



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:53 AM UTC

PDB ID : 7AMY / pdb_00007amy
EMDB ID : EMD-11827
Title : Nonameric cytoplasmic domain of FlhA from *Vibrio parahaemolyticus*
Authors : Kuhlen, L.; Johnson, S.; Lea, S.
Deposited on : 2020-10-09
Resolution : 3.75 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

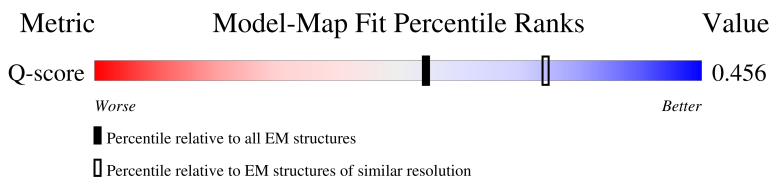
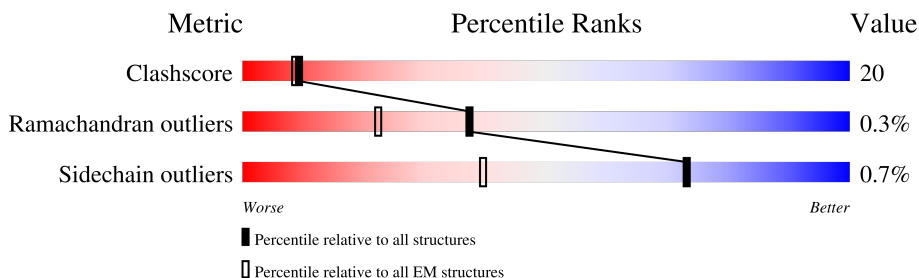
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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	10301 (3.25 - 4.25)

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	702	24% 30% 20% 50%
1	B	702	23% 30% 21% 50%
1	C	702	23% 30% 20% 50%
1	D	702	23% 30% 20% 50%

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Mol	Chain	Length	Quality of chain
1	E	702	23% 29% 21% 50%
1	F	702	23% 30% 20% 50%
1	G	702	23% 30% 20% 50%
1	H	702	23% 30% 20% 50%
1	I	702	23% 30% 21% 50%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 24849 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 Flagellar biosynthesis protein FlhA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	B	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	C	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	D	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	E	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	F	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	G	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	H	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		
1	I	353	Total	C	N	O	S	0	0
			2761	1750	480	523	8		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	696	GLU	-	expression tag	UNP A0A0F5SXE4
A	697	ASN	-	expression tag	UNP A0A0F5SXE4
A	698	LEU	-	expression tag	UNP A0A0F5SXE4
A	699	TYR	-	expression tag	UNP A0A0F5SXE4
A	700	PHE	-	expression tag	UNP A0A0F5SXE4
A	701	GLN	-	expression tag	UNP A0A0F5SXE4
B	696	GLU	-	expression tag	UNP A0A0F5SXE4
B	697	ASN	-	expression tag	UNP A0A0F5SXE4
B	698	LEU	-	expression tag	UNP A0A0F5SXE4
B	699	TYR	-	expression tag	UNP A0A0F5SXE4
B	700	PHE	-	expression tag	UNP A0A0F5SXE4
B	701	GLN	-	expression tag	UNP A0A0F5SXE4

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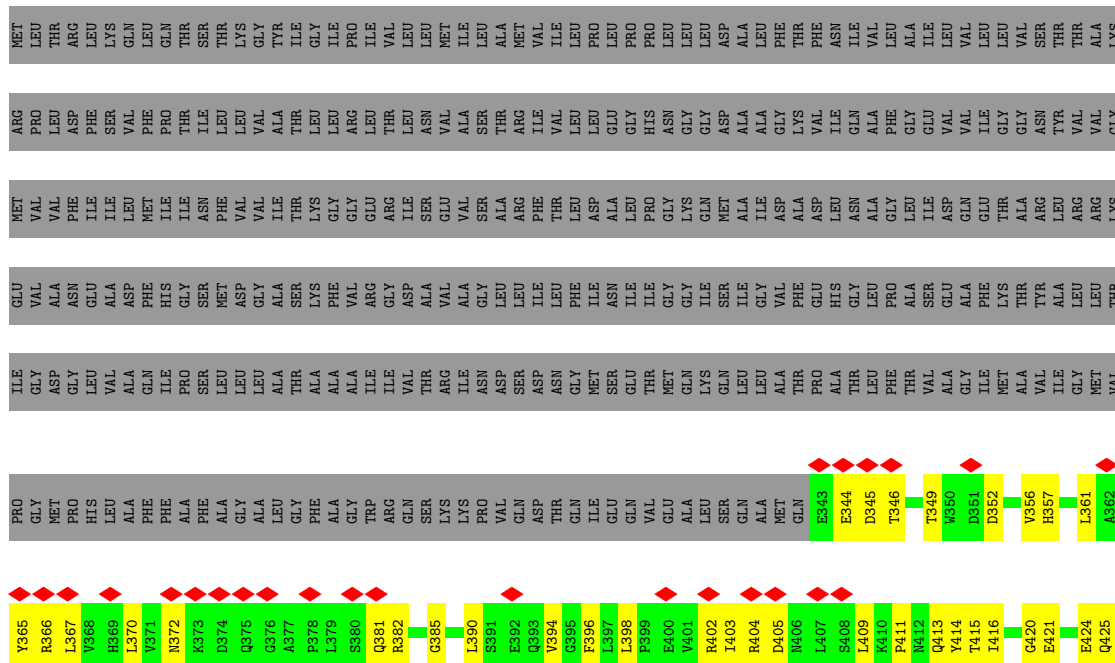
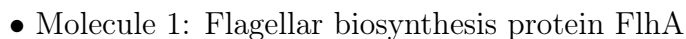
Chain	Residue	Modelled	Actual	Comment	Reference
C	696	GLU	-	expression tag	UNP A0A0F5SXE4
C	697	ASN	-	expression tag	UNP A0A0F5SXE4
C	698	LEU	-	expression tag	UNP A0A0F5SXE4
C	699	TYR	-	expression tag	UNP A0A0F5SXE4
C	700	PHE	-	expression tag	UNP A0A0F5SXE4
C	701	GLN	-	expression tag	UNP A0A0F5SXE4
D	696	GLU	-	expression tag	UNP A0A0F5SXE4
D	697	ASN	-	expression tag	UNP A0A0F5SXE4
D	698	LEU	-	expression tag	UNP A0A0F5SXE4
D	699	TYR	-	expression tag	UNP A0A0F5SXE4
D	700	PHE	-	expression tag	UNP A0A0F5SXE4
D	701	GLN	-	expression tag	UNP A0A0F5SXE4
E	696	GLU	-	expression tag	UNP A0A0F5SXE4
E	697	ASN	-	expression tag	UNP A0A0F5SXE4
E	698	LEU	-	expression tag	UNP A0A0F5SXE4
E	699	TYR	-	expression tag	UNP A0A0F5SXE4
E	700	PHE	-	expression tag	UNP A0A0F5SXE4
E	701	GLN	-	expression tag	UNP A0A0F5SXE4
F	696	GLU	-	expression tag	UNP A0A0F5SXE4
F	697	ASN	-	expression tag	UNP A0A0F5SXE4
F	698	LEU	-	expression tag	UNP A0A0F5SXE4
F	699	TYR	-	expression tag	UNP A0A0F5SXE4
F	700	PHE	-	expression tag	UNP A0A0F5SXE4
F	701	GLN	-	expression tag	UNP A0A0F5SXE4
G	696	GLU	-	expression tag	UNP A0A0F5SXE4
G	697	ASN	-	expression tag	UNP A0A0F5SXE4
G	698	LEU	-	expression tag	UNP A0A0F5SXE4
G	699	TYR	-	expression tag	UNP A0A0F5SXE4
G	700	PHE	-	expression tag	UNP A0A0F5SXE4
G	701	GLN	-	expression tag	UNP A0A0F5SXE4
H	696	GLU	-	expression tag	UNP A0A0F5SXE4
H	697	ASN	-	expression tag	UNP A0A0F5SXE4
H	698	LEU	-	expression tag	UNP A0A0F5SXE4
H	699	TYR	-	expression tag	UNP A0A0F5SXE4
H	700	PHE	-	expression tag	UNP A0A0F5SXE4
H	701	GLN	-	expression tag	UNP A0A0F5SXE4
I	696	GLU	-	expression tag	UNP A0A0F5SXE4
I	697	ASN	-	expression tag	UNP A0A0F5SXE4
I	698	LEU	-	expression tag	UNP A0A0F5SXE4
I	699	TYR	-	expression tag	UNP A0A0F5SXE4
I	700	PHE	-	expression tag	UNP A0A0F5SXE4
I	701	GLN	-	expression tag	UNP A0A0F5SXE4

