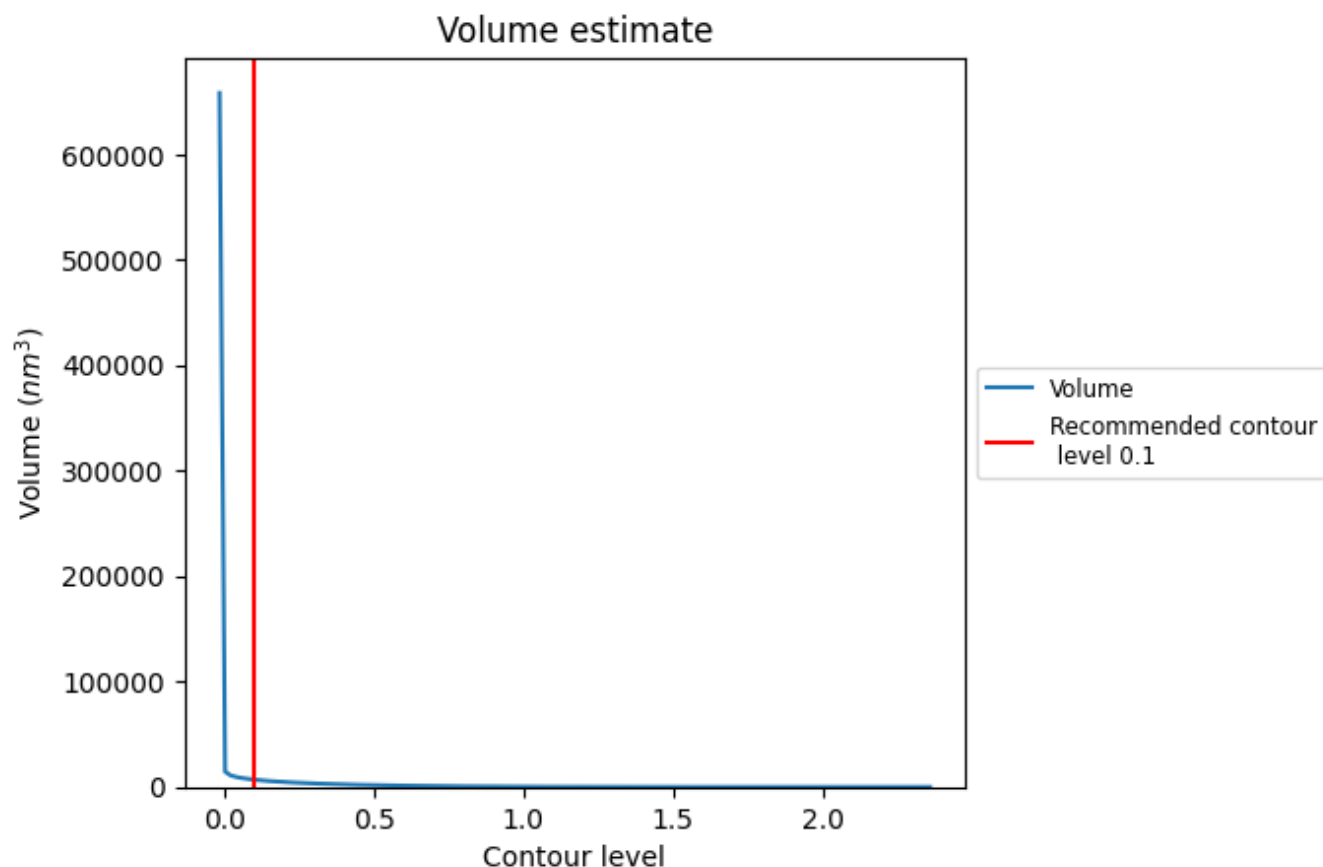
This section contains the results of statistical analysis of the map.

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.

