



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 08:10 PM UTC

PDB ID : 8WX0 / pdb_00008wx0
EMDB ID : EMD-37896
Title : PNPase of M.tuberculosis with its RNA substrate
Authors : Wang, N.; Sheng, Y.N.
Deposited on : 2023-10-27
Resolution : 3.70 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:

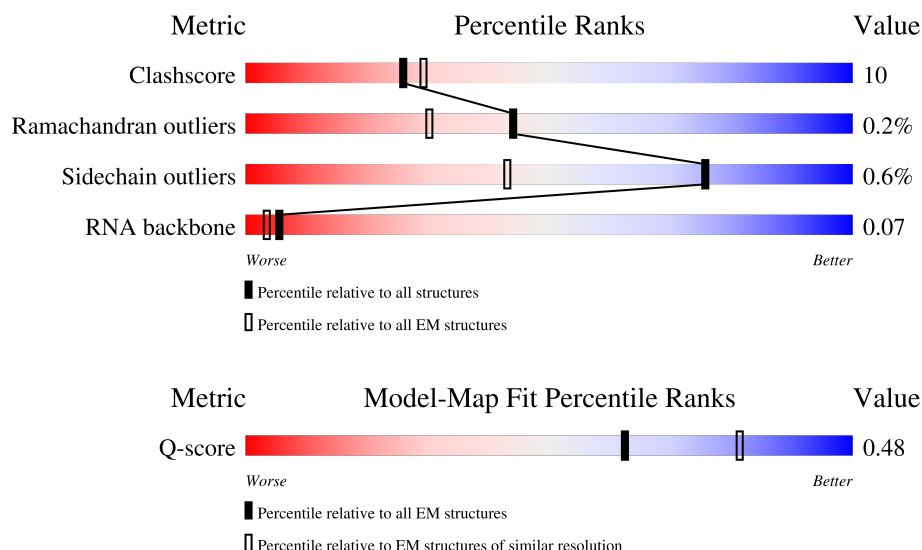
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	773	
1	B	773	
1	C	773	

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Mol	Chain	Length	Quality of chain
2	E	24	 25% 75%
3	D	24	 88%
3	F	24	 8% 88%
3	G	24	 8% 88%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13672 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 Bifunctional guanosine pentaphosphate synthetase/polyribonucleotide nucleotidyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	597	Total	C	N	O	S	0	0
			4478	2811	770	880	17		
1	B	592	Total	C	N	O	S	0	0
			4447	2792	765	874	16		
1	C	593	Total	C	N	O	S	0	0
			4452	2796	766	874	16		

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP A0A9Q6P703
A	-19	GLY	-	expression tag	UNP A0A9Q6P703
A	-18	SER	-	expression tag	UNP A0A9Q6P703
A	-17	SER	-	expression tag	UNP A0A9Q6P703
A	-16	HIS	-	expression tag	UNP A0A9Q6P703
A	-15	HIS	-	expression tag	UNP A0A9Q6P703
A	-14	HIS	-	expression tag	UNP A0A9Q6P703
A	-13	HIS	-	expression tag	UNP A0A9Q6P703
A	-12	HIS	-	expression tag	UNP A0A9Q6P703
A	-11	HIS	-	expression tag	UNP A0A9Q6P703
A	-10	SER	-	expression tag	UNP A0A9Q6P703
A	-9	SER	-	expression tag	UNP A0A9Q6P703
A	-8	GLY	-	expression tag	UNP A0A9Q6P703
A	-7	LEU	-	expression tag	UNP A0A9Q6P703
A	-6	VAL	-	expression tag	UNP A0A9Q6P703
A	-5	PRO	-	expression tag	UNP A0A9Q6P703
A	-4	ARG	-	expression tag	UNP A0A9Q6P703
A	-3	GLY	-	expression tag	UNP A0A9Q6P703
A	-2	SER	-	expression tag	UNP A0A9Q6P703
A	-1	HIS	-	expression tag	UNP A0A9Q6P703
A	0	MET	-	expression tag	UNP A0A9Q6P703
B	-20	MET	-	initiating methionine	UNP A0A9Q6P703
B	-19	GLY	-	expression tag	UNP A0A9Q6P703

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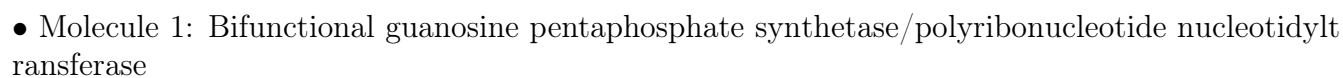
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	SER	-	expression tag	UNP A0A9Q6P703
B	-17	SER	-	expression tag	UNP A0A9Q6P703
B	-16	HIS	-	expression tag	UNP A0A9Q6P703
B	-15	HIS	-	expression tag	UNP A0A9Q6P703
B	-14	HIS	-	expression tag	UNP A0A9Q6P703
B	-13	HIS	-	expression tag	UNP A0A9Q6P703
B	-12	HIS	-	expression tag	UNP A0A9Q6P703
B	-11	HIS	-	expression tag	UNP A0A9Q6P703
B	-10	SER	-	expression tag	UNP A0A9Q6P703
B	-9	SER	-	expression tag	UNP A0A9Q6P703
B	-8	GLY	-	expression tag	UNP A0A9Q6P703
B	-7	LEU	-	expression tag	UNP A0A9Q6P703
B	-6	VAL	-	expression tag	UNP A0A9Q6P703
B	-5	PRO	-	expression tag	UNP A0A9Q6P703
B	-4	ARG	-	expression tag	UNP A0A9Q6P703
B	-3	GLY	-	expression tag	UNP A0A9Q6P703
B	-2	SER	-	expression tag	UNP A0A9Q6P703
B	-1	HIS	-	expression tag	UNP A0A9Q6P703
B	0	MET	-	expression tag	UNP A0A9Q6P703
C	-20	MET	-	initiating methionine	UNP A0A9Q6P703
C	-19	GLY	-	expression tag	UNP A0A9Q6P703
C	-18	SER	-	expression tag	UNP A0A9Q6P703
C	-17	SER	-	expression tag	UNP A0A9Q6P703
C	-16	HIS	-	expression tag	UNP A0A9Q6P703
C	-15	HIS	-	expression tag	UNP A0A9Q6P703
C	-14	HIS	-	expression tag	UNP A0A9Q6P703
C	-13	HIS	-	expression tag	UNP A0A9Q6P703
C	-12	HIS	-	expression tag	UNP A0A9Q6P703
C	-11	HIS	-	expression tag	UNP A0A9Q6P703
C	-10	SER	-	expression tag	UNP A0A9Q6P703
C	-9	SER	-	expression tag	UNP A0A9Q6P703
C	-8	GLY	-	expression tag	UNP A0A9Q6P703
C	-7	LEU	-	expression tag	UNP A0A9Q6P703
C	-6	VAL	-	expression tag	UNP A0A9Q6P703
C	-5	PRO	-	expression tag	UNP A0A9Q6P703
C	-4	ARG	-	expression tag	UNP A0A9Q6P703
C	-3	GLY	-	expression tag	UNP A0A9Q6P703
C	-2	SER	-	expression tag	UNP A0A9Q6P703
C	-1	HIS	-	expression tag	UNP A0A9Q6P703
C	0	MET	-	expression tag	UNP A0A9Q6P703

