



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:43 AM UTC

PDB ID : 8C8N / pdb_00008c8n
EMDB ID : EMD-16487
Title : In situ structure of the Nitrosopumilus maritimus S-layer - Two-fold symmetry (C2)
Authors : von Kuegelgen, A.; Bharat, T.
Deposited on : 2023-01-20
Resolution : 3.40 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

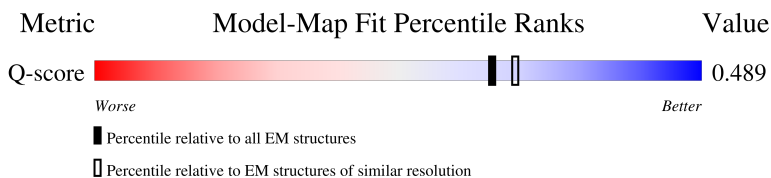
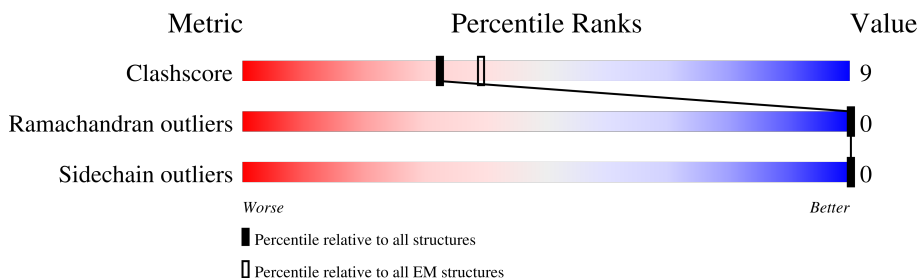
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	1734	 19% 5% 76%
1	B	1734	 20% 5% 76%
1	C	1734	 19% 5% 76%
1	D	1734	 19% 5% 76%

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Mol	Chain	Length	Quality of chain
1	E	1734	 20% 76%
1	F	1734	 19% 5% 76%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18342 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.

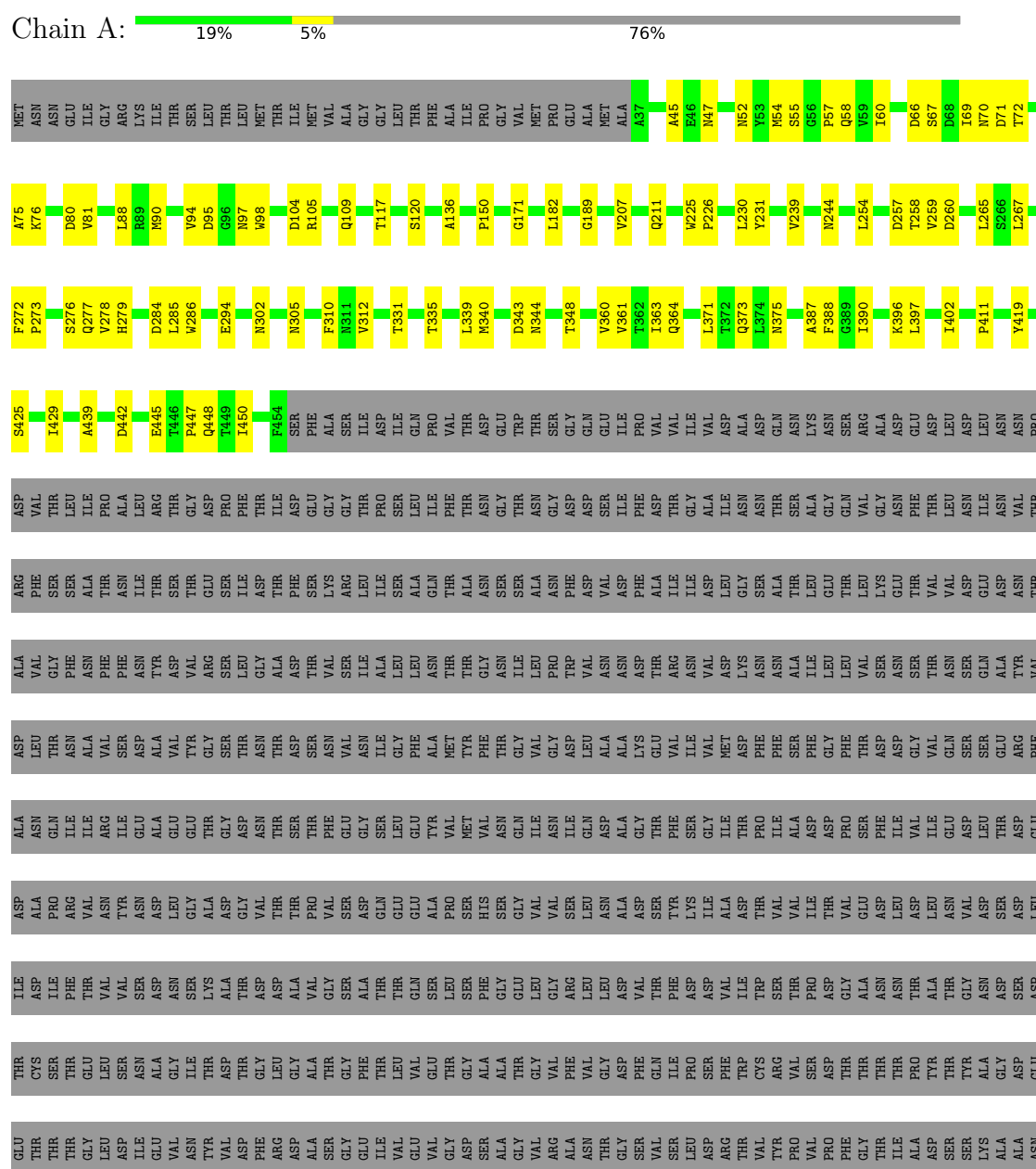
- Molecule 1 is a protein called Cell surface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	418	Total 3057	C 1876	N 506	O 668	S 7	0	0
1	B	418	Total 3057	C 1876	N 506	O 668	S 7	0	0
1	C	418	Total 3057	C 1876	N 506	O 668	S 7	0	0
1	D	418	Total 3057	C 1876	N 506	O 668	S 7	0	0
1	E	418	Total 3057	C 1876	N 506	O 668	S 7	0	0
1	F	418	Total 3057	C 1876	N 506	O 668	S 7	0	0