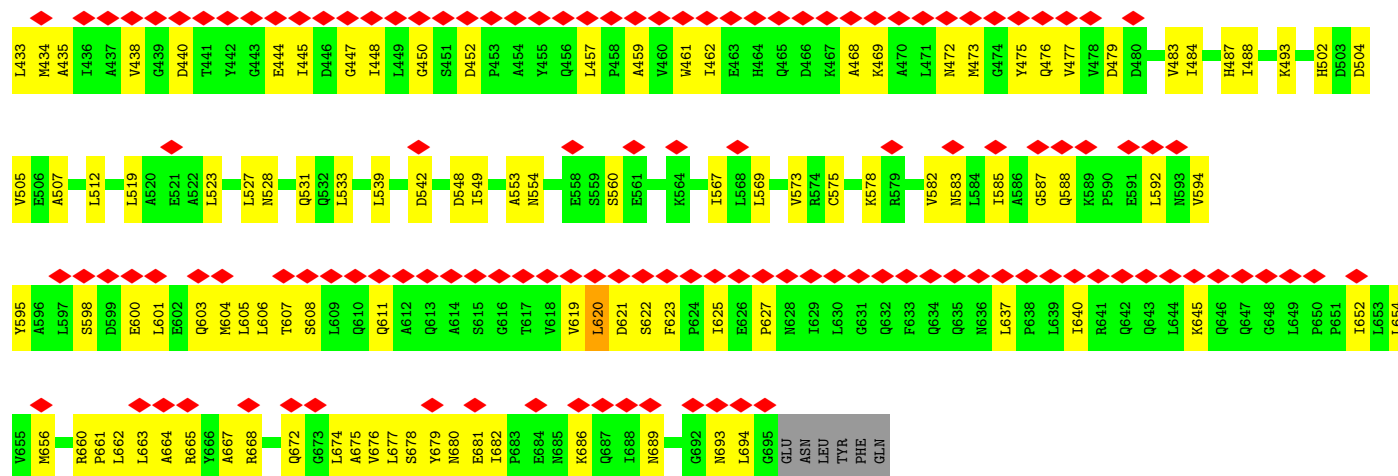
Chain B:

[illegible][illegible]

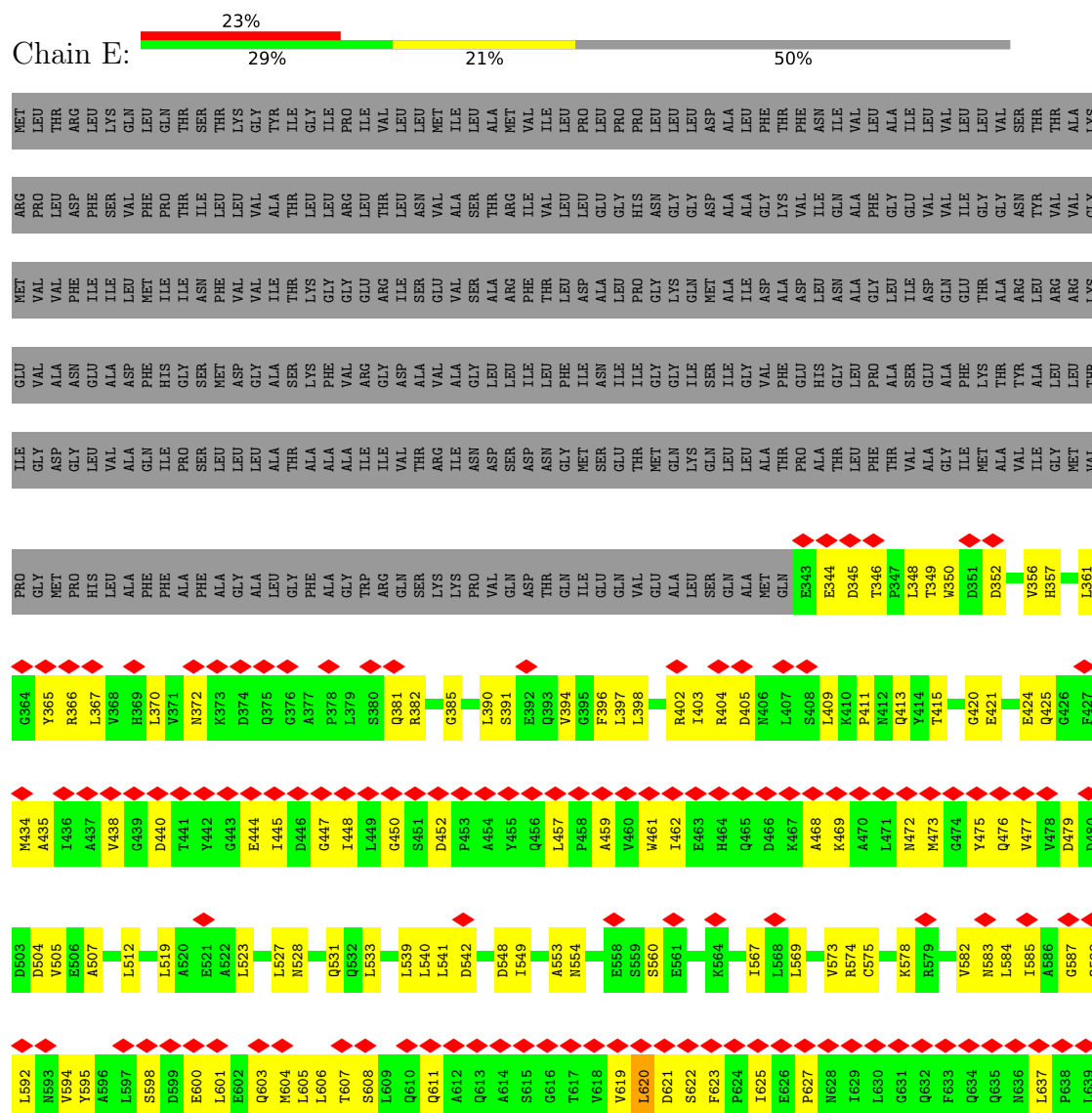
Chain C:

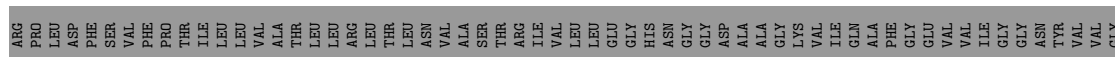
[illegible]

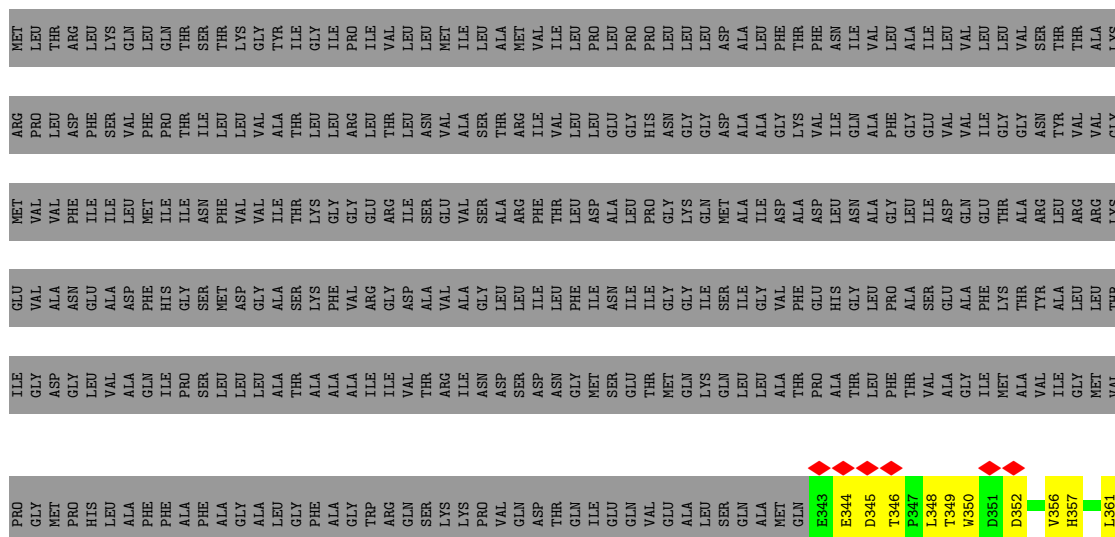
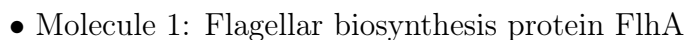


