



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 10:42 AM UTC

PDB ID : 9JOR / pdb_00009jor
EMDB ID : EMD-61683
Title : structure of phage T4 topoisomerase II central domain bound with DNA
Authors : Chen, Y.T.; Xin, Y.H.
Deposited on : 2024-09-25
Resolution : 3.09 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

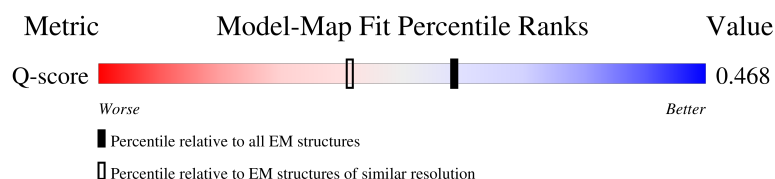
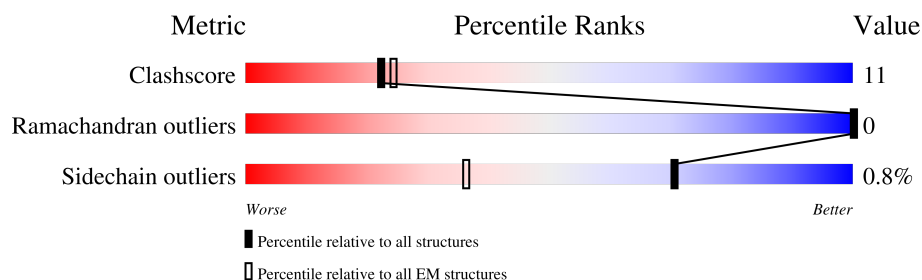
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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	14003 (2.59 - 3.59)

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	C	452	
1	D	452	
2	A	682	
2	B	682	

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Mol	Chain	Length	Quality of chain
3	E	24	 58% 42%
4	F	24	 33% 67%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12697 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 DNA topoisomerase medium subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	442	Total	C	N	O	S	0	0
			3563	2273	610	670	10		
1	D	442	Total	C	N	O	S	0	0
			3563	2273	610	670	10		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	443	HIS	-	expression tag	UNP P07065
C	444	HIS	-	expression tag	UNP P07065
C	445	HIS	-	expression tag	UNP P07065
C	446	HIS	-	expression tag	UNP P07065
C	447	HIS	-	expression tag	UNP P07065
C	448	HIS	-	expression tag	UNP P07065
C	449	HIS	-	expression tag	UNP P07065
C	450	HIS	-	expression tag	UNP P07065
C	451	HIS	-	expression tag	UNP P07065
C	452	HIS	-	expression tag	UNP P07065
D	443	HIS	-	expression tag	UNP P07065
D	444	HIS	-	expression tag	UNP P07065
D	445	HIS	-	expression tag	UNP P07065
D	446	HIS	-	expression tag	UNP P07065
D	447	HIS	-	expression tag	UNP P07065
D	448	HIS	-	expression tag	UNP P07065
D	449	HIS	-	expression tag	UNP P07065
D	450	HIS	-	expression tag	UNP P07065
D	451	HIS	-	expression tag	UNP P07065
D	452	HIS	-	expression tag	UNP P07065

- Molecule 2 is a protein called DNA topoisomerase large subunit,DNA topoisomerase small subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	284	Total	C	N	O	S	0	0
			2292	1466	382	432	12		
2	B	284	Total	C	N	O	S	0	0
			2292	1466	382	432	12		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	677	HIS	-	expression tag	UNP P23992
A	678	HIS	-	expression tag	UNP P23992
A	679	HIS	-	expression tag	UNP P23992
A	680	HIS	-	expression tag	UNP P23992
A	681	HIS	-	expression tag	UNP P23992
A	682	HIS	-	expression tag	UNP P23992
B	677	HIS	-	expression tag	UNP P23992
B	678	HIS	-	expression tag	UNP P23992
B	679	HIS	-	expression tag	UNP P23992
B	680	HIS	-	expression tag	UNP P23992
B	681	HIS	-	expression tag	UNP P23992
B	682	HIS	-	expression tag	UNP P23992

- Molecule 3 is a DNA chain called DNA (5'-D(P*TP*GP*TP*GP*TP*GP*TP*AP*TP*AP*TP*AP*TP*AP*CP*AP*CP*AP*TP*AP*TP*AP*TP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	24	Total	C	N	O	P	0	0
			493	238	86	145	24		

- Molecule 4 is a DNA chain called DNA (5'-D(P*AP*TP*AP*TP*AP*TP*GP*TP*GP*TP*AP*TP*AP*TP*AP*TP*AP*CP*AP*CP*AP*CP*AP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	24	Total	C	N	O	P	0	0
			491	237	87	143	24		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	2	Total	Mg	0
			2	2	
5	B	1	Total	Mg	0
			1	1	

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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58418	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.712	Depositor
Minimum map value	-1.153	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	249.59999, 249.59999, 249.59999	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	C	0.14	0/3635	0.28	0/4897
1	D	0.14	0/3635	0.31	0/4897
2	A	0.21	0/2340	0.35	0/3150
2	B	0.29	0/2340	0.46	3/3150 (0.1%)
3	E	0.24	0/552	0.46	0/850
4	F	0.24	0/550	0.40	0/846
All	All	0.20	0/13052	0.35	3/17790 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	619	PRO	CA-N-CD	-6.51	102.88	112.00
2	B	619	PRO	N-CD-CG	-5.90	94.34	103.20
2	B	543	LYS	N-CA-C	-5.06	105.23	111.40

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	C	3563	0	3568	80	0
1	D	3563	0	3568	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2292	0	2276	62	0
2	B	2292	0	2276	61	0
3	E	493	0	275	8	0
4	F	491	0	274	16	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
All	All	12697	0	12237	284	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 11.

