



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:37 AM UTC

PDB ID : 8VG0 / pdb_00008vg0
EMDB ID : EMD-43196
Title : Cryo-EM structure of GATA4 in complex with ALBN1 nucleosome
Authors : Zhou, B.R.; Bai, Y.
Deposited on : 2023-12-22
Resolution : 3.07 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

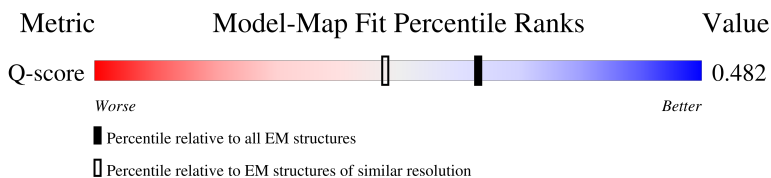
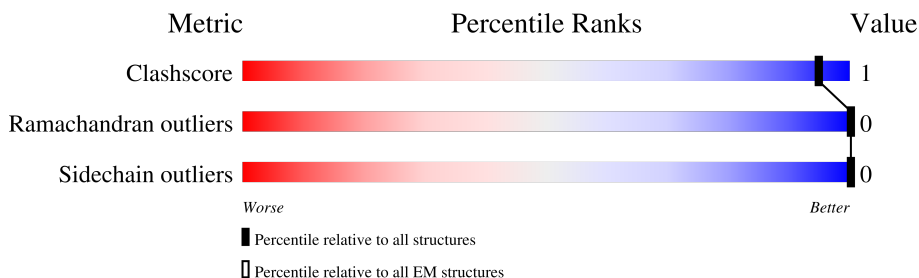
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.07 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	13977 (2.57 - 3.57)

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	I	186	
2	J	186	
3	A	136	
3	E	136	

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Mol	Chain	Length	Quality of chain
4	B	103	 79% 19%
4	F	103	 80% 19%
5	C	130	 82% 16%
5	G	130	 82% 15%
6	D	126	 72% 25%
6	H	126	 71% 5% 25%
7	T	835	 6% 94%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13042 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 DNA chain called DNA (159-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	159	Total	C	N	O	P	0	0
			3258	1556	583	960	159		

- Molecule 2 is a DNA chain called DNA (159-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	159	Total	C	N	O	P	0	0
			3261	1555	599	948	159		

- Molecule 3 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	97	Total	C	N	O	S	0	0
			799	505	153	137	4		
3	E	97	Total	C	N	O	S	0	0
			799	505	153	137	4		

- Molecule 4 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
4	F	83	Total	C	N	O	S	0	0
			662	418	129	114	1		

- Molecule 5 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	C	109	Total	C	N	O	0	0
			840	529	166	145		
5	G	111	Total	C	N	O	0	0
			856	539	169	148		

- Molecule 6 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	95	Total	C	N	O	S	0	0
			745	468	136	139	2		
6	H	95	Total	C	N	O	S	0	0
			745	468	136	139	2		

- Molecule 7 is a protein called Maltose/maltodextrin-binding periplasmic protein,Transcripti on factor GATA-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	53	Total	C	N	O	S	0	0
			414	253	83	72	6		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-392	MET	-	initiating methionine	UNP P0AEX9
T	-391	GLY	-	expression tag	UNP P0AEX9
T	-390	SER	-	expression tag	UNP P0AEX9
T	-389	SER	-	expression tag	UNP P0AEX9
T	-388	HIS	-	expression tag	UNP P0AEX9
T	-387	HIS	-	expression tag	UNP P0AEX9
T	-386	HIS	-	expression tag	UNP P0AEX9
T	-385	HIS	-	expression tag	UNP P0AEX9
T	-384	HIS	-	expression tag	UNP P0AEX9
T	-383	HIS	-	expression tag	UNP P0AEX9
T	-382	GLY	-	expression tag	UNP P0AEX9
T	-381	SER	-	expression tag	UNP P0AEX9
T	-380	SER	-	expression tag	UNP P0AEX9
T	-379	MET	-	expression tag	UNP P0AEX9
T	-12	ASN	-	linker	UNP P0AEX9
T	-11	GLY	-	linker	UNP P0AEX9
T	-10	ILE	-	linker	UNP P0AEX9
T	-9	GLU	-	linker	UNP P0AEX9
T	-8	GLU	-	linker	UNP P0AEX9
T	-7	ASN	-	linker	UNP P0AEX9
T	-6	LEU	-	linker	UNP P0AEX9
T	-5	TYR	-	linker	UNP P0AEX9
T	-4	PHE	-	linker	UNP P0AEX9
T	-3	GLN	-	linker	UNP P0AEX9
T	-2	SER	-	linker	UNP P0AEX9
T	-1	ASN	-	linker	UNP P0AEX9
T	0	ALA	-	linker	UNP P0AEX9

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
8	T	1	Total 1	Zn 1	0

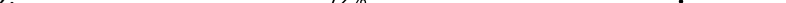
MET
SER
GLY
ARG
GLY
LYS
GLY
GLY
LYS
GLY
LEU
GLY
LYS
GLY
GLY
ALA
LYS
ARG
HIS
ARG
K20
N25
G102

- Chain C: 82% . 16%

Met SER GLY ARG GLY LYS GLN GLY LYS A10 S40 V54 K118 LYS THR GLU SER HIS HIS LYS ALA LYS LYS

- Chain G:  82% 15%

MET	SER	GLY	ARG	GLY	LYS	GLN	GLY	GLY	LYS	A10	S18	S19	R20	F25	V54	T120	GLU	SER	HIS	HIS	LYS	ALA	LYS	GLY	LYS
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- Chain D:  72% . 25%

MET	PRO	GLU	PRO	PRO	ALA	LYS	SER	ALA	PRO	ALA	LYS	LYS	GLY	SER	LYS	LYS	ALA	VAL	THR	LYS	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	ARG	R30	R31	S32	I89	R92	V98	A124	LYS
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- Chain H:  71% 5% 25%

MET	PRO	GLU	PRO	ALA	LYS	SER	ALA	PRO	ALA	LYS	LYS	GLY	SER	LYS	ALA	VAL	THR	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	LYS	ARG	K30	R31	S32	D51	E93	V98	E113	A124	LYS
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- Chain T: 6% 94%