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: Cell surface protein







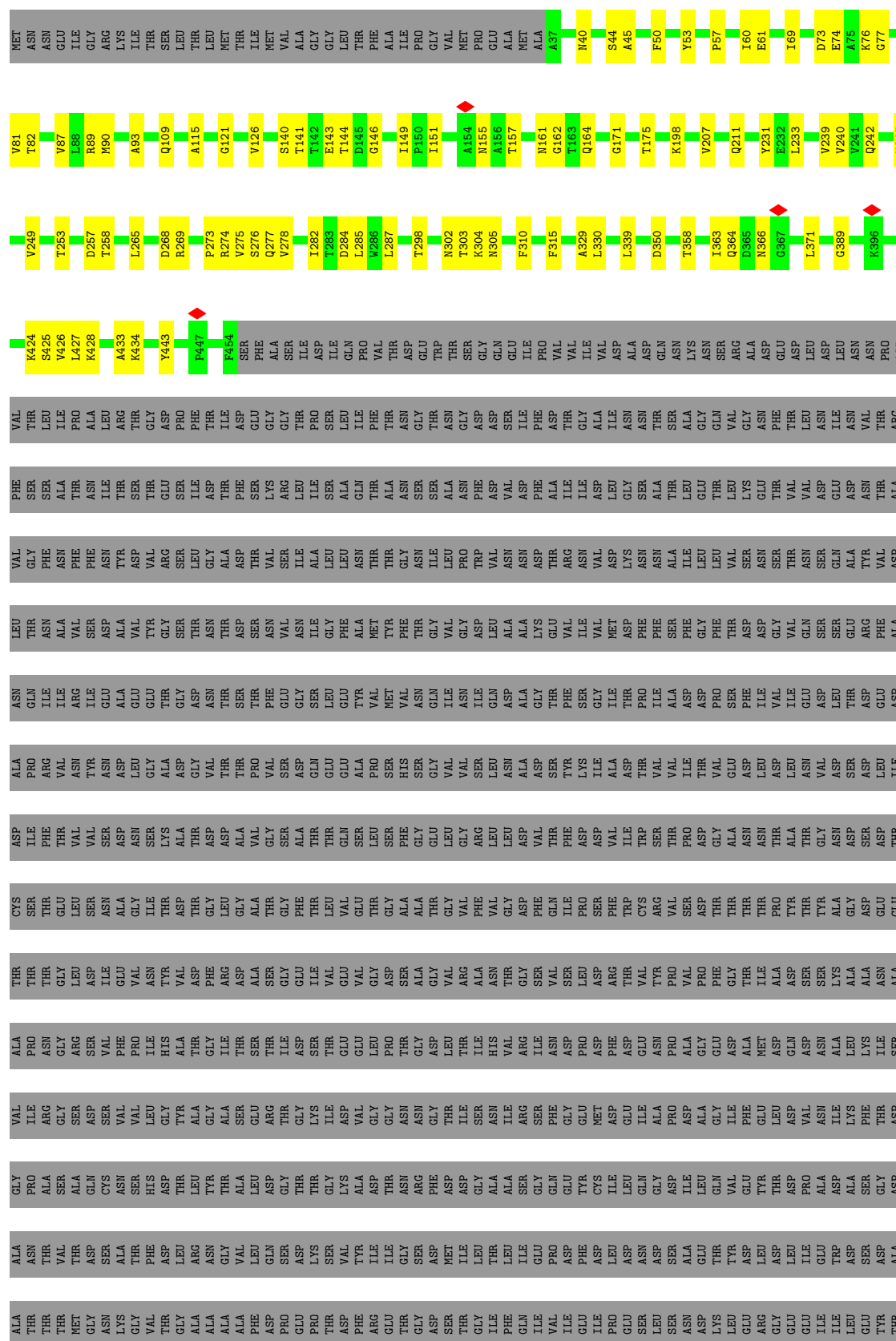
- Molecule 1: Cell surface protein

Chain F:

19%

5%

76%



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	108621	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; PseudoSubtomograms as described in Zivanov 2022 (https://elifesciences.org/articles/83724)	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	121	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.205	Depositor
Minimum map value	-0.120	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.02557	Depositor
Map size ($\text{\AA}$)	265.4, 265.4, 265.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.327, 1.327, 1.327	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	0.12	0/3103	0.30	0/4245
1	B	0.11	0/3103	0.28	0/4245
1	C	0.11	0/3103	0.30	0/4245
1	D	0.12	0/3103	0.31	0/4245
1	E	0.12	0/3103	0.30	0/4245
1	F	0.12	0/3103	0.30	0/4245
All	All	0.12	0/18618	0.30	0/25470

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	3057	0	2894	57	0
1	B	3057	0	2894	46	0
1	C	3057	0	2894	56	0
1	D	3057	0	2894	54	0
1	E	3057	0	2894	50	0
1	F	3057	0	2894	54	0
All	All	18342	0	17364	305	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 9.

The worst 5 of 305 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:B:105:ARG:HA	1:B:230:LEU:HD12	1.60	0.83
1:A:81:VAL:HG11	1:A:90:MET:HE2	1.60	0.82
1:E:105:ARG:HA	1:E:230:LEU:HD12	1.60	0.81
1:D:105:ARG:HA	1:D:230:LEU:HD12	1.70	0.74
1:A:302:ASN:HB2	1:A:402:ILE:H	1.53	0.73

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	416/1734 (24%)	401 (96%)	15 (4%)	0	100	100
1	B	416/1734 (24%)	398 (96%)	18 (4%)	0	100	100
1	C	416/1734 (24%)	397 (95%)	19 (5%)	0	100	100
1	D	416/1734 (24%)	403 (97%)	13 (3%)	0	100	100
1	E	416/1734 (24%)	397 (95%)	19 (5%)	0	100	100
1	F	416/1734 (24%)	395 (95%)	21 (5%)	0	100	100
All	All	2496/10404 (24%)	2391 (96%)	105 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	341/1438 (24%)	341 (100%)	0	100	100
1	B	341/1438 (24%)	341 (100%)	0	100	100
1	C	341/1438 (24%)	341 (100%)	0	100	100
1	D	341/1438 (24%)	341 (100%)	0	100	100
1	E	341/1438 (24%)	341 (100%)	0	100	100
1	F	341/1438 (24%)	341 (100%)	0	100	100
All	All	2046/8628 (24%)	2046 (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 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	409	GLN
1	F	409	GLN
1	D	70	ASN
1	E	288	ASN
1	D	47	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

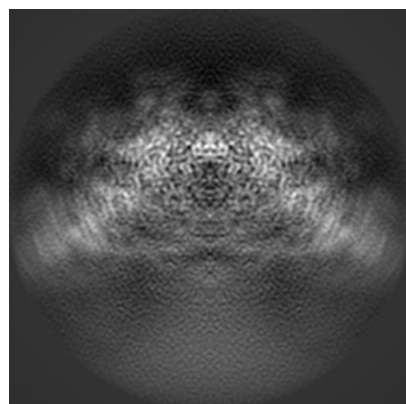
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16487. These allow visual inspection of the internal detail of the map and identification of artifacts.