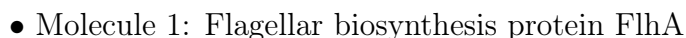


• Molecule 1: Flagellar biosynthesis protein FlhA

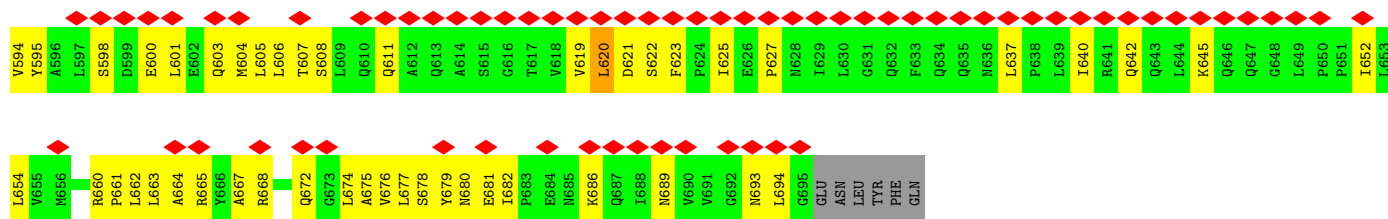








H502	E431	G364	PRO
D503	R432	Y365	GLY
D504	L433	R366	PRO
E505	M434	L367	HIS
E506	A435		
A507		Y368	LEU
	L436	R369	ALA
L512	A437	L370	PHE
	V438	V371	PHE
L519	G439	K372	ALA
A520	D440	K373	PHE
E521		D374	ALA
A522	T441		GLY
L523	Y442	K375	ALA
	G443	G376	LEU
L527	G444	A377	GLY
M528	L445	P378	PHE
	L446	L379	ALA
Q531	D446	L390	GLY
Q532	G447	S391	TRP
L533	L448	S380	ARG
		G381	GLN
L539	L449	R382	GLN
L540	G450		LYS
L541		G385	LYS
D542	S451		PRO
	D452	L390	VAL
D548	P453	S391	GLN
L549	A454	R392	ASP
	K455	K393	THR
A553	Y455	V394	GLN
M554	G456	G395	ILE
	L457	R396	GLU
	P458	L397	GLN
E558	S559	L398	VAL
S560	A459	P399	GLU
	Y460	E400	ALA
E561	W461	V401	LEU
K564	L462	R402	SER
	E463	I403	GLN
L567	H464	R404	ALA
L568	Q465	D405	MET
V573	D466		
R574	R467	H406	GLN
	A468	L409	
R579	K469	K410	
	A470	P411	P347
V582	L471	N412	L348
M583	N472	Q413	T349
L584	M473	Y414	W380
L585	G474	T415	
A586		L416	D351
	G587	G420	D352
Q588	Y475	E421	
K589	Q476	A424	V356
P590	V477	Q425	V357
E591	D479	G426	
L592	D480	L428	
	G481	E429	
N593	T482	P430	



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C9	Depositor
Number of particles used	9756	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.048	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0146	Depositor
Map size ($\text{\AA}$)	348.528, 348.528, 348.528	wwPDB
Map dimensions	424, 424, 424	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.822, 0.822, 0.822	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	0.43	0/2806	0.50	1/3819 (0.0%)
1	B	0.43	0/2806	0.50	1/3819 (0.0%)
1	C	0.43	0/2806	0.50	1/3819 (0.0%)
1	D	0.43	0/2806	0.50	1/3819 (0.0%)
1	E	0.43	0/2806	0.50	1/3819 (0.0%)
1	F	0.43	0/2806	0.50	1/3819 (0.0%)
1	G	0.43	0/2806	0.50	1/3819 (0.0%)
1	H	0.43	0/2806	0.50	1/3819 (0.0%)
1	I	0.43	0/2806	0.50	1/3819 (0.0%)
All	All	0.43	0/25254	0.50	9/34371 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	345	ASP	N-CA-C	-6.45	106.14	112.97
1	G	345	ASP	N-CA-C	-6.44	106.14	112.97
1	I	345	ASP	N-CA-C	-6.42	106.17	112.97
1	B	345	ASP	N-CA-C	-6.42	106.17	112.97
1	E	345	ASP	N-CA-C	-6.40	106.19	112.97

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	2761	0	2832	120	0
1	B	2761	0	2832	117	0
1	C	2761	0	2832	113	0
1	D	2761	0	2832	111	0
1	E	2761	0	2832	123	0
1	F	2761	0	2832	115	0
1	G	2761	0	2832	118	0
1	H	2761	0	2832	118	0
1	I	2761	0	2832	118	0
All	All	24849	0	25488	1020	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 20.

The worst 5 of 1020 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:LEU:HB2	1:A:413:GLN:HE21	1.34	0.93
1:B:409:LEU:HB2	1:B:413:GLN:HE21	1.34	0.92
1:I:409:LEU:HB2	1:I:413:GLN:HE21	1.34	0.91
1:C:409:LEU:HB2	1:C:413:GLN:HE21	1.34	0.91
1:E:409:LEU:HB2	1:E:413:GLN:HE21	1.34	0.91

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	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
1	B	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	36	66
1	C	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	36	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
1	E	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
1	F	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
1	G	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
1	H	351/702 (50%)	301 (86%)	49 (14%)	1 (0%)	36	66
1	I	351/702 (50%)	302 (86%)	48 (14%)	1 (0%)	36	66
All	All	3159/6318 (50%)	2715 (86%)	435 (14%)	9 (0%)	37	66

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	GLY
1	B	420	GLY
1	C	420	GLY
1	D	420	GLY
1	E	420	GLY

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	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	B	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	C	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	D	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	E	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	F	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	G	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	H	305/584 (52%)	303 (99%)	2 (1%)	76	77
1	I	305/584 (52%)	303 (99%)	2 (1%)	76	77
All	All	2745/5256 (52%)	2727 (99%)	18 (1%)	73	77

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	488	ILE
1	I	620	LEU
1	I	488	ILE
1	E	488	ILE
1	G	620	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	413	GLN
1	I	646	GLN
1	H	425	GLN
1	I	413	GLN
1	D	413	GLN

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 ⓘ

There are no chain breaks in this entry.

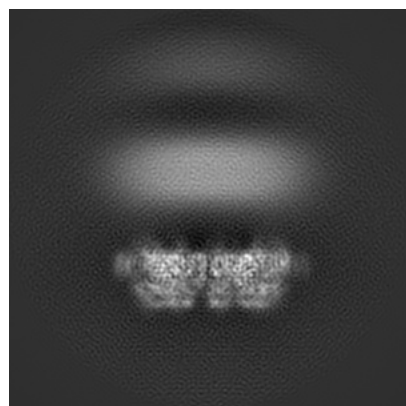
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11827. These allow visual inspection of the internal detail of the map and identification of artifacts.

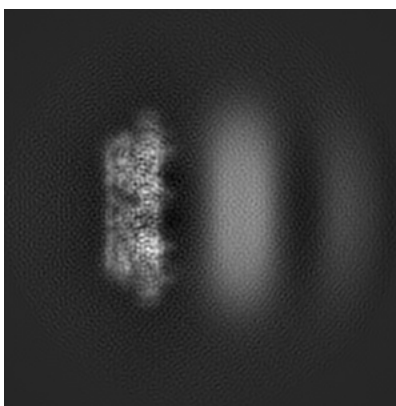
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