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

PRO	ILE	ALA	ALA	VAL	GLU	ALA	LEU	SER	LEU	ILE	TYR	ASN	LYS	ASP	LEU	PRO	PRO	ASN	PRO	PRO	THR	LYS	TRP	GLU	GLU	ILE	PRO	ALA	ALA	LYS	ASP	LYS	GLY	LYS	SER	ALA	LEU	MET	PHE	ASN	LEU	GLN	GLU	PRO	TYR	PHE	THR	TRP	PRO	LEU	ILE	ALA	ALA	ALA	GLY
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[illegible]

ASN	GLY	PRO	PRO	TRP	ALA	TRP	SER	ASN	ASN	ILE	ASP	THR	SER	LYS	VAL	ASN	GLY	VAL	THR	VAL	LEU	PRO	THR	PHE	LYS	GLN	GLY	PRO	SER	LYS	PRO	PHE	VAL	VAL	GLY	VAL	LEU	SER	ALA	GLY	ILE	ASN	ALA	ALA	SER	PRO	ASN	LYS	LEU	GLU	ALA	LYS	GLU	LEU	PHE	GLU	ASN	ASN	LYR	LEU	LEU
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[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97849	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.859	Depositor
Minimum map value	-2.421	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.35	Depositor
Map size ($\text{\AA}$)	316.8, 316.8, 316.8	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.056, 1.056, 1.056	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: ZN

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	I	0.24	0/3652	0.51	0/5635
2	J	0.24	0/3660	0.49	0/5646
3	A	0.15	0/811	0.32	0/1088
3	E	0.16	0/811	0.31	0/1088
4	B	0.16	0/669	0.34	0/894
4	F	0.17	0/669	0.33	0/894
5	C	0.17	0/850	0.37	0/1146
5	G	0.15	0/866	0.32	0/1167
6	D	0.18	0/756	0.37	0/1015
6	H	0.16	0/756	0.31	0/1015
7	T	0.16	0/420	0.34	0/564
All	All	0.21	0/13920	0.43	0/20152

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	3258	0	1798	11	0
2	J	3261	0	1792	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	799	0	838	2	0
3	E	799	0	838	2	0
4	B	662	0	709	2	0
4	F	662	0	709	1	0
5	C	840	0	902	2	0
5	G	856	0	922	3	0
6	D	745	0	771	4	0
6	H	745	0	771	6	0
7	T	414	0	425	3	0
8	T	1	0	0	0	0
All	All	13042	0	10475	26	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 1.

The worst 5 of 26 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:I:53:DC:OP1	7:T:284:ARG:NH1	2.23	0.72
4:B:52:GLU:N	4:B:52:GLU:OE2	2.23	0.71
2:J:103:DG:OP1	6:D:32:SER:OG	2.08	0.69
5:G:18:SER:OG	5:G:25:PHE:O	2.11	0.68
1:I:67:DT:OP1	6:H:30:LYS:NZ	2.26	0.68

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	
3	A	95/136 (70%)	94 (99%)	1 (1%)	0	100	100
3	E	95/136 (70%)	95 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	81/103 (79%)	79 (98%)	2 (2%)	0	100	100
4	F	81/103 (79%)	81 (100%)	0	0	100	100
5	C	107/130 (82%)	107 (100%)	0	0	100	100
5	G	109/130 (84%)	109 (100%)	0	0	100	100
6	D	93/126 (74%)	93 (100%)	0	0	100	100
6	H	93/126 (74%)	91 (98%)	2 (2%)	0	100	100
7	T	51/835 (6%)	49 (96%)	2 (4%)	0	100	100
All	All	805/1825 (44%)	798 (99%)	7 (1%)	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	
3	A	85/111 (77%)	85 (100%)	0	100	100
3	E	85/111 (77%)	85 (100%)	0	100	100
4	B	68/79 (86%)	68 (100%)	0	100	100
4	F	68/79 (86%)	68 (100%)	0	100	100
5	C	85/100 (85%)	85 (100%)	0	100	100
5	G	87/100 (87%)	87 (100%)	0	100	100
6	D	81/105 (77%)	81 (100%)	0	100	100
6	H	81/105 (77%)	81 (100%)	0	100	100
7	T	45/633 (7%)	45 (100%)	0	100	100
All	All	685/1423 (48%)	685 (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. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	39	HIS
5	C	110	ASN
4	F	75	HIS

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](#)

Of 1 ligands modelled in this entry, 1 is 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.

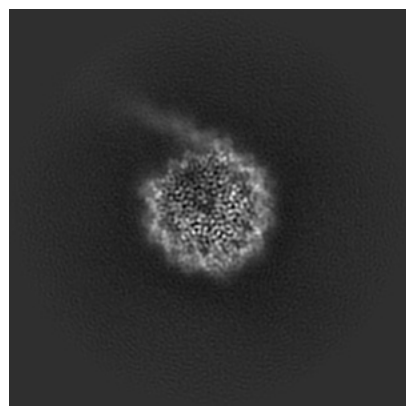
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43196. These allow visual inspection of the internal detail of the map and identification of artifacts.

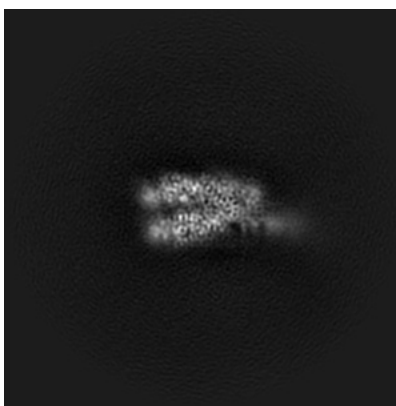
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

