



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 03:58 AM UTC

PDB ID : 8HWH / pdb_00008hwh
EMDB ID : EMD-35058
Title : Cryo-EM Structure of D5 Apo-ssDNA form
Authors : Li, Y.N.; Zhu, J.; Guo, Y.Y.; Yan, R.H.
Deposited on : 2022-12-29
Resolution : 3.60 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

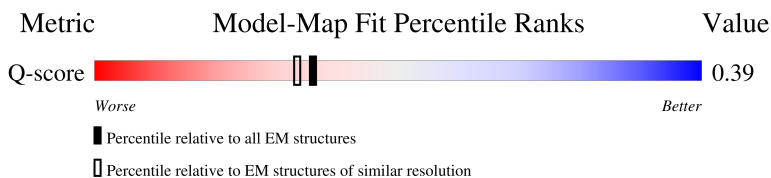
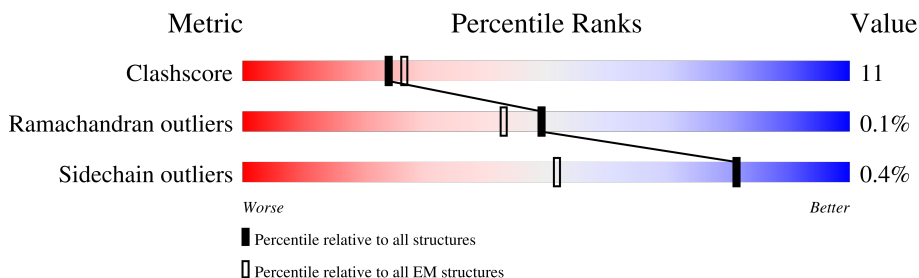
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	 35% 10% 55%
1	B	785	 34% 12% 55%
1	C	785	 37% 9% 54%
1	D	785	 34% 12% 54%

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Mol	Chain	Length	Quality of chain
1	E	785	 31%11%58%
1	F	785	 28%12%60%
2	S	6	 17%83%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16948 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.

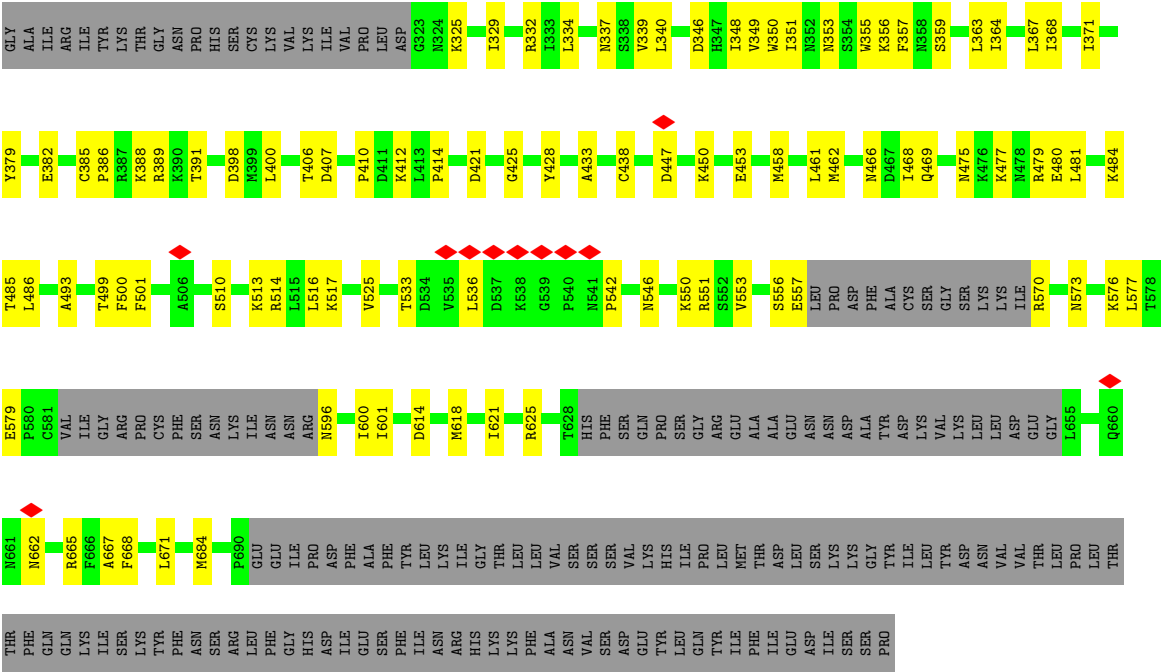
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	353	Total	C	N	O	S	0	0
			2858	1828	485	529	16		
1	B	357	Total	C	N	O	S	0	0
			2887	1845	489	537	16		
1	C	361	Total	C	N	O	S	0	0
			2920	1868	495	541	16		
1	D	363	Total	C	N	O	S	0	0
			2940	1881	497	546	16		
1	E	329	Total	C	N	O	S	0	0
			2662	1697	455	495	15		
1	F	316	Total	C	N	O	S	0	0
			2561	1636	434	477	14		

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*TP*TP*TP*TP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S	6	Total	C	N	O	P	0	0
			120	60	12	42	6		