The worst 5 of 284 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:D:5:ASN:ND2	2:B:536:ASN:HD22	1.17	1.37
1:D:5:ASN:HD21	2:B:536:ASN:ND2	1.35	1.21
1:D:5:ASN:ND2	2:B:536:ASN:ND2	1.89	1.15
2:A:431:LEU:O	2:A:432:HIS:ND1	2.05	0.88
2:A:474:PHE:HB3	2:A:545:SER:HB2	1.56	0.86

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	C	440/452 (97%)	414 (94%)	26 (6%)	0	100	100
1	D	440/452 (97%)	403 (92%)	37 (8%)	0	100	100
2	A	282/682 (41%)	254 (90%)	28 (10%)	0	100	100
2	B	282/682 (41%)	260 (92%)	22 (8%)	0	100	100
All	All	1444/2268 (64%)	1331 (92%)	113 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	382/392 (97%)	380 (100%)	2 (0%)	81	85
1	D	382/392 (97%)	382 (100%)	0	100	100
2	A	249/593 (42%)	244 (98%)	5 (2%)	48	72
2	B	249/593 (42%)	246 (99%)	3 (1%)	63	78
All	All	1262/1970 (64%)	1252 (99%)	10 (1%)	70	81

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	472	LYS
2	B	543	LYS
2	B	546	SER
2	A	546	SER
2	A	547	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	81	GLN
1	D	144	HIS
1	D	125	ASN
1	D	214	GLN
1	C	214	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

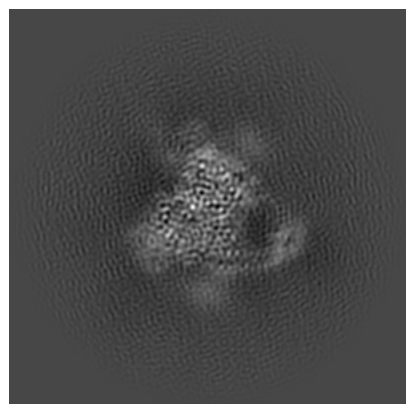
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61683. These allow visual inspection of the internal detail of the map and identification of artifacts.

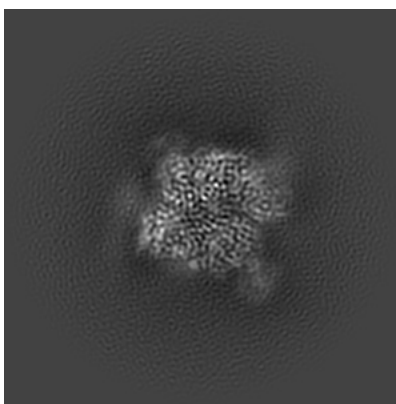
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

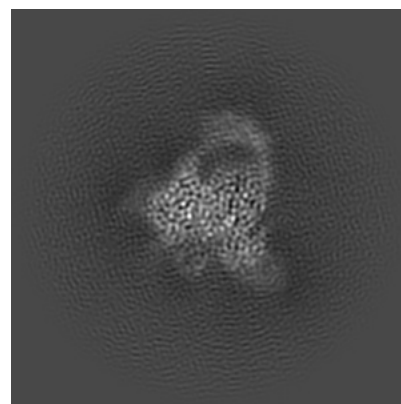
6.1.1 Primary map



X

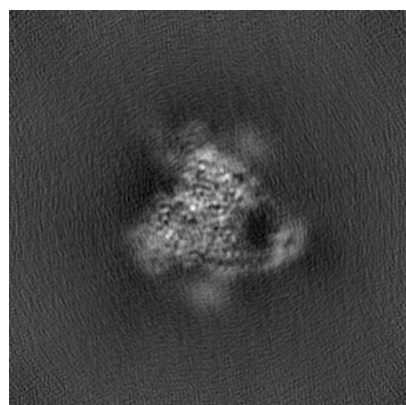


Y

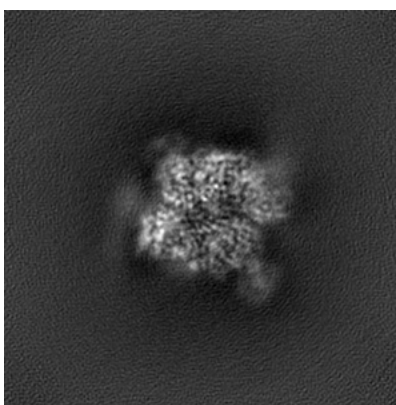


Z

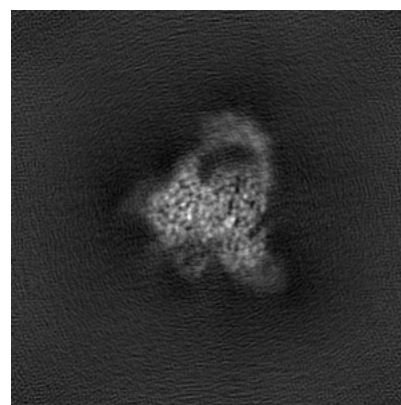
6.1.2 Raw map



X



Y

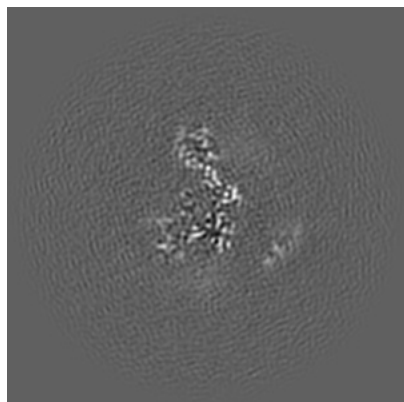


Z

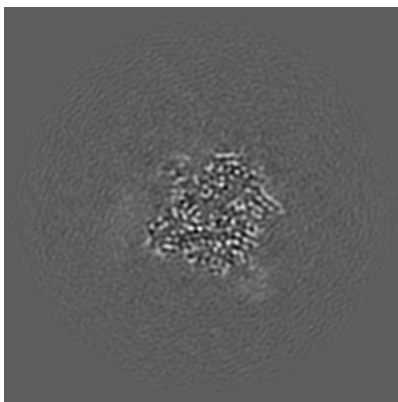
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

