



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 05:25 AM UTC

PDB ID : 9CTT / pdb_00009ctt
EMDB ID : EMD-45918
Title : Best1 + GABA closed state
Authors : Owji, A.P.; Kittredge, A.; Zhang, Y.; Yang, T.
Deposited on : 2024-07-25
Resolution : 2.50 Å(reported)
Based on initial model : 8D1I

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:

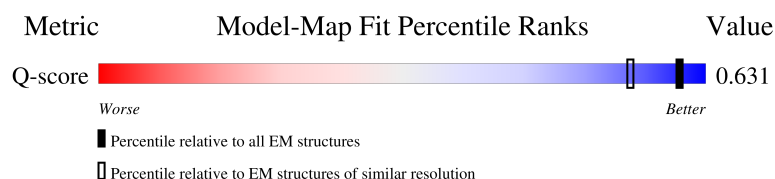
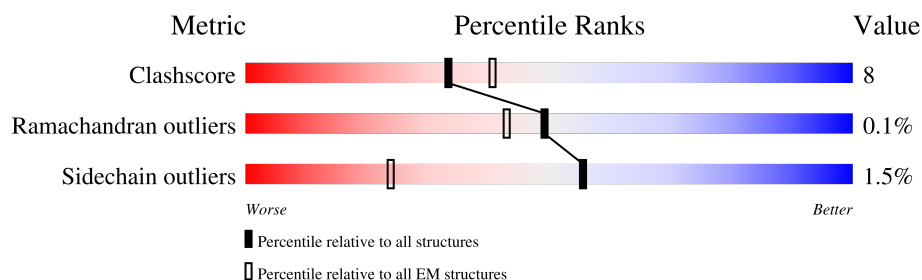
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.50 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	7115 (2.00 - 3.00)

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	584	
1	B	584	
1	C	584	
1	D	584	

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Mol	Chain	Length	Quality of chain
1	E	584	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: a green segment representing 51%, a yellow segment representing 13%, and a grey segment representing 36%. The percentages are labeled below each segment.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15595 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 Bestrophin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	376	Total 3118	C 2052	N 510	O 540	S 16	0	0
1	B	376	Total 3118	C 2052	N 510	O 540	S 16	0	0
1	E	376	Total 3118	C 2052	N 510	O 540	S 16	0	0
1	A	376	Total 3118	C 2052	N 510	O 540	S 16	0	0
1	C	376	Total 3118	C 2052	N 510	O 540	S 16	0	0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
2	D	1	Total 1	Ca 1	0
2	B	1	Total 1	Ca 1	0
2	E	1	Total 1	Ca 1	0
2	A	1	Total 1	Ca 1	0
2	C	1	Total 1	Ca 1	0

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

• Molecule 1: Bestrophin-1

Chain E:  51% 13% 36%

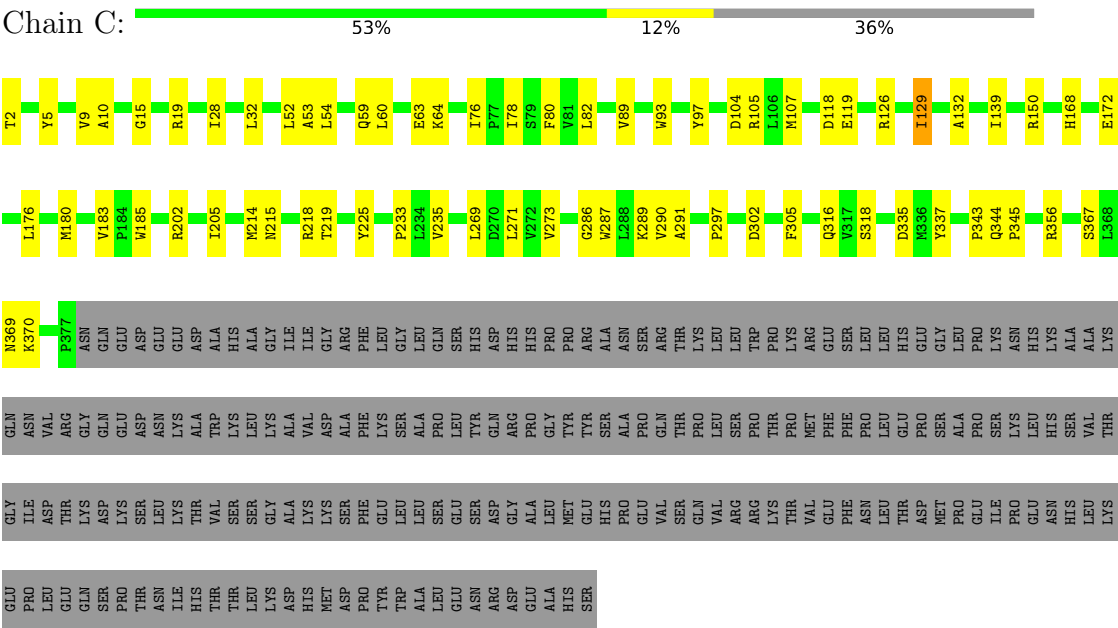
T2	Y5	V9	A10	R13	L14	G15	S16	R19	I28	L32	Y43	I49	Y50	R51	L52	A53	L54	Q58	M61	F62	E63	L67	D70	S71	Y72	I73	Q74	L75	I76	P77	F80	W93	Y97	D104	R105	L106	M107	V114	R125	I129								
	A132	I139	R150	K169	K173	W185	F188	M214	N215	R218	T219	Y225	A226	P233	L234	V235	Q238	S246	F247	F248	L249	T250	R255	Y264	H267	L271	V272	V273	P274	V275	L279	Q280	F281	Y284	V285	G286	K289	V290	L294									
I295	N296	P297	F305	Q316	Y317	S318	R331	M332	E333	M336	Y337	P343	L368	M373	E374	P377	ASN	GLN	GLY	ASP	GLY	ASP	GLY	ILE	ILE	GLY	ASP	ALA	ARG	PHE	LEU	GLY	LEU	GLN	SER	HIS	ASP	HIS	PRO	PRO	ARG	ALA	ASN	SER	ARG	THR	LYS	LEU
LEU	TRP	PRO	LYS	ARG	GLY	SER	LEU	HIS	GLY	ASP	GLY	PRO	PRO	LYS	ASN	HIS	LYS	ALA	ALA	LYS	GLN	ASN	VAL	ARG	GLY	ASN	GLN	SER	THR	LYS	LEU	ALA	PRO	GLY	ALA	PRO	TYR	THR	GLY	TYR	SER	ALA	PRO	GLN	THR	PRO	VAL	
SER	PRO	THR	LYS	VAL	PHE	PHE	PRO	LEU	GLY	ASP	SER	ALA	PRO	SER	LYS	ASN	HIS	VAL	THR	GLY	ILE	ASP	VAL	LYS	LYS	VAL	LYS	SER	PHE	GLY	LEU	SER	LEU	SER	GLY	LEU	MET	HIS	GLY	PRO	GLY	VAL	SER	GLN	VAL			
ARG	ARG	THR	VAL	GLY	PHE	ASN	THR	THR	ASP	MET	PRO	GLY	ILE	PRO	PRO	ASN	LEU	LEU	GLY	GLN	SER	PRO	THR	ILE	ILE	GLY	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	