ARG	HIS	GLY	ILE	ILE	GLY	D334	L420	GLY	ILE	ARG	SER	ALA	ALA	THR	LEU	SER	ALA	THR	ASP	MET
HIS	LYS	THR	GLY	THR	ILE	V535	D421	ALA	SER	VAL	THR	TYR	TYR	THR	THR	THR	SER	ALA	ASP	ASP
LYS	PHE	LEU	THR	LEU	THR	L536	L422	ILE	PHE	VAL	THR	ILE	ILE	THR	THR	THR	ILE	ARG	ASP	ASP
PHE	LEU	SER	LEU	LEU	GLN	D537	V423	ILE	ARG	THR	SER	VAL	VAL	THR	THR	THR	ARG	ARG	GLY	GLY
ALA	VAL	PRO	VAL	VAL	PRO	K538	G425	TYR	ALA	ARG	THR	ARG	ALA	THR	THR	THR	ARG	ARG	GLY	GLY
ASN	SER	SER	SER	SER	SER	G539	M426	LYS	ILE	LYS	THR	LYS	ILE	THR	THR	THR	ILE	ASN	ASN	ASN
VAL	SER	GLY	GLY	GLY	GLY	P540		THR	ARG	ASN	GLY	LYS	ILE	THR	THR	THR	ILE	PHE	ASN	ASN
SER	SER	ARG	SER	SER	GLU	K550	D454	GLY	ARG	PRO	ASN	VAL	VAL	THR	THR	THR	PHE	ASP	ASP	ASP
ASP	GLY	GLU	VAL	VAL	ALA	R551	S455	PRO	VAL	ASN	ASN	VAL	VAL	THR	THR	THR	VAL	VAL	VAL	VAL
TYR	GLY	ALA	LYS	LYS	ALA		P456	HIS	LYS	CYS	LYS	LYS	LYS	THR	THR	THR	ASP	ASP	ASP	ASP
LEU	LEU	GLU	ILE	ILE	GLU	S556	E457	SER	ILE	THR	ILE	ILE	ILE	THR	THR	THR	PHE	ASP	ASP	ASP
GLN	GLY	ASN	PRO	PRO	ASN	E557	M458	CYS	PHE	ILE	ILE	ILE	ILE	THR	THR	THR	HIS	ASP	ASP	ASP
TYR	LEU	ASN	LEU	LEU	ASN		E460	LYS	ILE	ILE	ILE	ILE	ILE	THR	THR	THR	HIS	ASP	ASP	ASP
ILE	ILE	MET	ASP	ASP	ASP	F561	L461	VAL	ASN	VAL	ASN	VAL	VAL	THR	THR	THR	ILE	ASN	ASN	ASN
PHE	PHE	THR	ALA	ALA	ALA	A562	M462	LYS	SER	VAL	SER	LYS	LYS	THR	THR	THR	MET	ASN	ASN	ASN
ILE	ILE	ASP	TYR	TYR	TYR	M463	T462	ILE	ILE	GLN	ILE	ILE	ILE	THR	THR	THR	GLY	GLY	GLY	GLY
GLY	GLU	LEU	ASP	ASP	ASP	C563	I464	VAL	ILE	PRO	ILE	ILE	ILE	THR	THR	THR	ASP	ASP	ASP	ASP
ASP	ASP	LYS	LYS	LYS	VAL	S564	I465	PRO	ASN	PRO	ASN	VAL	VAL	THR	THR	THR	ILE	ILE	ILE	ILE
LYS	LYS	VAL	LYS	LYS	VAL		M466	LEU	PHE	HIS	TYR	TYR	TYR	THR	THR	THR	ASP	ASP	ASP	ASP
LYS	LYS	LYS	LYS	LYS	LYS	K567	D467	ASP	ASN	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLY	LEU	LEU	GLY	LEU	LEU	K568	I468	ASP	ASP	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
TYR	LEU	LEU	TYR	LEU	LEU	I569	Q469	GLY	LEU	GLU	MET	LEU	LEU	THR	THR	THR	THR	THR	THR	THR
ILE	ASP	ASP	ILE	ILE	ASP	D572	P470	ILE	ASP	GLY	ASP	GLY	GLY	THR	THR	THR	ASP	ASP	ASP	ASP
TYR	GLY	GLY	TYR	TYR	GLY		L471	GLY	ASP	TYR	ILE	ILE	ILE	THR	THR	THR	GLY	GLY	GLY	GLY
ASP	LEU	LEU	ASP	ASP	LEU	K576	T472	ASP	ASN	TYR	ASN	ASN	ASN	THR	THR	THR	LEU	LEU	LEU	LEU
ASN	ASN	ASN	ASN	ASN	ASN	D556	N478	ASN	PHE	PHE	ASN	ASN	ASN	THR	THR	THR	LEU	LEU	LEU	LEU
VAL	VAL	VAL	VAL	VAL	VAL	G557	R479	THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU
THR	THR	THR	THR	THR	THR	K658	E579	THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU
LEU	LEU	LEU	LEU	LEU	LEU		E483	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY
PRO	PRO	PRO	PRO	PRO	PRO	N661	C489	PRO	PRO	ASP	MET	LEU								

[illegible]



● Molecule 2: DNA (5'-D(P*TP*TP*TP*TP*TP*T)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56953	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	3.045	Depositor
Minimum map value	-1.689	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.074	Depositor
Recommended contour level	0.25	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	0.16	0/2918	0.43	0/3940
1	B	0.14	0/2947	0.41	0/3979
1	C	0.14	0/2980	0.38	0/4022
1	D	0.17	0/3001	0.43	1/4051 (0.0%)
1	E	0.15	0/2714	0.40	0/3660
1	F	0.15	0/2610	0.42	0/3521
2	S	0.37	0/131	0.72	0/200
All	All	0.15	0/17301	0.42	1/23373 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	362	PRO	CA-N-CD	-5.10	104.86	112.00

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	2858	0	2885	51	0
1	B	2887	0	2909	68	0
1	C	2920	0	2955	54	0
1	D	2940	0	2968	72	0
1	E	2662	0	2691	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2561	0	2591	67	0
2	S	120	0	73	8	0
All	All	16948	0	17072	367	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 367 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:F:421:ASP:O	1:F:425:GLY:HA2	1.83	0.77
1:D:389:ARG:NH1	1:E:398:ASP:OD2	2.20	0.74
1:A:510:SER:HB2	1:A:514:ARG:HH21	1.53	0.73
1:B:693:ILE:HB	1:B:696:PHE:HB2	1.71	0.72
1:A:411:ASP:OD1	1:A:412:LYS:NZ	2.23	0.72

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	349/785 (44%)	329 (94%)	19 (5%)	1 (0%)	36	65
1	B	353/785 (45%)	336 (95%)	17 (5%)	0	100	100
1	C	357/785 (46%)	344 (96%)	13 (4%)	0	100	100
1	D	359/785 (46%)	332 (92%)	26 (7%)	1 (0%)	36	65
1	E	323/785 (41%)	310 (96%)	13 (4%)	0	100	100
1	F	308/785 (39%)	296 (96%)	12 (4%)	0	100	100
All	All	2049/4710 (44%)	1947 (95%)	100 (5%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	532	LEU
1	A	523	LEU

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	A	324/725 (45%)	323 (100%)	1 (0%)	86	83
1	B	327/725 (45%)	327 (100%)	0	100	100
1	C	331/725 (46%)	330 (100%)	1 (0%)	86	83
1	D	333/725 (46%)	331 (99%)	2 (1%)	78	79
1	E	302/725 (42%)	302 (100%)	0	100	100
1	F	291/725 (40%)	288 (99%)	3 (1%)	68	75
All	All	1908/4350 (44%)	1901 (100%)	7 (0%)	81	81

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	606	TYR
1	F	371	ILE
1	F	468	ILE
1	F	461	LEU
1	D	531	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	347	HIS
1	E	353	ASN
1	F	615	ASN
1	E	466	ASN
1	D	590	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.

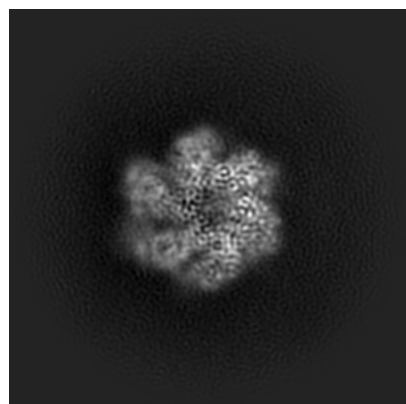
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35058. These allow visual inspection of the internal detail of the map and identification of artifacts.