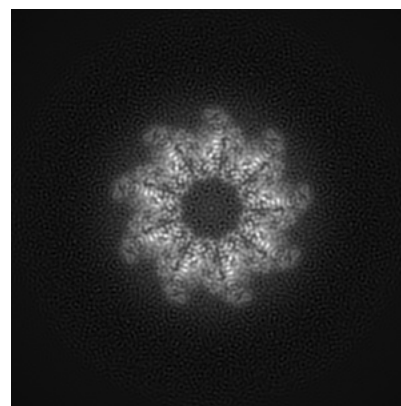
6.1.1 Primary map



X

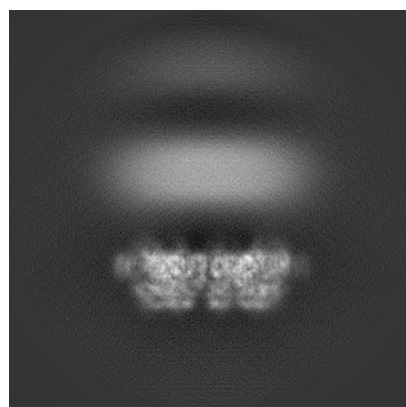


Y

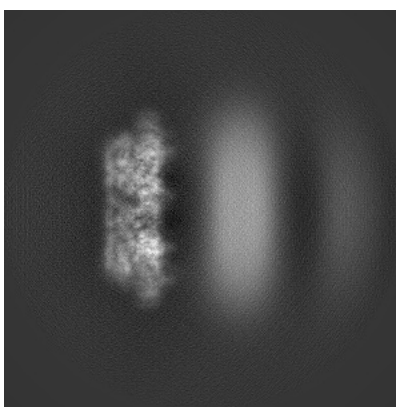


Z

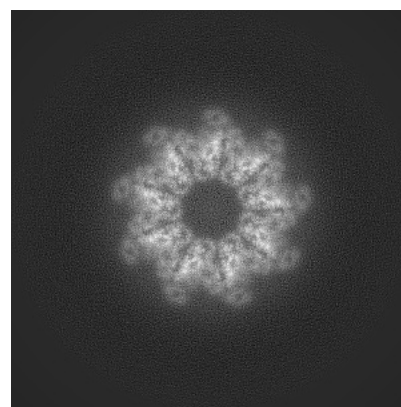
6.1.2 Raw map



X



Y

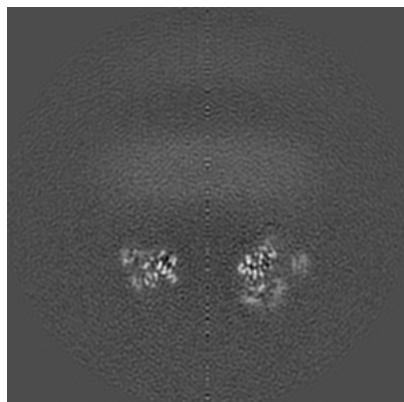


Z

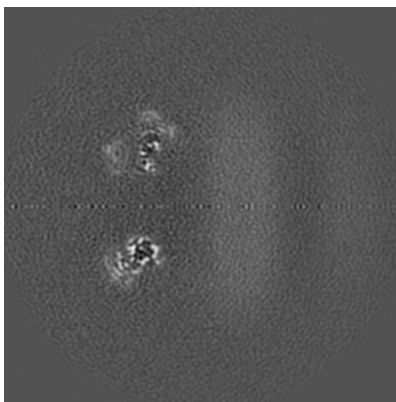
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

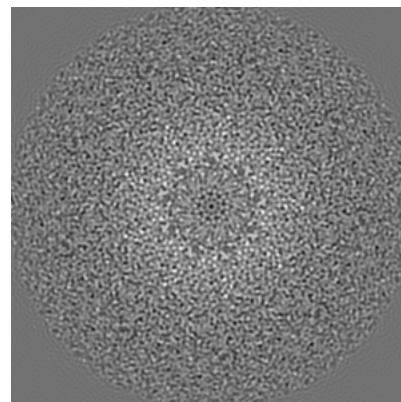
6.2.1 Primary map



X Index: 212

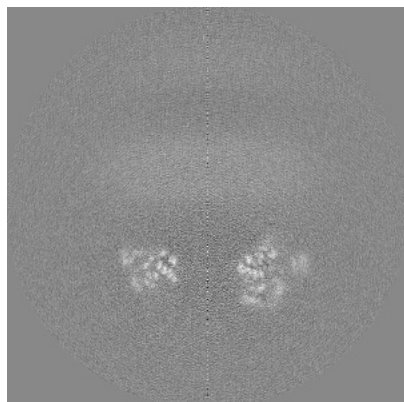


Y Index: 212

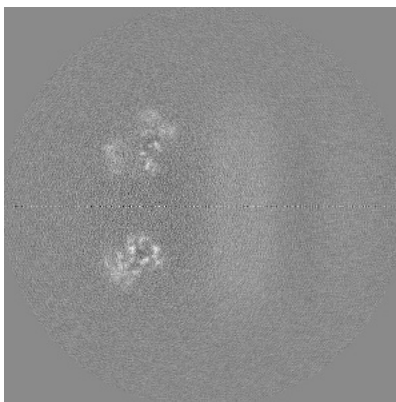


Z Index: 212

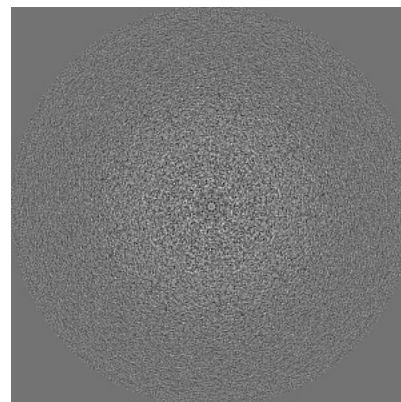
6.2.2 Raw map



X Index: 212



Y Index: 212

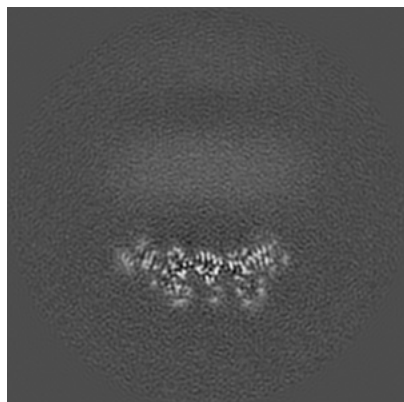


Z Index: 212

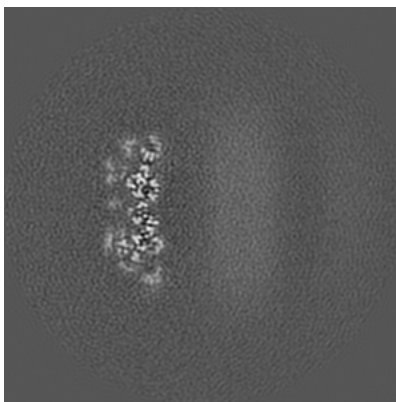
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

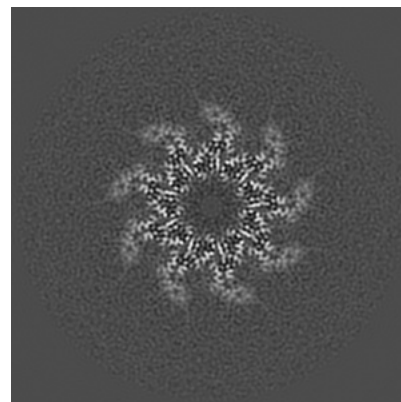
6.3.1 Primary map



X Index: 168

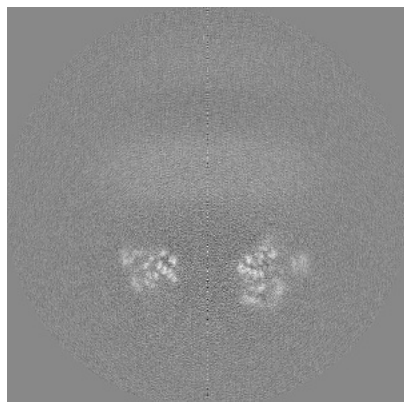


Y Index: 250

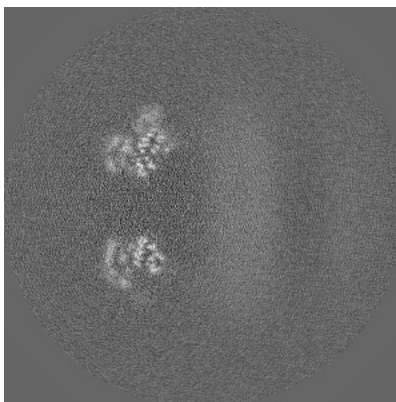


Z Index: 152

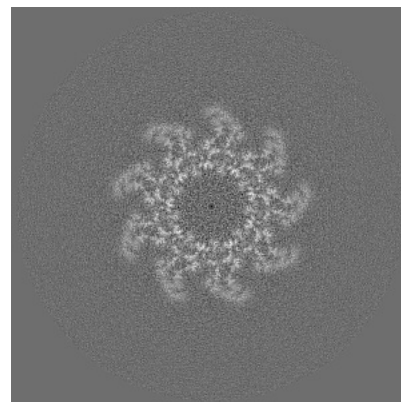
6.3.2 Raw map



X Index: 212



Y Index: 219

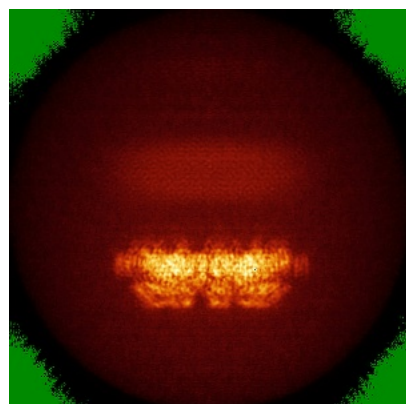


Z Index: 158

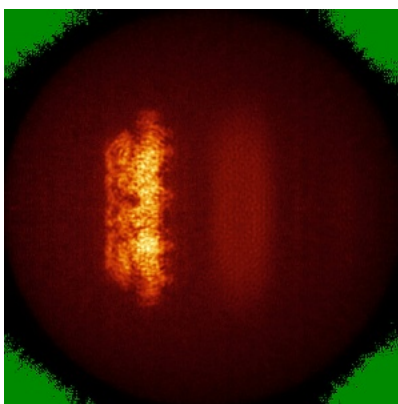
The images above show the largest variance slices of the map in three orthogonal directions.

