



wwPDB EM Validation Summary Report ⓘ

Sep 15, 2025 – 06:09 PM EDT

PDB ID : 9Q3I / pdb_00009q3i
EMDB ID : EMD-72194
Title : Cryo-EM Structure of the Class II Cyclase Domain in the Bifunctional Copalyl Diphosphate Synthase from *Penicillium verruculosum*
Authors : Gaynes, M.N.; Christianson, D.W.
Deposited on : 2025-08-18
Resolution : 2.90 Å(reported)
Based on initial model : .

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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

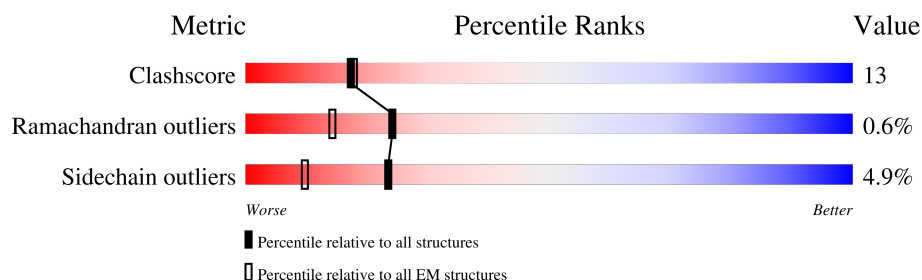
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	987	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3635 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 Copalyl diphosphate synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	494	Total	C	N	O	S	0	0
			3635	2343	602	676	14		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP A0A348FUE1
A	-22	GLY	-	expression tag	UNP A0A348FUE1
A	-21	SER	-	expression tag	UNP A0A348FUE1
A	-20	SER	-	expression tag	UNP A0A348FUE1
A	-19	HIS	-	expression tag	UNP A0A348FUE1
A	-18	HIS	-	expression tag	UNP A0A348FUE1
A	-17	HIS	-	expression tag	UNP A0A348FUE1
A	-16	HIS	-	expression tag	UNP A0A348FUE1
A	-15	HIS	-	expression tag	UNP A0A348FUE1
A	-14	HIS	-	expression tag	UNP A0A348FUE1
A	-13	SER	-	expression tag	UNP A0A348FUE1
A	-12	SER	-	expression tag	UNP A0A348FUE1
A	-11	GLY	-	expression tag	UNP A0A348FUE1
A	-10	GLU	-	expression tag	UNP A0A348FUE1
A	-9	ASN	-	expression tag	UNP A0A348FUE1
A	-8	LEU	-	expression tag	UNP A0A348FUE1
A	-7	TYR	-	expression tag	UNP A0A348FUE1
A	-6	PHE	-	expression tag	UNP A0A348FUE1
A	-5	GLN	-	expression tag	UNP A0A348FUE1
A	-4	GLY	-	expression tag	UNP A0A348FUE1
A	-3	HIS	-	expression tag	UNP A0A348FUE1
A	-2	MET	-	expression tag	UNP A0A348FUE1
A	-1	ALA	-	expression tag	UNP A0A348FUE1
A	0	SER	-	expression tag	UNP A0A348FUE1

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	381049	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 ($e^-/\text{\AA}^2$)	33	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	192.6, 192.6, 192.6	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0/3711	0.29	0/5062

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	3635	0	3365	94	0
All	All	3635	0	3365	94	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 13.

The worst 5 of 94 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:409:MET:HG3	1:A:474:LEU:HB3	1.63	0.81
1:A:86:SER:HB2	1:A:145:LEU:HD13	1.73	0.70
1:A:185:LYS:HG3	1:A:189:LEU:HD12	1.79	0.65
1:A:311:ASP:N	1:A:311:ASP:OD1	2.31	0.63
1:A:460:TRP:HD1	1:A:469:THR:HG23	1.64	0.62

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	474/987 (48%)	452 (95%)	19 (4%)	3 (1%)	22 52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	ILE
1	A	75	TYR
1	A	520	LYS

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	347/857 (40%)	330 (95%)	17 (5%)	21 53

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	474	LEU
1	A	520	LYS
1	A	266	TRP
1	A	278	LEU
1	A	311	ASP

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	A	327	GLN
1	A	358	ASN
1	A	401	ASN
1	A	292	HIS
1	A	98	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.

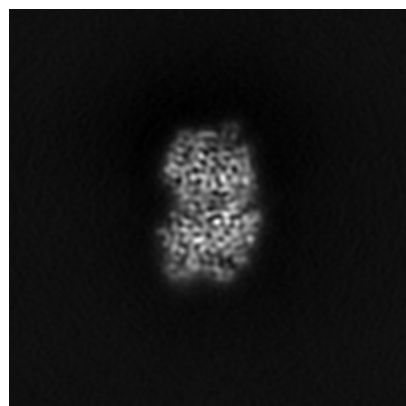
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72194. These allow visual inspection of the internal detail of the map and identification of artifacts.

