



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:36 AM UTC

PDB ID : 8HWC / pdb_00008hwc
EMDB ID : EMD-35053
Title : Cryo-EM Structure of D5 Apo
Authors : Li, Y.N.; Zhu, J.; Guo, Y.Y.; Yan, R.H.
Deposited on : 2022-12-29
Resolution : 3.30 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

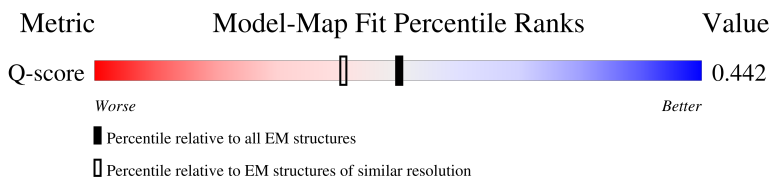
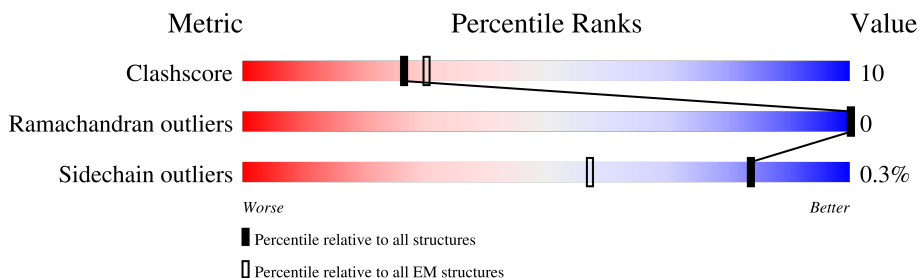
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	785	
1	B	785	
1	C	785	
1	D	785	

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Mol	Chain	Length	Quality of chain
1	E	785	 28% 8% 64%
1	F	785	 30% 9% 61%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14943 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.

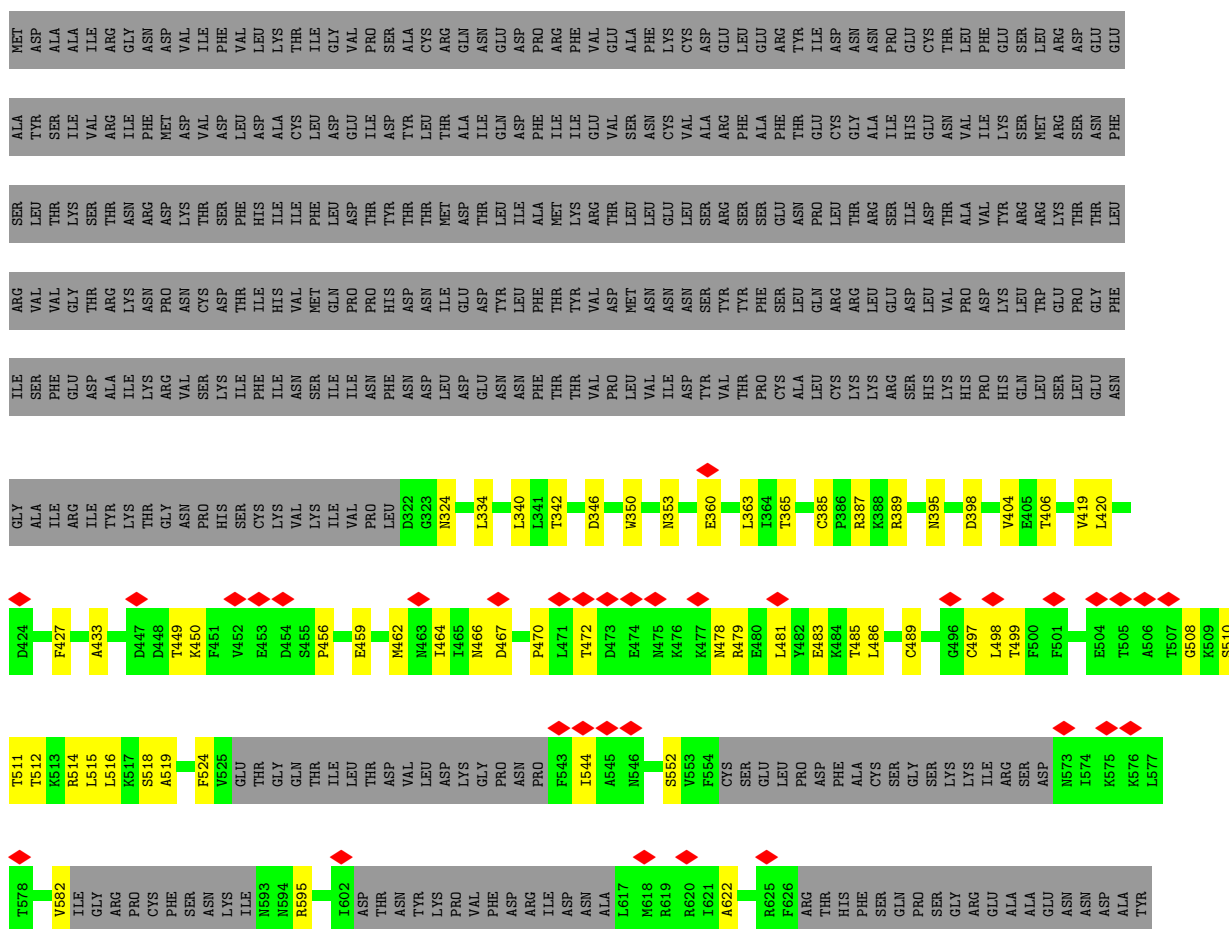
- Molecule 1 is a protein called Primase D5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	284	Total	C	N	O	S	0	0
			2313	1480	394	425	14		
1	F	308	Total	C	N	O	S	0	0
			2514	1608	429	463	14		
1	D	266	Total	C	N	O	S	0	0
			2178	1399	372	394	13		
1	C	280	Total	C	N	O	S	0	0
			2283	1466	388	416	13		
1	B	320	Total	C	N	O	S	0	0
			2610	1672	440	484	14		
1	A	378	Total	C	N	O	S	0	0
			3045	1939	518	572	16		

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



- Molecule 1: Primase D5





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	779993	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.851	Depositor
Minimum map value	-3.371	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	280.32, 280.32, 280.32	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.095, 1.095, 1.095	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	0/3108	0.42	1/4198 (0.0%)
1	B	0.14	0/2660	0.34	0/3587
1	C	0.13	0/2324	0.35	1/3126 (0.0%)
1	D	0.14	0/2216	0.34	0/2977
1	E	0.13	0/2354	0.30	0/3165
1	F	0.12	0/2562	0.30	0/3453
All	All	0.14	0/15224	0.35	2/20506 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	544	ILE	N-CA-C	-5.67	106.78	113.42
1	C	675	TRP	N-CA-CB	-5.07	102.38	109.94

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	3045	0	3055	79	0
1	B	2610	0	2630	50	0
1	C	2283	0	2324	51	0
1	D	2178	0	2227	39	0
1	E	2313	0	2345	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2514	0	2544	53	0
All	All	14943	0	15125	302	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 10.