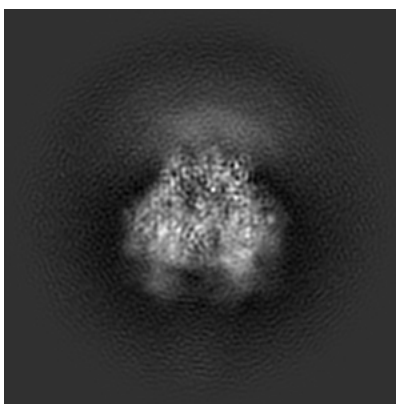
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

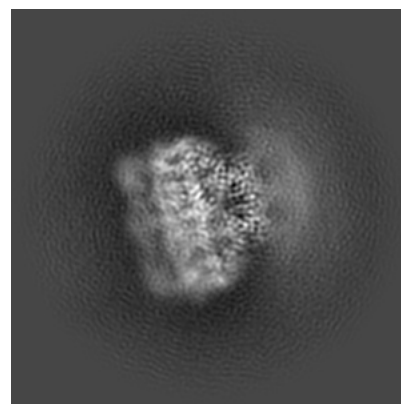
6.1.1 Primary map



X

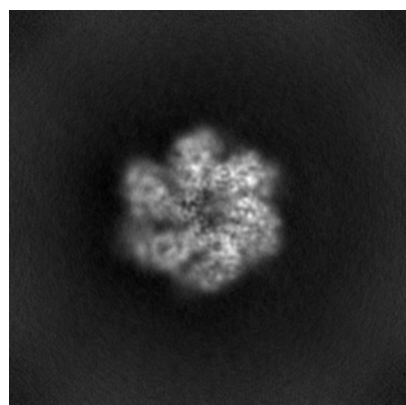


Y

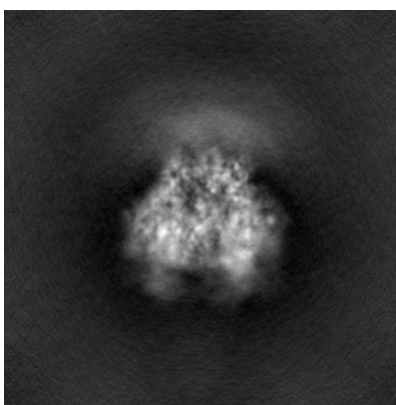


Z

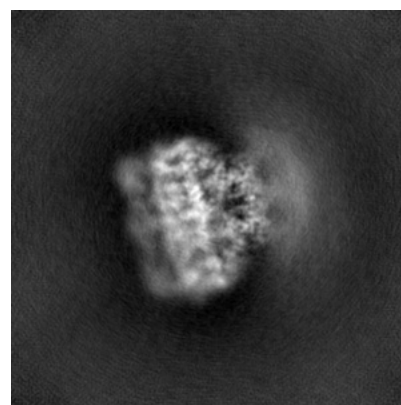
6.1.2 Raw map



X



Y

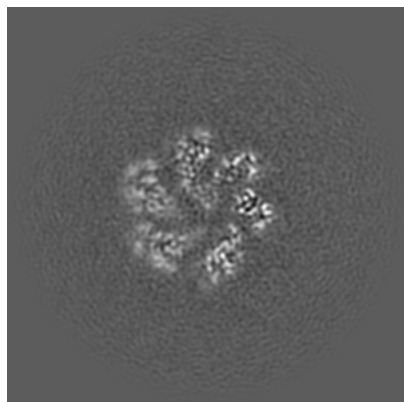


Z

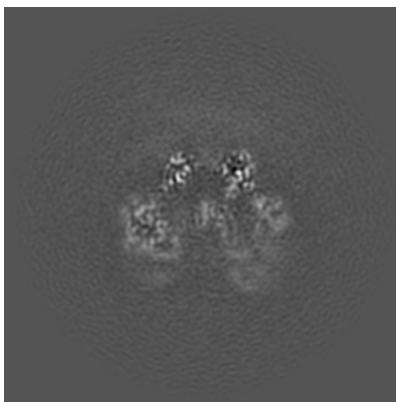
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