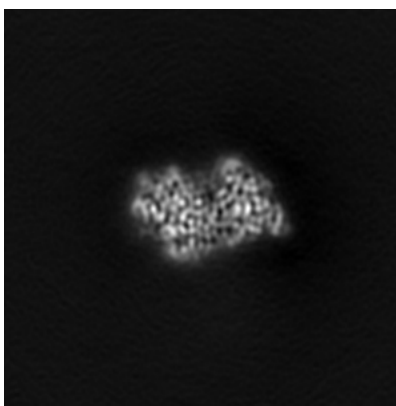
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

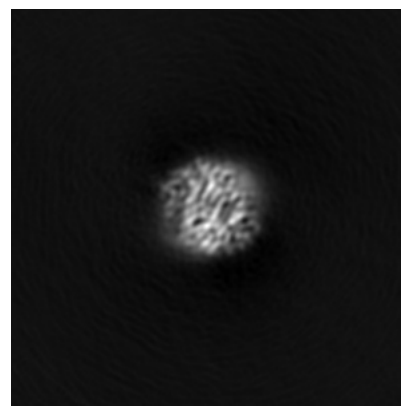
6.1.1 Primary map



X

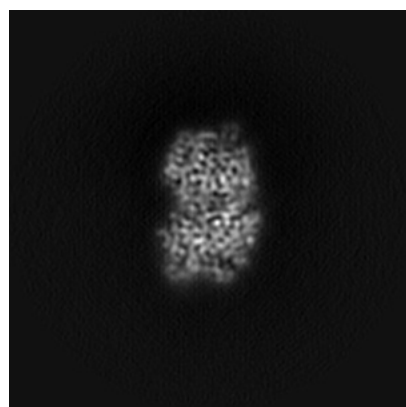


Y

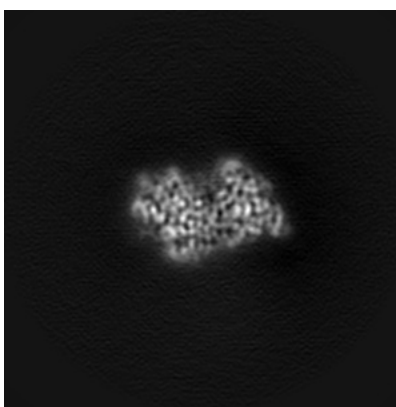


Z

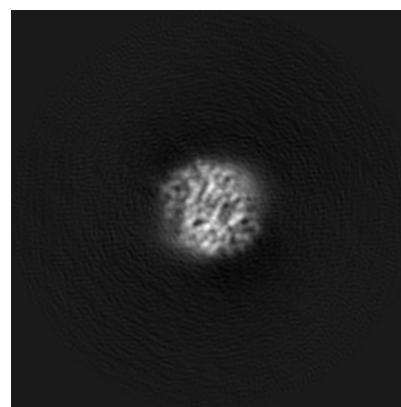
6.1.2 Raw map



X



Y

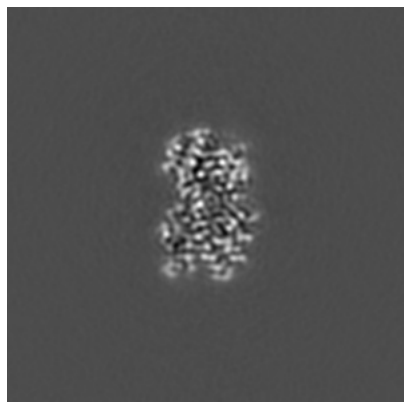


Z

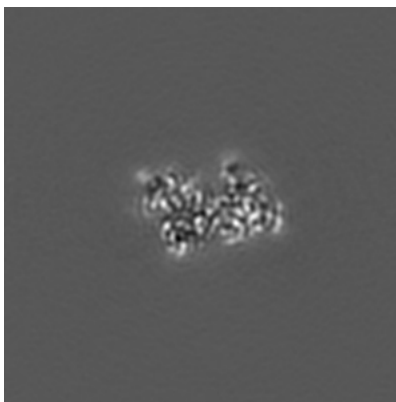
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