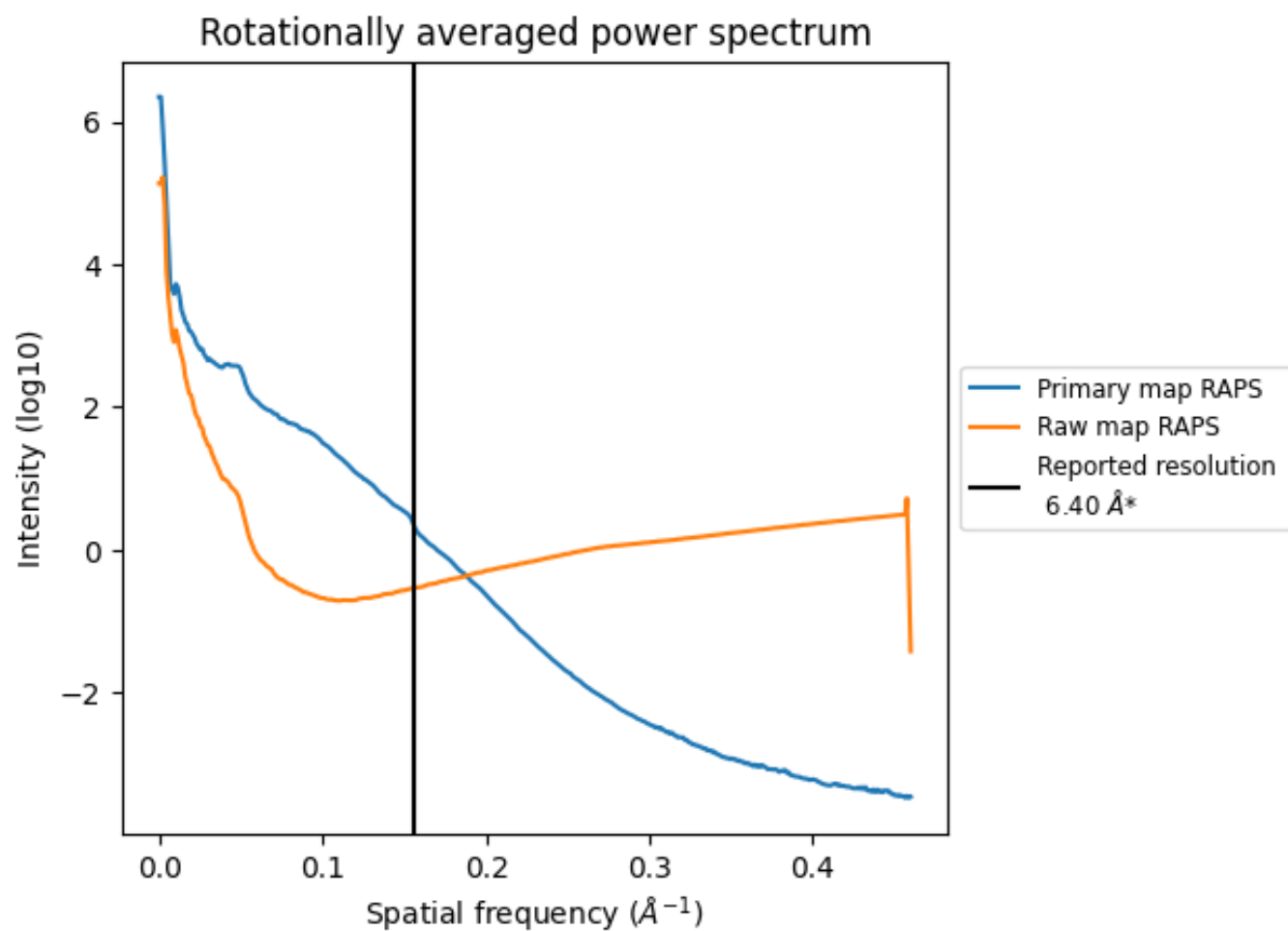
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 6910 nm^3 ; this corresponds to an approximate mass of 6242 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 ⓘ