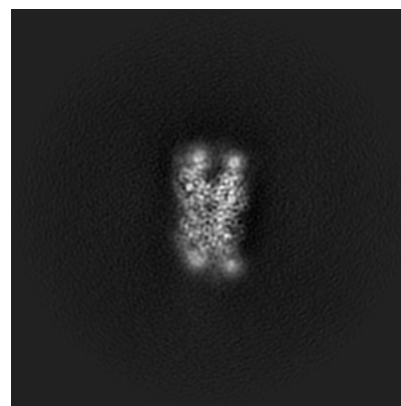
6.1.1 Primary map



X

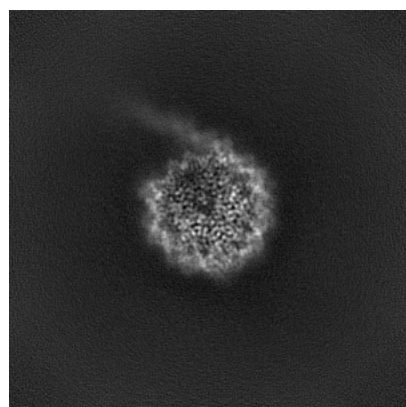


Y

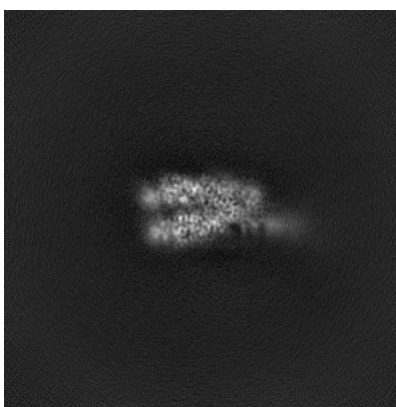


Z

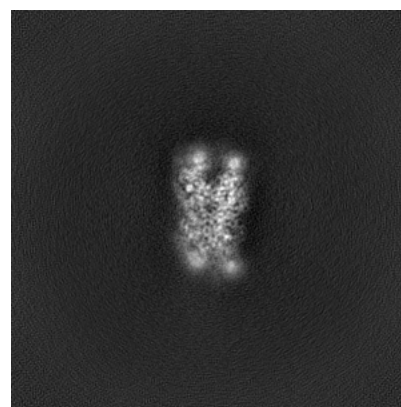
6.1.2 Raw map



X



Y

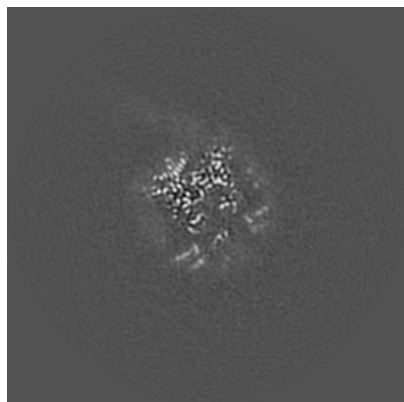


Z

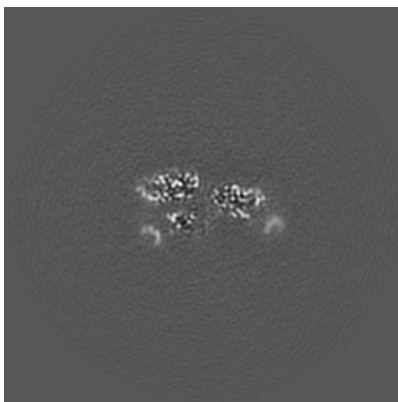
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

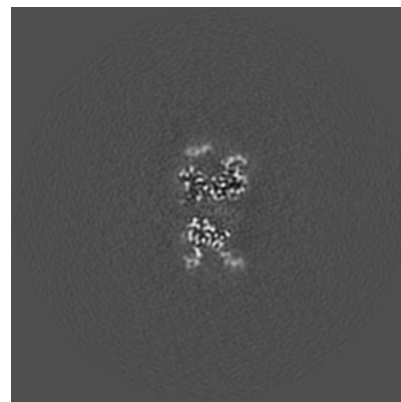
6.2.1 Primary map



X Index: 150

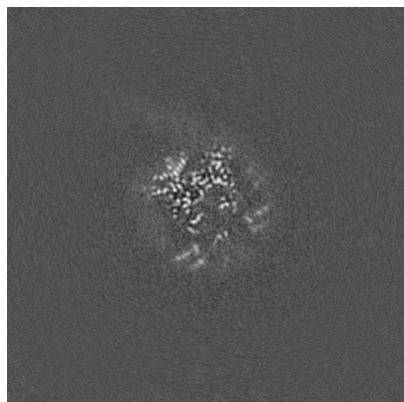


Y Index: 150

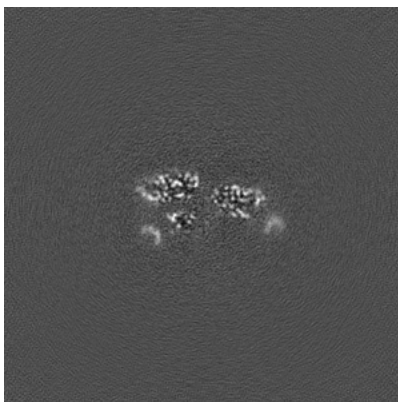


Z Index: 150

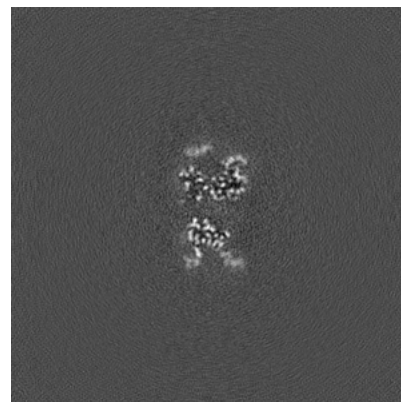
6.2.2 Raw map



X Index: 150



Y Index: 150

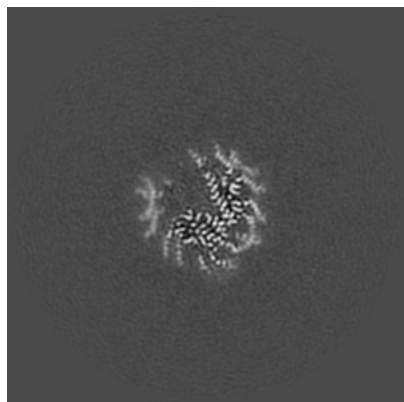


Z Index: 150

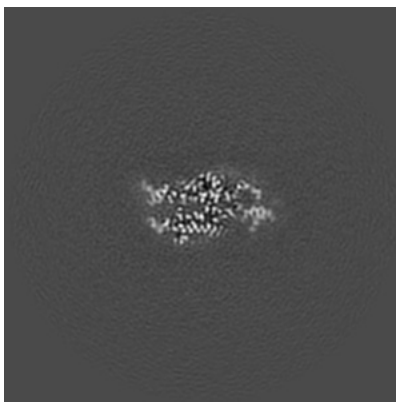
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