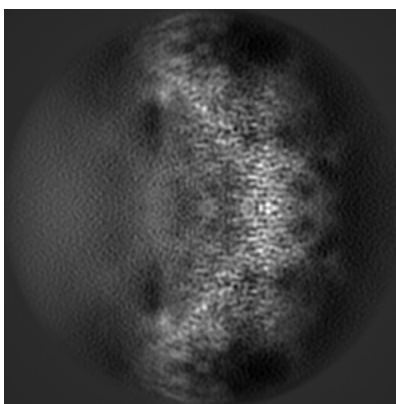
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

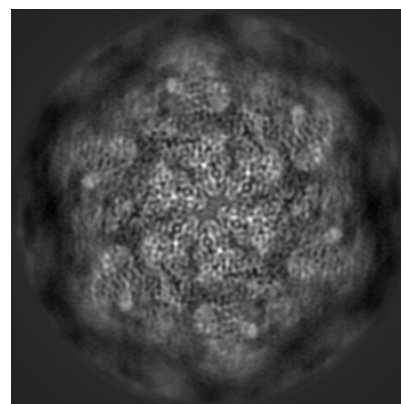
6.1.1 Primary map



X

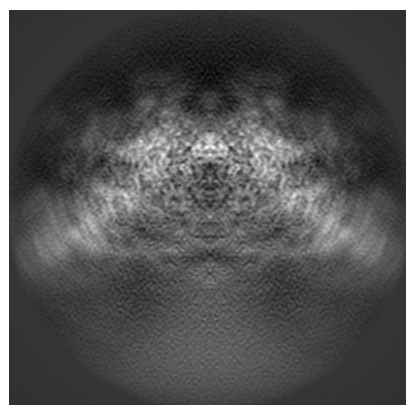


Y

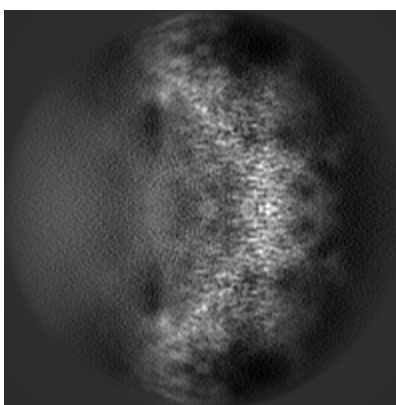


Z

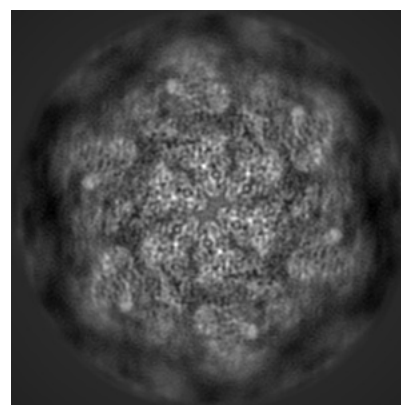
6.1.2 Raw map



X



Y

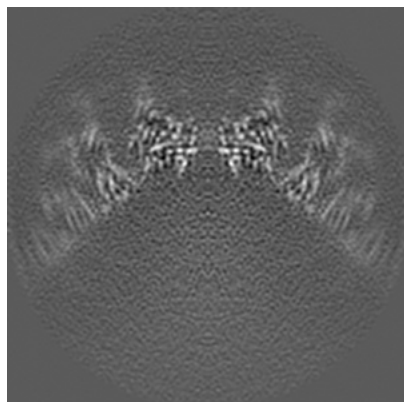


Z

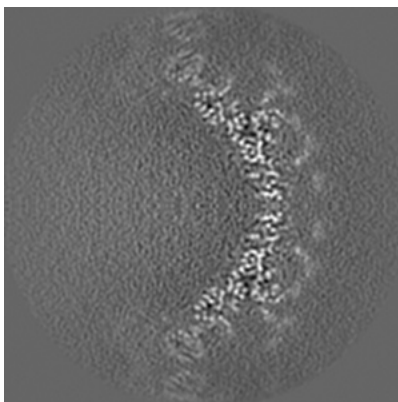
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

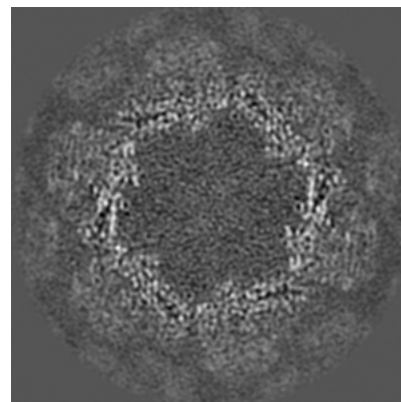
6.2.1 Primary map



X Index: 100

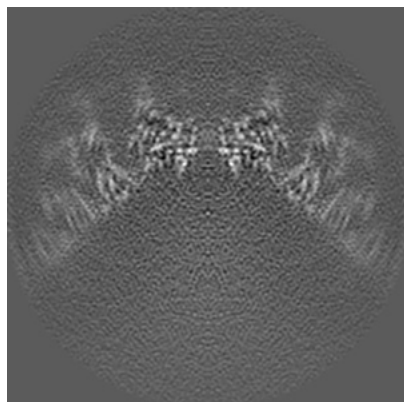


Y Index: 100

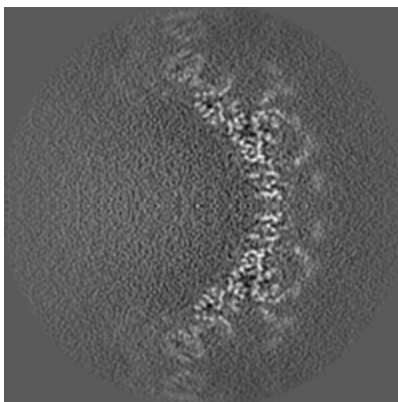


Z Index: 100

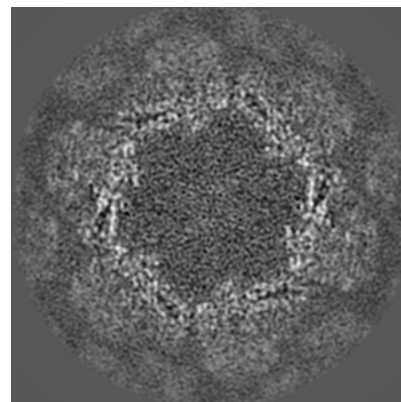
6.2.2 Raw map



X Index: 100



Y Index: 100

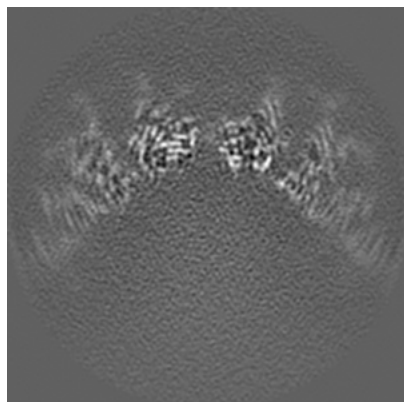


Z Index: 100

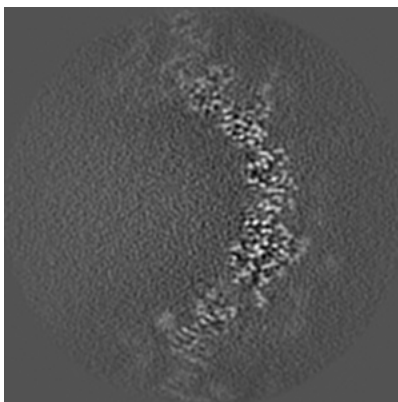
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

