



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:08 PM UTC

PDB ID : 8DGI / pdb_00008dgi
EMDB ID : EMD-27423
Title : Structural Basis of MicroRNA Biogenesis by Dicer-1 and Its Partner Protein
Loqs-PB - complex Ia
Authors : Jouravleva, K.; Golovenko, D.; Demo, G.; Dutcher, R.C.; Tanaka Hall, T.M.;
Zamore, P.D.; Korostelev, A.A.
Deposited on : 2022-06-23
Resolution : 3.94 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

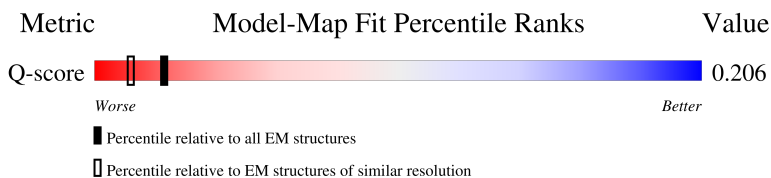
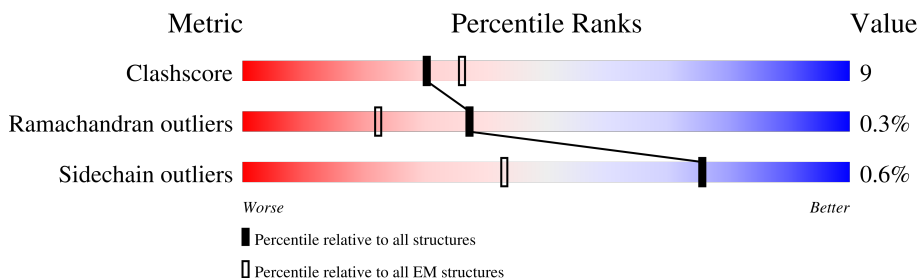
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.94 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	7757 (3.44 - 4.43)

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	2249	
2	N	465	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13580 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 Dcr-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1582	Total	C	N	O	S	0	0
			12733	8073	2236	2354	70		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	134	ARG	SER	conflict	UNP Q9VCU9
A	205	SER	THR	conflict	UNP Q9VCU9
A	416	LEU	MET	conflict	UNP Q9VCU9
A	702	SER	ALA	conflict	UNP Q9VCU9
A	796	CYS	SER	conflict	UNP Q9VCU9
A	1332	VAL	ALA	conflict	UNP Q9VCU9
A	1338	ALA	PRO	conflict	UNP Q9VCU9
A	1339	ILE	THR	conflict	UNP Q9VCU9
A	1345	ILE	LEU	conflict	UNP Q9VCU9

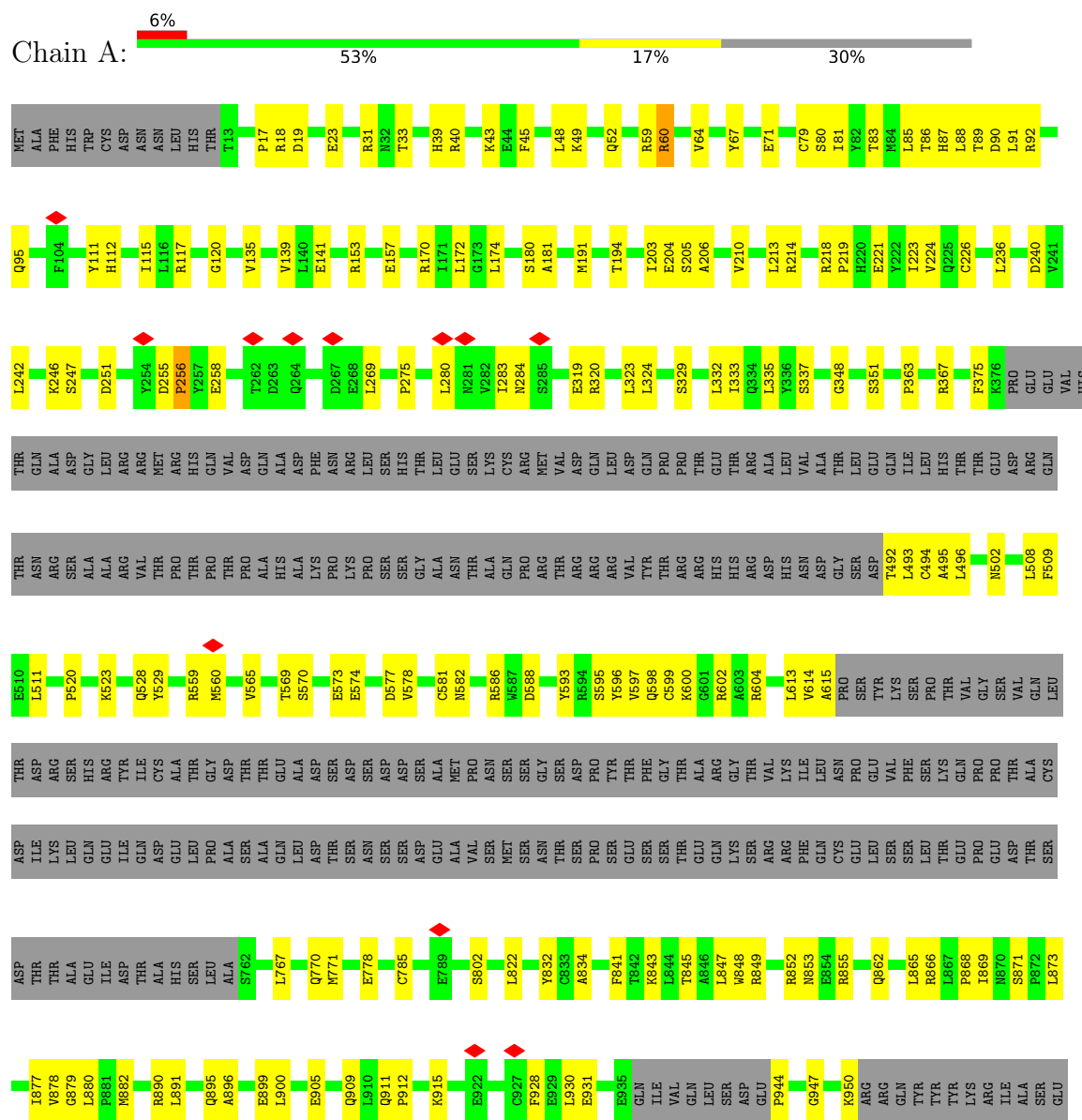
- Molecule 2 is a protein called Loquacious, isoform B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	108	Total	C	N	O	S	0	0
			847	535	148	160	4		