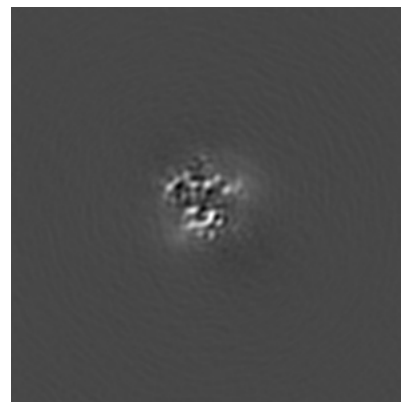
6.2.1 Primary map



X Index: 90

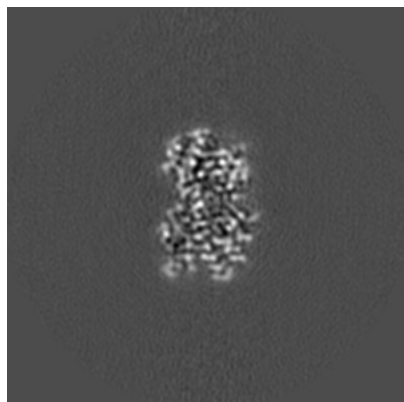


Y Index: 90

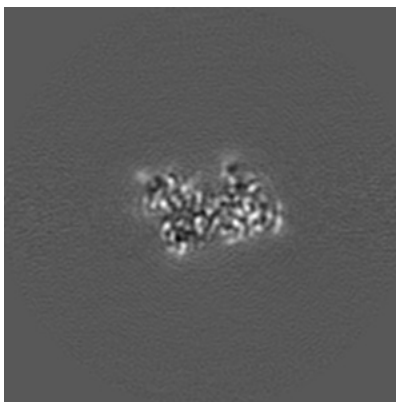


Z Index: 90

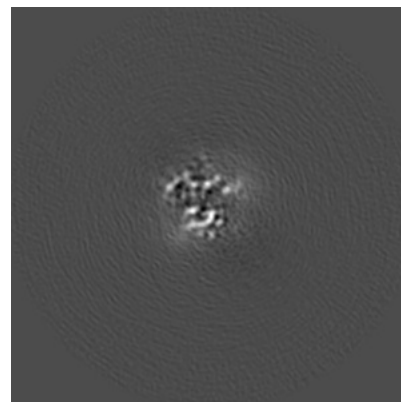
6.2.2 Raw map



X Index: 90



Y Index: 90

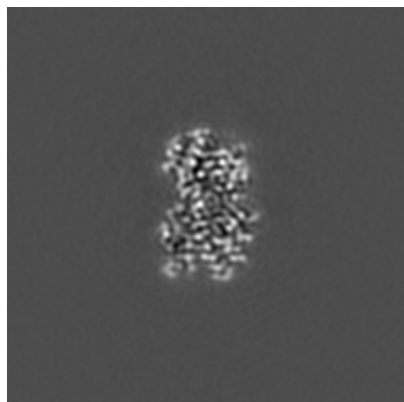


Z Index: 90

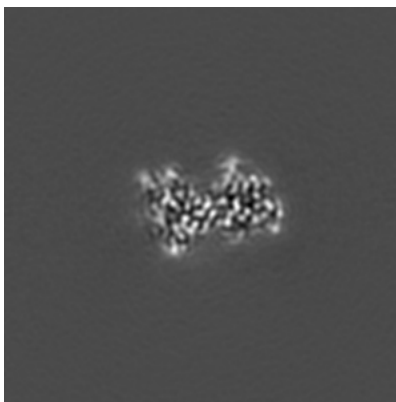
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

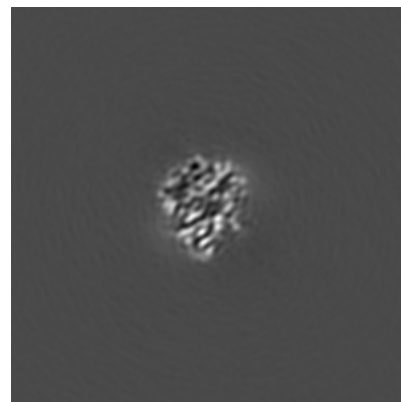
6.3.1 Primary map



X Index: 90

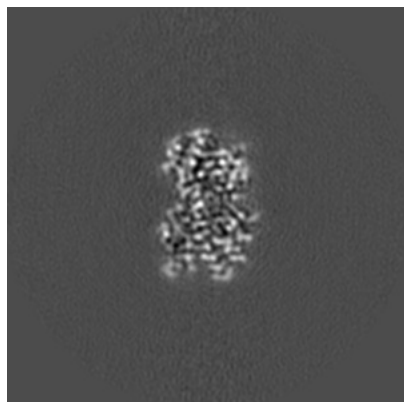


Y Index: 87

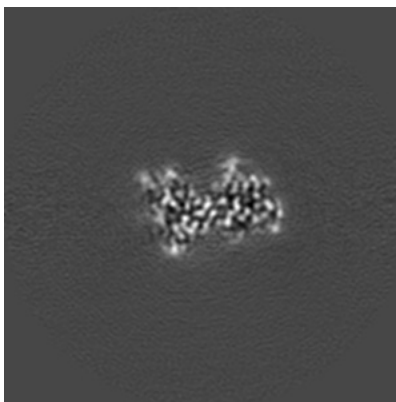


Z Index: 80

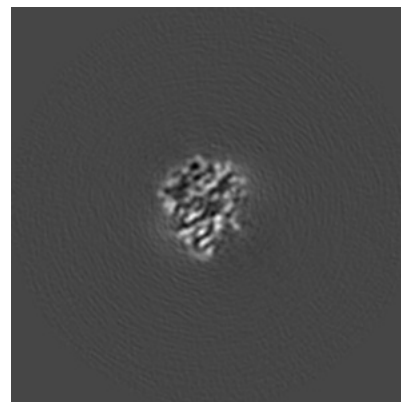
6.3.2 Raw map



X Index: 90



Y Index: 87

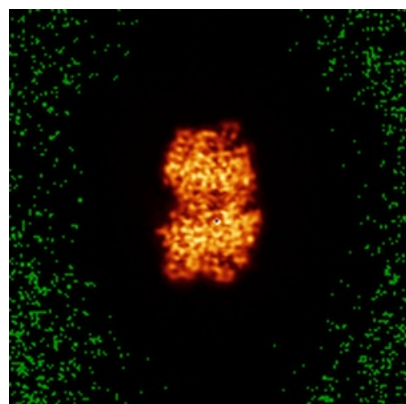


Z Index: 80

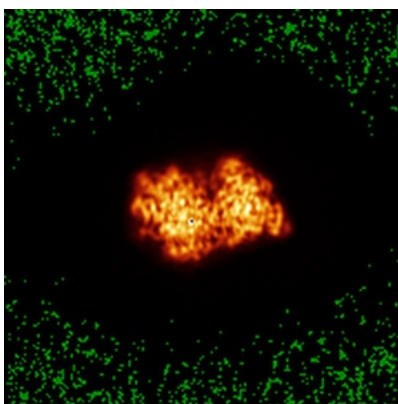
The images above show the largest variance slices of the map in three orthogonal directions.