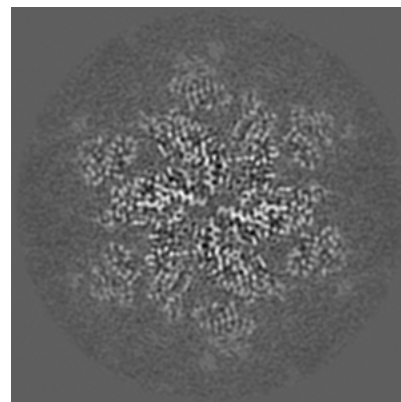
6.3.1 Primary map



X Index: 101

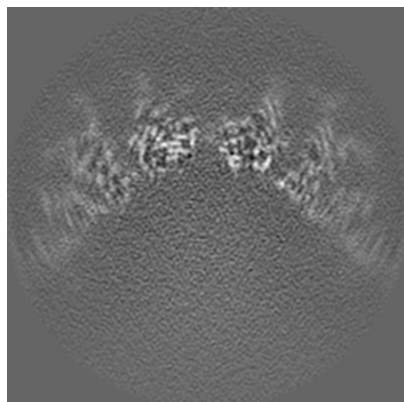


Y Index: 108

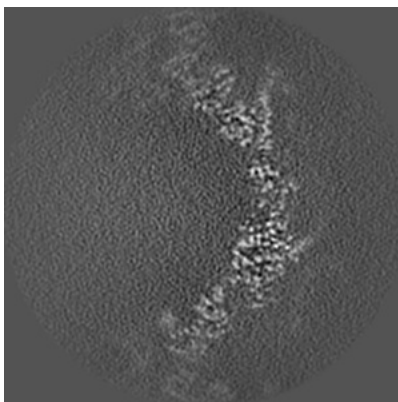


Z Index: 127

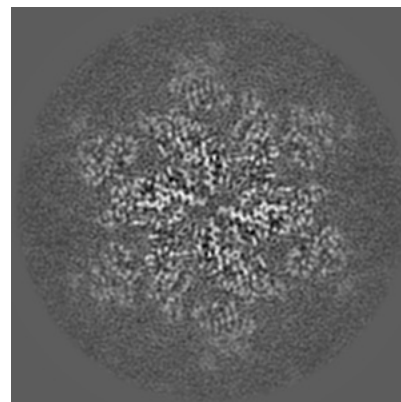
6.3.2 Raw map



X Index: 101



Y Index: 106

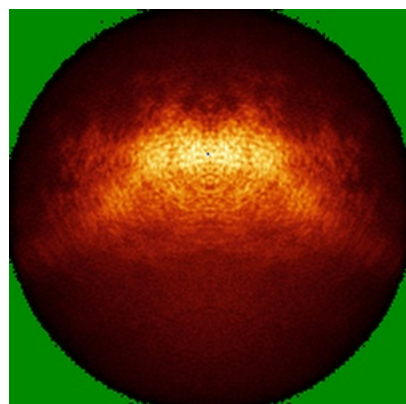


Z Index: 127

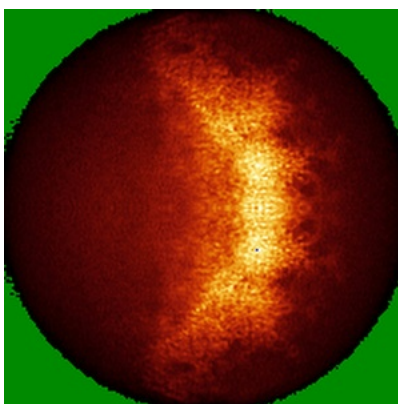
The images above show the largest variance slices of the map in three orthogonal directions.

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

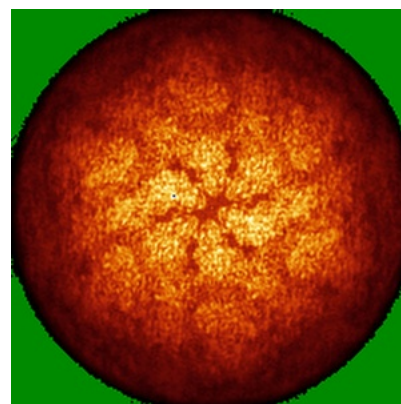
6.4.1 Primary map



X

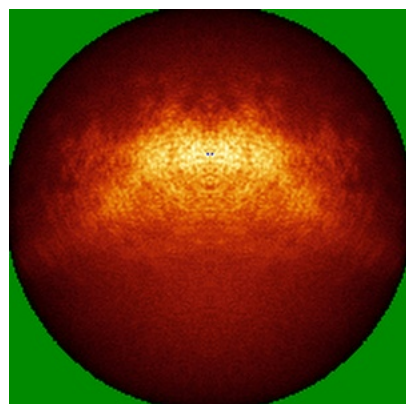


Y

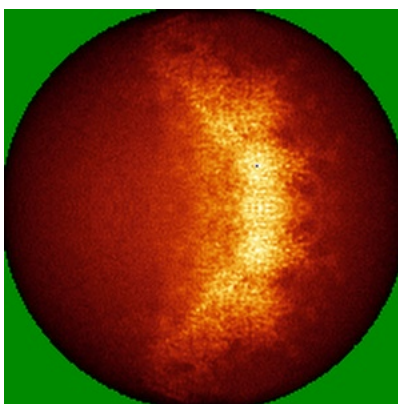


Z

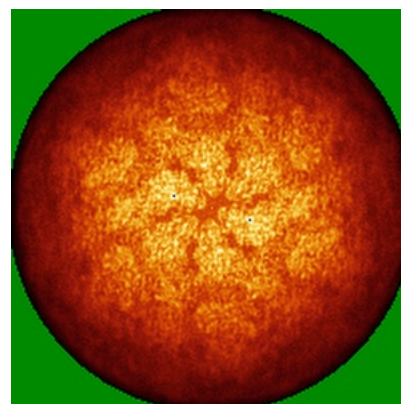
6.4.2 Raw map



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.