The worst 5 of 302 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:B:612:ARG:HH12	1:B:614:ASP:HB3	1.41	0.86
1:A:652:ASP:HB3	1:A:655:LEU:HB2	1.69	0.74
1:C:483:GLU:HA	1:C:675:TRP:HZ3	1.55	0.71
1:F:501:PHE:HB2	1:F:603:ASP:HA	1.73	0.69
1:A:406:THR:O	1:A:595:ARG:NH1	2.26	0.69

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	376/785 (48%)	347 (92%)	29 (8%)	0	100	100
1	B	310/785 (40%)	294 (95%)	16 (5%)	0	100	100
1	C	268/785 (34%)	250 (93%)	18 (7%)	0	100	100
1	D	252/785 (32%)	236 (94%)	16 (6%)	0	100	100
1	E	272/785 (35%)	252 (93%)	20 (7%)	0	100	100
1	F	298/785 (38%)	282 (95%)	16 (5%)	0	100	100
All	All	1776/4710 (38%)	1661 (94%)	115 (6%)	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	343/725 (47%)	341 (99%)	2 (1%)	78	81
1	B	295/725 (41%)	295 (100%)	0	100	100
1	C	258/725 (36%)	257 (100%)	1 (0%)	84	84
1	D	247/725 (34%)	245 (99%)	2 (1%)	73	79
1	E	262/725 (36%)	262 (100%)	0	100	100
1	F	285/725 (39%)	285 (100%)	0	100	100
All	All	1690/4350 (39%)	1685 (100%)	5 (0%)	84	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	449	THR
1	D	478	ASN
1	C	478	ASN
1	A	359	SER
1	A	515	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	596	ASN
1	A	475	ASN
1	A	478	ASN
1	D	475	ASN
1	D	478	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.

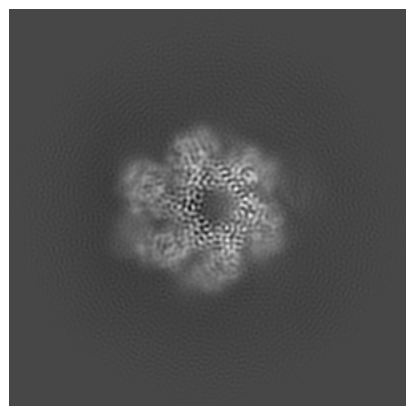
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35053. These allow visual inspection of the internal detail of the map and identification of artifacts.

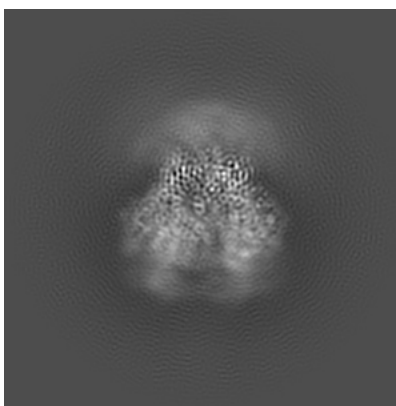
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

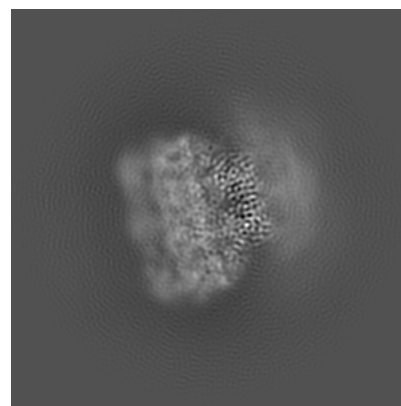
6.1.1 Primary map



X

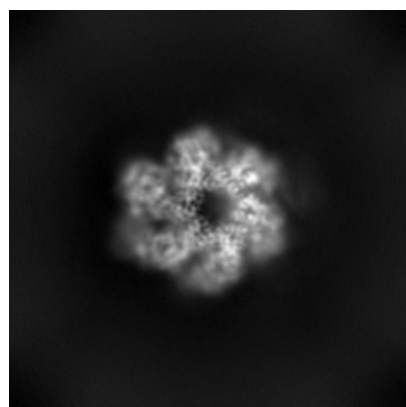


Y

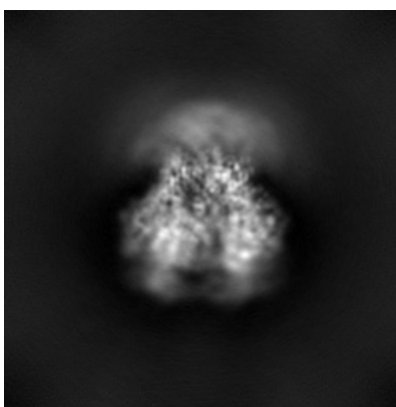


Z

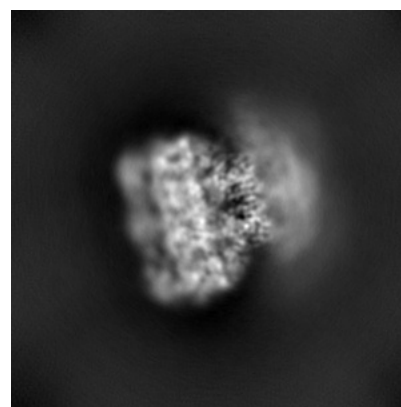
6.1.2 Raw map



X



Y

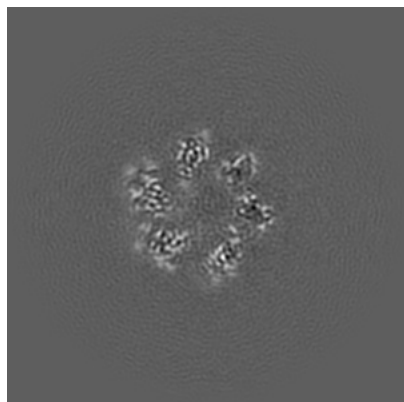


Z

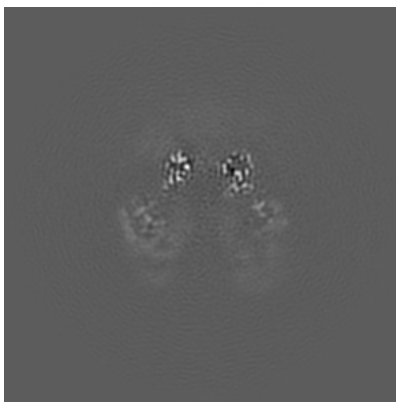
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

