wwPDB EM Validation Summary Report

Nov 10, 2026 – 12:11 PM JST

PDB ID	:	47NP / pdb_000047np
EMDB ID	:	EMD-84557
Title	:	Cryo-EM structure of Dicer in the compact apo state
Authors	:	Nguyen, P.D.; Nguyen, T.A.
Deposited on	:	2026-10-27
Resolution	:	3.71 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:

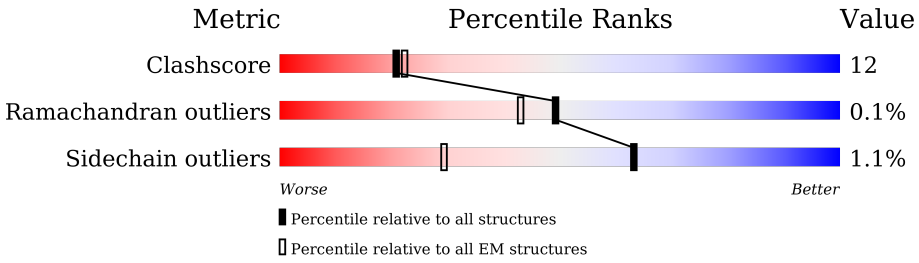
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

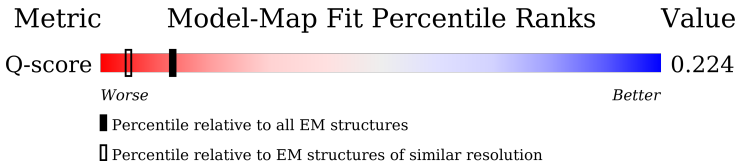
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.71 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	10534 (3.21 - 4.21)

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 <=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	1909	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 10516 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 Endoribonuclease Dicer.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1309	10516	6701	1798	1959	58	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	MET	-	initiating methionine	UNP Q9UPY3
A	15	GLY	-	expression tag	UNP Q9UPY3
A	16	HIS	-	expression tag	UNP Q9UPY3
A	17	HIS	-	expression tag	UNP Q9UPY3
A	18	HIS	-	expression tag	UNP Q9UPY3
A	19	HIS	-	expression tag	UNP Q9UPY3
A	20	HIS	-	expression tag	UNP Q9UPY3
A	21	HIS	-	expression tag	UNP Q9UPY3
A	22	HIS	-	expression tag	UNP Q9UPY3
A	23	HIS	-	expression tag	UNP Q9UPY3
A	24	HIS	-	expression tag	UNP Q9UPY3
A	25	HIS	-	expression tag	UNP Q9UPY3

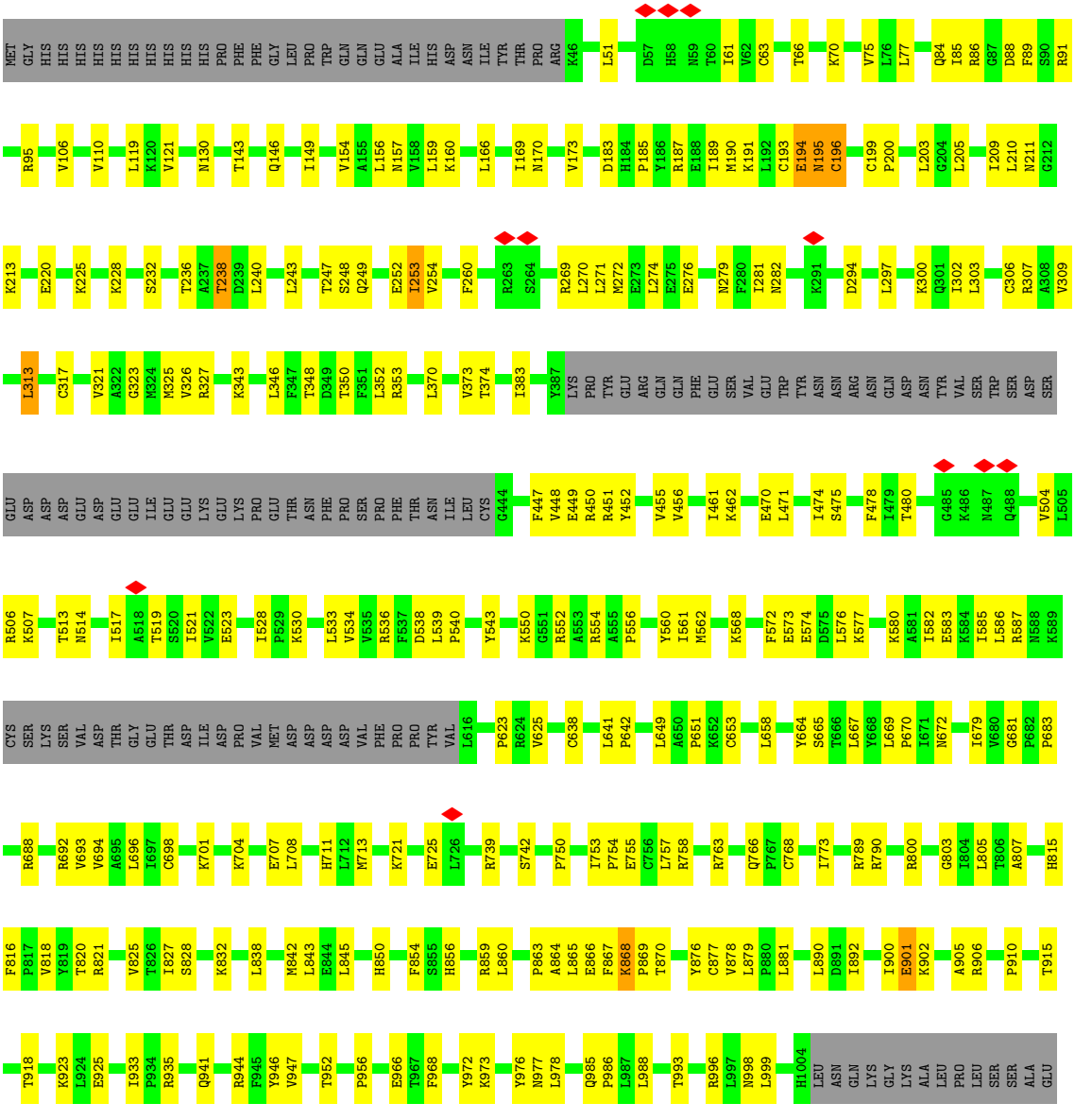
3 Residue-property plots (i)

