



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:16 AM UTC

PDB ID : 7YZ4 / pdb_00007yz4
EMDB ID : EMD-14387
Title : Mouse endoribonuclease Dicer (composite structure)
Authors : Zanova, M.; Zapletal, D.; Kubicek, K.; Stefl, R.; Pinkas, M.; Novacek, J.
Deposited on : 2022-02-18
Resolution : 3.84 Å (reported)

This is a Full wwPDB EM Validation 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

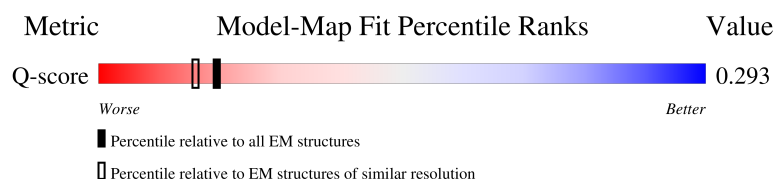
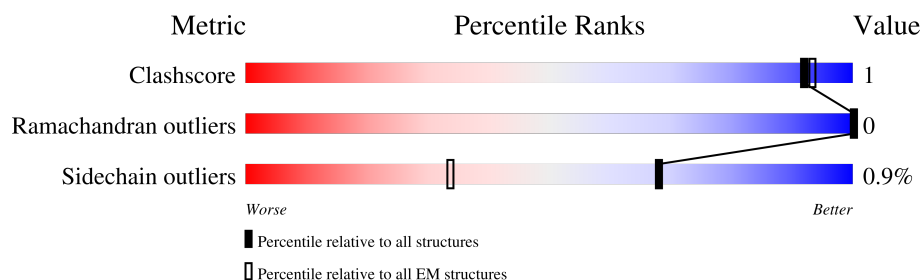
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.84 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	9033 (3.34 - 4.34)

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	2004	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19805 atoms, of which 9953 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
1	A	1234	Total 19805	C 6325	H 9953	N 1675	O 1797	S 55	0	0

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-52	MET	-	initiating methionine	UNP Q8R418
A	-51	VAL	-	expression tag	UNP Q8R418
A	-50	TRP	-	expression tag	UNP Q8R418
A	-49	SER	-	expression tag	UNP Q8R418
A	-48	HIS	-	expression tag	UNP Q8R418
A	-47	PRO	-	expression tag	UNP Q8R418
A	-46	GLN	-	expression tag	UNP Q8R418
A	-45	PHE	-	expression tag	UNP Q8R418
A	-44	GLU	-	expression tag	UNP Q8R418
A	-43	LYS	-	expression tag	UNP Q8R418
A	-42	GLY	-	expression tag	UNP Q8R418
A	-41	GLY	-	expression tag	UNP Q8R418
A	-40	GLY	-	expression tag	UNP Q8R418
A	-39	SER	-	expression tag	UNP Q8R418
A	-38	GLY	-	expression tag	UNP Q8R418
A	-37	GLY	-	expression tag	UNP Q8R418
A	-36	GLY	-	expression tag	UNP Q8R418
A	-35	SER	-	expression tag	UNP Q8R418
A	-34	GLY	-	expression tag	UNP Q8R418
A	-33	GLY	-	expression tag	UNP Q8R418
A	-32	SER	-	expression tag	UNP Q8R418
A	-31	ALA	-	expression tag	UNP Q8R418
A	-30	TRP	-	expression tag	UNP Q8R418
A	-29	SER	-	expression tag	UNP Q8R418
A	-28	HIS	-	expression tag	UNP Q8R418
A	-27	PRO	-	expression tag	UNP Q8R418
A	-26	GLN	-	expression tag	UNP Q8R418
A	-25	PHE	-	expression tag	UNP Q8R418

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	GLU	-	expression tag	UNP Q8R418
A	-23	LYS	-	expression tag	UNP Q8R418
A	-22	GLY	-	expression tag	UNP Q8R418
A	-21	ASP	-	expression tag	UNP Q8R418
A	-20	TYR	-	expression tag	UNP Q8R418
A	-19	PRO	-	expression tag	UNP Q8R418
A	-18	TYR	-	expression tag	UNP Q8R418
A	-17	ASP	-	expression tag	UNP Q8R418
A	-16	VAL	-	expression tag	UNP Q8R418
A	-15	PRO	-	expression tag	UNP Q8R418
A	-14	ASP	-	expression tag	UNP Q8R418
A	-13	TYR	-	expression tag	UNP Q8R418
A	-12	ALA	-	expression tag	UNP Q8R418
A	-11	GLY	-	expression tag	UNP Q8R418
A	-10	THR	-	expression tag	UNP Q8R418
A	-9	GLU	-	expression tag	UNP Q8R418
A	-8	ASN	-	expression tag	UNP Q8R418
A	-7	LEU	-	expression tag	UNP Q8R418
A	-6	TYR	-	expression tag	UNP Q8R418
A	-5	PHE	-	expression tag	UNP Q8R418
A	-4	GLN	-	expression tag	UNP Q8R418
A	-3	GLY	-	expression tag	UNP Q8R418
A	-2	LEU	-	expression tag	UNP Q8R418
A	-1	VAL	-	expression tag	UNP Q8R418
A	0	ASP	-	expression tag	UNP Q8R418
A	1110	SER	THR	conflict	UNP Q8R418
A	1560	ALA	GLU	conflict	UNP Q8R418
A	1619	SER	ALA	conflict	UNP Q8R418
A	1807	ALA	GLU	conflict	UNP Q8R418
A	1917	GLY	-	expression tag	UNP Q8R418
A	1918	ARG	-	expression tag	UNP Q8R418
A	1919	GLY	-	expression tag	UNP Q8R418
A	1920	GLU	-	expression tag	UNP Q8R418
A	1921	ASN	-	expression tag	UNP Q8R418
A	1922	LEU	-	expression tag	UNP Q8R418
A	1923	TYR	-	expression tag	UNP Q8R418
A	1924	PHE	-	expression tag	UNP Q8R418
A	1925	GLN	-	expression tag	UNP Q8R418
A	1926	GLY	-	expression tag	UNP Q8R418
A	1927	ALA	-	expression tag	UNP Q8R418
A	1928	SER	-	expression tag	UNP Q8R418
A	1929	ASP	-	expression tag	UNP Q8R418

