



wwPDB EM Validation Summary Report ⓘ

Apr 20, 2026 – 01:27 PM EDT

PDB ID : 9Z04 / pdb_00009z04
EMDB ID : EMD-73693
Title : Structure of human lymphoid-specific helicase HELLS in its auto-inhibitory state
Authors : Kaur, G.; Horton, J.R.; Cheng, X.
Deposited on : 2025-10-31
Resolution : 2.99 Å(reported)
Based on initial model : .

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

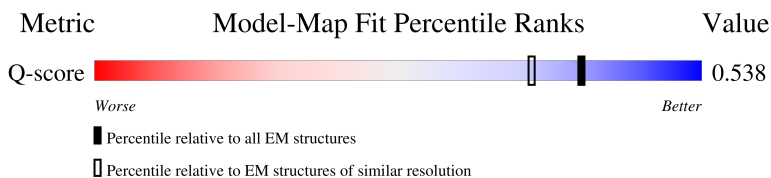
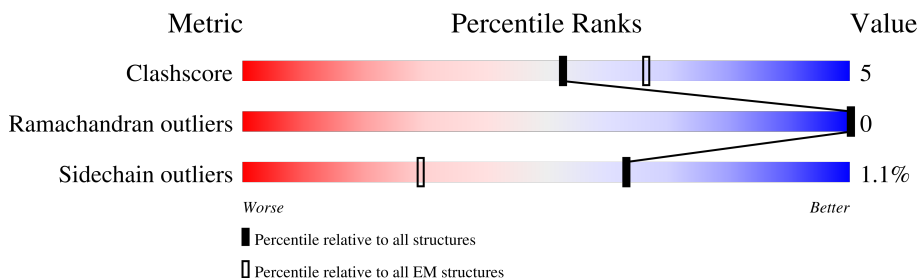
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.99 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	-
Q-score	-	25397	13287 (2.49 - 3.49)

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	A	838	
1	B	838	
1	C	838	
1	D	838	

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Mol	Chain	Length	Quality of chain
1	E	838	 34%5%61%
1	F	838	 34%5%61%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16158 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 Lymphoid-specific helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		
1	B	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		
1	C	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		
1	D	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		
1	E	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		
1	F	329	Total	C	N	O	S	1	0
			2693	1723	469	484	17		

LEU	LEU	LEU	ASP	ASP	ASP	GLY	ASP	GLN	ASN
GLU	GLU	ASP	ASP	CYS	CYS	GLY	GLY	GLU	GLU
ASN	ASN	PRO	PRO	ARG	ARG	SER	SER	PHE	LEU
SER	SER	GLY	GLY	HIS	HIS	MET	MET	ILE	LYS
ASP	ASP	LEU	ILE	ILE	ILE	TYR	TYR	ASP	LEU
SER	SER	MET	GLY	GLY	GLY	SER	SER	GLU	ILE
SER	SER	GLU	GLU	THR	THR	GLU	GLU	GLU	SER
PRO	PRO	LEU	LEU	THR	THR	ARG	ARG	LEU	GLN
GLU	GLU	LEU	LYS	LYS	PRO	LYS	LYS	THR	GLN
CYS	CYS	LYS	VAL	VAL	VAL	ASN	ASN	ASN	PRO
LEU	LEU	ARG	VAL	VAL	VAL	MET	SER	SER	GLU
PHE	PHE	ARG	VAL	VAL	VAL	HIS	HIS	GLY	VAL
		TYR	TYR	TYR	TYR	SER	SER	LYS	ASP
		GLU	GLU	ARG	ARG	PHE	PHE	GLU	ARG
		ARG	LEU	LEU	LEU	ASN	ASN	LEU	GLU
		GLU	VAL	VAL	THR	THR	THR	ILE	ARG
		ILE	THR	THR	ASP	ASP	ASP	LEU	ALA
		LYS	ALA	ALA	PRO	PRO	PRO	ASP	VAL
		GLY	ASN	ASN	GLU	GLU	GLU	ARG	VAL
		SER	THR	THR	VAL	VAL	VAL	MET	GLU
		ARG	ILE	ILE	PHE	PHE	LEU	VAL	VAL
		GLU	ASP	ILE	ILE	ILE	GLY	LEU	ASN
		LYS	GLN	GLN	PHE	PHE	ILE	GLU	ASN
		VAL	LYS	ILE	VAL	VAL	VAL	LEU	VAL
		ILE	ILE	ILE	THR	THR	THR	GLU	PRO
		SER	VAL	VAL	SER	SER	SER	LYS	VAL
		ASP	GLU	GLU	THR	THR	THR	ARG	SER
		LYS	ARG	ARG	ARG	ARG	ARG	GLY	GLU
		ASP	ALA	ALA	ALA	ALA	ALA	HIS	VAL
		LEU	ALA	ALA	GLY	GLY	GLY	LYS	ASN
		GLU	ALA	ALA	LEU	LEU	LEU	VAL	LEU
		LEU	LYS	LYS	LEU	LEU	LEU	LYS	LYS
		LEU	ARG	ARG	GLY	GLY	GLY	LEU	LEU
		LEU	LYS	LYS	ILE	ILE	ASP	PHE	GLN
		ASP	LEU	LEU	THR	THR	THR	LEU	ASN
		ARG	GLU	GLU	LEU	LEU	LEU	ARG	ASN
		SER	LYS	LYS	THR	THR	THR	MET	ILE
		ASP	ARG	ARG	ASP	ASP	ASP	MET	GLN
		LEU	ILE	ILE	ILE	ILE	ILE	LEU	CYS
		LEU	GLN	GLN	VAL	VAL	VAL	ASP	LYS
		ASP	HIS	HIS	ILE	ILE	ILE	LEU	CYS
		ALA	PHE	PHE	TYR	TYR	TYR	MET	ASN
		SER	LYS	LYS	ASP	ASP	ASP	ASP	HIS
		GLY	GLY	GLY	SER	SER	SER	TYR	TYR
		PRO	GLY	GLY	ASP	ASP	CYS	GLY	LEU
		ILE	ILE	GLN	TRP	TRP	HIS	HIS	LEU
		GLY	SER	SER	ASN	ASN	LEU	LEU	ILE
		GLU	GLY	GLY	PRO	PRO	ARG	ASP	TYR
		LYS	LEU	LEU	GLN	GLN	ASP	ASP	TYR
		MET	ASN	ASN	SER	SER	PHE	PHE	PRO
		GLY	LEU	LEU	ASP	ASP	GLY	GLY	ILE
		ILE	ILE	SER	LEU	LEU	LEU	LEU	ASN
		PHE	LYS	LYS	GLN	GLN	SER	SER	PRO
		LYS	ASN	ASN	ALA	ALA	ARG	ARG	VAL
		THR	PHE	PHE	GLN	GLN	LEU	LEU	THR

