



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 11:58 AM UTC

PDB ID : 8EKY / pdb_00008eky
EMDB ID : EMD-28217
Title : Cryo-EM structure of the human PRDX4-ErP46 complex
Authors : Su, C.C.
Deposited on : 2022-09-22
Resolution : 3.47 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

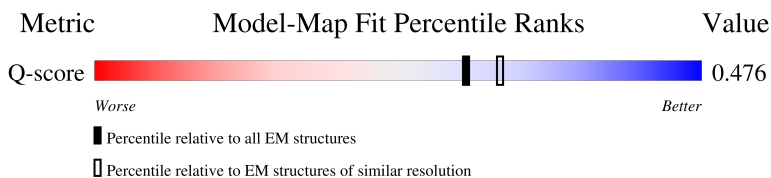
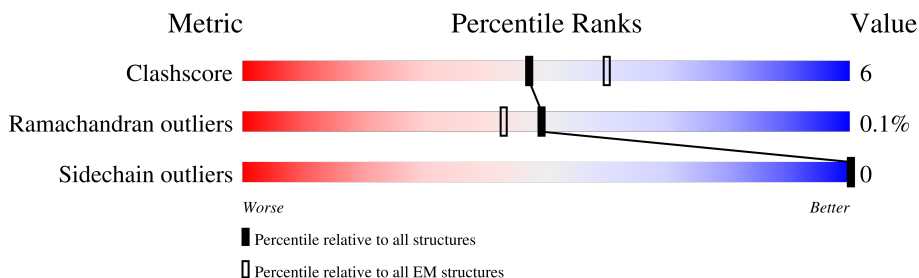
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.47 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	13733 (2.97 - 3.97)

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	271	
1	B	271	
1	C	271	
1	D	271	

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Mol	Chain	Length	Quality of chain
1	E	271	 52%10%38%
1	F	271	 52%11%37%
1	G	271	 56%6%38%
1	H	271	 54%8%38%
1	I	271	 54%10%37%
1	J	271	 50%12%38%
2	M	432	 19%6%75%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14605 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 Peroxiredoxin-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	171	Total	C	N	O	S	0	0
			1378	890	231	254	3		
1	B	168	Total	C	N	O	S	0	0
			1356	877	228	249	2		
1	C	187	Total	C	N	O	S	0	0
			1493	965	249	276	3		
1	D	171	Total	C	N	O	S	0	0
			1378	890	231	254	3		
1	E	168	Total	C	N	O	S	0	0
			1356	877	228	249	2		
1	F	171	Total	C	N	O	S	0	0
			1378	890	231	254	3		
1	G	167	Total	C	N	O	S	0	0
			1346	871	225	248	2		
1	H	167	Total	C	N	O	S	0	0
			1346	871	225	248	2		
1	I	171	Total	C	N	O	S	0	0
			1378	890	231	254	3		
1	J	168	Total	C	N	O	S	0	0
			1356	877	228	249	2		

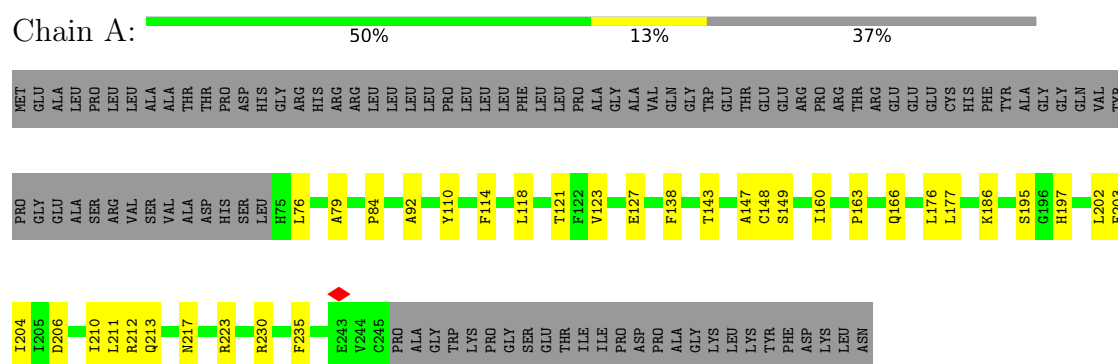
- Molecule 2 is a protein called Thioredoxin domain-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	106	Total	C	N	O	S	0	0
			840	537	144	156	3		

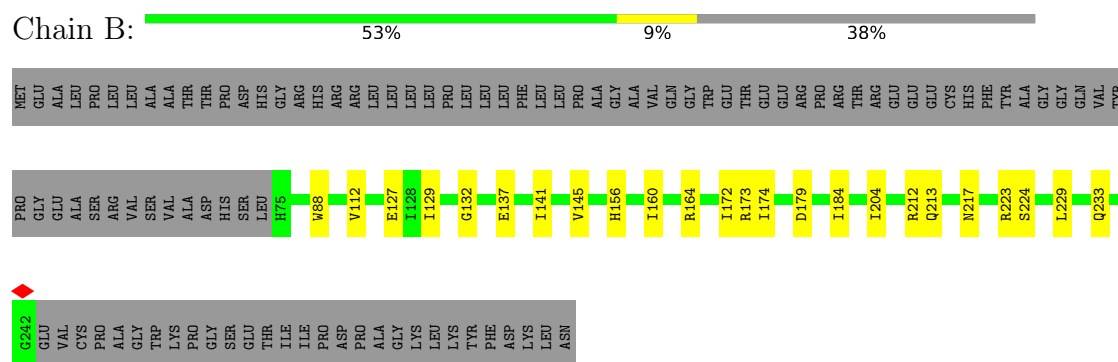
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

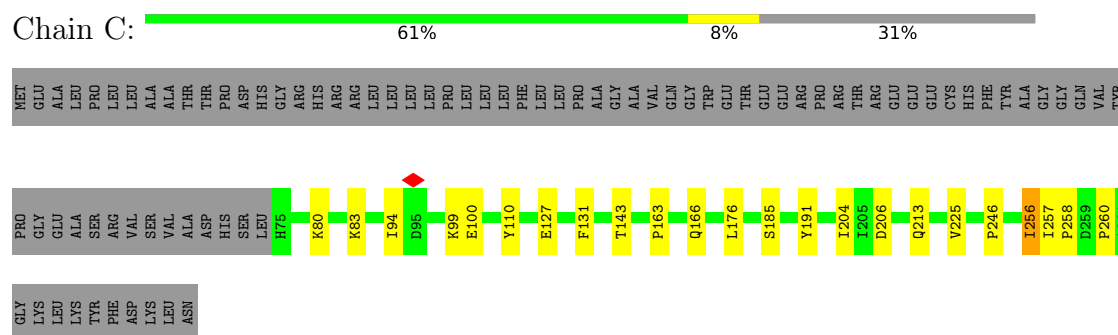
• Molecule 1: Peroxiredoxin-4



• Molecule 1: Peroxiredoxin-4



• Molecule 1: Peroxiredoxin-4



- Molecule 1: Peroxiredoxin-4

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GLU	THR	ILE	ILE	PRO	ASP	PRO	PRO	GLY	LEU	LEU	LYS	THR	THR	PRO	ASP	HIS	THR	ALA	LEU	PRO	GLU	ALA	GLU	MET																							
161	168	176	184	192	200	208	216	224	232	240	248	256	264	272	280	288	296	304	312	320	328	336	344																								
PRO	GLY	GLU	ALA	SER	ARG	VAL	SER	ALA	VAL	ALA	ASP	HIS	SER	HIS	HIS	L76	T61	W88	F115	E127	R165	D179	I184	D194	F203	I204	L211	R212	Q213	T214	N217	R223	R230	L231	G242	GLU	VAL	CYS	HIS	PHE	TYR	ALA	GLY	TRP	LYS	PRO	GLY