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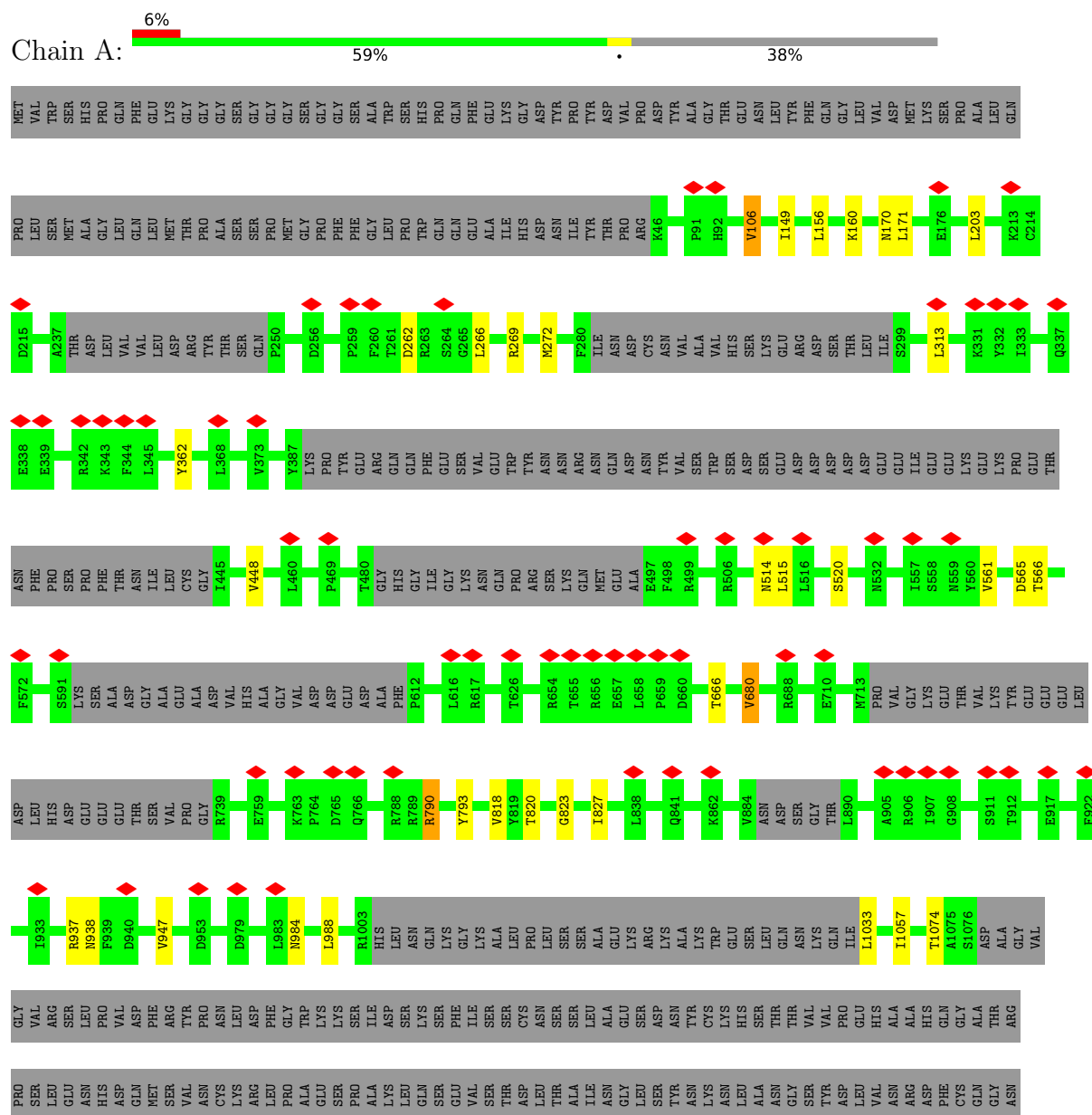
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Chain	Residue	Modelled	Actual	Comment	Reference
A	1930	TYR	-	expression tag	UNP Q8R418
A	1931	LYS	-	expression tag	UNP Q8R418
A	1932	ASP	-	expression tag	UNP Q8R418
A	1933	HIS	-	expression tag	UNP Q8R418
A	1934	ASP	-	expression tag	UNP Q8R418
A	1935	GLY	-	expression tag	UNP Q8R418
A	1936	ASP	-	expression tag	UNP Q8R418
A	1937	TYR	-	expression tag	UNP Q8R418
A	1938	LYS	-	expression tag	UNP Q8R418
A	1939	ASP	-	expression tag	UNP Q8R418
A	1940	HIS	-	expression tag	UNP Q8R418
A	1941	ASP	-	expression tag	UNP Q8R418
A	1942	GLY	-	expression tag	UNP Q8R418
A	1943	SER	-	expression tag	UNP Q8R418
A	1944	HIS	-	expression tag	UNP Q8R418
A	1945	HIS	-	expression tag	UNP Q8R418
A	1946	HIS	-	expression tag	UNP Q8R418
A	1947	HIS	-	expression tag	UNP Q8R418
A	1948	HIS	-	expression tag	UNP Q8R418
A	1949	HIS	-	expression tag	UNP Q8R418
A	1950	HIS	-	expression tag	UNP Q8R418
A	1951	HIS	-	expression tag	UNP Q8R418

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



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92906	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.684	Depositor
Minimum map value	-0.800	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.103	Depositor
Map size (Å)	317.952, 317.952, 317.952	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	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	0.19	0/10066	0.44	1/13634 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	313	LEU	N-CA-C	5.77	115.46	107.73

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	790	ARG	Sidechain

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	9852	9953	9952	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9852	9953	9952	29	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 1.