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: Endoribonuclease Dcr-1



R2023	F1926	I1E	ASP	GLY	PHE	SER	K1227	N1142	I1052	PHE
C2027	M1927	CYS	VAL	PHE	ILE	ILE	R1228	Q1143	N1053	CYS
R2030	A1928	GLU	ALA	GLY	GLU	GLU	E1229	D1144	L1056	ASP
F2033	W1929	MET	ASP	GLY	ILE	THR	M1230	Q1145	L1057	CYS
L2039	L1930	VAL	ILE	THR	THR	TRP	Q1233	Y1148	Y1058	ARG
D2040	G1931	ARG	ASP	SER	SER	LYS	L1237	A1152	T1059	PRO
L2042	V1932	GLY	ALA	LYS	ASN	ASP	G1242	P1166	F1060	VAL
T2043	R1933	LYS	GLY	GLN	ASN	ASP	T1243	H1157	T1061	ALA
T2044	V1934	ALA	ILE	LYS	THR	THR	V1244	L1158	N1062	ALA
L2047	L1935	ALA	ALA	GLY	ASP	ASP	H1245	L1161	Y977	ALA
D2050	G1936	GLY	THR	THR	PHE	GLY	T1254	L1168	L1064	ALA
H2054	R1943	LEU	THR	THR	THR	GLY	A1255	K1173	F978	ALA
L2059	G1944	GLU	ALA	GLY	GLY	GLY	V1256	K1179	F979	ALA
T2060	G1945	GLU	ALA	GLY	ALA	VAL	C1257	Y1180	Q980	ALA
D2062	N1946	GLU	ALA	GLY	ALA	VAL	T1265	T1183	Q984	ALA
S2064	Q1947	GLY	ALA	GLY	ASN	VAL	G1267	I1184	C985	ALA
A2065	R1948	GLY	ALA	GLY	ASN	VAL	A1271	Q1185	P986	ALA
L2066	I1949	GLY	ALA	GLY	ASN	VAL	R1275	T1187	F987	ALA
A2076	S1953	GLY	ALA	GLY	ASN	VAL	V1278	S1188	P988	ALA
F2081	G1949	GLY	ALA	GLY	ASN	VAL	L1282	Q1189	E989	ALA
H2082	L1944	GLY	ALA	GLY	ASN	VAL	L1284	L1191	Q991	ALA
K2083	A1945	GLY	ALA	GLY	ASN	VAL	Q1288	D1088	G995	ALA
F2085	W1946	GLY	ALA	GLY	ASN	VAL	ILE	W1099	B996	ALA
R2086	L1947	GLY	ALA	GLY	ASN	VAL	ASP	V1193	F1008	ALA
H2087	I1948	GLY	ALA	GLY	ASN	VAL	GLU	Q1100	T1012	ALA
L2088	V1949	GLY	ALA	GLY	ASN	VAL	ASP	F1101	I1016	ALA
S2089	G1950	GLY	ALA	GLY	ASN	VAL	GLU	S1020	S1020	ALA
C2091	R1951	GLY	ALA	GLY	ASN	VAL	PHE	I1024	I1024	ALA
D2094	L1952	GLY	ALA	GLY	ASN	VAL	GLU	F1025	F1025	ALA
F2099	A1953	GLY	ALA	GLY	ASN	VAL	GLU	T1026	T1026	ALA
V2100	W1954	GLY	ALA	GLY	ASN	VAL	GLU	R1027	R1027	ALA
Q2103	L1955	GLY	ALA	GLY	ASN	VAL	GLU	S1028	S1028	ALA
N2106	G1956	GLY	ALA	GLY	ASN	VAL	GLU	G1029	G1029	ALA
G2107	R1957	GLY	ALA	GLY	ASN	VAL	GLU	E1030	E1030	ALA
H2108	V1958	GLY	ALA	GLY	ASN	VAL	GLU	V1031	V1031	ALA
C2109	L1959	GLY	ALA	GLY	ASN	VAL	GLU	K1032	K1032	ALA
I2110	T2001	GLY	ALA	GLY	ASN	VAL	GLU	V1033	V1033	ALA
S2111	A2002	GLY	ALA	GLY	ASN	VAL	GLU	S1034	S1034	ALA
V2114	W2003	GLY	ALA	GLY	ASN	VAL	GLU	L1035	L1035	ALA
Y2115	L2004	GLY	ALA	GLY	ASN	VAL	GLU	R1041	R1041	ALA
	Q2005	GLY	ALA	GLY	ASN	VAL	GLU	L1044	L1044	ALA
	R2006	GLY	ALA	GLY	ASN	VAL	GLU	T1045	T1045	ALA
	D2007	GLY	ALA	GLY	ASN	VAL	GLU	S1046	S1046	ALA
	L2010	GLY	ALA	GLY	ASN	VAL	GLU	Q1047	Q1047	ALA
	L2011	GLY	ALA	GLY	ASN	VAL	GLU	I1049	I1049	ALA
	Q2012	GLY	ALA	GLY	ASN	VAL	GLU	V1050	V1050	ALA
	M2014	GLY	ALA	GLY	ASN	VAL	GLU	P1126	P1126	ALA
	T2015	GLY	ALA	GLY	ASN	VAL	GLU	F1127	F1127	ALA
	H2016	GLY	ALA	GLY	ASN	VAL	GLU	P1128	P1128	ALA
	Y2019	GLY	ALA	GLY	ASN	VAL	GLU	Q1129	Q1129	ALA
	T2020	GLY	ALA	GLY	ASN	VAL	GLU	F1130	F1130	ALA
	P2021	GLY	ALA	GLY	ASN	VAL	GLU	F1131	F1131	ALA
	N2022	GLY	ALA	GLY	ASN	VAL	GLU	P1138	P1138	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112398	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.06	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	57471	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.496	Depositor
Minimum map value	-0.340	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0262	Depositor
Map size ($\text{\AA}$)	360.18, 360.18, 360.18	wwPDB
Map dimensions	414, 414, 414	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87, 0.87, 0.87	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	0.26	0/13020	0.64	4/17661 (0.0%)
2	N	0.24	0/859	0.63	1/1153 (0.1%)
All	All	0.26	0/13879	0.64	5/18814 (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	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	2030	ARG	N-CA-C	-6.48	106.58	114.75
1	A	1566	ARG	CA-CB-CG	5.60	125.30	114.10
1	A	256	PRO	N-CD-CG	-5.31	95.23	103.20
1	A	256	PRO	CA-N-CD	-5.22	104.69	112.00
2	N	406	GLN	CA-CB-CG	5.11	124.32	114.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1205	THR	Peptide
1	A	2116	LEU	Peptide

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	12733	0	12650	235	0
2	N	847	0	873	8	0
All	All	13580	0	13523	243	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 243 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:1278:VAL:O	1:A:1282:LEU:HB3	1.79	0.81
1:A:1920:PRO:O	1:A:1923:ALA:HB3	1.83	0.78
1:A:1529:LEU:O	1:A:1533:GLN:HB2	1.84	0.78
1:A:2117:LEU:O	1:A:2121:GLU:HB3	1.92	0.70
1:A:59:ARG:HB3	1:A:1991:SER:HB3	1.77	0.67

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	1562/2249 (70%)	1460 (94%)	97 (6%)	5 (0%)	36	70
2	N	106/465 (23%)	105 (99%)	1 (1%)	0	100	100
All	All	1668/2714 (62%)	1565 (94%)	98 (6%)	5 (0%)	37	70

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1667	TYR
1	A	2117	LEU
1	A	1535	THR
1	A	1233	GLN
1	A	1216	LEU

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	1407/1994 (71%)	1398 (99%)	9 (1%)	78	81
2	N	94/380 (25%)	94 (100%)	0	100	100
All	All	1501/2374 (63%)	1492 (99%)	9 (1%)	76	81

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2117	LEU
1	A	2141	ILE
1	A	882	MET
1	A	1657	VAL
1	A	2041	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	N	390	ASN
1	A	2170	GLN
1	A	1614	GLN
1	A	2106	ASN
1	A	1235	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 [i](#)

There are no chain breaks in this entry.