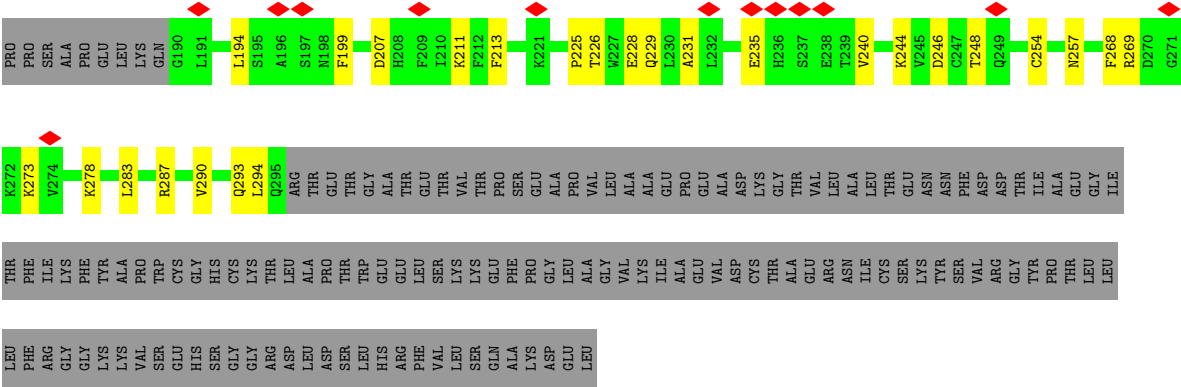
Chain H:

Position	Amino Acid	Conservation (%)
1	MET	54%
2	GLU	54%
3	ALA	54%
4	LEU	54%
5	PRO	54%
6	LEU	54%
7	LEU	54%
8	ALA	54%
9	ALA	54%
10	THR	54%
11	THR	54%
12	PRO	54%
13	ASP	54%
14	HIS	54%
15	GLY	54%
16	ARG	54%
17	HIS	54%
18	ARG	54%
19	ARG	54%
20	LEU	54%
21	LEU	54%
22	LEU	54%
23	LEU	54%
24	PRO	54%
25	LEU	54%
26	LEU	54%
27	PHE	54%
28	LEU	54%
29	LEU	54%
30	ALA	54%
31	GLY	54%
32	ALA	54%
33	VAL	54%
34	GLN	54%
35	GLY	54%
36	TRP	54%
37	GLU	54%
38	THR	54%
39	GLU	54%
40	ARG	54%
41	GLU	54%
42	ARG	54%
43	THR	54%
44	ARG	54%
45	GLU	54%
46	GLU	54%
47	CYS	54%
48	HIS	54%
49	PHE	54%
50	TYR	54%
51	ALA	54%
52	GLY	54%
53	GLN	54%
54	VAL	54%
55	TYR	54%
56	PRO	54%
57	ASP	54%
58	PRO	54%
59	ASP	54%
60	LEU	54%
61	LEU	54%
62	LEU	54%
63	LEU	54%
64	LEU	54%
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150	LEU	54%
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152	LEU	54%
153	LEU	54%
154	LEU	54%
155	LEU	54%
156	LEU	54%
157	LEU	54%
158	LEU	54%
1		

[illegible][illegible]

Chain M:

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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22035	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 ($e^-/\text{\AA}^2$)	29.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.027	Depositor
Minimum map value	-0.560	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.17	0/1412	0.38	0/1915
1	B	0.18	0/1390	0.35	0/1885
1	C	0.23	0/1533	0.48	0/2084
1	D	0.18	0/1412	0.38	0/1915
1	E	0.17	0/1390	0.39	0/1885
1	F	0.17	0/1412	0.33	0/1915
1	G	0.17	0/1379	0.33	0/1870
1	H	0.16	0/1379	0.35	0/1870
1	I	0.18	0/1412	0.35	0/1915
1	J	0.20	0/1390	0.40	0/1885
2	M	0.17	0/861	0.48	0/1163
All	All	0.18	0/14970	0.38	0/20302

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	1378	0	1366	21	0
1	B	1356	0	1346	16	0
1	C	1493	0	1477	16	0
1	D	1378	0	1366	18	0
1	E	1356	0	1346	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1378	0	1366	21	0
1	G	1346	0	1339	12	0
1	H	1346	0	1339	13	0
1	I	1378	0	1366	17	0
1	J	1356	0	1346	19	0
2	M	840	0	795	16	0
All	All	14605	0	14452	175	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 175 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:256:ILE:HG23	1:C:258:PRO:HD2	1.65	0.78
1:F:224:SER:HB2	1:G:230:ARG:HH12	1.53	0.74
1:D:127:GLU:OE2	1:D:200:ARG:NH1	2.21	0.73
1:A:230:ARG:HH12	1:B:224:SER:HB2	1.58	0.69
1:F:213:GLN:NE2	1:G:217:ASN:OD1	2.23	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	169/271 (62%)	164 (97%)	5 (3%)	0	100	100
1	B	166/271 (61%)	161 (97%)	5 (3%)	0	100	100
1	C	185/271 (68%)	179 (97%)	5 (3%)	1 (0%)	24	58
1	D	169/271 (62%)	164 (97%)	5 (3%)	0	100	100
1	E	166/271 (61%)	161 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	169/271 (62%)	163 (96%)	6 (4%)	0	100	100
1	G	165/271 (61%)	161 (98%)	4 (2%)	0	100	100
1	H	165/271 (61%)	158 (96%)	7 (4%)	0	100	100
1	I	169/271 (62%)	164 (97%)	5 (3%)	0	100	100
1	J	166/271 (61%)	159 (96%)	7 (4%)	0	100	100
2	M	104/432 (24%)	101 (97%)	3 (3%)	0	100	100
All	All	1793/3142 (57%)	1735 (97%)	57 (3%)	1 (0%)	49	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	256	ILE

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	151/232 (65%)	151 (100%)	0	100	100
1	B	148/232 (64%)	148 (100%)	0	100	100
1	C	163/232 (70%)	163 (100%)	0	100	100
1	D	151/232 (65%)	151 (100%)	0	100	100
1	E	148/232 (64%)	148 (100%)	0	100	100
1	F	151/232 (65%)	151 (100%)	0	100	100
1	G	147/232 (63%)	147 (100%)	0	100	100
1	H	147/232 (63%)	147 (100%)	0	100	100
1	I	151/232 (65%)	151 (100%)	0	100	100
1	J	148/232 (64%)	148 (100%)	0	100	100
2	M	86/351 (24%)	86 (100%)	0	100	100
All	All	1591/2671 (60%)	1591 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	142	ASN
2	M	229	GLN
1	F	75	HIS
2	M	249	GLN
1	I	142	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.

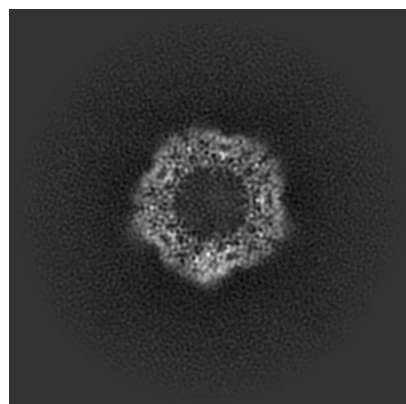
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28217. These allow visual inspection of the internal detail of the map and identification of artifacts.