- Molecule 2 is a RNA chain called RNA (24-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	6	Total	C	N	O	P	0	0
			122	56	19	42	5		

- Molecule 3 is a RNA chain called RNA (24-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	3	Total	C	N	O	P	0	0
			57	27	6	22	2		
3	G	3	Total	C	N	O	P	0	0
			57	27	6	22	2		
3	D	3	Total	C	N	O	P	0	0
			59	27	6	24	2		



K333	K334	L335	V336	R337	D343	H344	F345	R346	T347	D348	G349	R350	G351	L352	T353	D354	R355	E361	H369	L373	R376	Q380	T386	M392	L399	G400	P401	R406	Y411	R423	S426	F427	K428	E439	V443	P447	F452	P453	Y454	R457				
M203	M204	V205	E206	A207	E211	N212	P224	T225	D226	A246	Q247	Q248	E249	L250	A251	D252	A253	K256	S257	G258	K259	P260	D263	F264	D269	D273	S279	S280	V281	A282	T283	E297	R298	D299	O300	R301	I302	L313	A314	E321	K322	E323	L328	L331
I85	S88	R91	R105	I107	D108	R109	P110	L111	R112	P113	S114	D117	I123	V127	D139	A142	I143	A148	S149	T150	L155	I161	R165	V166	A167	L168	I169	W173	V179	A185	D188	M189	A192	G193	R194	I195	V196	E197	G198	D199				
MET	GLY	SER	SER	HIS	HIS	HIS	HIS	SER	SER	GLY	VAL	PRO	ARG	GLY	HIS	MET	MET	SER	ALA	ALA	GLU	I6	D7	V10	F11	E12	A15	D18	T24	R28	F29	E30	Y45	L46	N50	S54	A55	T56	K63	E64	F69	V75	E76	E77

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	348409	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.22	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.246	Depositor
Minimum map value	-2.437	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.145	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	211.2, 211.2, 211.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	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	0.13	0/4549	0.31	0/6177
1	B	0.14	0/4518	0.32	0/6135
1	C	0.15	0/4523	0.32	0/6143
2	E	0.11	0/135	0.21	0/208
3	D	0.52	0/62	0.86	0/94
3	F	0.08	0/62	0.21	0/94
3	G	0.05	0/62	0.11	0/94
All	All	0.14	0/13911	0.32	0/18945

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	4478	0	4480	83	0
1	B	4447	0	4444	102	0
1	C	4452	0	4454	97	0
2	E	122	0	65	1	0
3	D	59	0	32	2	0
3	F	57	0	32	0	0
3	G	57	0	32	1	0
All	All	13672	0	13539	278	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 278 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:A:326:ALA:HA	1:A:329:ARG:HE	1.32	0.94
1:C:525:LEU:H	1:C:528:GLU:HB2	1.42	0.81
1:A:209:ALA:HB1	1:A:213:VAL:HG21	1.64	0.80
1:A:506:VAL:O	1:A:512:GLY:HA2	1.82	0.79
1:C:46:LEU:HD23	1:C:50:ASN:HD22	1.51	0.76

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	595/773 (77%)	566 (95%)	28 (5%)	1 (0%)	43	72
1	B	590/773 (76%)	562 (95%)	27 (5%)	1 (0%)	43	72
1	C	591/773 (76%)	565 (96%)	25 (4%)	1 (0%)	43	72
All	All	1776/2319 (77%)	1693 (95%)	80 (4%)	3 (0%)	44	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	ILE
1	B	510	VAL
1	C	511	ASP

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	471/611 (77%)	466 (99%)	5 (1%)	65	73
1	B	468/611 (77%)	466 (100%)	2 (0%)	84	81
1	C	469/611 (77%)	468 (100%)	1 (0%)	87	86
All	All	1408/1833 (77%)	1400 (99%)	8 (1%)	76	79

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	77	GLU
1	B	189	MET
1	A	466	ASN
1	A	341	LEU
1	B	10	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	409	HIS
1	C	247	GLN
1	C	549	GLN
1	A	344	HIS
1	A	247	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	5/24 (20%)	5 (100%)	0
3	D	2/24 (8%)	1 (50%)	0
3	F	2/24 (8%)	1 (50%)	0
3	G	2/24 (8%)	1 (50%)	0
All	All	11/96 (11%)	8 (72%)	0

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	2	U
2	E	3	U
2	E	4	A
2	E	5	G
2	E	6	U

There are no RNA pucker outliers to report.

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.

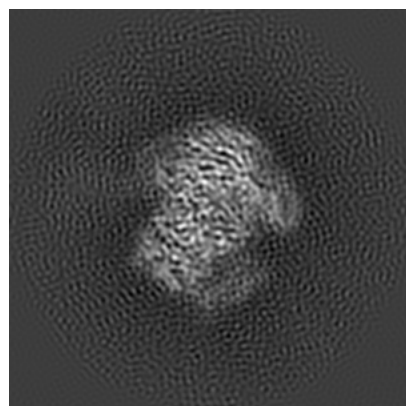
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37896. These allow visual inspection of the internal detail of the map and identification of artifacts.

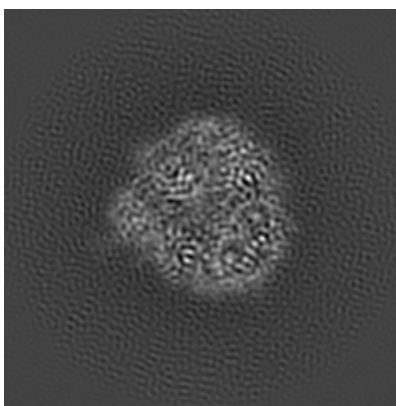
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