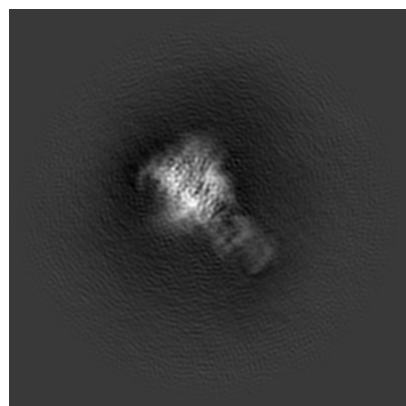
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27423. These allow visual inspection of the internal detail of the map and identification of artifacts.

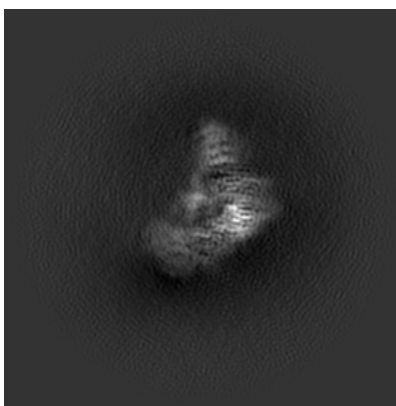
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

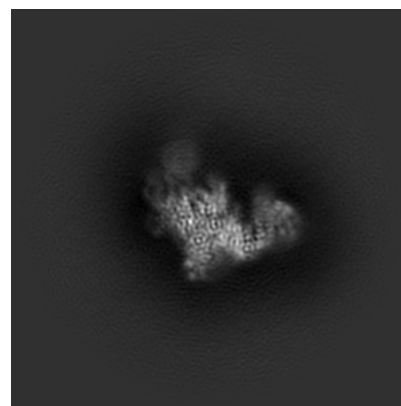
6.1.1 Primary map



X

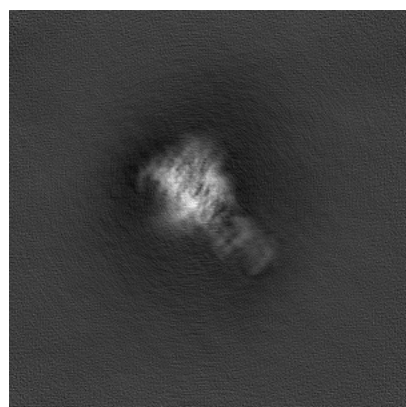


Y

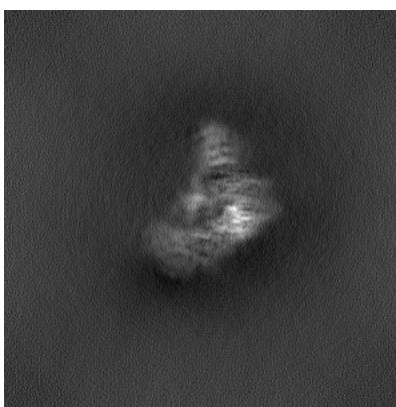


Z

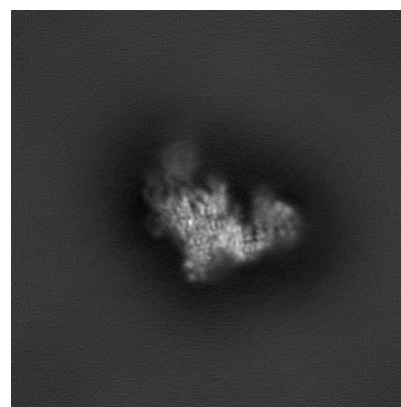
6.1.2 Raw map



X



Y

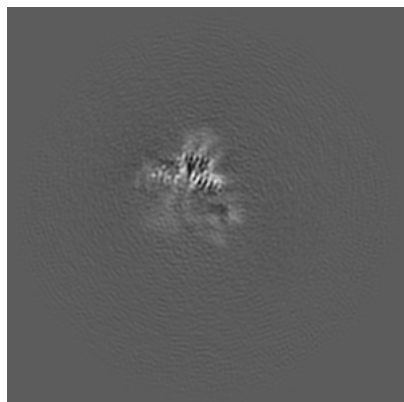


Z

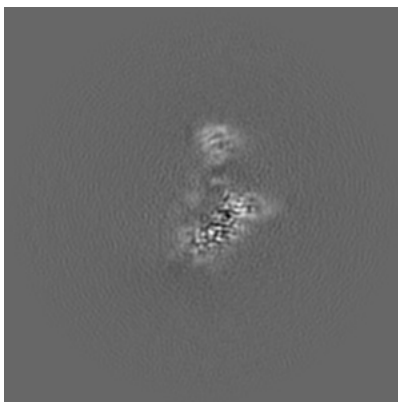
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