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

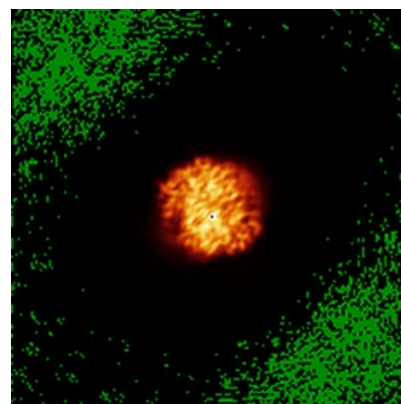
6.4.1 Primary map



X

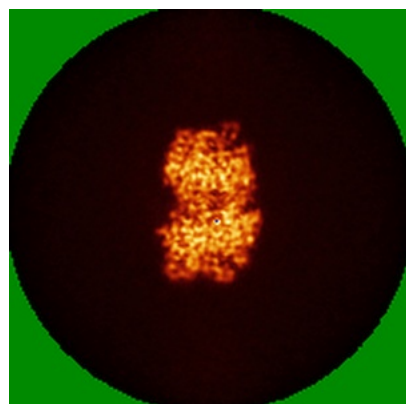


Y

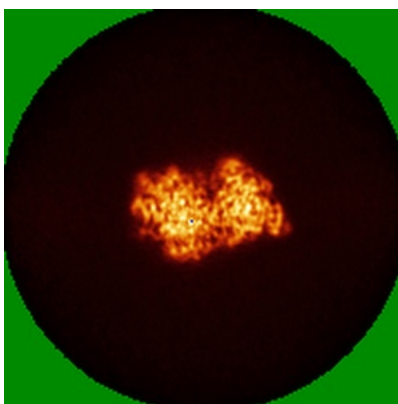


Z

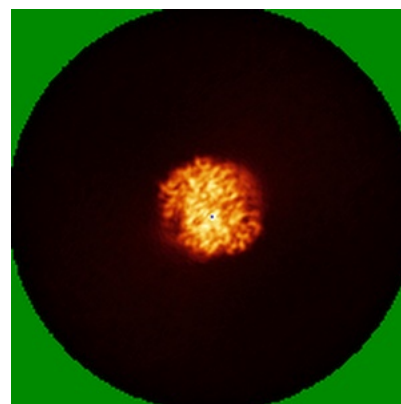
6.4.2 Raw map



X



Y

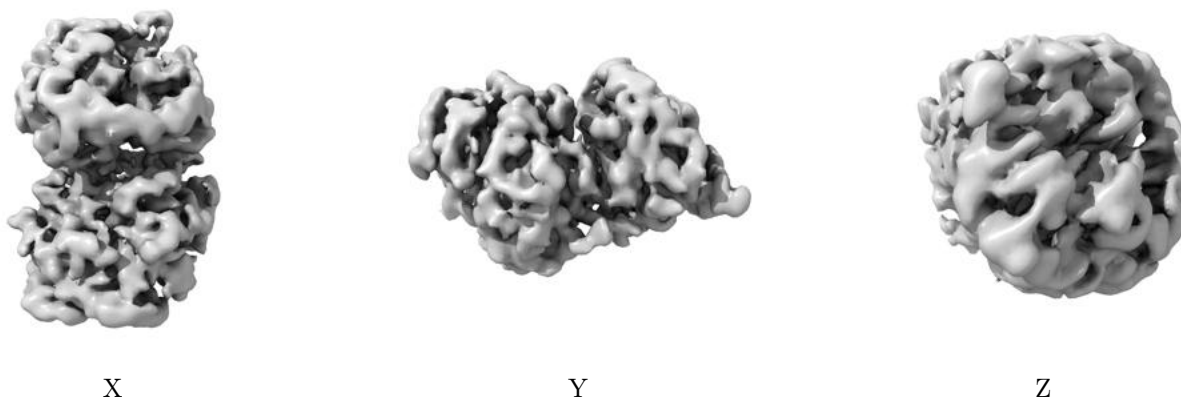


Z

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.

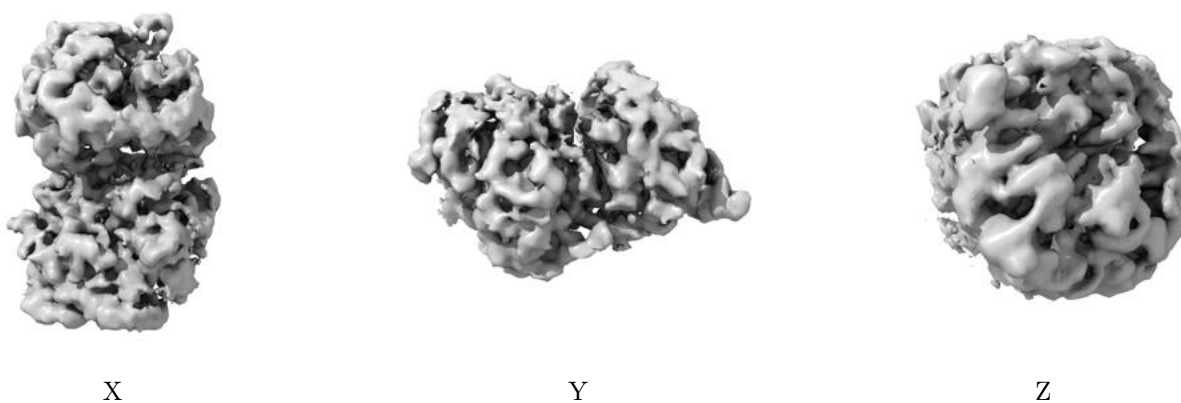
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