- Molecule 1: Lymphoid-specific helicase



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Response	Percentage
Yes	34%
No	5%
Don't know	61%



Response	Percentage
Yes	34%
No	5%
Don't know	61%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	338516	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 ($e^-/\text{\AA}^2$)	58.51	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.891	Depositor
Minimum map value	-1.890	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.178	Depositor
Map size (Å)	317.568, 317.568, 317.568	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82699996, 0.82699996, 0.82699996	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	A	0.18	0/2751	0.27	0/3711
1	B	0.18	0/2751	0.27	0/3711
1	C	0.17	0/2751	0.27	0/3711
1	D	0.18	0/2751	0.27	0/3711
1	E	0.17	0/2751	0.27	0/3711
1	F	0.17	0/2751	0.26	0/3711
All	All	0.17	0/16506	0.27	0/22266

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	A	2693	0	2711	32	0
1	B	2693	0	2711	34	0
1	C	2693	0	2711	31	0
1	D	2693	0	2711	32	0
1	E	2693	0	2711	30	0
1	F	2693	0	2711	27	0
All	All	16158	0	16266	171	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 5.

The worst 5 of 171 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)
1:A:34:GLU:HG3	1:D:280:LEU:HD22	1.68	0.74
1:A:280:LEU:HD22	1:D:34:GLU:HG3	1.77	0.65
1:B:356:GLY:HA3	1:B:380:LEU:HD11	1.80	0.64
1:C:356:GLY:HA3	1:C:380:LEU:HD11	1.80	0.63
1:C:80:LYS:HG3	1:D:428:ILE:HD11	1.81	0.62

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	A	326/838 (39%)	321 (98%)	5 (2%)	0	100	100
1	B	326/838 (39%)	320 (98%)	6 (2%)	0	100	100
1	C	326/838 (39%)	320 (98%)	6 (2%)	0	100	100
1	D	326/838 (39%)	322 (99%)	4 (1%)	0	100	100
1	E	326/838 (39%)	322 (99%)	4 (1%)	0	100	100
1	F	326/838 (39%)	320 (98%)	6 (2%)	0	100	100
All	All	1956/5028 (39%)	1925 (98%)	31 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	A	291/768 (38%)	289 (99%)	2 (1%)	76	86
1	B	291/768 (38%)	286 (98%)	5 (2%)	53	78
1	C	291/768 (38%)	289 (99%)	2 (1%)	76	86
1	D	291/768 (38%)	285 (98%)	6 (2%)	47	75
1	E	291/768 (38%)	288 (99%)	3 (1%)	68	84
1	F	291/768 (38%)	289 (99%)	2 (1%)	76	86
All	All	1746/4608 (38%)	1726 (99%)	20 (1%)	63	83

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	439	MET
1	E	387	GLN
1	F	325	ILE
1	F	280	LEU
1	B	439	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	344	GLN
1	D	387	GLN
1	E	217	HIS
1	E	344	GLN
1	F	344	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

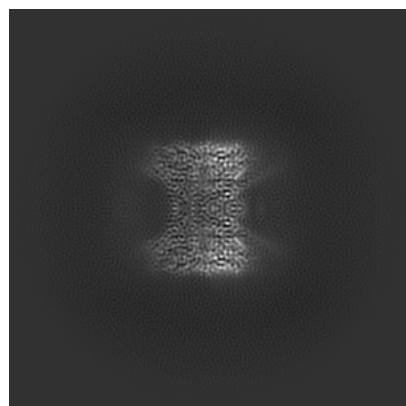
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73693. These allow visual inspection of the internal detail of the map and identification of artifacts.

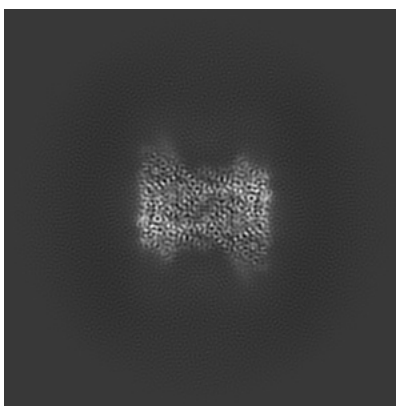
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