All (29) 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:514:ASN:OD1	1:A:515:LEU:N	2.28	0.66
1:A:1679:GLN:NE2	1:A:1693:ASP:OD1	2.29	0.66
1:A:269:ARG:NH1	1:A:272:MET:SD	2.75	0.60
1:A:1312:LEU:HD11	1:A:1561:ALA:CB	2.34	0.57
1:A:1373:ILE:O	1:A:1379:ASN:ND2	2.38	0.56
1:A:156:LEU:O	1:A:160:LYS:HG2	2.05	0.56
1:A:790:ARG:NH2	1:A:793:TYR:OH	2.40	0.54
1:A:827:ILE:HD13	1:A:1057:ILE:HG12	1.89	0.53
1:A:106:VAL:HG13	1:A:149:ILE:HG22	1.91	0.52
1:A:448:VAL:O	1:A:520:SER:N	2.43	0.51
1:A:1651:LYS:O	1:A:1655:HIS:ND1	2.43	0.50
1:A:1074:THR:OG1	1:A:1566:TYR:OH	2.25	0.50
1:A:820:THR:N	1:A:823:GLY:O	2.45	0.49
1:A:262:ASP:OD2	1:A:266:LEU:N	2.46	0.49
1:A:170:ASN:OD1	1:A:171:LEU:N	2.46	0.48
1:A:937:ARG:NH1	1:A:938:ASN:OD1	2.46	0.48
1:A:1734:VAL:O	1:A:1734:VAL:HG12	2.13	0.48
1:A:818:VAL:CG1	1:A:827:ILE:HD11	2.47	0.45
1:A:203:LEU:O	1:A:203:LEU:HD23	2.17	0.45
1:A:1885:LYS:O	1:A:1901:ARG:NH1	2.48	0.44
1:A:947:VAL:HG13	1:A:947:VAL:O	2.18	0.44
1:A:666:THR:HG22	1:A:680:VAL:HG12	2.00	0.44
1:A:565:ASP:OD1	1:A:566:THR:N	2.51	0.43
1:A:1755:VAL:HG12	1:A:1755:VAL:O	2.17	0.43
1:A:984:ASN:OD1	1:A:984:ASN:N	2.53	0.42
1:A:1323:LEU:HD13	1:A:1579:LEU:HD21	2.02	0.42
1:A:988:LEU:O	1:A:1033:LEU:N	2.53	0.41
1:A:160:LYS:HA	1:A:160:LYS:HE3	2.03	0.41
1:A:1578:PHE:CE2	1:A:1582:LEU:HD11	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1208/2004 (60%)	1165 (96%)	43 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1089/1772 (62%)	1079 (99%)	10 (1%)	70	75

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	VAL
1	A	362	TYR
1	A	561	VAL
1	A	680	VAL
1	A	1350	LYS
1	A	1372	SER
1	A	1586	VAL
1	A	1726	LEU
1	A	1753	LYS
1	A	1770	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	A	532	ASN
1	A	1689	ASN
1	A	1761	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.

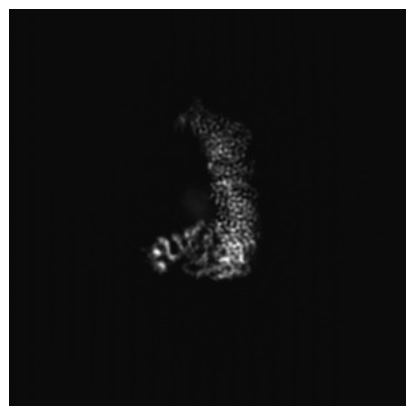
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14387. These allow visual inspection of the internal detail of the map and identification of artifacts.

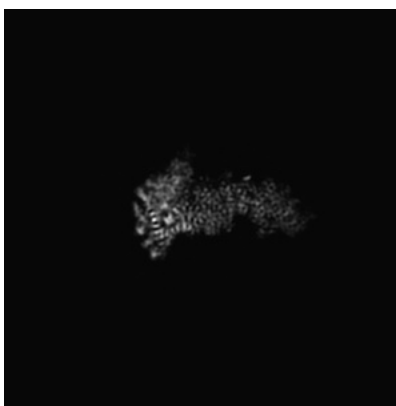
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