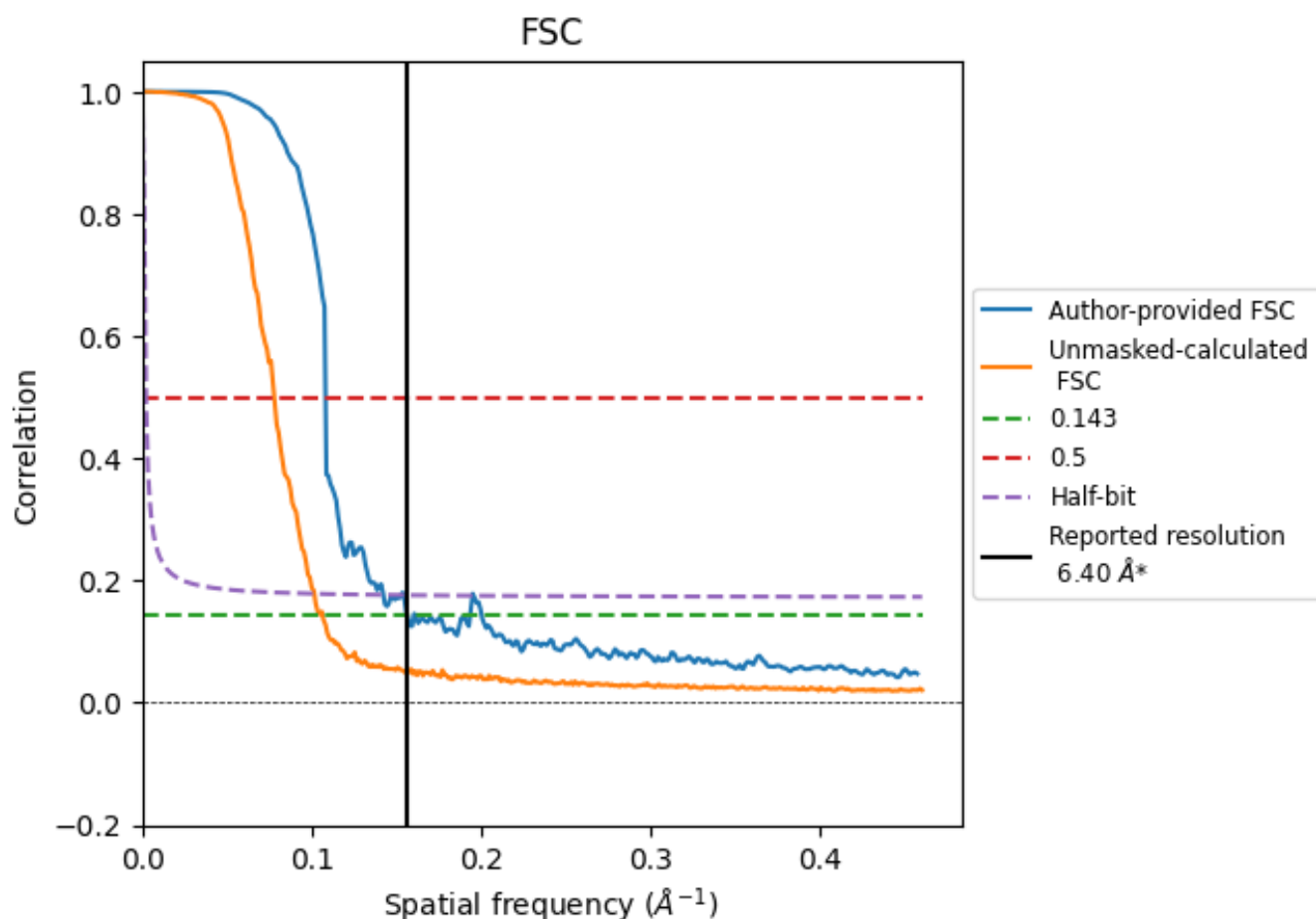


*Reported resolution corresponds to spatial frequency of 0.156 $\text{\AA}^{-1}$

7 Fourier-Shell correlation ⓘ

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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.156 $\text{\AA}^{-1}$

7.2 Resolution estimates [i](#)

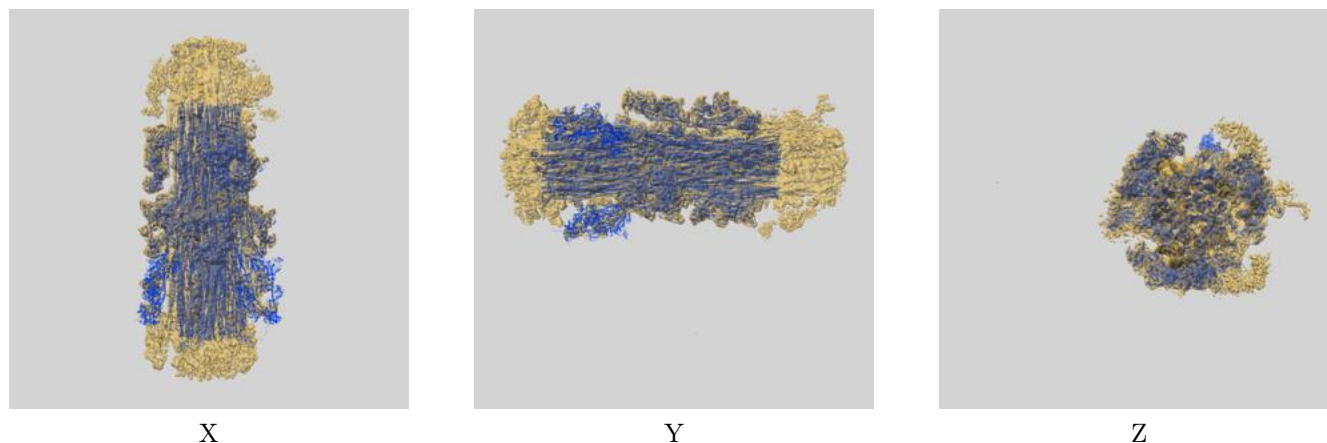
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.40	-	-
Author-provided FSC curve	6.41	9.25	7.03
Unmasked-calculated*	9.41	12.84	9.86