• Molecule 1: Bestrophin-1

Chain A:  52% 12% 36%

SER		GLY	A349		V183		T2	
ALA	LEU	PRO	ALA	A350	P184	Y5		
PRO	GLY	PRO	GLY	S351	W185			
ILE	SER	LYS	ASN	A352		V9		
PRO	LYS	LYS	HIS	Q353	W214	A10		
GLY	LEU	LEU	HIS					
ASN	HIS	ASN	ALA		G15			
HIS	SER	ALA	LYS	R356	R218			
LEU	VAL	ALA	ALA		T219			
LYS	THR	LYS	GLY	K370	Y225	R19		
GLY	GLY	GLN	ASN		A226	L20		
PRO	ILE	ASN	VAL	M373		L21		
GLY	THR	THR	ARG		P233	I28		
LYS	LYS	GLY	GLY	P377				
ASP	ASP	GLN	GLN	ASN	Q238	L31		
PRO	LYS	GLY	GLY	GLU		L32		
THR	SER	ASP	ASP	ASP	V242	Y43		
ASN	LEU	GLY	GLY	GLU	S246			
ILE	LYS	LYS	ALA	ASP	F247	R51		
THR	VAL	THR	THR	ALA	F248	L52		
THR	SER	SER	LYS	HIS	L249	A53		
LEU	SER	LEU	LEU	ALA	T250	L54		
GLY	GLY	LYS	GLY	GLY	F257	T55		
ALA	ALA	ALA	ILE	ILE	L258	E56		
LYS	LYS	VAL	VAL	ILE	F257	E57		
LYS	LYS	ASP	ASP	GLY	Q58			
ASP	ASP	ALA	ALA	GLY	Y264	Q59		
PRO	PHE	PHE	PHE	PHE	H267	L60		
TRP	GLY	LYS	LEU	GLY		M61		
LEU	LEU	SER	LEU	GLY	F62			
LEU	ALA	ALA	ALA	LEU	P274	E63		
LEU	SER	PRO	PRO	LEU				
GLY	GLY	LEU	GLN	GLN	T277	I76		
ASN	SER	TYR	TYR	SER	F278			
ARG	ASP	GLN	GLN	HIS	L279	F80		
ASP	GLY	ARG	ARG	ASP	Q280			
GLY	ALA	ALA	PRO	HIS	F281	F84		
ALA	ALA	GLY	GLY	PRO				
HIS	MET	TYR	TYR	PRO	G286	V69		
SER	GLY	TYR	TYR	ARG				
	HIS	SER	SER	ARG	K289	W93		
	PRO	ALA	ALA	ALA	V290			
	GLY	PRO	PRO	ASN	A291	Y97		
	VAL	GLN	GLN	SER				
	SER	THR	THR	ARG	THR			
	GLN	PRO	PRO	LYS	L294	D104		
	VAL	LEU	LEU	LEU	I295	R105		
	ARG	SER	SER	LEU	N296	L106		
	ARG	PRO	PRO	LEU	P297	M107		
	LYS	THR	THR	THR	F305	R126		
	THR	PRO	PRO	LYS				
	VAL	MET	MET	ARG	Q316	I129		
	GLY	PHE	PHE	GLY				
	SER	ASN	ASN	SER	Y337	I139		
	LEU	LEU	LEU	LEU				
	THR	GLY	GLY	LEU	P343	L176		
	ASP	PRO	PRO	HIS	Q344			
					P345			

● Molecule 1: Bestrophin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52529	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.560	Depositor
Minimum map value	-1.888	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.097	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	332.0, 332.0, 332.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: CA

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	0.14	0/3213	0.31	0/4377
1	B	0.20	0/3213	0.36	0/4377
1	C	0.19	0/3213	0.36	0/4377
1	D	0.14	0/3213	0.32	0/4377
1	E	0.15	0/3213	0.31	0/4377
All	All	0.16	0/16065	0.33	0/21885

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	A	3118	0	3089	56	0
1	B	3118	0	3089	76	0
1	C	3118	0	3089	58	0
1	D	3118	0	3089	57	0
1	E	3118	0	3089	70	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
2	E	1	0	0	0	0
All	All	15595	0	15445	257	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 8.

The worst 5 of 257 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:C:52:LEU:HD12	1:C:52:LEU:O	1.18	1.26
1:C:52:LEU:O	1:C:52:LEU:CD1	2.06	1.03
1:B:51:ARG:HH12	1:B:259:ASN:HB3	1.27	0.96
1:B:51:ARG:HH12	1:B:259:ASN:CB	1.93	0.81
1:B:51:ARG:NH2	1:B:257:PHE:O	2.16	0.77

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	374/584 (64%)	366 (98%)	8 (2%)	0	100	100
1	B	374/584 (64%)	366 (98%)	8 (2%)	0	100	100
1	C	374/584 (64%)	368 (98%)	5 (1%)	1 (0%)	36	55
1	D	374/584 (64%)	370 (99%)	4 (1%)	0	100	100
1	E	374/584 (64%)	368 (98%)	6 (2%)	0	100	100
All	All	1870/2920 (64%)	1838 (98%)	31 (2%)	1 (0%)	49	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	53	ALA

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	339/523 (65%)	336 (99%)	3 (1%)	70	87
1	B	339/523 (65%)	333 (98%)	6 (2%)	51	77
1	C	339/523 (65%)	331 (98%)	8 (2%)	43	70
1	D	339/523 (65%)	335 (99%)	4 (1%)	63	83
1	E	339/523 (65%)	335 (99%)	4 (1%)	63	83
All	All	1695/2615 (65%)	1670 (98%)	25 (2%)	55	80

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	C	54	LEU
1	C	367	SER
1	A	242	VAL
1	C	60	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	GLN
1	C	259	ASN
1	A	223	HIS
1	C	133	ASN
1	C	296	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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

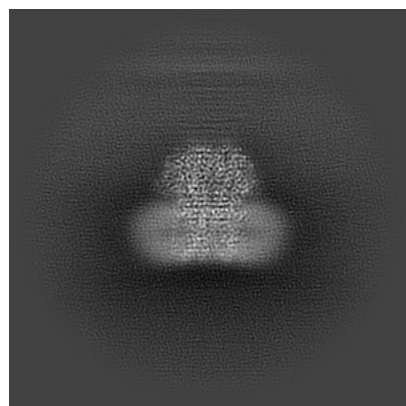
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45918. These allow visual inspection of the internal detail of the map and identification of artifacts.