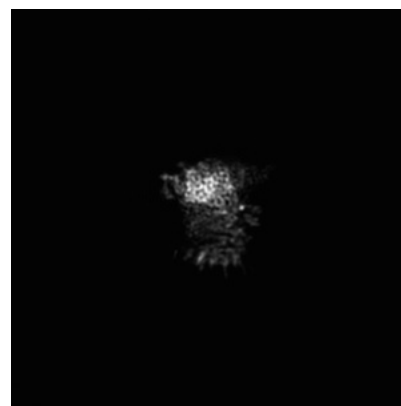
6.1.1 Primary map



X

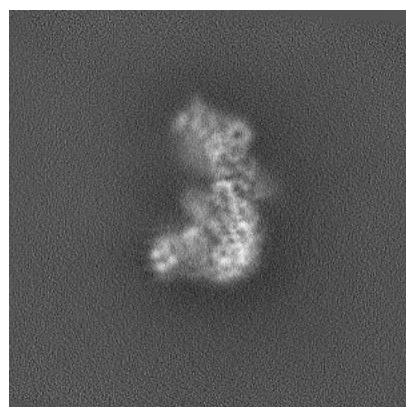


Y

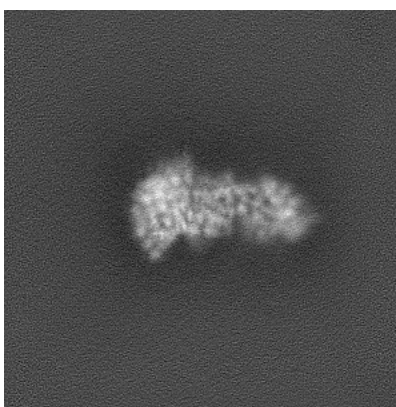


Z

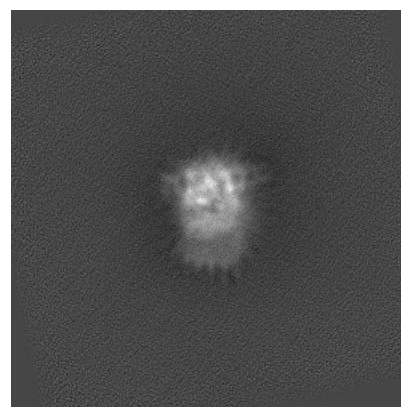
6.1.2 Raw map



X



Y

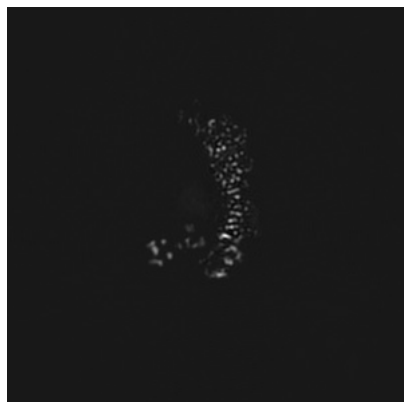


Z

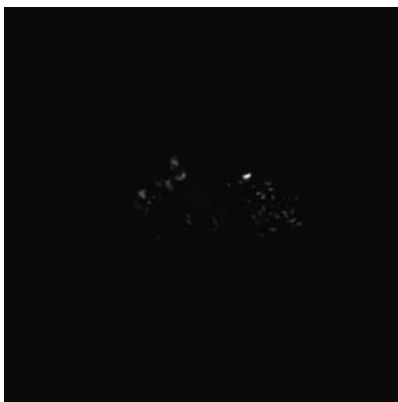
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

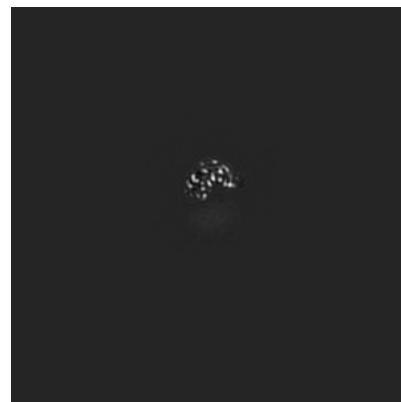
6.2.1 Primary map



X Index: 192

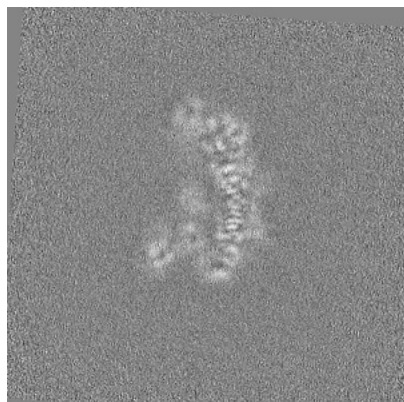


Y Index: 192

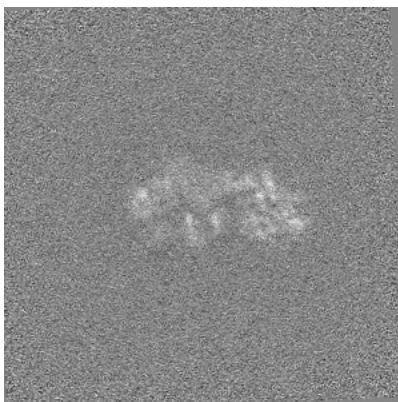


Z Index: 192

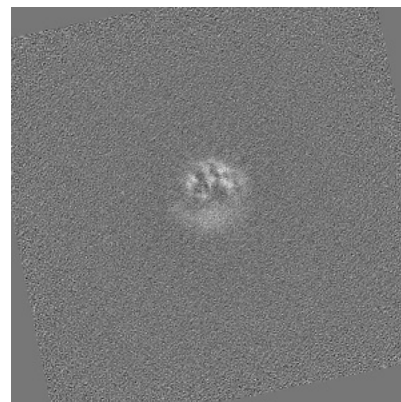
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