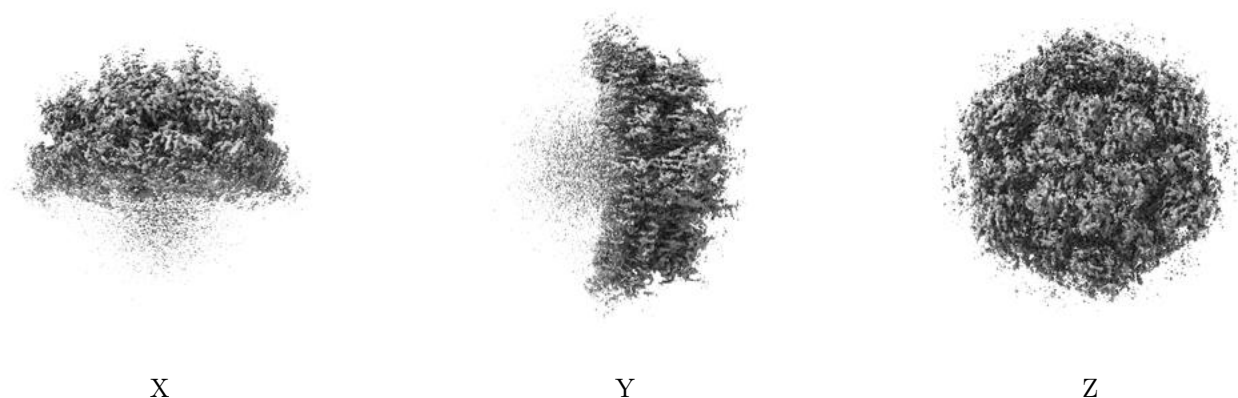
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02557. 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.

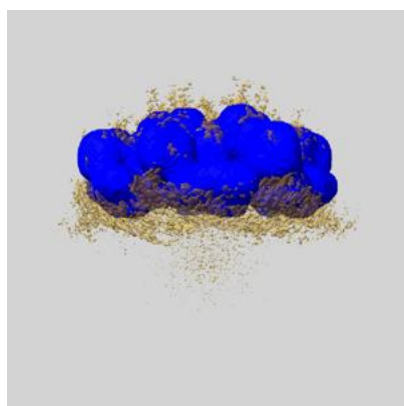
6.6 Mask visualisation [i](#)

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

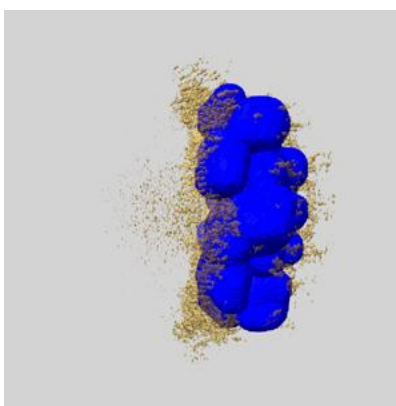
A mask typically either:

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

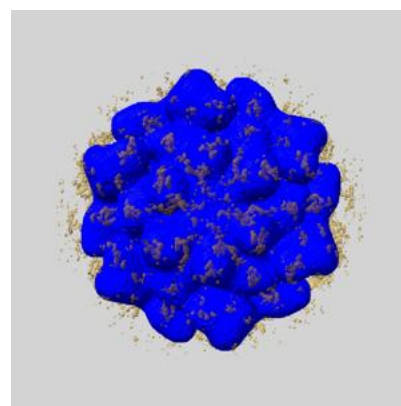
6.6.1 emd_16487_msk_1.map [i](#)