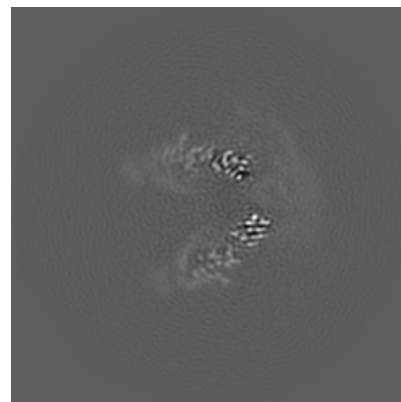
6.2.1 Primary map



X Index: 128

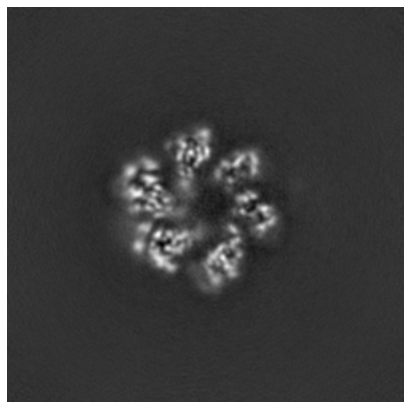


Y Index: 128

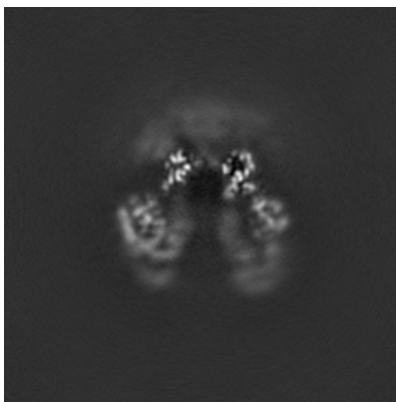


Z Index: 128

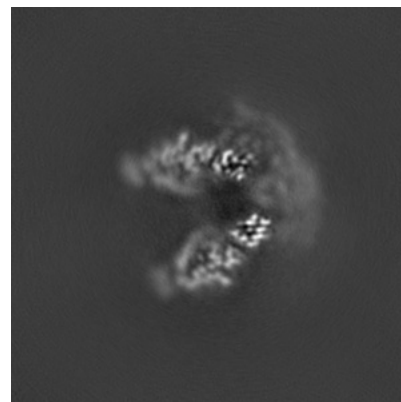
6.2.2 Raw map



X Index: 128



Y Index: 128

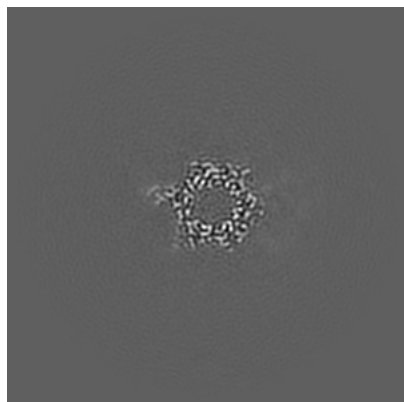


Z Index: 128

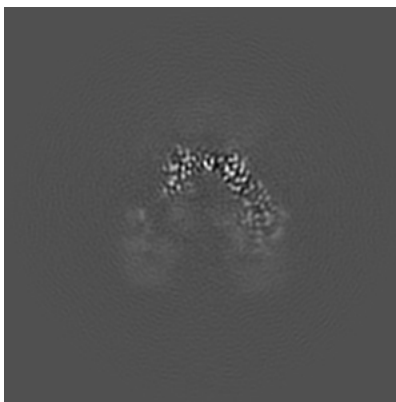
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

