



wwPDB EM Validation Summary Report ⓘ

Oct 20, 2026 – 05:44 pm BST

PDB ID : 9THH / pdb_00009thh
EMDB ID : EMD-55927
Title : OmRV WT infectious clone
Authors : Wang, H.; Okamoto, K.
Deposited on : 2025-12-03
Resolution : 3.10 Å(reported)
Based on initial model : 6S2C

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

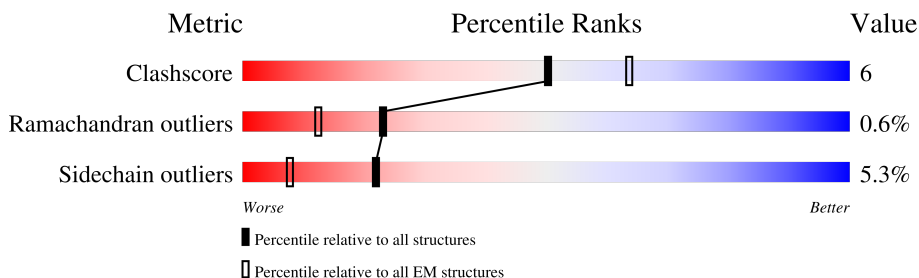
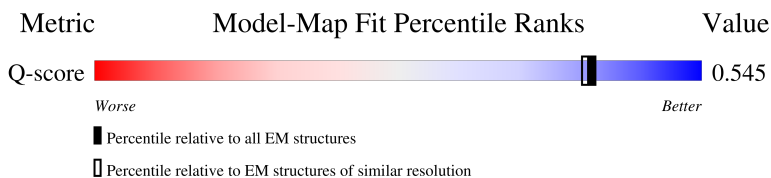
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	 41% 9% 50%
1	B	1685	 43% 8% 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		

S1665	D1666	P1667	S1668	N1669	V1670	L1671	S1672	Q1673	P1674	A1675	P1676	L1677	M1678	SER	PRO	PRO	THR	SER	SER	SER																															
E1549	I1553	E1554	D1569	Y1576	N1594	Y1606	ALA	GLU	PRO	ALA	LEU	GLN	ALA	GLN	GLY	ASP	GLU	VAL	E1619	D1620	A1621	F1622	D1623	N1627	F1630	L1631	D1632	V1633	A1634	K1635	S1636	V1637	A1638	E1639	S1640	A1641	G1642	E1643	A1646	T1647	K1648	A1649	L1650	T1651	D1652	L1653	D1657	V1658	S1659	S1660	
Q1261	A1264	V1268	Y1269	D1270	T1271	D1272	T1275	K1278	V1279	A1286	A1287	N1288	L1289	E1292	Q1293	S1294	M1295	D1296	V1297	P1298	F1299	V1300	V1301	T1306	E1310	T1332	Y1339	T1343	L1347	V1351	V1361	G1362	T1363	I1364	R1368	Y1369	G1370	C1374	K1378	H1382											
G1106	R1116	R1117	E1118	I1119		N1122	P1123	T1124	T1125	L1126	M1132	Q1138	P1141	A1145	G1146	A1147	G1153	N1157	P1164	A1165	E1168	L1171	R1181	T1187	Y1204	L1210	L1214	M1221	T1222	G1227	A1233	R1251	F1256	P1257	L1258	A1259	N1260														
R926	D927	N928	T929	S930	L931	Q932	N935	I939	I946	L947	P948	N949	G950	L951	S955	M956	L957	L963	R978	S979	V983	V989	A994	M1013	M1014	P1015	I1026	V1030	T1034	D1037	P1048	Q1052	A1053	T1054	S1055	D1056	V1078	D1084	L1085	A1086	G1087										
LEU	MET	HIS	ALA	TYR	THR	ASN	CYS	P794	E798	N799	A800	P801	E808	N809	T810	D811	E812	V813	L814	E821	T826	T827	G831	D832	Q850	Y851	S852	A864	I865	P866	N879	E892	E897	Y898	Y899	I904	M911	D914	Q915	N919	W924	R925									
PRO	LYS	THR	GLN	GLU	ASP	VAL	GLU	ARG	LYS	PHE	ASN	ASP	ILE	ASP	GLU	ALA	ILE	ASP	THR	ARG	LEU	LYS	THR	THR	ARG	PRO	THR	LYS	THR	ASP	MET	LYS	PHE	ALA	VAL	GLY	VAL	GLN	PRO	ALA	VAL	GLY	VAL	GLN	PRO	GLN	PRO	GLN	PRO	GLN	PRO
THR	THR	ASN	ARG	PHE	GLU	ASP	VAL	MET	LYS	ASP	VAL	VAL	MET	LYS	GLU	VAL	THR	GLY	THR	ARG	LEU	LYS	THR	THR	ARG	VAL	ARG	VAL	ARG	VAL	GLY	ALA	PHE	ALA	VAL	VAL	GLY	VAL	GLN	PRO	ALA	VAL	THR	VAL	GLN	GLN	GLN	GLN	GLN	GLN	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31506	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	2.900	Depositor
Minimum map value	-1.951	Depositor
Average map value	0.050	Depositor
Map value standard deviation	0.193	Depositor
Recommended contour level	0.774	Depositor
Map size (Å)	599.76, 599.76, 599.76	wwPDB
Map dimensions	630, 630, 630	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	0.17	0/6644	0.41	0/9088
1	B	0.16	0/6849	0.39	1/9373 (0.0%)
All	All	0.16	0/13493	0.40	1/18461 (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
1	B	0	1
All	All	0	2