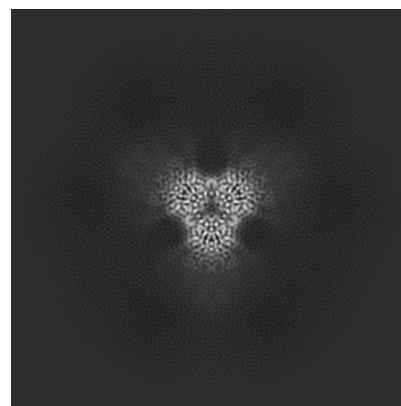
6.1.1 Primary map



X

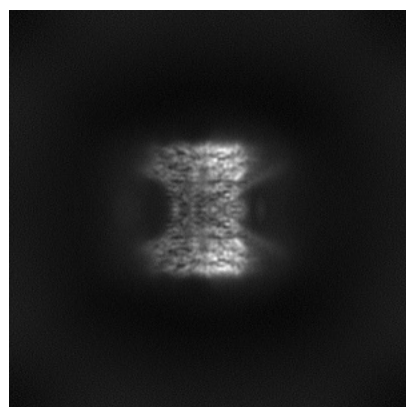


Y

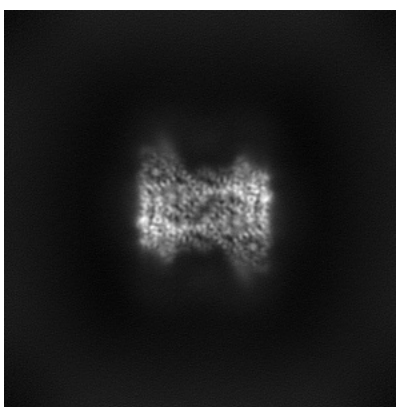


Z

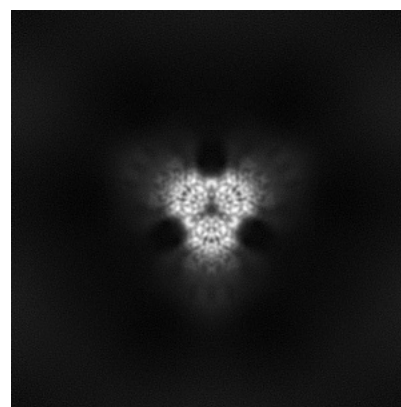
6.1.2 Raw map



X



Y

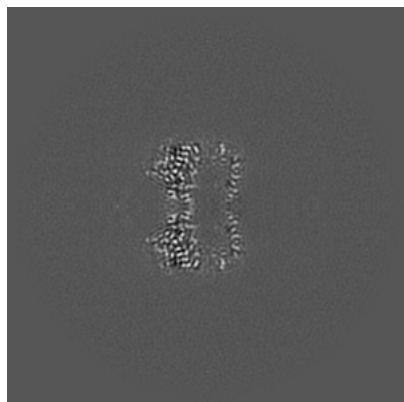


Z

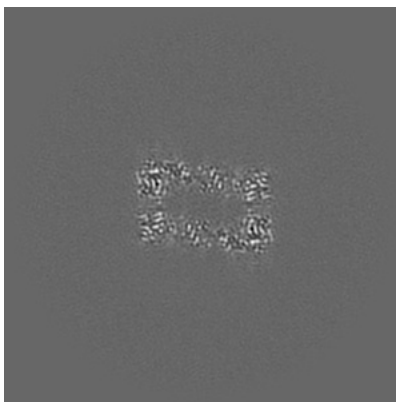
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

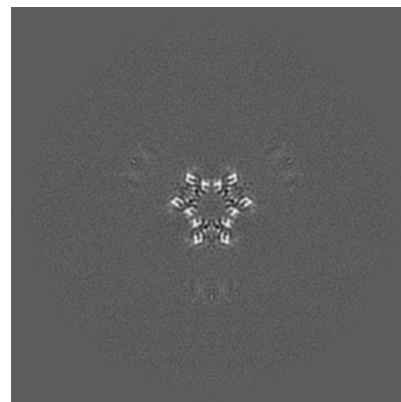
6.2.1 Primary map



X Index: 192

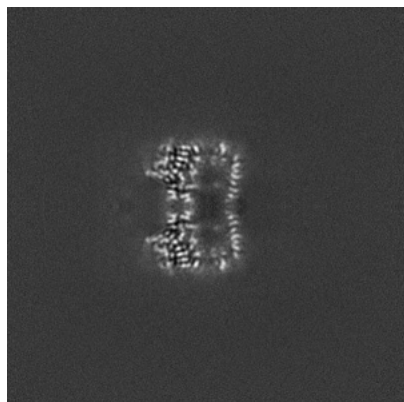


Y Index: 192

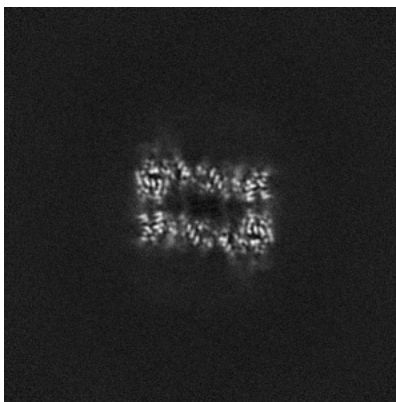


Z Index: 192

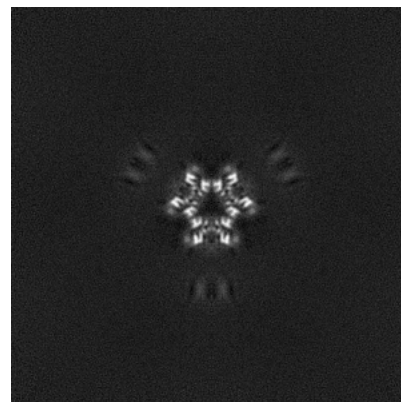
6.2.2 Raw map



X Index: 192



Y Index: 192

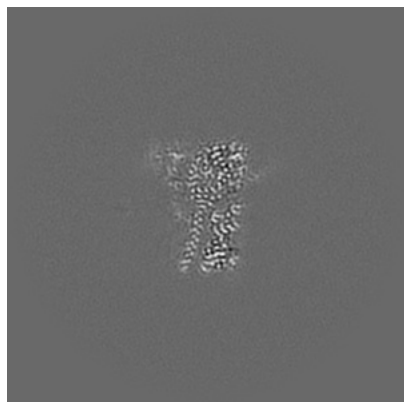


Z Index: 192

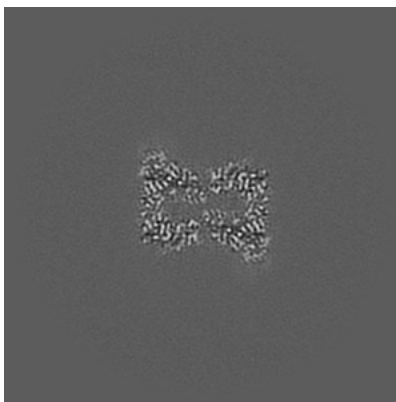
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