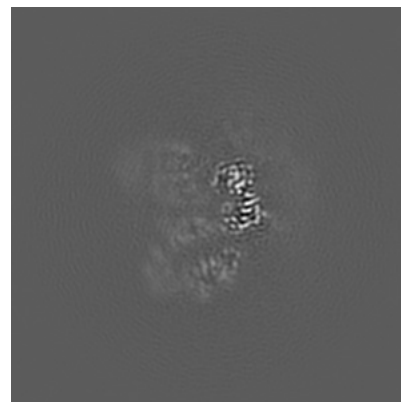
6.3.1 Primary map



X Index: 149

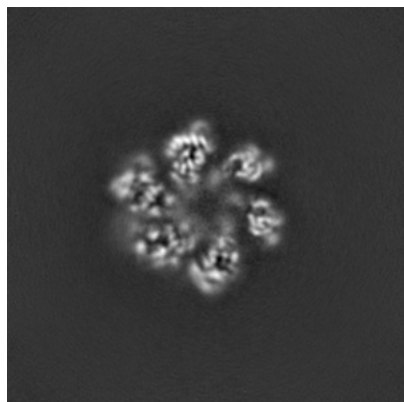


Y Index: 121

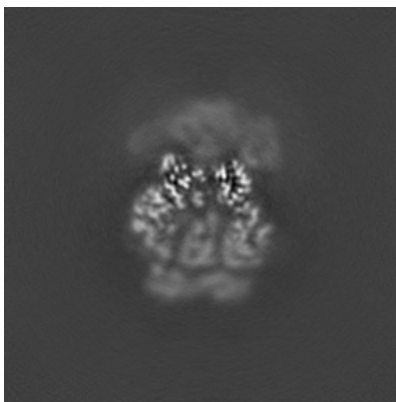


Z Index: 144

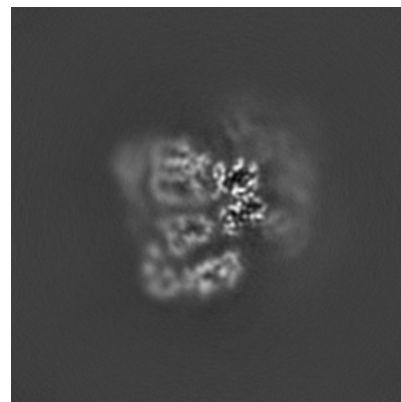
6.3.2 Raw map



X Index: 122



Y Index: 145

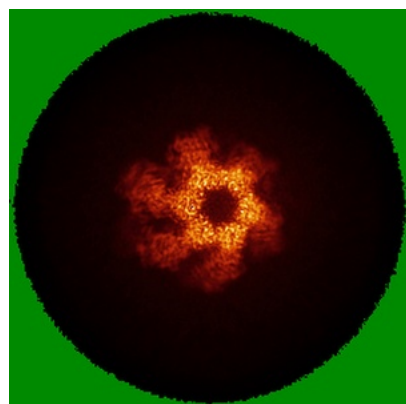


Z Index: 147

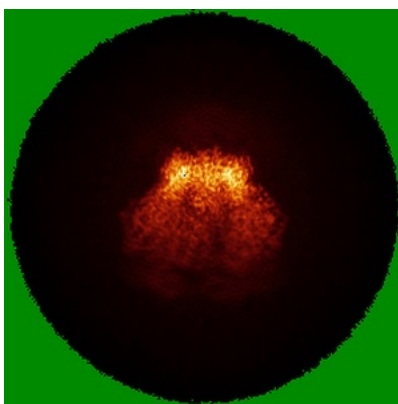
The images above show the largest variance slices of the map in three orthogonal directions.

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

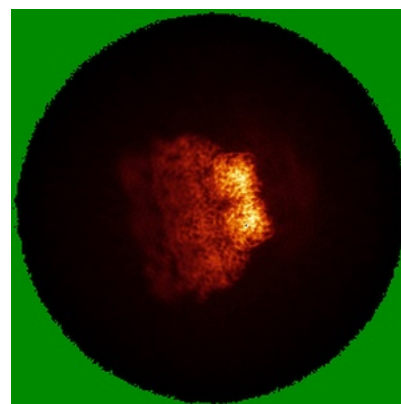
6.4.1 Primary map



X

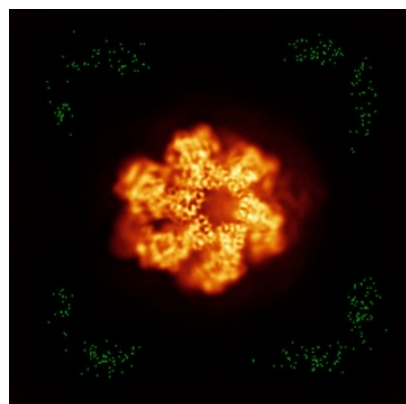


Y

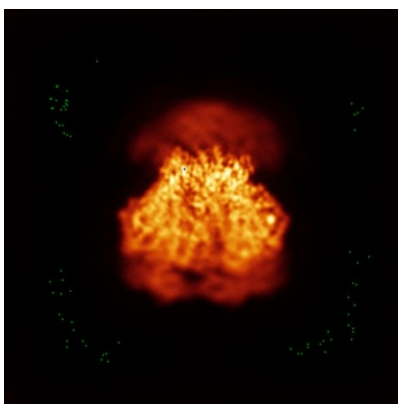


Z

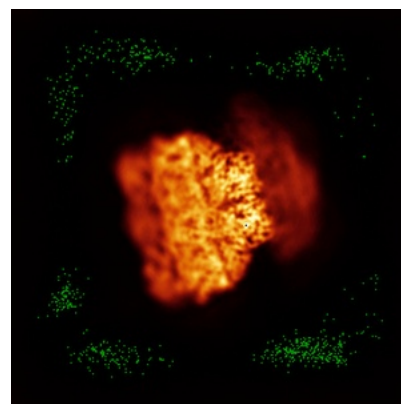
6.4.2 Raw map



X



Y

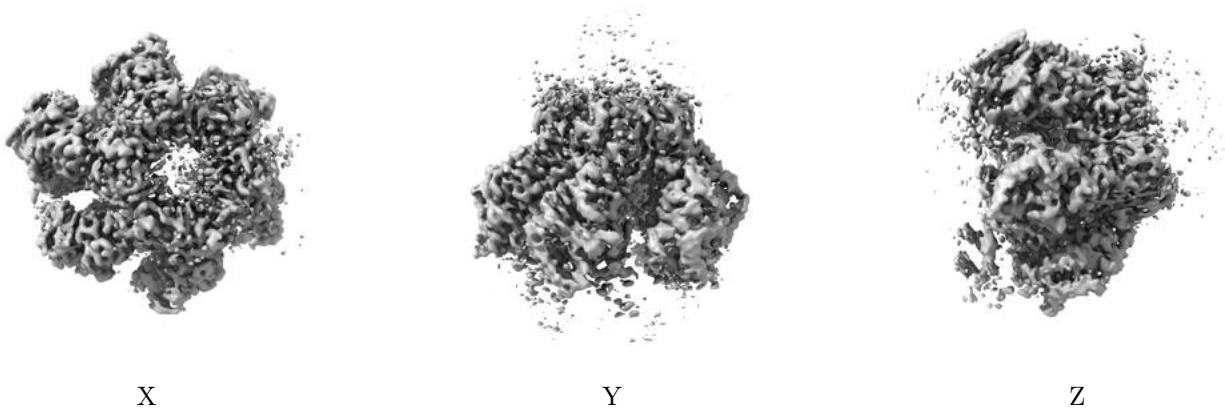


Z

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.