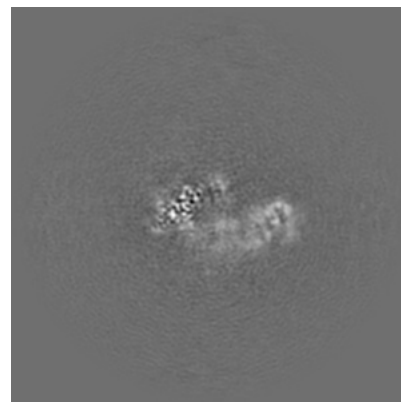
6.2.1 Primary map



X Index: 207

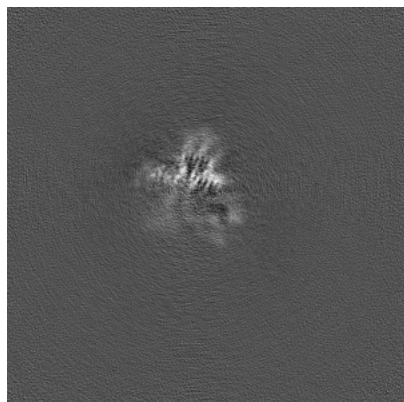


Y Index: 207

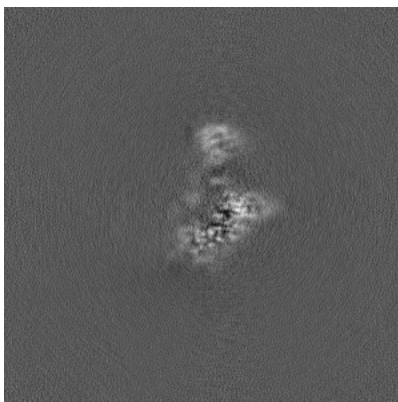


Z Index: 207

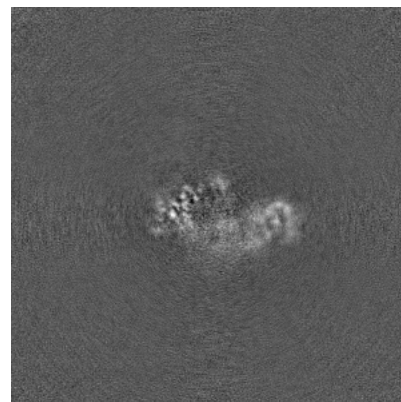
6.2.2 Raw map



X Index: 207



Y Index: 207

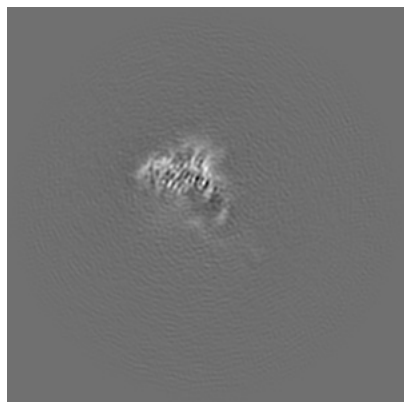


Z Index: 207

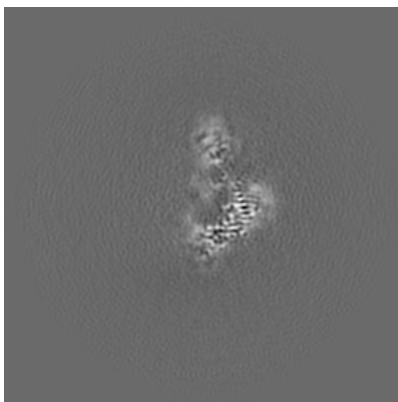
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

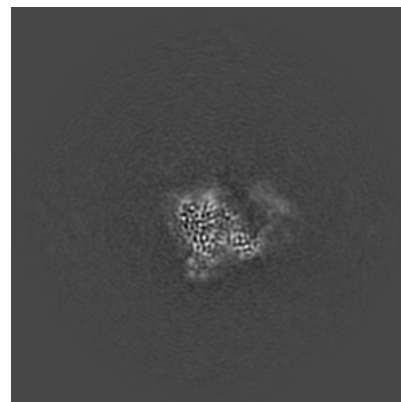
6.3.1 Primary map



X Index: 198

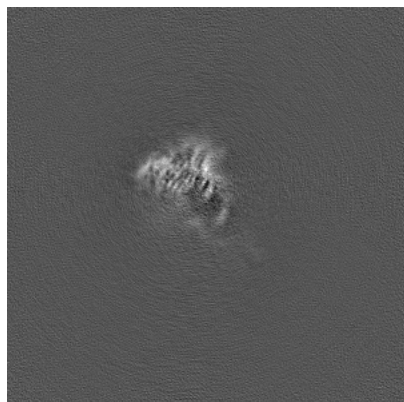


Y Index: 193

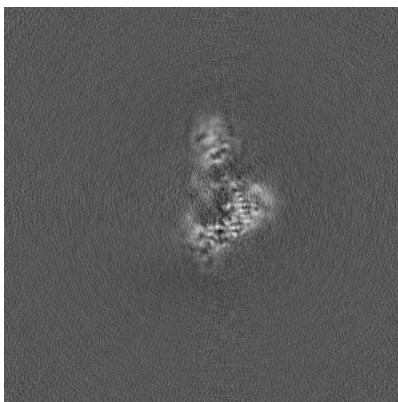


Z Index: 238

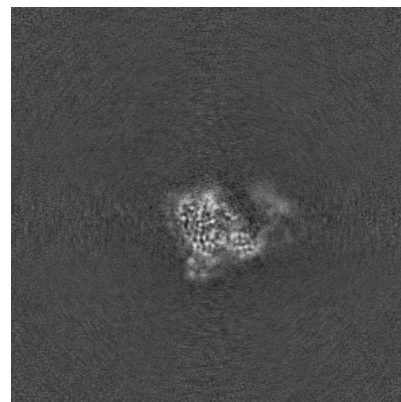
6.3.2 Raw map



X Index: 198



Y Index: 194

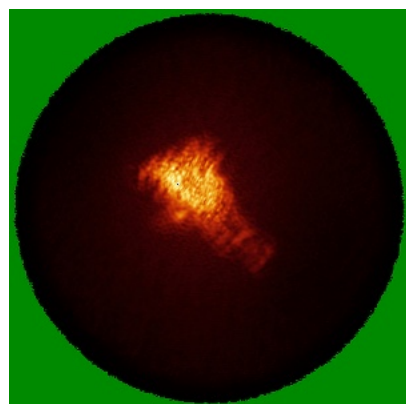


Z Index: 238

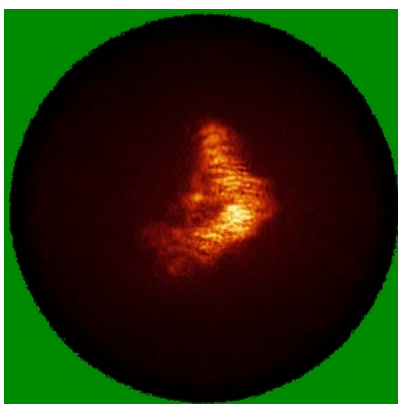
The images above show the largest variance slices of the map in three orthogonal directions.