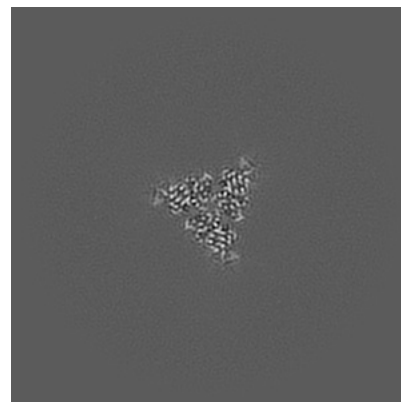
6.3.1 Primary map



X Index: 214

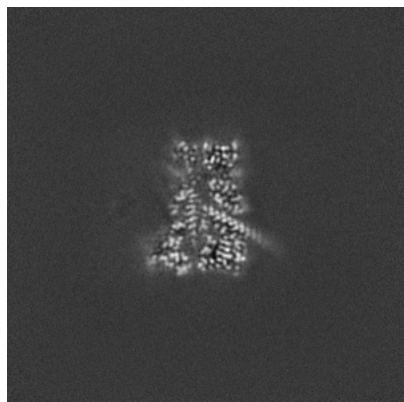


Y Index: 208

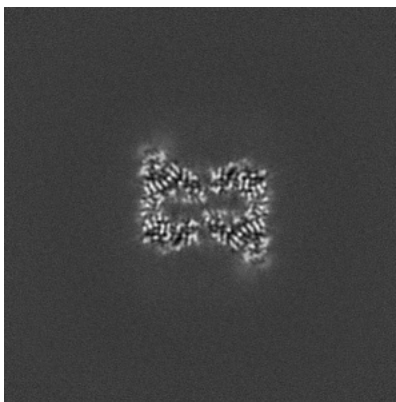


Z Index: 239

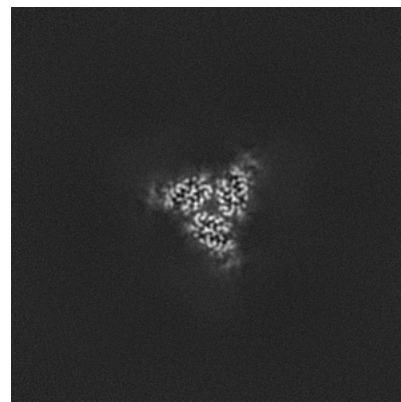
6.3.2 Raw map



X Index: 175



Y Index: 208

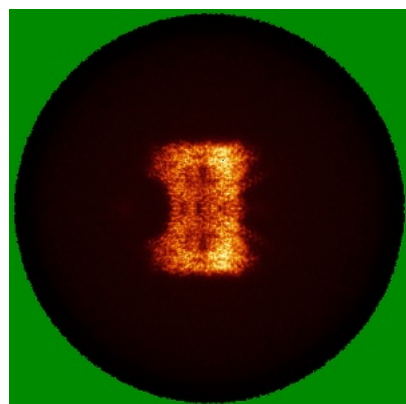


Z Index: 248

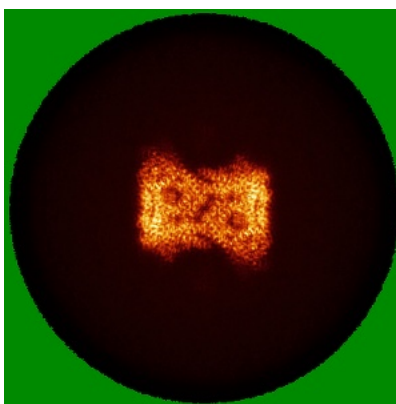
The images above show the largest variance slices of the map in three orthogonal directions.

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

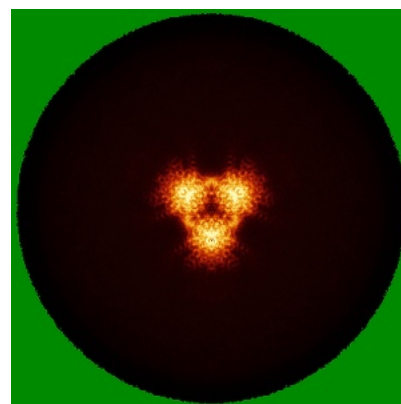
6.4.1 Primary map



X

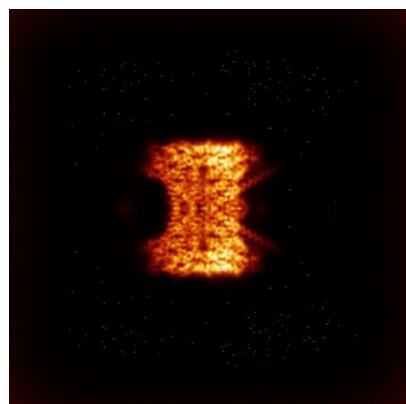


Y

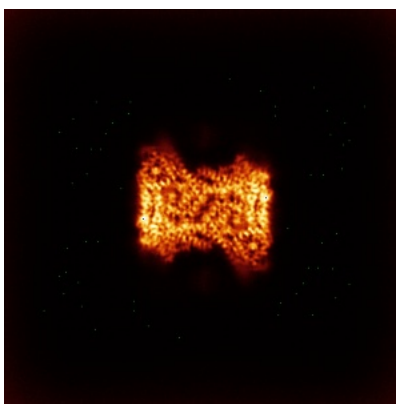


Z

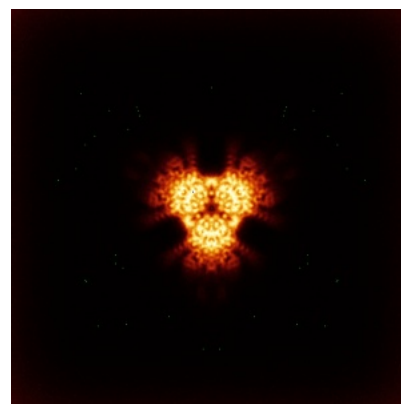
6.4.2 Raw map



X



Y

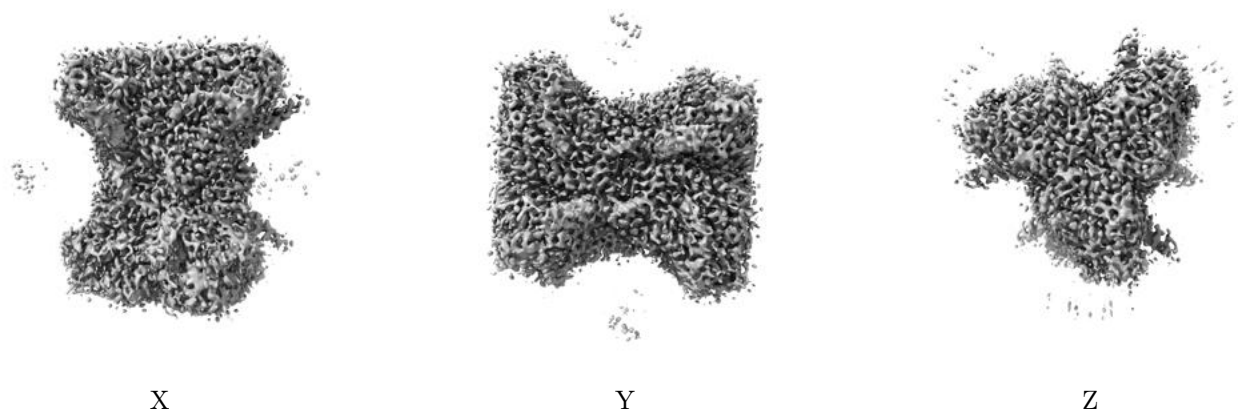


Z

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.

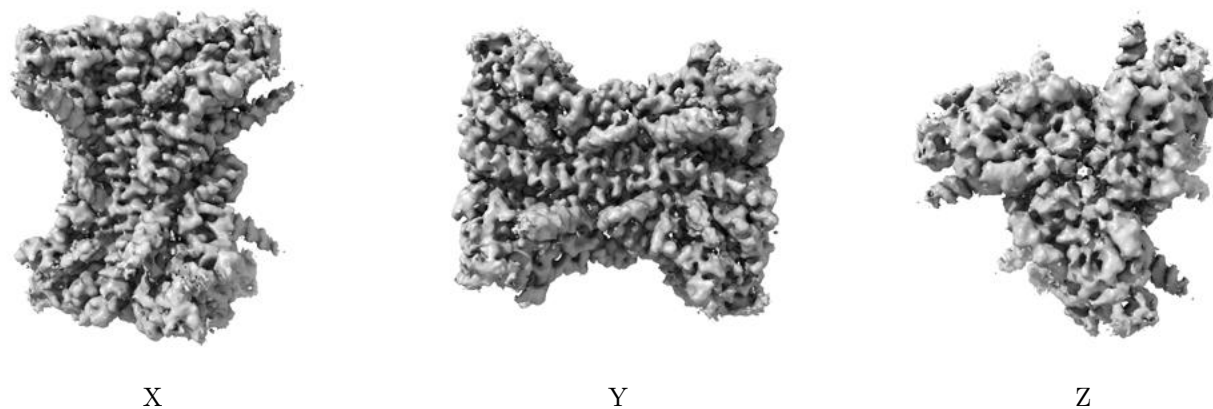
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.178. 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.