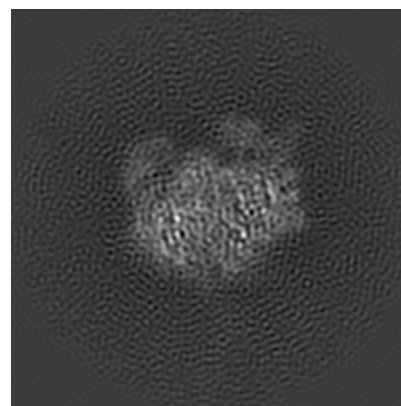
6.1.1 Primary map



X

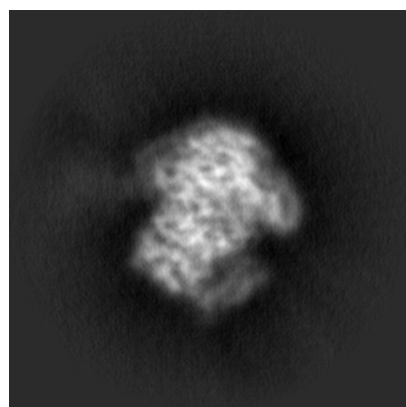


Y

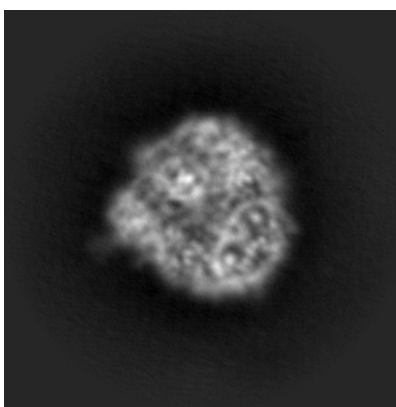


Z

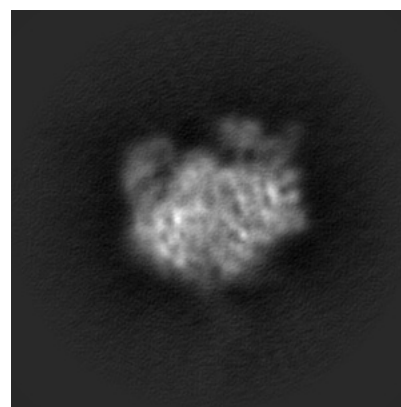
6.1.2 Raw map



X



Y

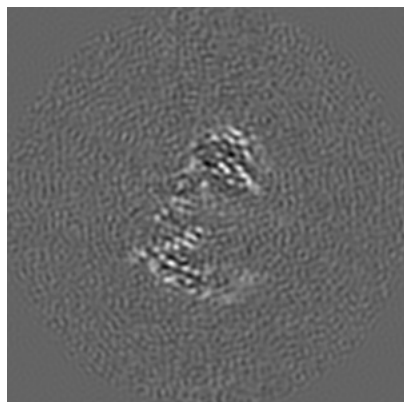


Z

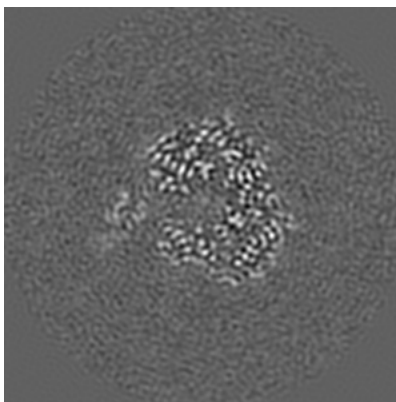
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

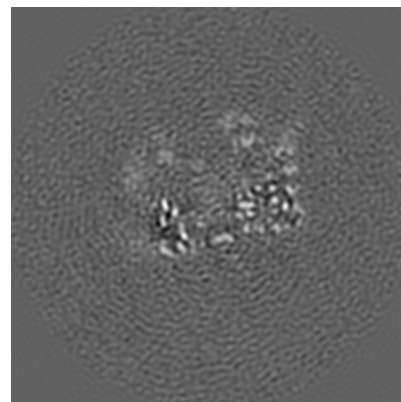
6.2.1 Primary map



X Index: 120

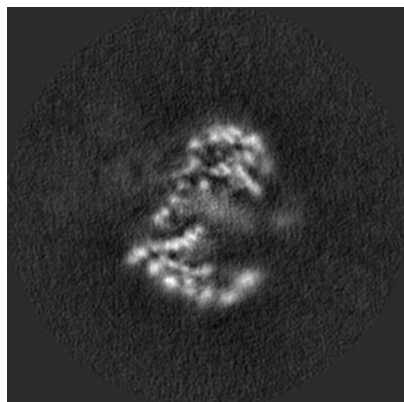


Y Index: 120

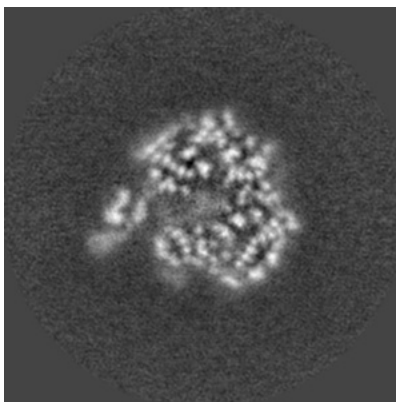


Z Index: 120

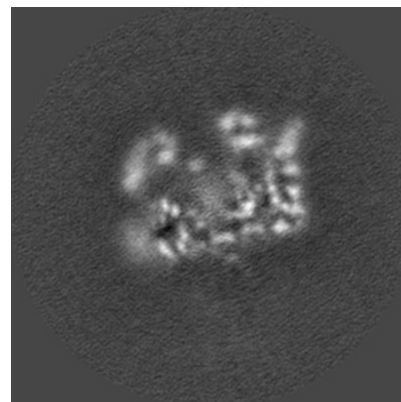
6.2.2 Raw map



X Index: 120



Y Index: 120

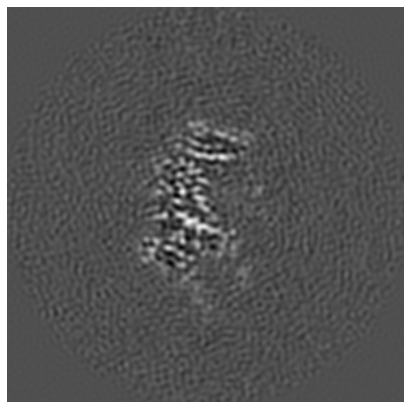


Z Index: 120

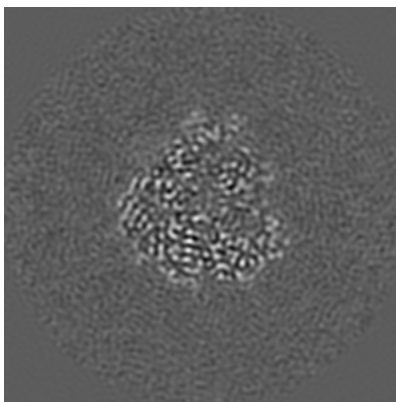
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