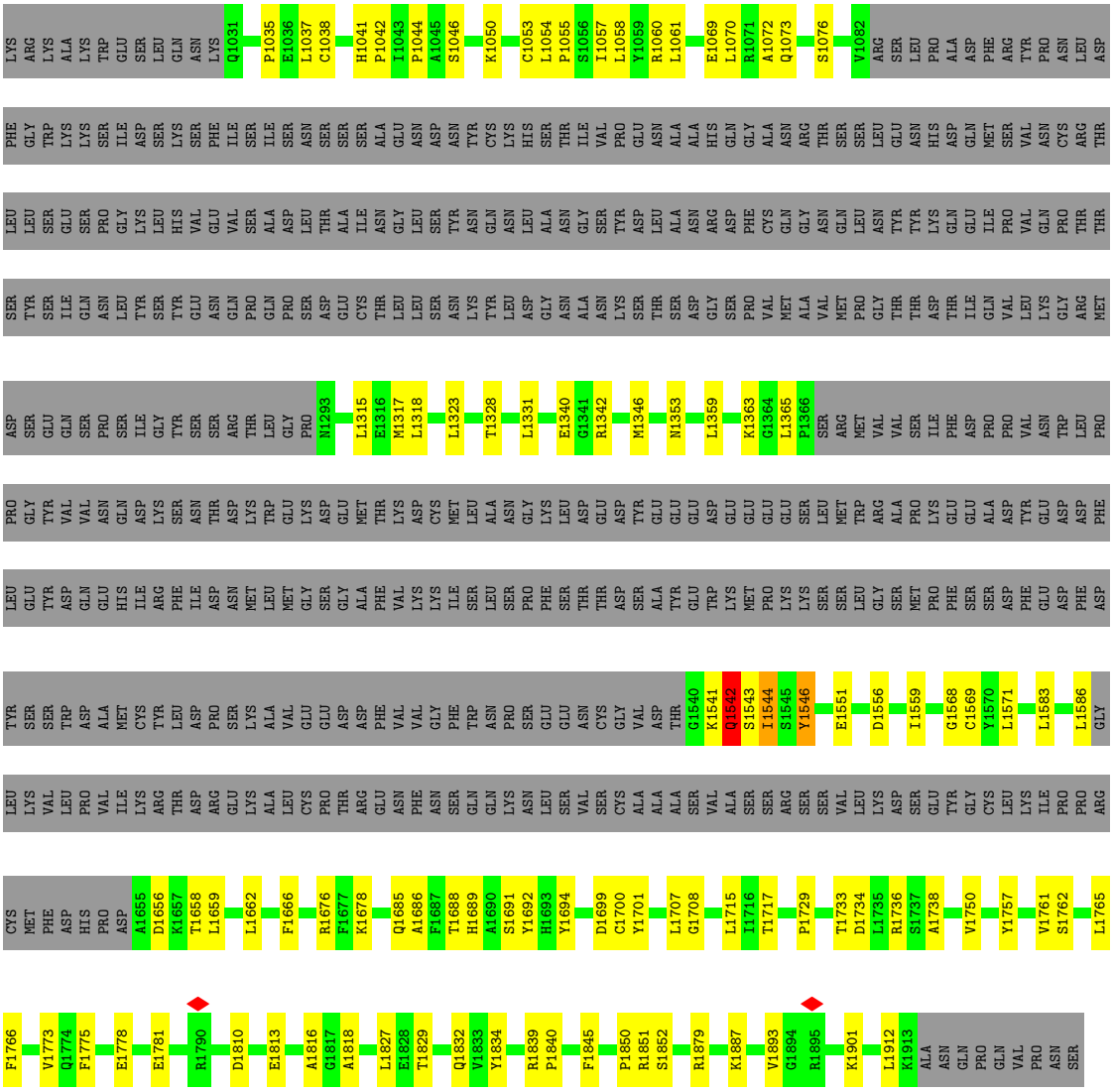
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Endoribonuclease Dicer

Chain A:






LYS ARG LYS ALA LYS TRP GLU SER LEU GLN ASN LYS Q1031 P1035 E1036 L1037 C1038 H1041 P1042 I1043 P1044 A1045 S1046 K1050 C1053 L1054 P1055 S1056 I1057 L1058 Y1059 R1060 L1061 E1069 L1070 R1071 A1072 Q1073 S1076 V1082 ARG SER LEU PRO ALA ASP PHE ARG TYR PRO ASN LEU ASP
PHE GLY TRP LYS LYS SER ILE ASP SER LYS SER PHE ILE SER ILE SER ASN SER SER SER ALA GLU ASN ASP ASN TYR CYS LYS HIS SER THR ILE VAL PRO GLU ASN ALA ALA HIS GLN GLY ALA ASN ARG THR SER SER LEU GLU ASN HIS ASP GLN MET SER VAL ASN CYS ARG THR
LEU LEU SER GLU SER PRO GLY LYS LEU HIS VAL GLU VAL SER ALA ASP LEU THR ALA ILE ASN GLY LEU SER TYR ASN GLN ASN LEU ALA ASN GLY SER TYR ASP LEU ALA ASN ARG ASP PHE CYS GLN GLY ASN GLY ARG THR GLN GLU ILE PRO VAL GLN PRO THR THR
SER TYR SER ILE GLN ASN LEU TYR SER TYR GLU ASN GLN PRO GLN PRO SER ASP GLU CYS THR LEU LEU SER ASN LYS TYR LEU ASP GLY ASN ALA ASN LYS SER THR SER ASP GLY SER PRO VAL MET ALA VAL MET MET PRO GLY THR THR ASP THR ILE GLN VAL LEU LYS GLY ARG MET
ASP SER GLU GLN SER PRO SER ILE GLY TYR SER SER ARG THR LEU GLY PRO N1293 L1315 E1316 M1317 L1318 L1323 T1328 L1331 E1340 G1341 R1342 M1346 N1353 L1359 K1363 G1364 L1365 P1366 SER ARG MET VAL VAL SER ILE PHE ASP PRO PRO VAL ASN TRP LEU PRO
PRO GLY TYR VAL VAL ASN GLN ASP LYS SER ASN THR ASP LYS TRP GLU LYS ASP GLU MET THR LYS ASP CYS MET LEU ALA ASN GLY LYS LEU ASP GLU ASP TYR GLU GLU GLU ASP GLU GLU GLU GLU SER LEU MET TRP ARG ALA PRO LYS GLU GLU ALA ASP TYR GLU ASP ASP PHE
LEU GLU TYR ASP GLN GLU HIS ILE ARG PHE ILE ASP ASN MET LEU MET GLY SER GLY ALA PHE VAL LYS LYS ILE SER LEU SER PRO PRO PHE SER THR THR ASP SER ALA TYR GLU TRP LYS MET PRO LYS LYS SER SER LEU GLY SER MET PRO PHE SER SER ASP PHE GLU ASP PHE ASP
TYR SER SER TRP ASP ALA MET CYS TYR LEU ASP PRO SER LYS ALA VAL GLU GLU ASP ASP PHE VAL VAL GLY PHE TRP ASN PRO SER GLU GLU ASN CYS GLY VAL ASP THR G1540 K1541 Q1542 S1543 I1544 S1545 Y1546 E1551 D1556 I1559 G1568 C1569 Y1570 L1571 L1583 L1586 GLY
LEU LYS VAL LEU PRO VAL ILE LYS ARG THR ASP ARG GLU LYS ALA LEU CYS PRO THR ARG GLU ASN PHE ASN SER GLN GLN LYS ASN LEU SER VAL SER CYS ALA ALA ALA SER VAL ALA SER SER ARG SER SER VAL LEU LYS ASP SER GLU TYR GLY CYS LEU LYS ILE PRO PRO ARG
CYS MET PHE ASP HIS PRO ASP A1655 D1656 K1657 T1658 L1659 L1662 F1666 R1676 F1677 K1678 Q1685 A1686 F1687 T1688 H1689 A1690 S1691 Y1692 H1693 Y1694 D1699 C1700 Y1701 L1707 G1708 L1715 I1716 T1717 P1729 T1733 D1734 L1735 R1736 S1737 A1738 V1750 Y1757 V1761 S1762 L1765
F1766 V1773 Q1774 F1775 E1778 E1781 R1790 D1810 E1813 A1816 G1817 A1818 L1827 E1828 T1829 Q1832 V1833 Y1834 R1839 P1840 F1845 P1850 R1851 S1852 R1879 K1887 V1893 G1894 R1895 K1901 L1912 K1913 ALA ASN GLN PRO GLN VAL PRO ASN SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	318300	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 ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.423	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.0396	Depositor
Map size (Å)	269.056, 269.056, 269.056	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.051, 1.051, 1.051	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.17	0/10734	0.37	5/14521 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	194	GLU	N-CA-C	-8.66	100.86	111.33
1	A	253	ILE	CA-C-N	-7.07	114.43	123.19
1	A	253	ILE	C-N-CA	-7.07	114.43	123.19
1	A	1546	TYR	N-CA-CB	-5.75	101.47	110.44
1	A	1542	GLN	N-CA-C	5.24	121.95	110.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	10516	0	10588	253	0
All	All	10516	0	10588	253	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 12.