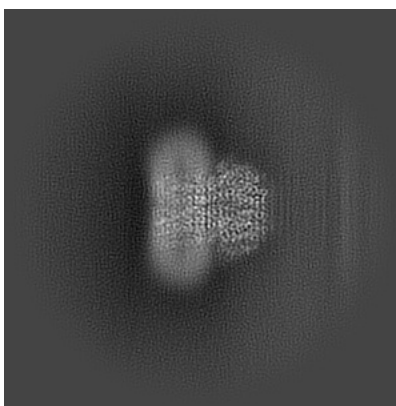
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

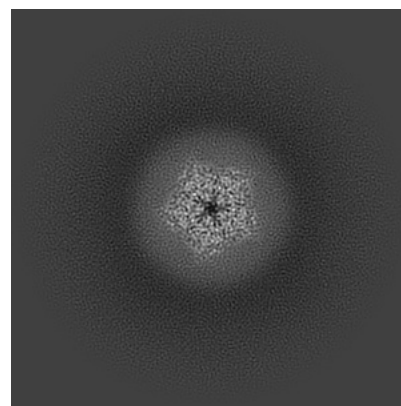
6.1.1 Primary map



X

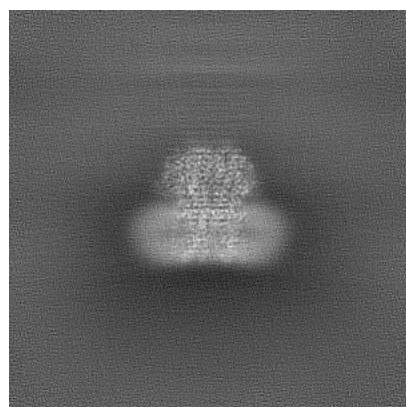


Y

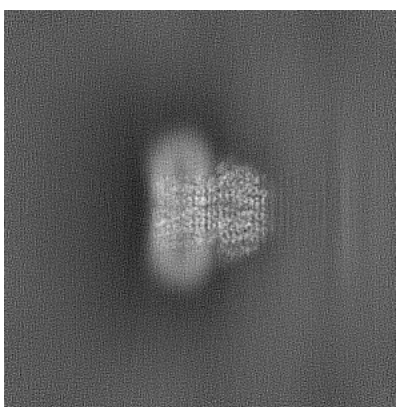


Z

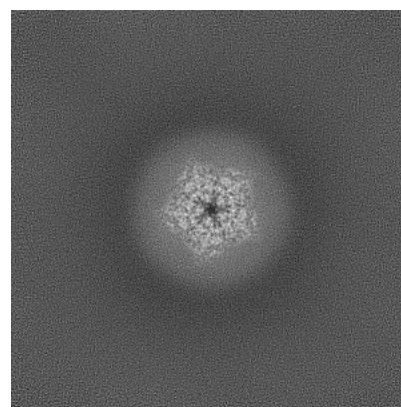
6.1.2 Raw map



X



Y

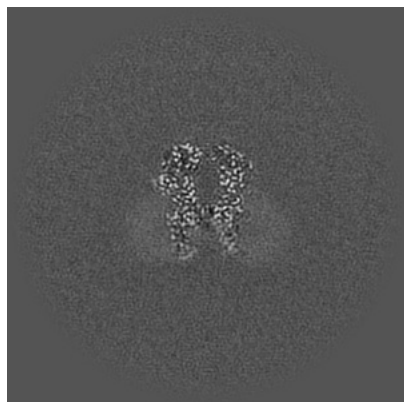


Z

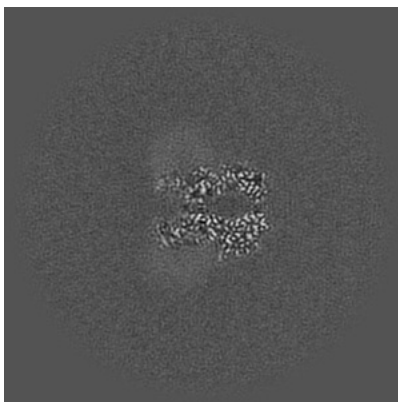
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

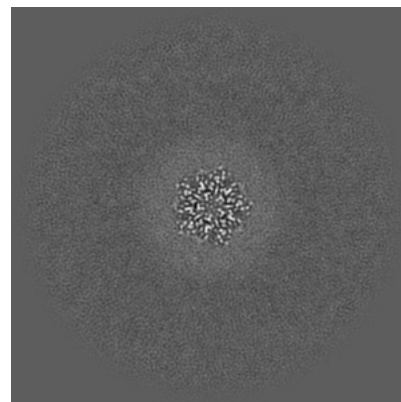
6.2.1 Primary map



X Index: 200

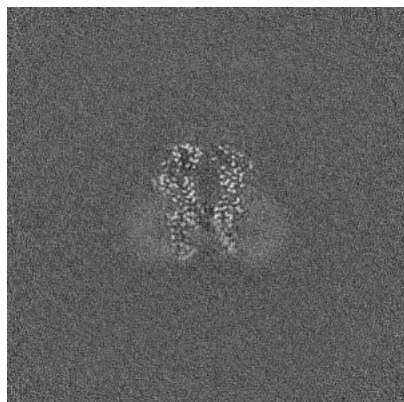


Y Index: 200

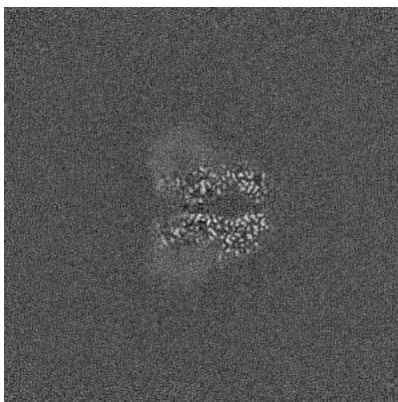


Z Index: 200

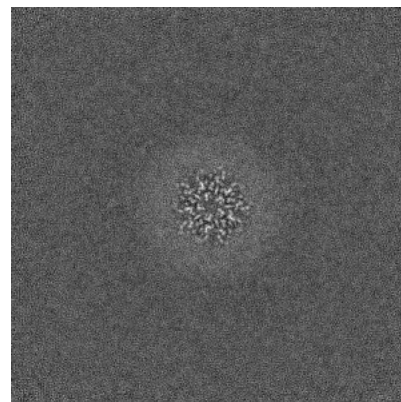
6.2.2 Raw map



X Index: 200



Y Index: 200

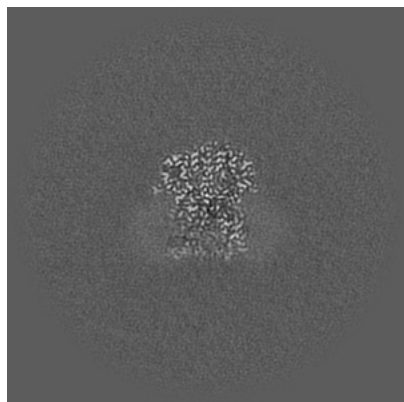


Z Index: 200

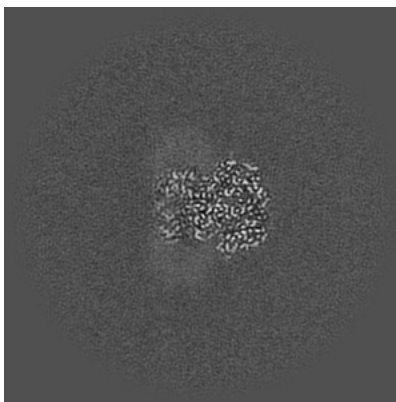
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