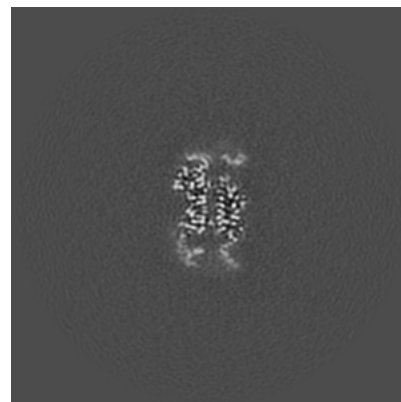
6.3.1 Primary map



X Index: 165

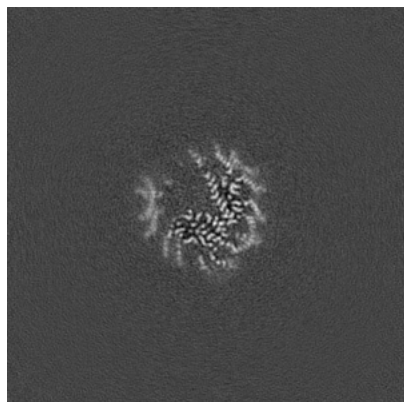


Y Index: 166

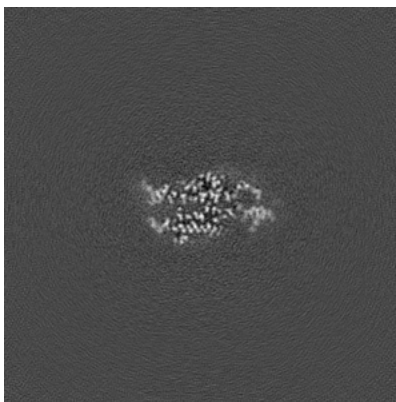


Z Index: 132

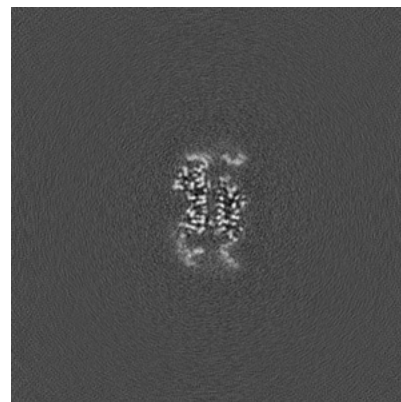
6.3.2 Raw map



X Index: 165



Y Index: 166

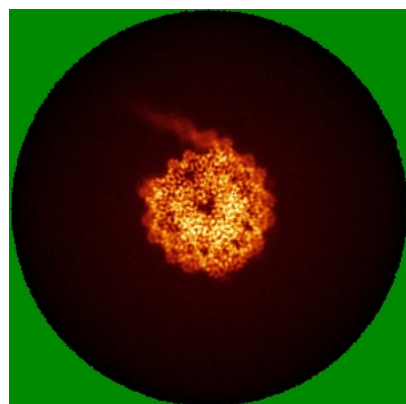


Z Index: 132

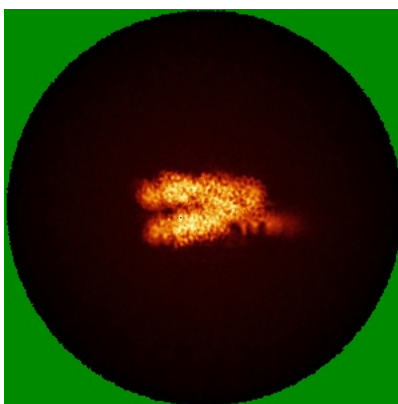
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

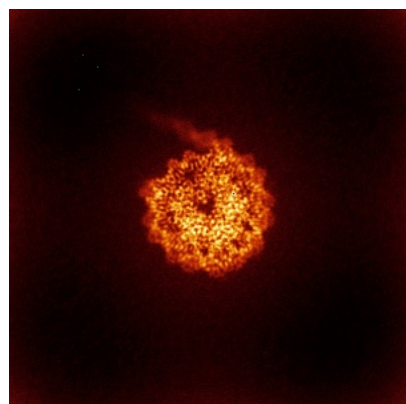


Y

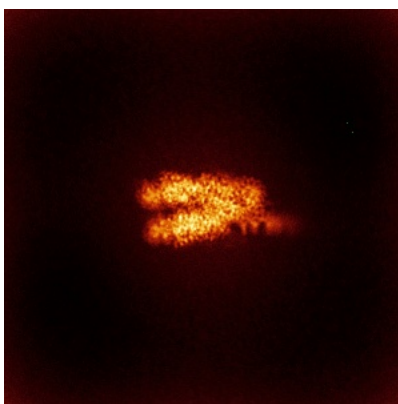


Z

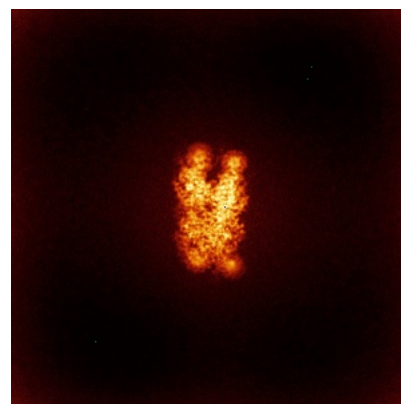
6.4.2 Raw map



X



Y

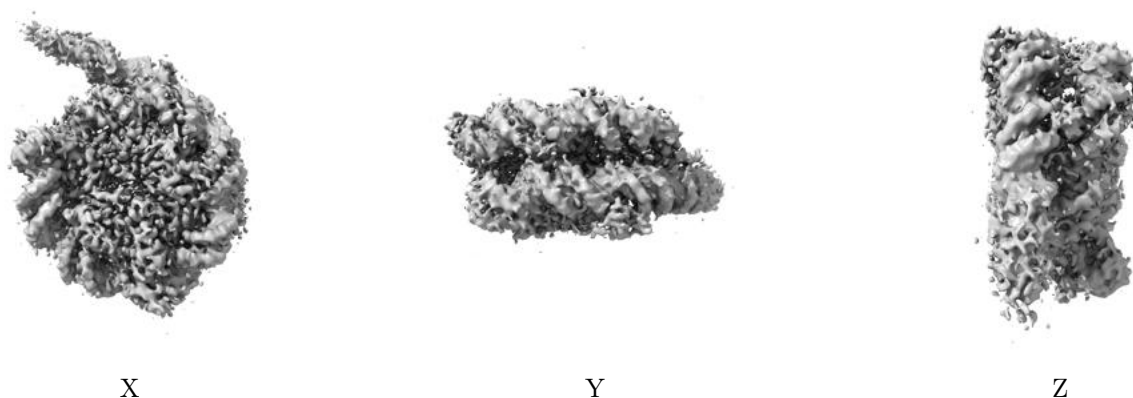


Z

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.