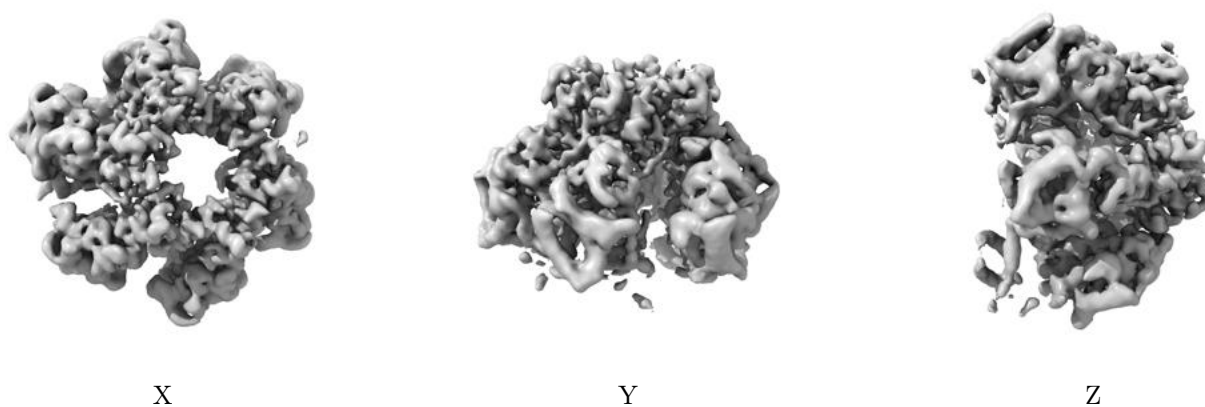
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

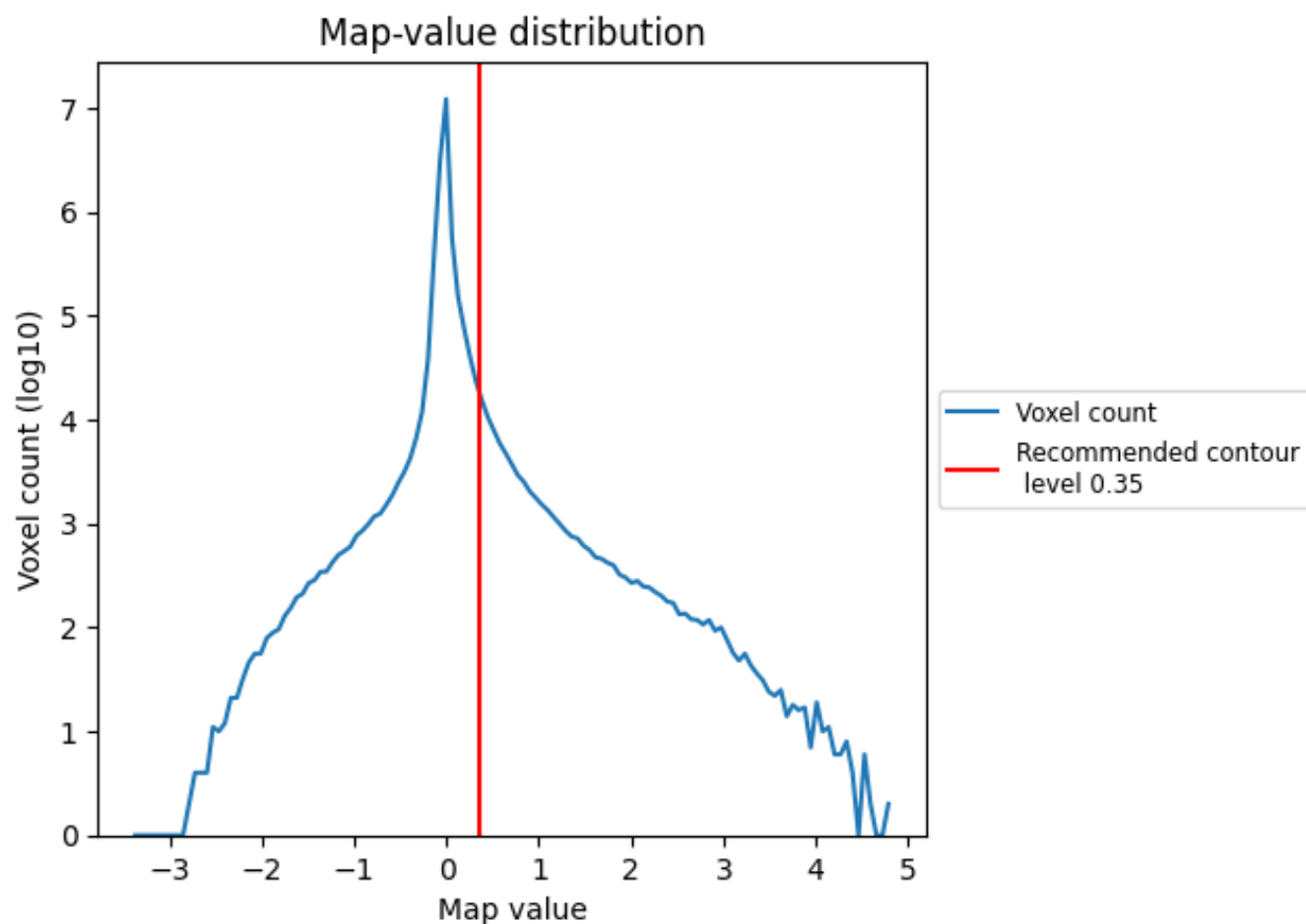
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