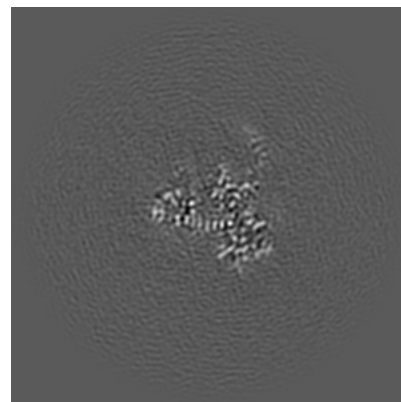
6.2.1 Primary map



X Index: 120

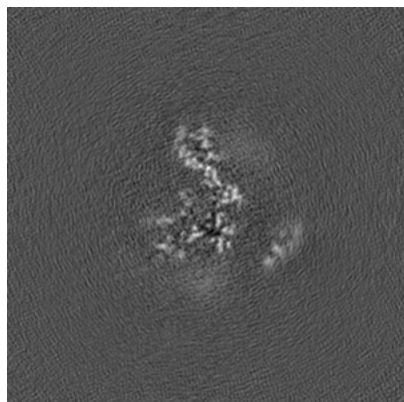


Y Index: 120

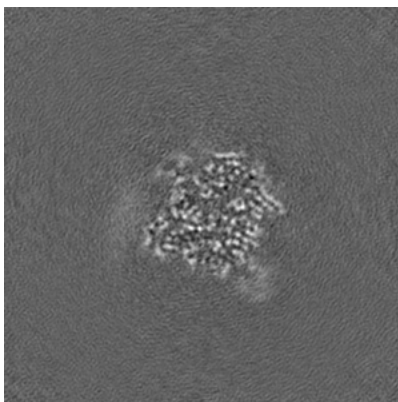


Z Index: 120

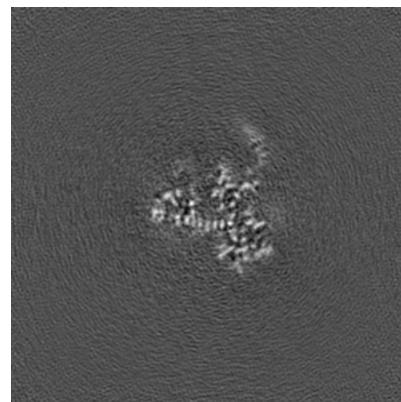
6.2.2 Raw map



X Index: 120



Y Index: 120

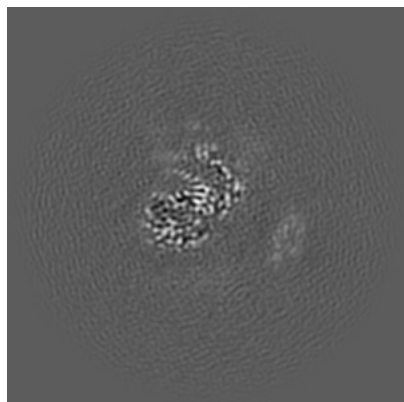


Z Index: 120

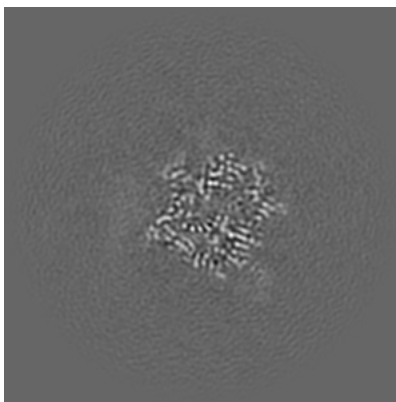
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

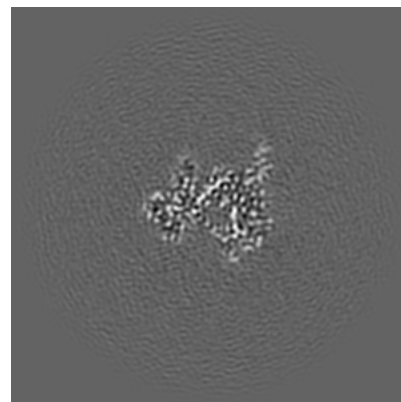
6.3.1 Primary map



X Index: 133

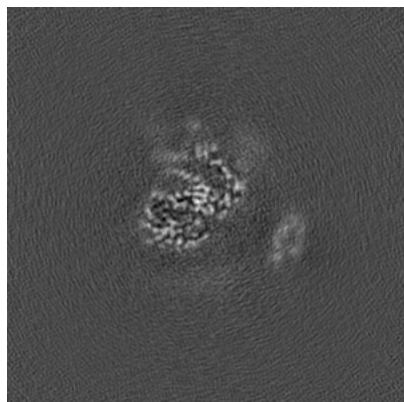


Y Index: 118

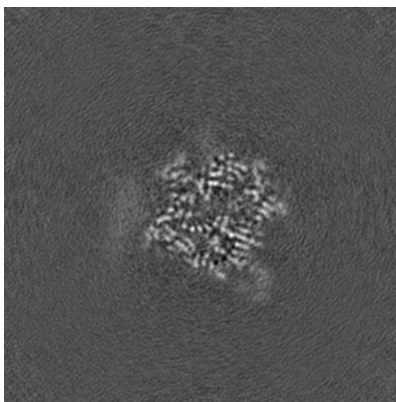


Z Index: 127

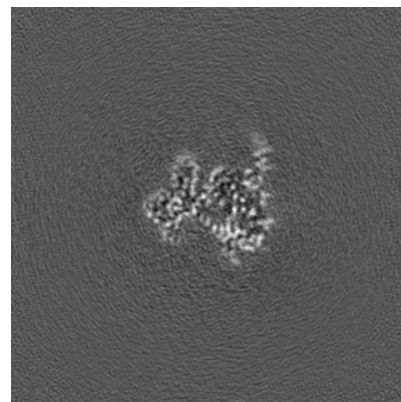
6.3.2 Raw map



X Index: 133



Y Index: 118

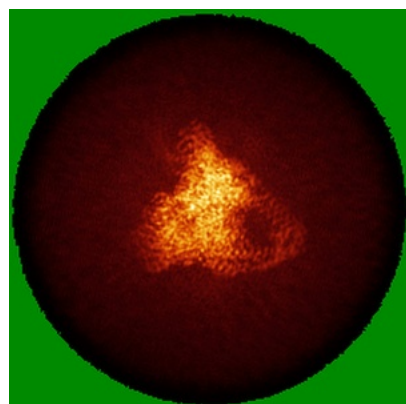


Z Index: 126

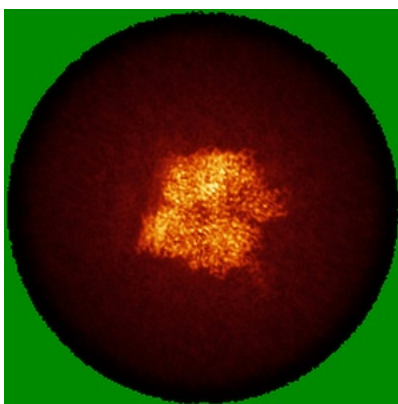
The images above show the largest variance slices of the map in three orthogonal directions.