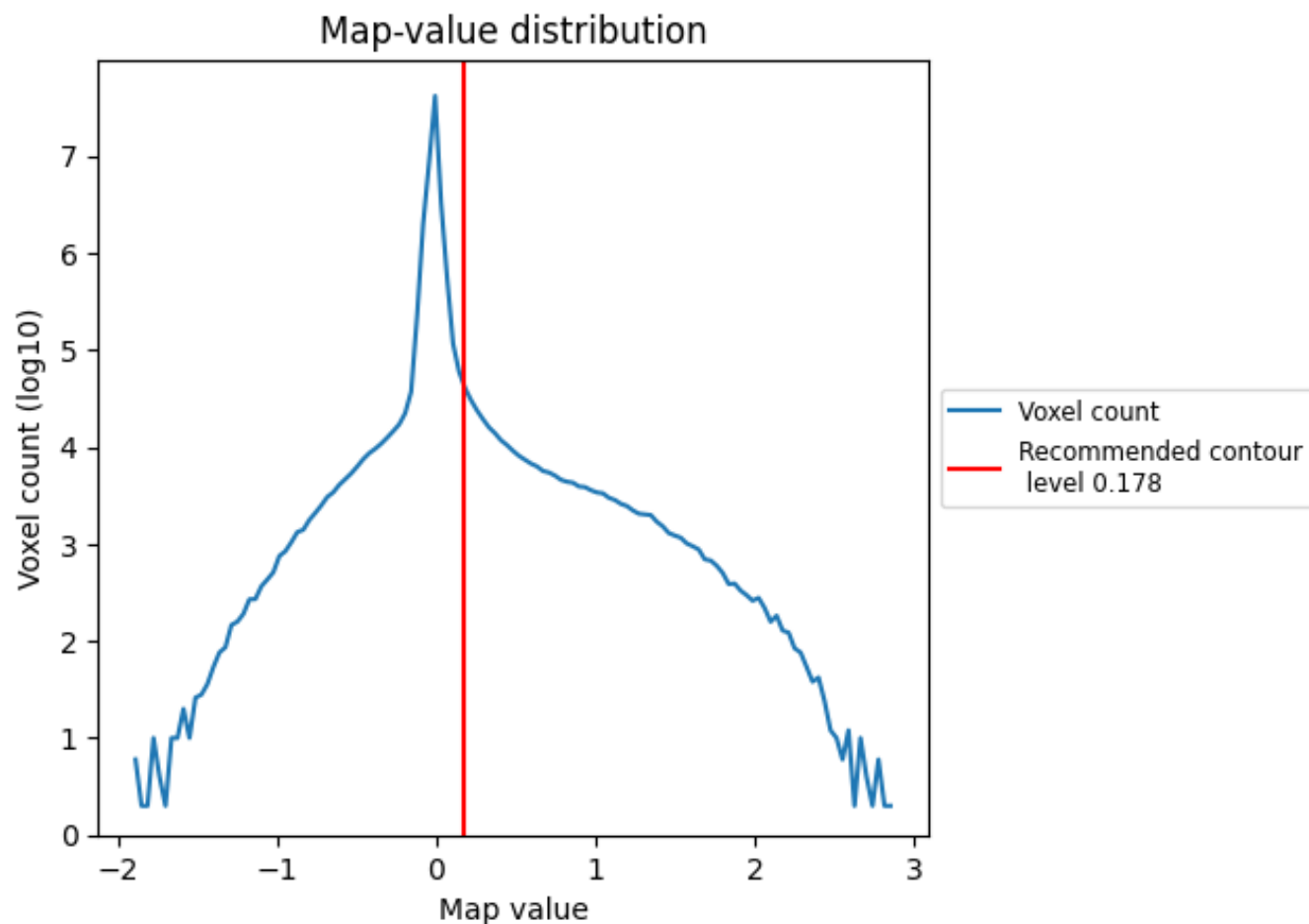
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

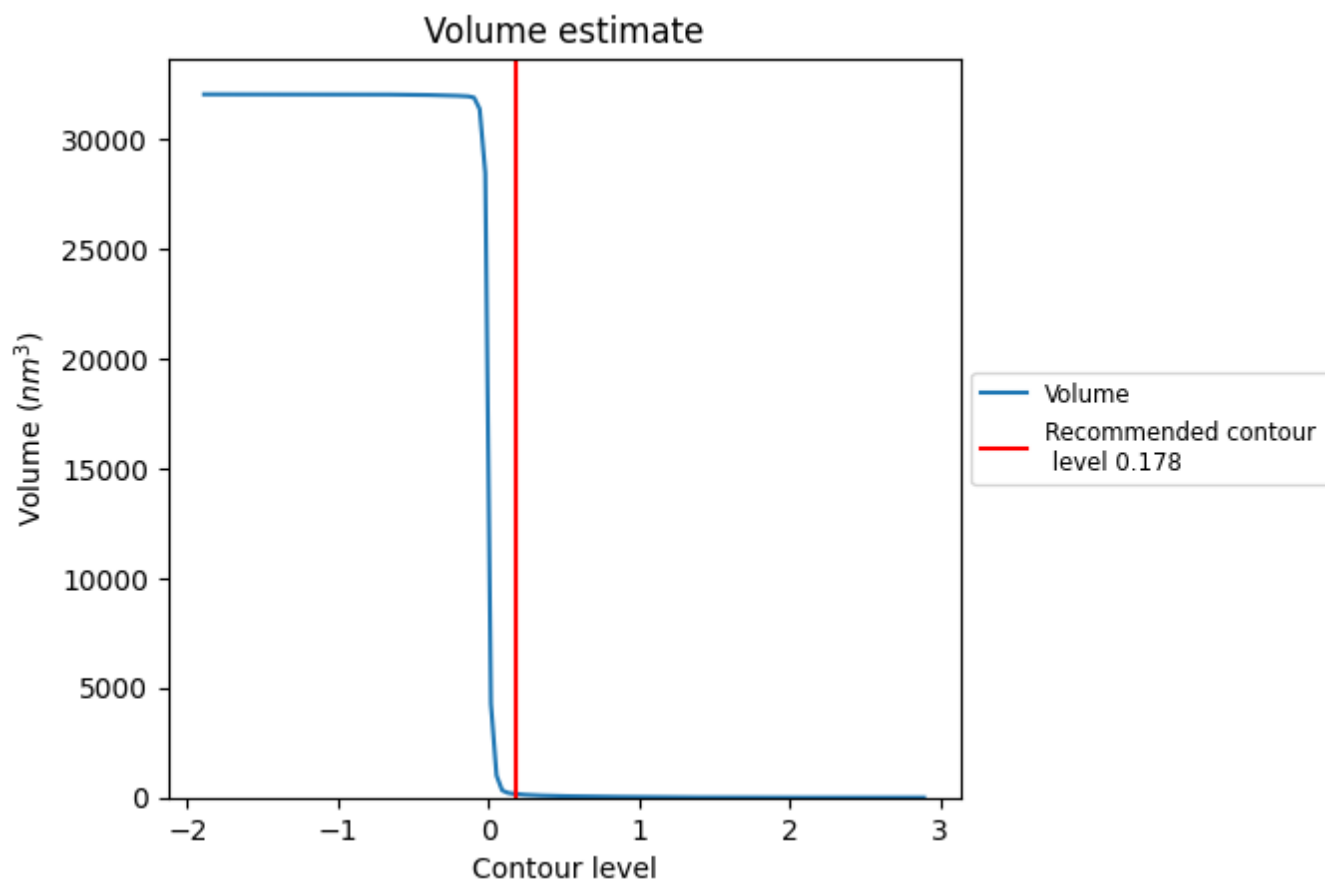
This section contains the results of statistical analysis of the map.