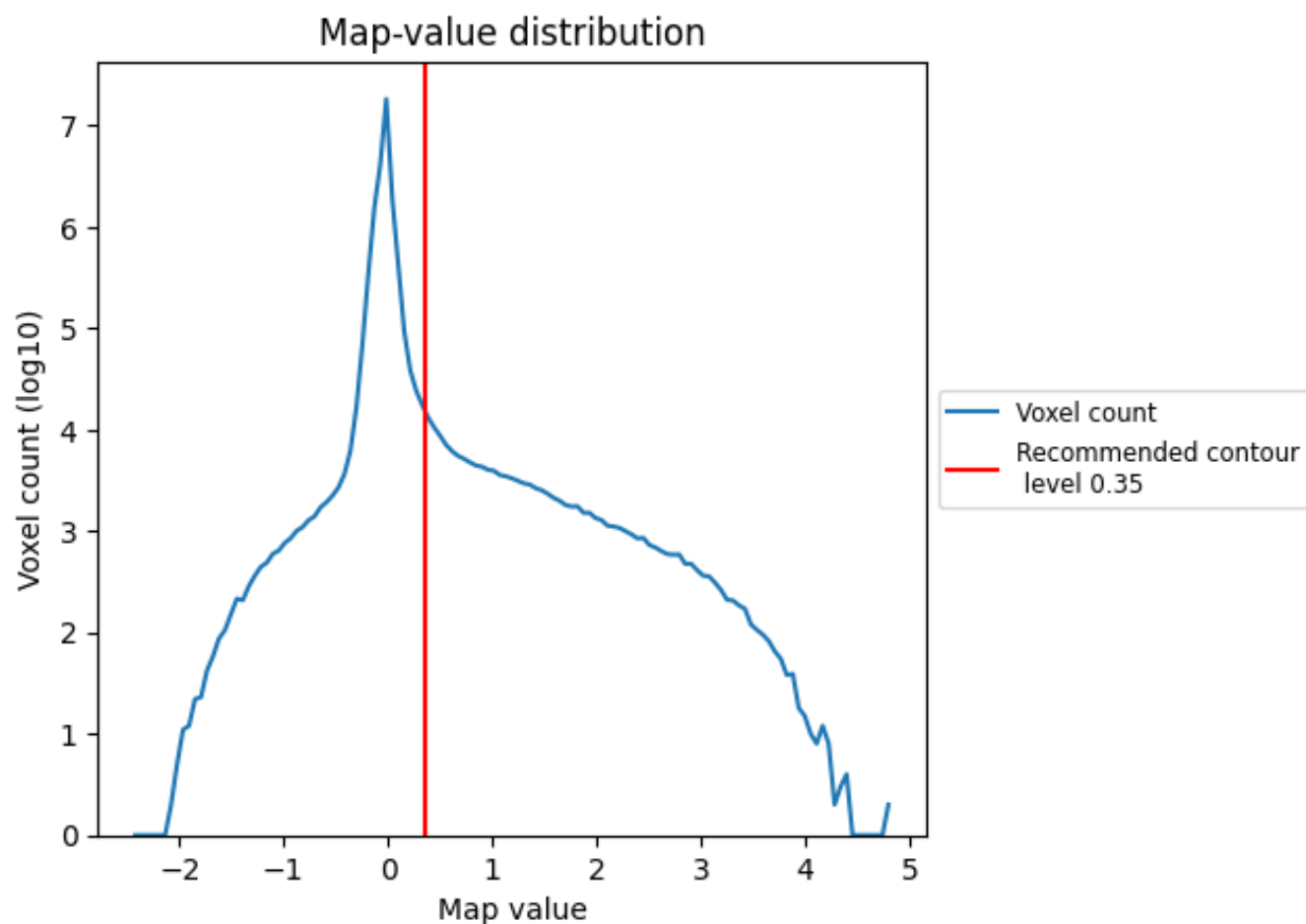
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

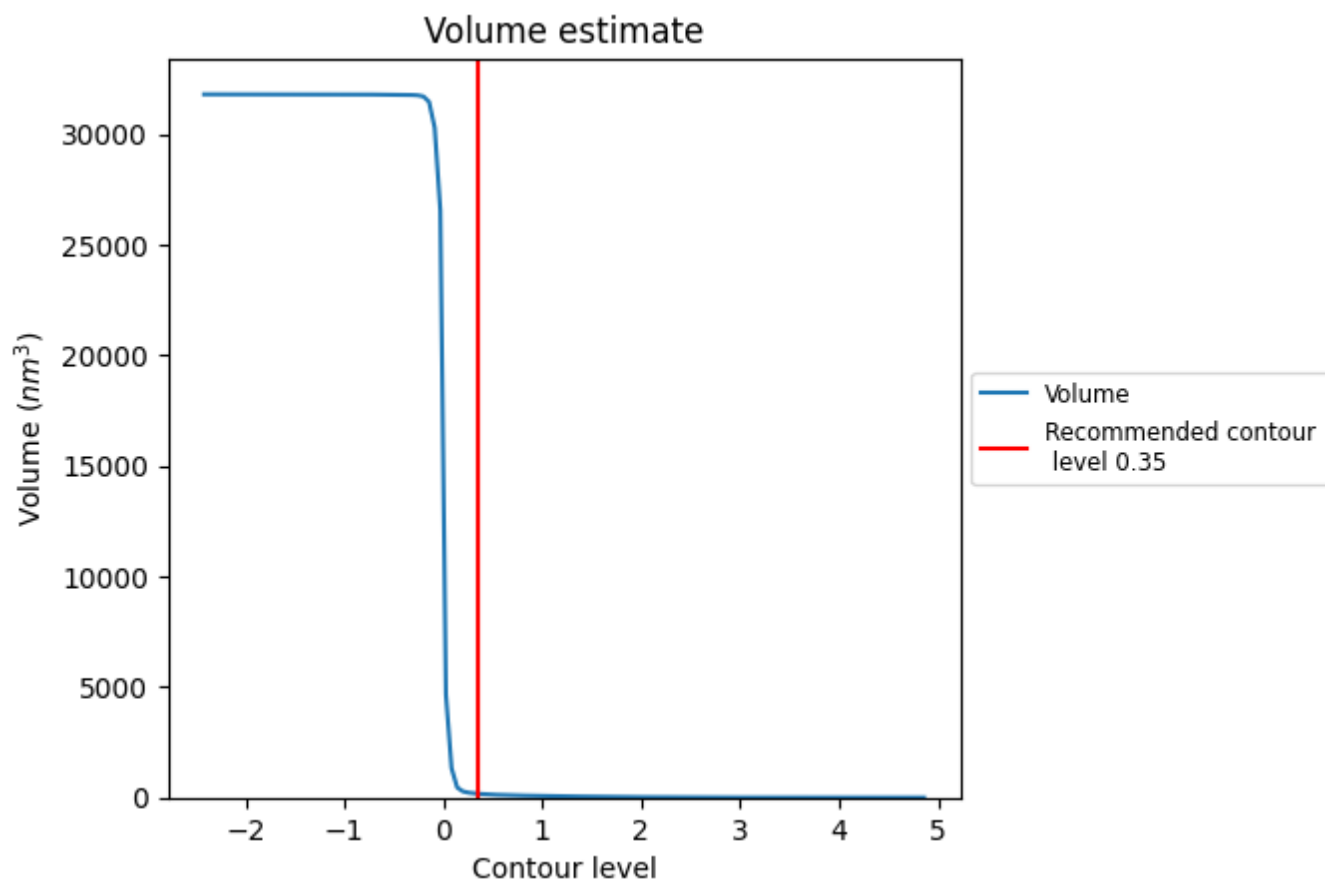
This section contains the results of statistical analysis of the map.