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

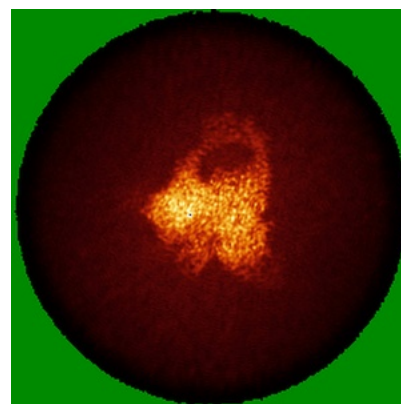
6.4.1 Primary map



X

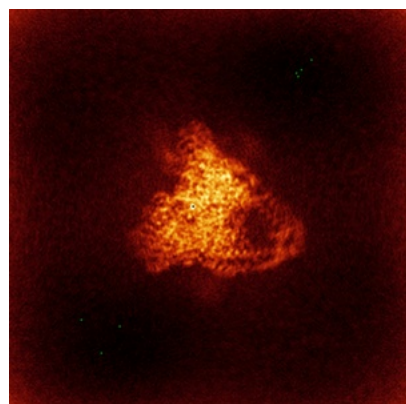


Y

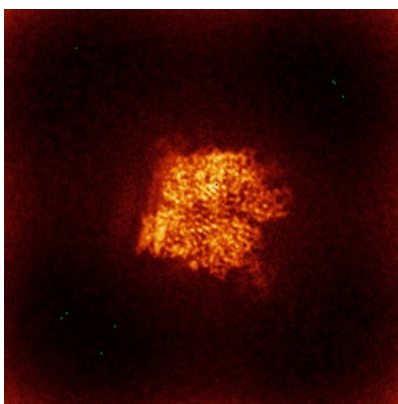


Z

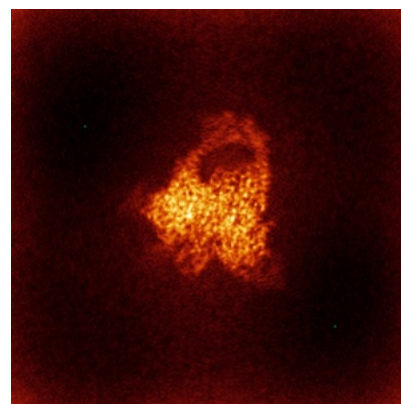
6.4.2 Raw map



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.

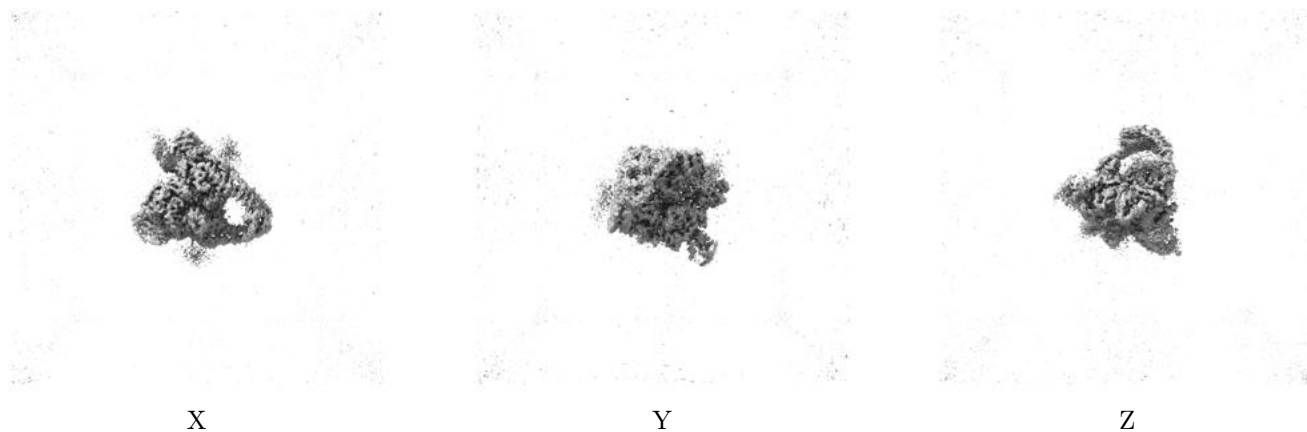
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