The worst 5 of 253 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:1541:LYS:O	1:A:1544:ILE:HD12	1.51	1.10
1:A:1541:LYS:O	1:A:1544:ILE:CD1	1.99	1.09
1:A:1072:ALA:O	1:A:1076:SER:HB3	1.70	0.92
1:A:193:CYS:HA	1:A:196:CYS:HB3	1.58	0.85
1:A:998:ASN:HA	1:A:1542:GLN:HE21	1.44	0.83

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	1295/1909 (68%)	1221 (94%)	73 (6%)	1 (0%)	48 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1542	GLN

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	1174/1721 (68%)	1161 (99%)	13 (1%)	65 73

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	867	PHE
1	A	868	LYS
1	A	1544	ILE
1	A	966	GLU
1	A	1542	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1542	GLN
1	A	1776	GLN
1	A	1780	ASN
1	A	249	GLN
1	A	856	HIS

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.

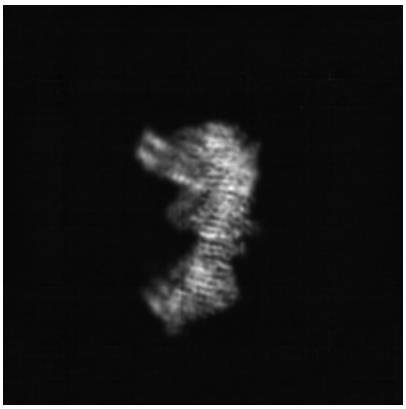
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-84557. These allow visual inspection of the internal detail of the map and identification of artifacts.

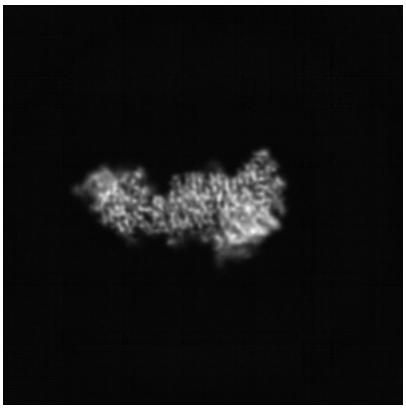
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