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	B	931	LEU	CB-CA-C	-5.18	110.62	116.63

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	926	ARG	Sidechain
1	B	1256	PHE	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	6488	0	6358	77	0
1	B	6689	0	6565	68	0
All	All	13177	0	12923	145	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 6.

The worst 5 of 145 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:866:PRO:HG2	1:B:1430:ILE:HG22	1.75	0.68
1:A:1387:TYR:HB2	1:A:1398:HIS:HB3	1.77	0.65
1:A:1232:ALA:HB3	1:A:1235:SER:HB3	1.78	0.63
1:B:1477:LEU:HD22	1:B:1576:TYR:HB3	1.80	0.63
1:A:988:THR:HG21	1:A:1093:GLN:HE22	1.64	0.63

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	845/1685 (50%)	781 (92%)	59 (7%)	5 (1%)	21	52
1	B	874/1685 (52%)	820 (94%)	49 (6%)	5 (1%)	21	52
All	All	1719/3370 (51%)	1601 (93%)	108 (6%)	10 (1%)	23	52

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1553	ILE

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Mol	Chain	Res	Type
1	B	994	ALA
1	B	1257	PRO
1	A	1360	SER
1	A	1489	SER

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%)	655 (95%)	36 (5%)	21	51
1	B	717/1408 (51%)	678 (95%)	39 (5%)	20	50
All	All	1408/2816 (50%)	1333 (95%)	75 (5%)	22	51

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1300	VAL
1	B	1488	ASN
1	B	1332	THR
1	B	1388	VAL
1	A	1410	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	982	GLN
1	B	1154	GLN
1	B	1673	GLN
1	B	1138	GLN
1	B	1216	GLN

5.3.3 RNA ⓘ

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.

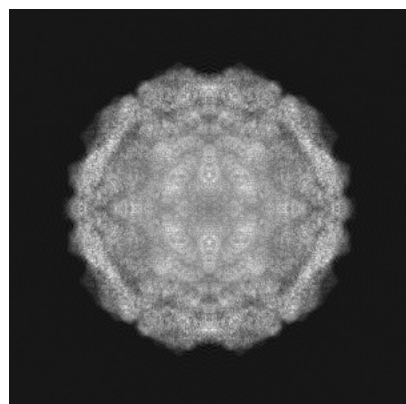
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55927. These allow visual inspection of the internal detail of the map and identification of artifacts.

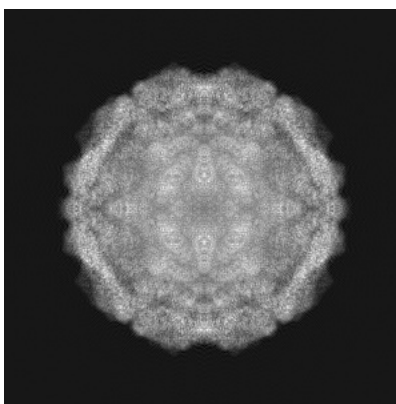
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