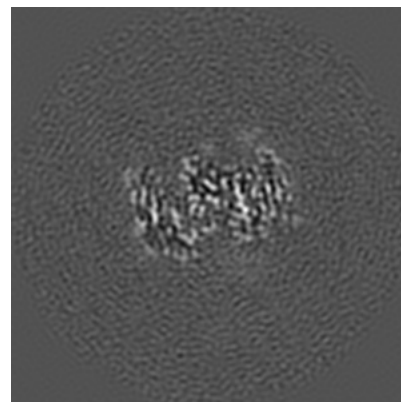
6.3.1 Primary map



X Index: 99

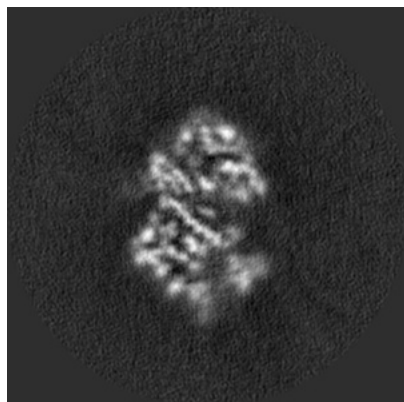


Y Index: 109

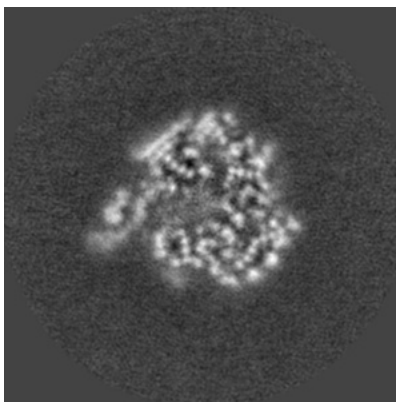


Z Index: 141

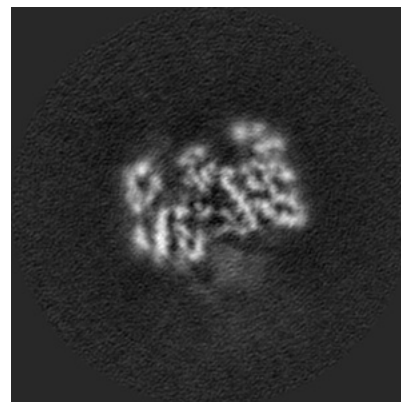
6.3.2 Raw map



X Index: 104



Y Index: 118

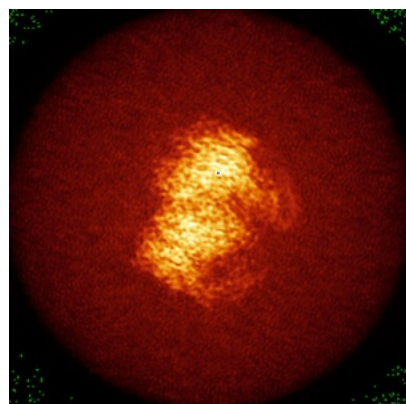


Z Index: 136

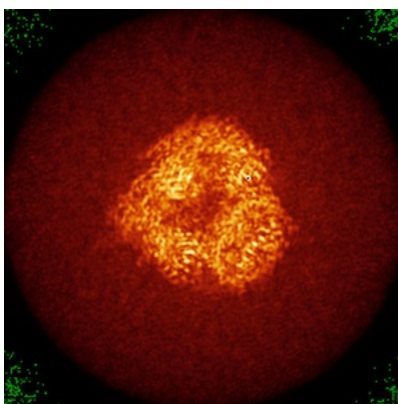
The images above show the largest variance slices of the map in three orthogonal directions.

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

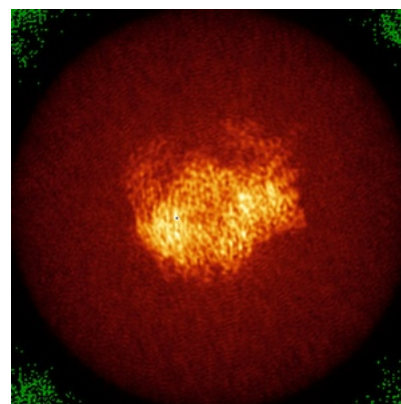
6.4.1 Primary map



X

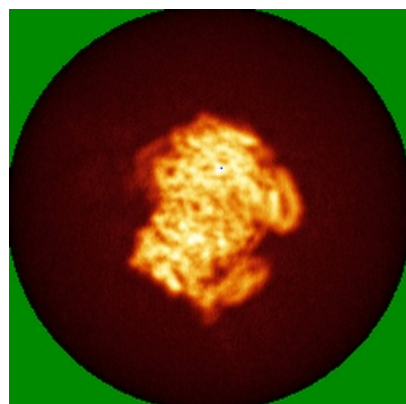


Y

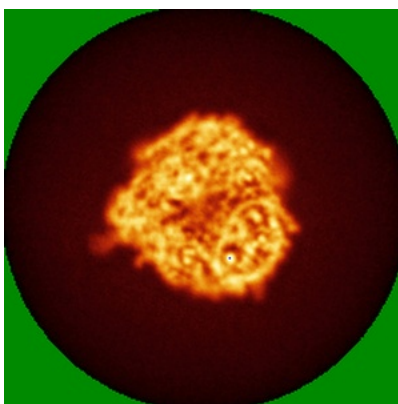


Z

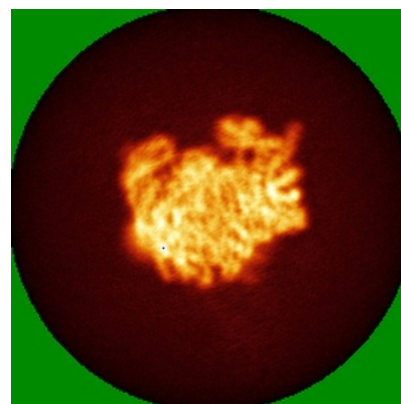
6.4.2 Raw map



X



Y

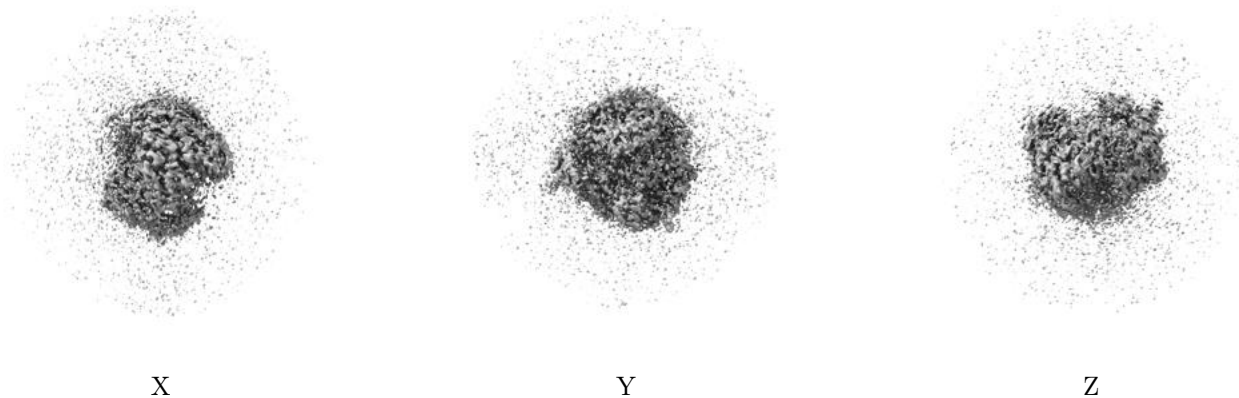


Z

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.