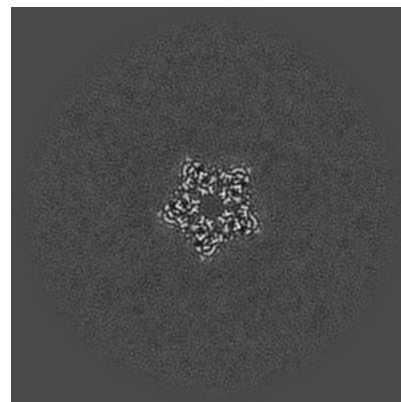
6.3.1 Primary map



X Index: 185

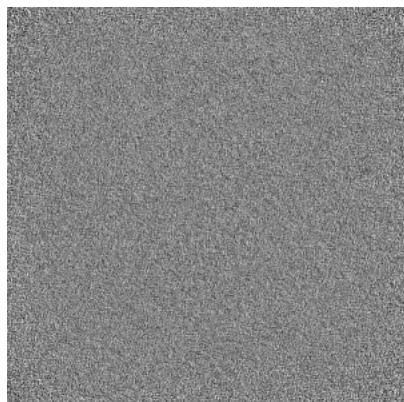


Y Index: 185

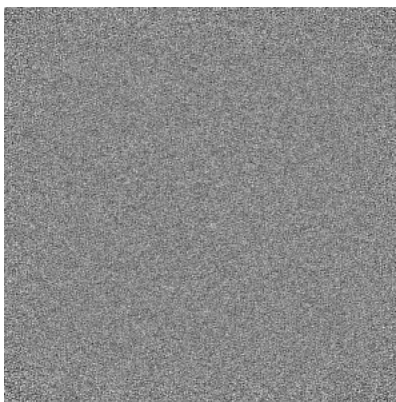


Z Index: 223

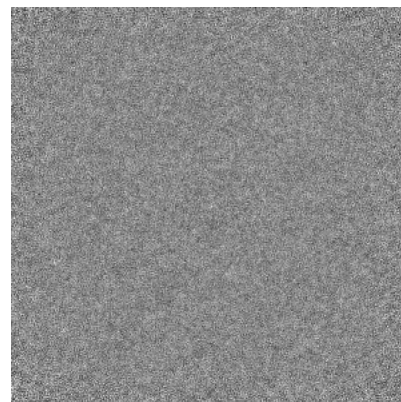
6.3.2 Raw map



X Index: 0



Y Index: 0

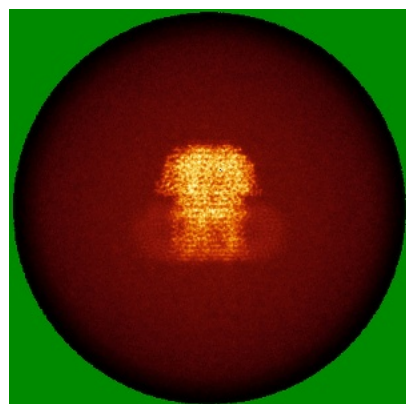


Z Index: 0

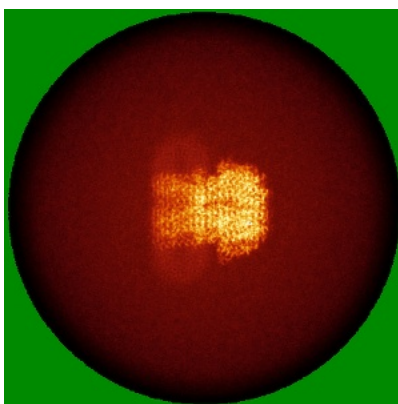
The images above show the largest variance slices of the map in three orthogonal directions.

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

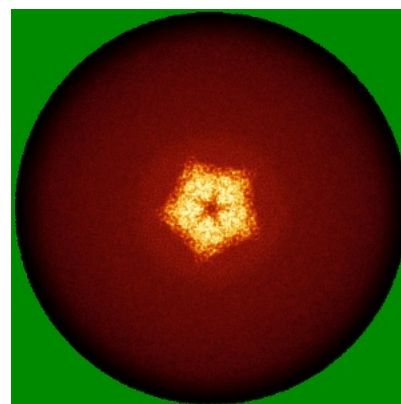
6.4.1 Primary map



X

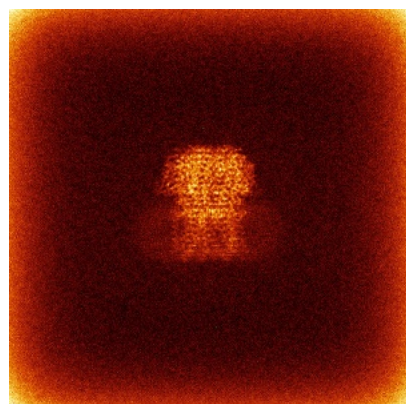


Y

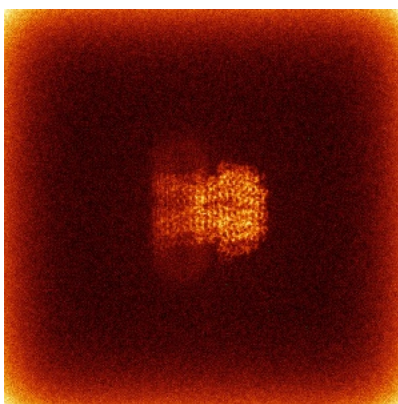


Z

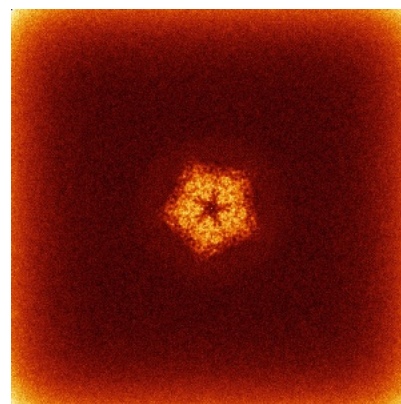
6.4.2 Raw map



X



Y

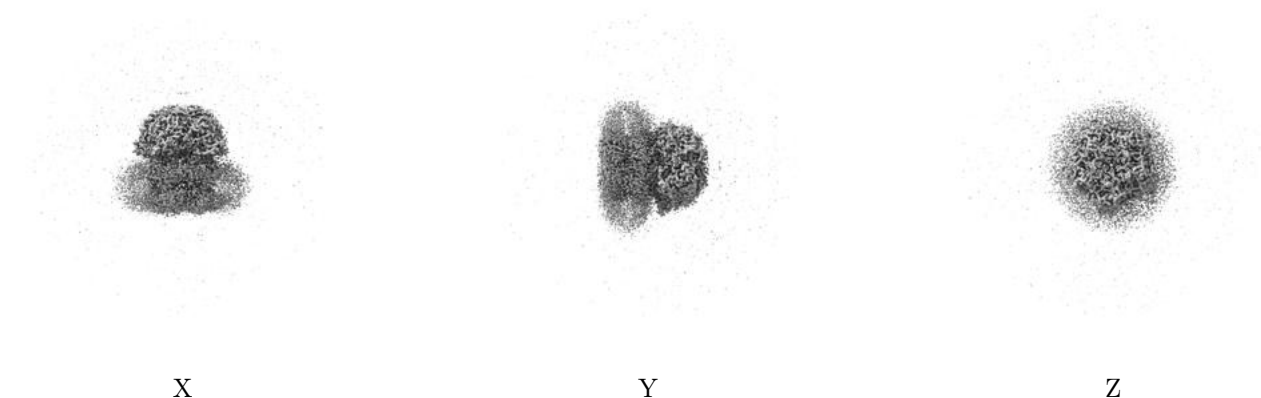


Z

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.