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

6.3 Largest variance slices [i](#)

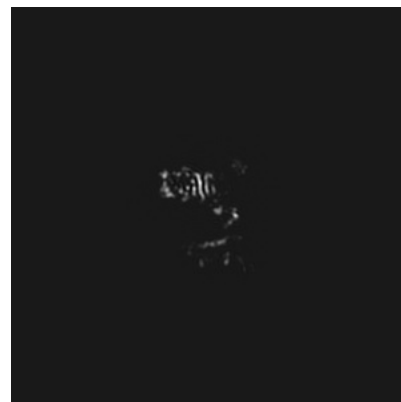
6.3.1 Primary map



X Index: 181

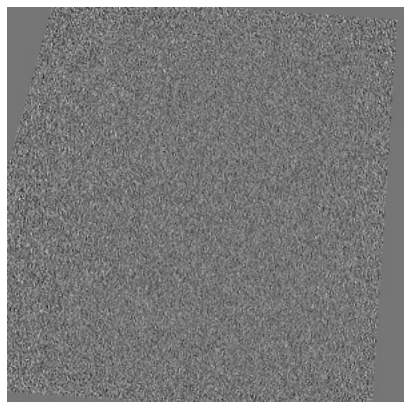


Y Index: 210

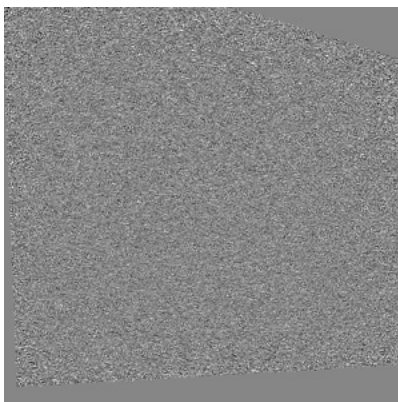


Z Index: 143

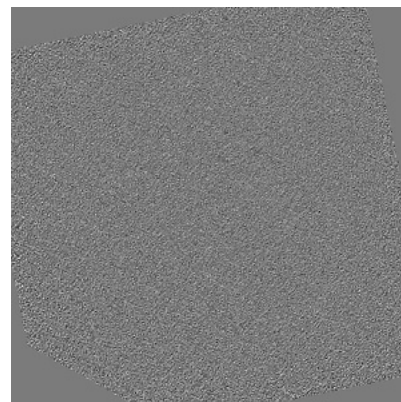
6.3.2 Raw map



X Index: 40



Y Index: 44

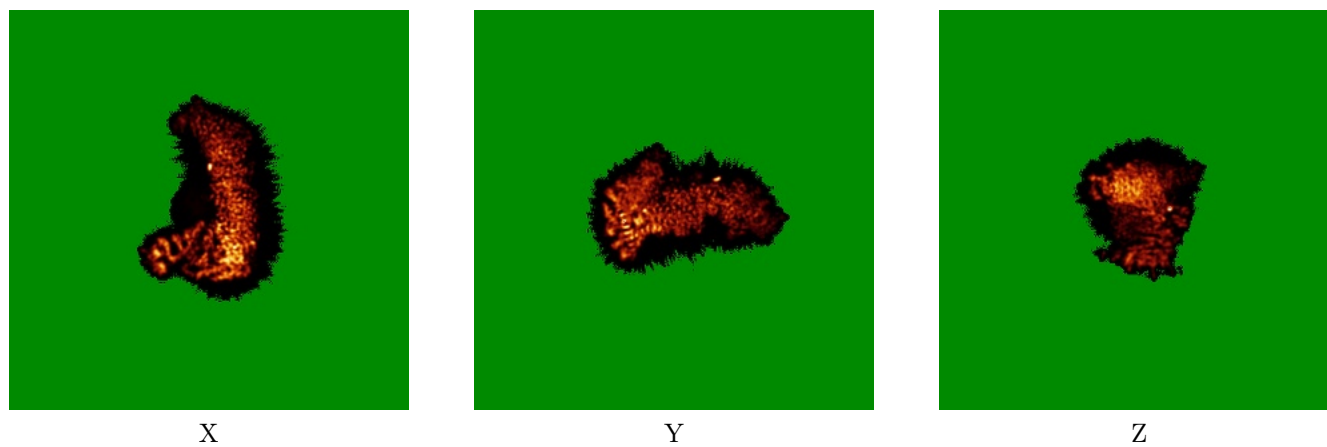


Z Index: 11

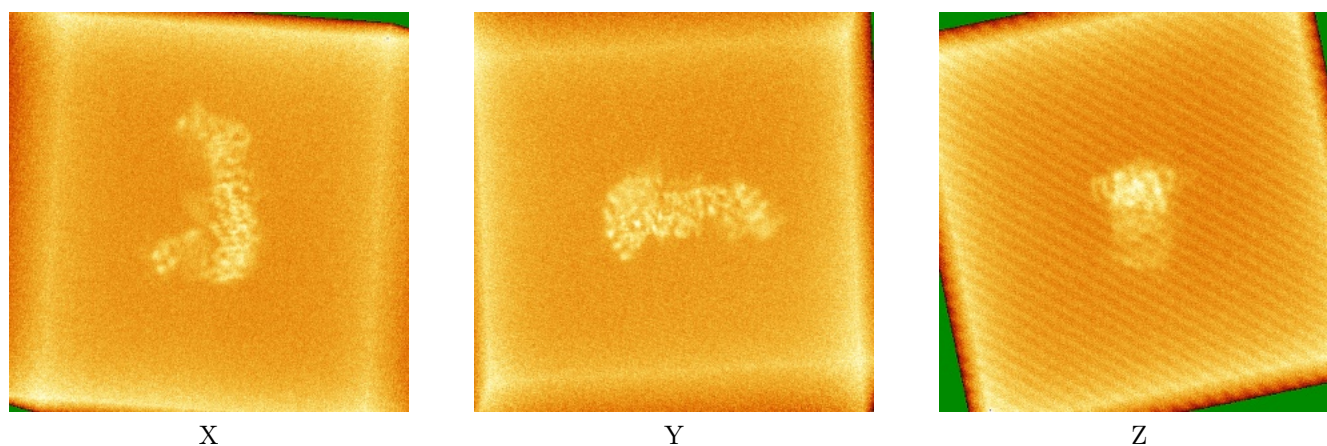
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

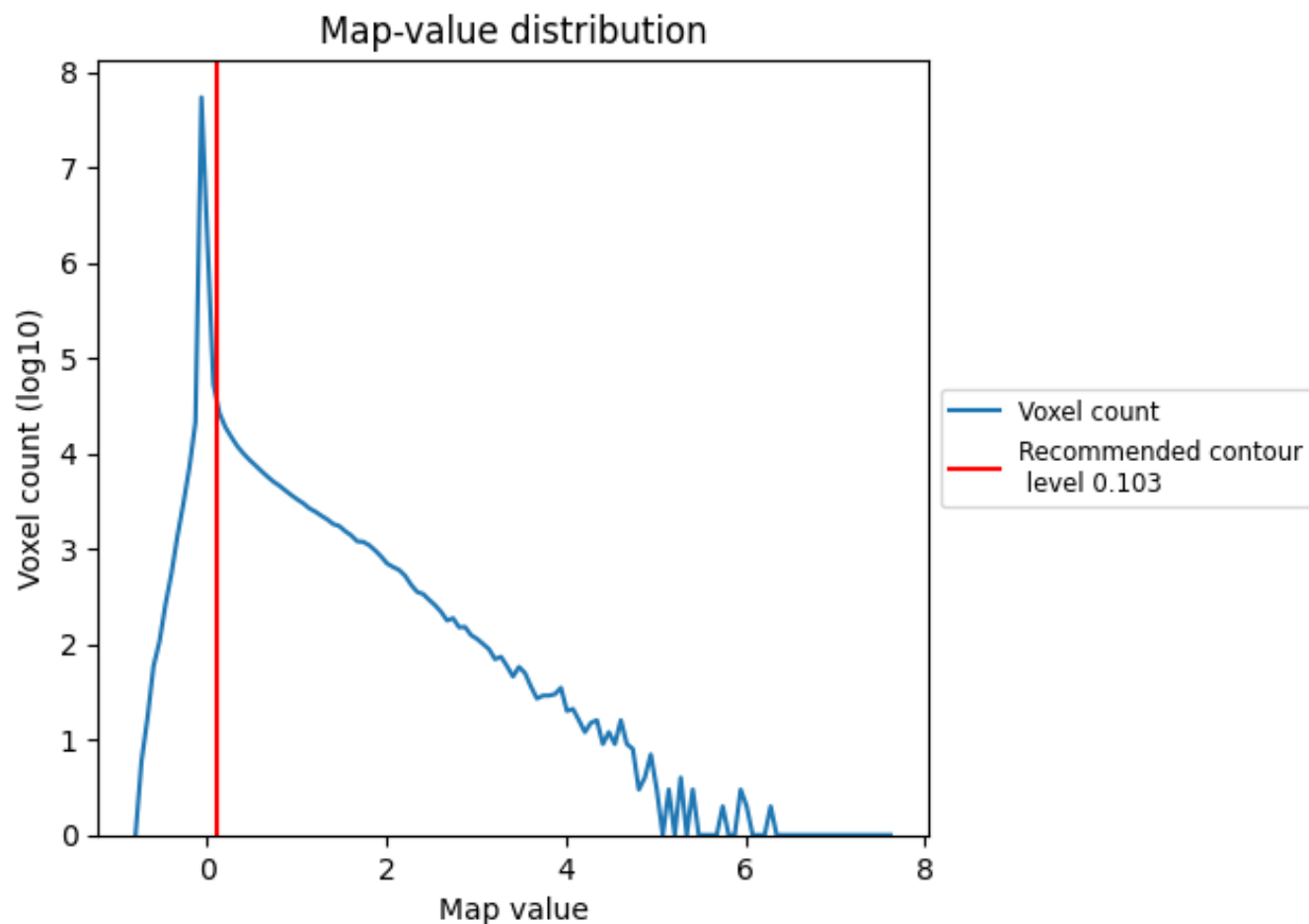
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

