



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:20 AM UTC

PDB ID : 8S92 / pdb_00008s92
EMDB ID : EMD-40235
Title : Structure of N-terminal domains of Walker B mutated MCM8/9 heterohexamer complex with ADP
Authors : Li, C.; Gao, Y.
Deposited on : 2023-03-27
Resolution : 4.06 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

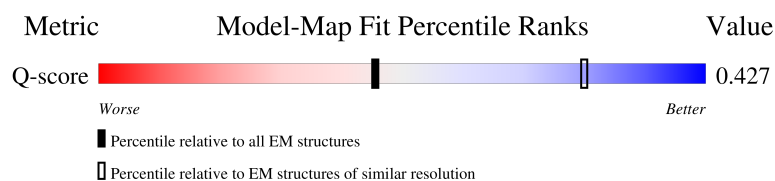
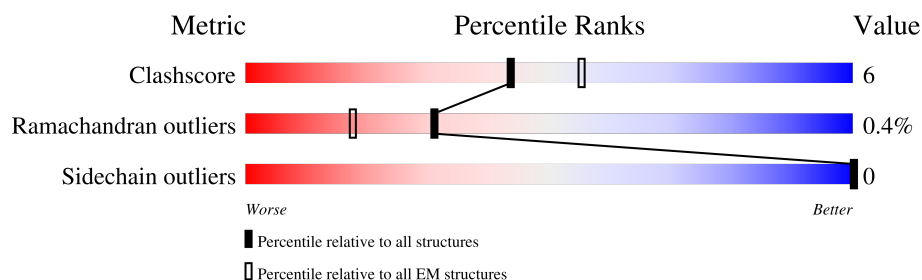
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.06 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	6515 (3.56 - 4.56)

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	840	
1	B	840	
1	C	840	
2	D	1143	

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Mol	Chain	Length	Quality of chain
2	E	1143	 18% 78%
2	F	1143	 18% 78%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12714 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 helicase MCM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	274	Total	C	N	O	S	0	0
			2168	1383	364	406	15		
1	B	274	Total	C	N	O	S	0	0
			2168	1383	364	406	15		
1	C	274	Total	C	N	O	S	0	0
			2168	1383	364	406	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	GLN	GLU	engineered mutation	UNP Q9UJA3
B	519	GLN	GLU	engineered mutation	UNP Q9UJA3
C	519	GLN	GLU	engineered mutation	UNP Q9UJA3

- Molecule 2 is a protein called DNA helicase MCM9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	256	Total	C	N	O	S	0	0
			2070	1310	349	394	17		
2	E	256	Total	C	N	O	S	0	0
			2070	1310	349	394	17		
2	F	256	Total	C	N	O	S	0	0
			2070	1310	349	394	17		

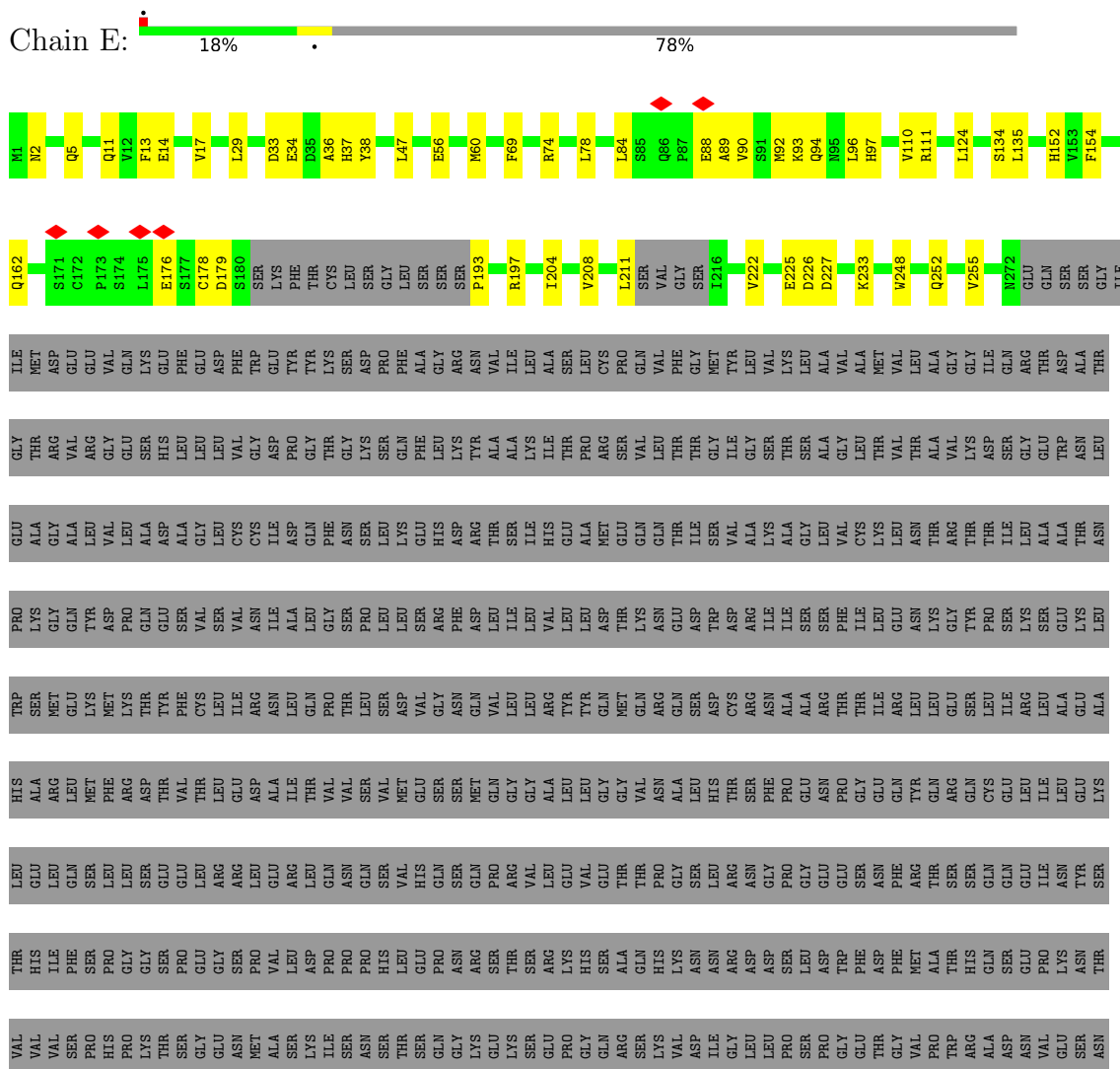
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	415	GLN	GLU	engineered mutation	UNP Q9NXL9
E	415	GLN	GLU	engineered mutation	UNP Q9NXL9
F	415	GLN	GLU	engineered mutation	UNP Q9NXL9