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

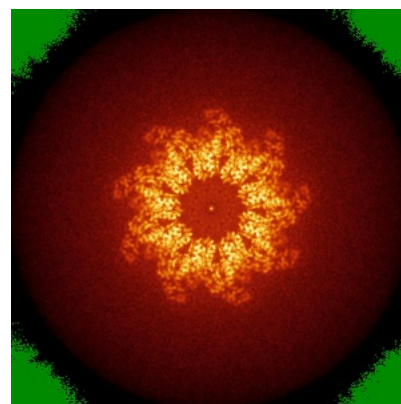
6.4.1 Primary map



X

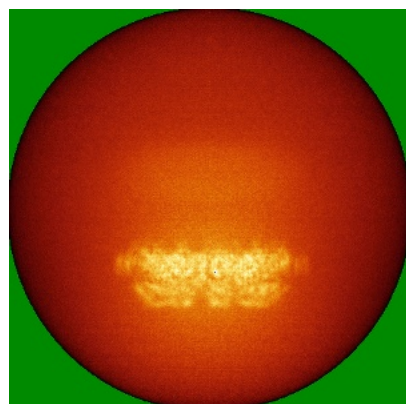


Y

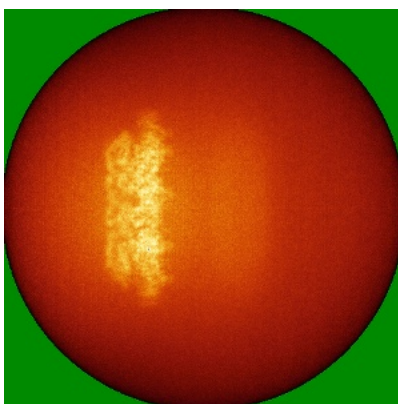


Z

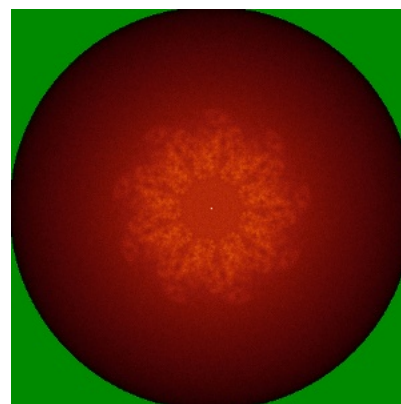
6.4.2 Raw map



X



Y

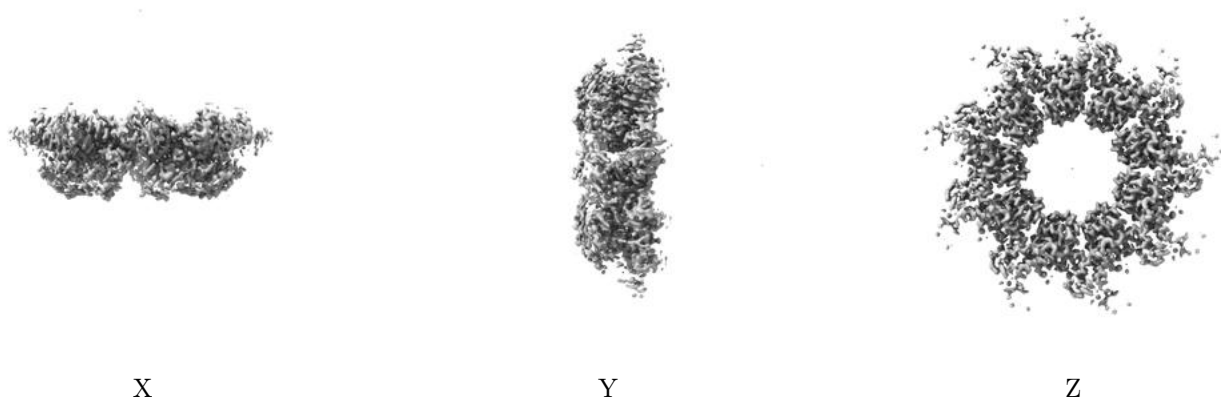


Z

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.

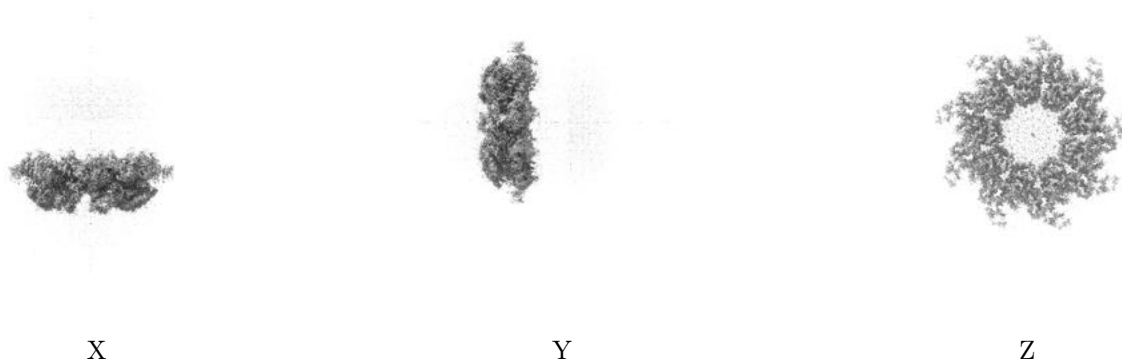
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0146. 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.

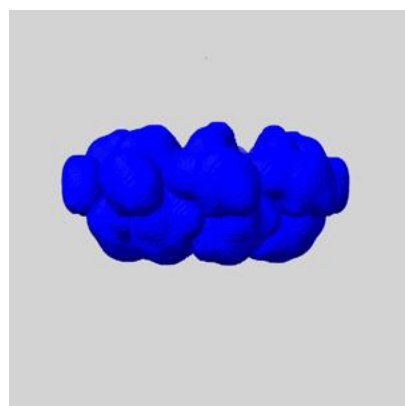
6.6 Mask visualisation [i](#)

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

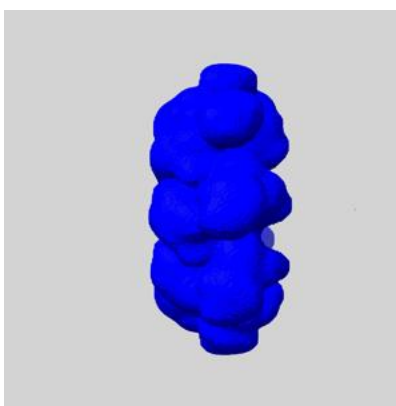
A mask typically either:

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

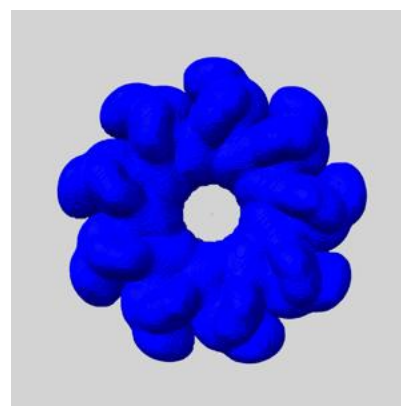
6.6.1 emd_11827_msk_1.map [i](#)