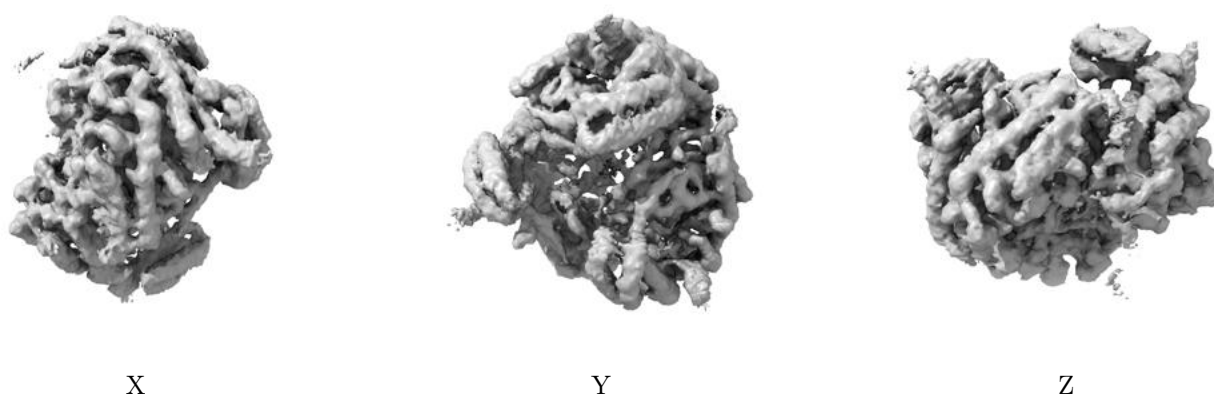
6.5 Orthogonal surface views [i](#)

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.

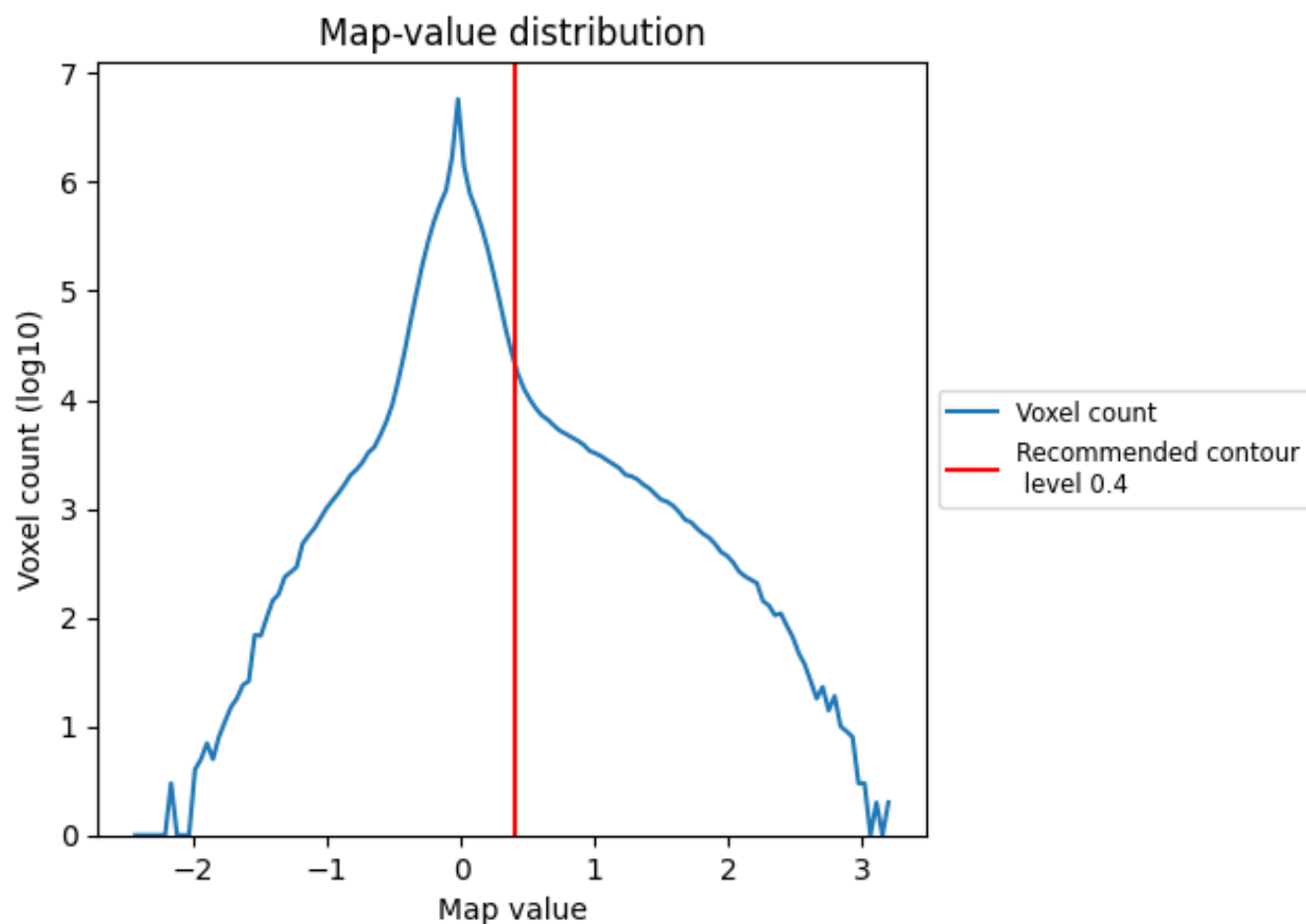
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