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.

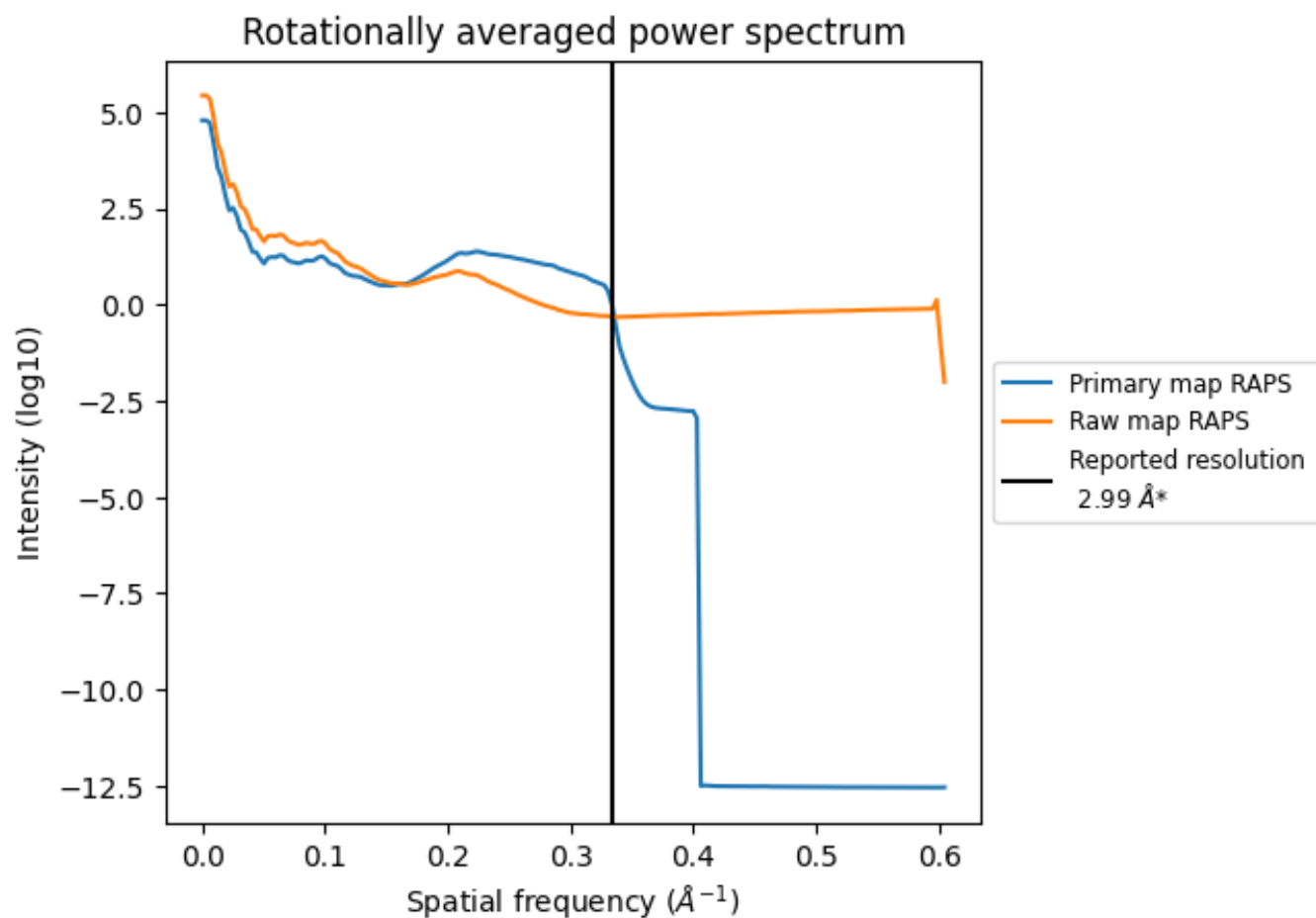
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 164 nm³; this corresponds to an approximate mass of 148 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 ⓘ