X



Y

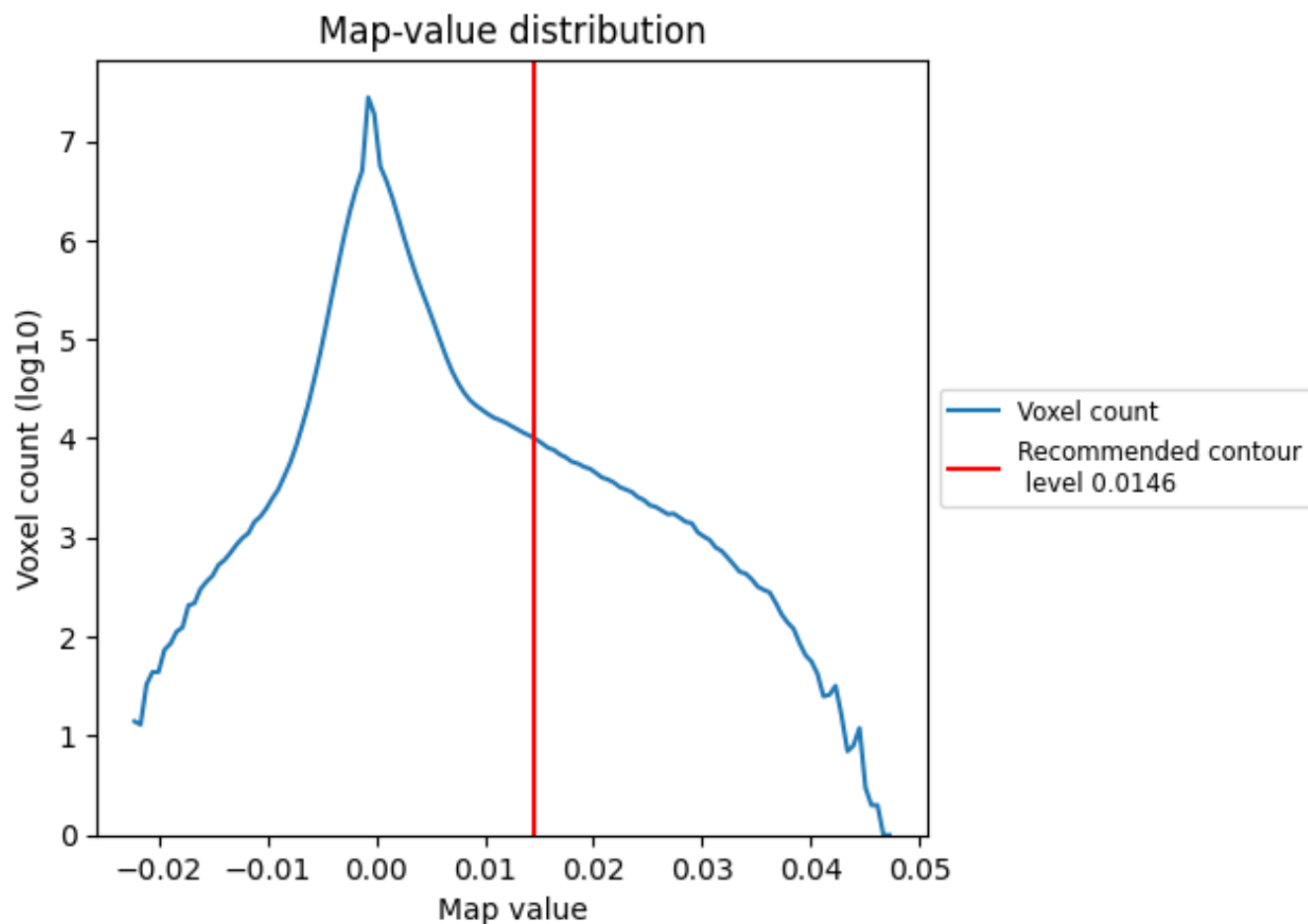


Z

7 Map analysis [i](#)

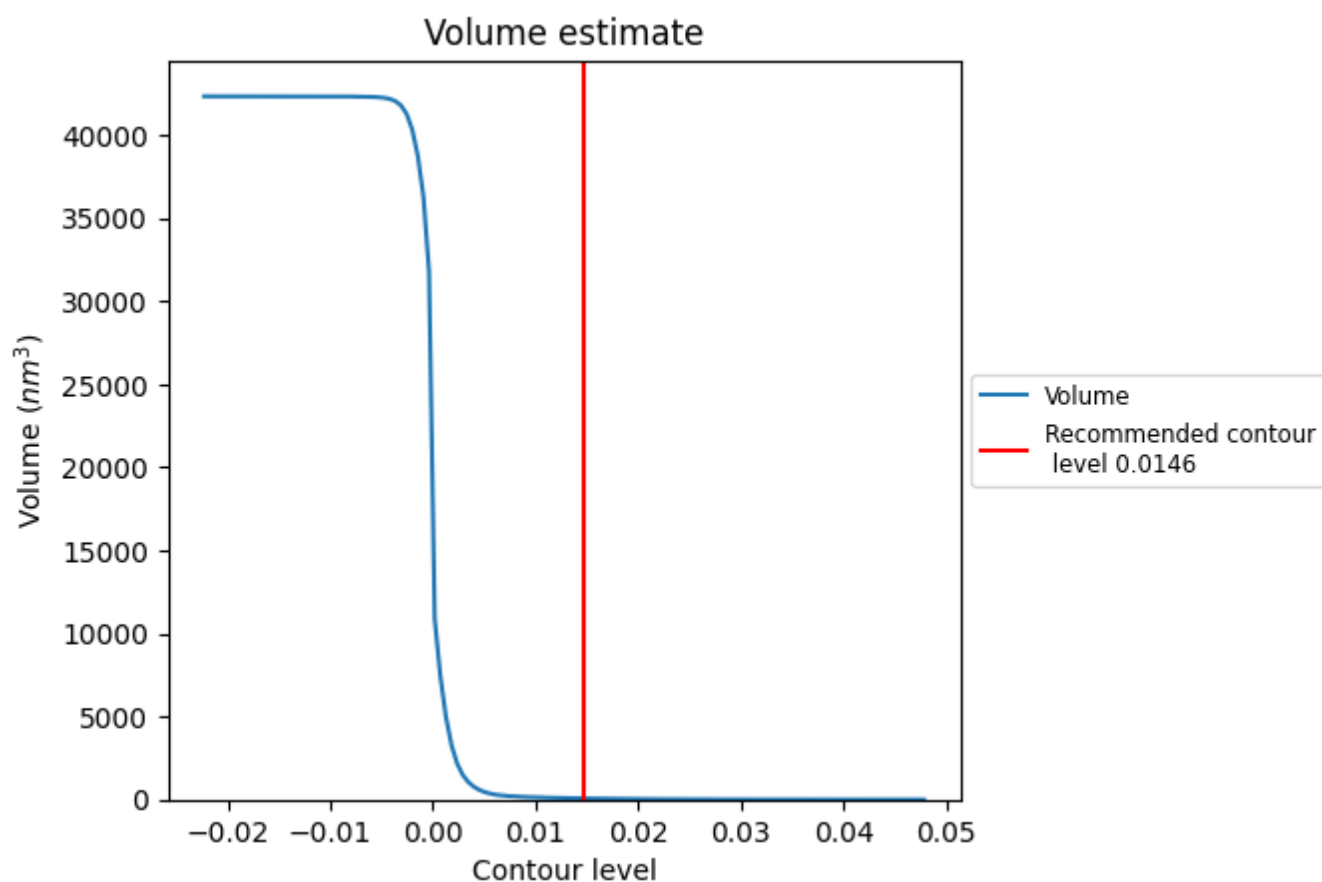
This section contains the results of statistical analysis of the map.

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.