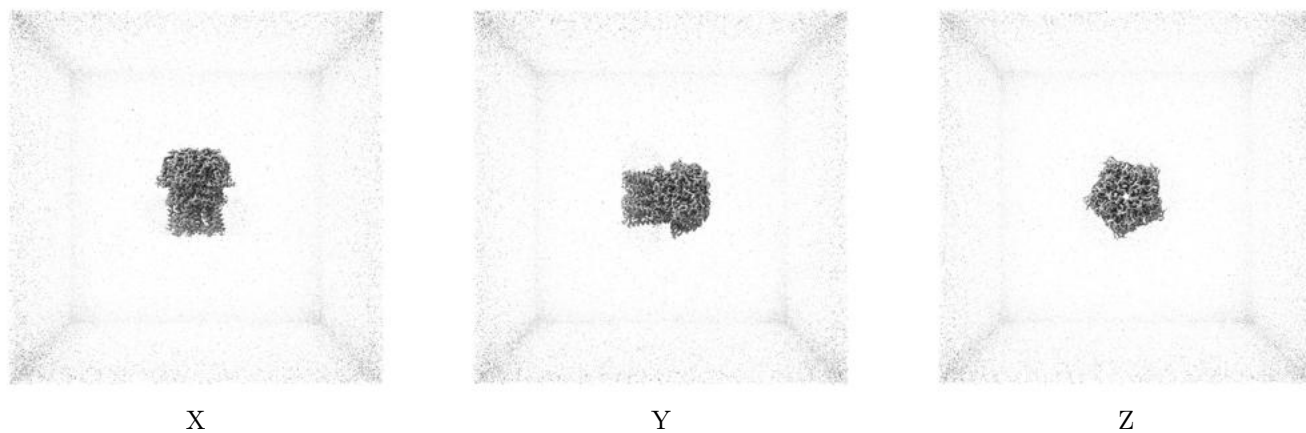
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

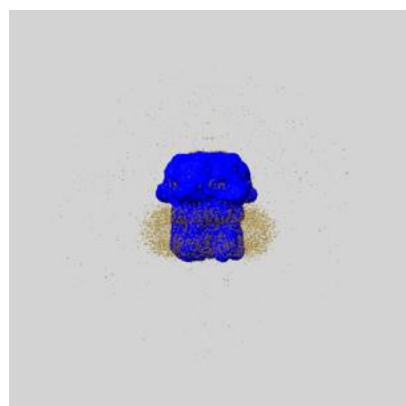
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

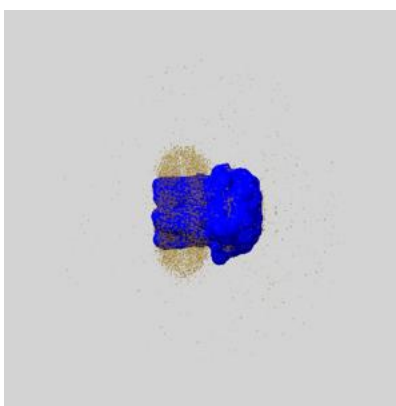
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

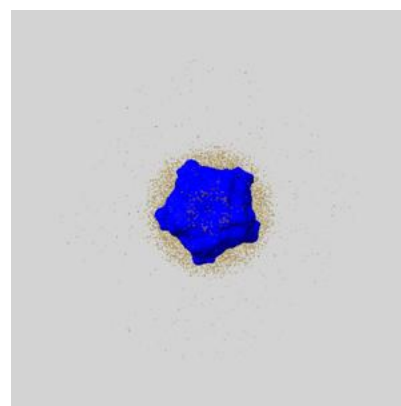
6.6.1 emd_45918_msk_1.map [i](#)