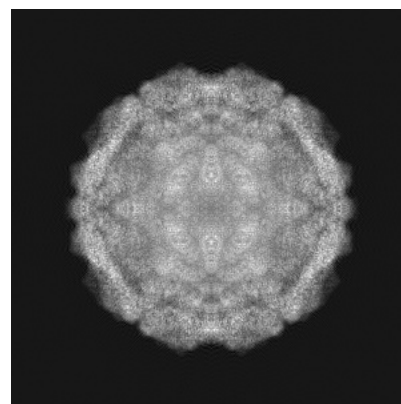
6.1.1 Primary map



X

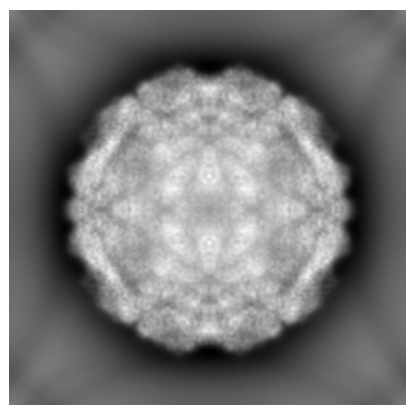


Y

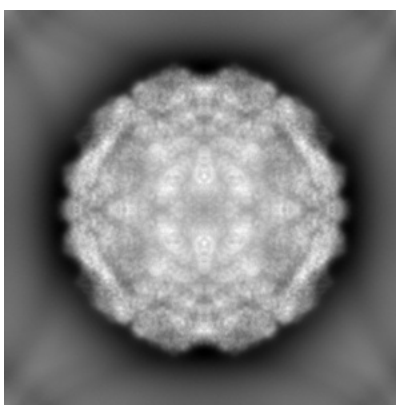


Z

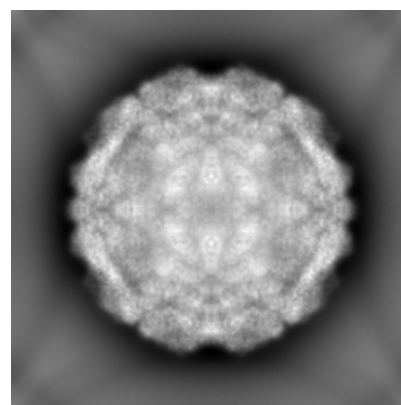
6.1.2 Raw map



X



Y

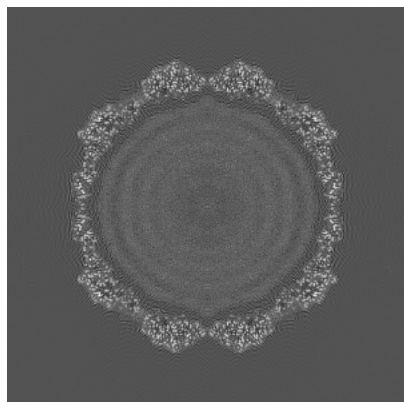


Z

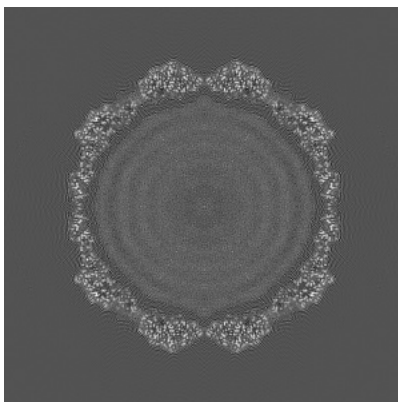
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