- Molecule 2: DNA helicase MCM9





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	227818	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.748	Depositor
Minimum map value	-1.196	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	355.2, 355.2, 355.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.11, 1.11, 1.11	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	0.13	0/2211	0.40	0/2994
1	B	0.13	0/2211	0.40	0/2994
1	C	0.13	0/2211	0.41	0/2994
2	D	0.16	0/2107	0.43	2/2847 (0.1%)
2	E	0.16	0/2107	0.44	2/2847 (0.1%)
2	F	0.12	0/2107	0.35	0/2847
All	All	0.14	0/12954	0.41	4/17523 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	193	PRO	CA-N-CD	-11.30	96.18	112.00
2	E	193	PRO	CA-N-CD	-10.83	96.84	112.00
2	D	193	PRO	N-CD-CG	-6.46	93.51	103.20
2	E	193	PRO	N-CD-CG	-6.45	93.52	103.20

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	2168	0	2188	33	0
1	B	2168	0	2188	30	0
1	C	2168	0	2188	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2070	0	2064	24	0
2	E	2070	0	2064	31	0
2	F	2070	0	2064	27	0
All	All	12714	0	12756	165	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 6.

The worst 5 of 165 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)
2:F:36:ALA:O	2:F:37:HIS:ND1	2.04	0.90
1:C:272:ARG:HD2	1:C:273:SER:H	1.36	0.89
1:C:207:LEU:HD12	1:C:295:GLU:HB2	1.72	0.71
1:A:207:LEU:HD12	1:A:295:GLU:HB2	1.72	0.70
1:B:207:LEU:HD12	1:B:295:GLU:HB2	1.72	0.70

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	268/840 (32%)	217 (81%)	49 (18%)	2 (1%)	18	55
1	B	268/840 (32%)	221 (82%)	45 (17%)	2 (1%)	18	55
1	C	268/840 (32%)	221 (82%)	45 (17%)	2 (1%)	18	55
2	D	250/1143 (22%)	227 (91%)	23 (9%)	0	100	100
2	E	250/1143 (22%)	226 (90%)	24 (10%)	0	100	100
2	F	250/1143 (22%)	226 (90%)	24 (10%)	0	100	100
All	All	1554/5949 (26%)	1338 (86%)	210 (14%)	6 (0%)	31	65

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	VAL
1	B	266	VAL
1	C	266	VAL
1	A	320	VAL
1	B	320	VAL

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	244/723 (34%)	244 (100%)	0	100	100
1	B	244/723 (34%)	244 (100%)	0	100	100
1	C	244/723 (34%)	244 (100%)	0	100	100
2	D	241/1020 (24%)	241 (100%)	0	100	100
2	E	241/1020 (24%)	241 (100%)	0	100	100
2	F	241/1020 (24%)	241 (100%)	0	100	100
All	All	1455/5229 (28%)	1455 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	86	GLN
2	E	266	ASN
2	F	266	ASN
2	F	5	GLN
2	D	95	ASN

5.3.3 RNA [i](#)

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](#)

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.

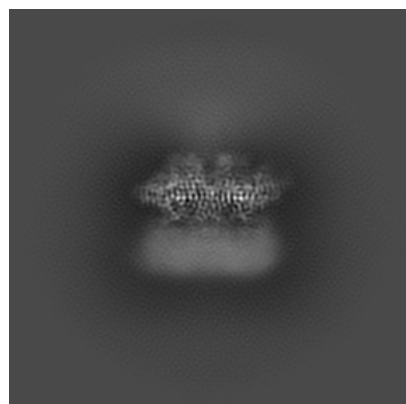
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40235. These allow visual inspection of the internal detail of the map and identification of artifacts.

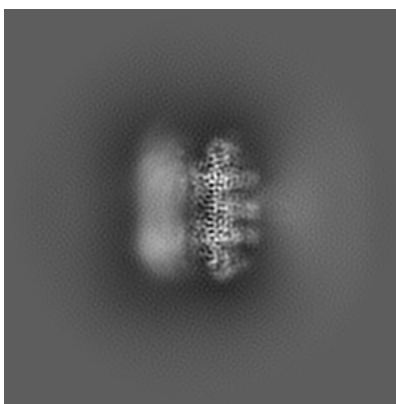
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

