



wwPDB EM Validation Summary Report ⓘ

Jul 19, 2026 – 08:22 pm BST

PDB ID : 9THI / pdb_00009thi
EMDB ID : EMD-55928
Title : OmRV Crown Protein Deletion mutant infectious clone
Authors : Wang, H.; Okamoto, K.
Deposited on : 2025-12-03
Resolution : 2.90 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 Phenix2.0
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) : 2.50

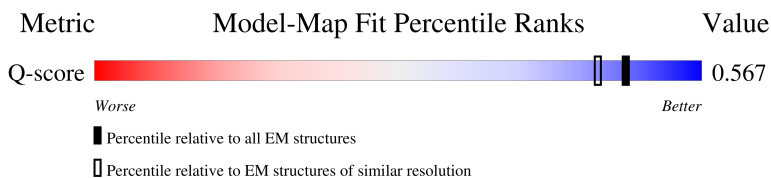
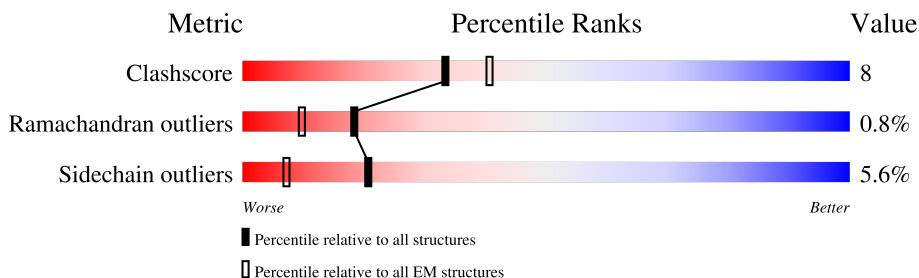
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

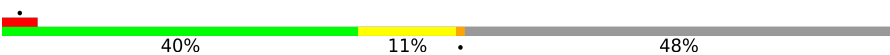
The reported resolution of this entry is 2.90 Å.

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	13054 (2.40 - 3.40)

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	1685	 38% 11% 50%
1	B	1685	 40% 11% 48%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13177 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.

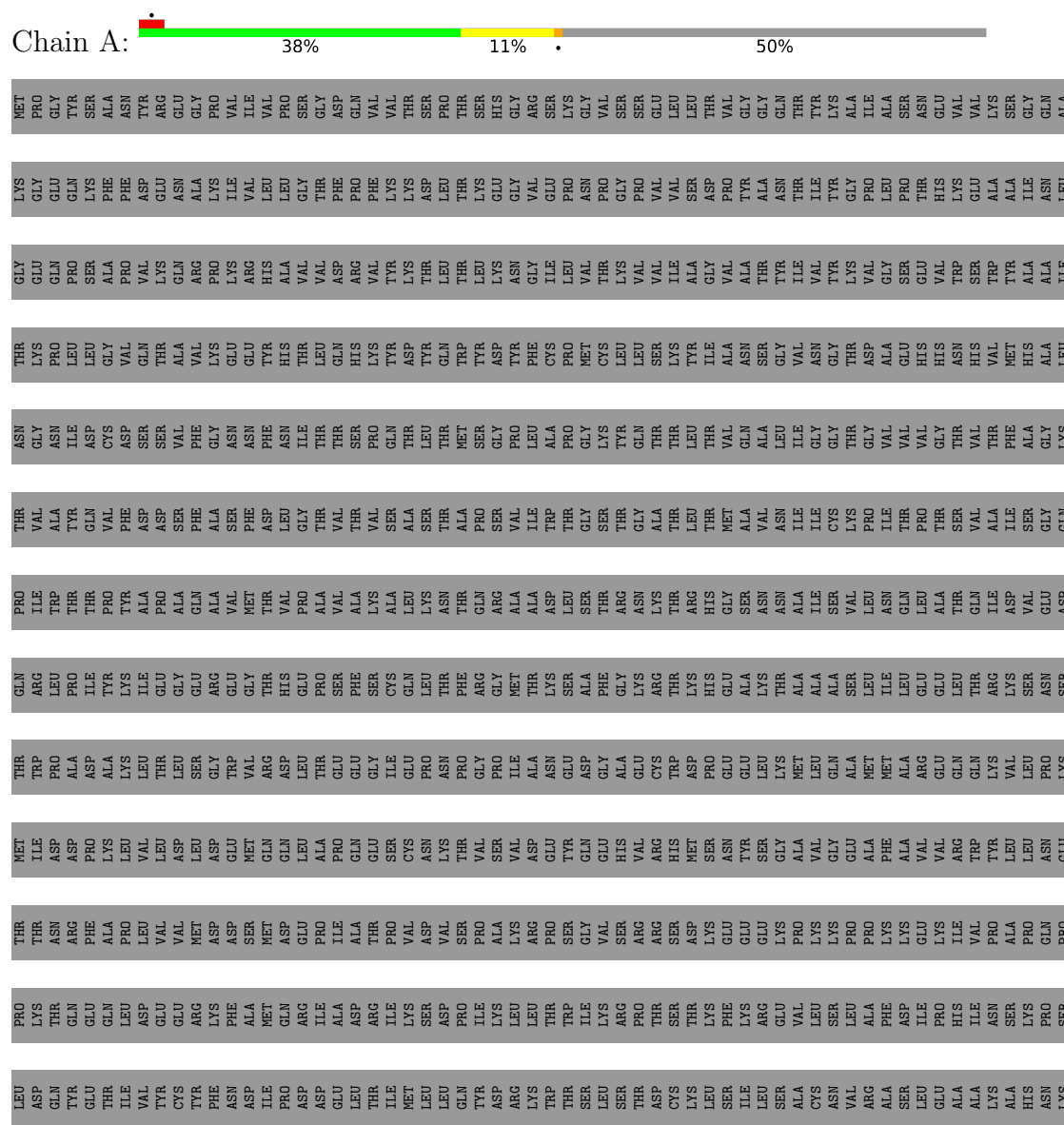
- Molecule 1 is a protein called Omono River Virus AK4 strain Subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	849	Total	C	N	O	S	0	0
			6488	4113	1112	1234	29		
1	B	878	Total	C	N	O	S	0	0
			6689	4237	1145	1277	30		

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: Omono River Virus AK4 strain Subunit A