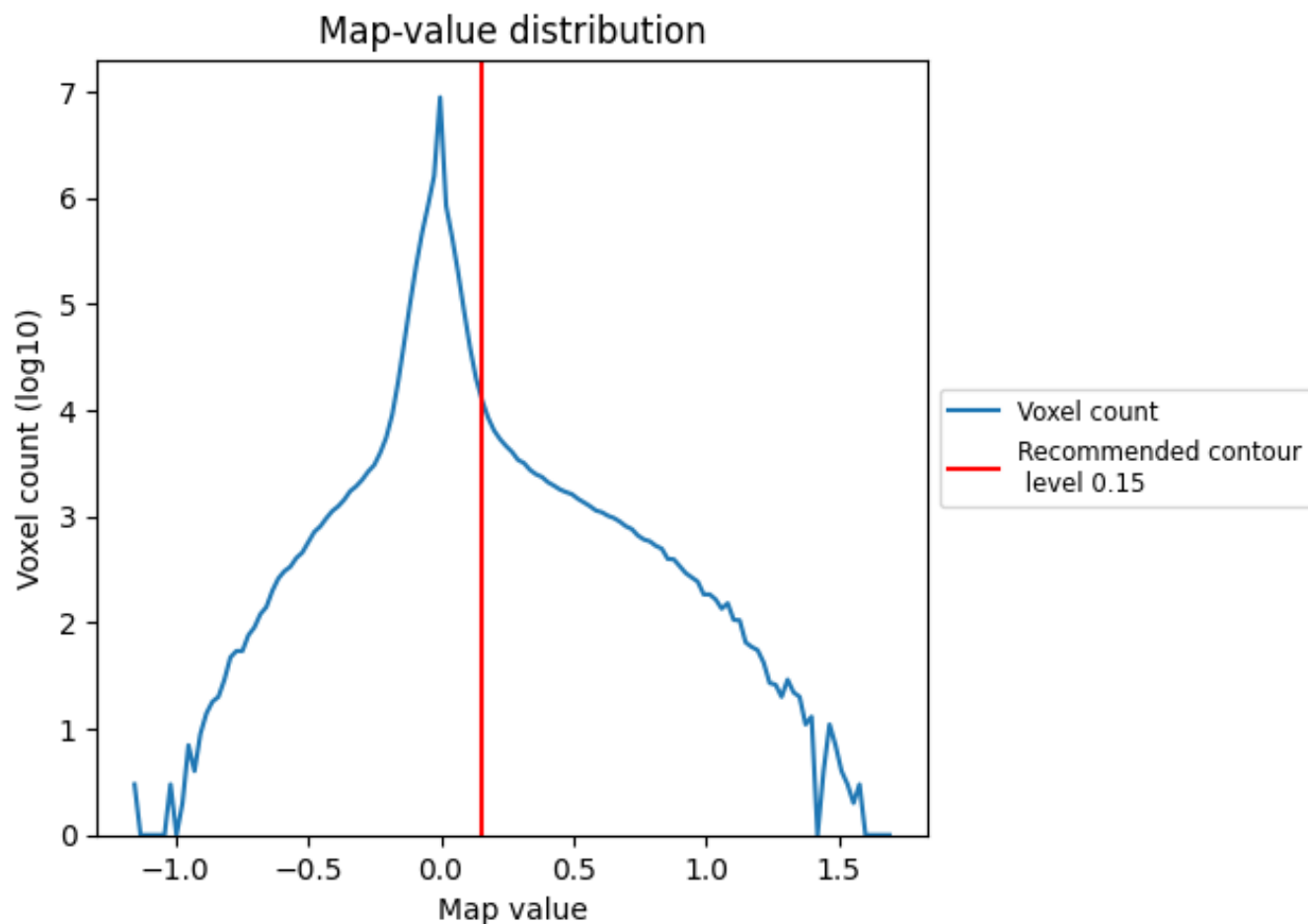
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

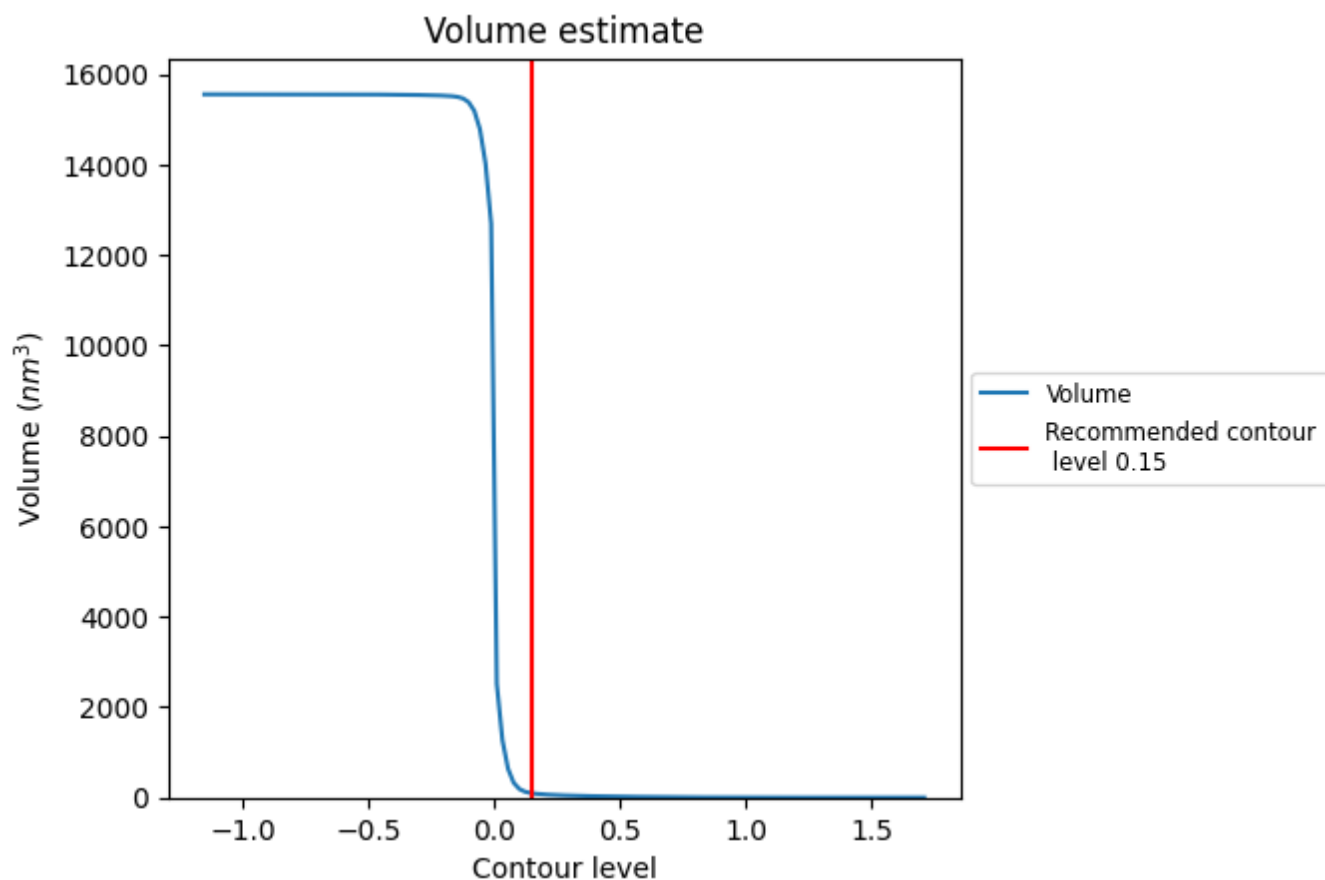
This section contains the results of statistical analysis of the map.