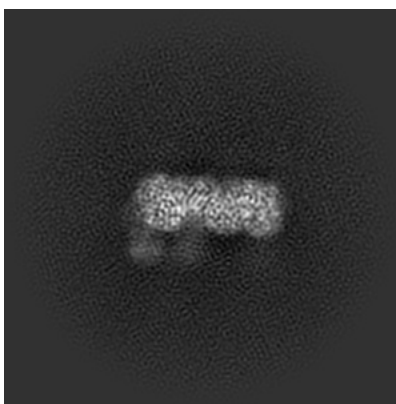
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

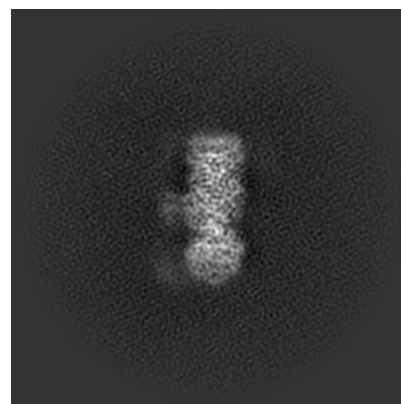
6.1.1 Primary map



X

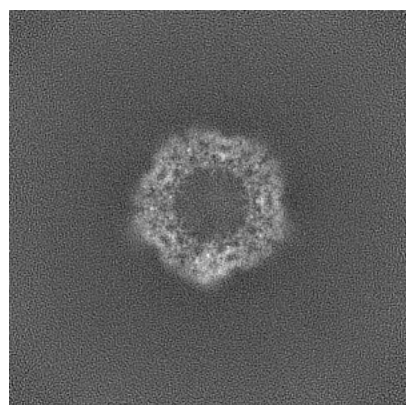


Y

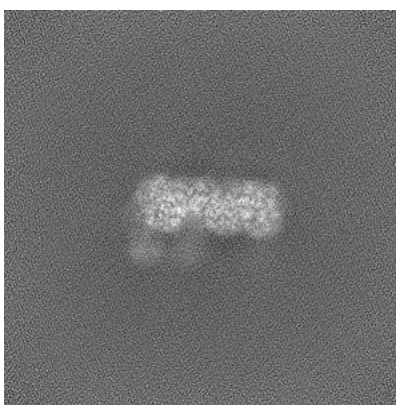


Z

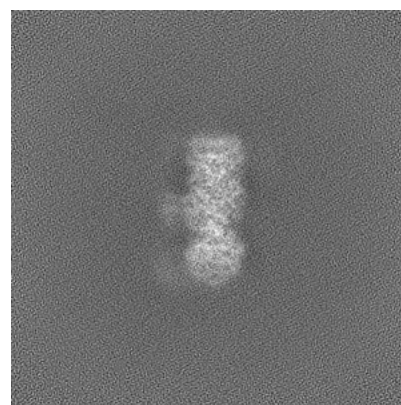
6.1.2 Raw map



X



Y

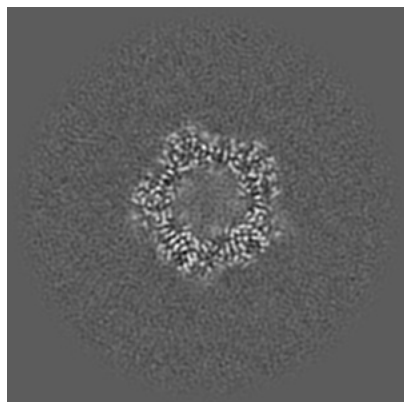


Z

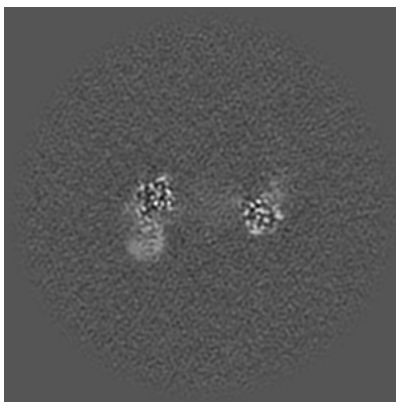
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

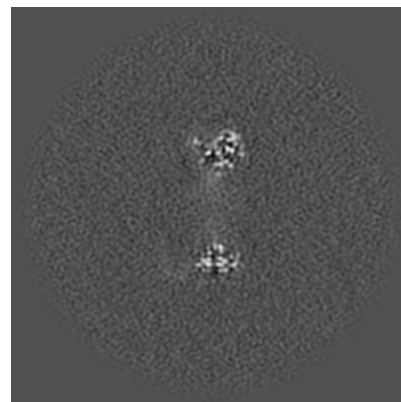
6.2.1 Primary map



X Index: 150

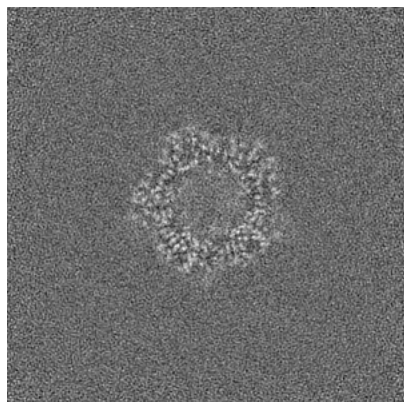


Y Index: 150

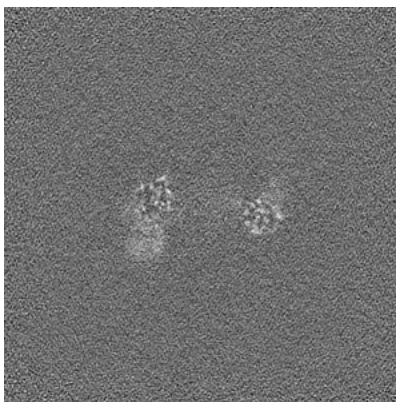


Z Index: 150

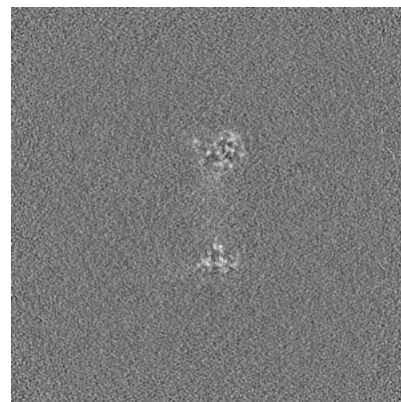
6.2.2 Raw map



X Index: 150



Y Index: 150

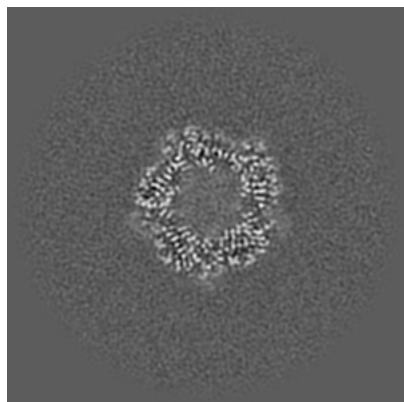


Z Index: 150

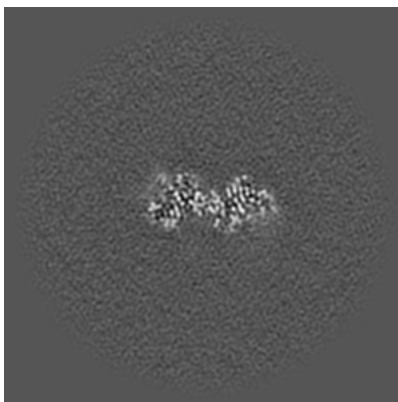
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