V1670	L1671	S1672	Q1673	P1674	A1675	P1676	L1677	M1678	SER	PRO	PRO	THR	SER	SER	SER	SER	VAL	E1619	D1620	A1621	F1622	D1623	S1629	F1630	L1631	D1632	V1633	A1634	K1635	S1636	V1637	A1638	E1639	S1640	A1641	G1642	E1643	V1644	T1647	K1648	A1649	L1650	T1651	D1652	L1653	V1656	D1657	V1658	S1659	S1663	T1664	S1665	D1666	P1667	S1668	N1669																																																																																																																																																																																																																																																																																																																																																																																																																					
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Y1437	F1438	T1439	L1442	P1443	L1444	F1445	S1457	T1458	K1459	L1467	Y1481	F1485	A1486	D1487	N1488	D1502	M1503	A1504	T1505	M1512	N1516	L1520	I1527	V1528	E1529	E1536	I1553	E1554	L1555	T1556	A1559	C1562	P1564	R1565	Y1566	T1573	F1574	T1575	R1591	N1594																																																																																																																																																																																																																																																																																																																																																																																																																																					
T1306	S1307	F1308	W1309	E1310	R1311	L1312	T1315	I1319	T1322	M1323	Y1324	Y1325	H1326	S1327	T1330	T1331	T1332	L1333	K1345	W1346	M1353	T1354	T1358	V1361	G1362	Y1369	I1372	M1380	F1381	H1382	R1383	A1384	V1414	V1422	F1425	S1426	P1427	V1428	L1429	I1430	P1431	D1432	C1435	Q1436																																																																																																																																																																																																																																																																																																																																																																																																																																	
S1173	Y1174	L1175	F1182	T1185	Y1190	M1191	L1194	A1195	T1196	M1197	V1198	Y1204	L1210	L1214	V1217	A1218	M1221	T1222	T1223	V1241	C1242	Y1243	V1249	F1256	P1257	Y1269	D1270	T1271	D1272	T1275	K1278	L1283	L1289	V1290	P1291	E1292	Q1293	S1294	M1295	P1298																																																																																																																																																																																																																																																																																																																																																																																																																																					
E1070	V1078	L1085	I1096	Q1099	T1101	H1102	S954	S955	M956	L957	L958	F812	W813	L814	M969	D972	S979	Q980	T988	A994	P1015	T1023	G1024	A1025	I1026	F1027	A1028	H1029	Q1154	L1155	F1156	M1157	M1158	I1161	G1162	A1163	P1164	A1165	F1166	E1167	W1169	P1170	L1171	T1172																																																																																																																																																																																																																																																																																																																																																																																																																																	
N918	W924	D927	N928	T929	S930	L931	L951	E954	S955	M956	L957	L958	F812	W813	L814	M969	D972	S979	Q980	T988	A994	P1015	T1023	G1024	A1025	I1026	F1027	A1028	H1029	Q1154	L1155	F1156	M1157	M1158	I1161	G1162	A1163	P1164	A1165	F1166	E1167	W1169	P1170	L1171	T1172																																																																																																																																																																																																																																																																																																																																																																																																																																
LEU	MET	HIS	ALA	TYR	ASN	GLY	ASN	P789	P793	F794	E798	F803	L957	F812	W813	L814	M969	D972	S979	Q980	T988	A994	P1015	T1023	G1024	A1025	I1026	F1027	A1028	H1029	Q1154	L1155	F1156	M1157	M1158	I1161	G1162	A1163	P1164	A1165	F1166	E1167	W1169	P1170	L1171	T1172																																																																																																																																																																																																																																																																																																																																																																																																																															
LEU	ASP	GLN	TYR	GLU	GLU	THR	ILE	VAL	TYR	TYR	TYR	PHE	ASN	ASP	ALA	ASP	GLU	LEU	THR	GLN	TYR	THR	ILE	ASP	PRO	ILE	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																																																																																		
THR	TRP	PRO	ALA	ASP	PRO	ALA	TYR	LEU	LEU	VAL	VAL	ASP	GLU	GLY	TRP	VAL	GLY	THR	ASP	GLN	ASP	GLU	LEU	THR	PRO	ALA	ILE	ASP	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR</

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12488	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.57	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	5.483	Depositor
Minimum map value	-3.100	Depositor
Average map value	0.037	Depositor
Map value standard deviation	0.244	Depositor
Recommended contour level	0.7329	Depositor
Map size (Å)	571.2, 571.2, 571.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.952, 0.952, 0.952	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	0.24	0/6644	0.57	8/9088 (0.1%)
1	B	0.23	0/6849	0.53	5/9373 (0.1%)
All	All	0.24	0/13493	0.55	13/18461 (0.1%)

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
1	B	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	920	GLN	N-CA-CB	-8.10	101.03	110.35
1	B	1652	ASP	N-CA-C	-7.85	104.22	113.88
1	A	914	ASP	CB-CA-C	-7.72	99.36	111.17
1	B	1124	THR	CA-C-N	7.45	135.76	121.54
1	B	1124	THR	C-N-CA	7.45	135.76	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	925	ARG	Sidechain
1	A	926	ARG	Sidechain
1	B	1256	PHE	Peptide

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	6488	0	6358	118	0
1	B	6689	0	6565	105	0
All	All	13177	0	12923	217	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 8.

The worst 5 of 217 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:1376:LEU:O	1:A:1380:MET:HB2	1.74	0.86
1:B:1124:THR:O	1:B:1125:THR:HG22	1.82	0.79
1:A:1465:GLN:HB3	1:A:1503:MET:HE1	1.66	0.75
1:B:1063:LEU:HB3	1:B:1182:PHE:CE1	2.24	0.72
1:A:1220:LYS:HD2	1:A:1415:TYR:HE2	1.55	0.70

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	845/1685 (50%)	776 (92%)	61 (7%)	8 (1%)	14	41
1	B	874/1685 (52%)	798 (91%)	71 (8%)	5 (1%)	21	51
All	All	1719/3370 (51%)	1574 (92%)	132 (8%)	13 (1%)	18	44

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	921	PHE
1	A	1233	ALA
1	A	1338	ALA
1	A	1364	ILE
1	B	1257	PRO

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	691/1408 (49%)	653 (94%)	38 (6%)	19	50
1	B	717/1408 (51%)	676 (94%)	41 (6%)	18	49
All	All	1408/2816 (50%)	1329 (94%)	79 (6%)	21	50

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1198	VAL
1	B	1575	THR
1	B	1283	LEU
1	B	1503	MET
1	B	1644	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	823	GLN
1	B	1002	ASN
1	B	980	GLN
1	B	1189	GLN
1	A	1413	ASN

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.

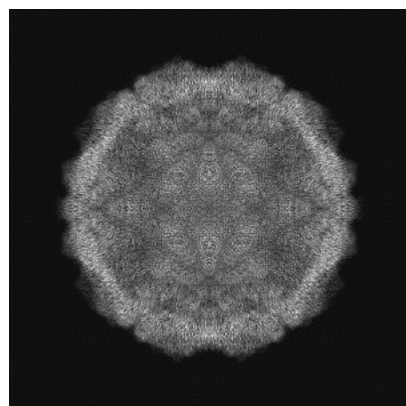
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55928. These allow visual inspection of the internal detail of the map and identification of artifacts.