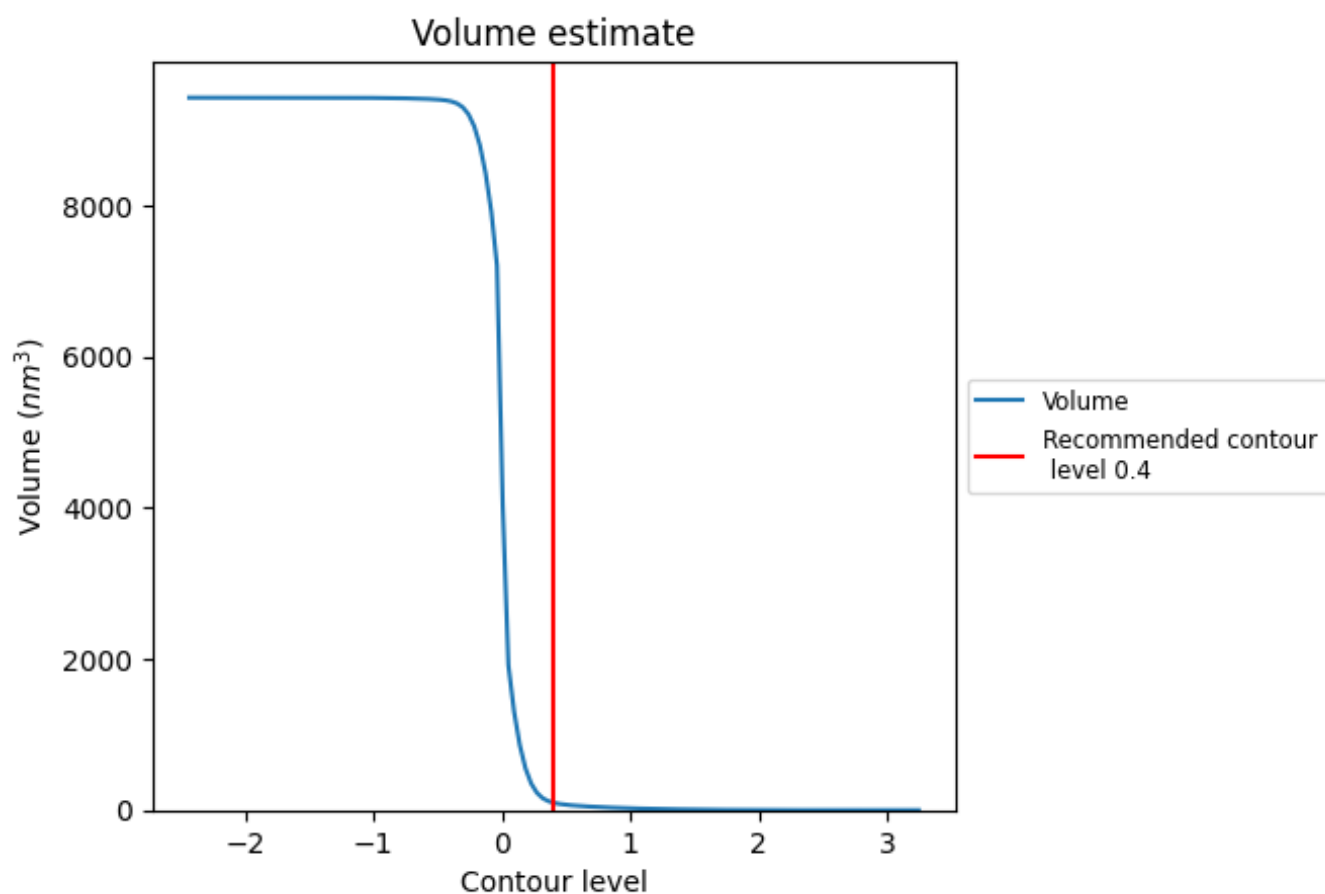
This section contains the results of statistical analysis of the map.

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.

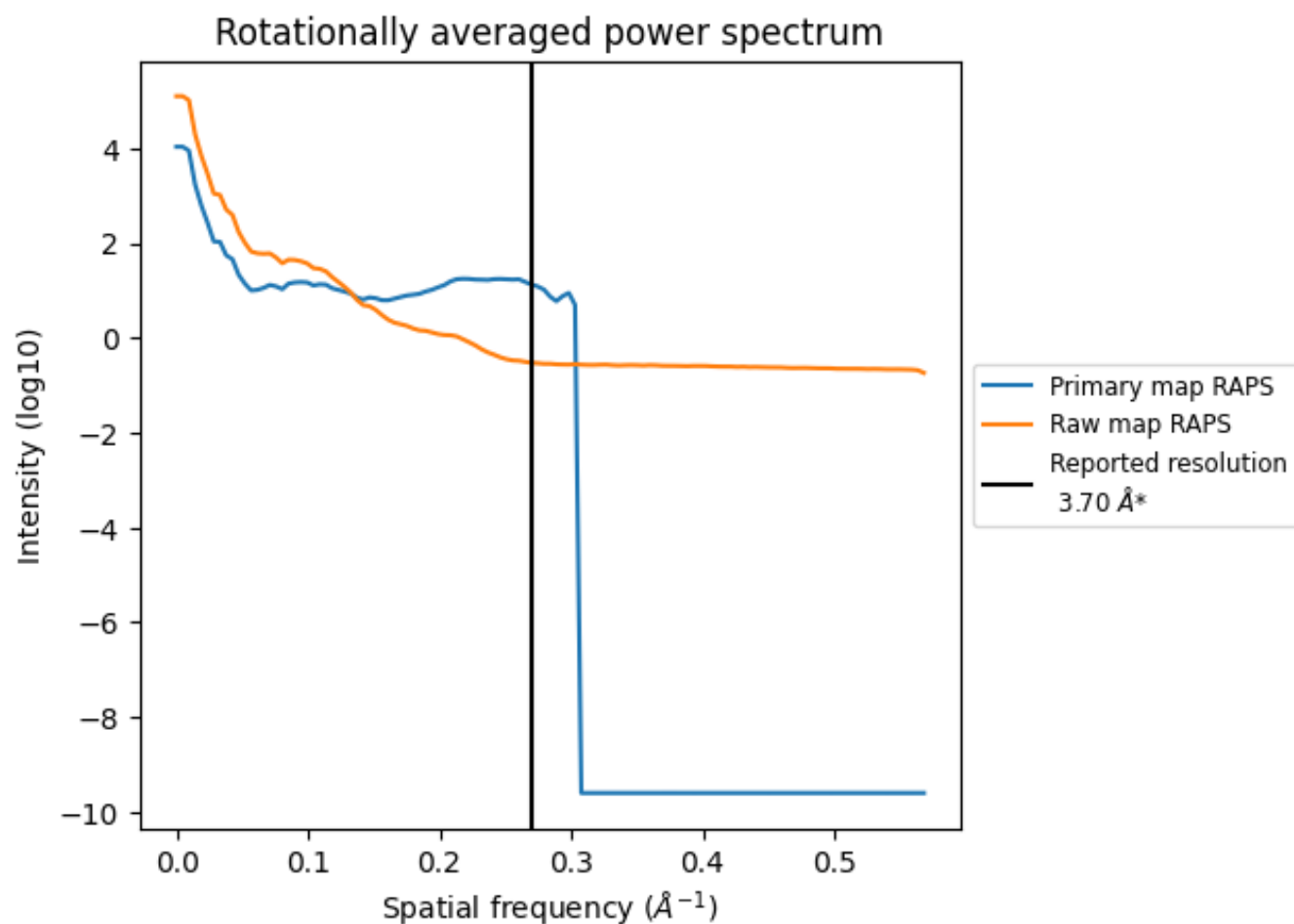
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 99 nm³; this corresponds to an approximate mass of 89 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 ⓘ