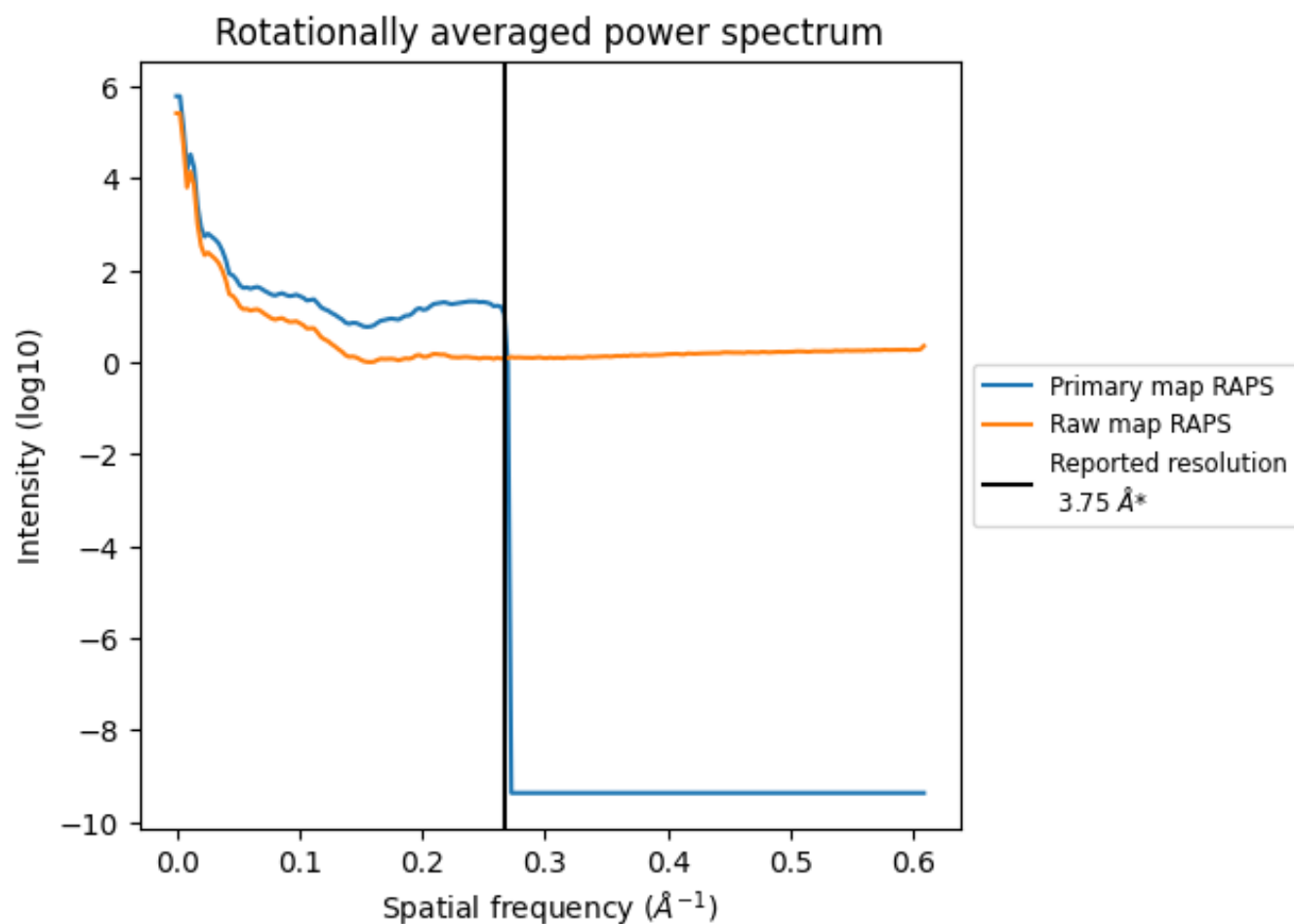
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 69 nm³; this corresponds to an approximate mass of 62 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 ⓘ

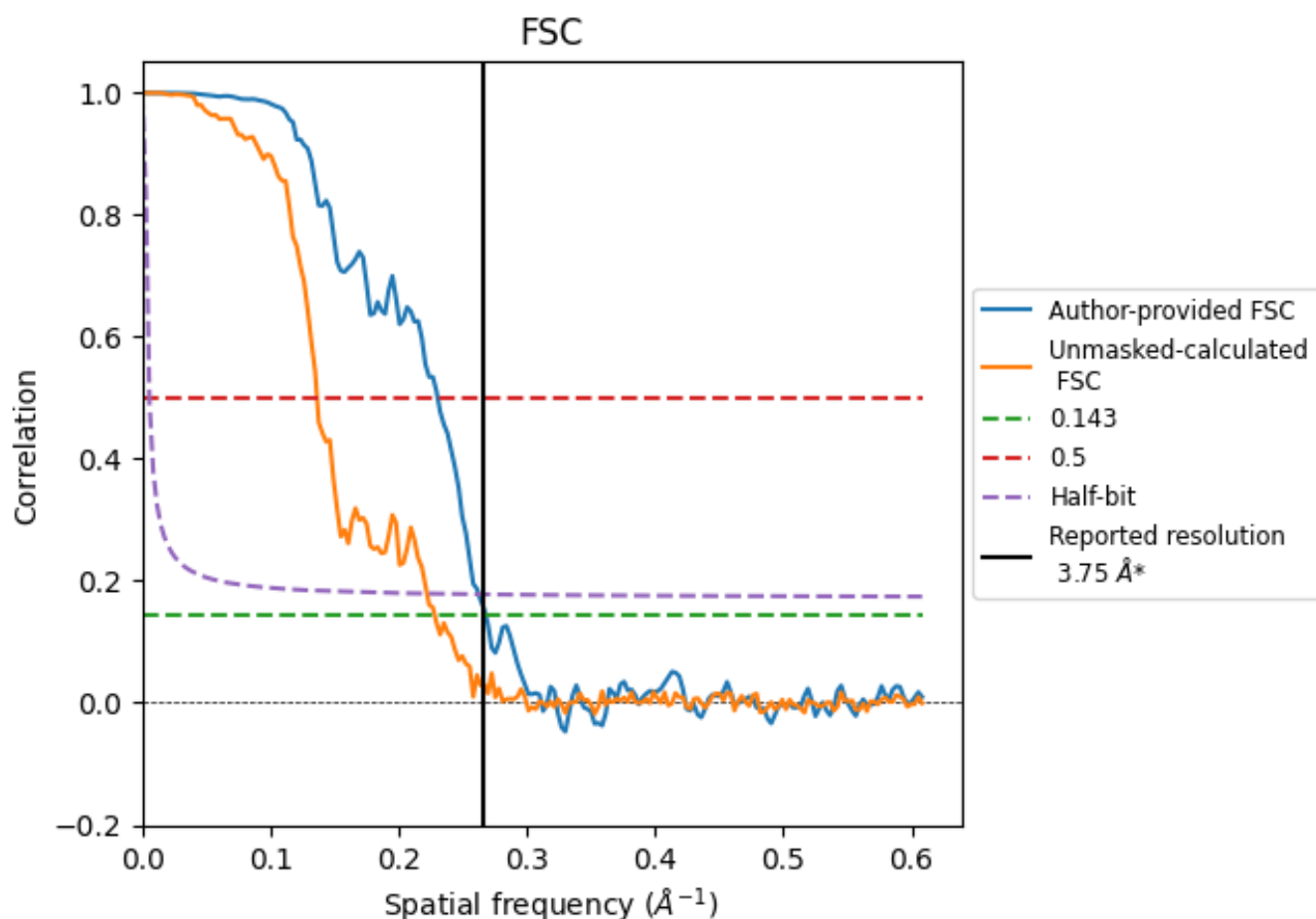


*Reported resolution corresponds to spatial frequency of 0.267 $\text{\AA}^{-1}$

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 0.267 Å⁻¹

8.2 Resolution estimates [i](#)

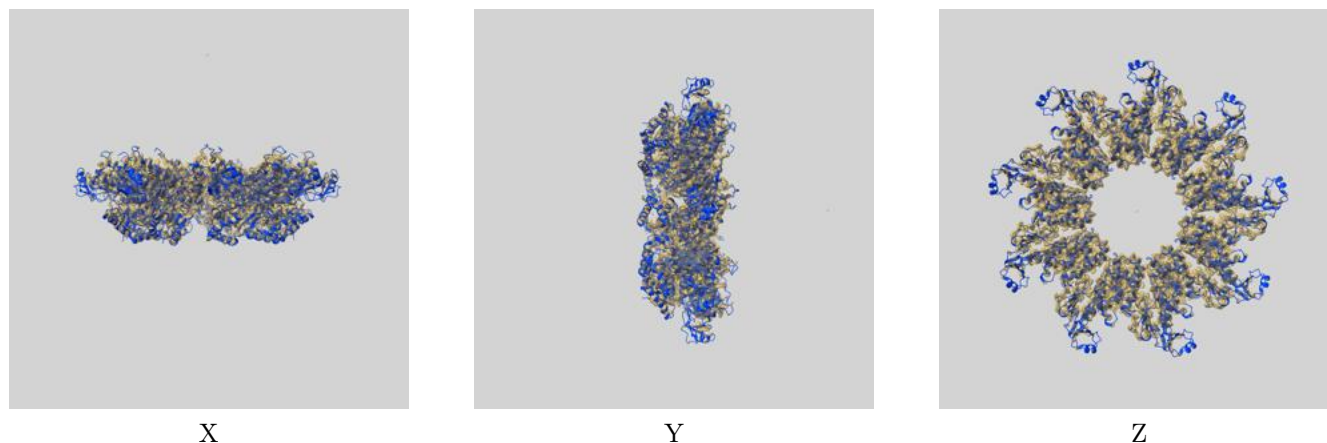
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.75	-	-
Author-provided FSC curve	3.73	4.34	3.81
Unmasked-calculated*	4.38	7.34	4.50