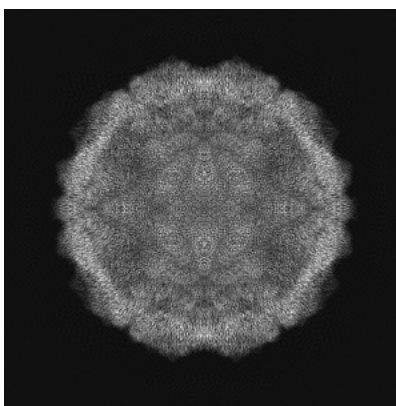
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

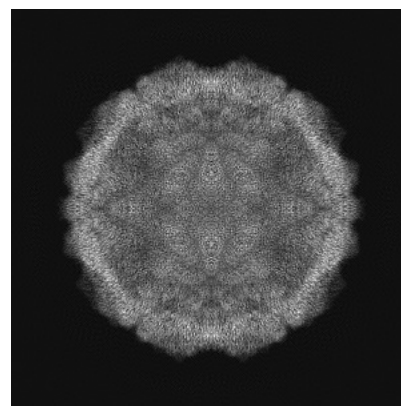
6.1.1 Primary map



X

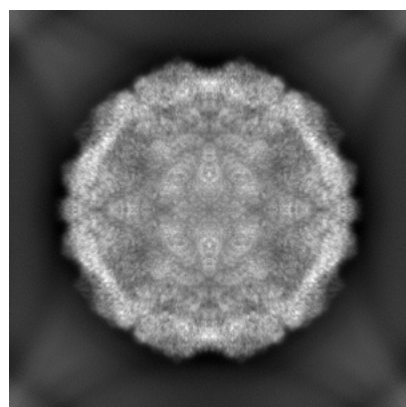


Y

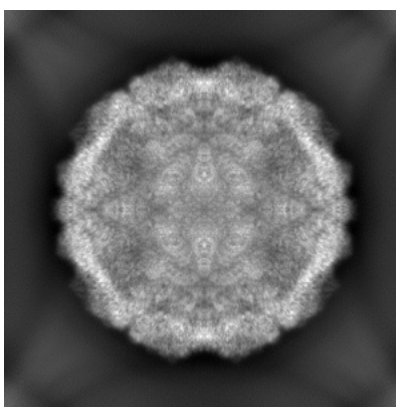


Z

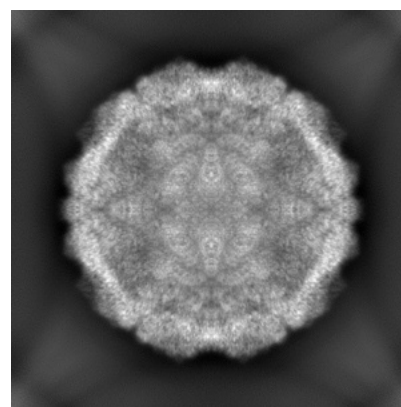
6.1.2 Raw map



X



Y

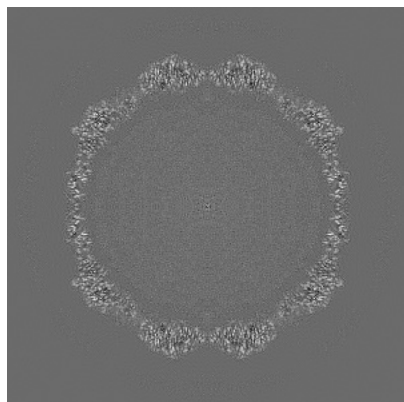


Z

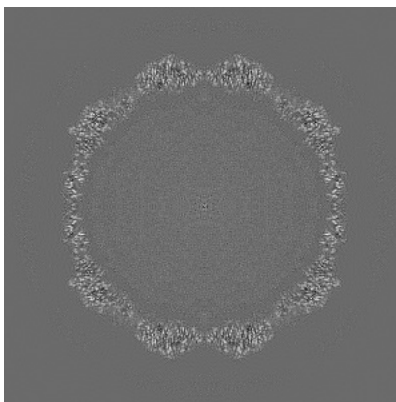
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