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

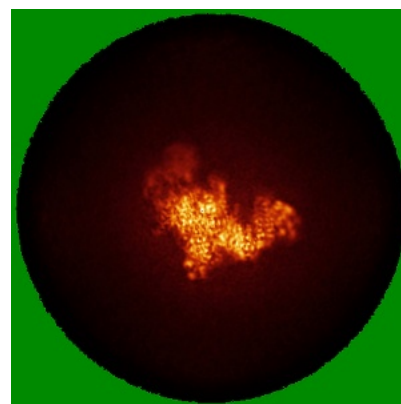
6.4.1 Primary map



X

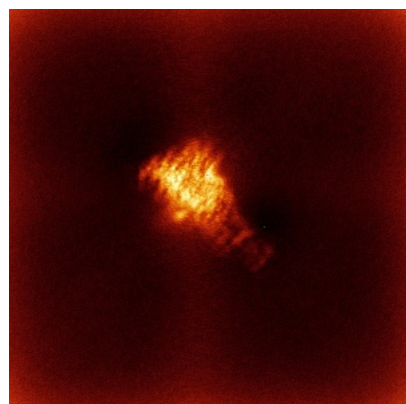


Y

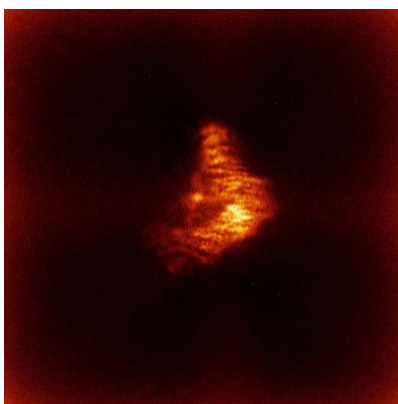


Z

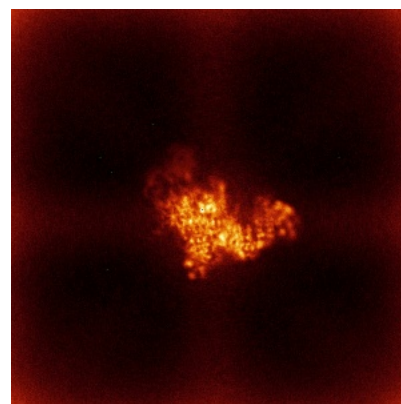
6.4.2 Raw map



X



Y

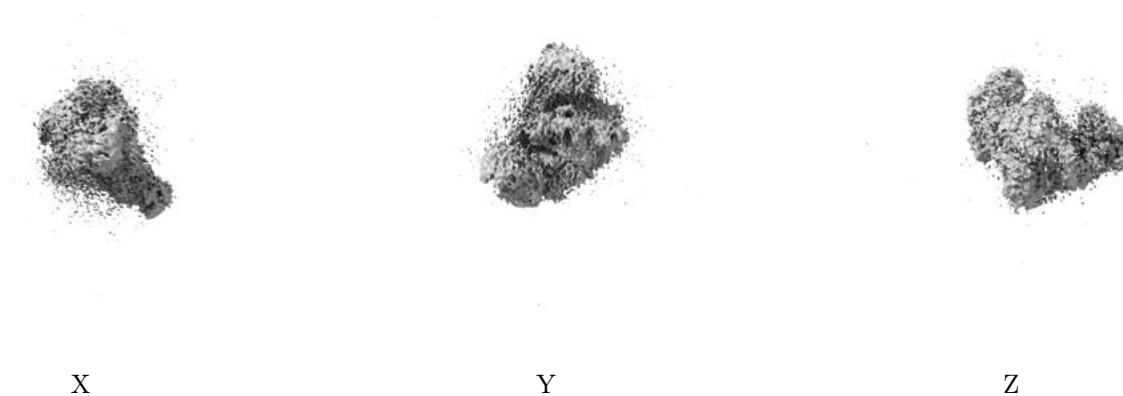


Z

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.

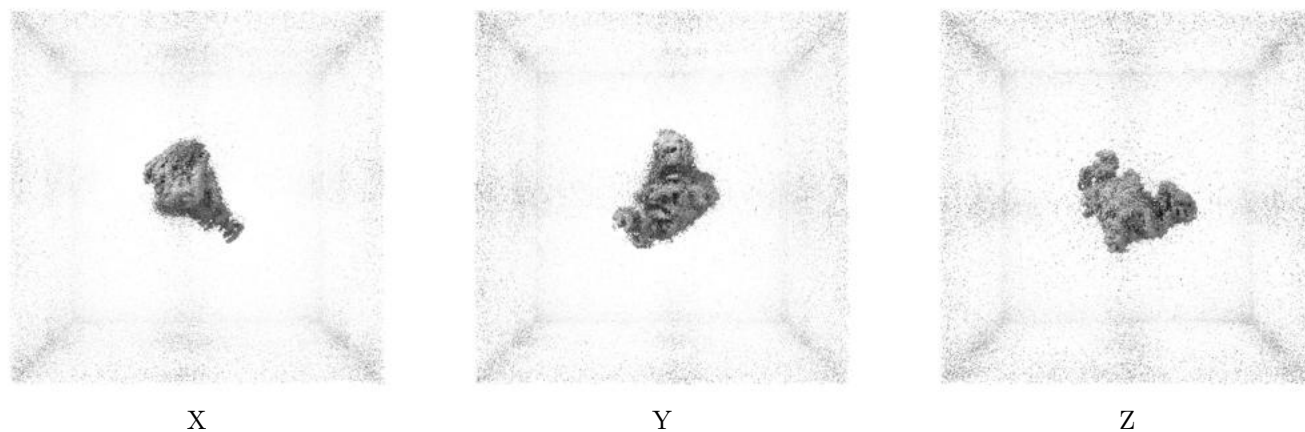
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0262. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

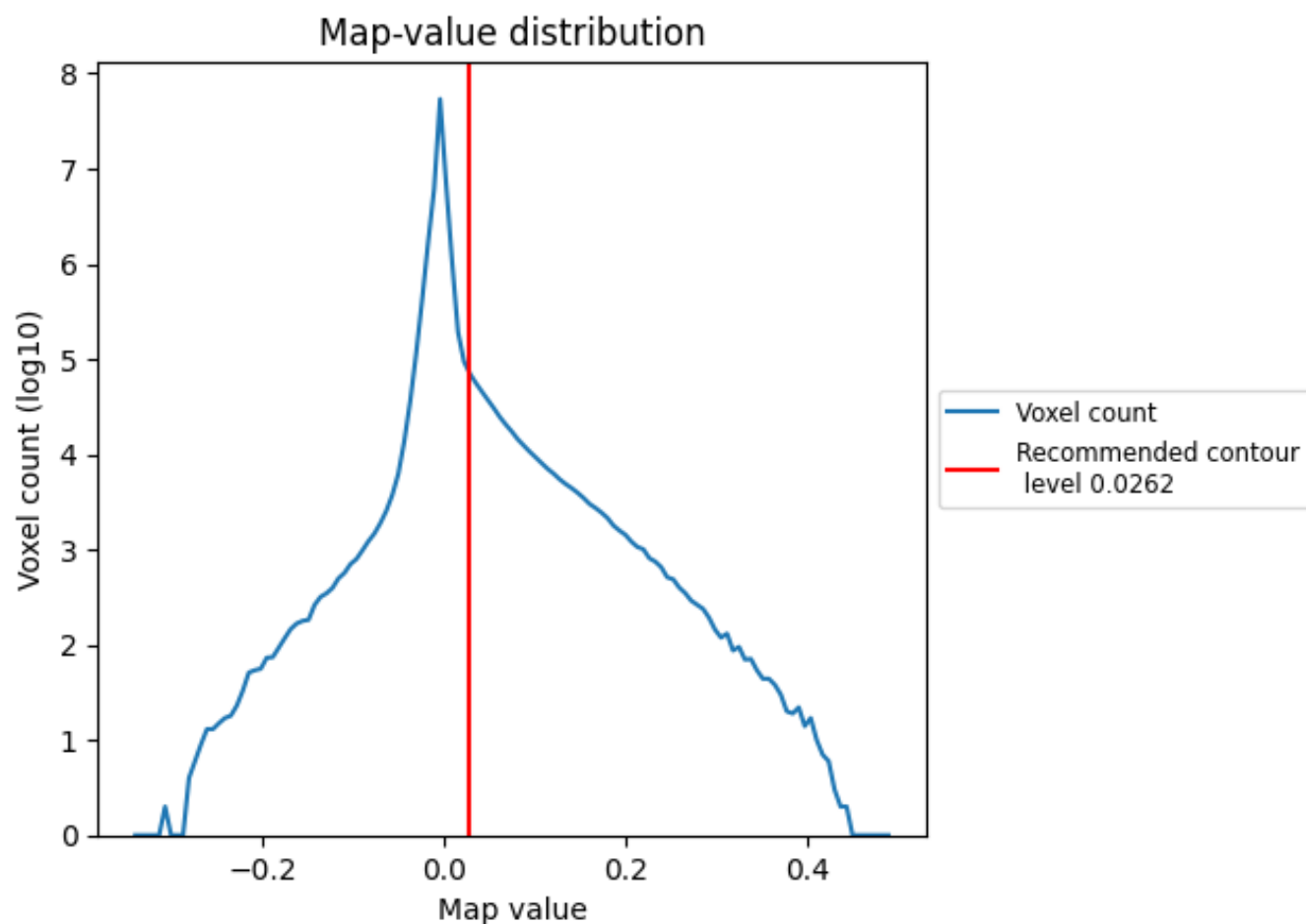
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