X



Y

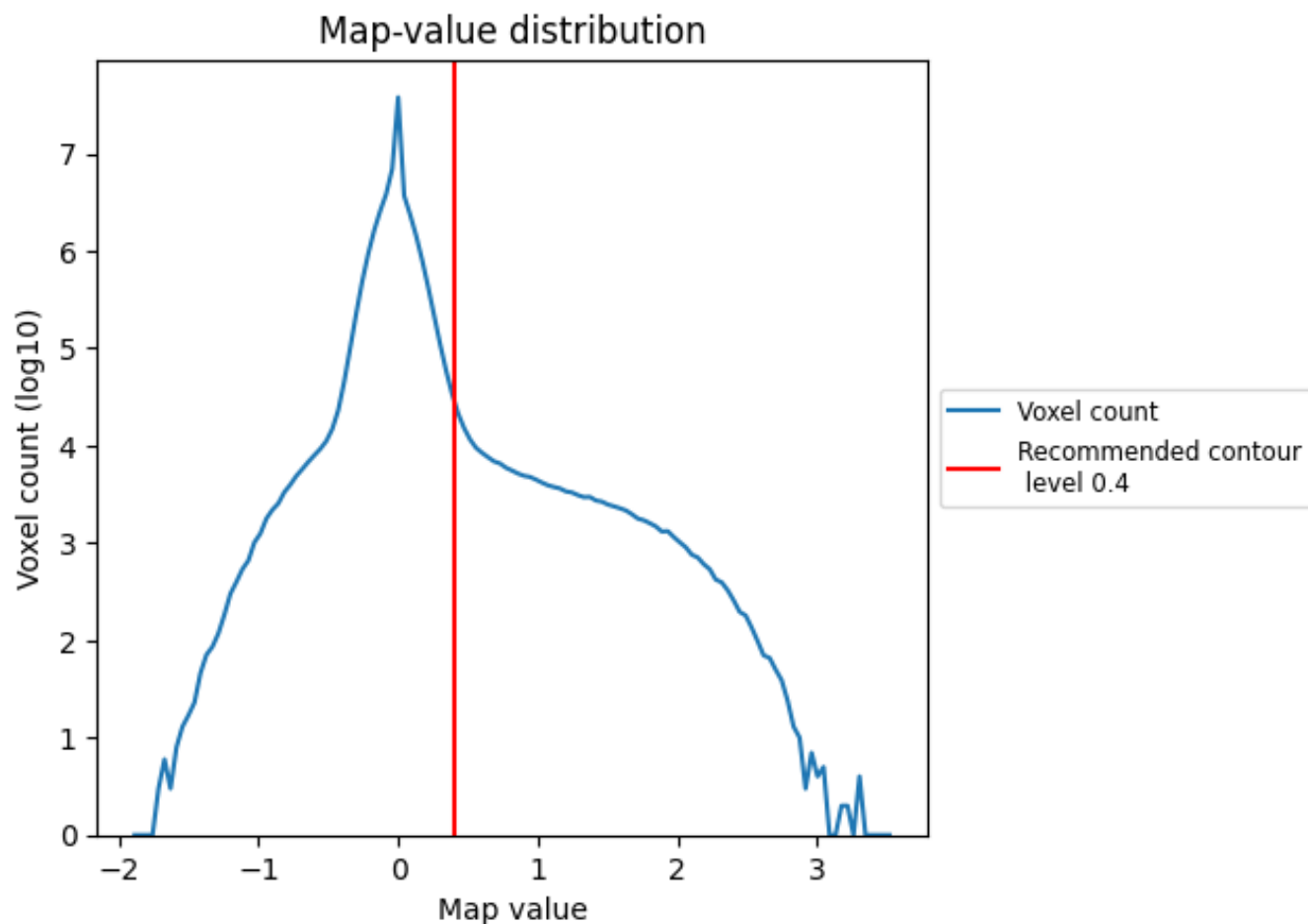


Z

7 Map analysis [i](#)

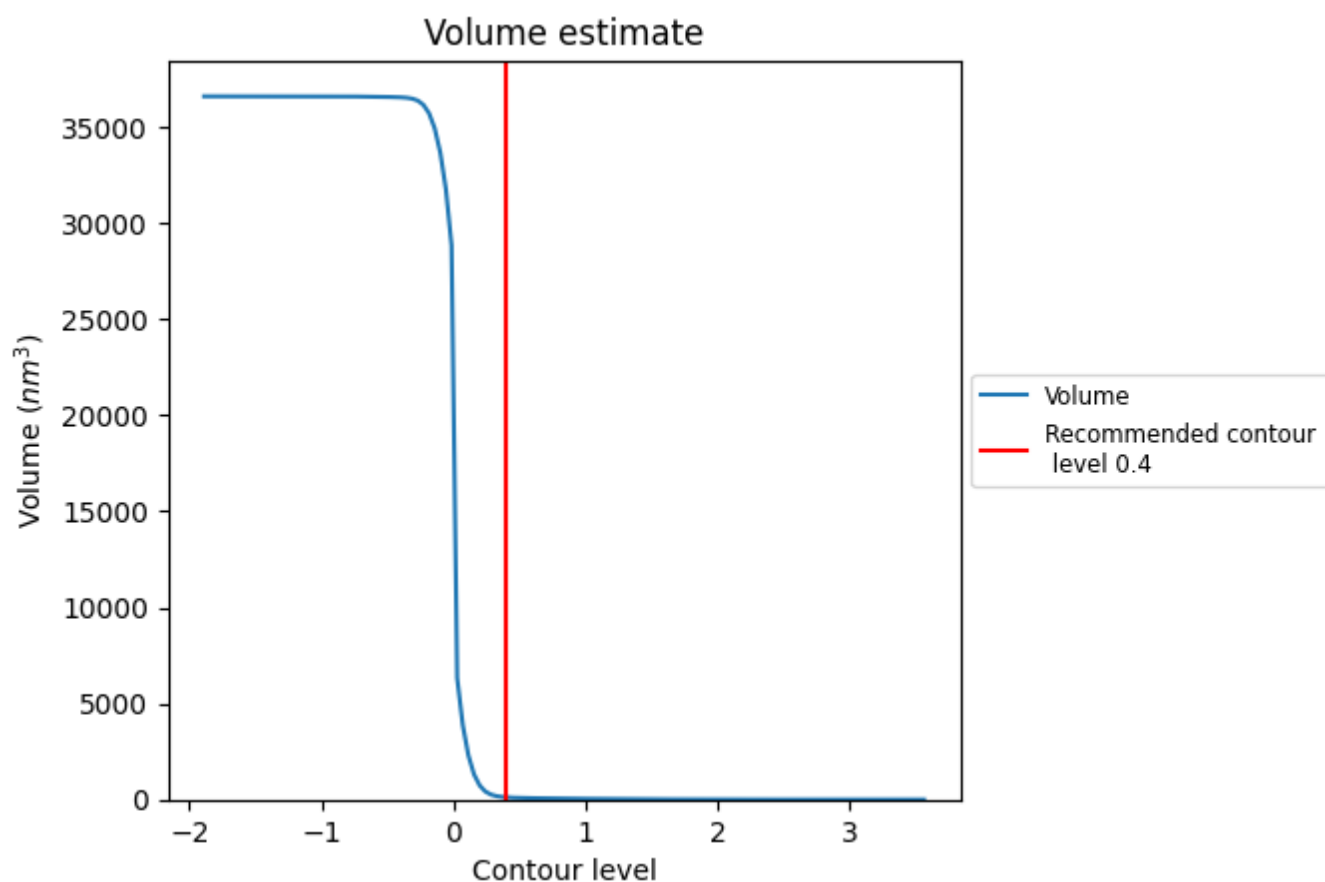
This section contains the results of statistical analysis of the map.

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.

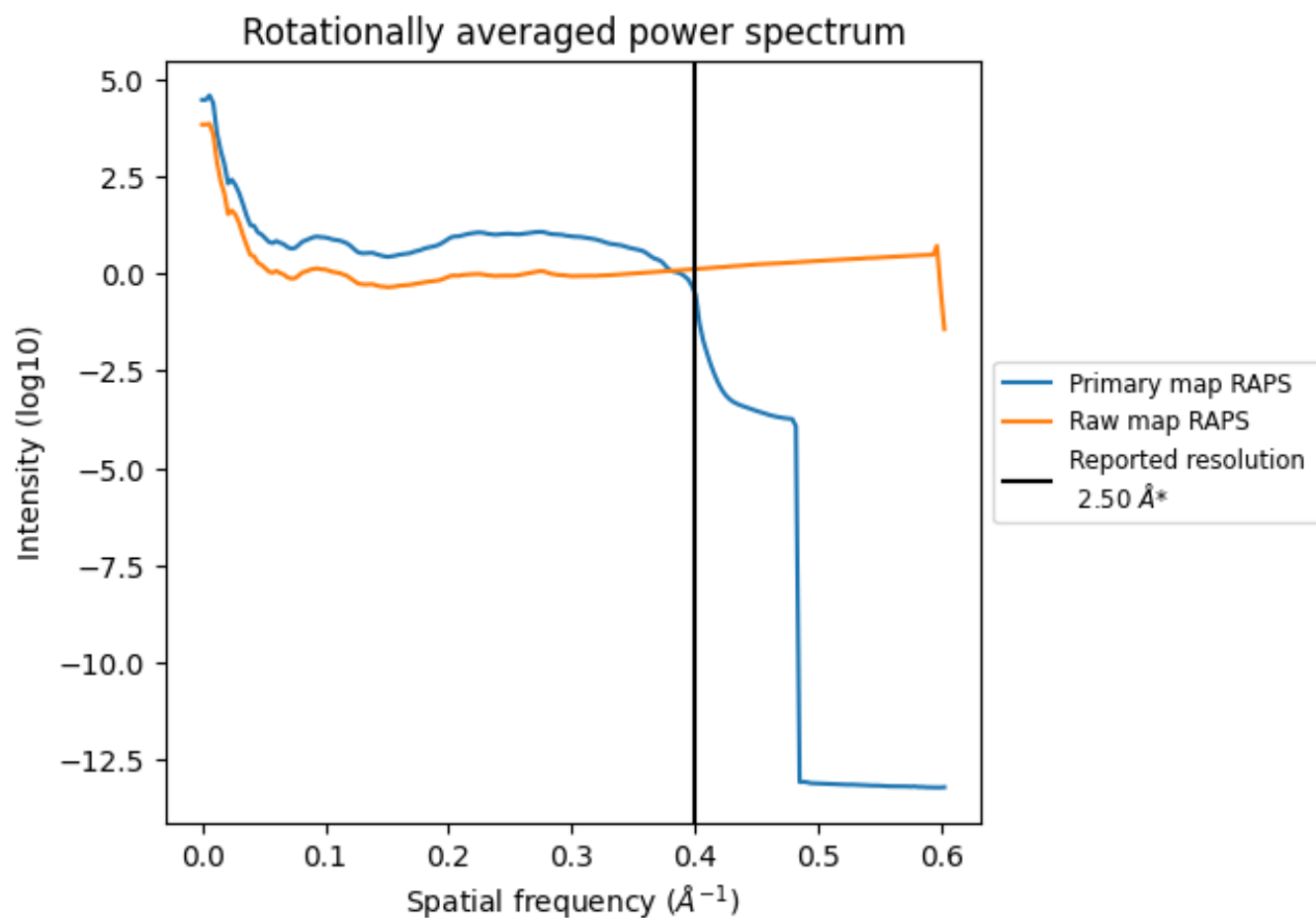
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm³; this corresponds to an approximate mass of 106 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 ⓘ