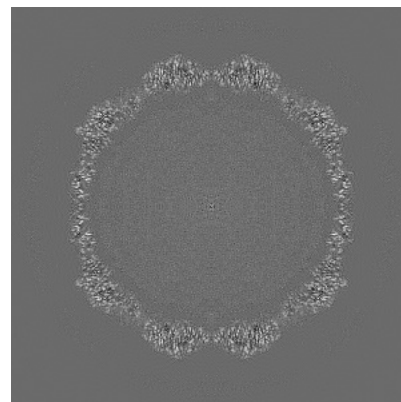
6.2.1 Primary map



X Index: 300

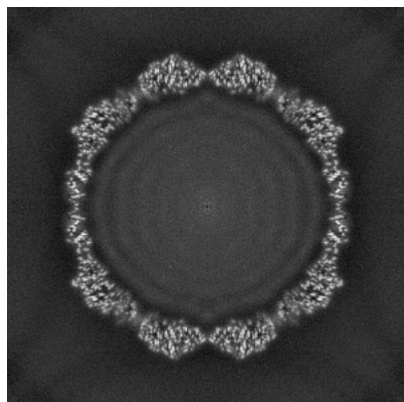


Y Index: 300

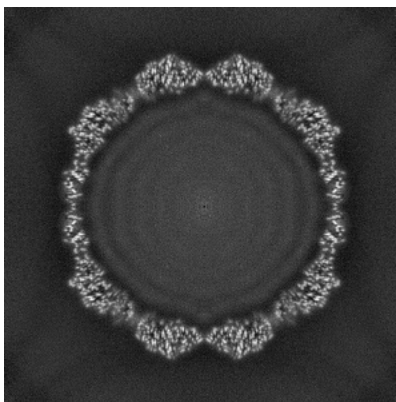


Z Index: 300

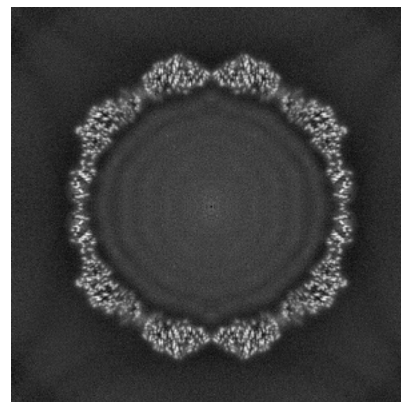
6.2.2 Raw map



X Index: 300



Y Index: 300

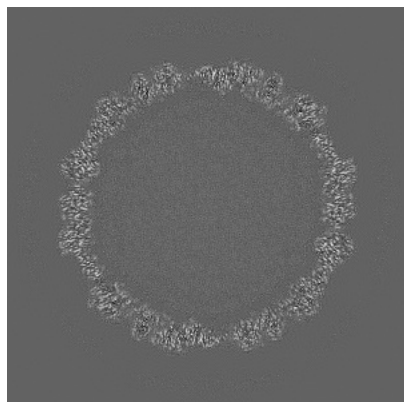


Z Index: 300

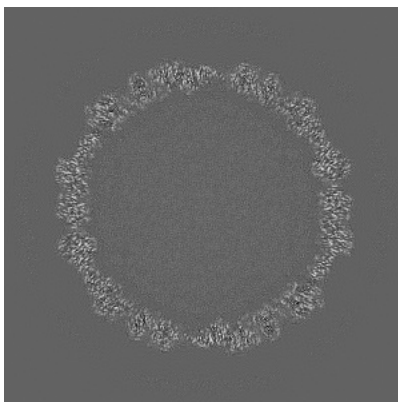
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

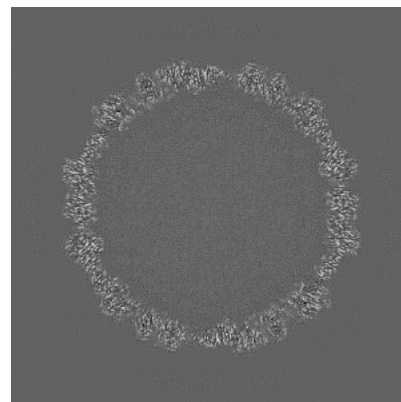
6.3.1 Primary map



X Index: 265

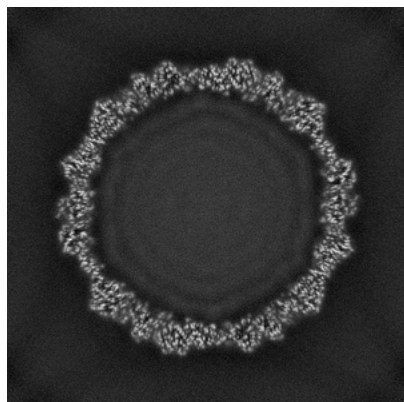


Y Index: 335

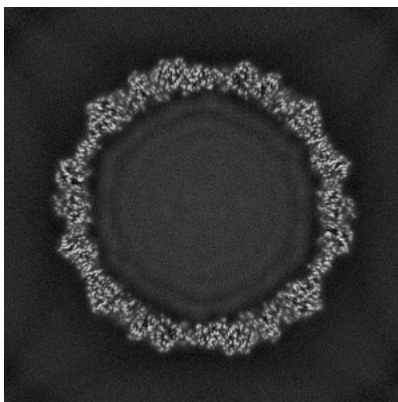


Z Index: 335

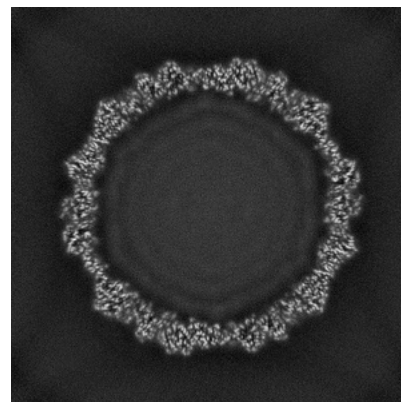
6.3.2 Raw map



X Index: 260



Y Index: 340

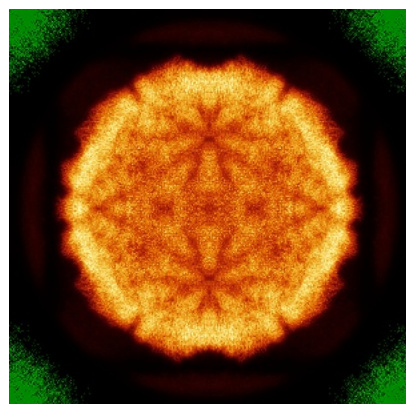


Z Index: 260

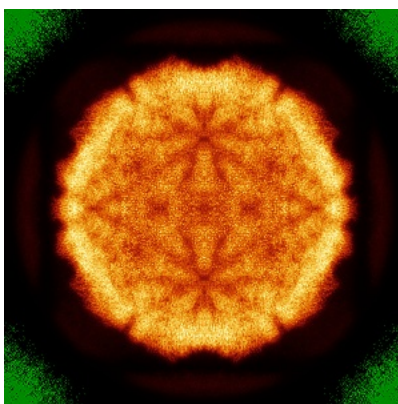
The images above show the largest variance slices of the map in three orthogonal directions.