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.

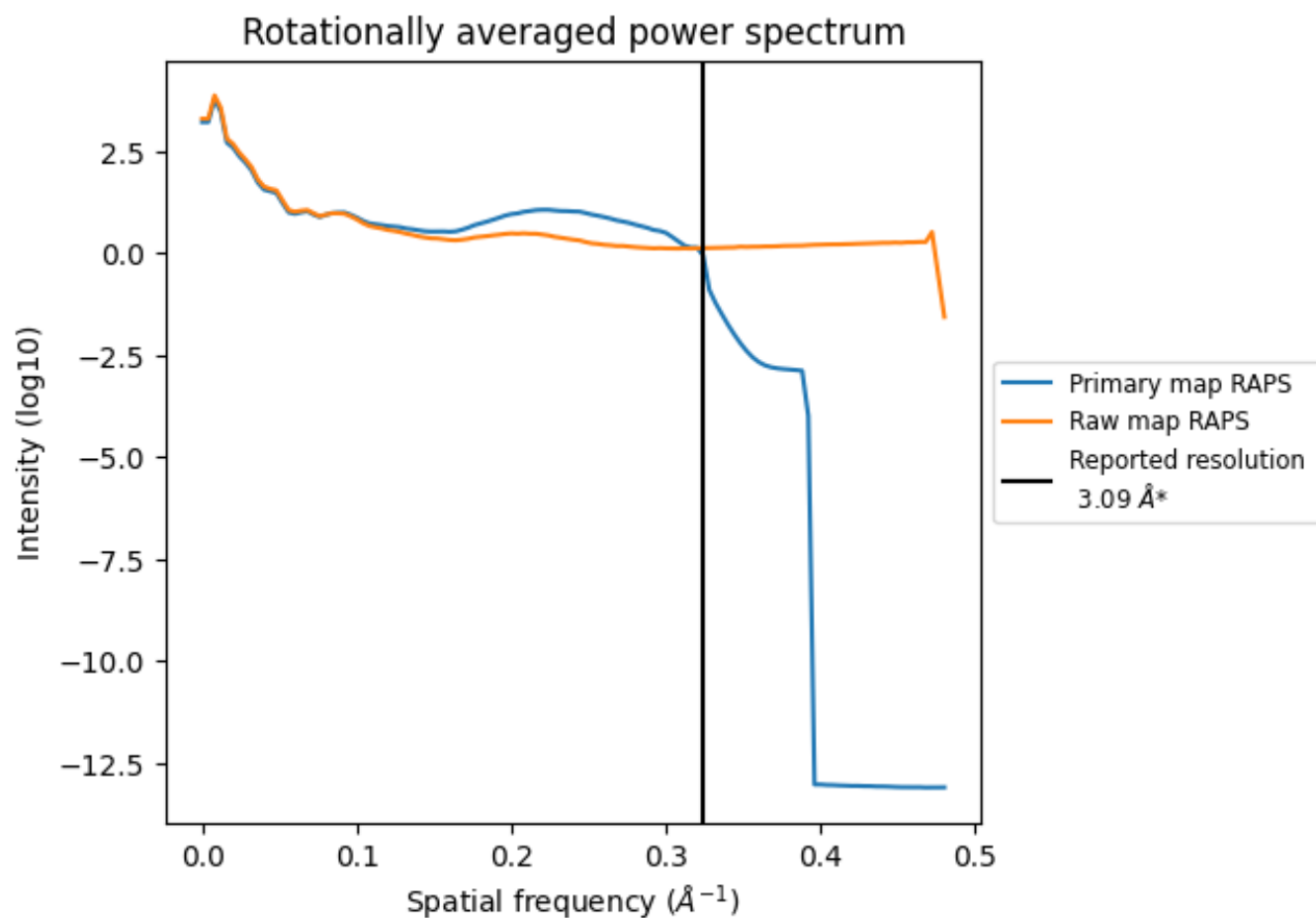
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 96 nm^3 ; this corresponds to an approximate mass of 87 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 ⓘ