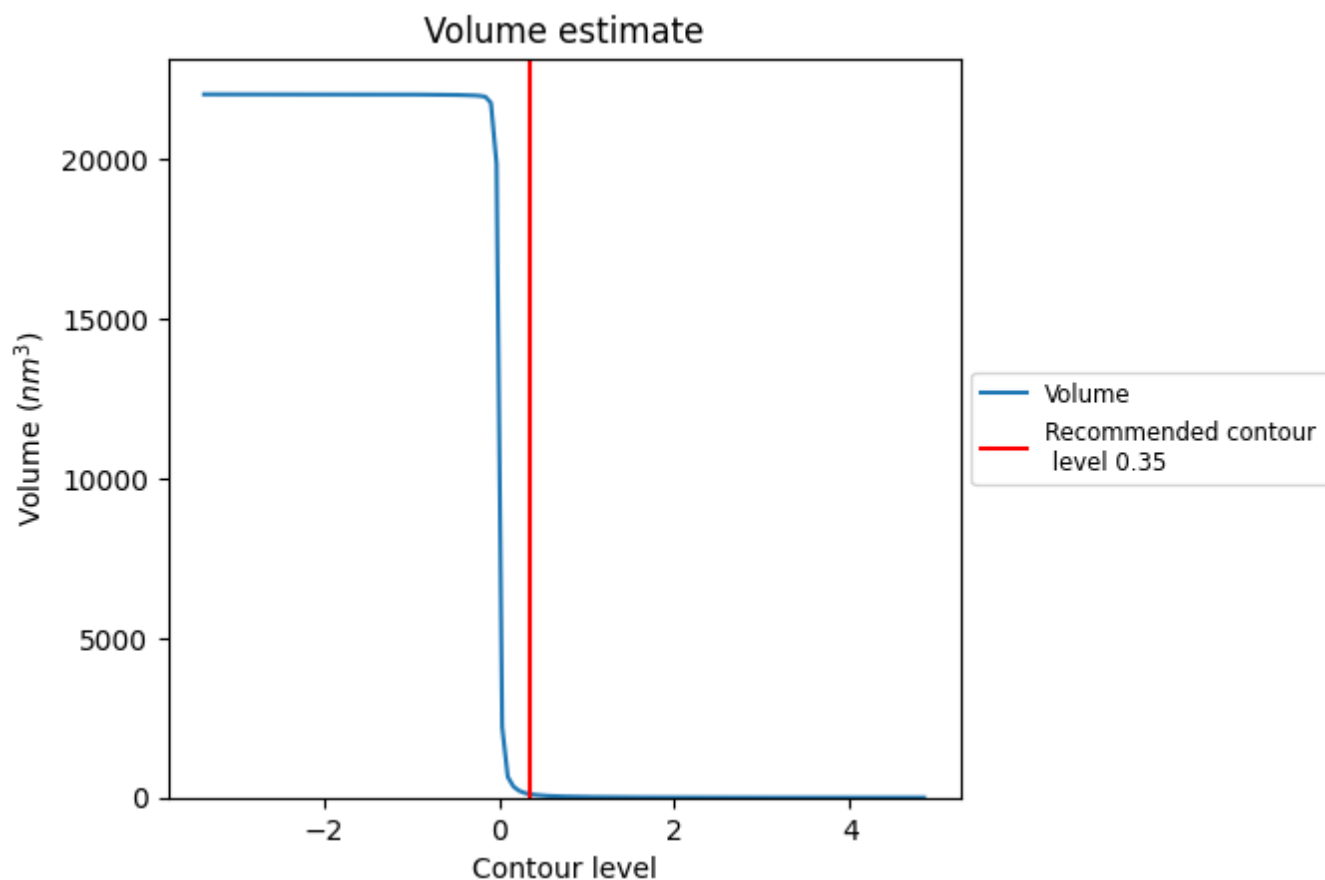
This section contains the results of statistical analysis of the map.

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.

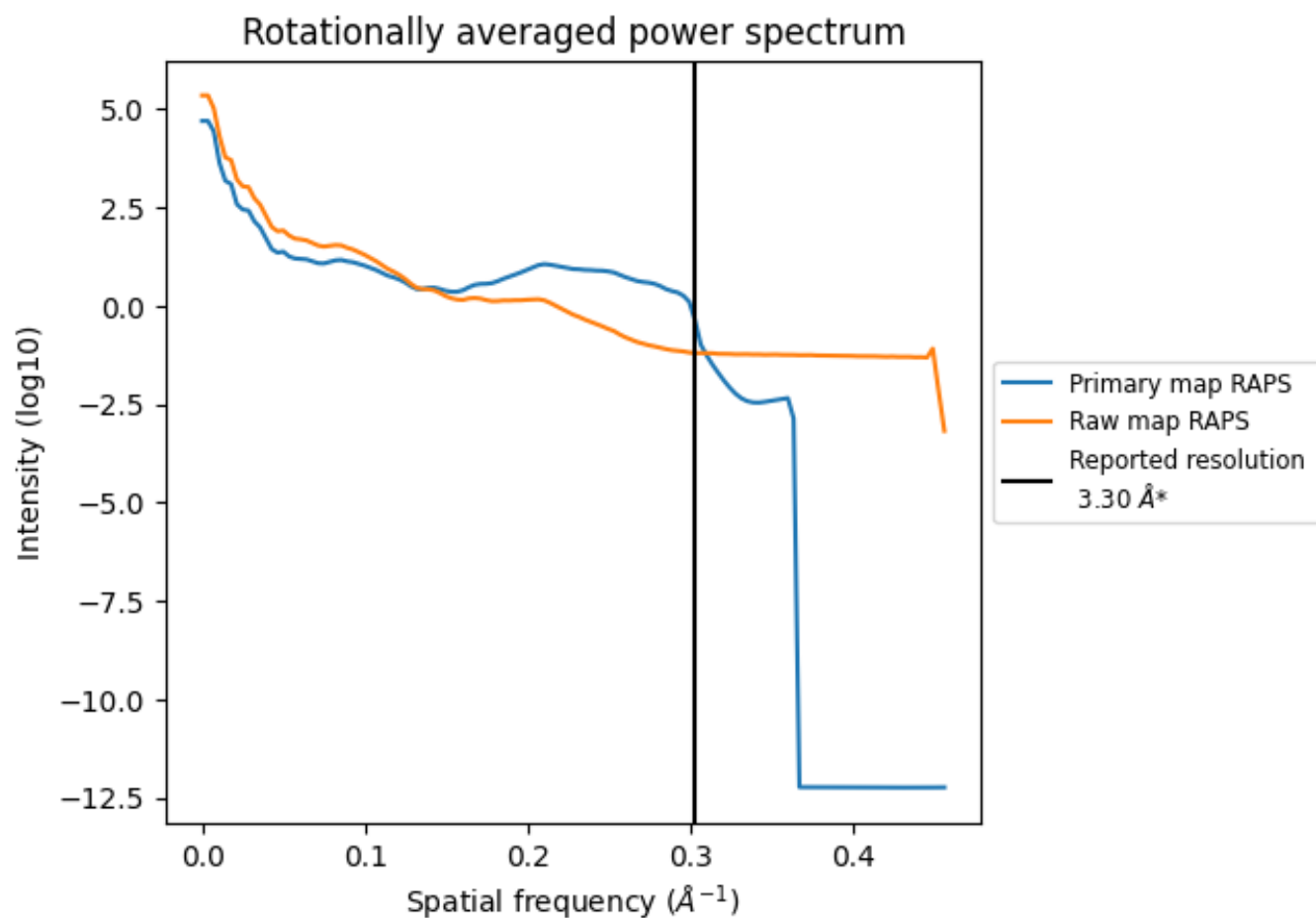
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 109 nm³; this corresponds to an approximate mass of 98 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 ⓘ