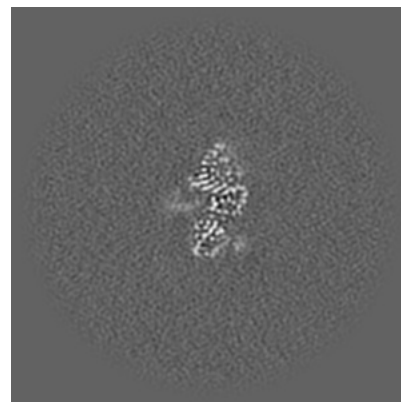
6.3.1 Primary map



X Index: 148

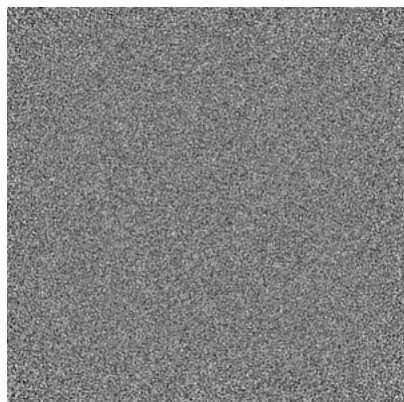


Y Index: 121

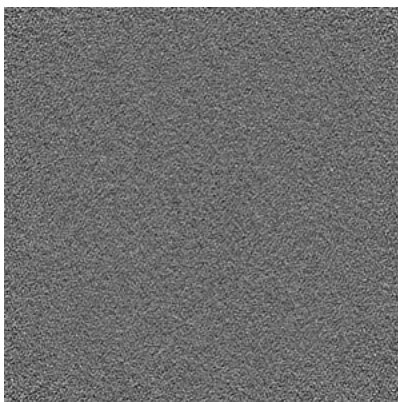


Z Index: 118

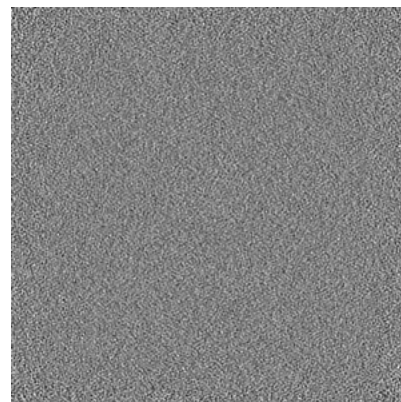
6.3.2 Raw map



X Index: 0



Y Index: 0

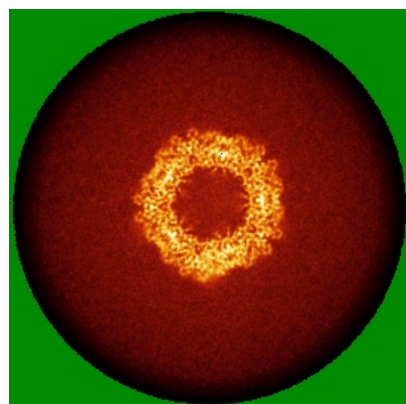


Z Index: 0

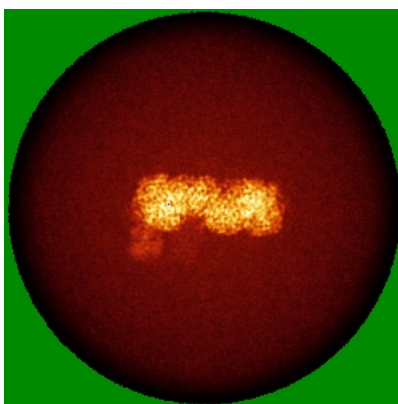
The images above show the largest variance slices of the map in three orthogonal directions.

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

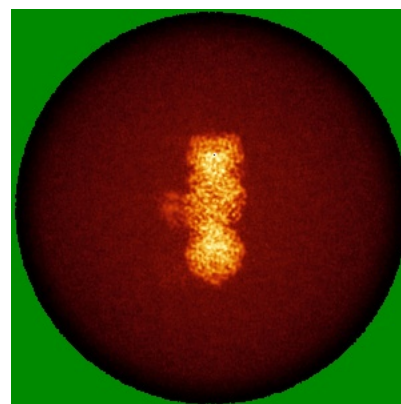
6.4.1 Primary map



X

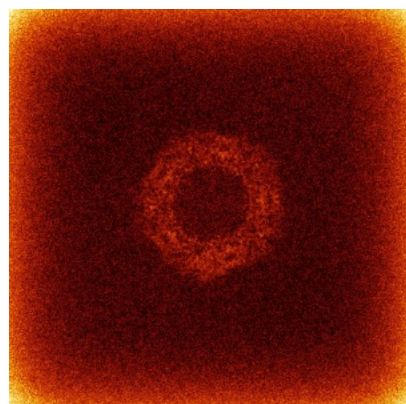


Y

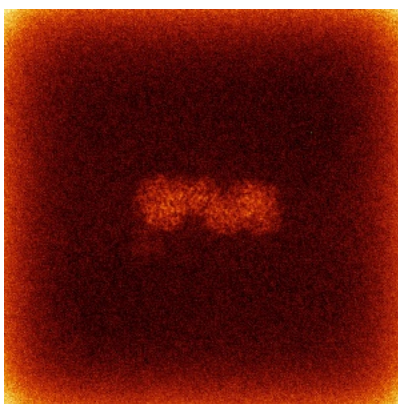


Z

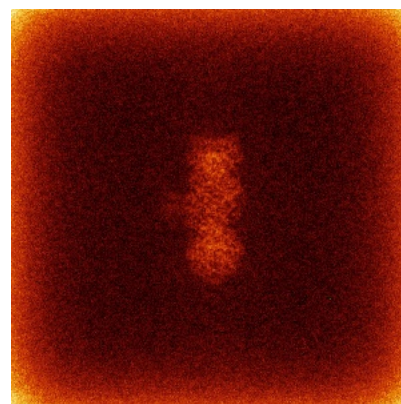
6.4.2 Raw map



X



Y

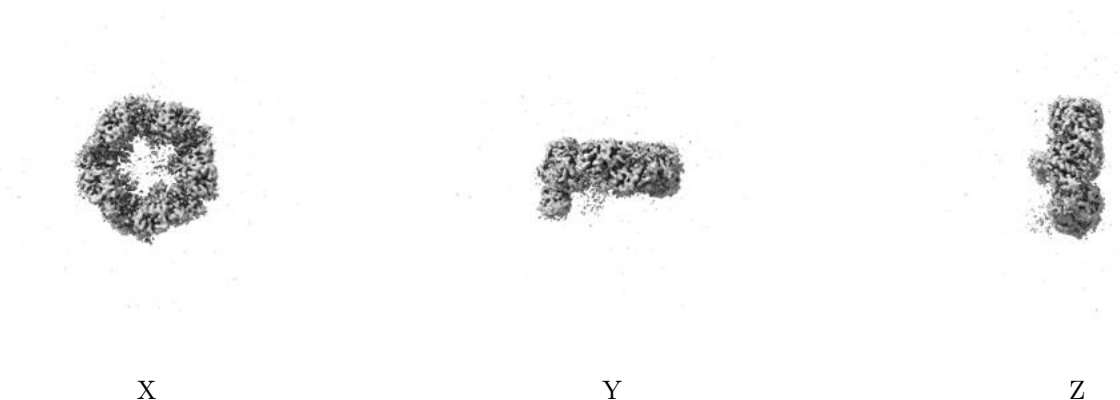


Z

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.