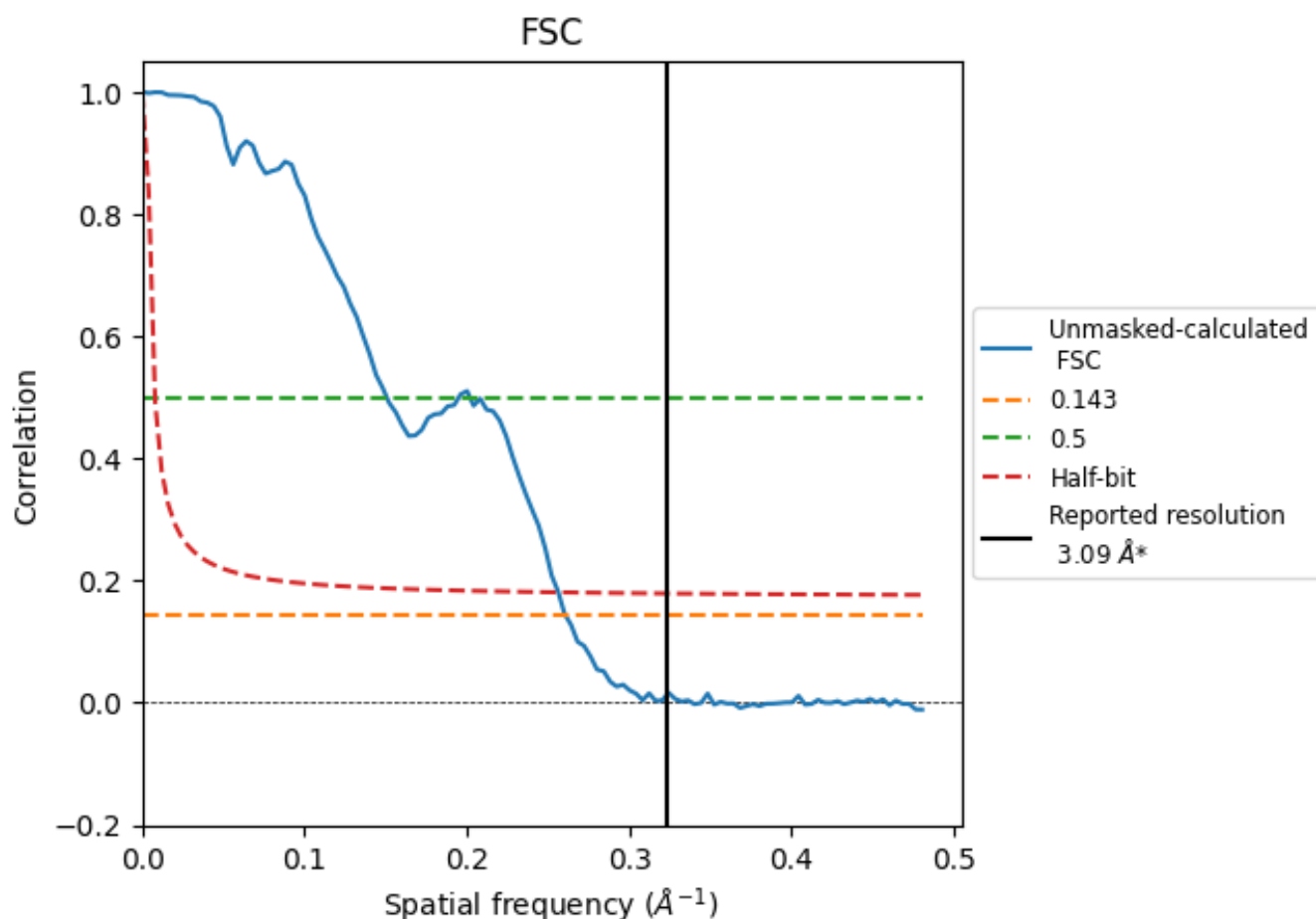


*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

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 0.324 Å⁻¹

8.2 Resolution estimates [i](#)

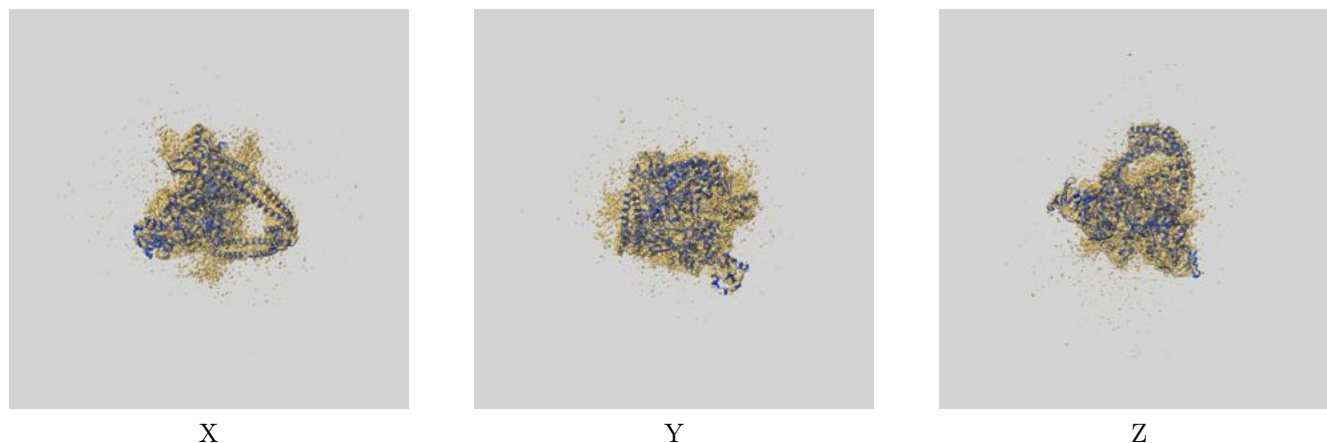
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.83	6.63	3.90

*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 3.83 differs from the reported value 3.09 by more than 10 %

9 Map-model fit [i](#)

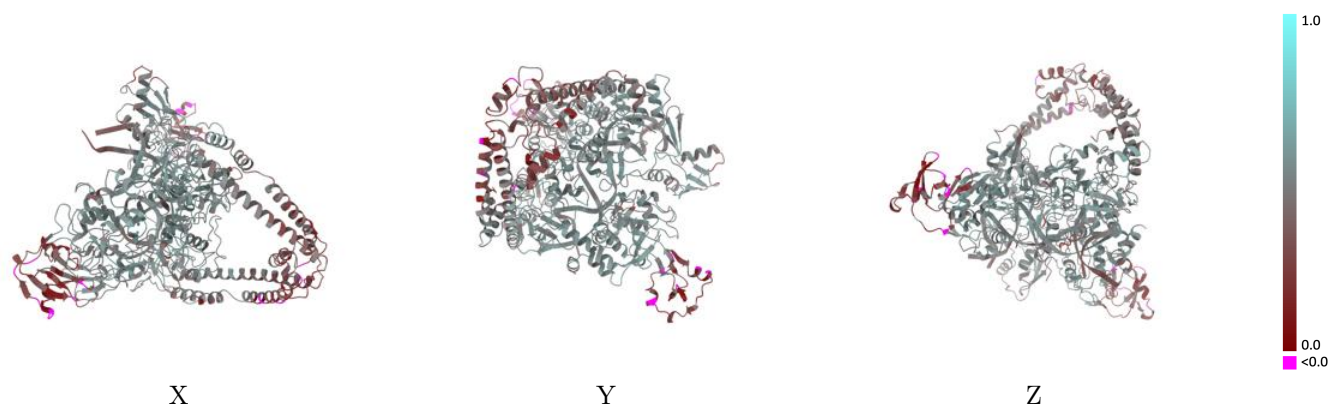
This section contains information regarding the fit between EMDB map EMD-61683 and PDB model 9JOR. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