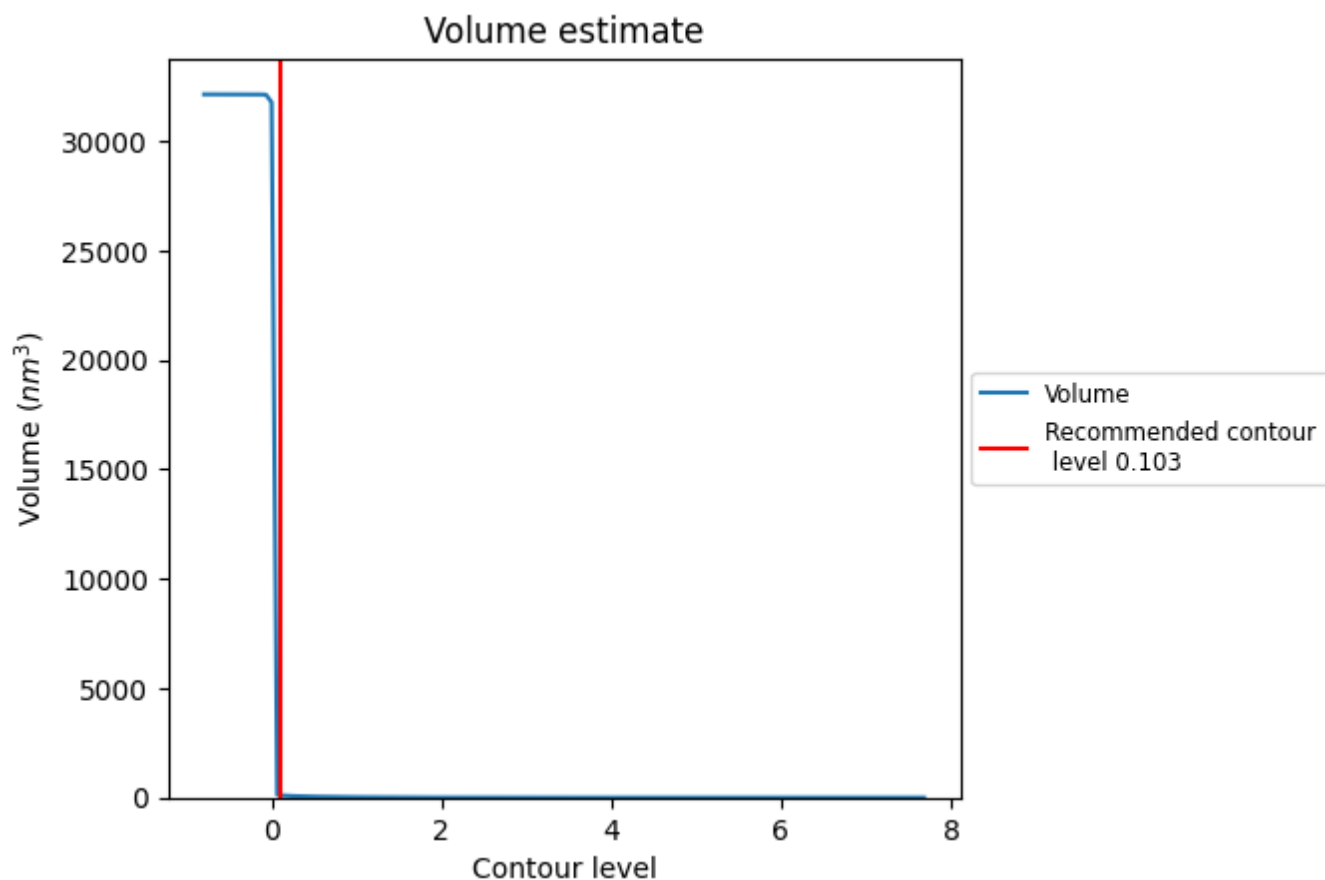
This section contains the results of statistical analysis of the map.

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.