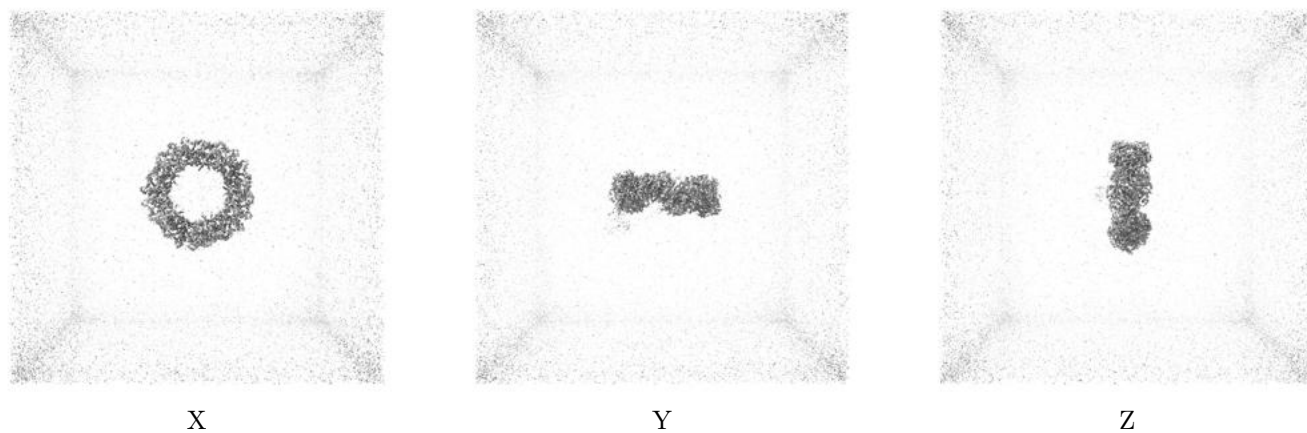
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

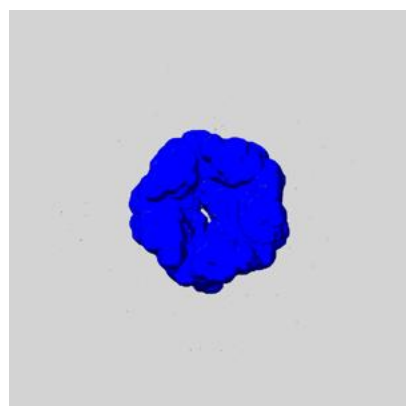
6.6 Mask visualisation [i](#)

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

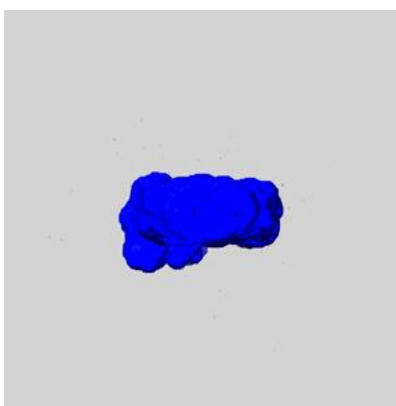
A mask typically either:

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

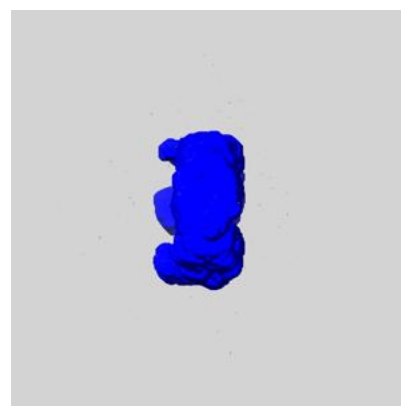
6.6.1 emd_28217_msk_1.map [i](#)