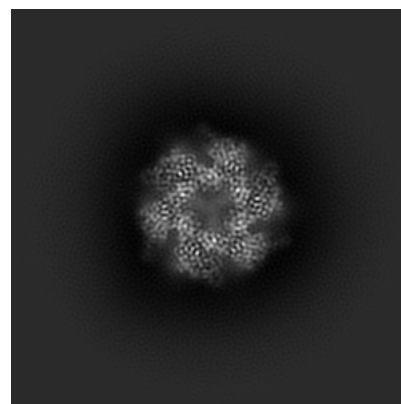
6.1.1 Primary map



X

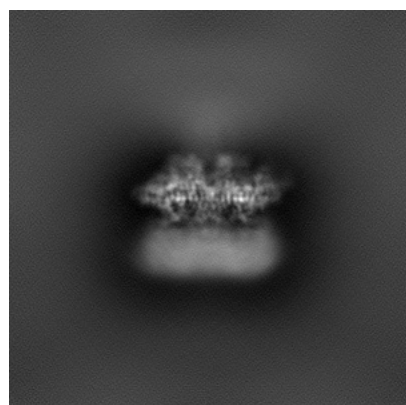


Y

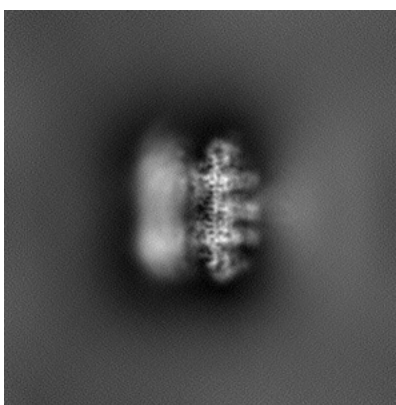


Z

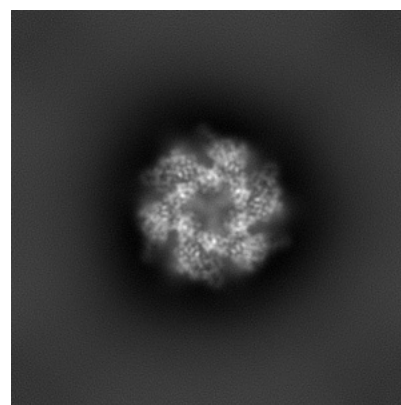
6.1.2 Raw map



X



Y

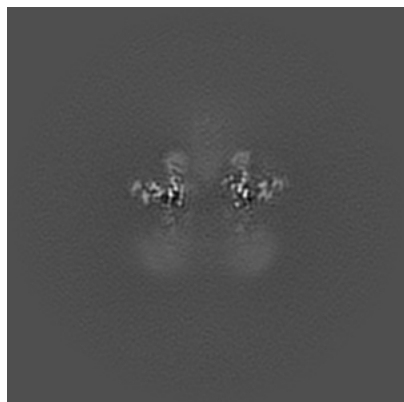


Z

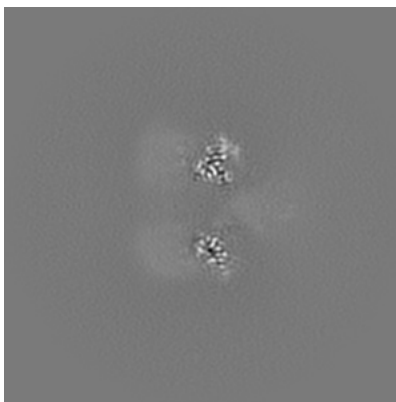
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

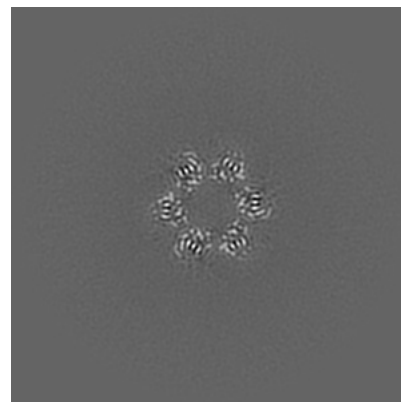
6.2.1 Primary map



X Index: 160

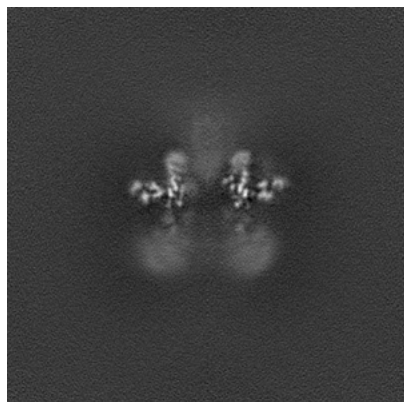


Y Index: 160

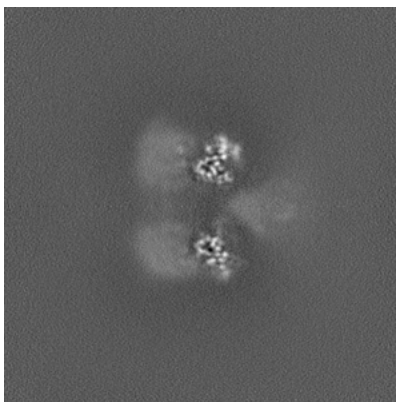


Z Index: 160

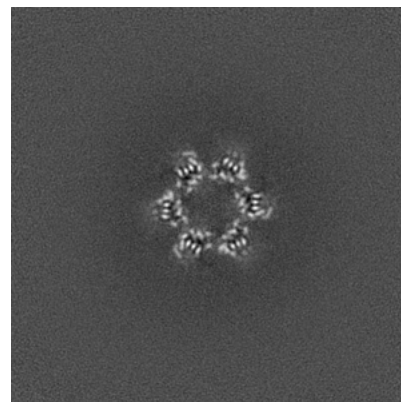
6.2.2 Raw map



X Index: 160



Y Index: 160

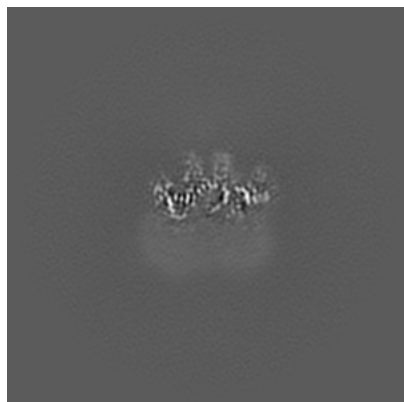


Z Index: 160

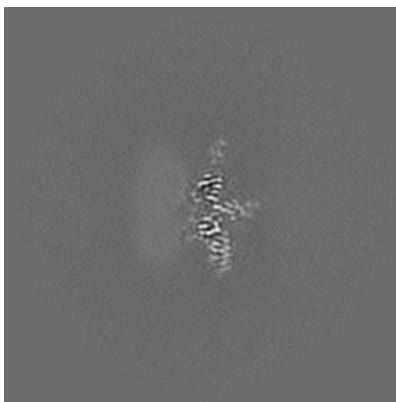
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