X



Y

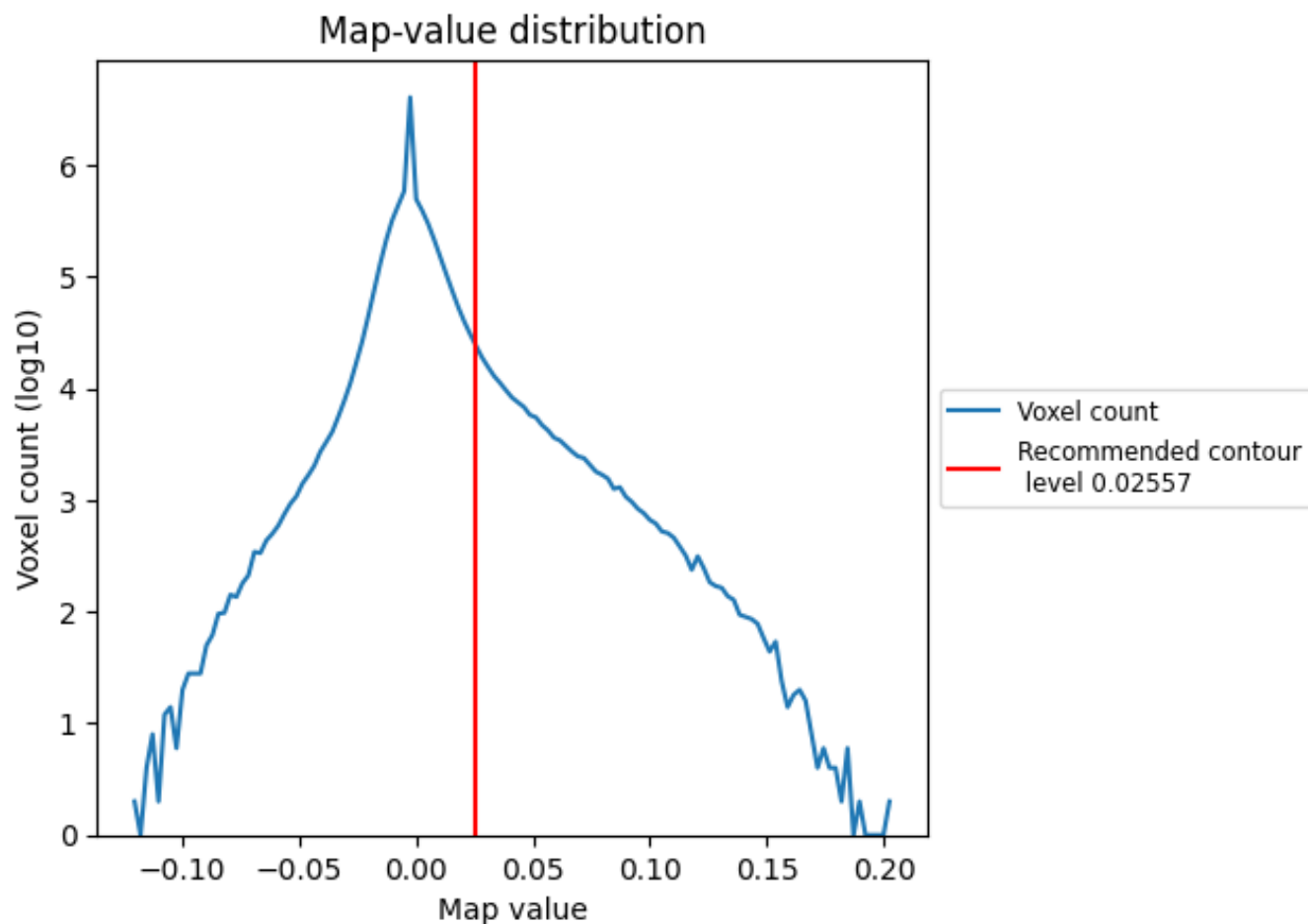


Z

7 Map analysis [i](#)

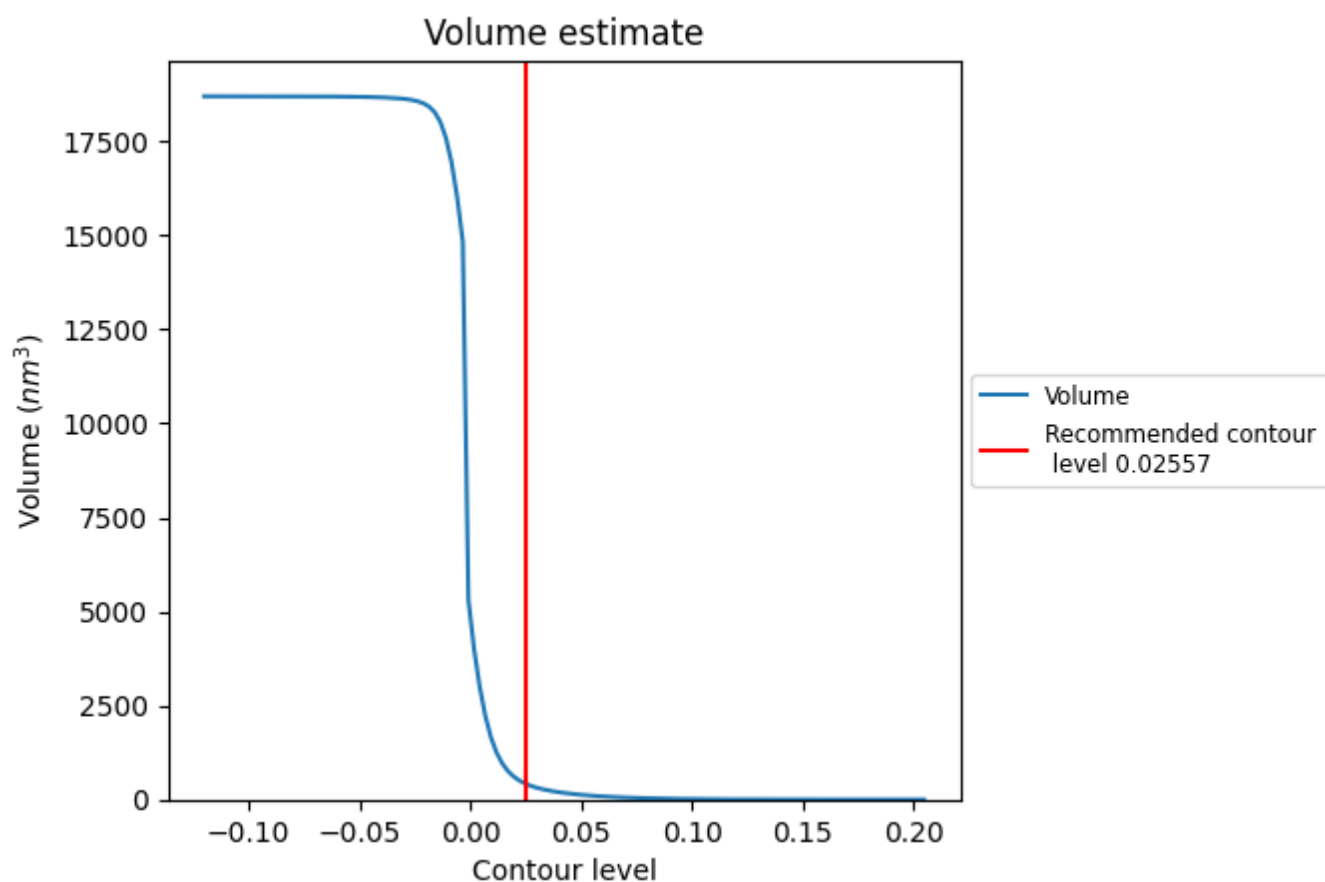
This section contains the results of statistical analysis of the map.

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.

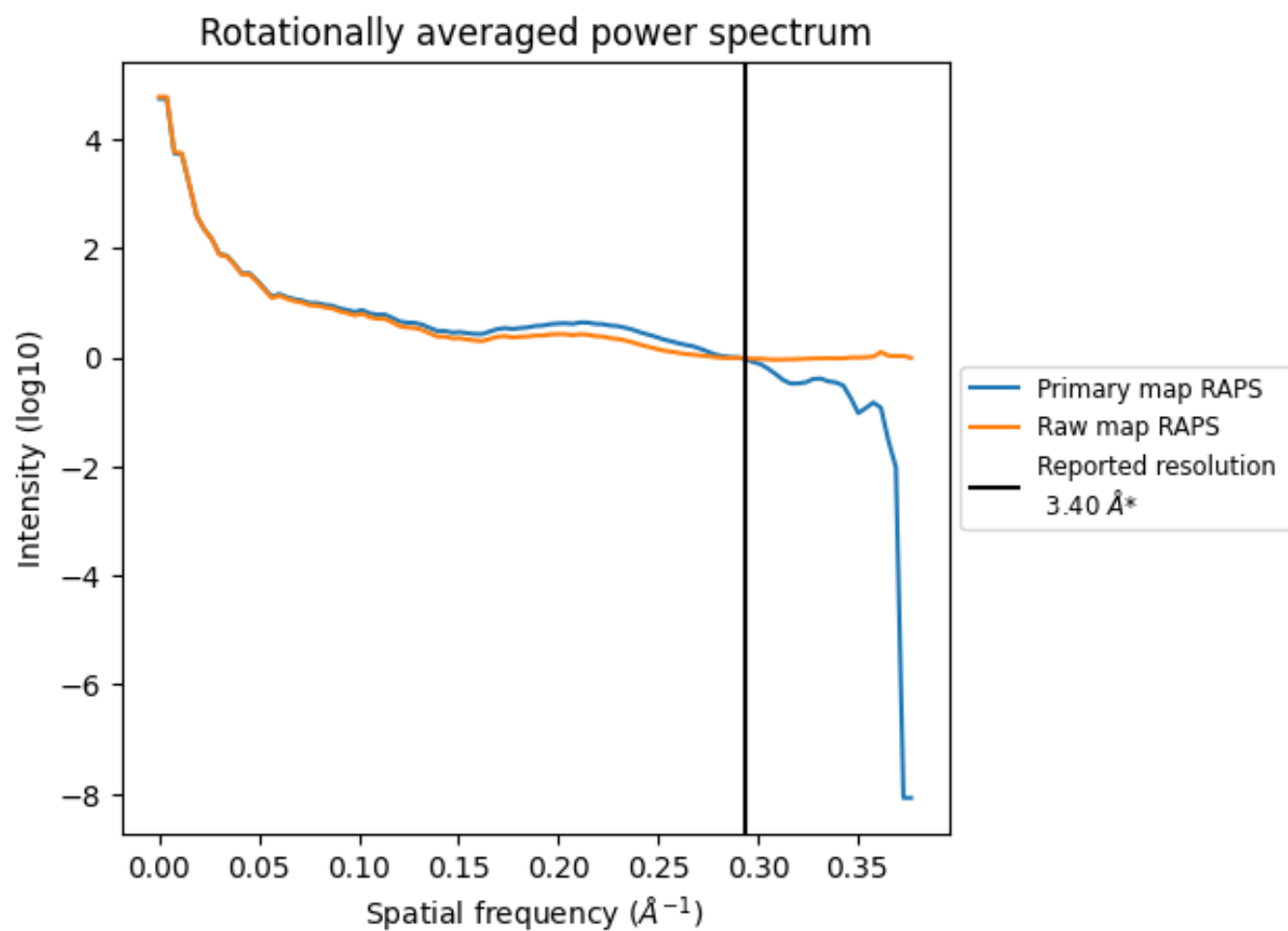
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 408 nm³; this corresponds to an approximate mass of 369 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 ⓘ