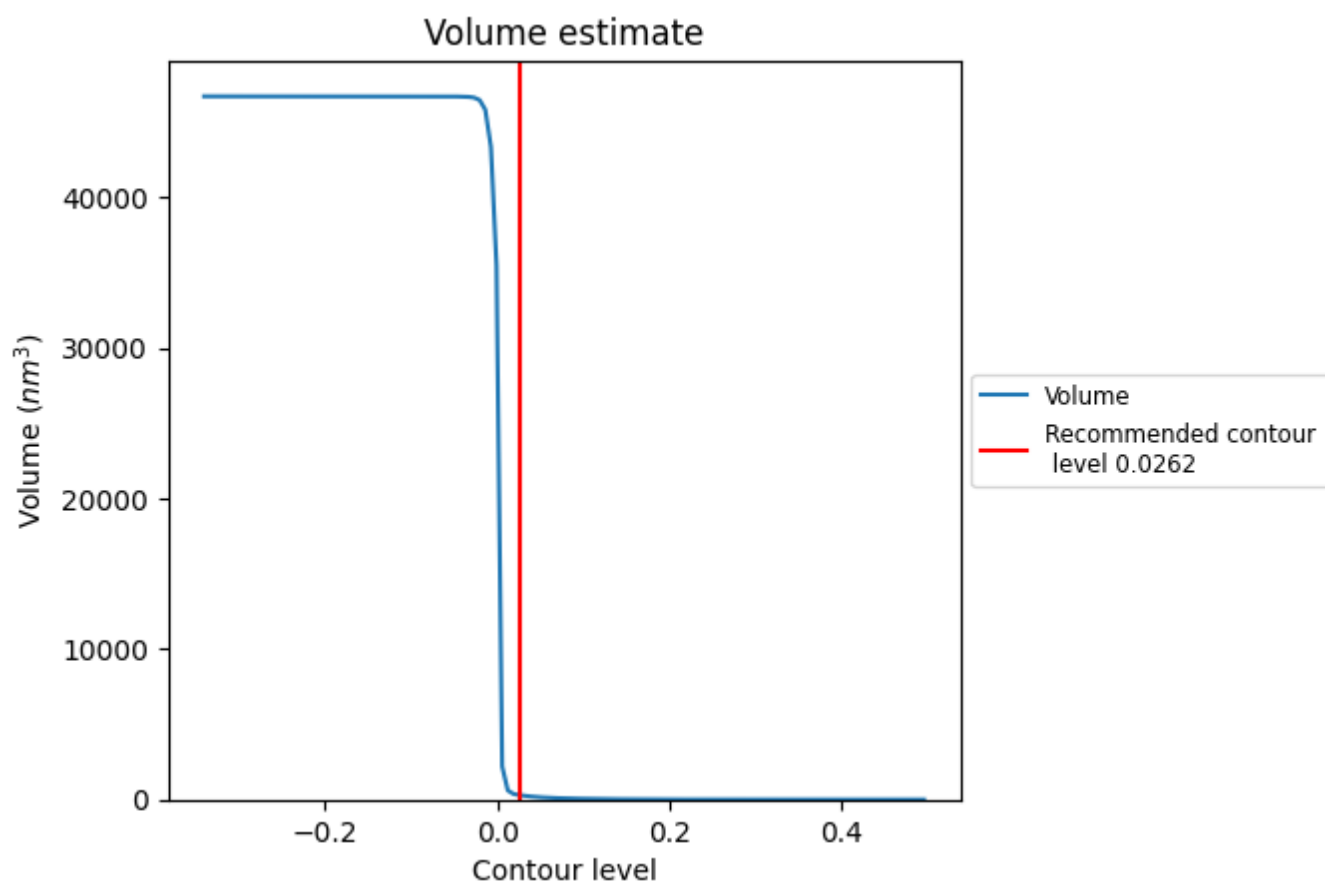
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

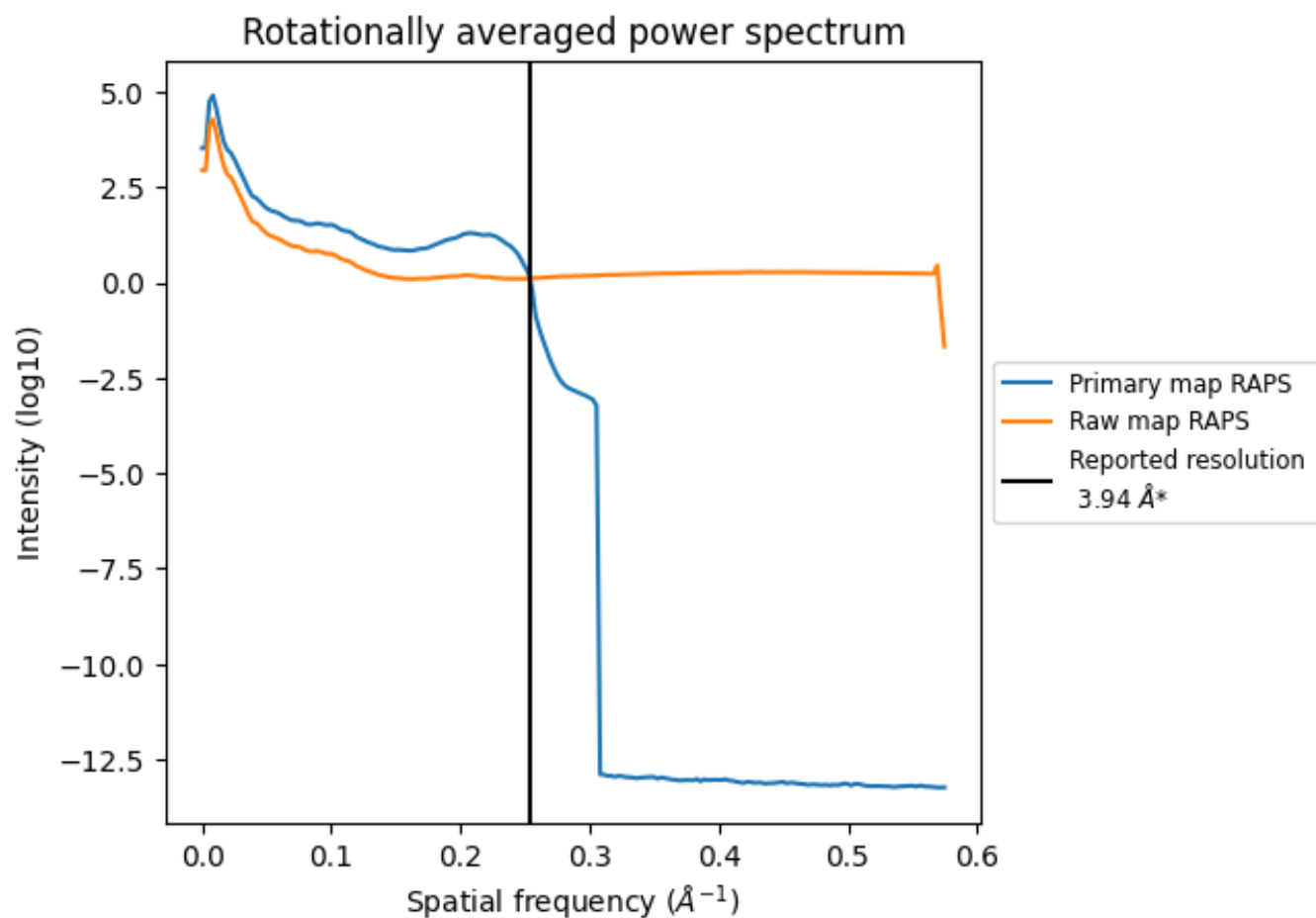
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 291 nm³; this corresponds to an approximate mass of 263 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 ⓘ