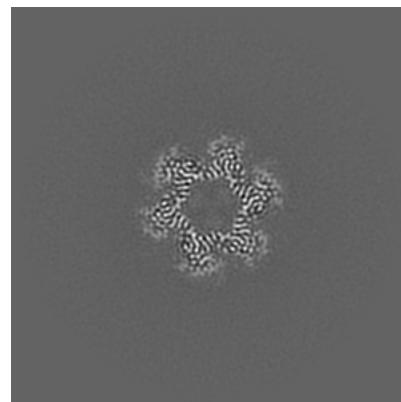
6.3.1 Primary map



X Index: 181

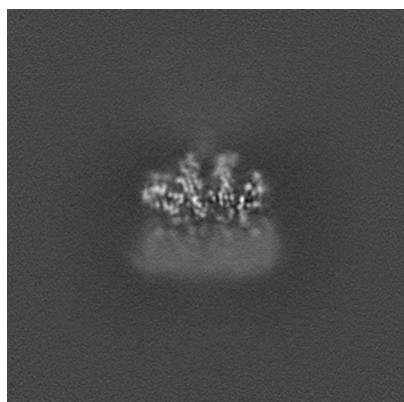


Y Index: 190

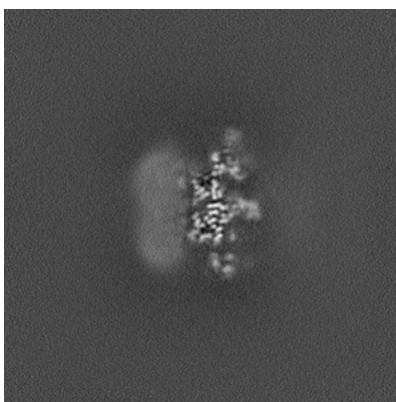


Z Index: 168

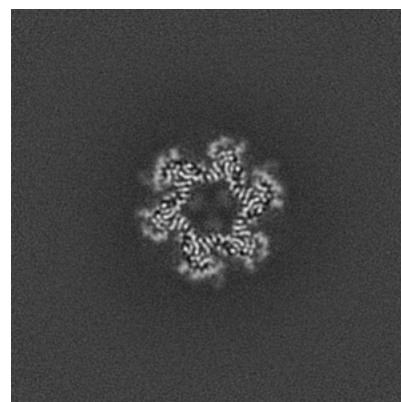
6.3.2 Raw map



X Index: 136



Y Index: 135

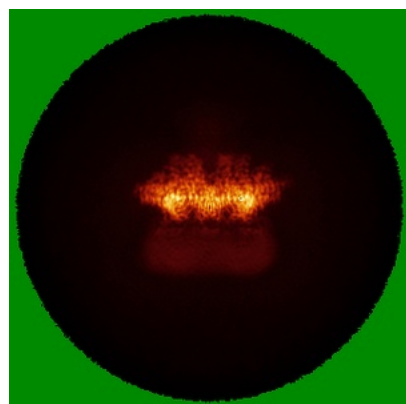


Z Index: 168

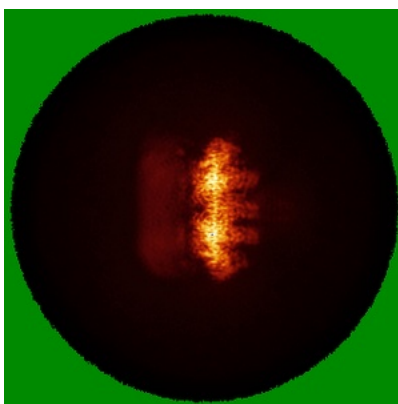
The images above show the largest variance slices of the map in three orthogonal directions.

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

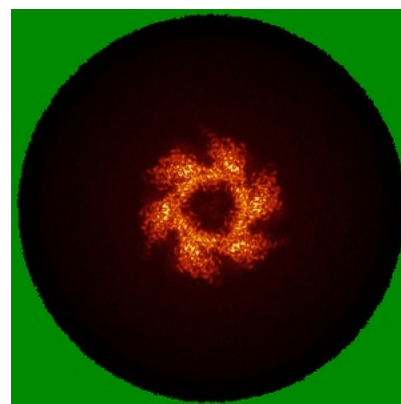
6.4.1 Primary map



X

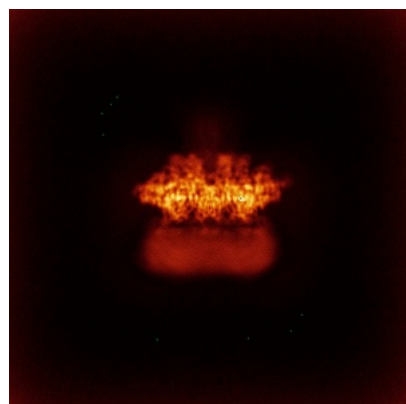


Y

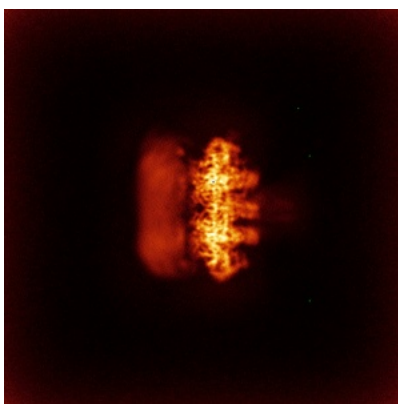


Z

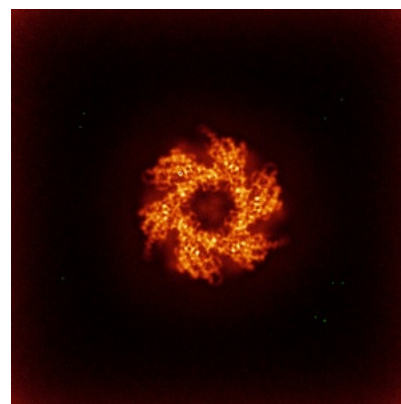
6.4.2 Raw map



X



Y

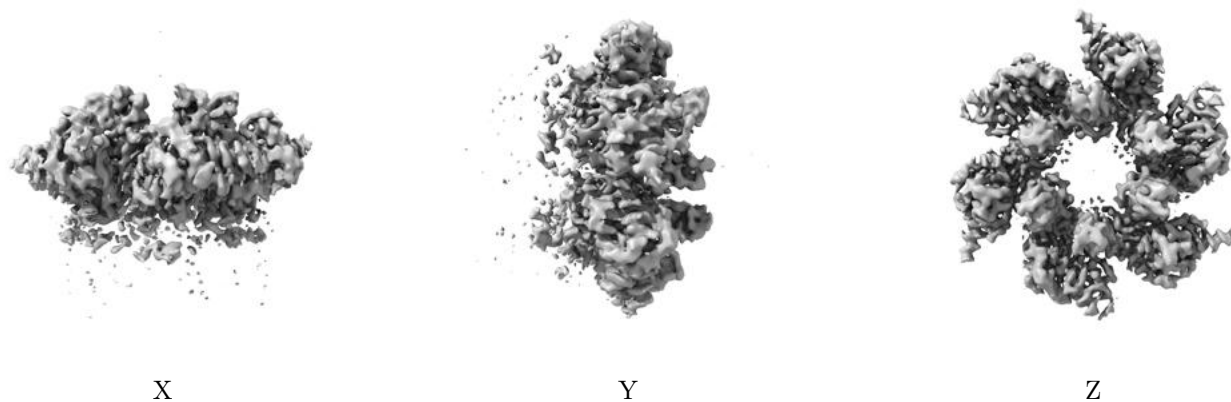


Z

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.