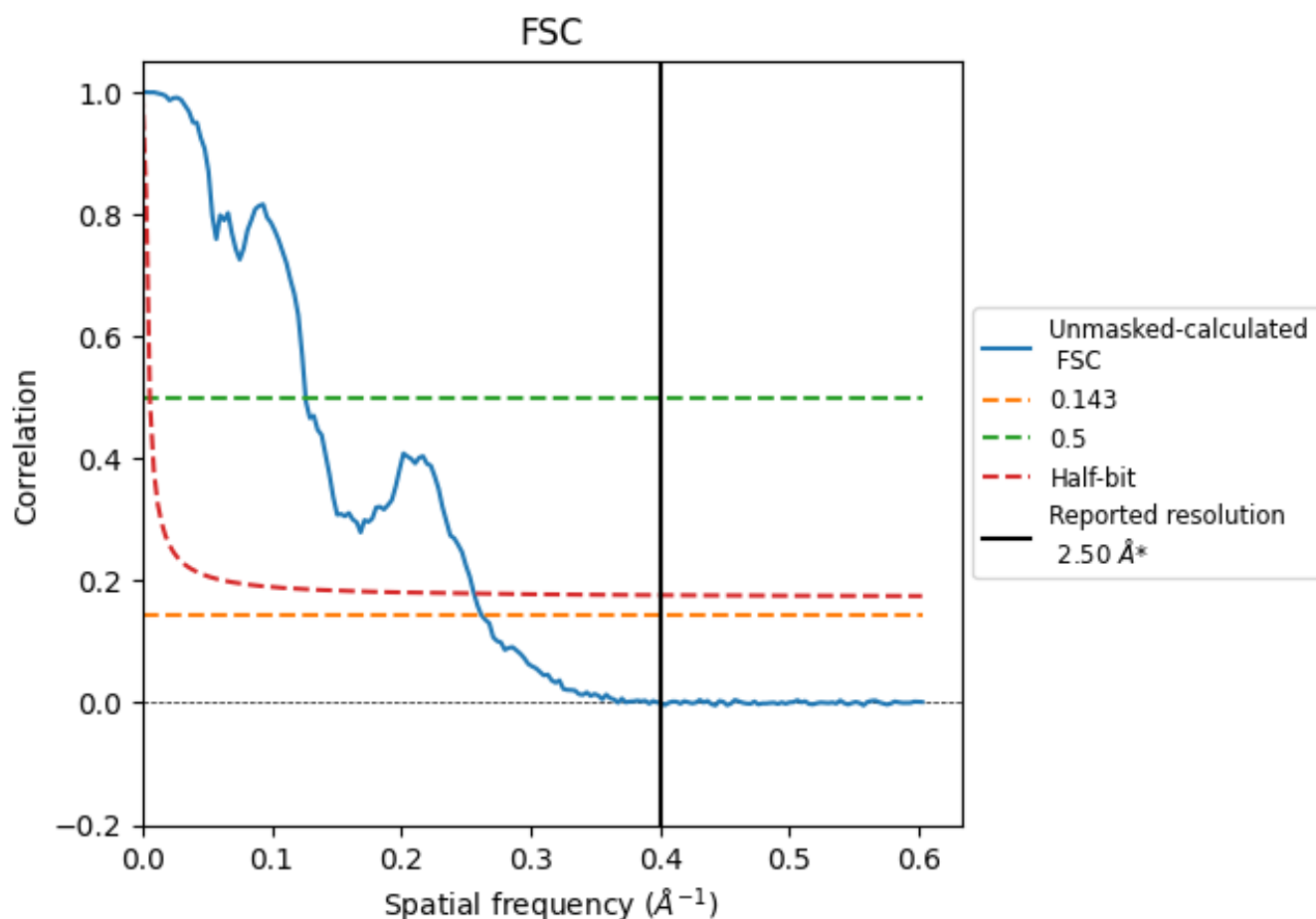


*Reported resolution corresponds to spatial frequency of 0.400 Å⁻¹

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 0.400 Å⁻¹

8.2 Resolution estimates [i](#)

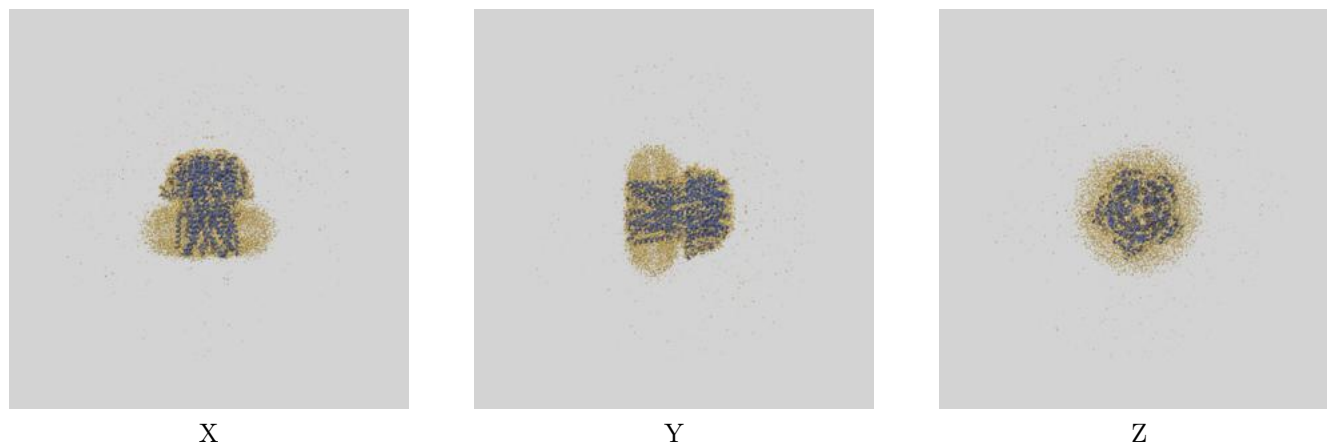
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	7.92	3.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.82 differs from the reported value 2.5 by more than 10 %