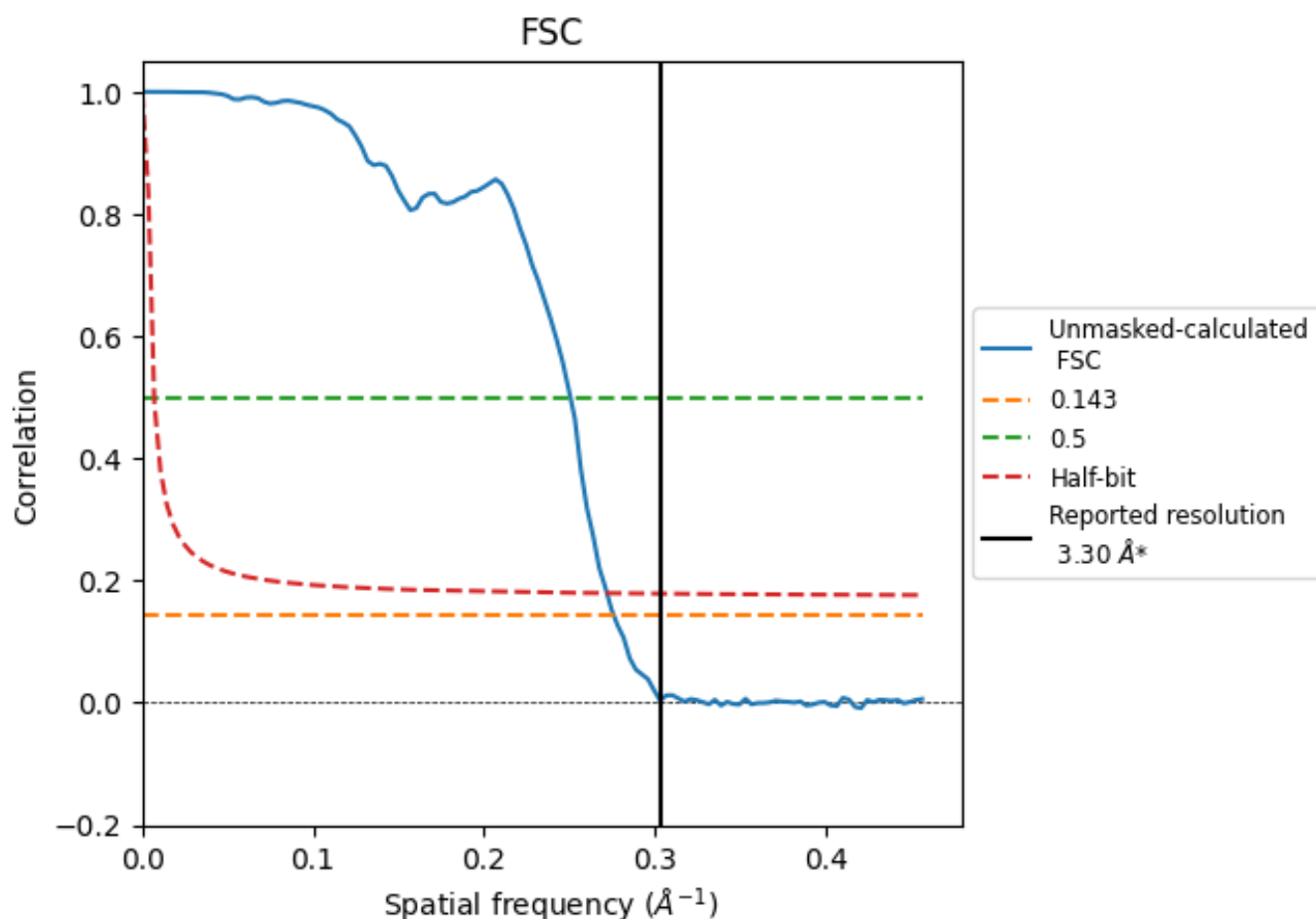


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

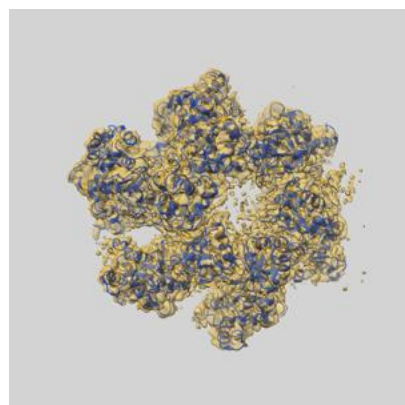
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.62	3.99	3.68

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

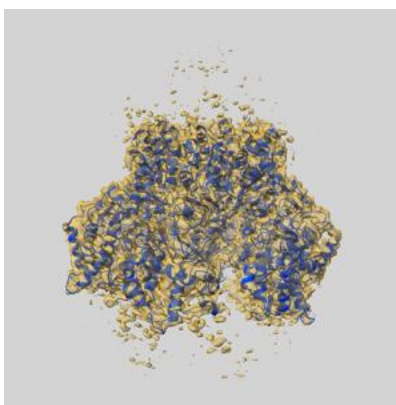
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35053 and PDB model 8HWC. Per-residue inclusion information can be found in section [3](#) on page [5](#).

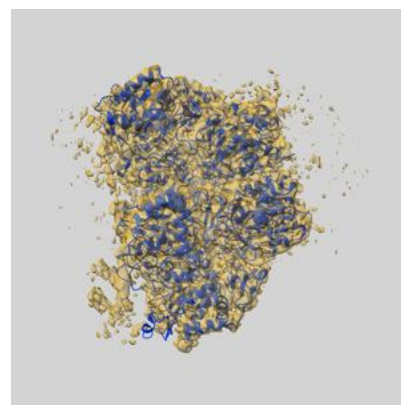
9.1 Map-model overlay [i](#)