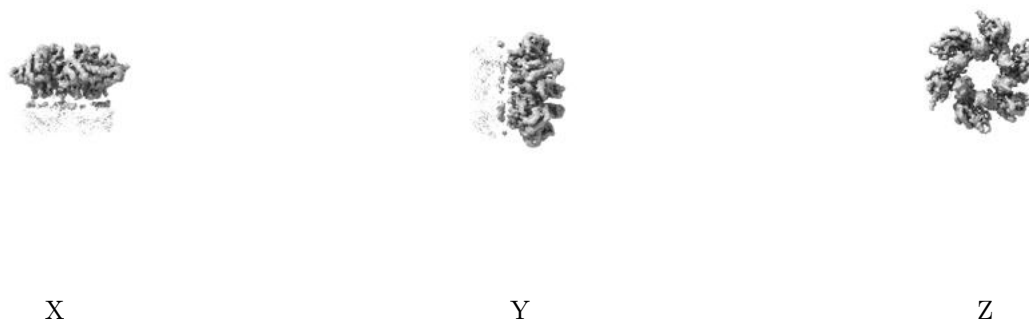
6.5 Orthogonal surface views [i](#)

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.

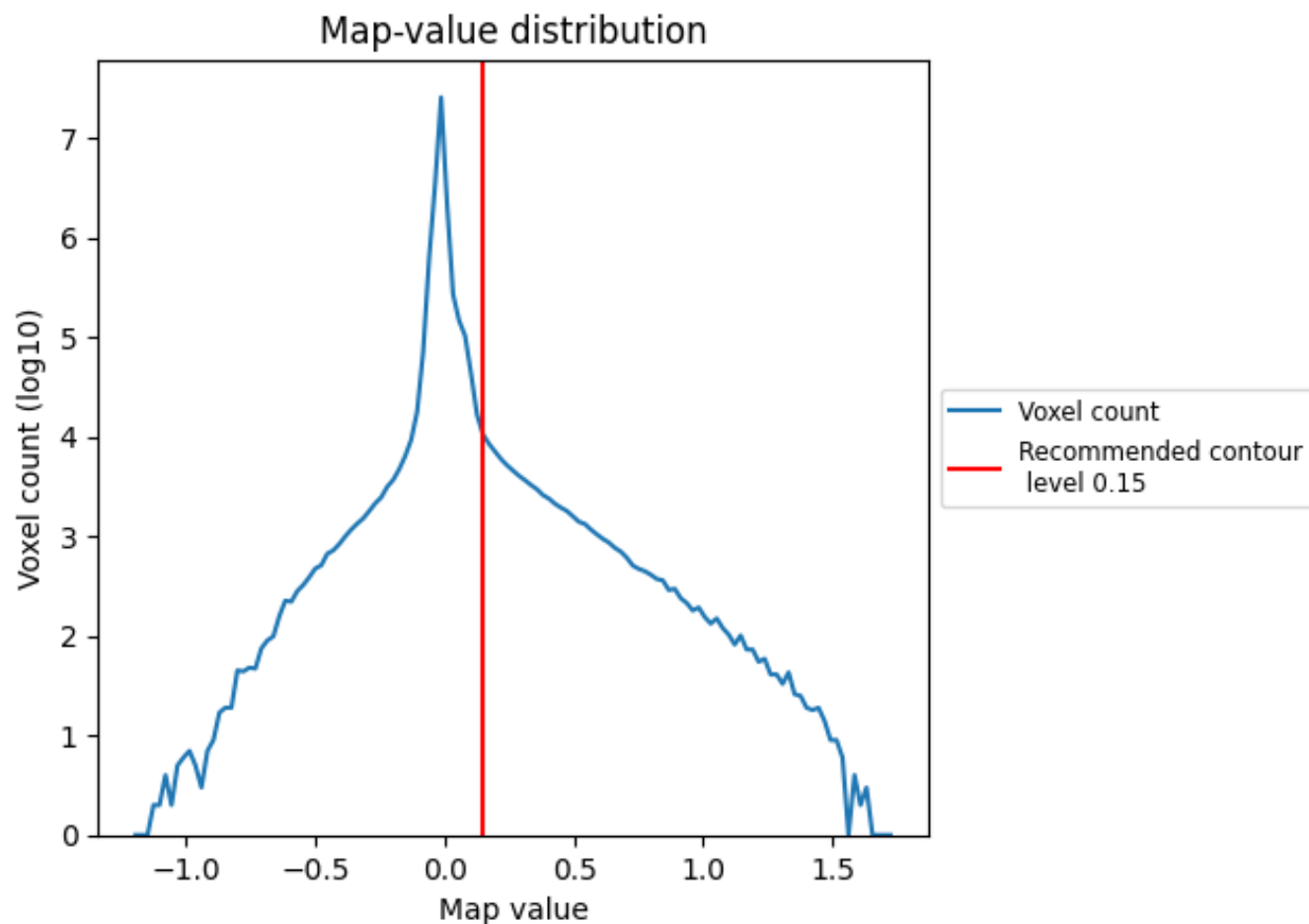
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