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

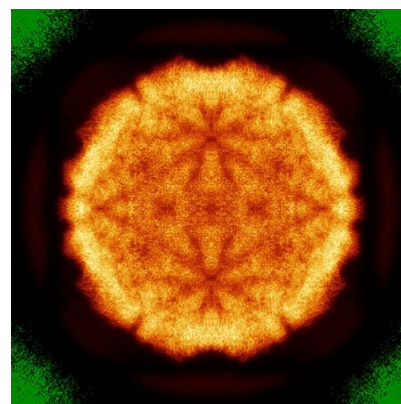
6.4.1 Primary map



X

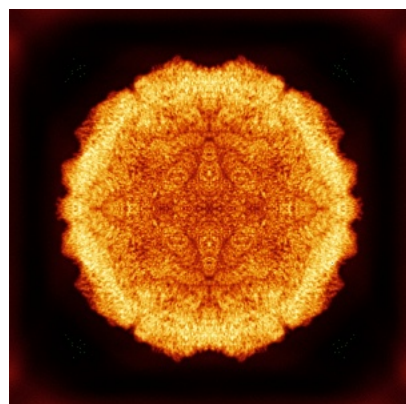


Y

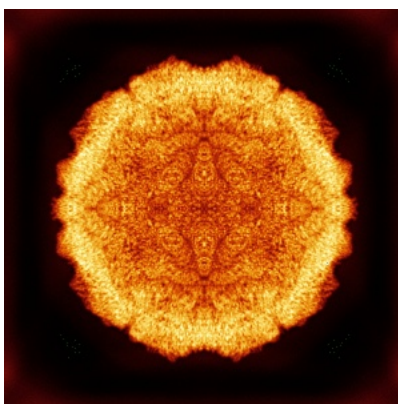


Z

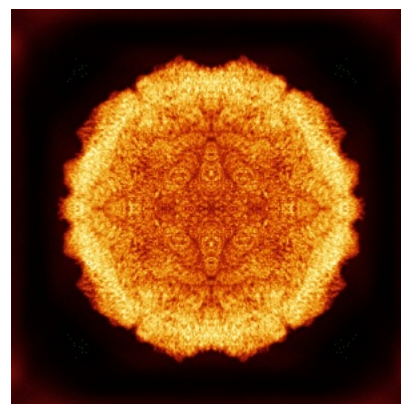
6.4.2 Raw map



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



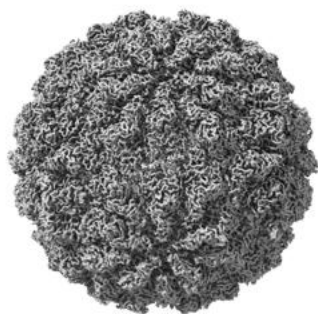
Y



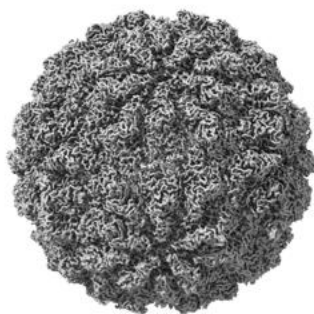
Z

The images above show the 3D surface view of the map at the recommended contour level 0.7329. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

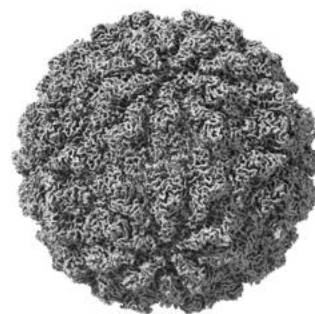
6.5.2 Raw map



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.

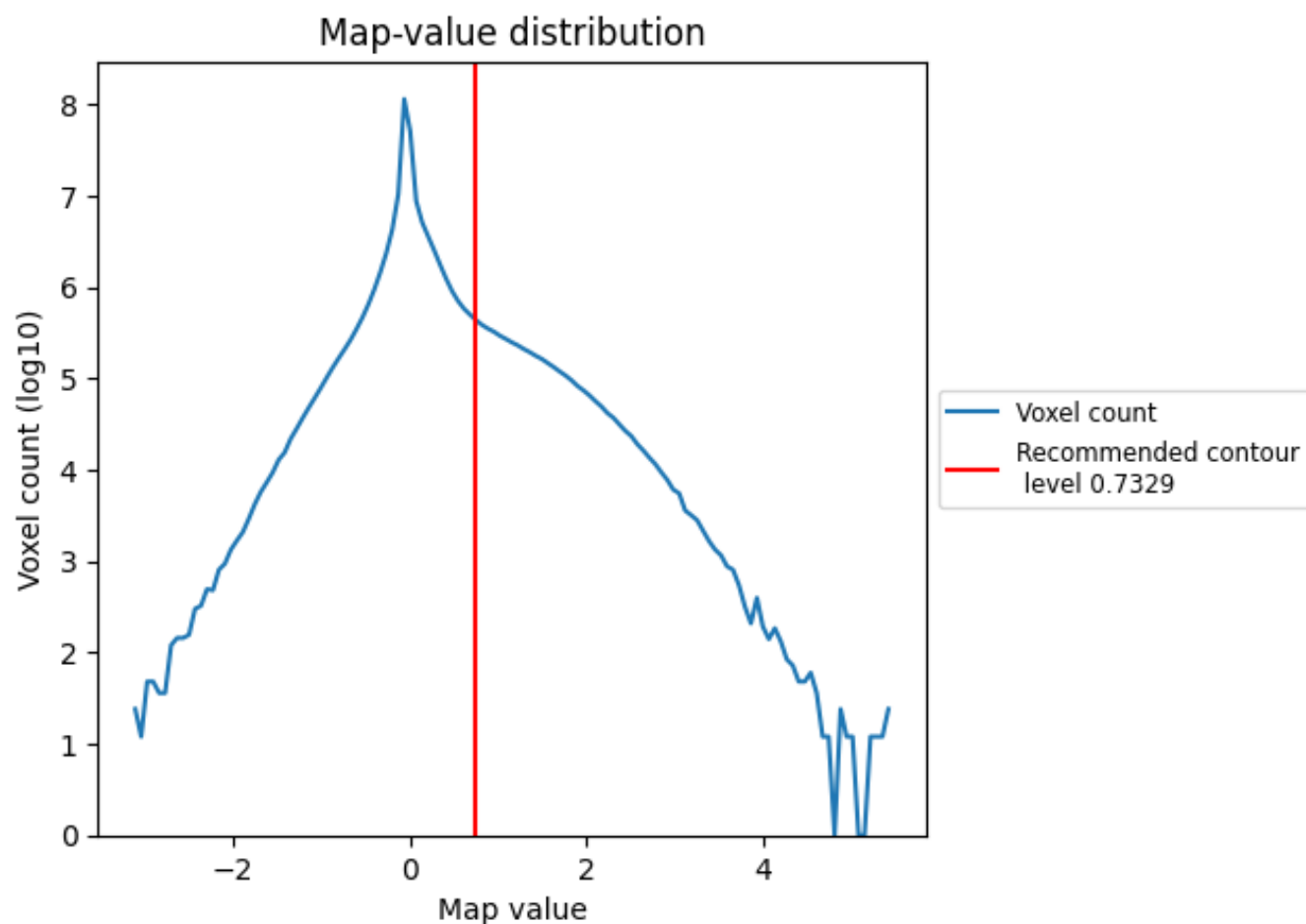
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