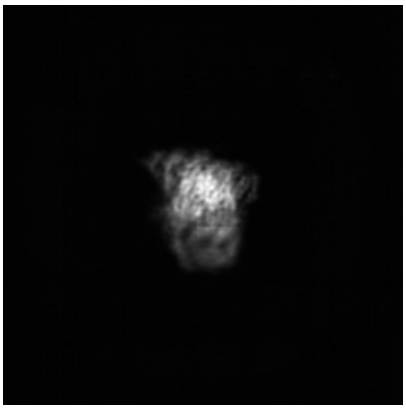
6.1.1 Primary map



X

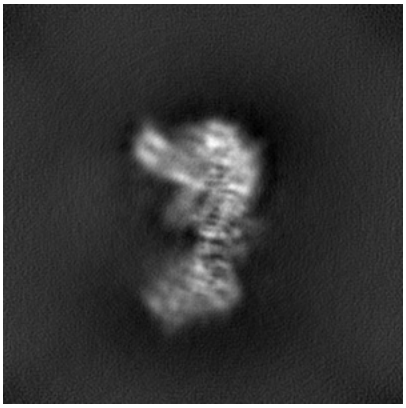


Y

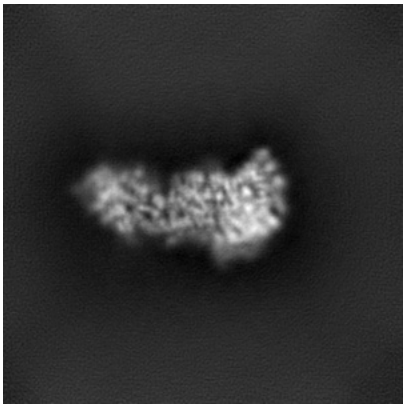


Z

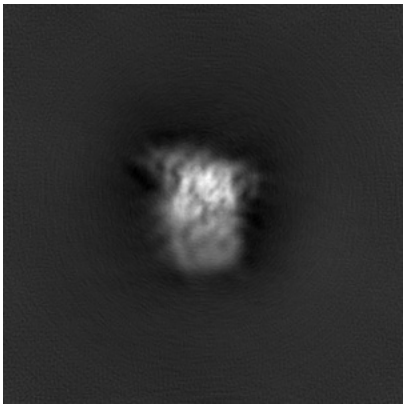
6.1.2 Raw map



X



Y

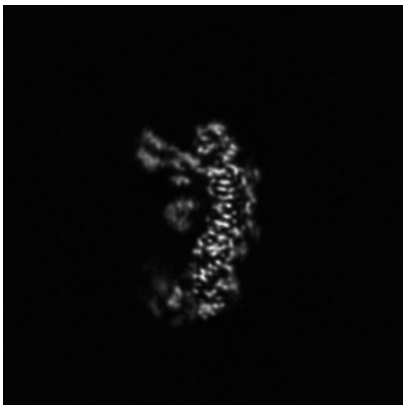


Z

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

6.2 Central slices (i)

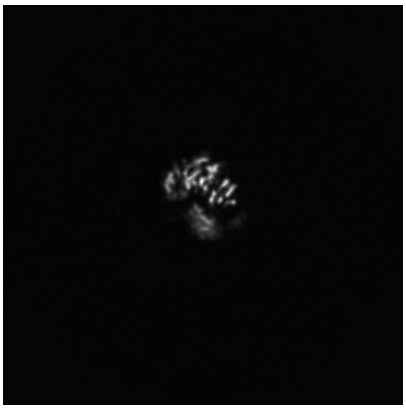
6.2.1 Primary map



X Index: 128



Y Index: 128

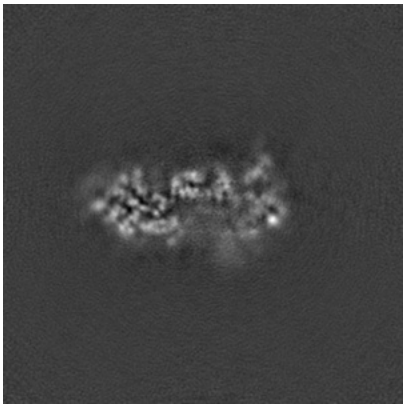


Z Index: 128

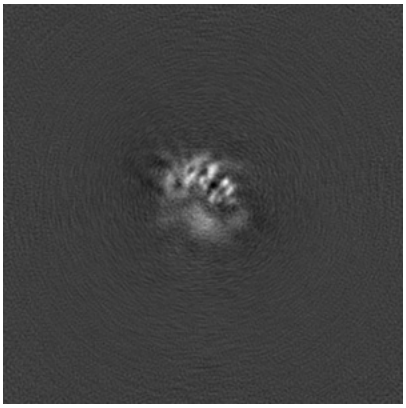
6.2.2 Raw map



X Index: 128



Y Index: 128

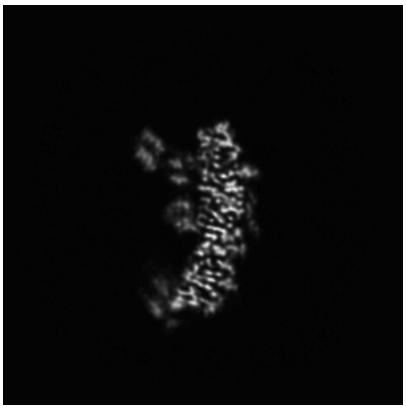


Z Index: 128

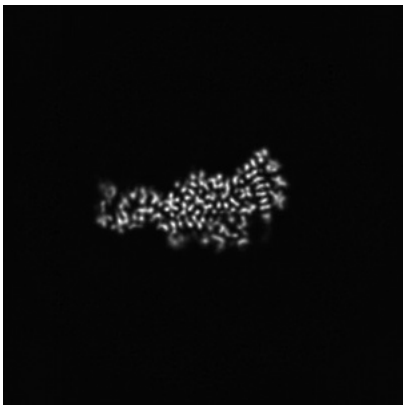
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

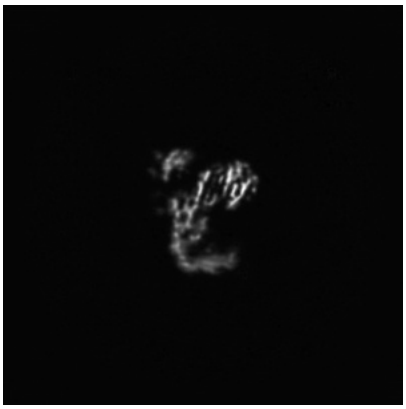
6.3.1 Primary map



X Index: 131



Y Index: 140

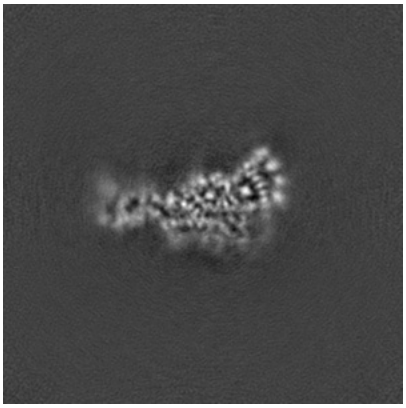


Z Index: 160

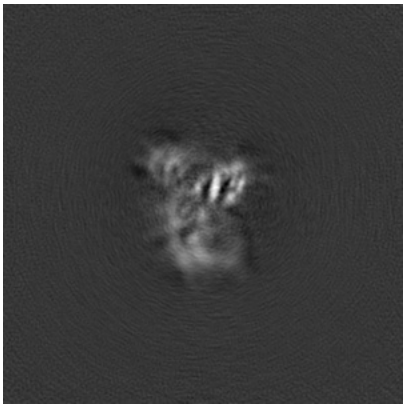
6.3.2 Raw map



X Index: 132



Y Index: 141

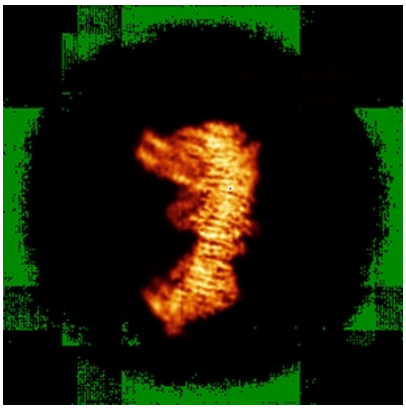


Z Index: 156

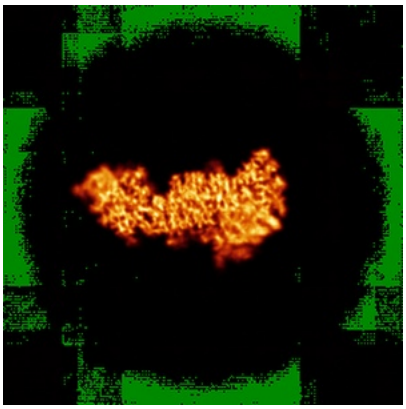
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