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.

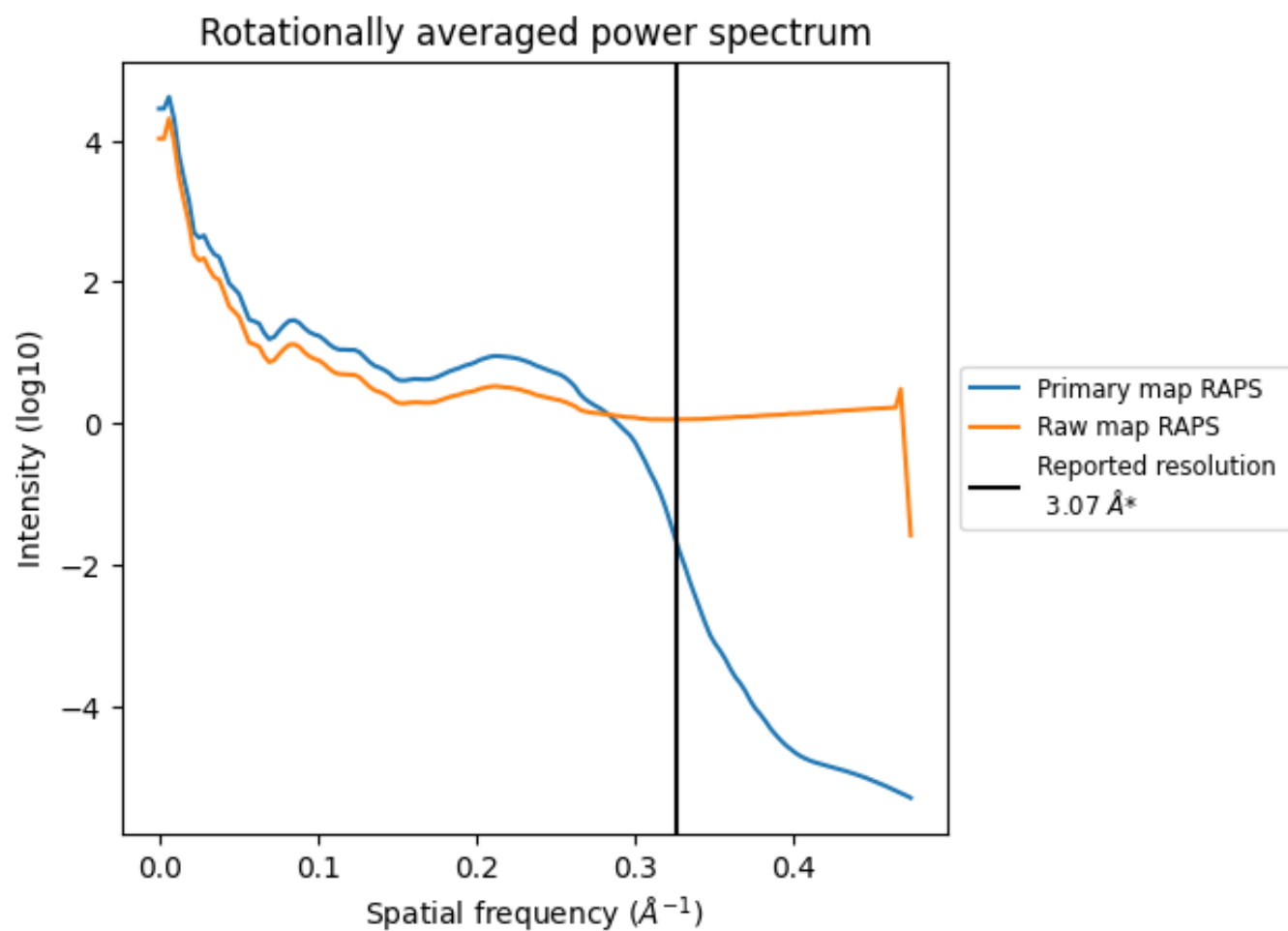
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 172 nm^3 ; this corresponds to an approximate mass of 155 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 ⓘ