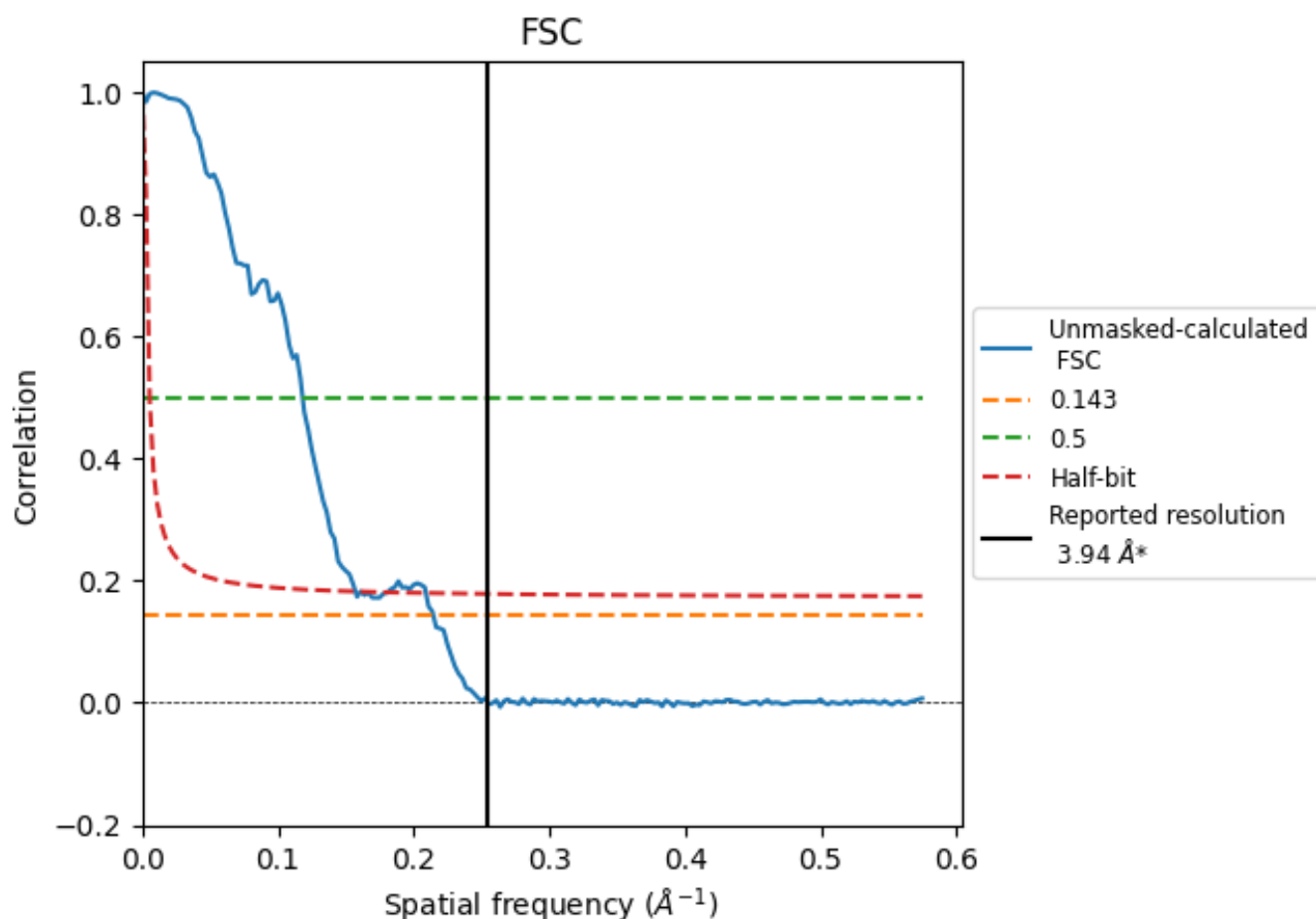


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 Å⁻¹

8.2 Resolution estimates [i](#)

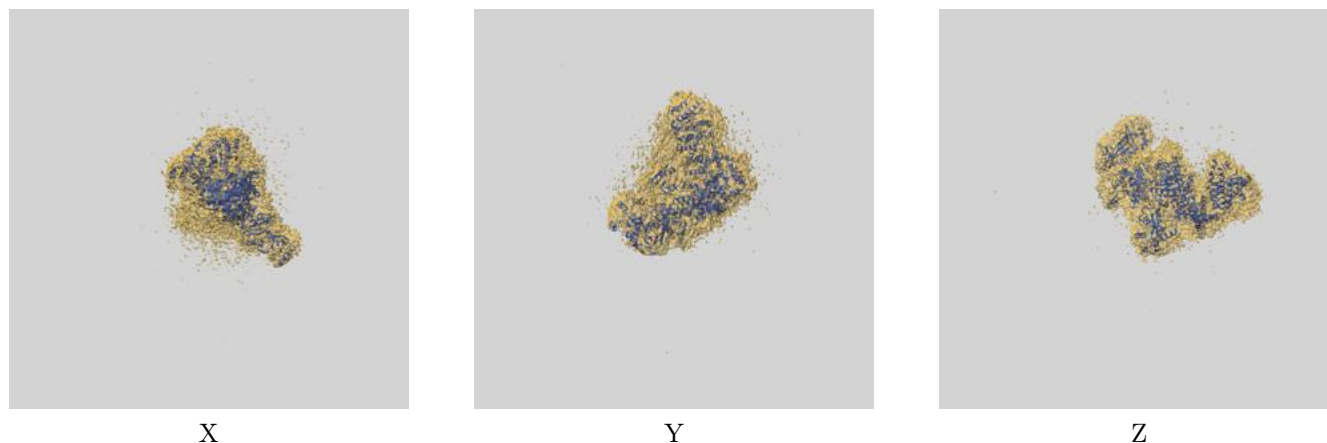
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.66	8.46	6.37

*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 4.66 differs from the reported value 3.94 by more than 10 %