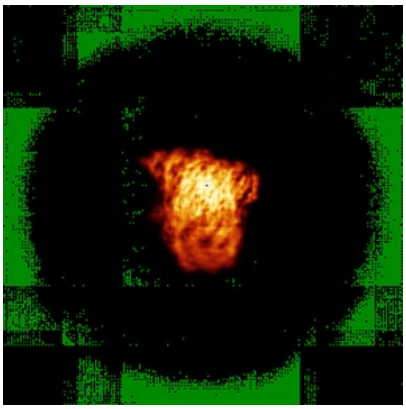
6.4.1 Primary map



X

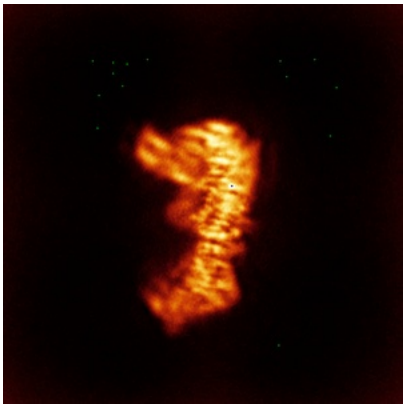


Y

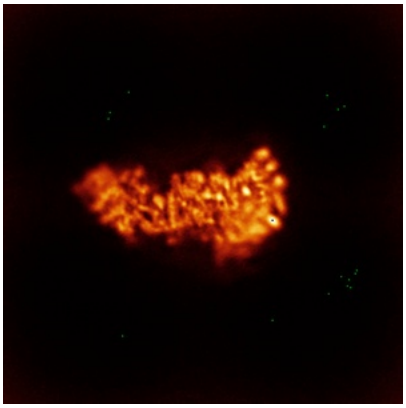


Z

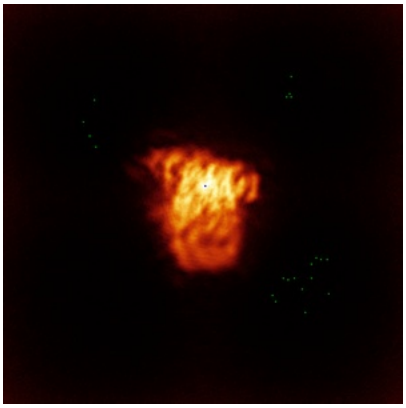
6.4.2 Raw map



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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0396. 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



X Y Z

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.

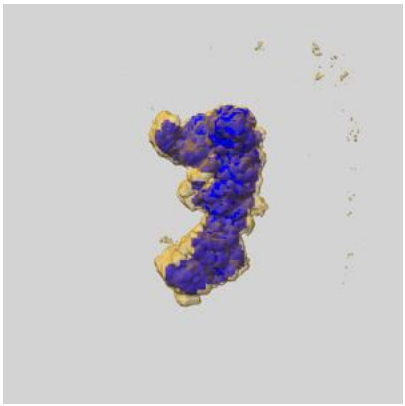
6.6 Mask visualisation (i)

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

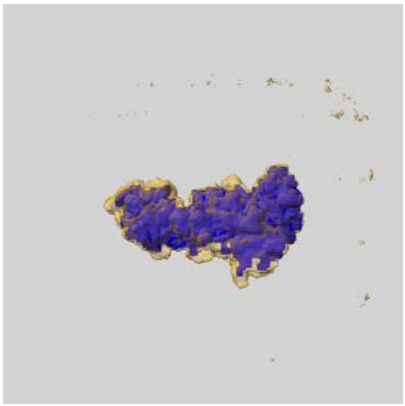
A mask typically either:

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

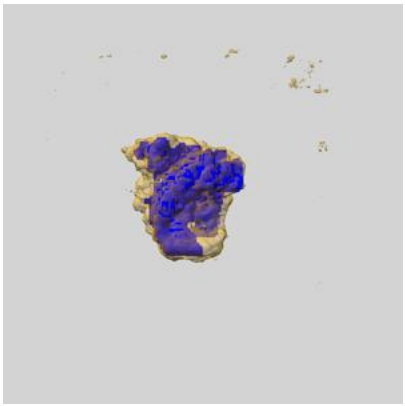
6.6.1 emd_84557_msk_1.map (i)