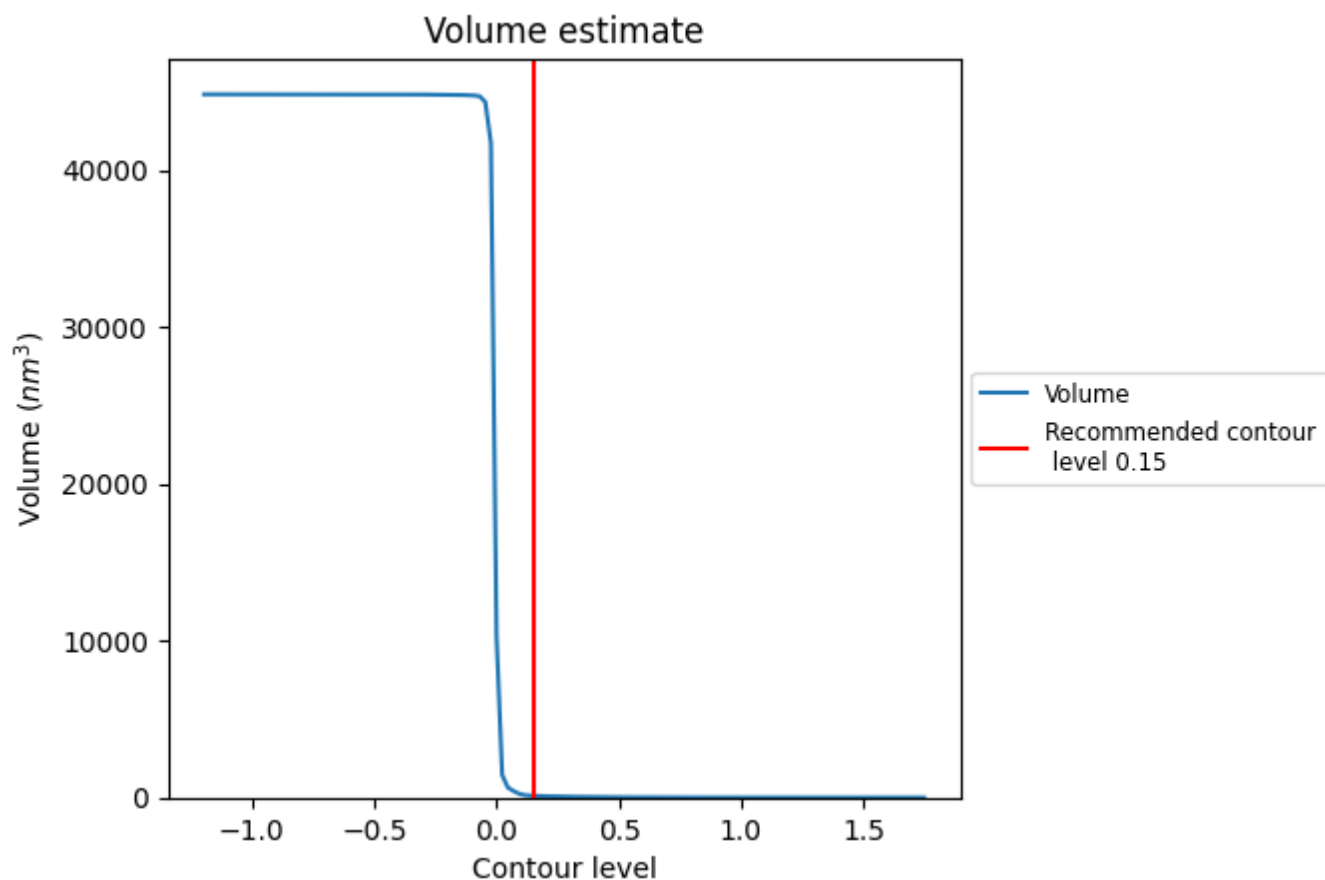
This section contains the results of statistical analysis of the map.

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.

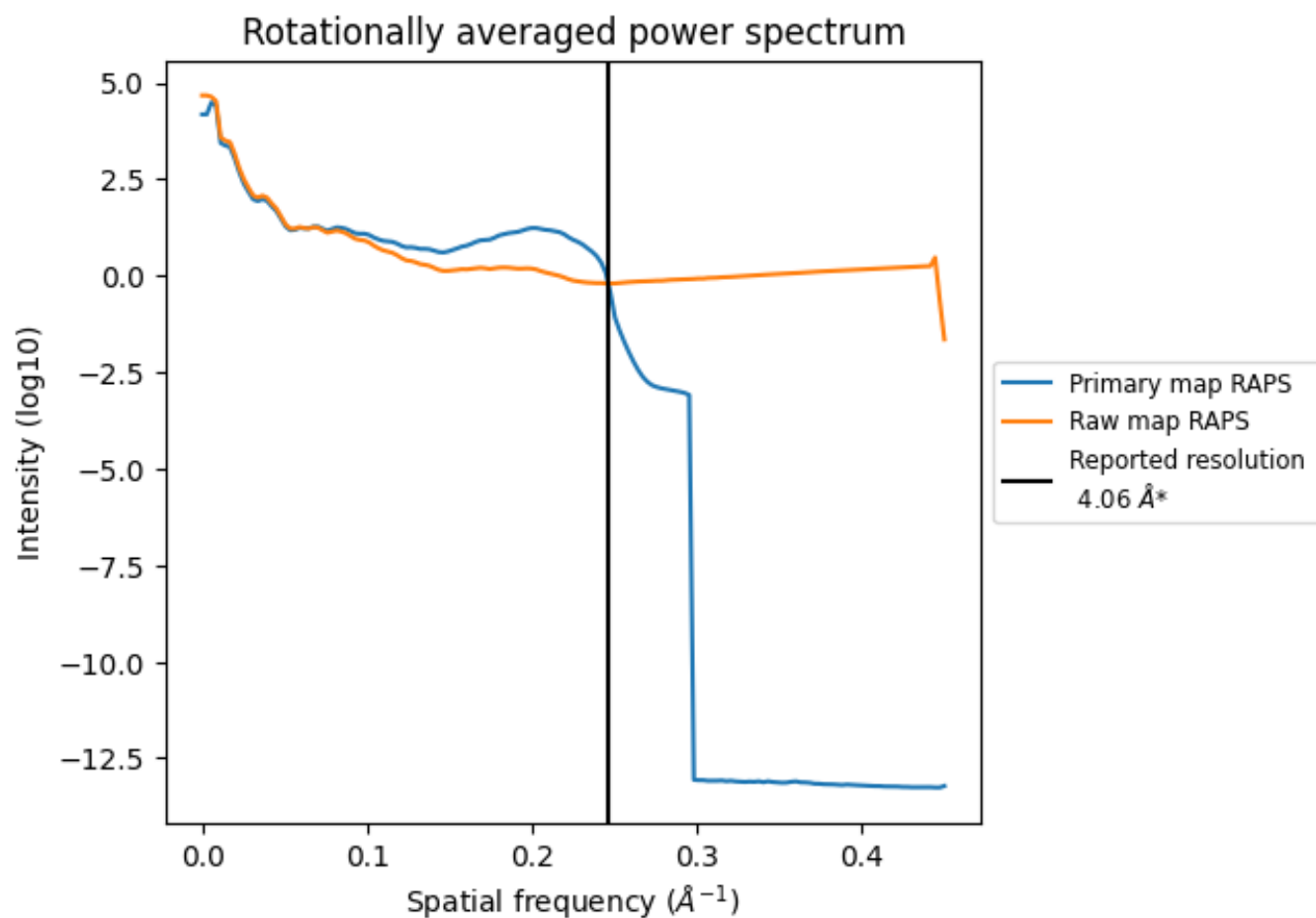
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 113 nm³; this corresponds to an approximate mass of 102 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 ⓘ