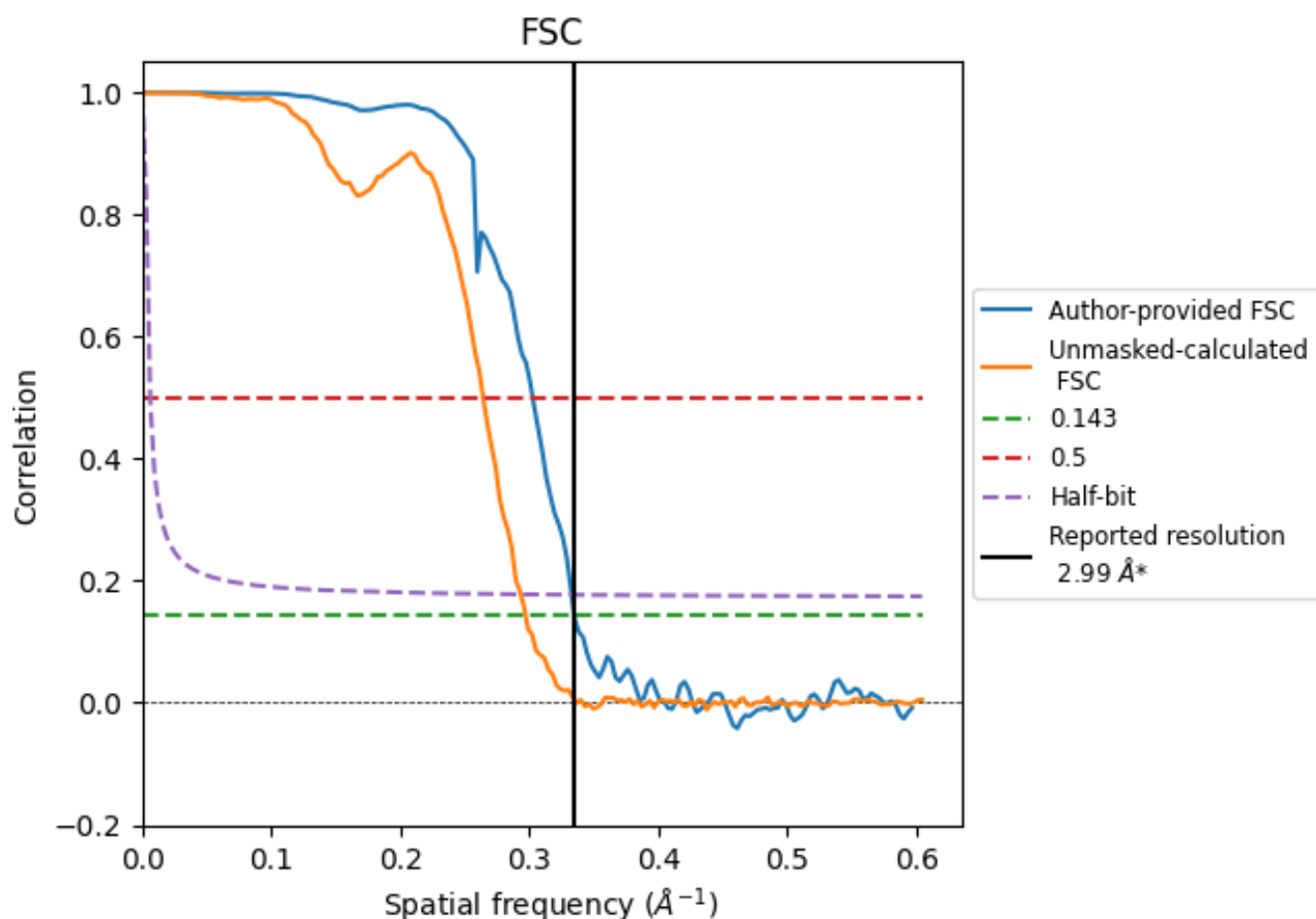


*Reported resolution corresponds to spatial frequency of 0.334 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.334 \AA^{-1}

8.2 Resolution estimates [i](#)

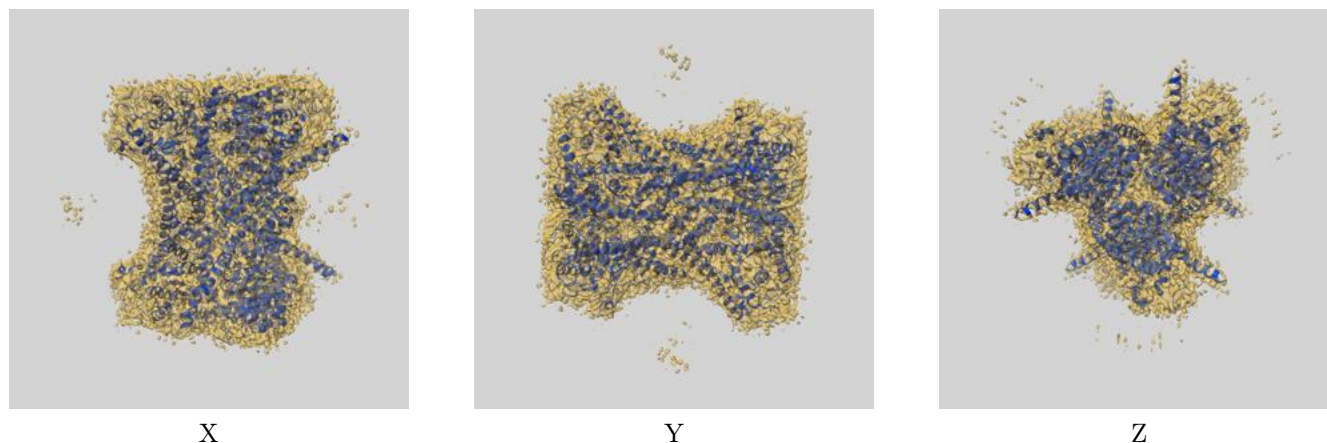
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.99	-	-
Author-provided FSC curve	2.99	3.30	3.00
Unmasked-calculated*	3.36	3.78	3.41

*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 3.36 differs from the reported value 2.99 by more than 10 %

9 Map-model fit [i](#)

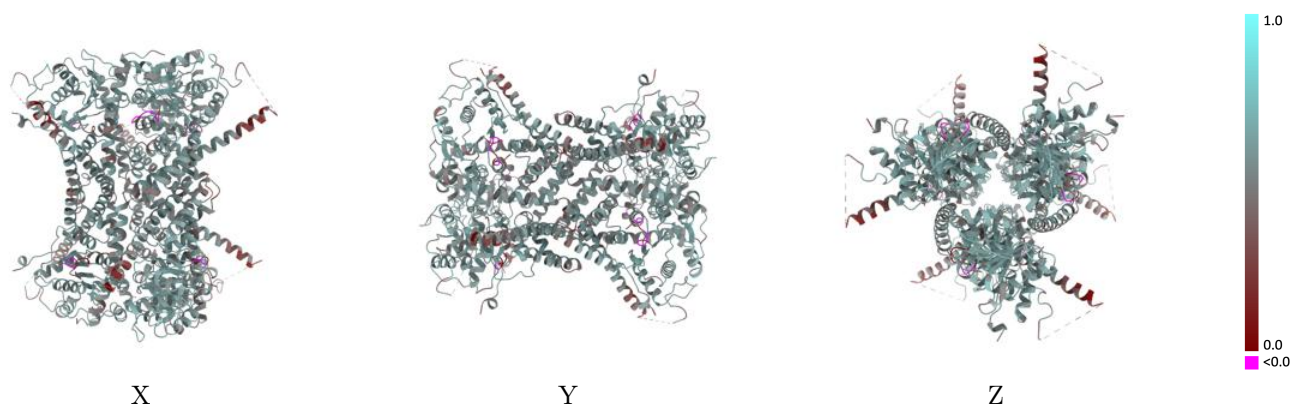
This section contains information regarding the fit between EMDB map EMD-73693 and PDB model 9Z04. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