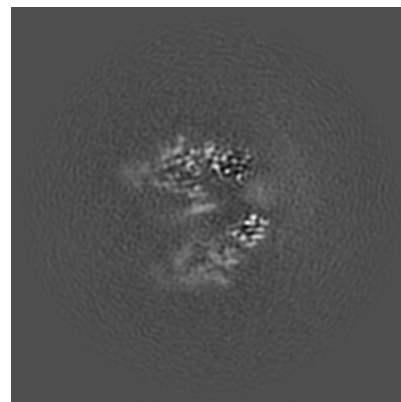
6.2.1 Primary map



X Index: 128

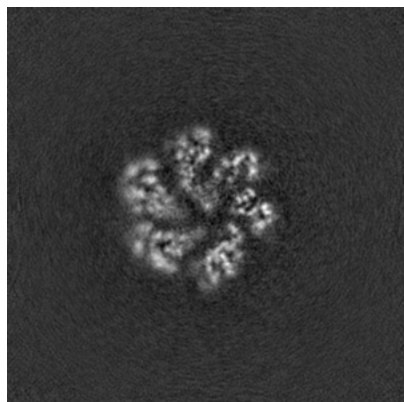


Y Index: 128

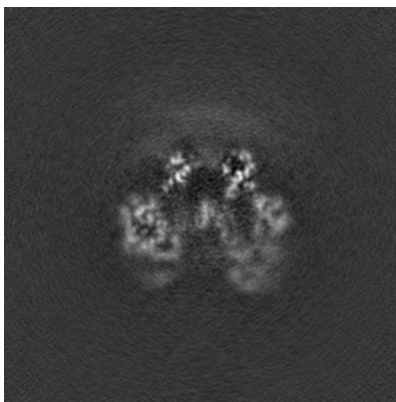


Z Index: 128

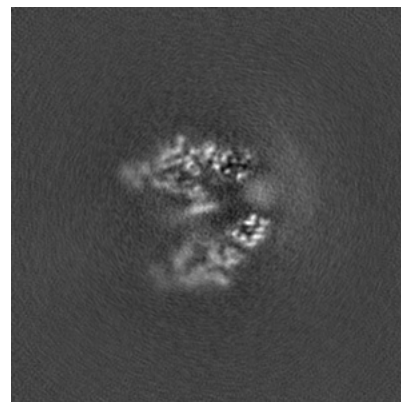
6.2.2 Raw map



X Index: 128



Y Index: 128

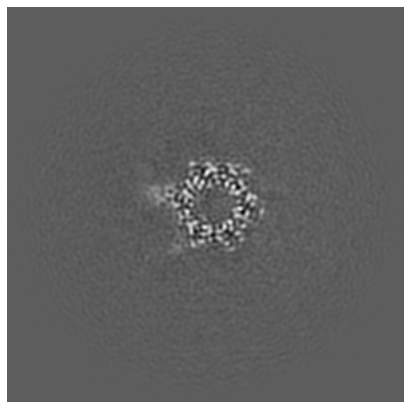


Z Index: 128

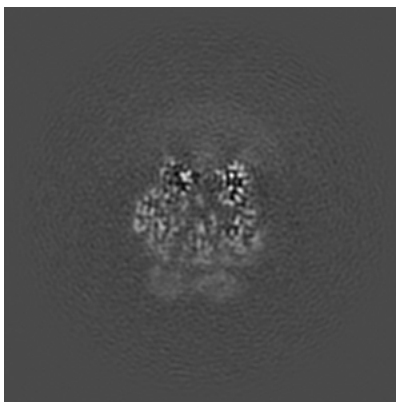
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

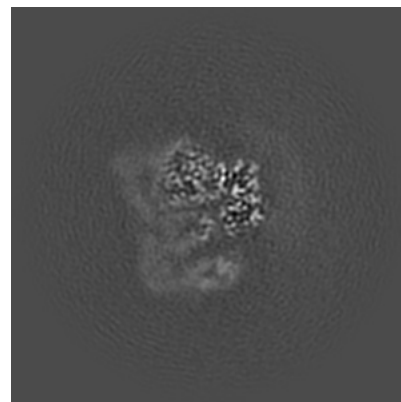
6.3.1 Primary map



X Index: 149

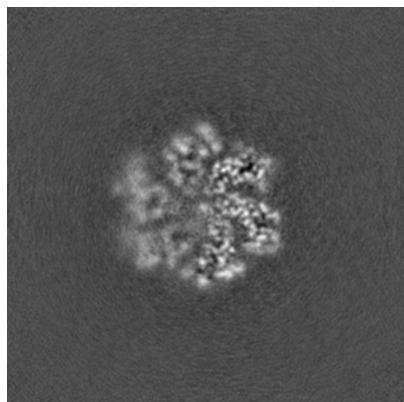


Y Index: 143

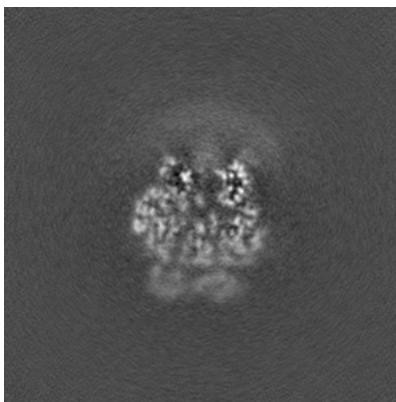


Z Index: 148

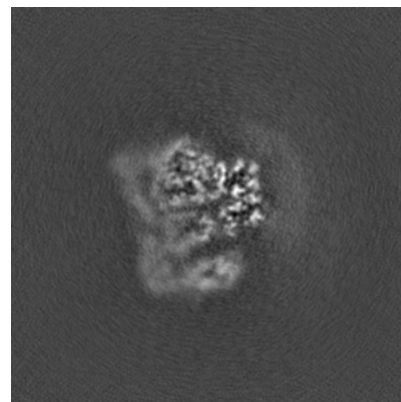
6.3.2 Raw map



X Index: 116



Y Index: 143

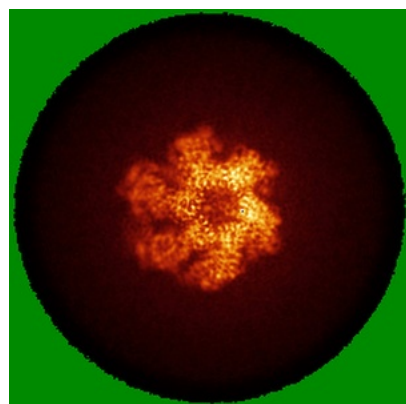


Z Index: 148

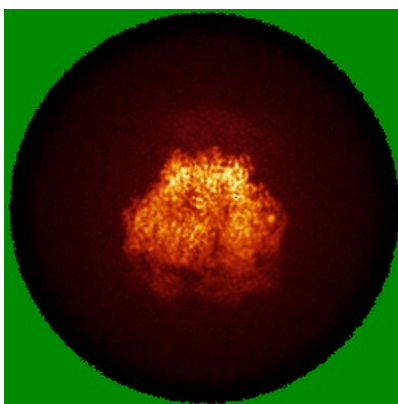
The images above show the largest variance slices of the map in three orthogonal directions.