*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 4.38 differs from the reported value 3.75 by more than 10 %

9 Map-model fit [i](#)

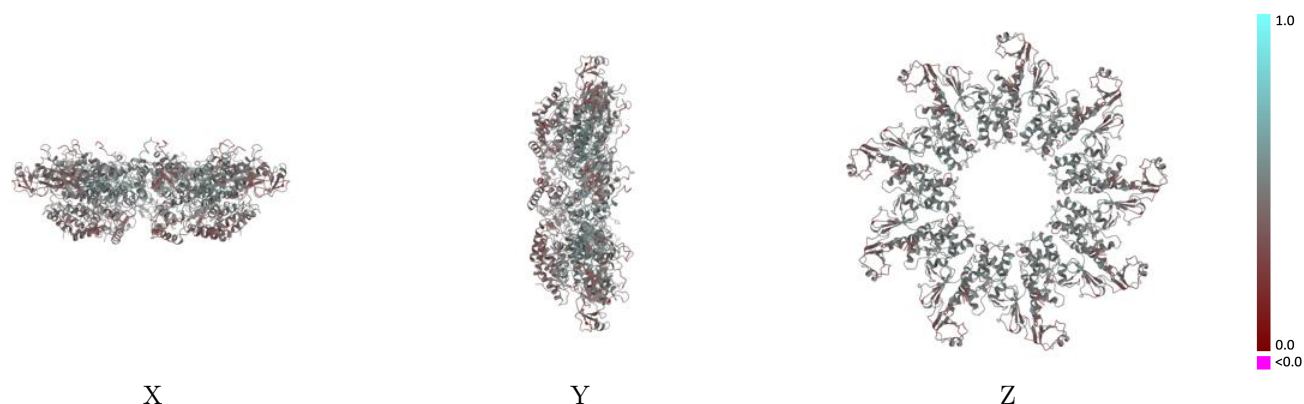
This section contains information regarding the fit between EMDB map EMD-11827 and PDB model 7AMY. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



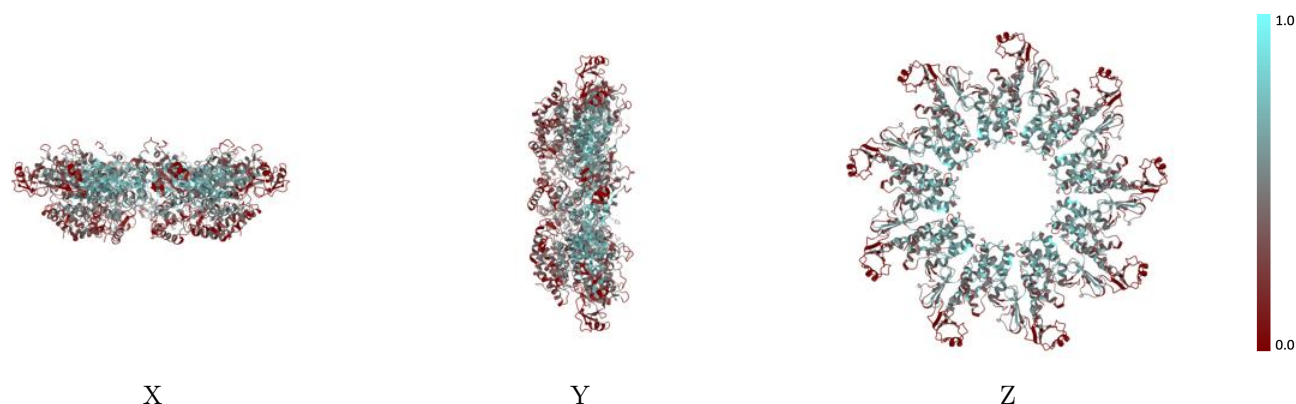
The images above show the 3D surface view of the map at the recommended contour level 0.0146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



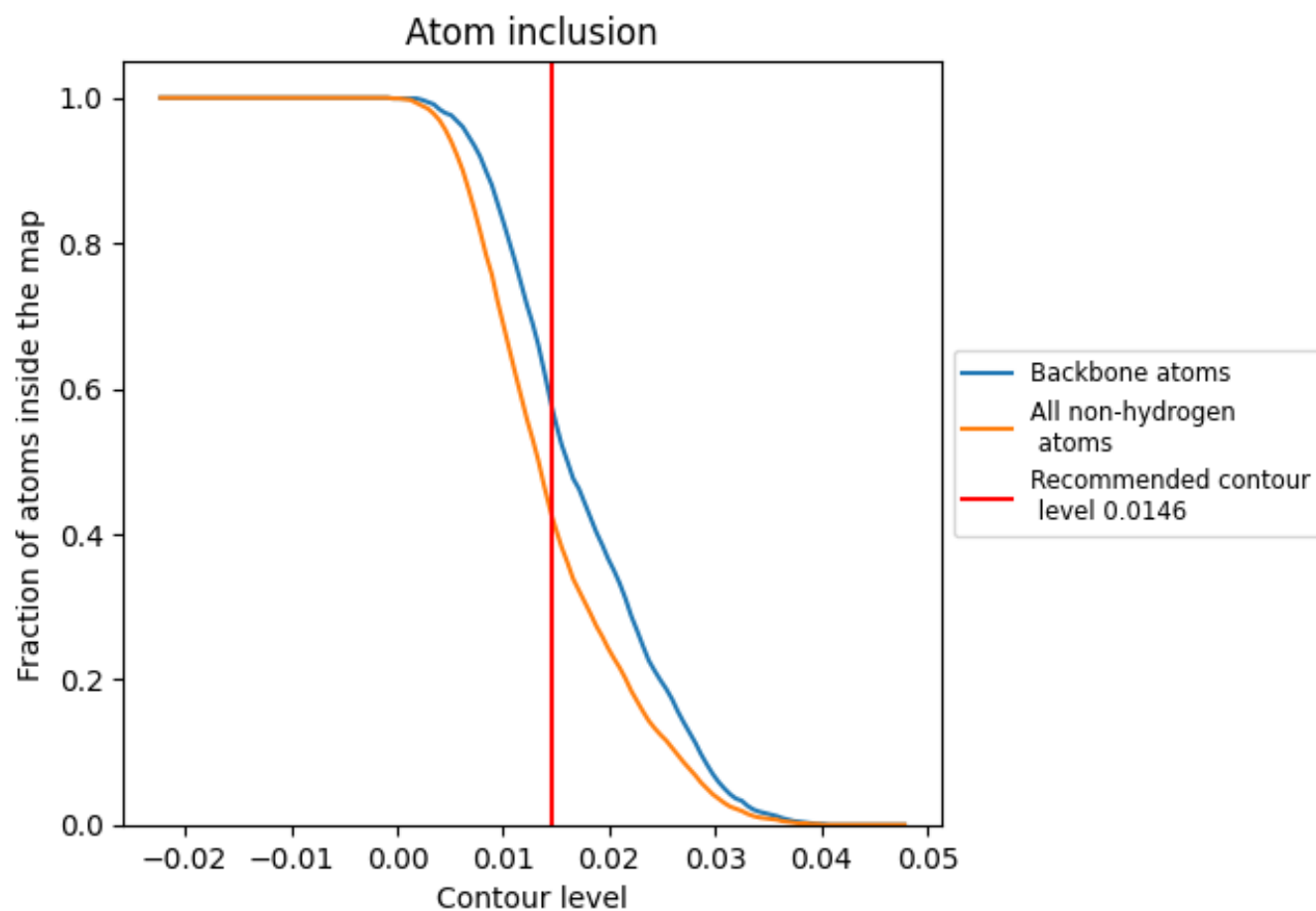
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0146).

9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 42% 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 (0.0146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4240	0.4560
A	0.4220	0.4560
B	0.4240	0.4560
C	0.4220	0.4550
D	0.4270	0.4560
E	0.4240	0.4560
F	0.4220	0.4560
G	0.4220	0.4560
H	0.4240	0.4560
I	0.4230	0.4570

1.0

0.0

<0.0