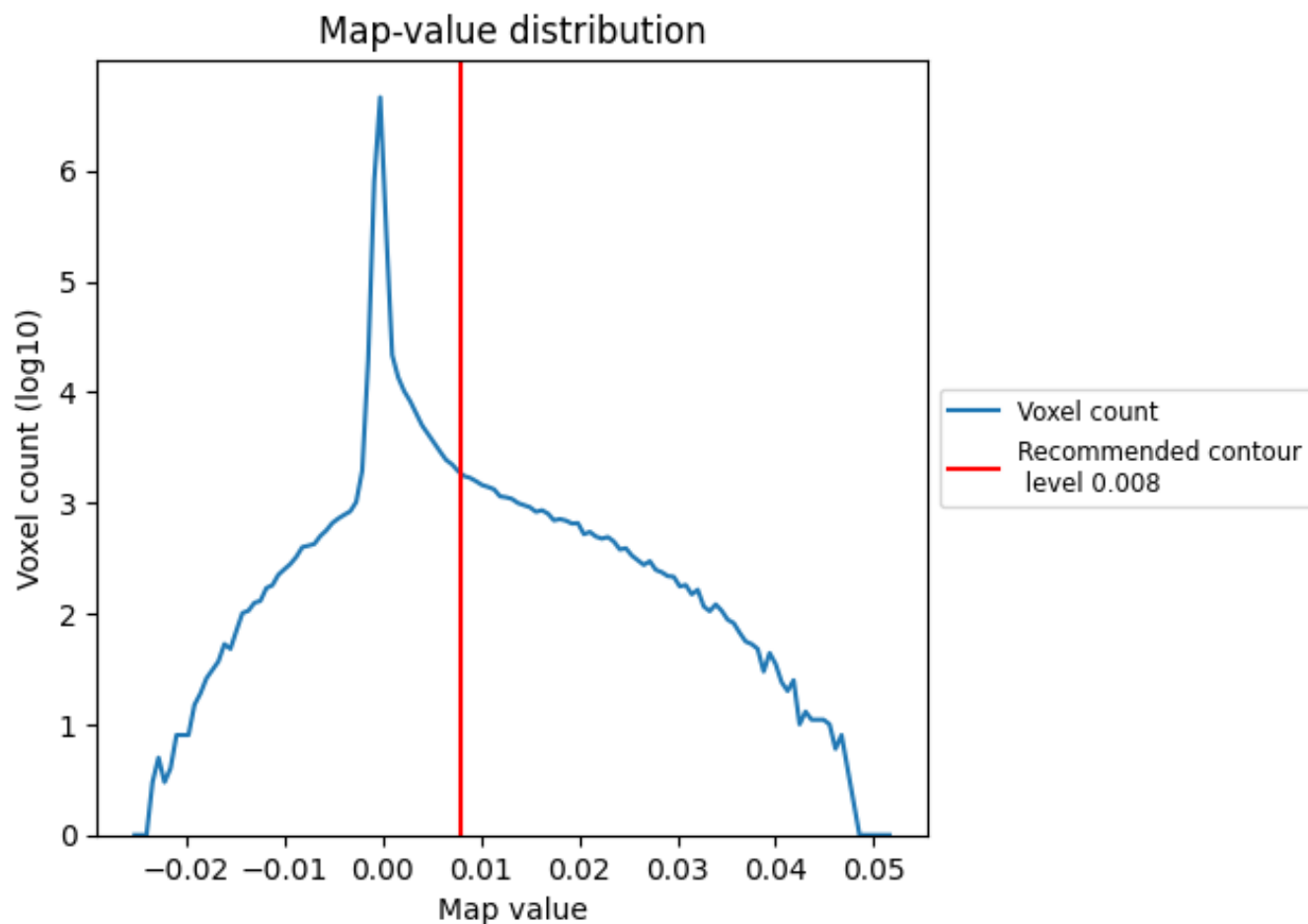
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

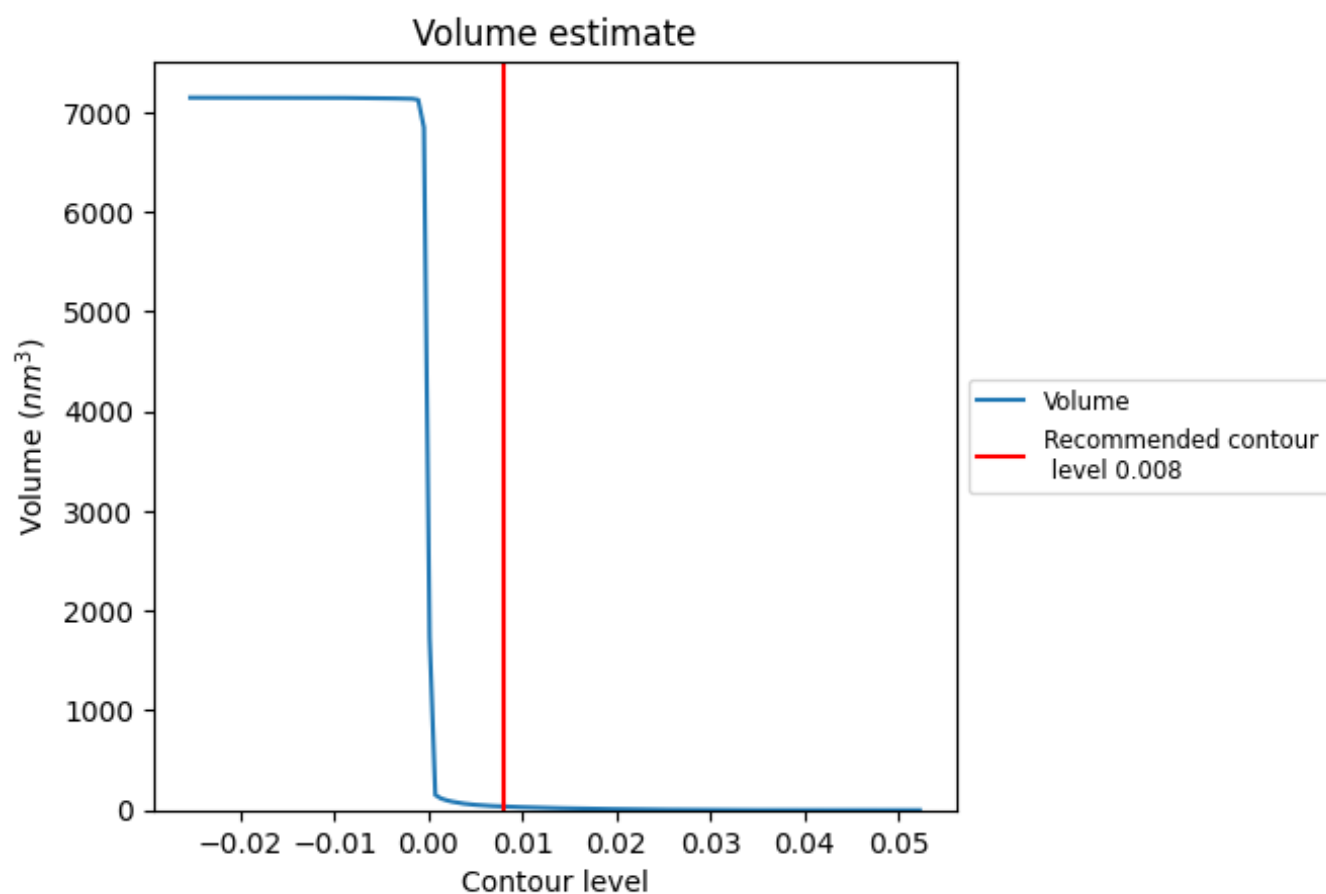
This section contains the results of statistical analysis of the map.