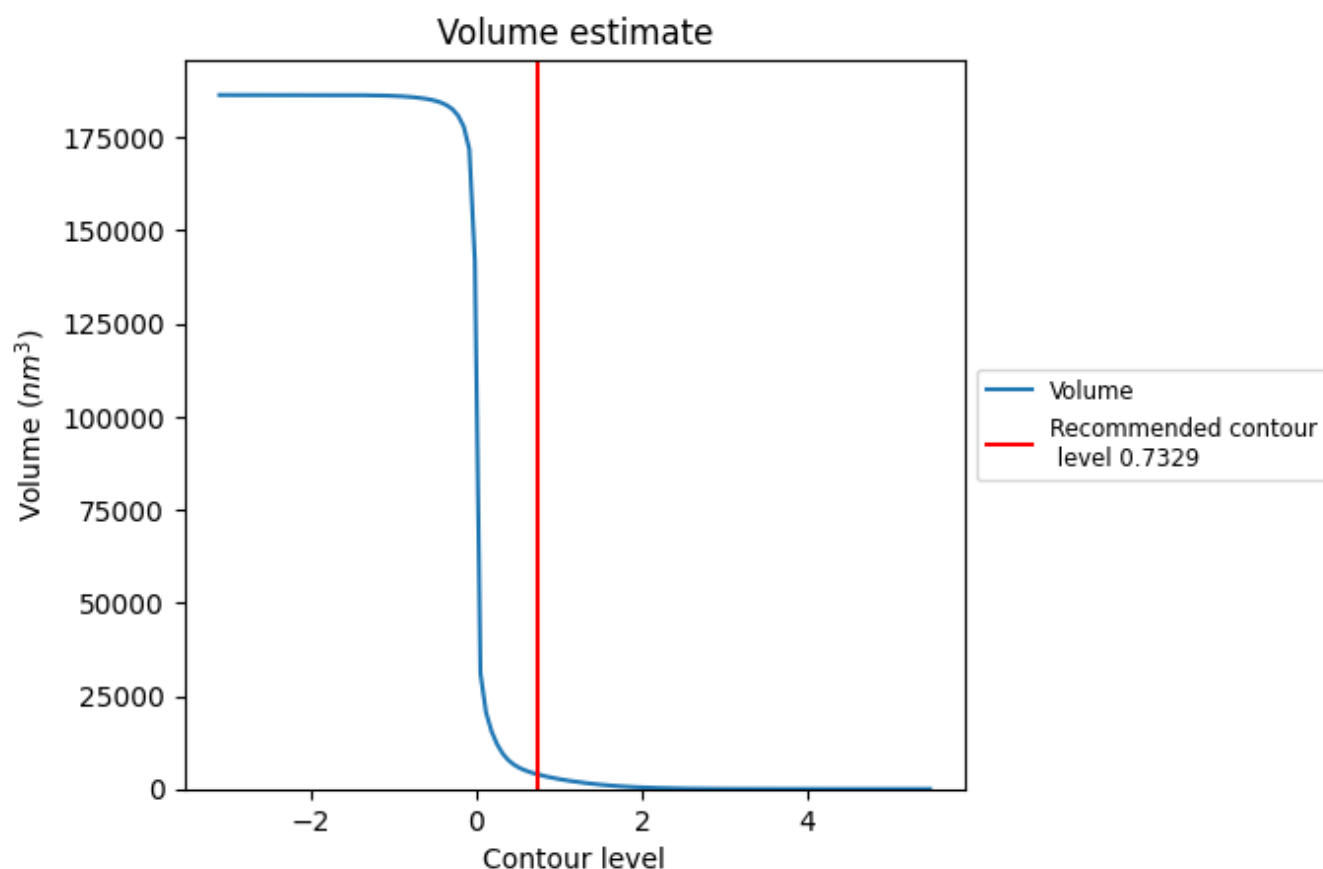
This section contains the results of statistical analysis of the map.

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.

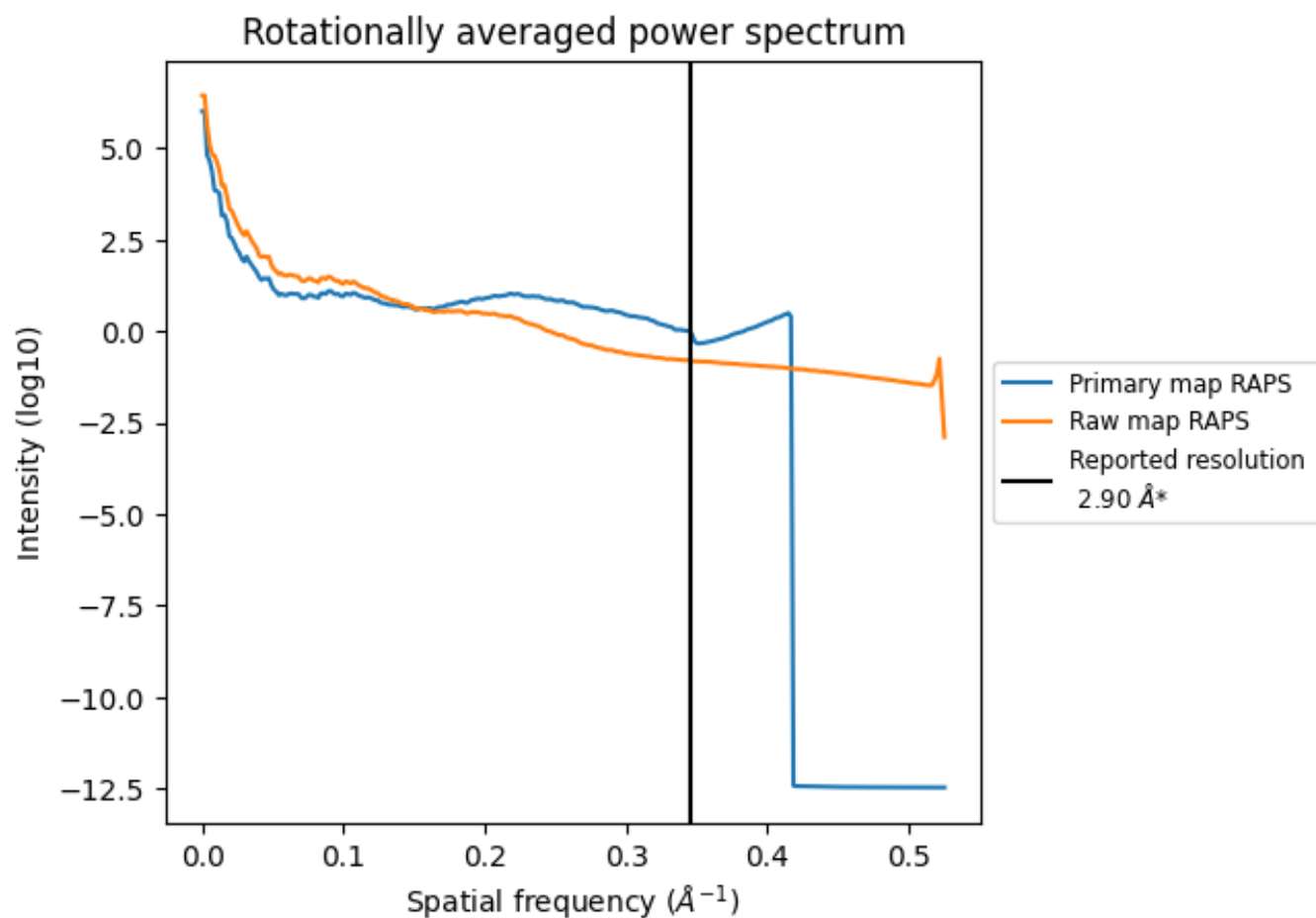
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3973 nm^3 ; this corresponds to an approximate mass of 3589 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 ⓘ