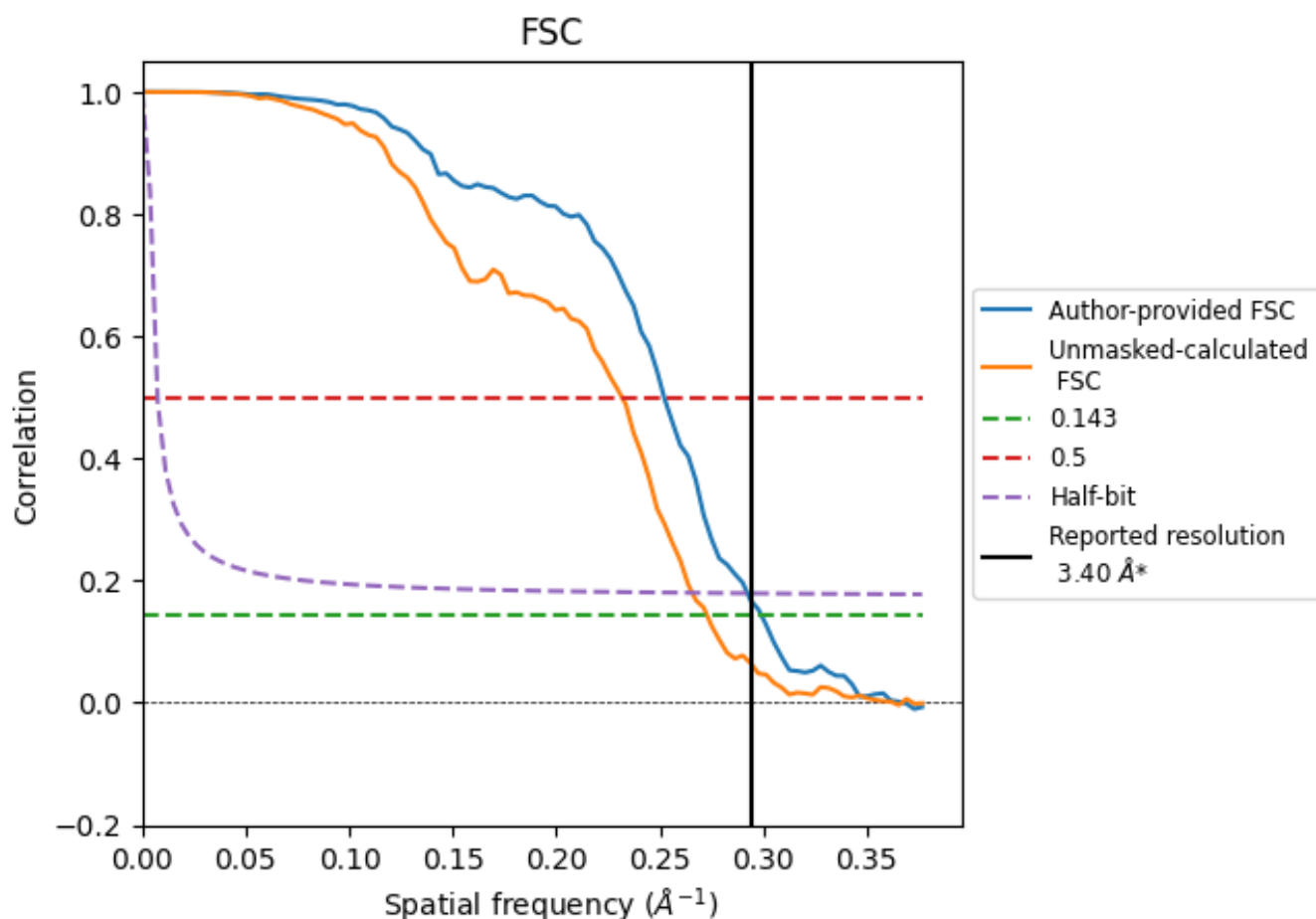


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

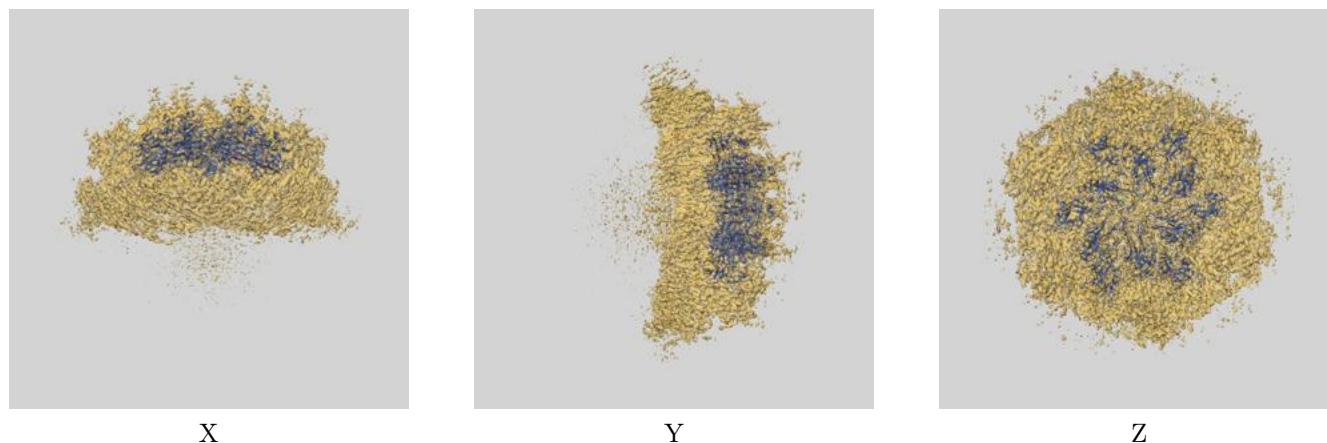
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.34	3.97	3.42
Unmasked-calculated*	3.66	4.31	3.76