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.

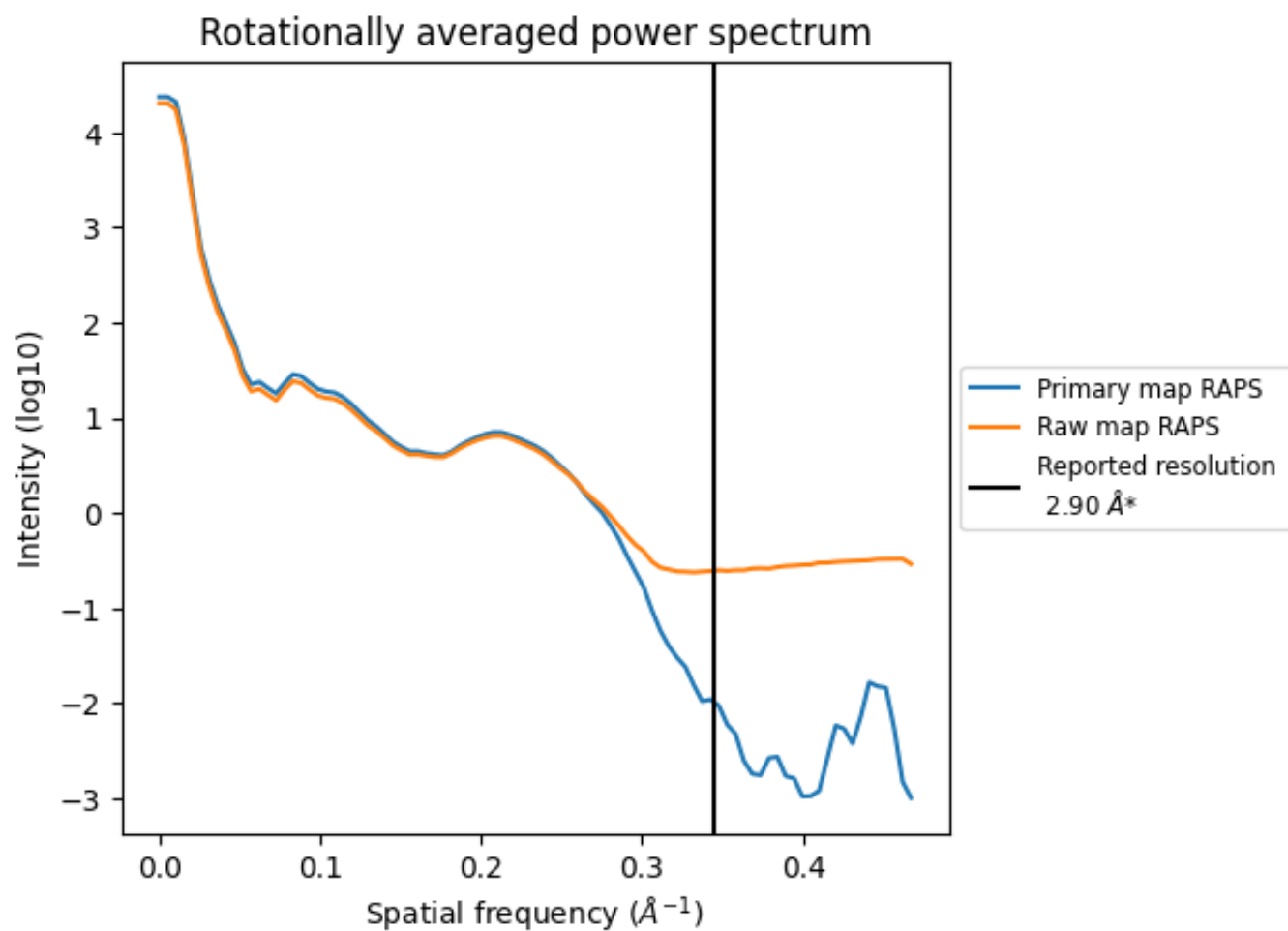
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 36 nm³; this corresponds to an approximate mass of 33 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 ⓘ