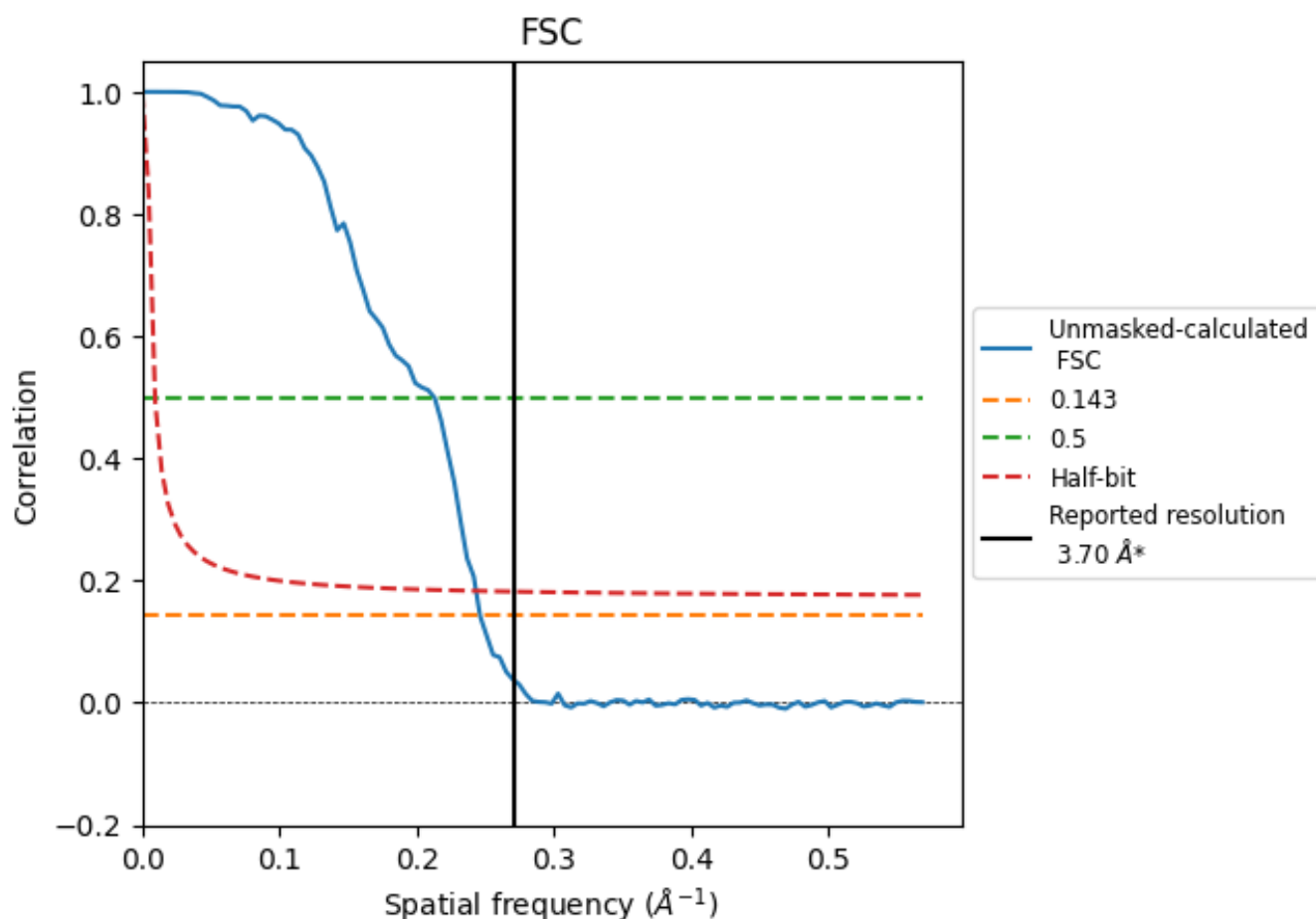


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

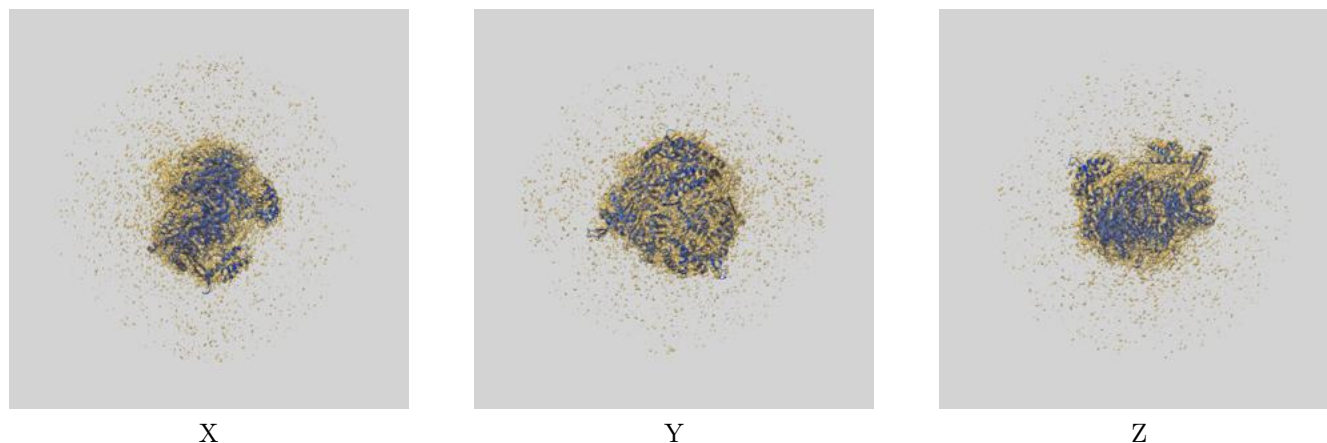
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.06	4.70	4.11