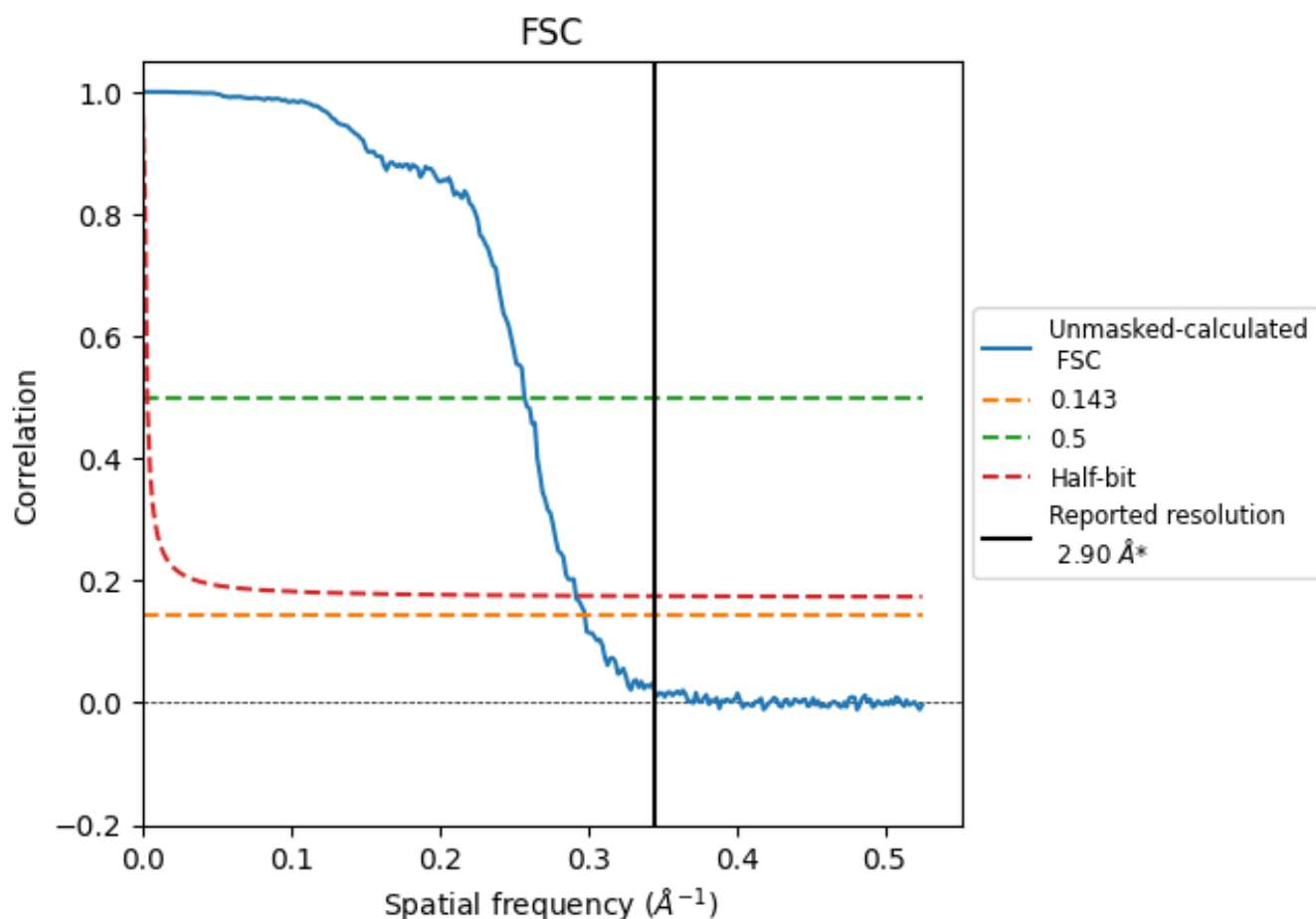


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

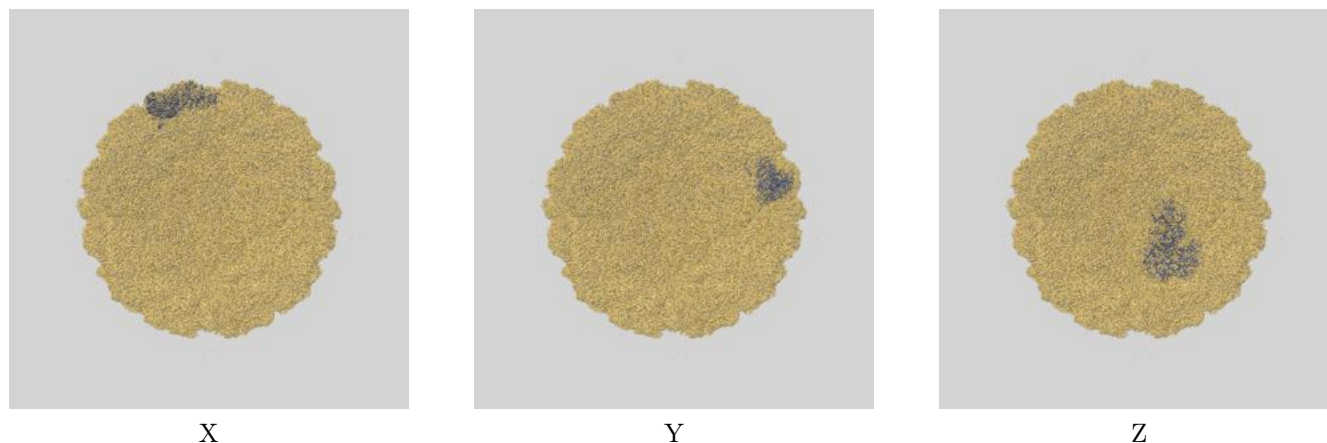
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.36	3.89	3.42

*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 3.36 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

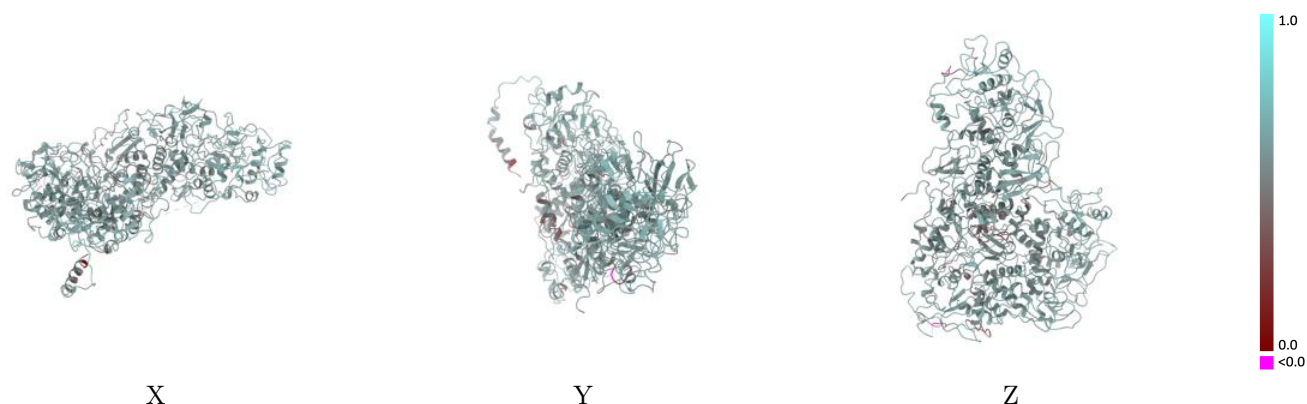
This section contains information regarding the fit between EMDB map EMD-55928 and PDB model 9THI. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