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

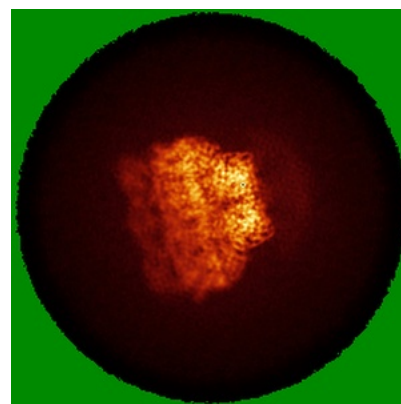
6.4.1 Primary map



X

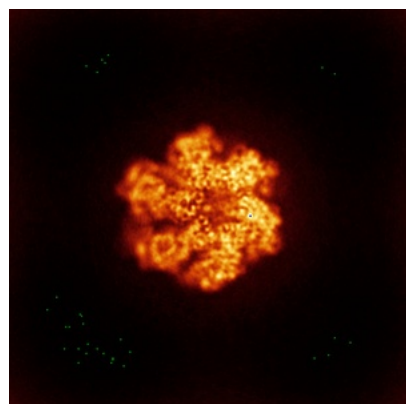


Y

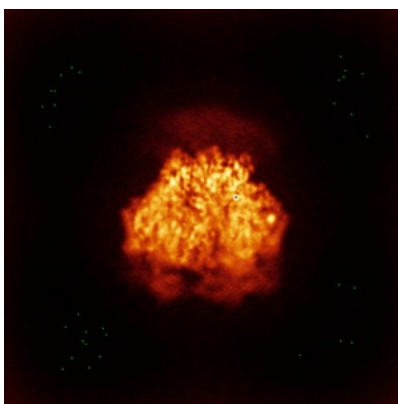


Z

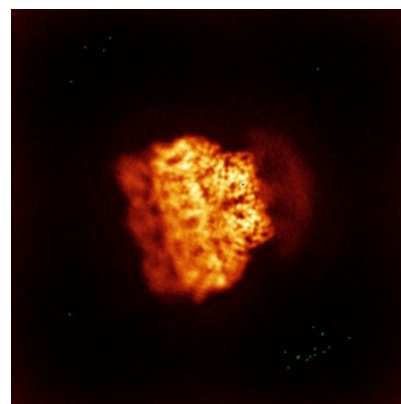
6.4.2 Raw map



X



Y

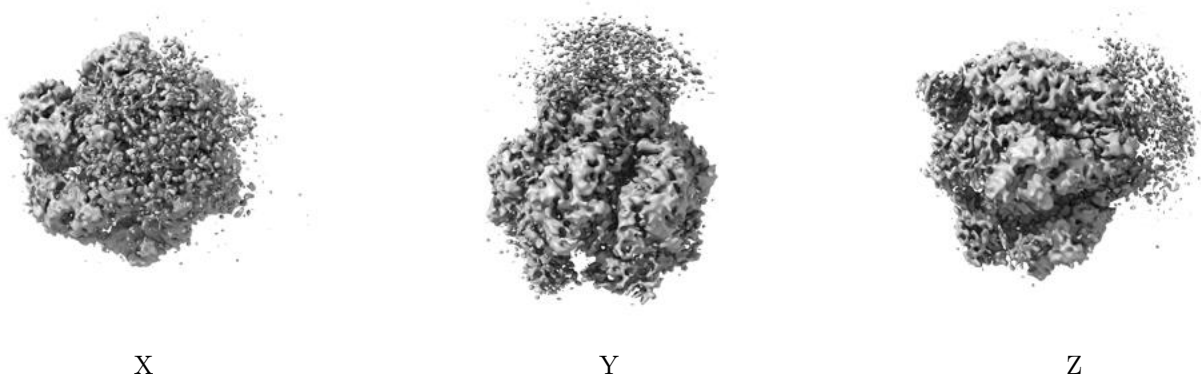


Z

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 0.25. 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.

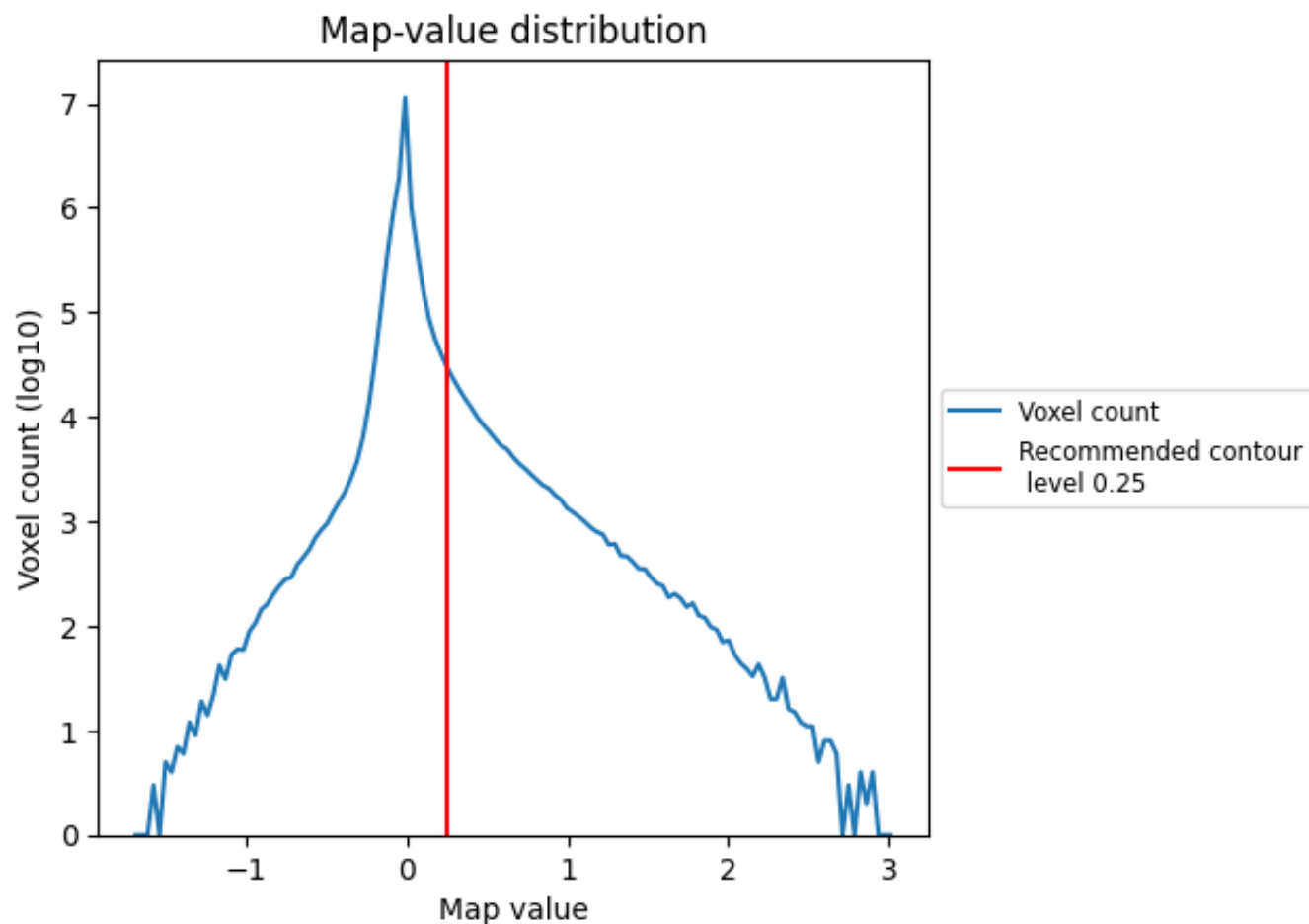
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