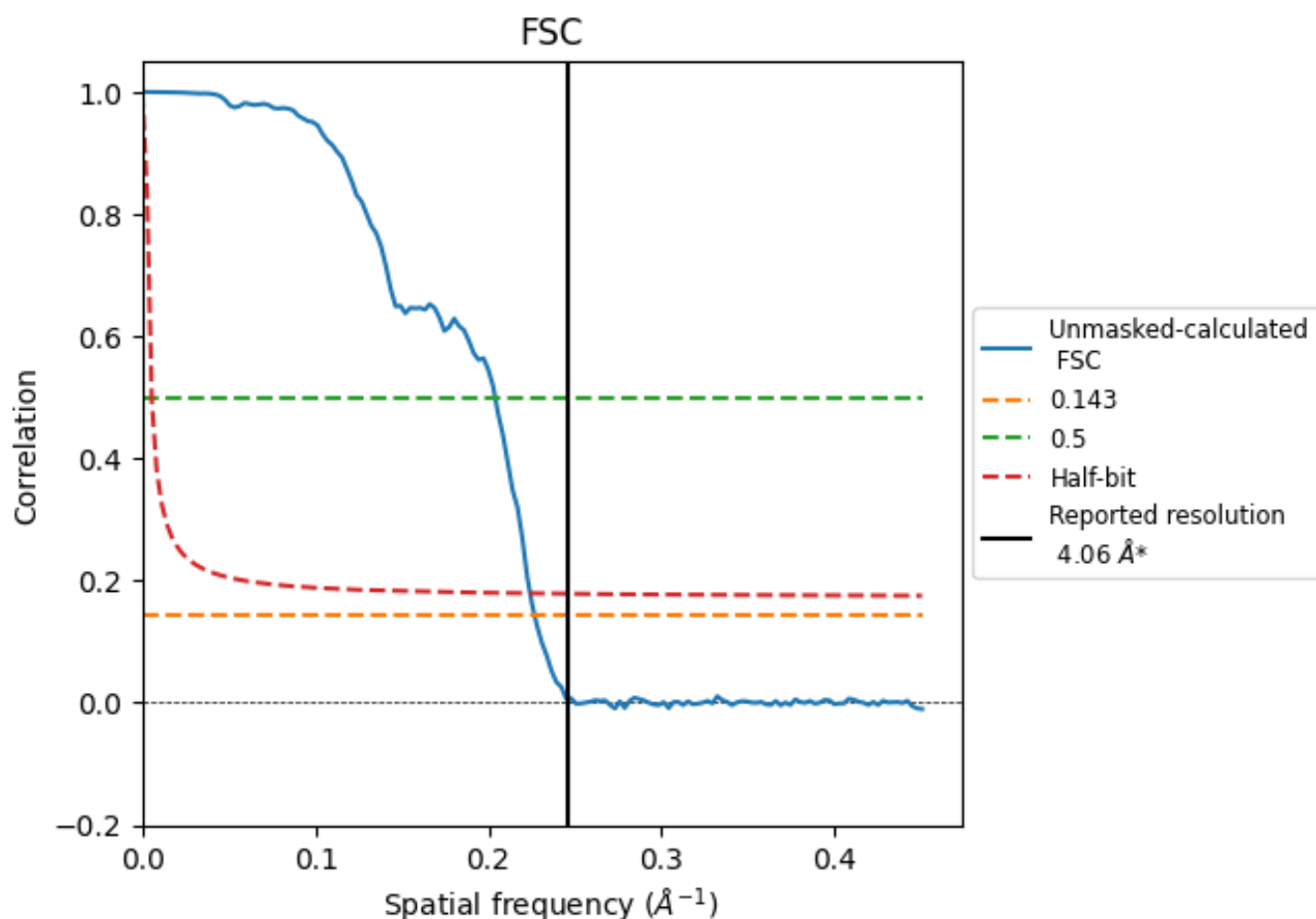


*Reported resolution corresponds to spatial frequency of 0.246 Å⁻¹

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 0.246 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

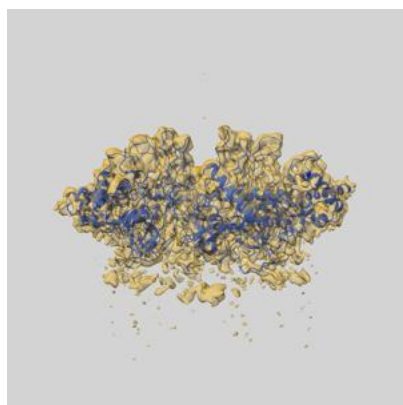
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.06	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.41	4.90	4.46

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

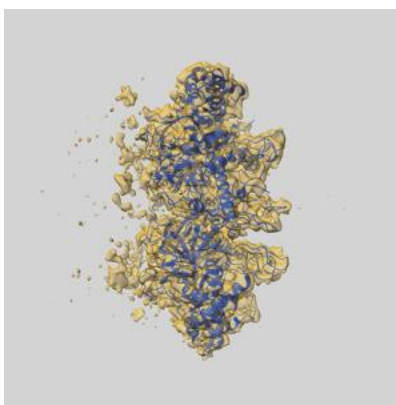
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40235 and PDB model 8S92. Per-residue inclusion information can be found in section [3](#) on page [5](#).

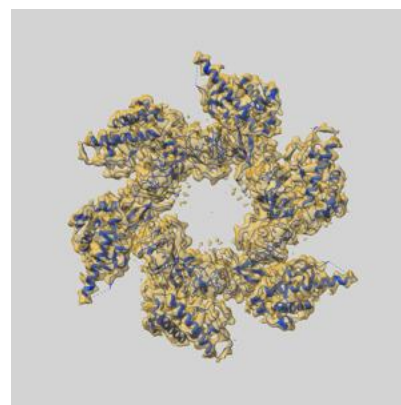
9.1 Map-model overlay [i](#)