*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 9.41 differs from the reported value 6.4 by more than 10 %

8 Map-model fit [i](#)

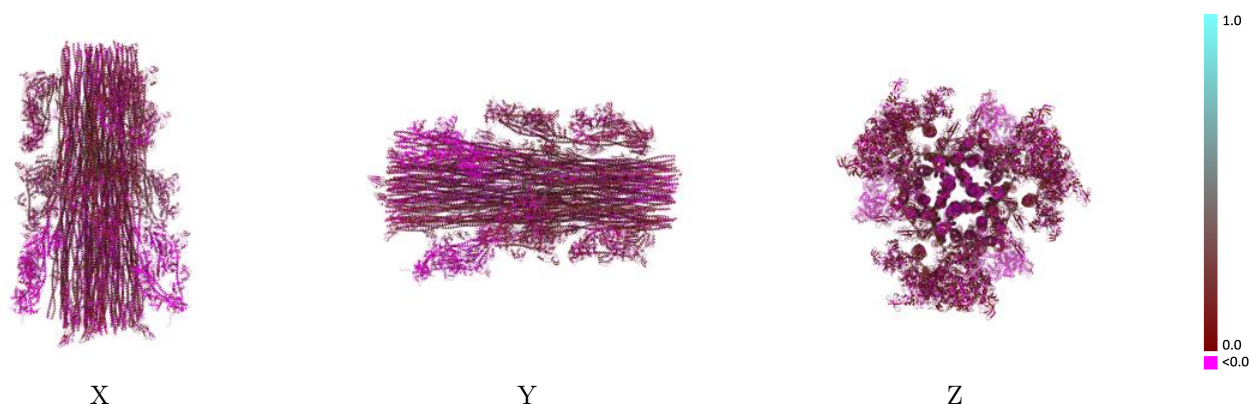
This section contains information regarding the fit between EMDB map EMD-29722 and PDB model 8G4L. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



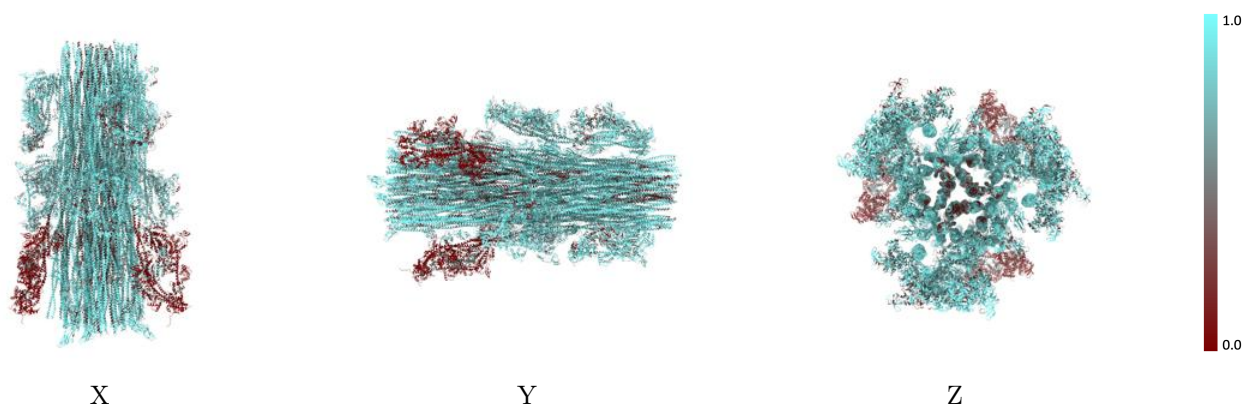
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