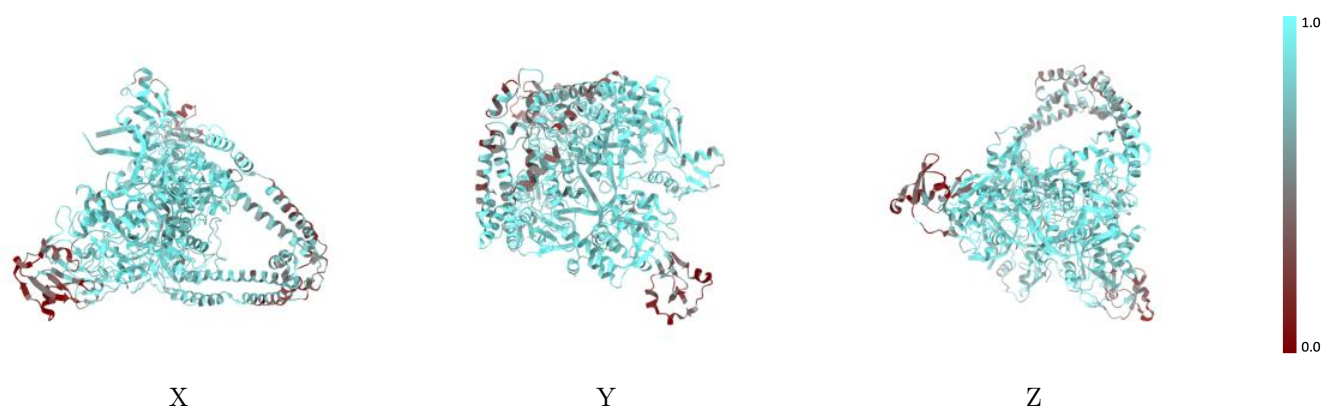
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



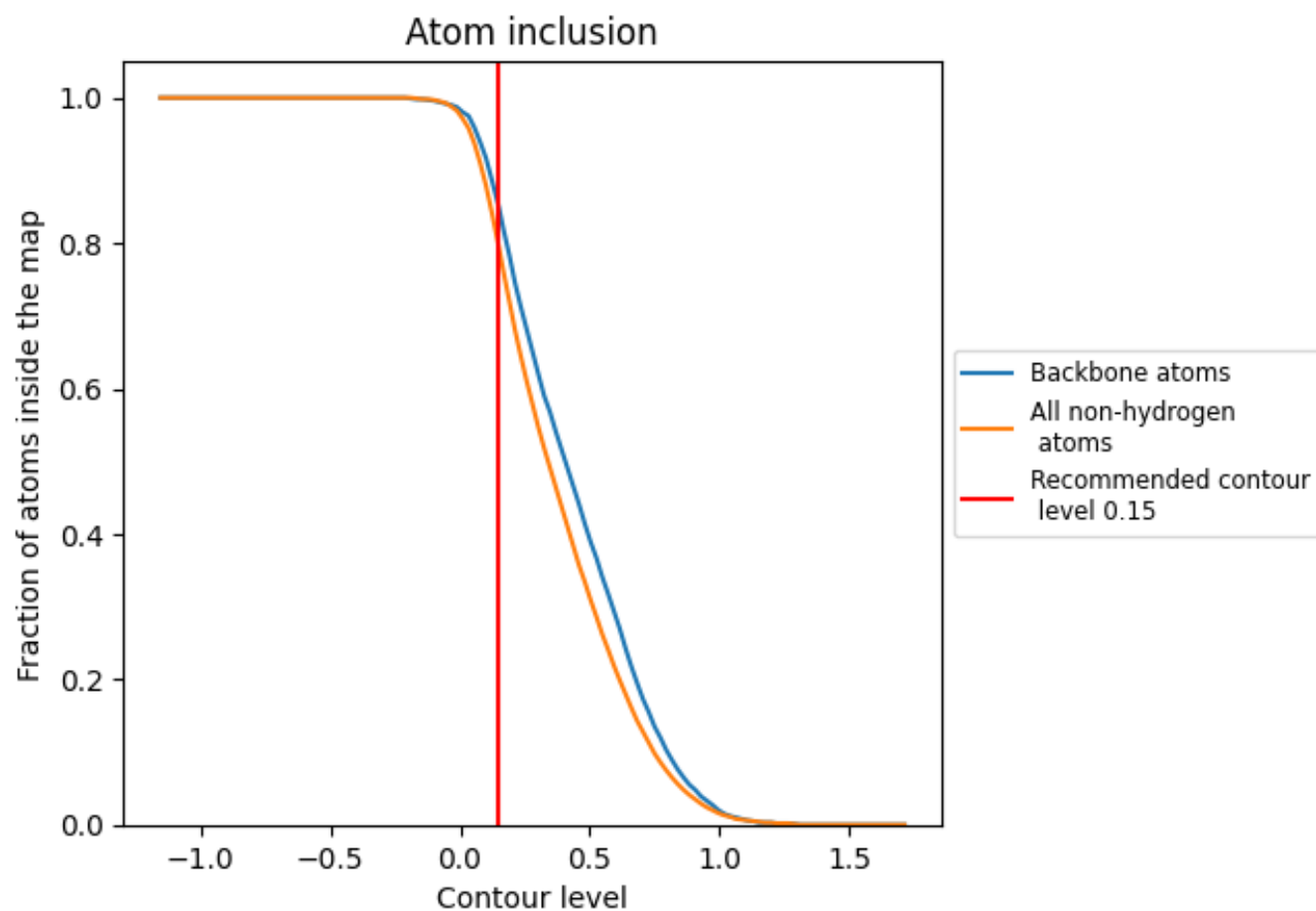
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 79% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7940	0.4680
A	0.7290	0.4460
B	0.7500	0.4510
C	0.8220	0.4830
D	0.8100	0.4760
E	0.8840	0.4840
F	0.8780	0.4690

1.0

0.0

<0.0