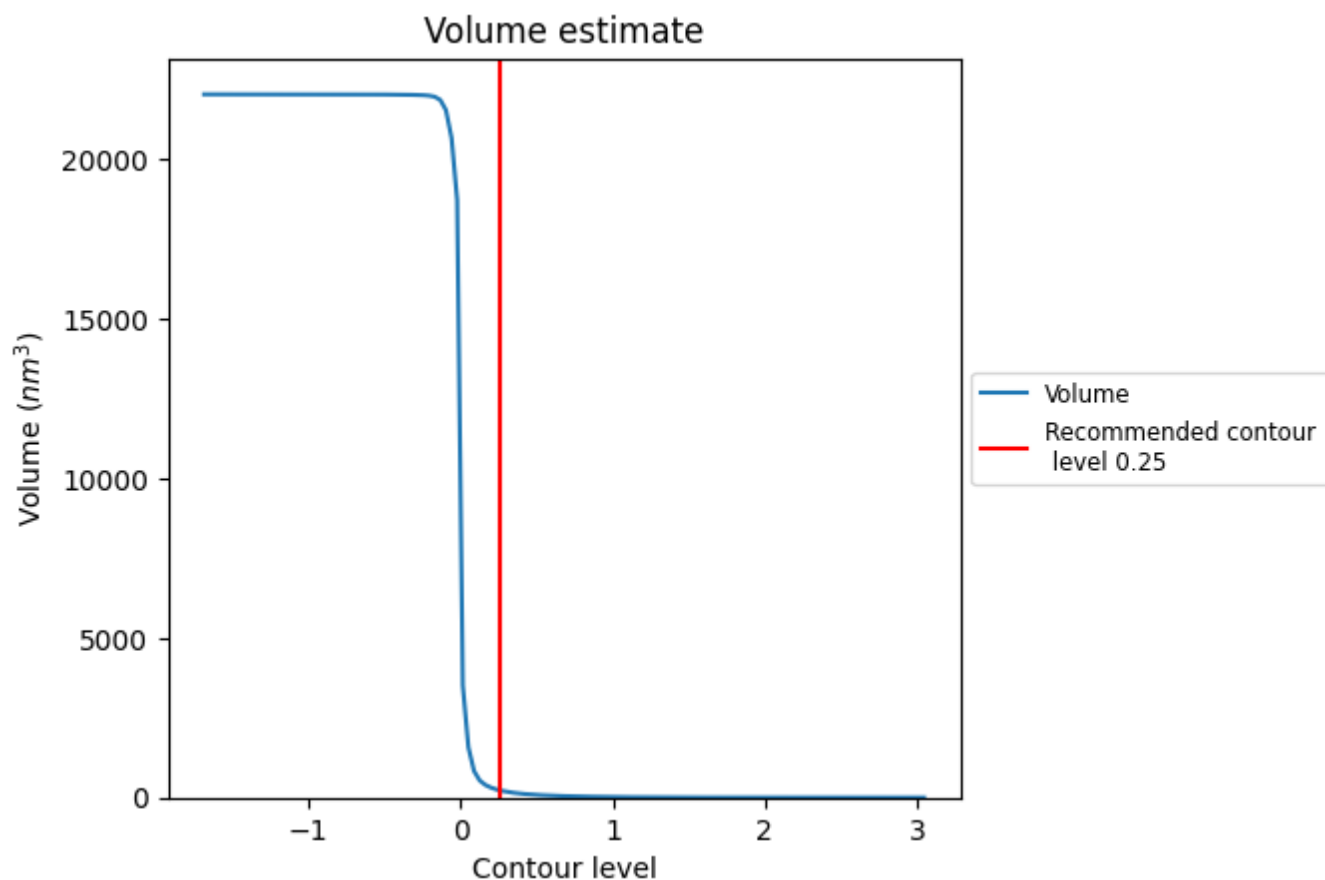
This section contains the results of statistical analysis of the map.

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.

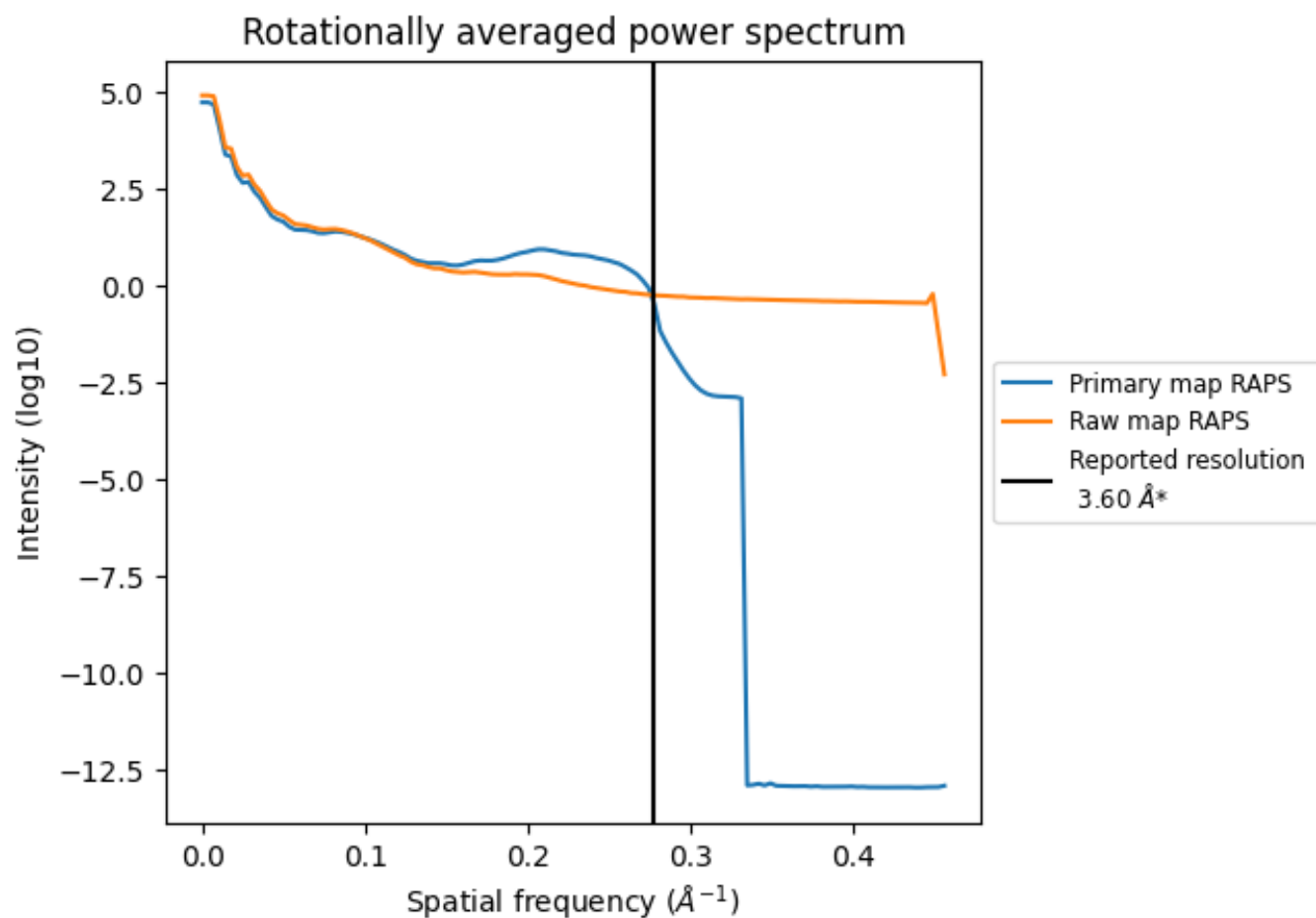
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 235 nm³; this corresponds to an approximate mass of 212 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 ⓘ