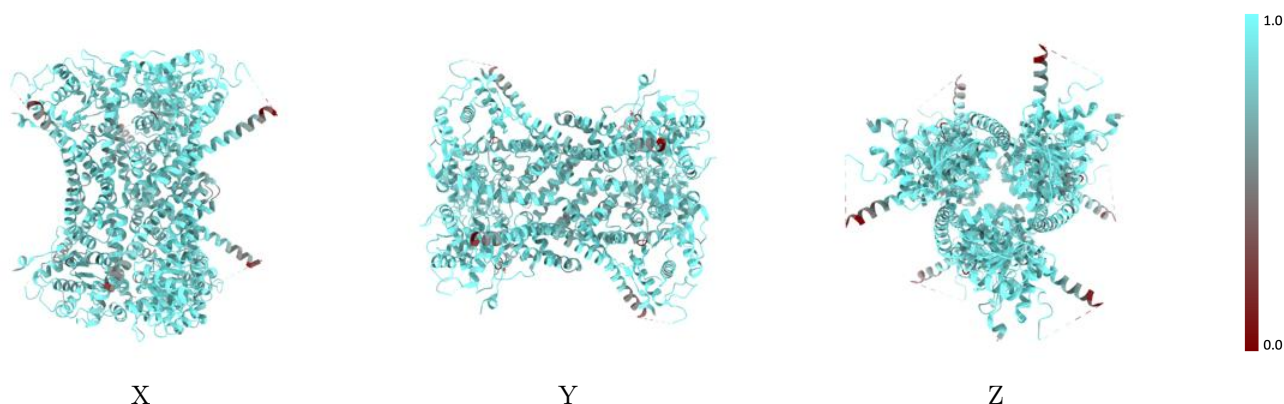
The images above show the 3D surface view of the map at the recommended contour level 0.178 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



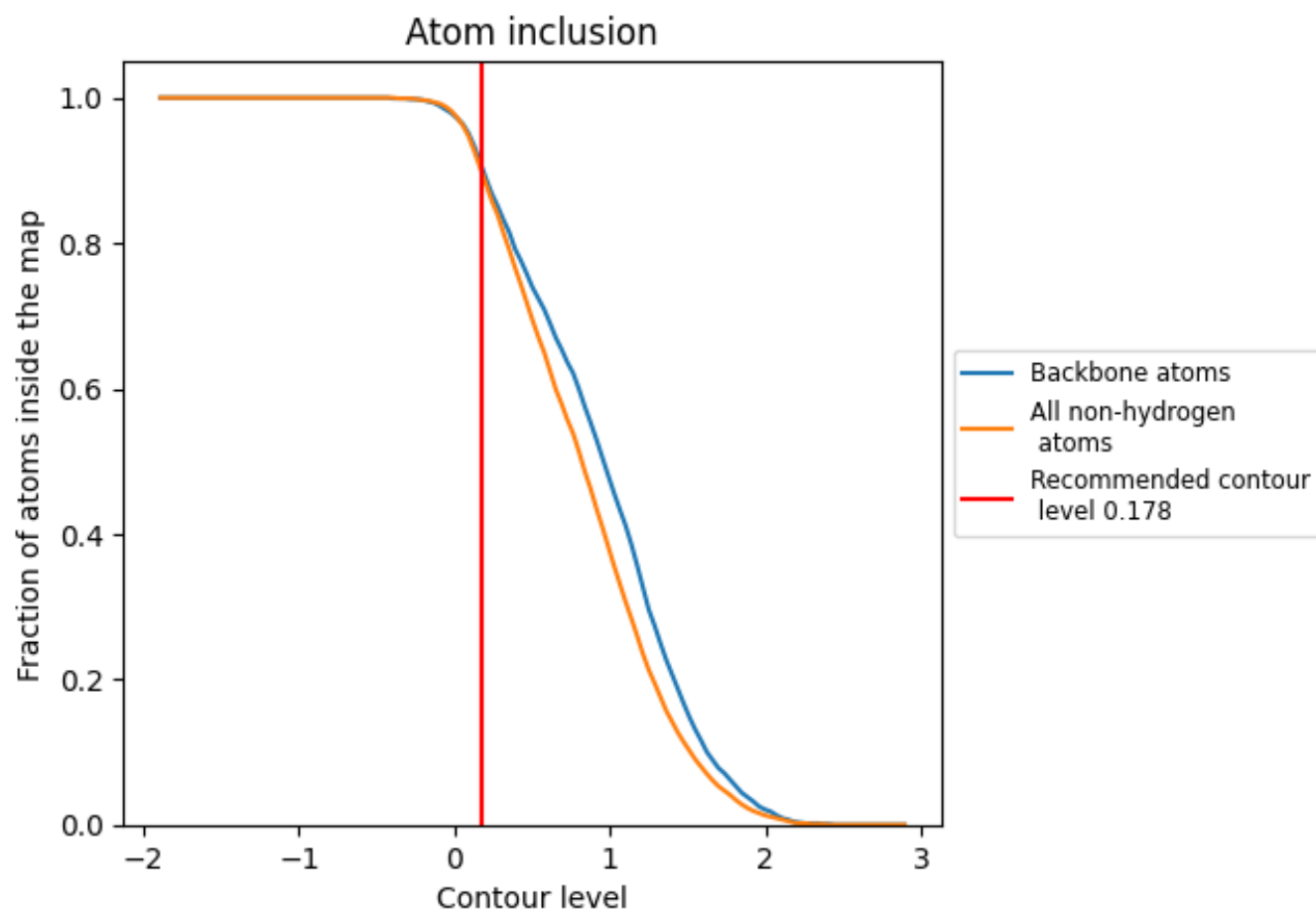
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.178).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.178) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8960	<div></div> 0.5380
A	<div></div> 0.8920	<div></div> 0.5380
B	<div></div> 0.9010	<div></div> 0.5380
C	<div></div> 0.8950	<div></div> 0.5370
D	<div></div> 0.8980	<div></div> 0.5370
E	<div></div> 0.8960	<div></div> 0.5400
F	<div></div> 0.8920	<div></div> 0.5370