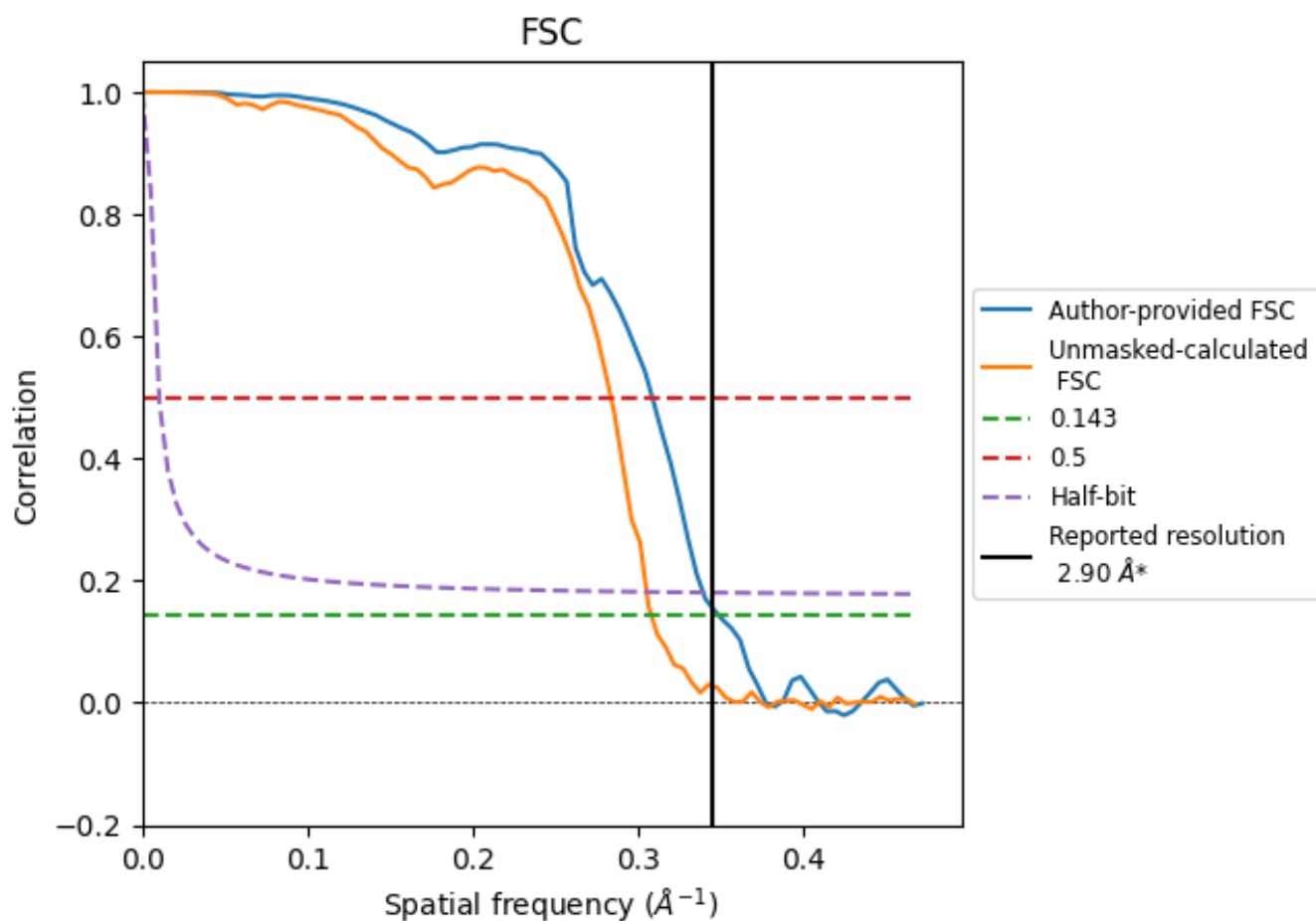


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 \AA^{-1}

8.2 Resolution estimates [i](#)

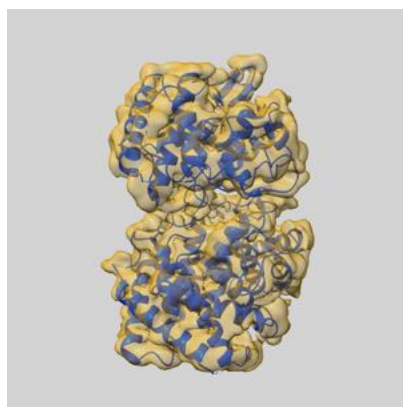
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.87	3.24	2.95
Unmasked-calculated*	3.25	3.53	3.28

*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 3.25 differs from the reported value 2.9 by more than 10 %

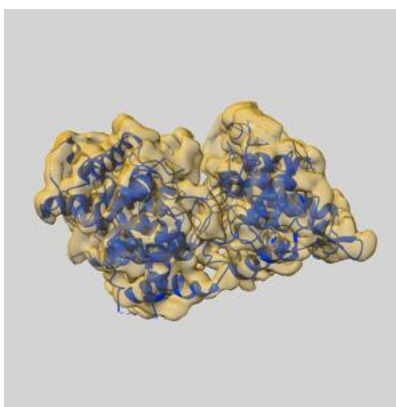
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72194 and PDB model 9Q3I. Per-residue inclusion information can be found in section 3 on page 4.