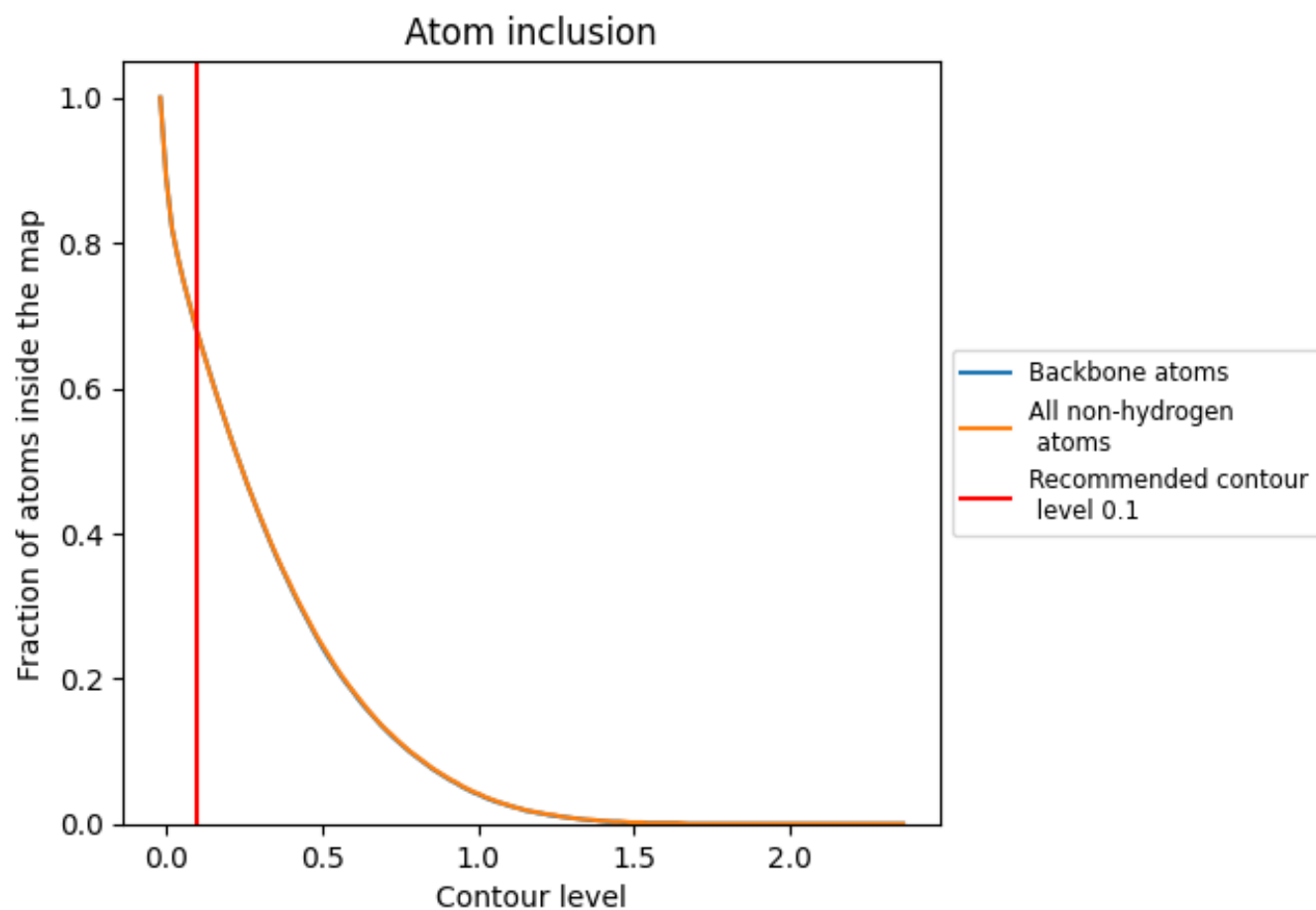
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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 (0.1).