X



Y

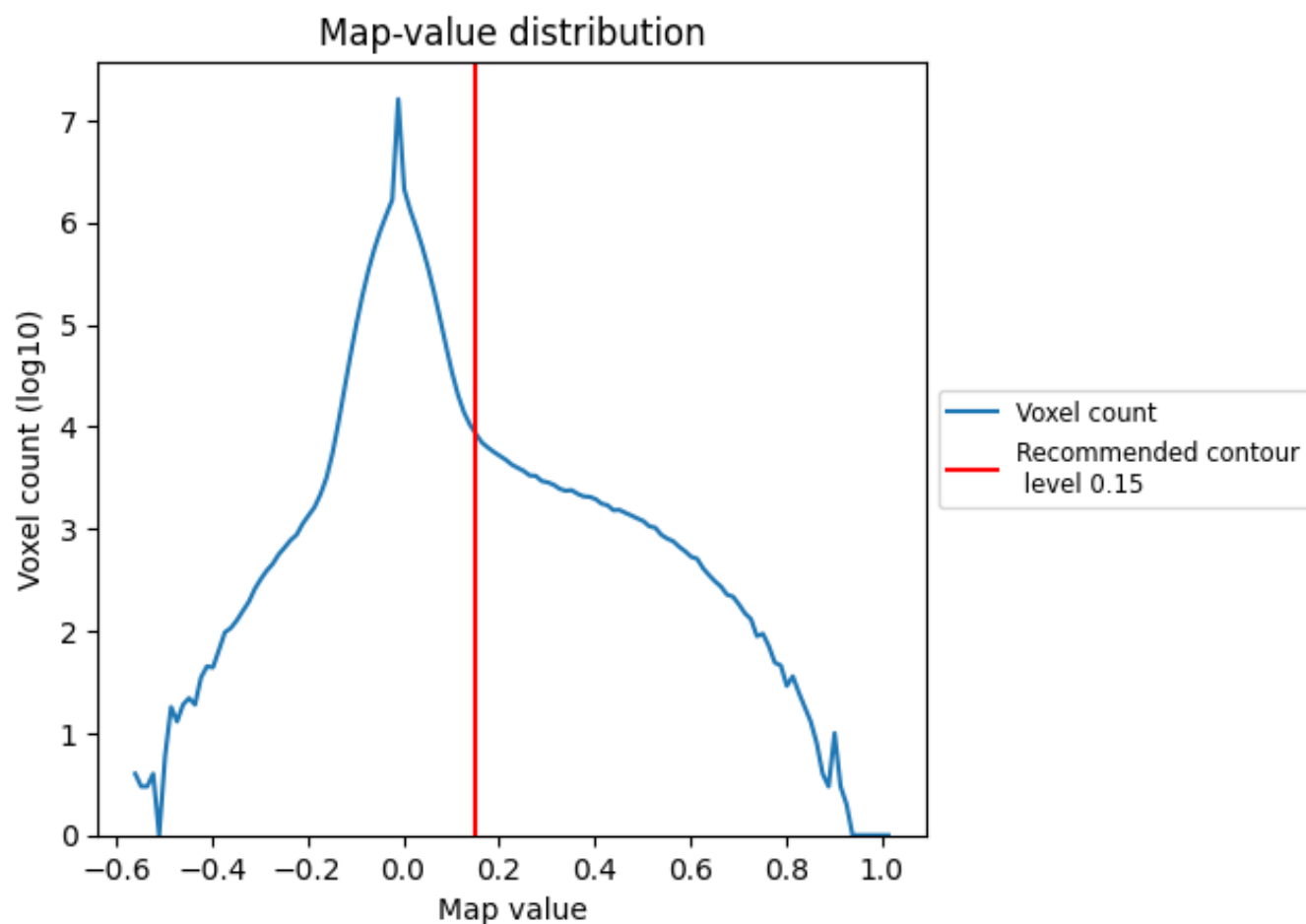


Z

7 Map analysis [i](#)

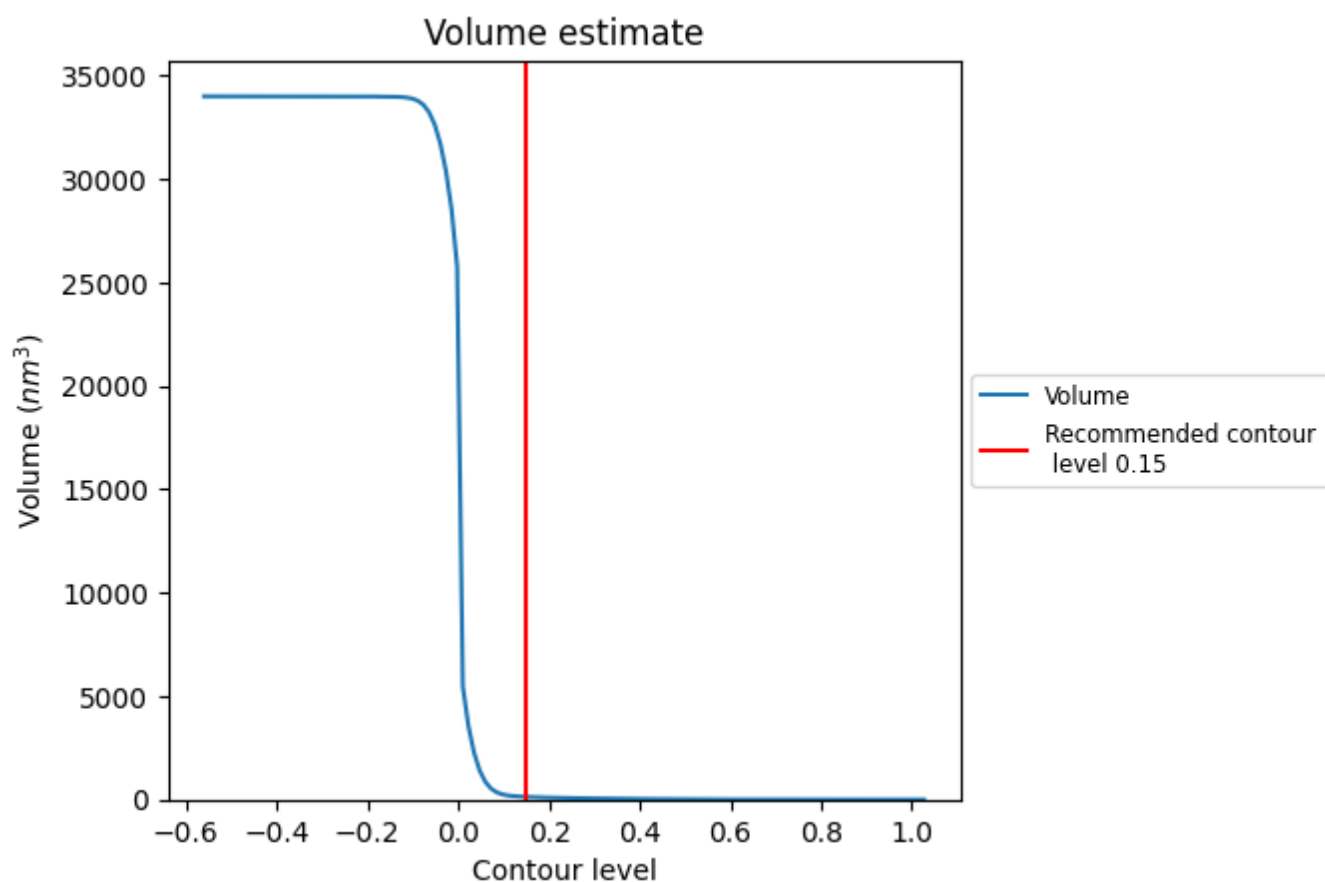
This section contains the results of statistical analysis of the map.

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.

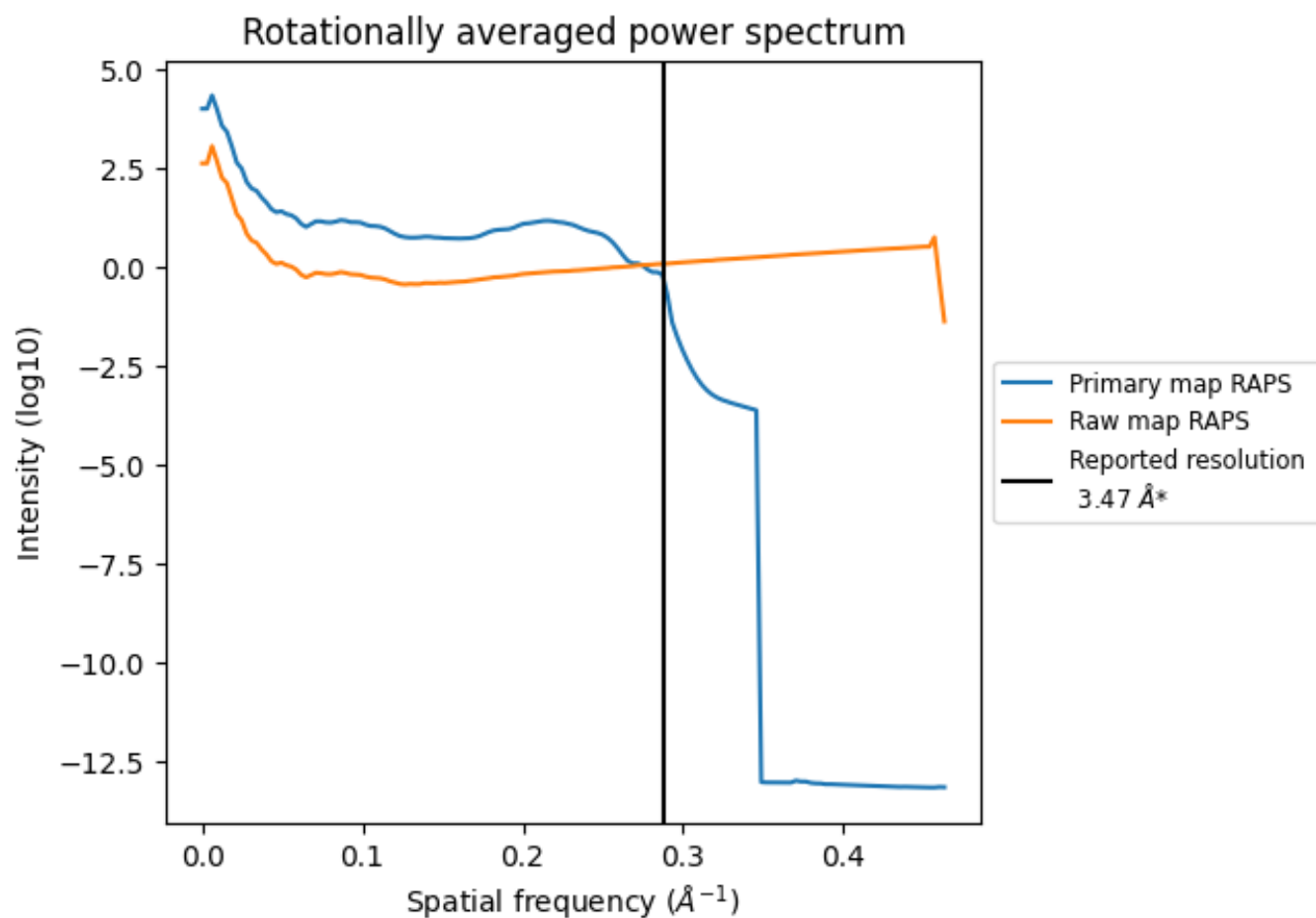
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130 nm³; this corresponds to an approximate mass of 117 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 ⓘ