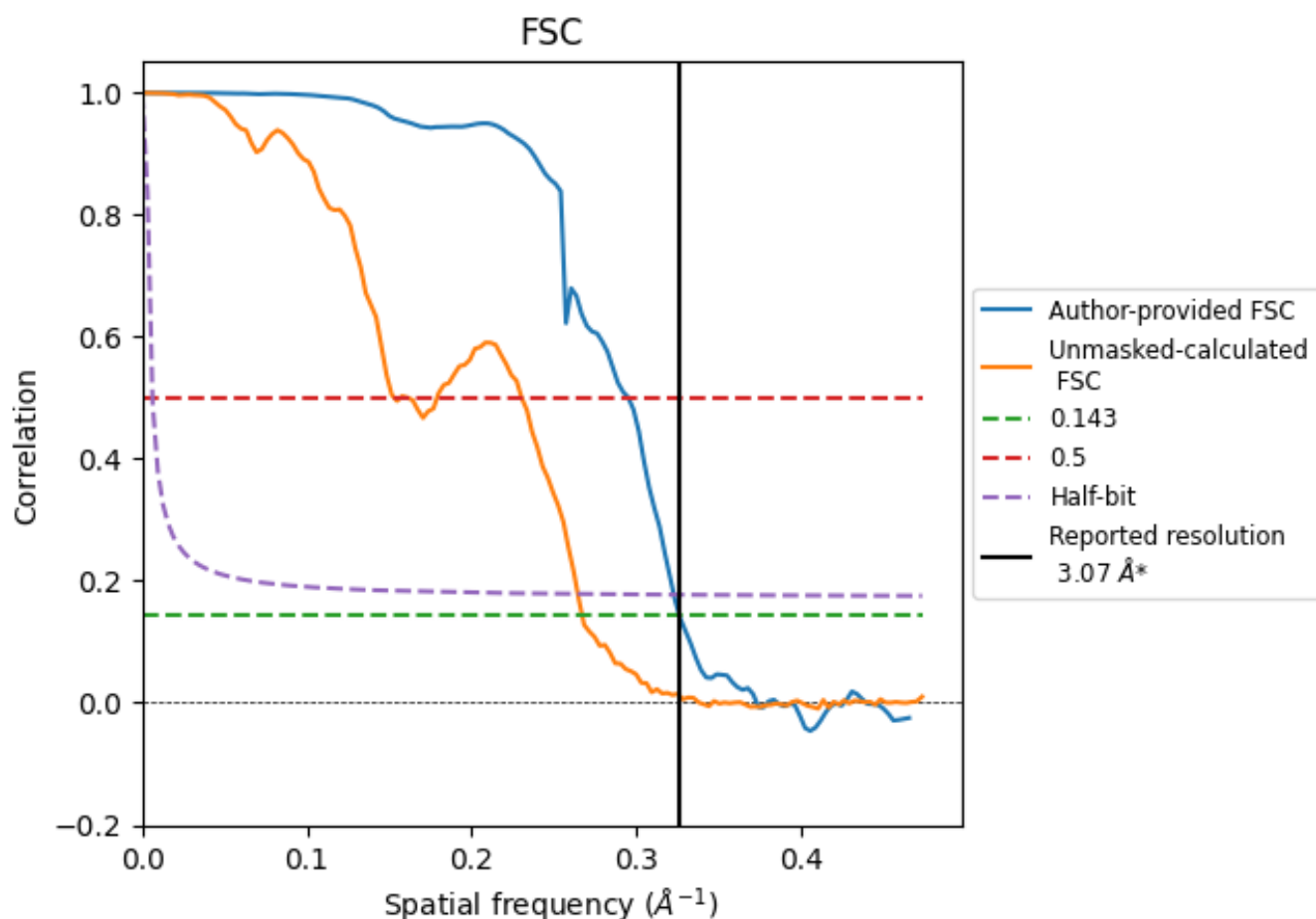


*Reported resolution corresponds to spatial frequency of 0.326 Å⁻¹

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 0.326 Å⁻¹

8.2 Resolution estimates [i](#)

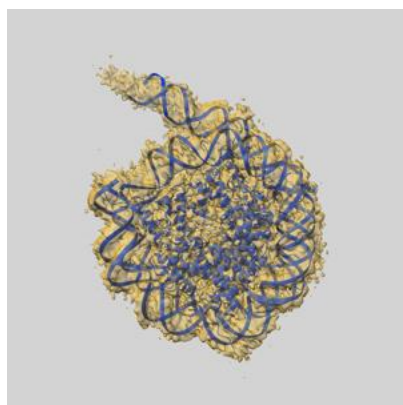
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.07	-	-
Author-provided FSC curve	3.07	3.39	3.10
Unmasked-calculated*	3.74	6.53	3.78

*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 3.74 differs from the reported value 3.07 by more than 10 %

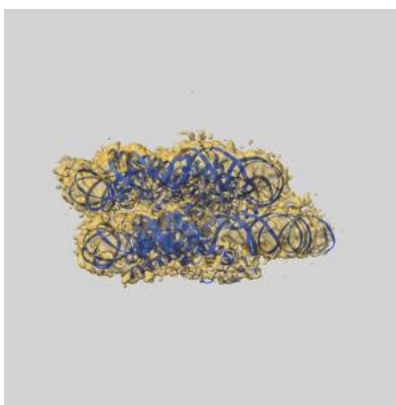
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43196 and PDB model 8VG0. Per-residue inclusion information can be found in section [3](#) on page [7](#).

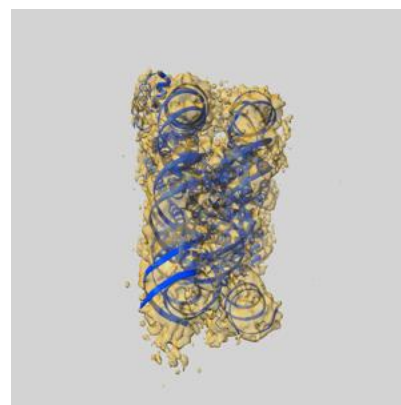
9.1 Map-model overlay [i](#)