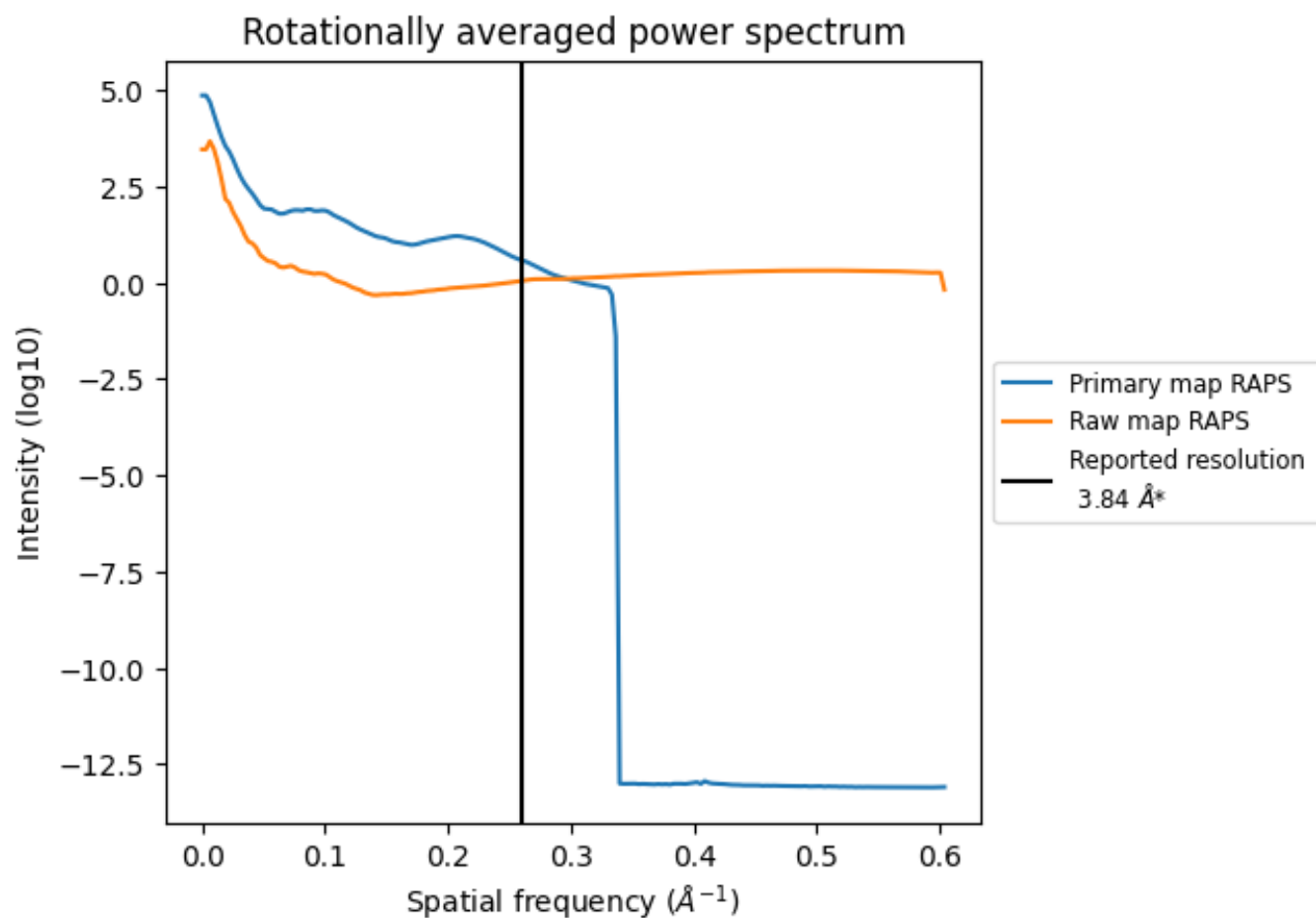
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 107 nm³; this corresponds to an approximate mass of 97 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 ⓘ

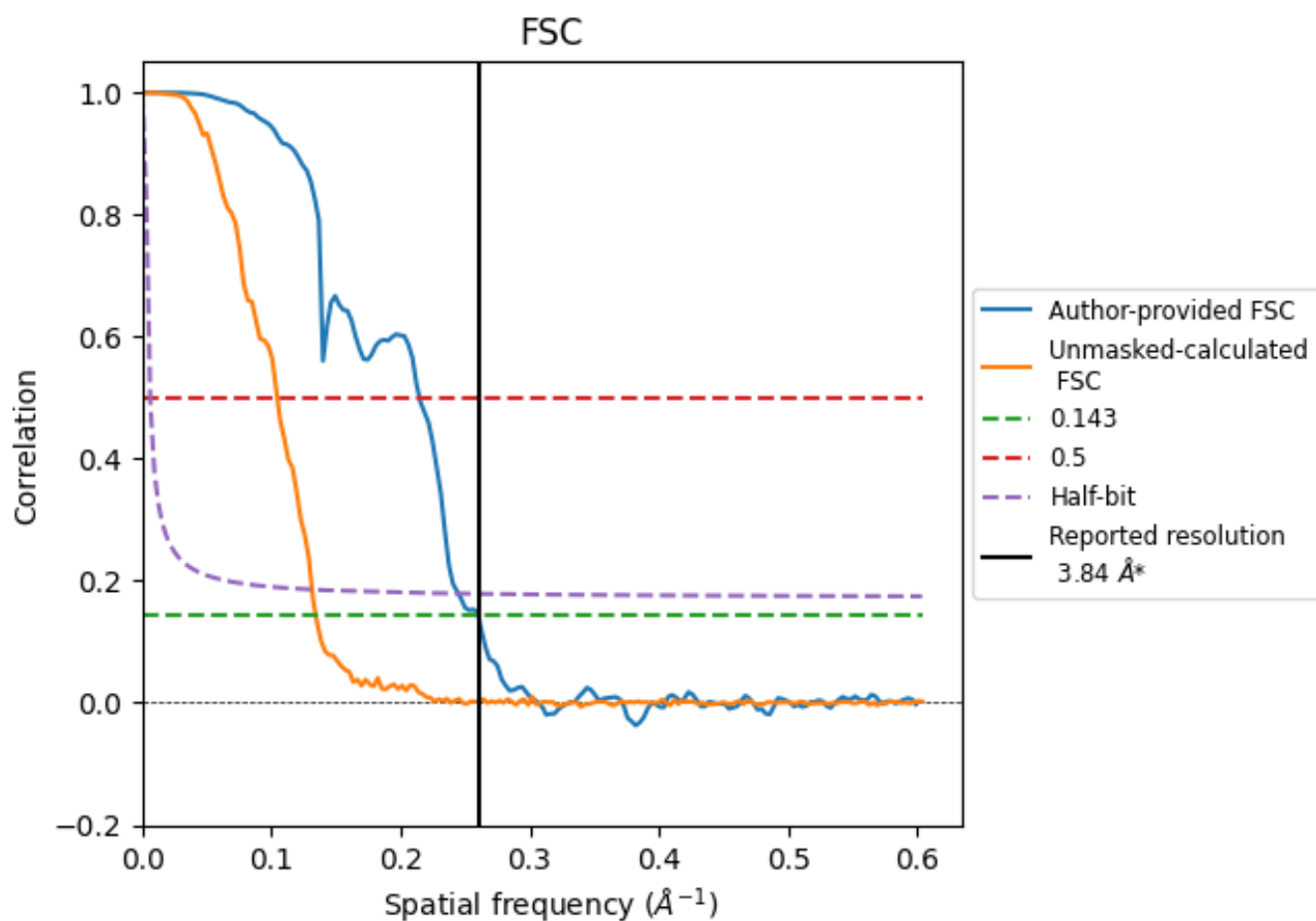


*Reported resolution corresponds to spatial frequency of 0.260 Å⁻¹

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 0.260 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.84	-	-
Author-provided FSC curve	3.84	4.66	4.08
Unmasked-calculated*	7.44	9.56	7.61