9 Map-model fit [i](#)

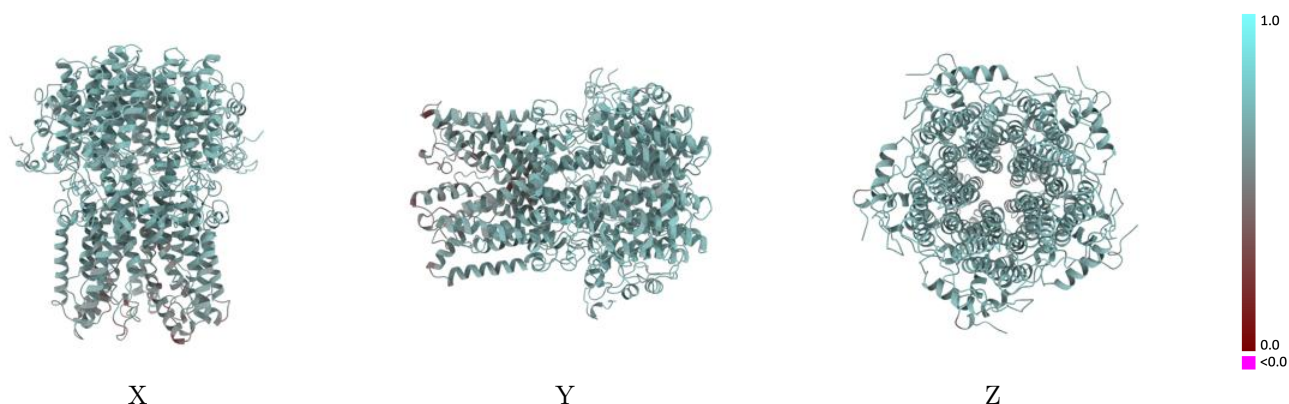
This section contains information regarding the fit between EMDB map EMD-45918 and PDB model 9CTT. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



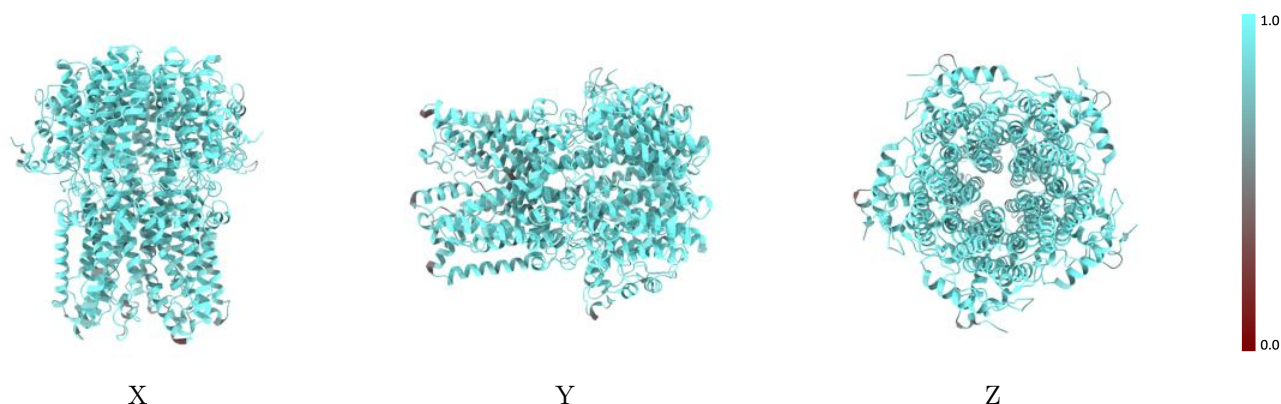
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



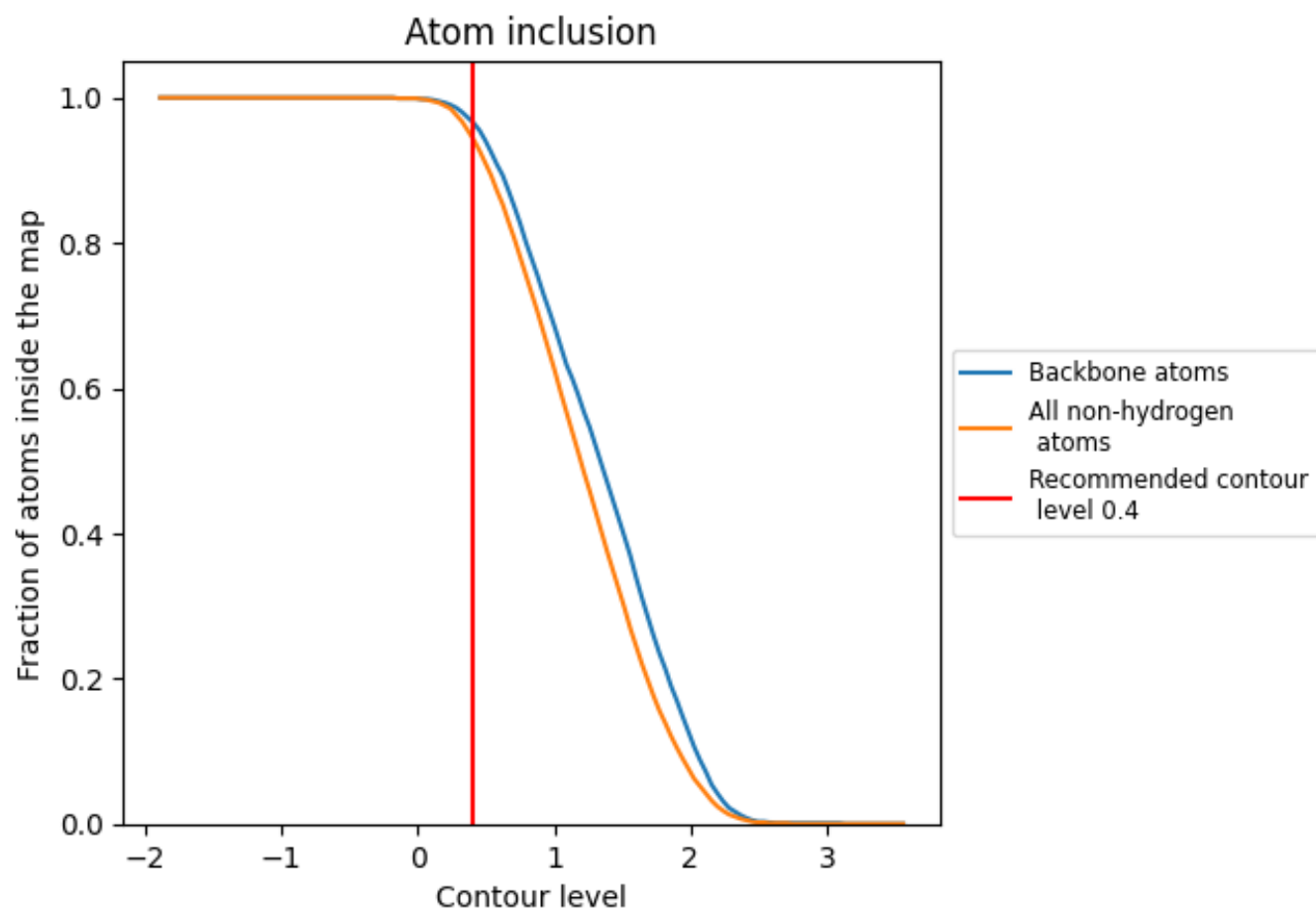
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9450	0.6310
A	0.9420	0.6290
B	0.9430	0.6300
C	0.9510	0.6330
D	0.9450	0.6330
E	0.9450	0.6300