X



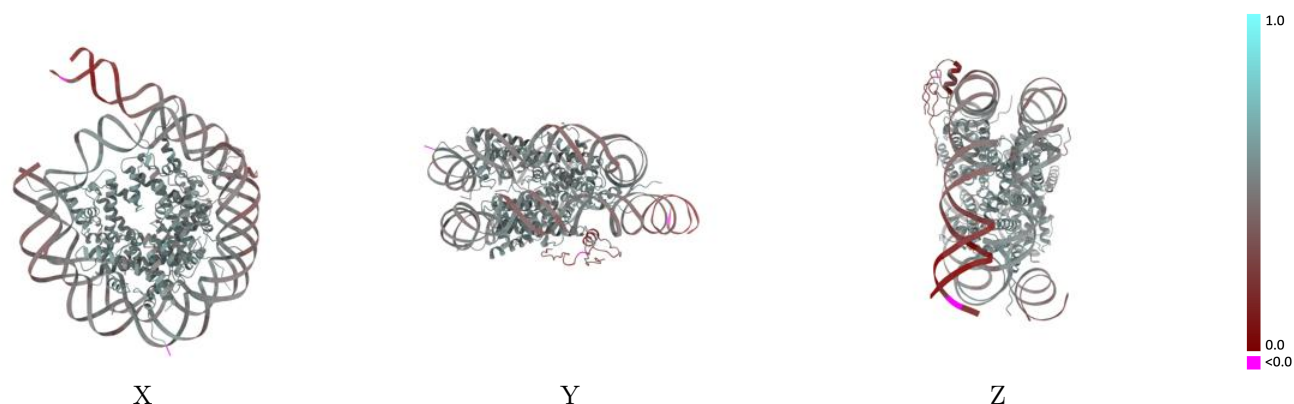
Y



Z

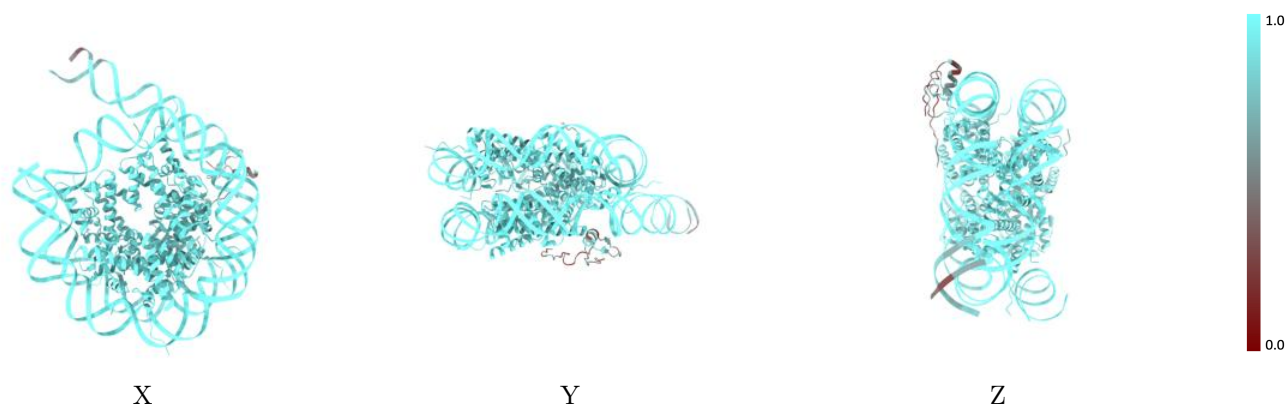
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



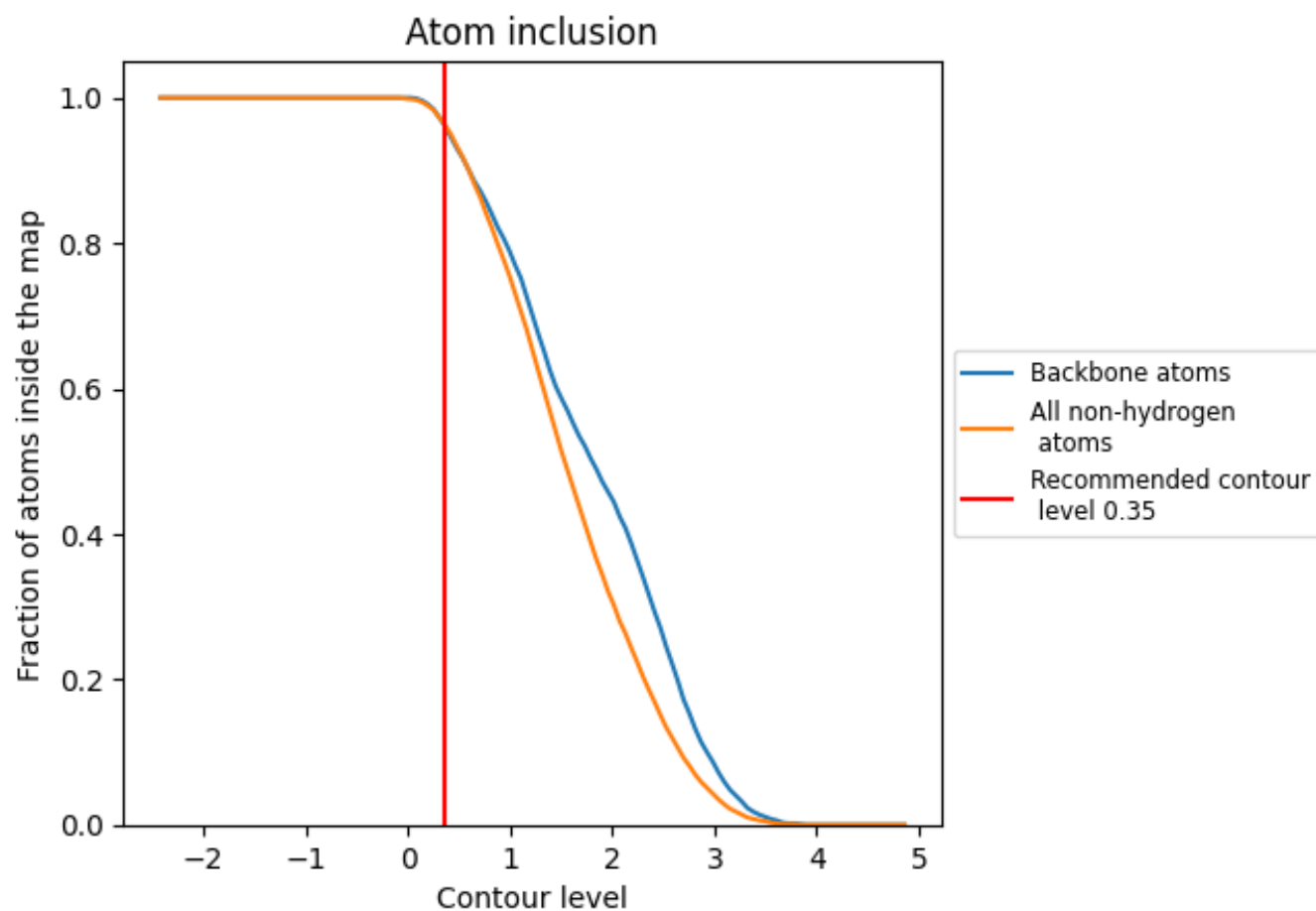
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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	0.9650	0.4820
A	0.9820	0.5490
B	0.9690	0.5420
C	0.9830	0.5460
D	0.9810	0.5320
E	0.9840	0.5530
F	0.9760	0.5450
G	0.9810	0.5460
H	0.9950	0.5400
I	0.9800	0.4380
J	0.9790	0.4350
T	0.4910	0.2660

1.0

0.0

<0.0