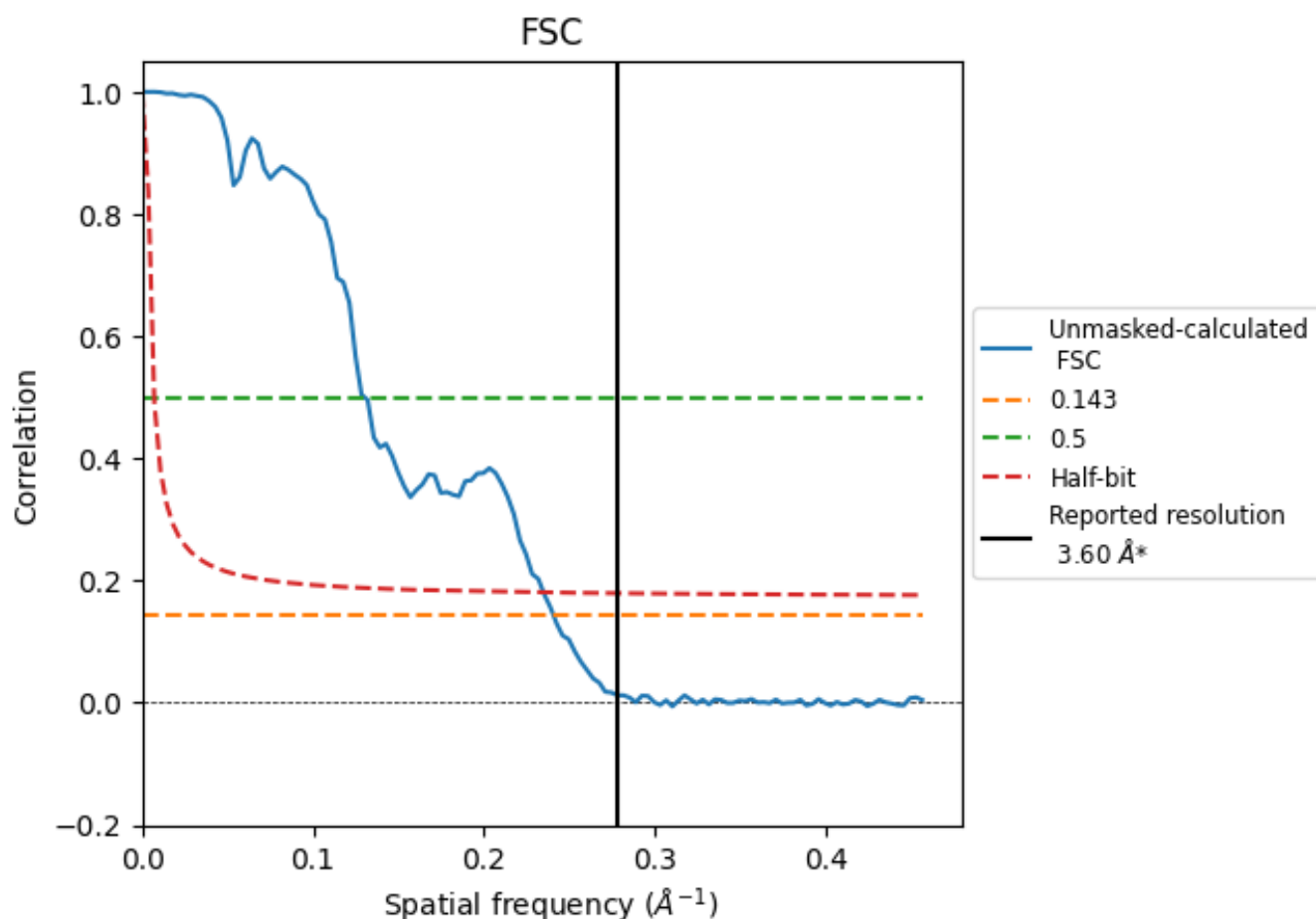


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

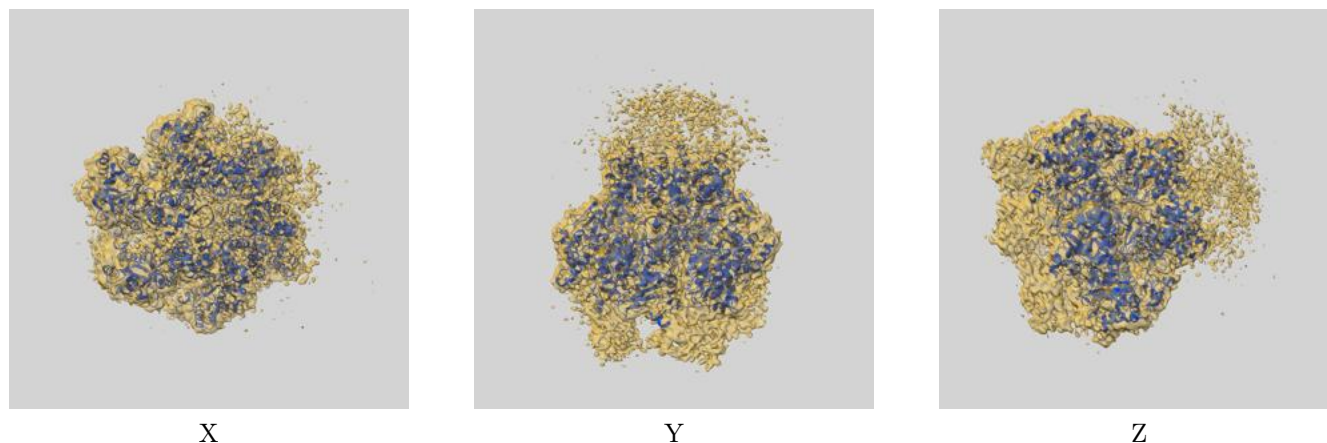
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.15	7.69	4.26

*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 4.15 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

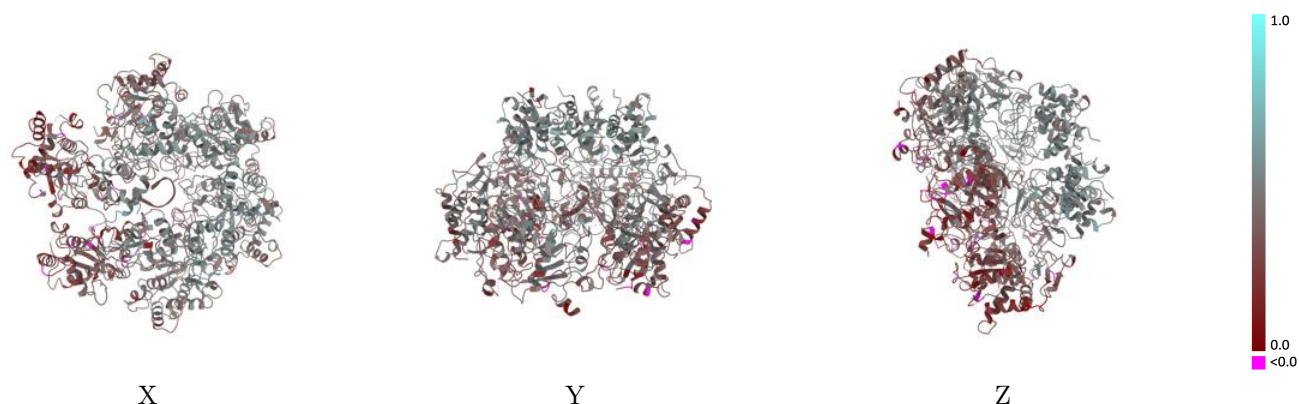
This section contains information regarding the fit between EMDB map EMD-35058 and PDB model 8HWH. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