9 Map-model fit [i](#)

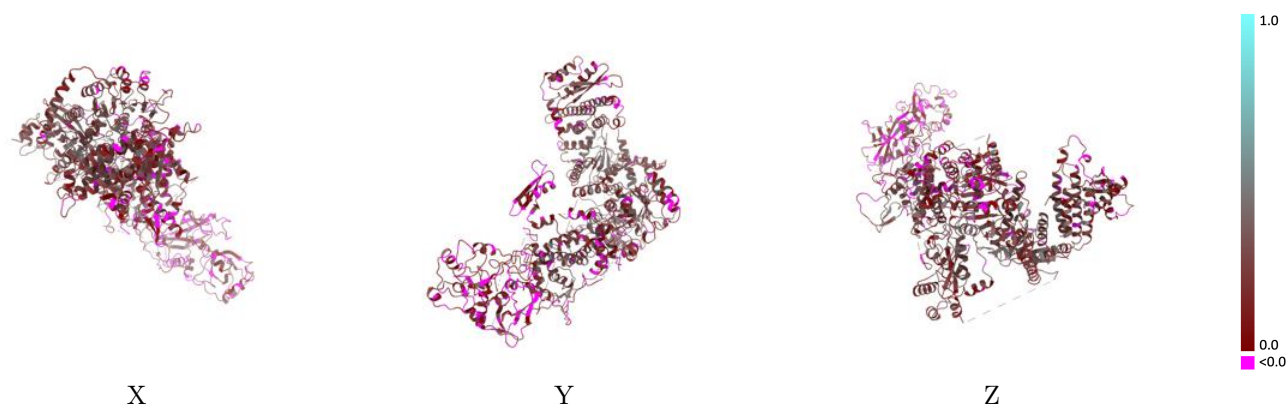
This section contains information regarding the fit between EMDB map EMD-27423 and PDB model 8DGI. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



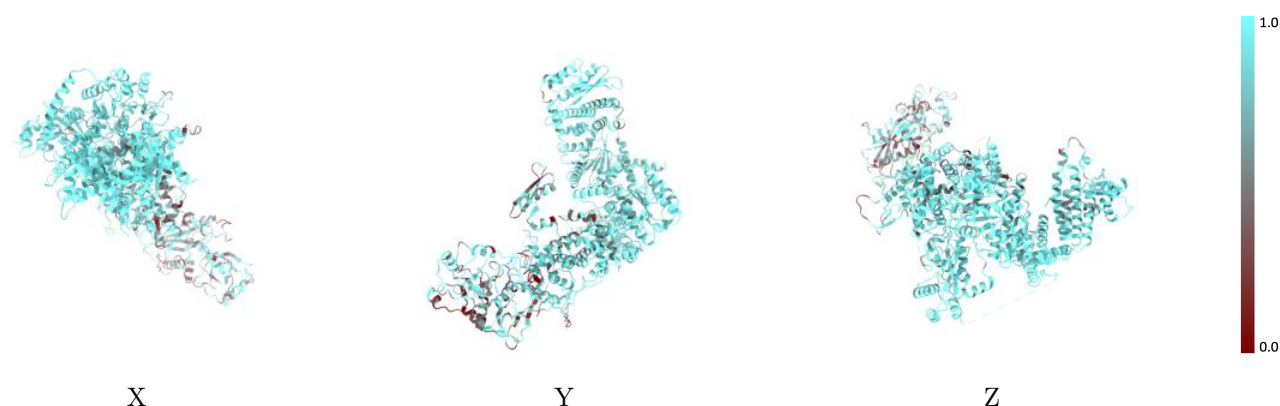
The images above show the 3D surface view of the map at the recommended contour level 0.0262 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



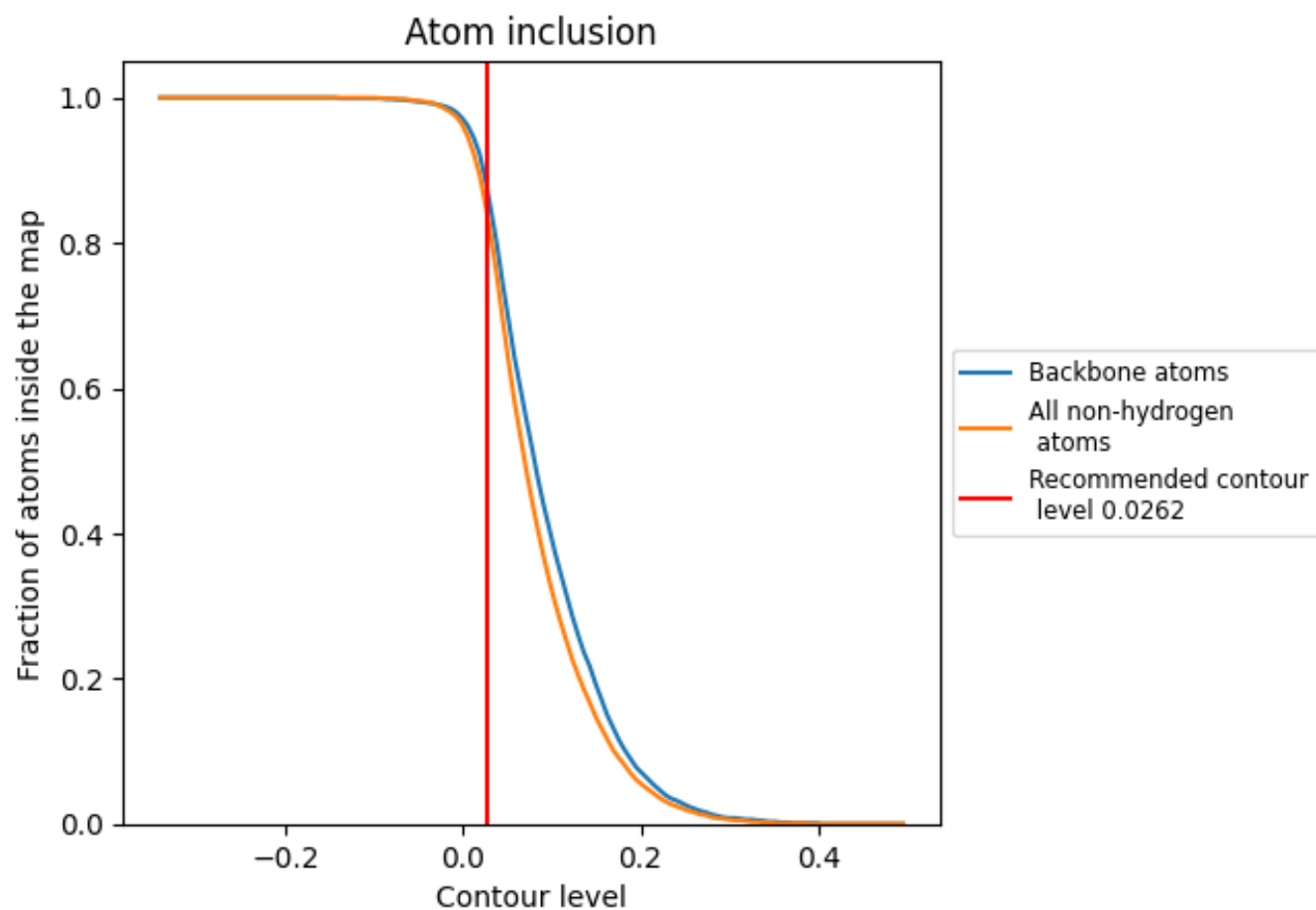
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0262).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% 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 (0.0262) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8490	0.2060
A	0.8430	0.2090
N	0.9420	0.1610