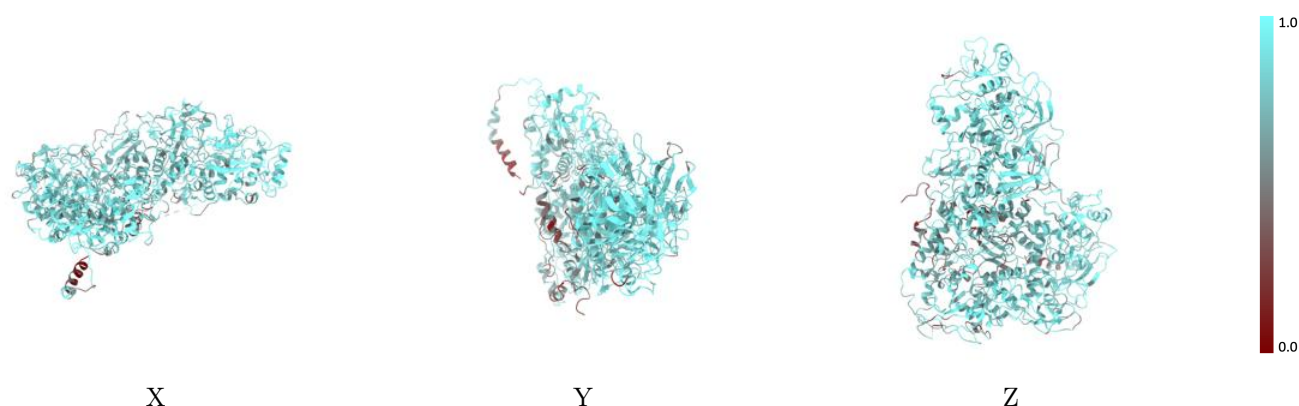
The images above show the 3D surface view of the map at the recommended contour level 0.7329 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



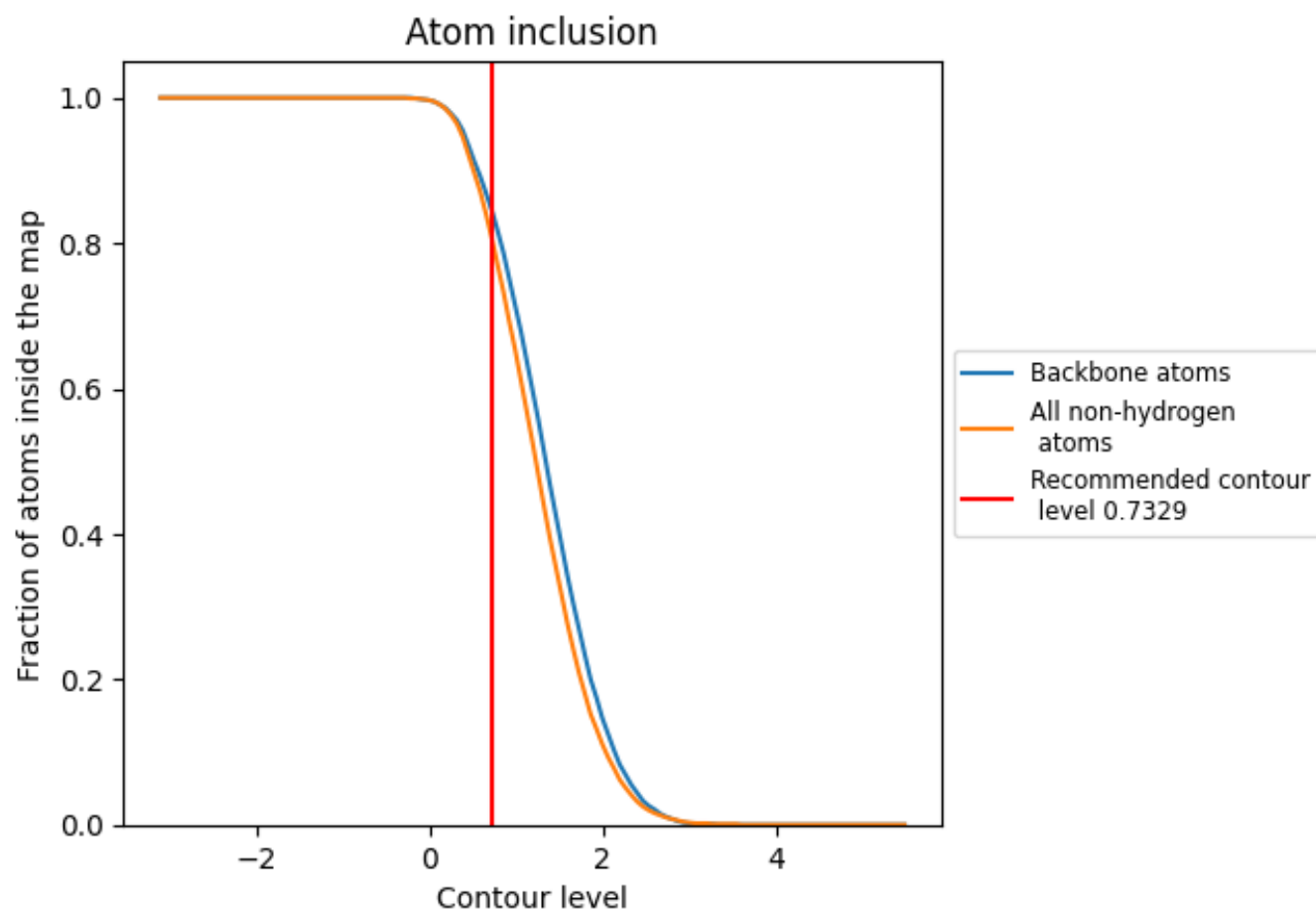
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7329).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.7329) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.5670
A	0.8040	0.5690
B	0.7980	0.5650