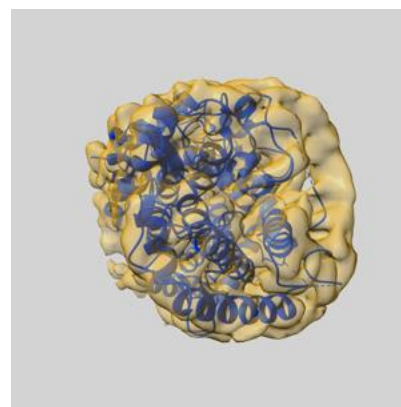
9.1 Map-model overlay [i](#)



X



Y



Z

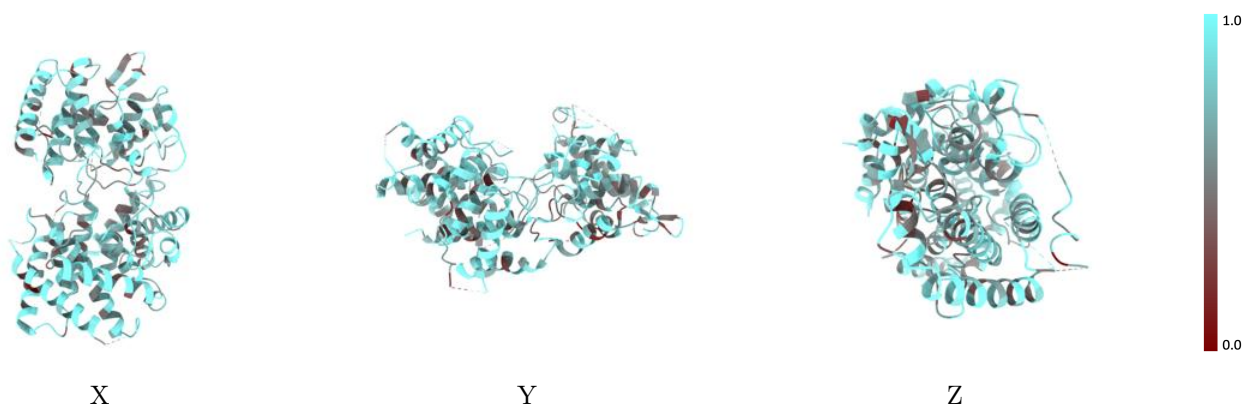
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



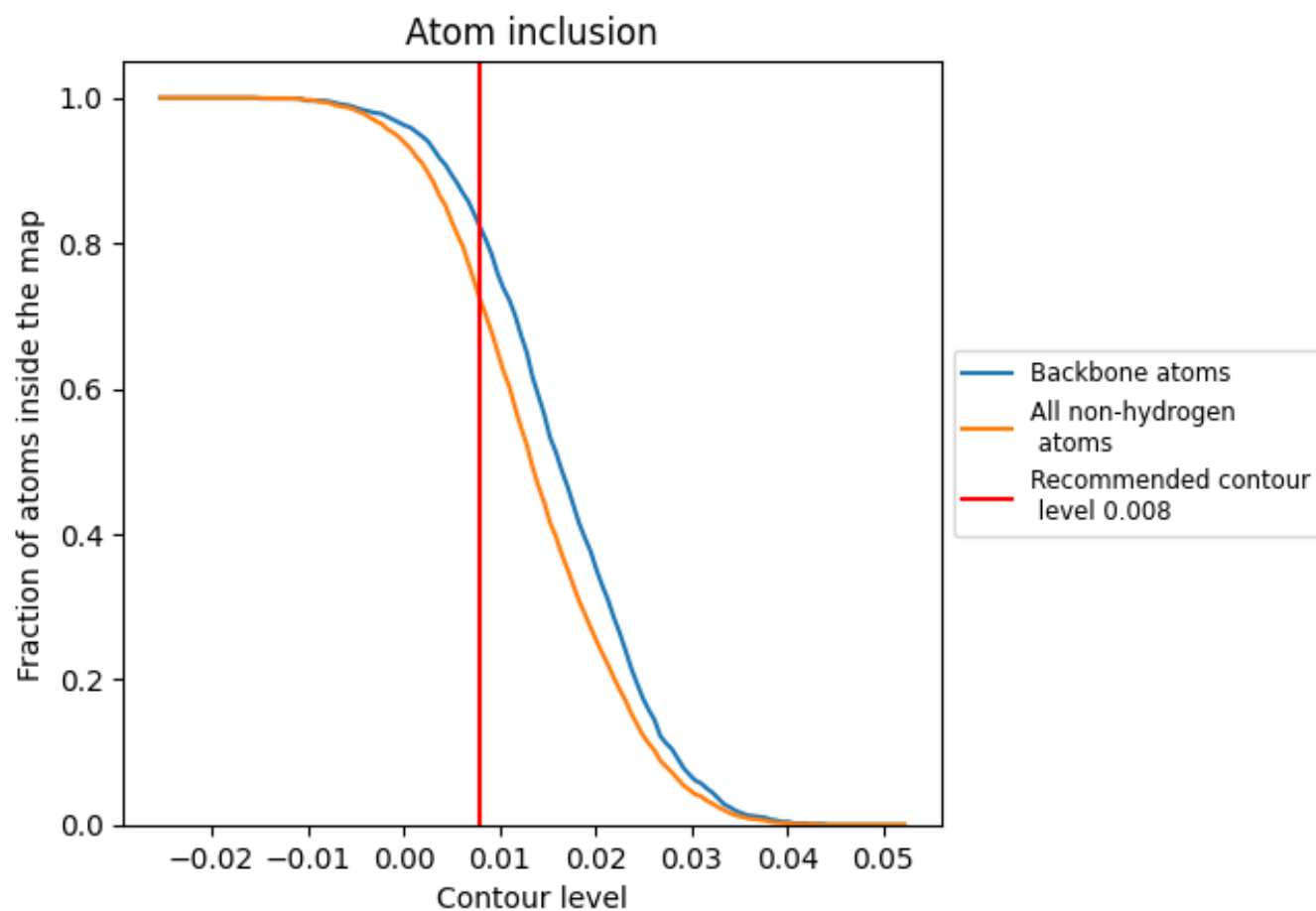
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 72% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7220	<div></div> 0.2210
A	<div></div> 0.7220	<div></div> 0.2210