8.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 68% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6810	 0.0790
A	 0.2650	 -0.0250
AA	 0.3430	 -0.0170
AB	 0.2210	 -0.0370
AE	 0.1360	 -0.0560
AF	 0.0470	 -0.0230
AG	 0.8700	 0.1190
AH	 0.8280	 0.1130
AI	 0.9140	 0.1360
AJ	 0.9200	 0.1450
AK	 0.8660	 0.1180
AL	 0.8090	 0.0960
AM	 0.5970	 0.0480
AN	 0.5480	 0.0270
AO	 0.8540	 0.1170
AP	 0.8470	 0.1070
AQ	 0.8280	 0.1020
AR	 0.8060	 0.1010
AS	 0.6000	 0.0520
AT	 0.6740	 0.0720
AU	 0.7840	 0.0970
AV	 0.7500	 0.0830
AW	 0.6910	 0.0580
AX	 0.7710	 0.0920
AY	 0.7880	 0.1070
AZ	 0.7950	 0.1310
B	 0.2460	 -0.0360
BA	 0.2410	 -0.0350
BB	 0.2940	 -0.0170
BE	 0.0480	 -0.0570
BF	 0.1030	 -0.0320
BG	 0.8580	 0.1180
BH	 0.8210	 0.1100
BI	 0.9000	 0.1350
BJ	 0.9150	 0.1440



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Chain	Atom inclusion	Q-score
BK	 0.8730	 0.1170
BL	 0.8090	 0.0940
BM	 0.6520	 0.0510
BN	 0.6230	 0.0340
BO	 0.8630	 0.1130
BP	 0.8610	 0.1140
BQ	 0.8260	 0.0970
BR	 0.8100	 0.1020
BS	 0.6620	 0.0540
BT	 0.7050	 0.0770
BU	 0.7720	 0.0900
BV	 0.7530	 0.0830
BW	 0.6920	 0.0600
BX	 0.7870	 0.0940
BY	 0.7550	 0.1010
BZ	 0.7730	 0.1250
E	 0.0840	 -0.0520
F	 0.0780	 -0.0230
G	 0.8420	 0.1140
H	 0.8320	 0.1150
I	 0.9020	 0.1370
J	 0.9260	 0.1440
K	 0.8740	 0.1230
L	 0.8080	 0.0920
M	 0.6410	 0.0510
N	 0.5670	 0.0180
O	 0.8680	 0.1230
P	 0.8520	 0.1060
Q	 0.8310	 0.1010
R	 0.8030	 0.0990
S	 0.5610	 0.0520
T	 0.6430	 0.0730
U	 0.8290	 0.1000
V	 0.7780	 0.0870
W	 0.7190	 0.0660
X	 0.7940	 0.0950
Y	 0.7630	 0.1030
Z	 0.7840	 0.1280
a	 0.6540	 0.0680
aa	 0.6300	 0.0580
ab	 0.7810	 0.1180
ac	 0.7780	 0.0770

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Chain	Atom inclusion	Q-score
ad	 0.7960	 0.1070
ae	 0.7370	 0.0900
af	 0.7700	 0.1050
ag	 0.4740	 0.0350
ah	 0.8570	 0.1060
ai	 0.6190	 0.0530
aj	 0.6560	 0.0620
ak	 0.5980	 0.0130
al	 0.6600	 0.0560
am	 0.7840	 0.1050
an	 0.9080	 0.1470
ao	 0.8150	 0.1500
aq	 0.0860	 -0.0700
ar	 0.0370	 -0.0590
b	 0.7620	 0.1120
ba	 0.6380	 0.0550
bb	 0.8040	 0.1230
bc	 0.7290	 0.0750
bd	 0.7790	 0.1030
be	 0.7170	 0.0870
bf	 0.8090	 0.1110
bg	 0.6160	 0.0500
bh	 0.8780	 0.1170
bi	 0.7290	 0.0460
bj	 0.7150	 0.0740
bk	 0.6390	 0.0250
bl	 0.7100	 0.0590
bm	 0.7780	 0.1020
bn	 0.9050	 0.1440
bo	 0.7900	 0.1420
bq	 0.1160	 -0.0660
br	 0.1350	 -0.0600
c	 0.7080	 0.0660
d	 0.7870	 0.1030
e	 0.7280	 0.0910
f	 0.8130	 0.1110
g	 0.5370	 0.0360
h	 0.8800	 0.1170
i	 0.5490	 0.0400
j	 0.6630	 0.0610
k	 0.5490	 0.0130
l	 0.6400	 0.0490

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Chain	Atom inclusion	Q-score
m	 0.7930	 0.1050
n	 0.9000	 0.1450
o	 0.7960	 0.1470
q	 0.0340	 -0.0740
r	 0.0680	 -0.0630