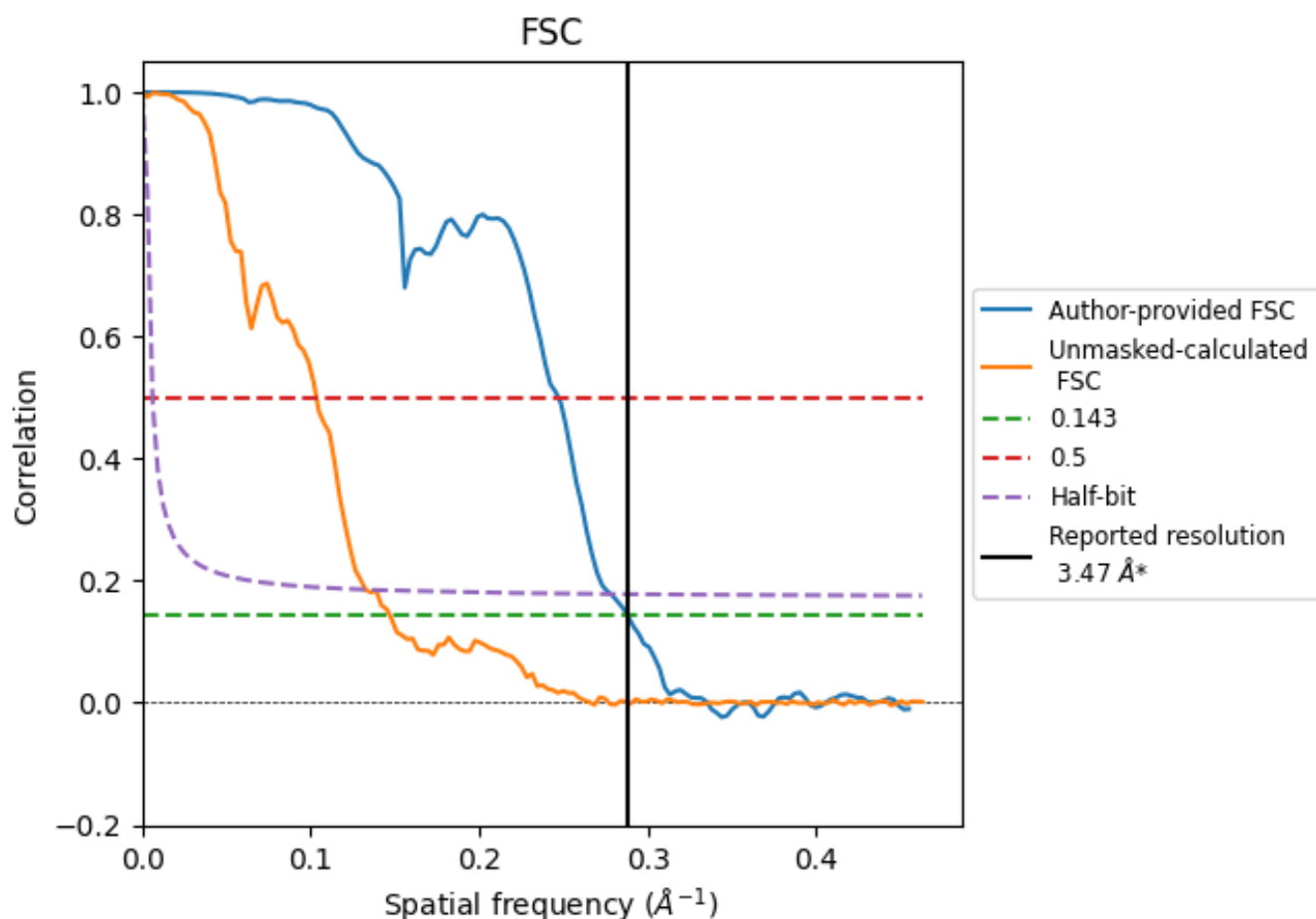


*Reported resolution corresponds to spatial frequency of 0.288 Å⁻¹

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 $0.288 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

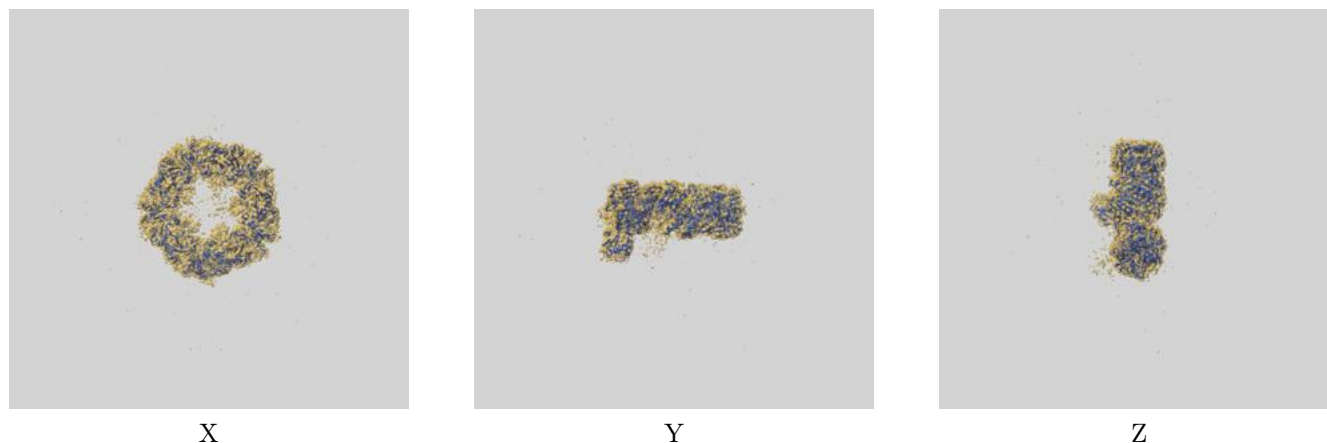
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.47	4.05	3.60
Unmasked-calculated*	6.80	9.67	7.54

*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 6.80 differs from the reported value 3.47 by more than 10 %