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

9 Map-model fit [i](#)

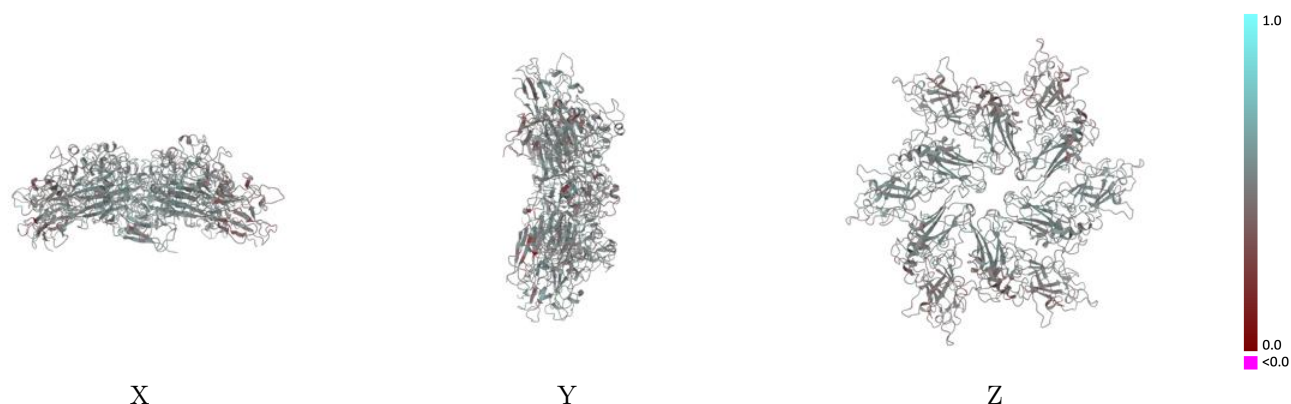
This section contains information regarding the fit between EMDB map EMD-16487 and PDB model 8C8N. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.02557 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](#)



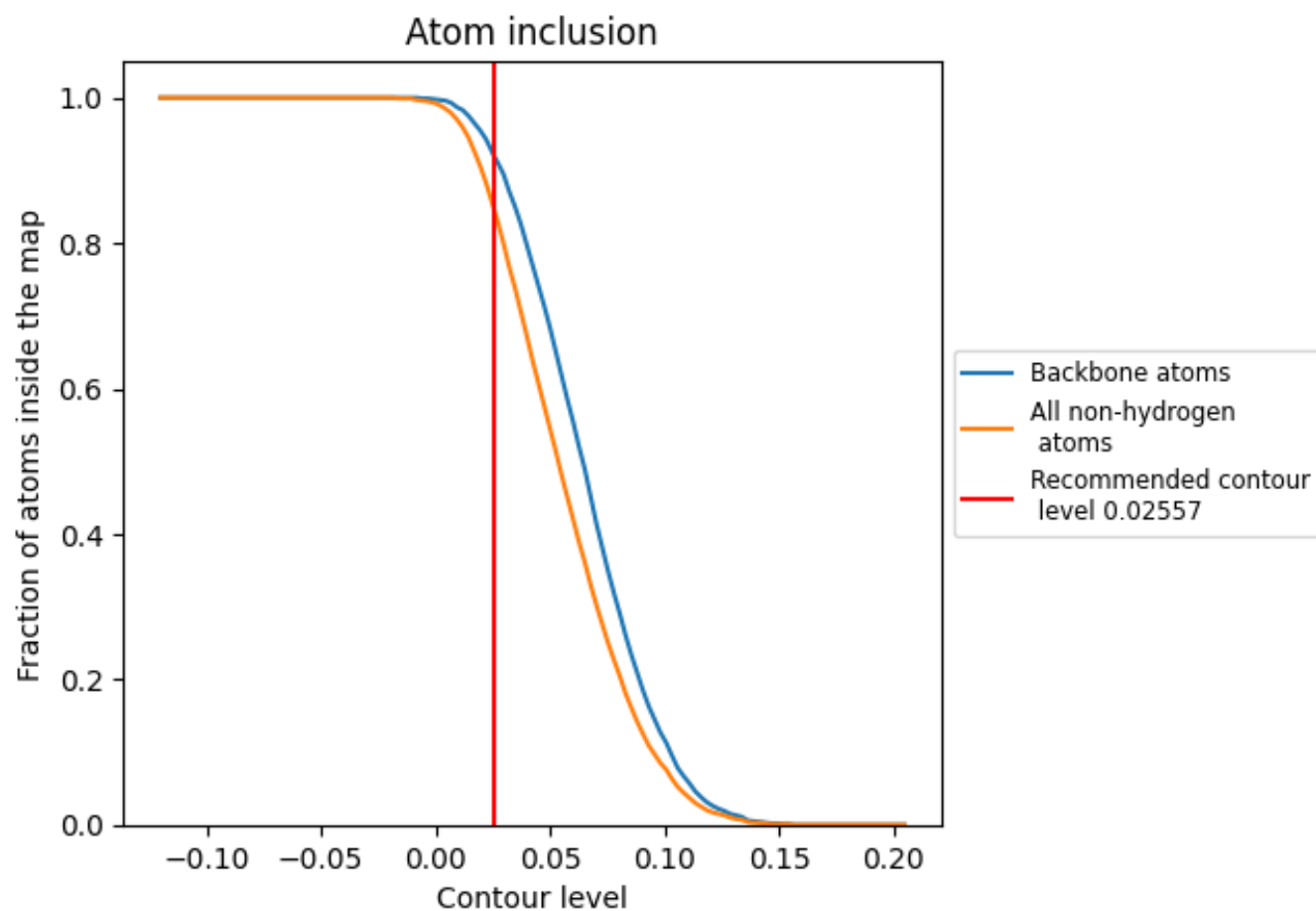
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02557).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (0.02557) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8460	0.4890
A	0.8870	0.5130
B	0.8390	0.4780
C	0.8160	0.4760
D	0.8800	0.5110
E	0.8390	0.4810
F	0.8170	0.4780