X



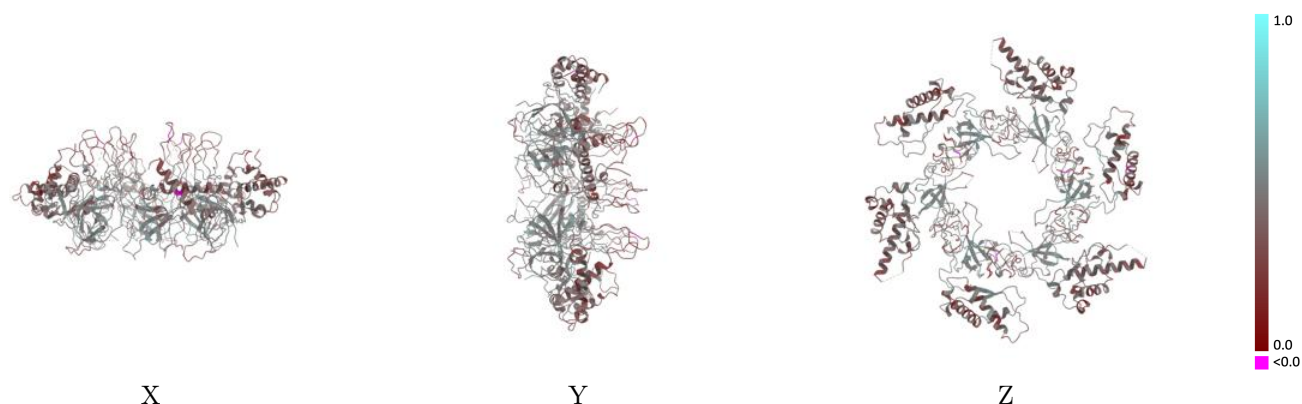
Y



Z

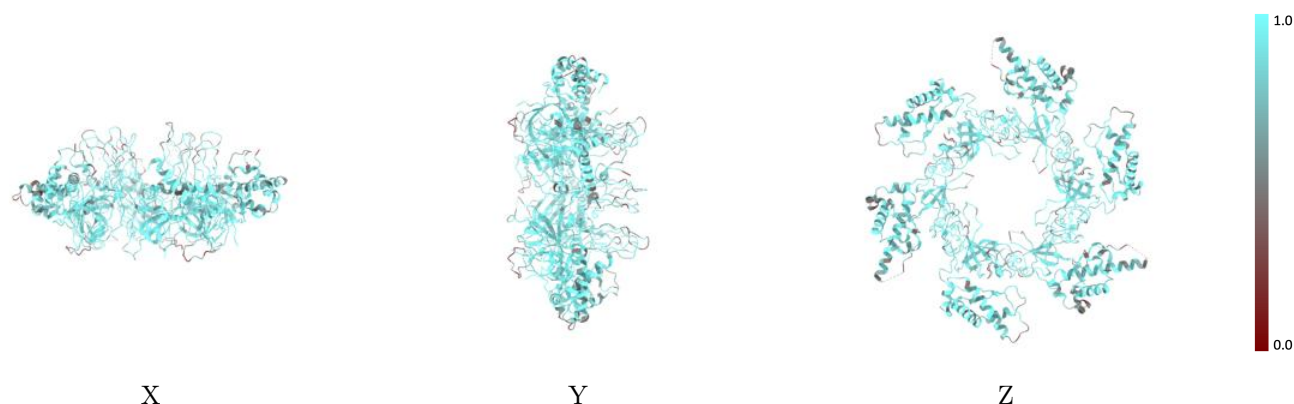
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



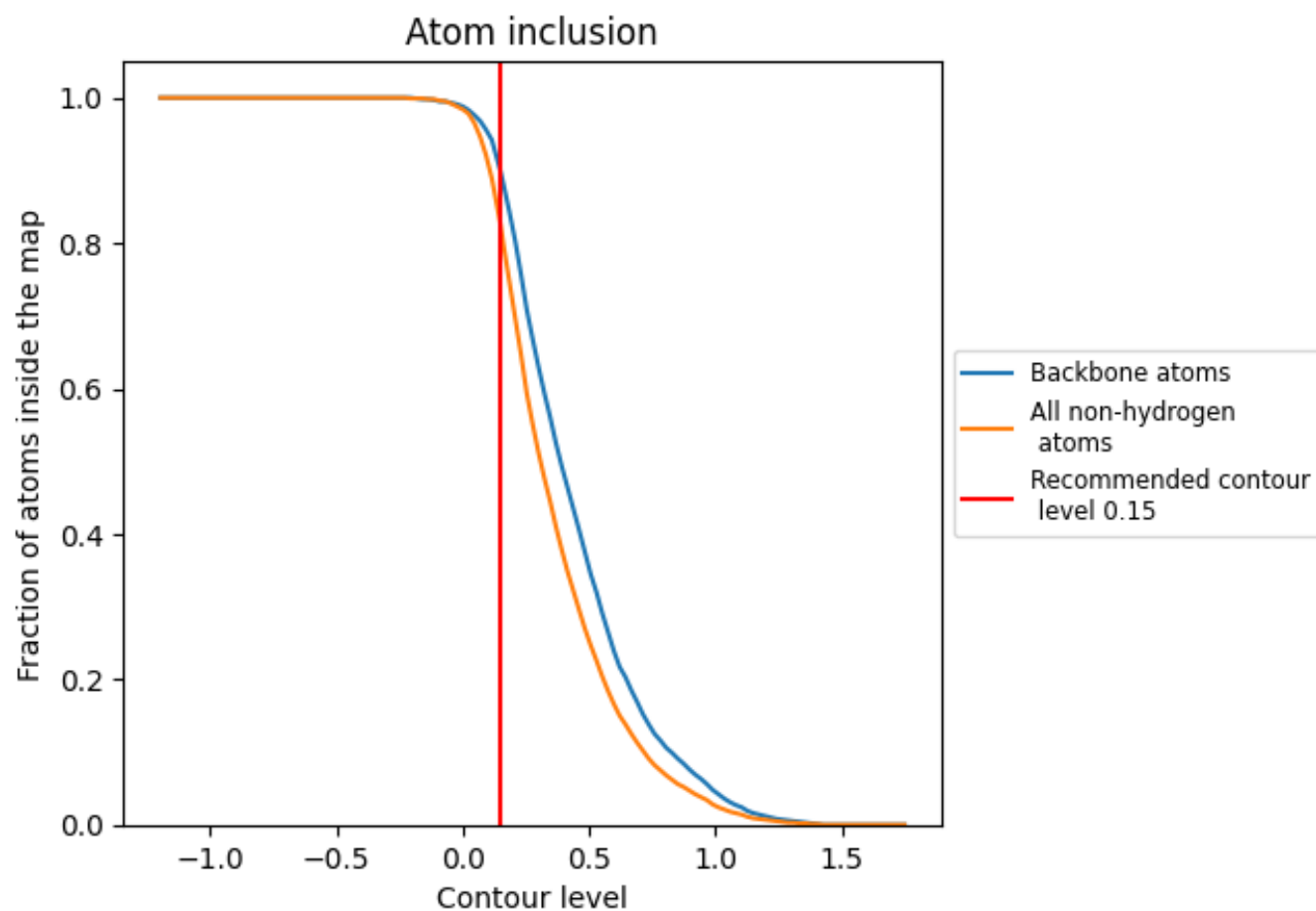
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% of all backbone atoms, 82% 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	0.8250	0.4270
A	0.8160	0.4220
B	0.8120	0.4240
C	0.8120	0.4210
D	0.8350	0.4320
E	0.8380	0.4320
F	0.8390	0.4310

1.0

0.0

<0.0