9 Map-model fit [i](#)

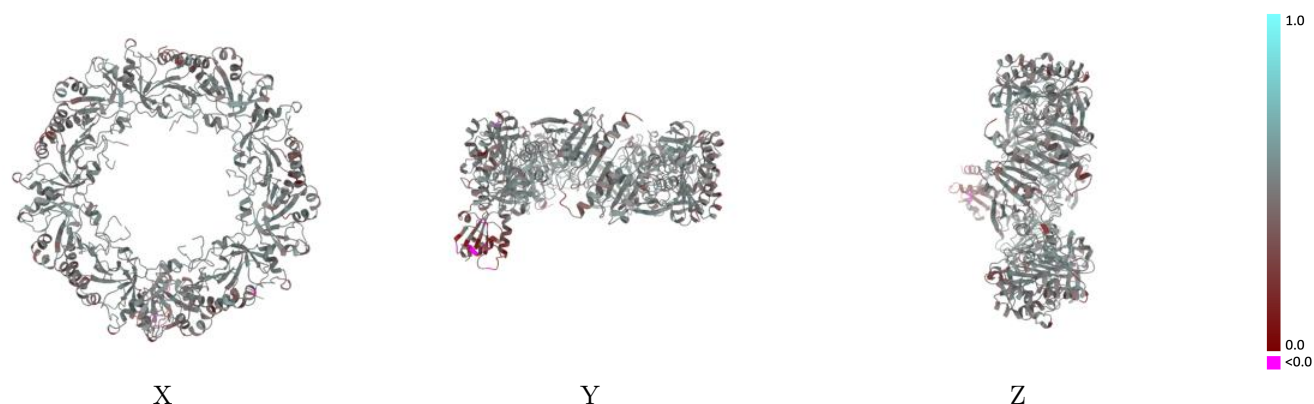
This section contains information regarding the fit between EMDB map EMD-28217 and PDB model 8EKY. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



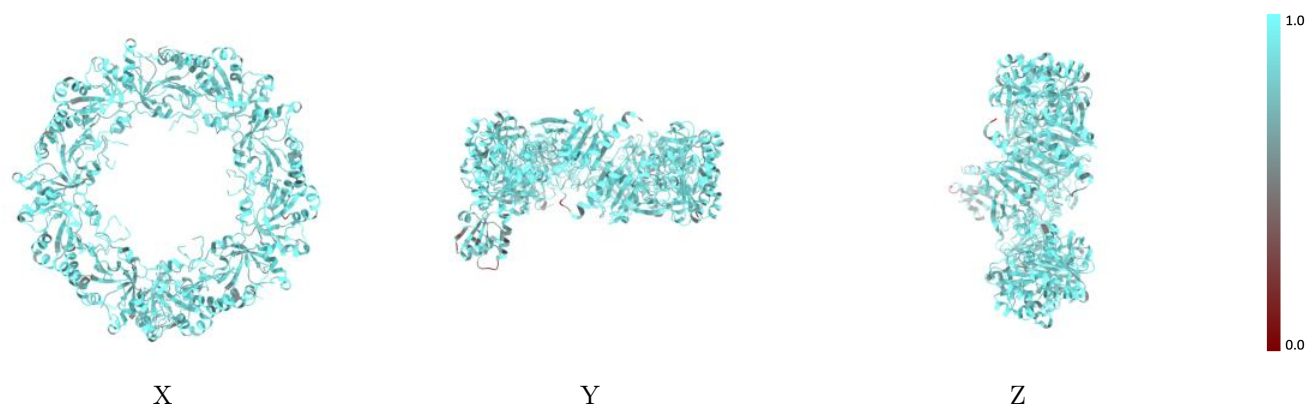
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



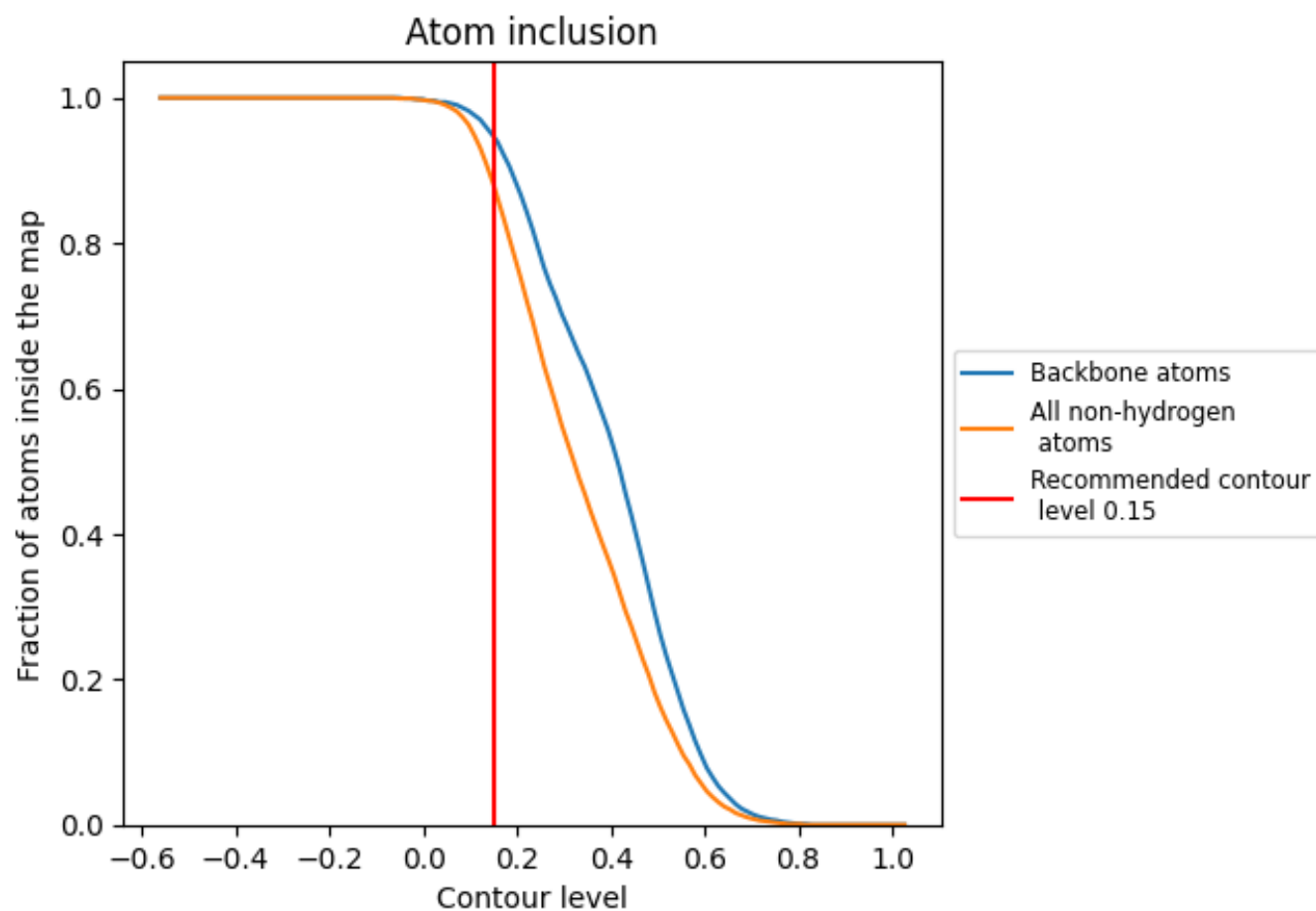
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.4760
A	0.8830	0.4890
B	0.8940	0.4860
C	0.8940	0.4870
D	0.8960	0.4870
E	0.8840	0.4940
F	0.8840	0.4840
G	0.8820	0.4810
H	0.8880	0.4850
I	0.9000	0.4810
J	0.8980	0.4890
M	0.7190	0.3070

1.0

0.0

<0.0