X



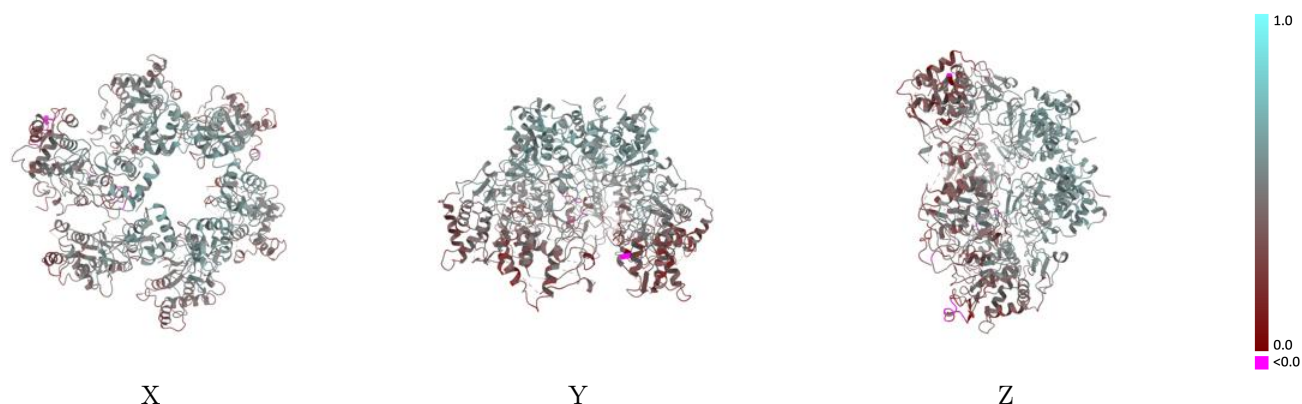
Y



Z

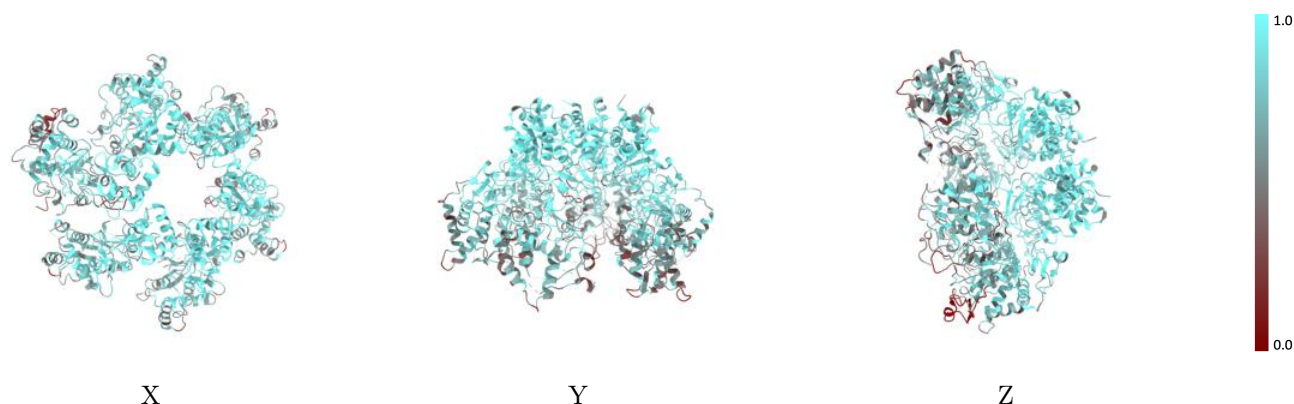
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



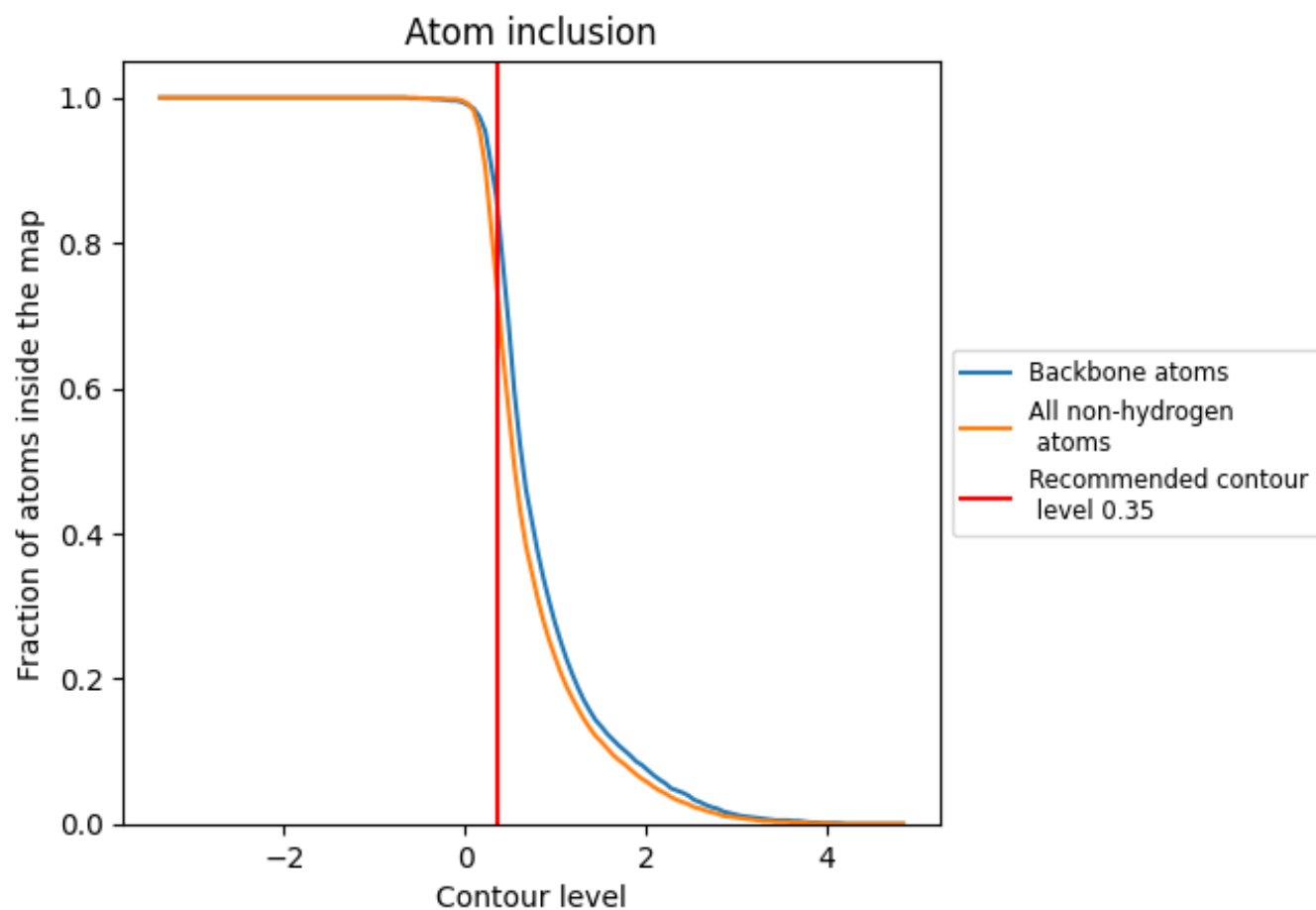
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 74% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7430	0.4420
A	0.6790	0.4100
B	0.7860	0.4680
C	0.7200	0.4290
D	0.7590	0.4510
E	0.7690	0.4520
F	0.7610	0.4460

1.0

0.0

<0.0