X



Y

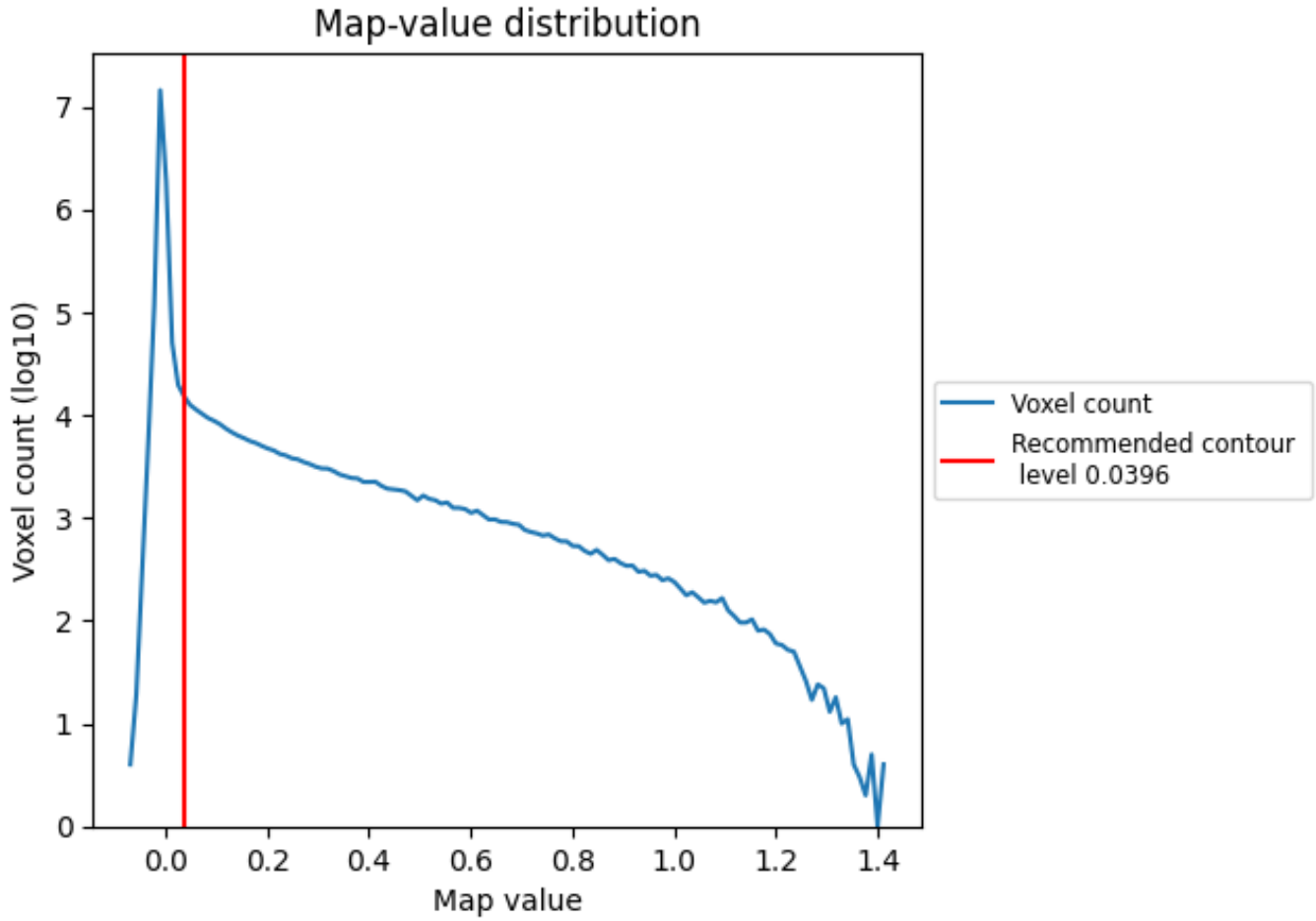


Z

7 Map analysis

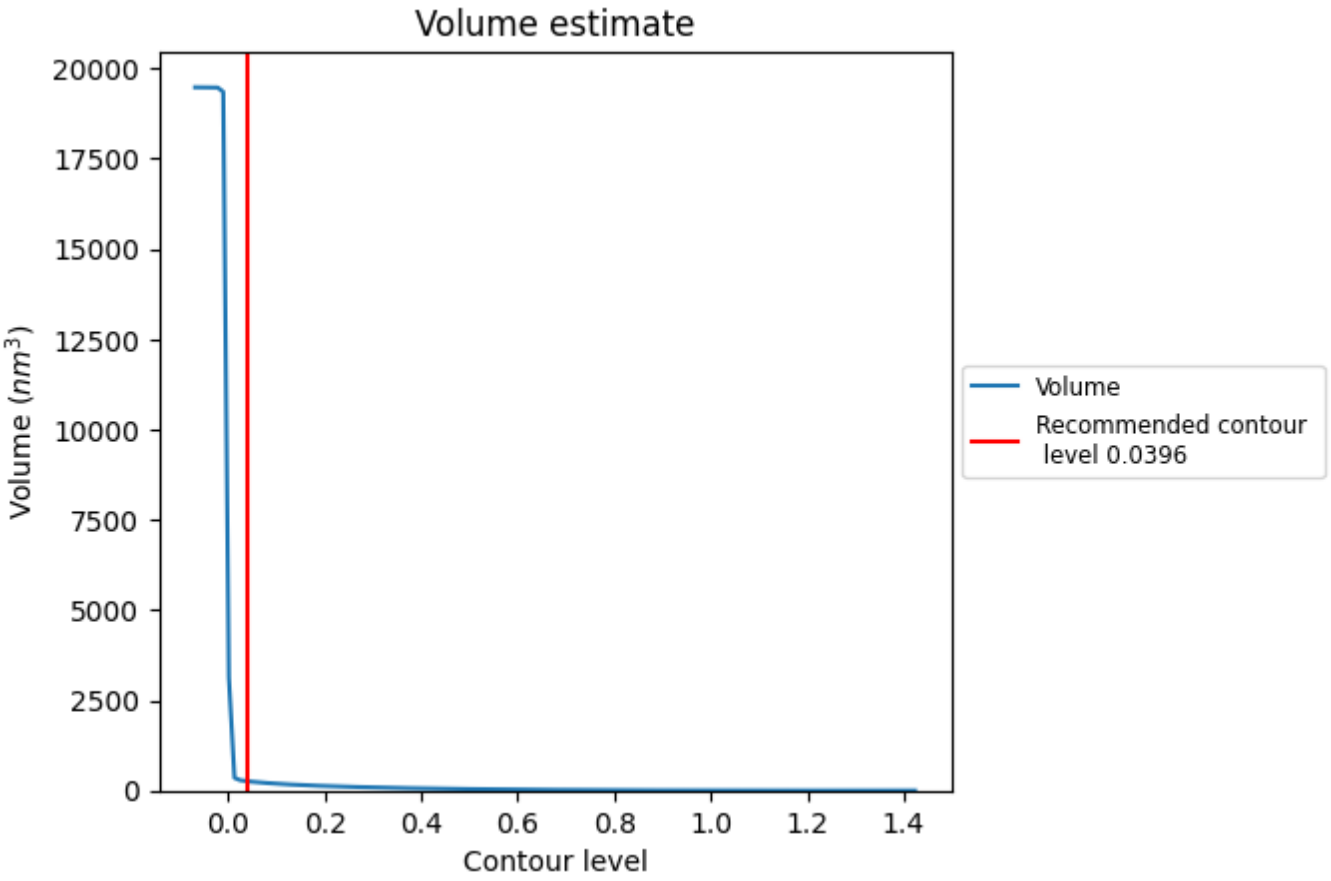
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

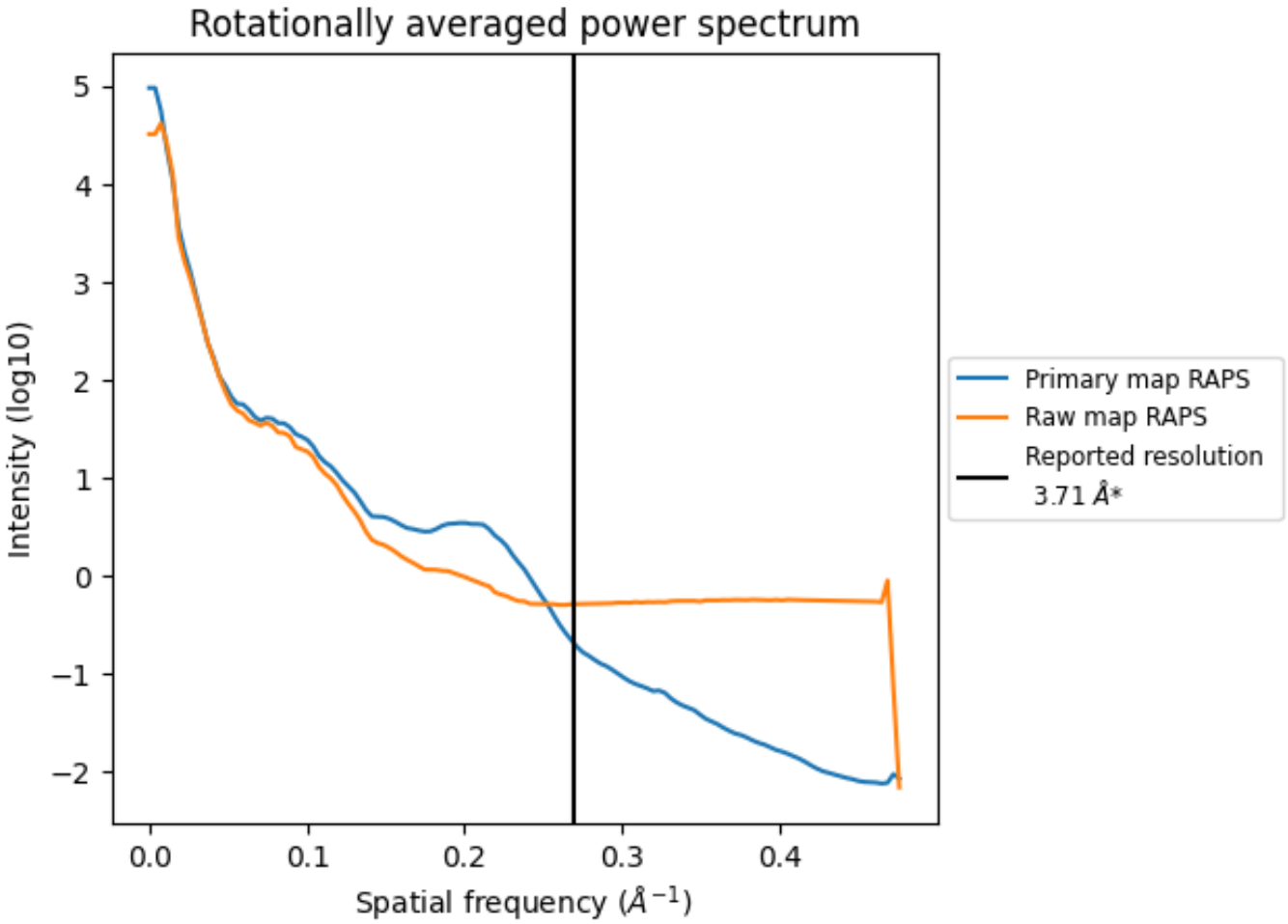
7.2 Volume estimate (i)