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

9 Map-model fit [i](#)

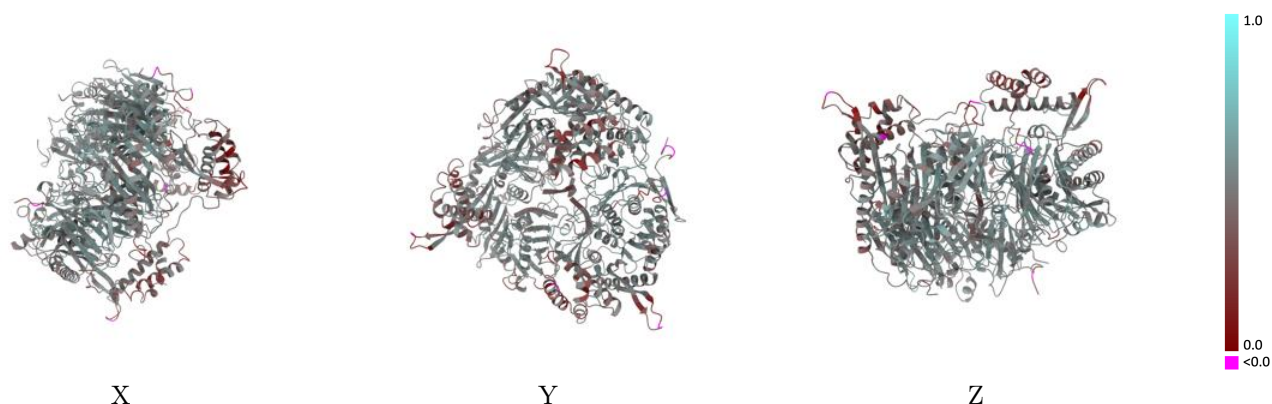
This section contains information regarding the fit between EMDB map EMD-37896 and PDB model 8WX0. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



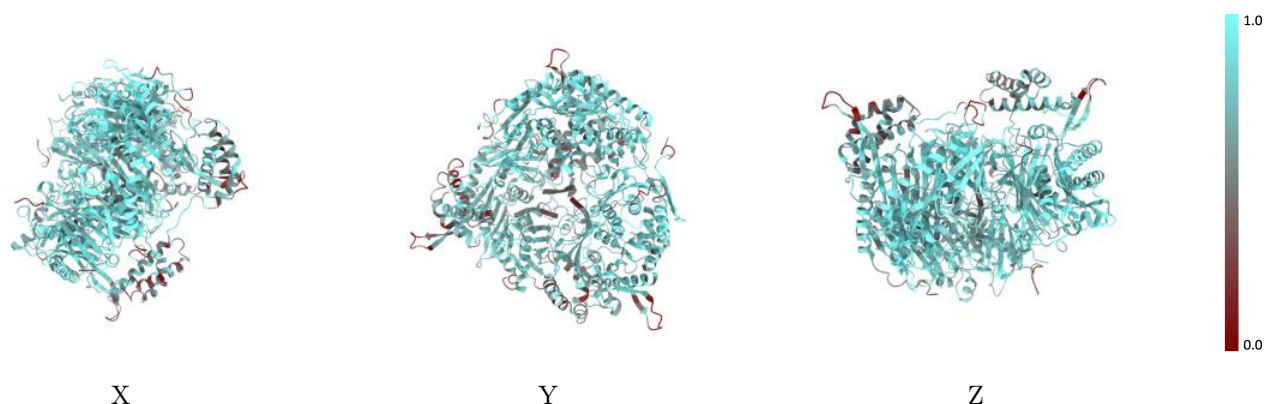
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



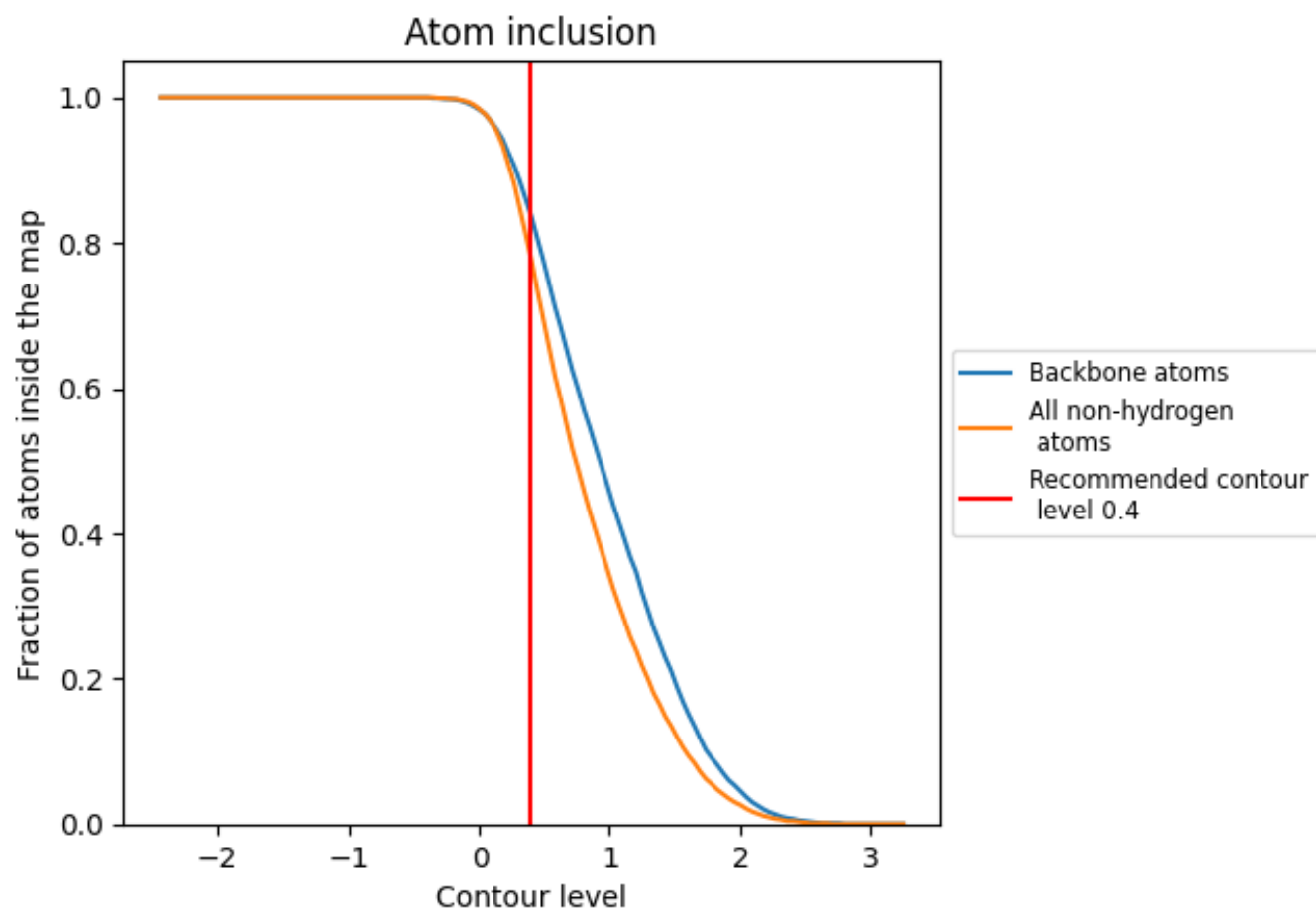
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% of all backbone atoms, 78% 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	0.7780	0.4800
A	0.7820	0.4790
B	0.7730	0.4800
C	0.7970	0.4850
D	0.4580	0.3990
E	0.5080	0.3870
F	0.4390	0.4250
G	0.7370	0.4880

1.0

0.0

<0.0