*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 7.44 differs from the reported value 3.84 by more than 10 %

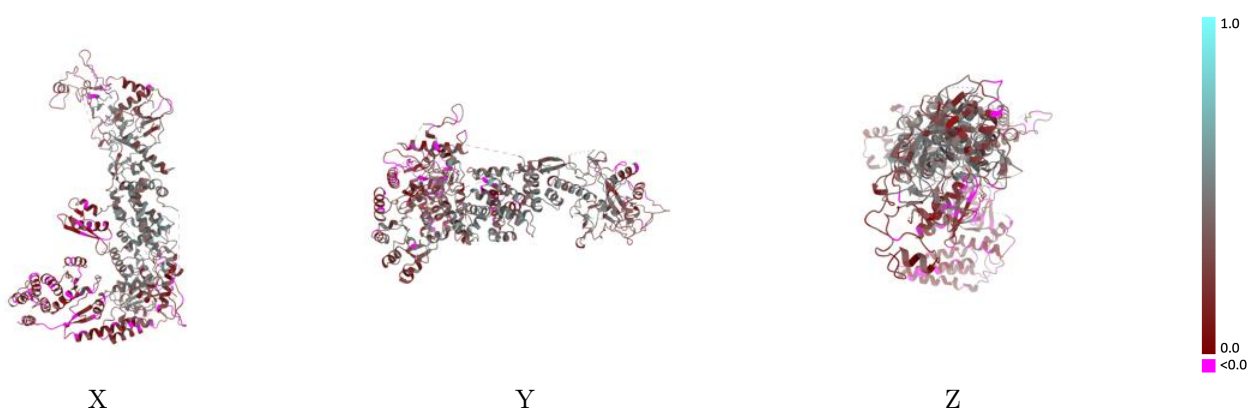
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14387 and PDB model 7YZ4. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

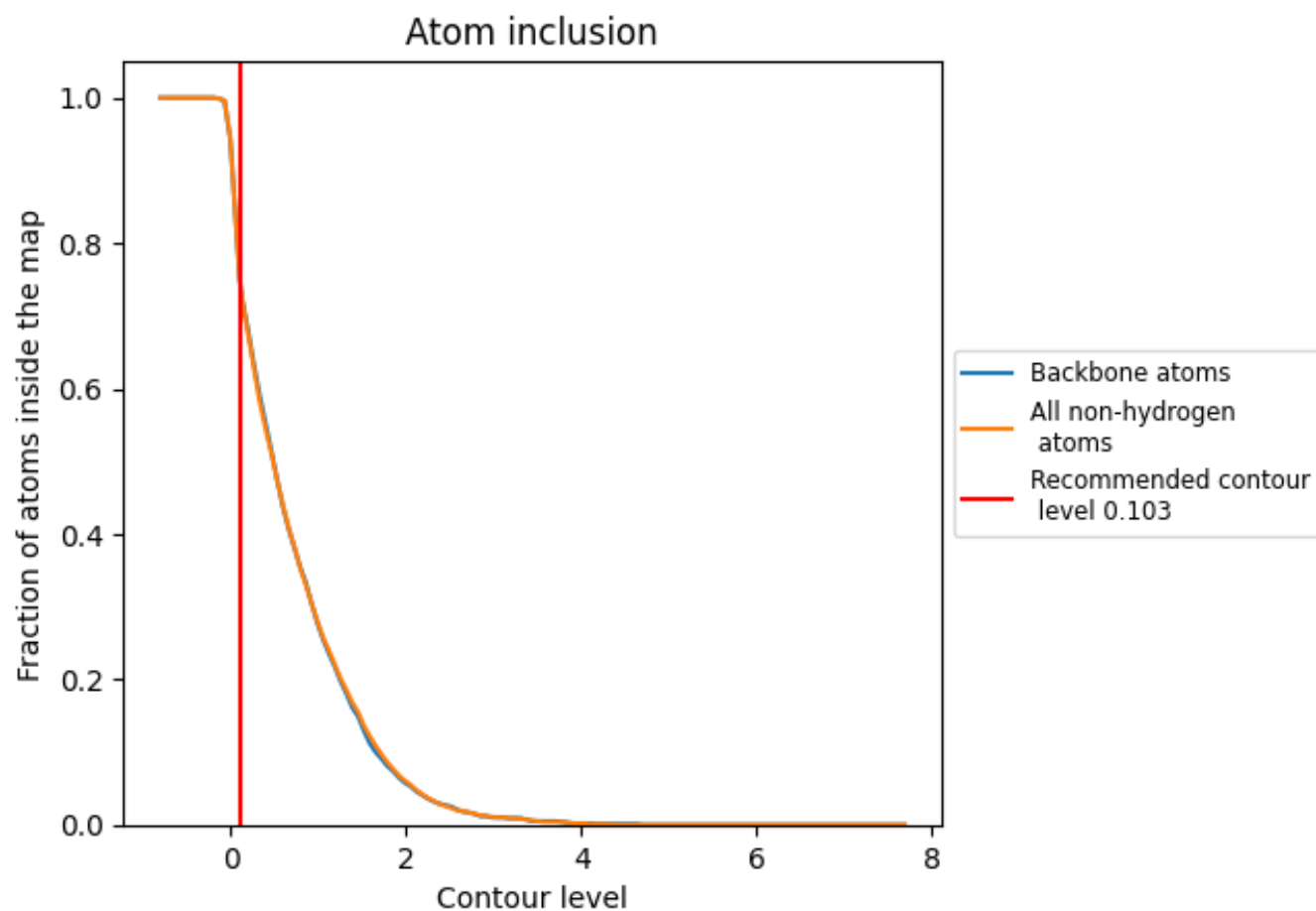


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 75% 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 (0.103) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7500	0.2930
A	0.7570	0.2930