The volume at the recommended contour level is 259 nm^3; this corresponds to an approximate mass of 234 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 (i)

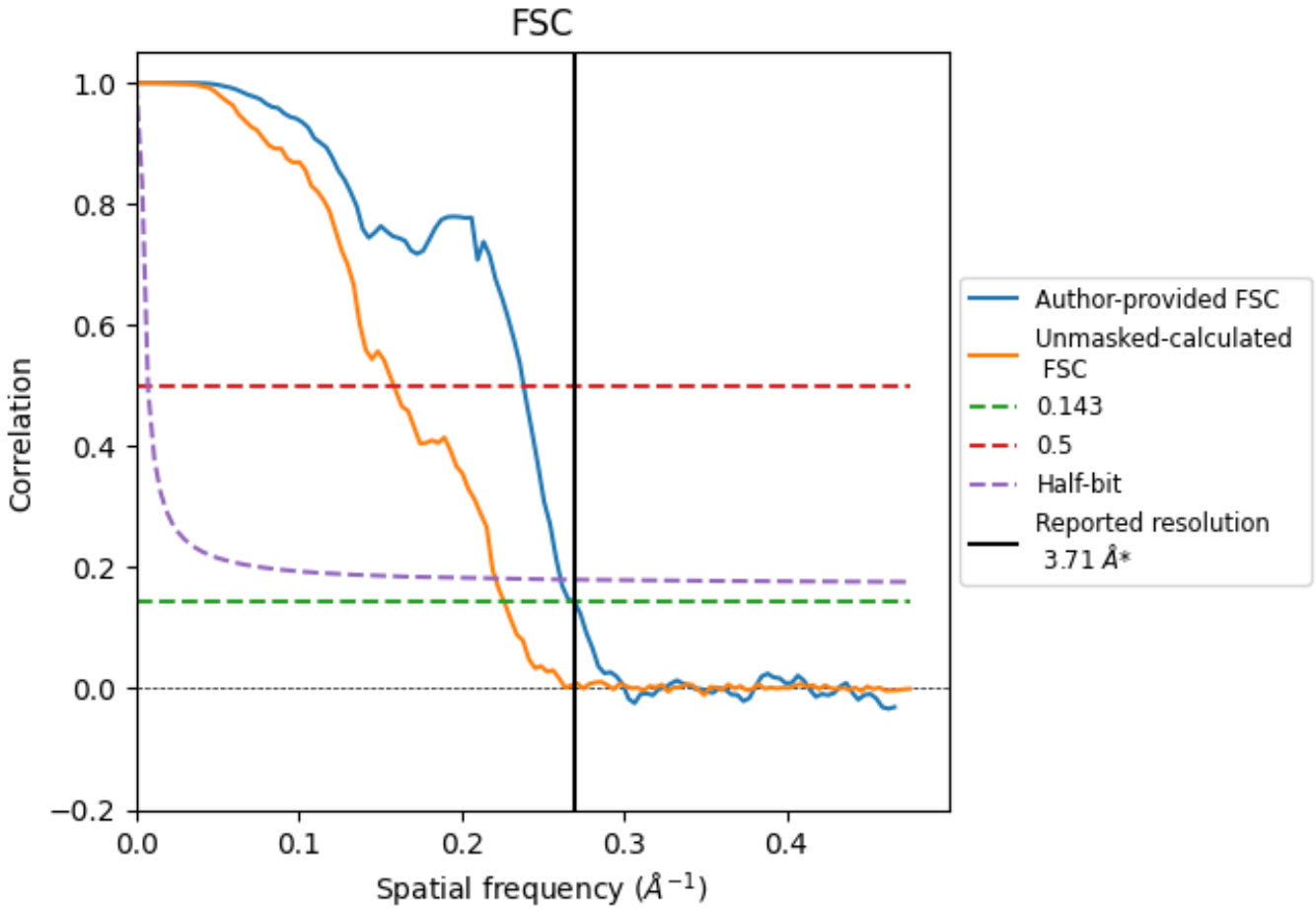


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

8.2 Resolution estimates (i)

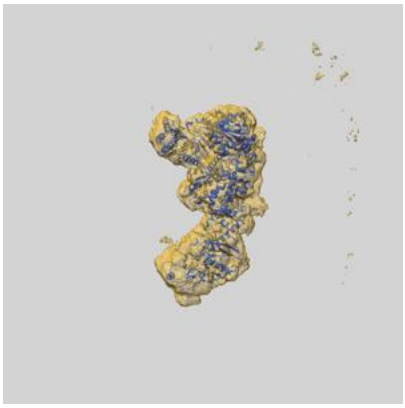
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.71	-	-
Author-provided FSC curve	3.71	4.19	3.83
Unmasked-calculated*	4.42	6.31	4.52

*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 4.42 differs from the reported value 3.71 by more than 10 %

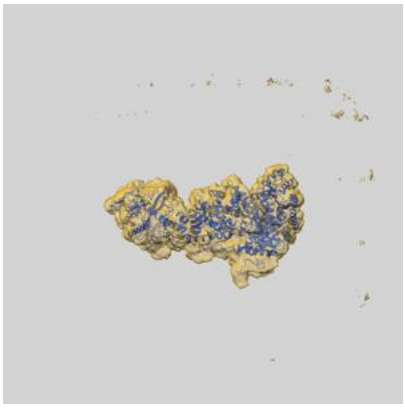
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-84557 and PDB model 47NP. Per-residue inclusion information can be found in section 3 on page 4.