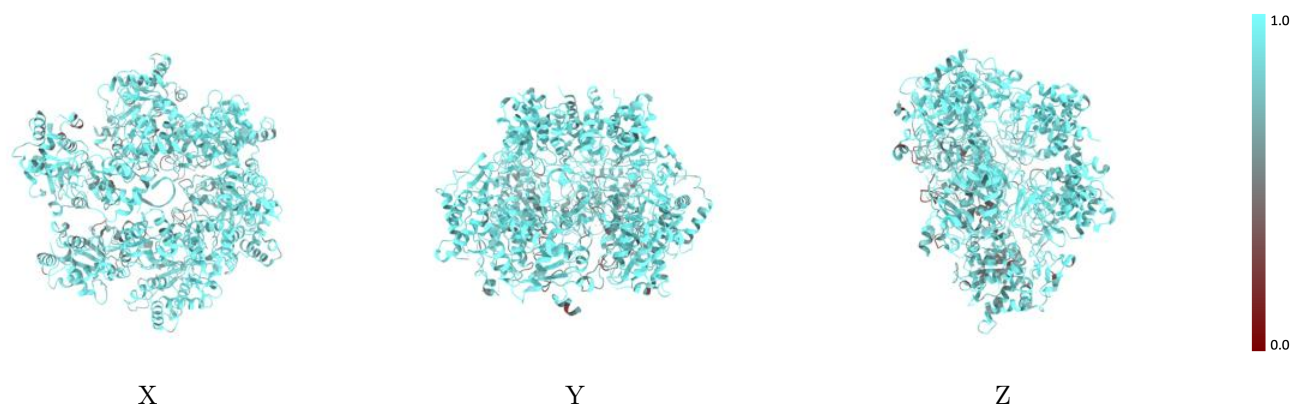
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



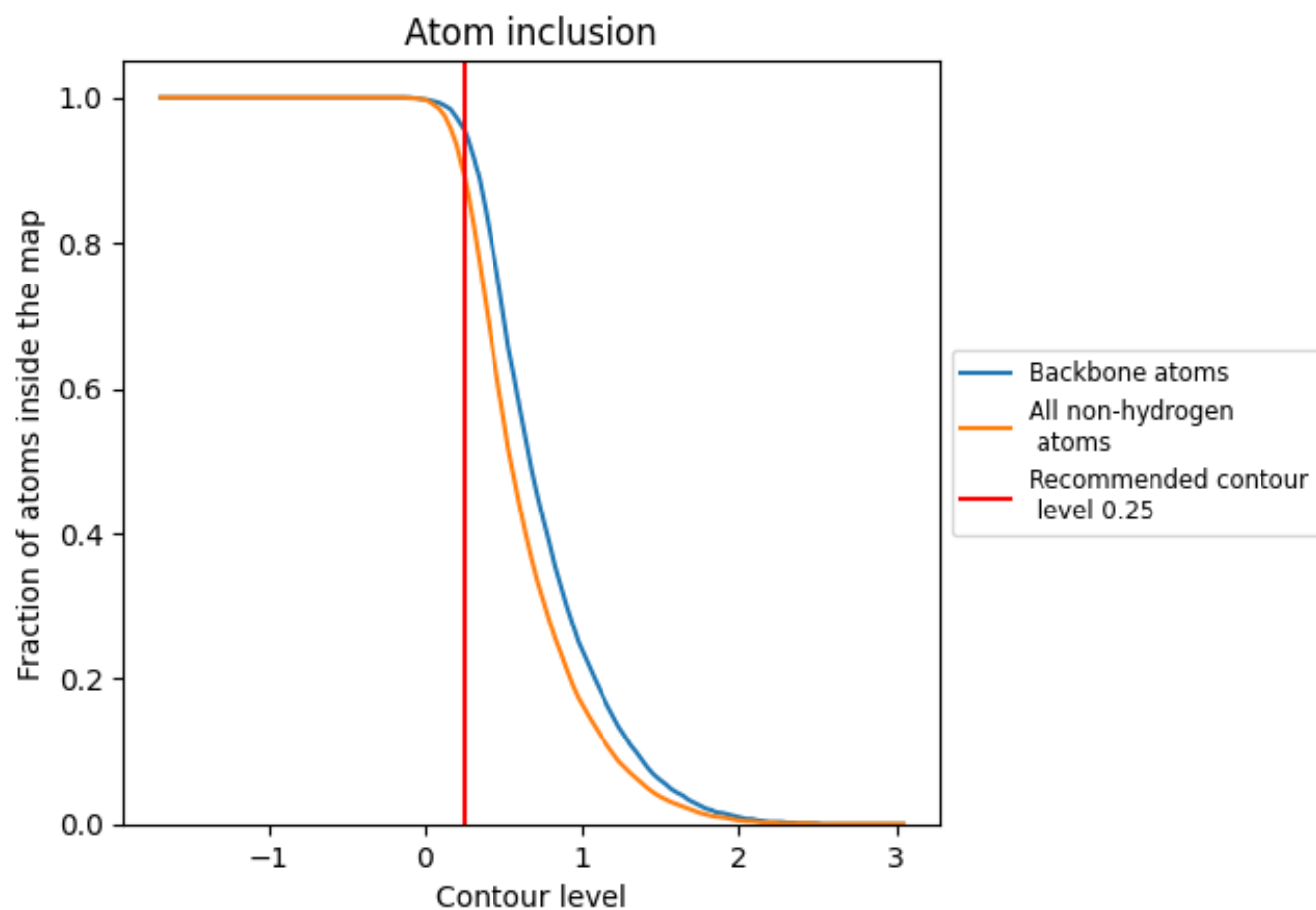
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 89% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8900	0.3900
A	0.8610	0.3770
B	0.9190	0.4300
C	0.9100	0.4450
D	0.9140	0.4260
E	0.8640	0.3220
F	0.8680	0.3290
S	0.8670	0.2980

1.0

0.0

<0.0