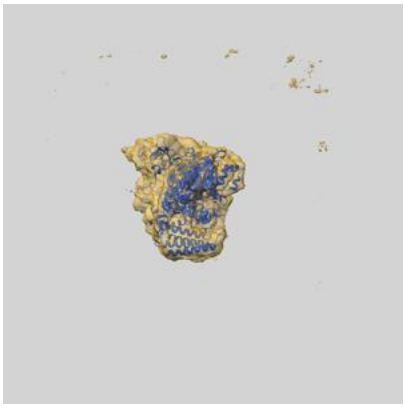
9.1 Map-model overlay



X



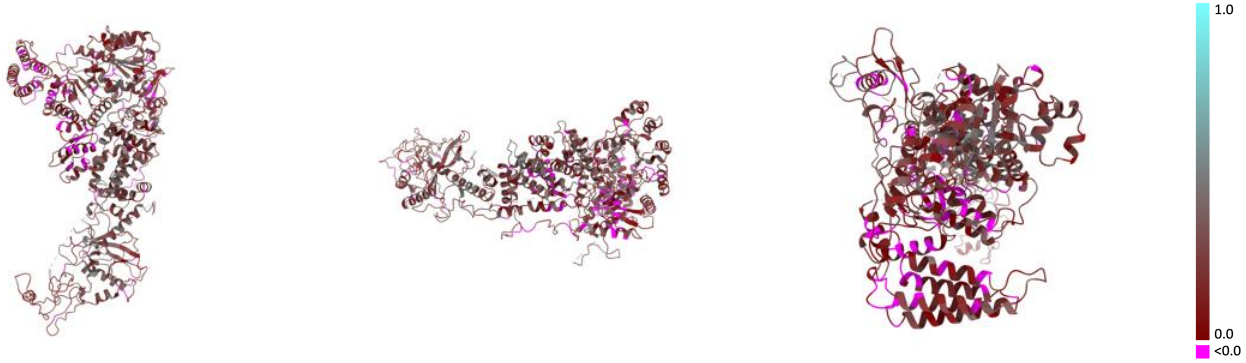
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0396 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.

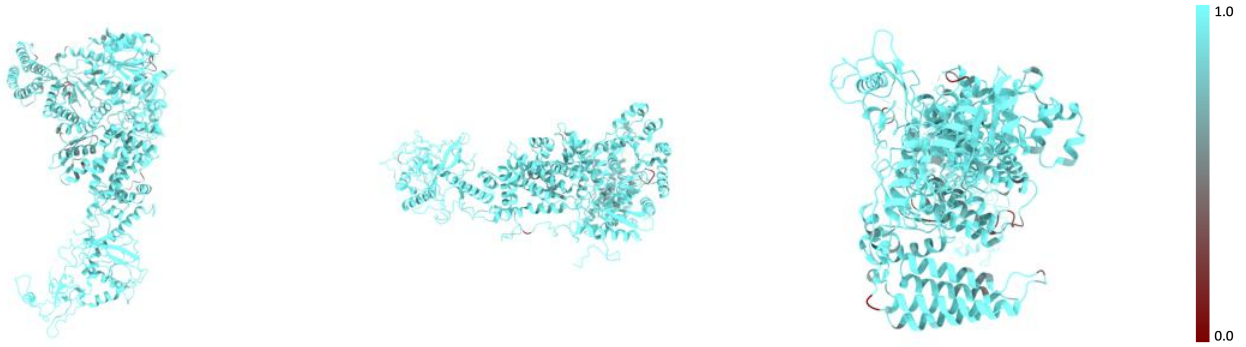
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

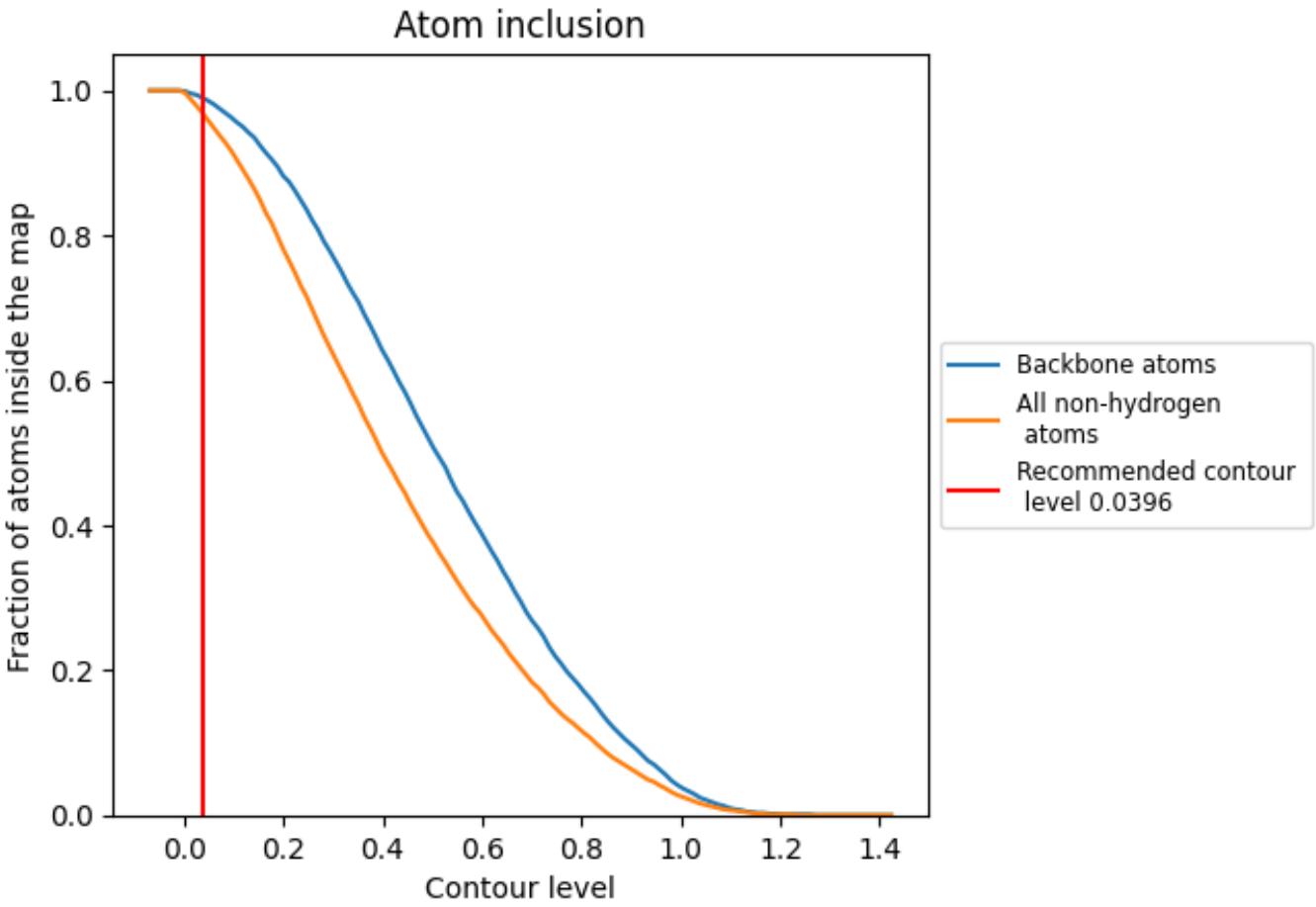
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0396).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.0396) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.9670	0.2240
A	0.9670	0.2240