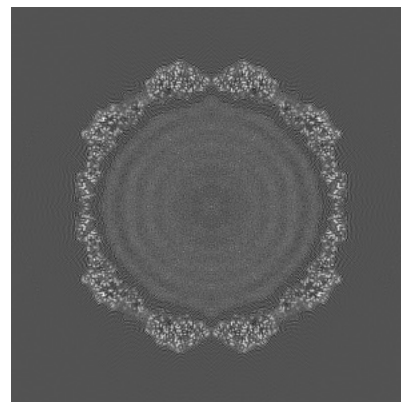
6.2.1 Primary map



X Index: 315

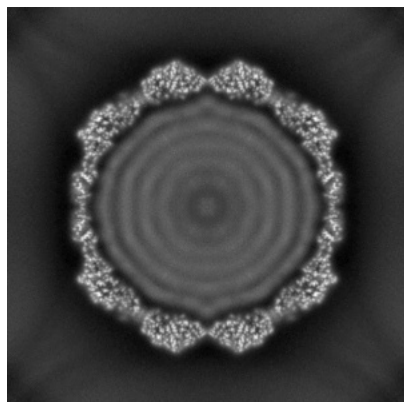


Y Index: 315

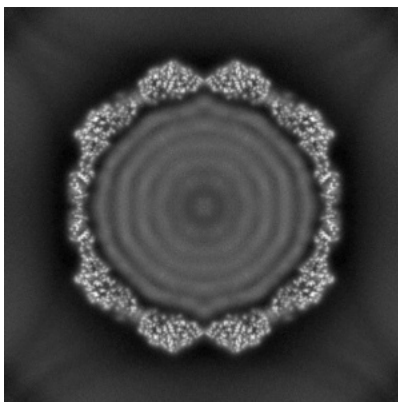


Z Index: 315

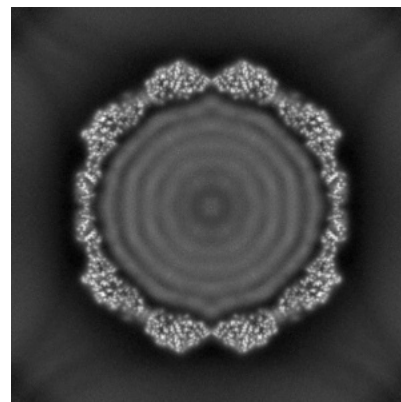
6.2.2 Raw map



X Index: 315



Y Index: 315

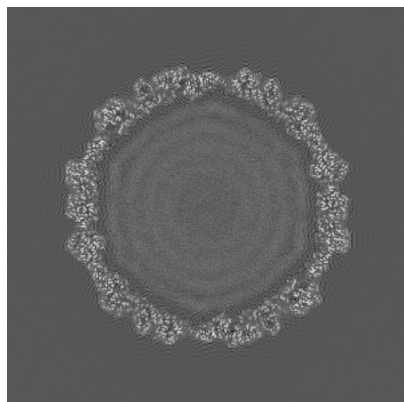


Z Index: 315

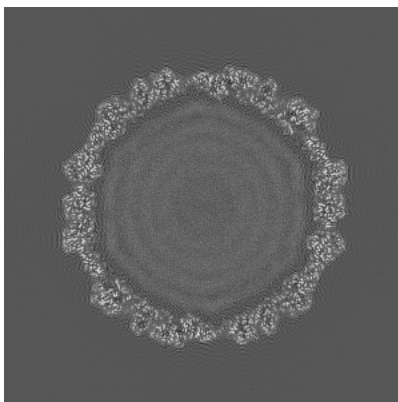
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

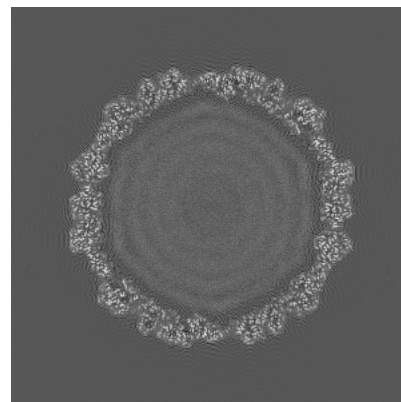
6.3.1 Primary map



X Index: 350

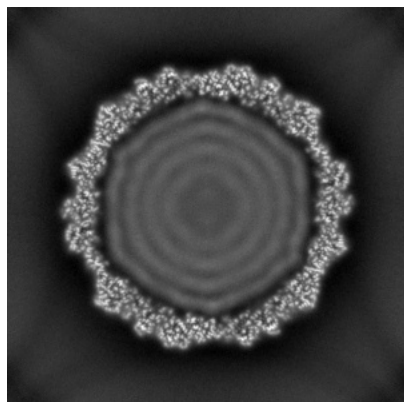


Y Index: 280

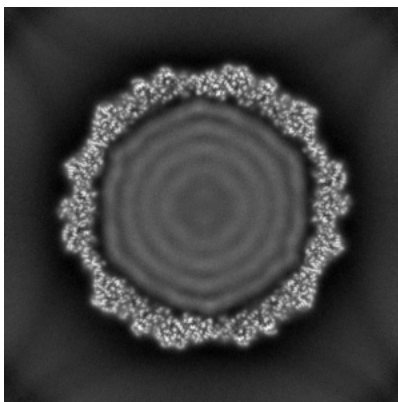


Z Index: 280

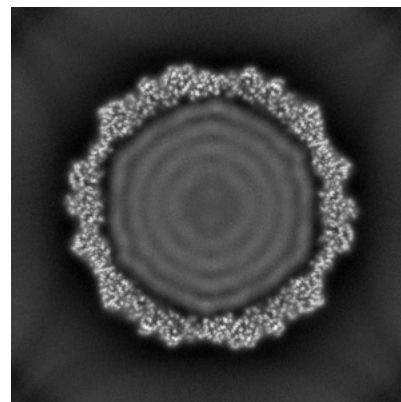
6.3.2 Raw map



X Index: 274



Y Index: 274

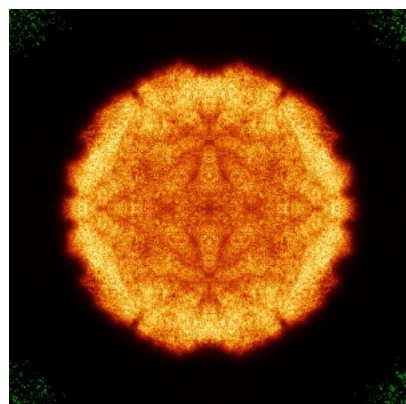


Z Index: 356

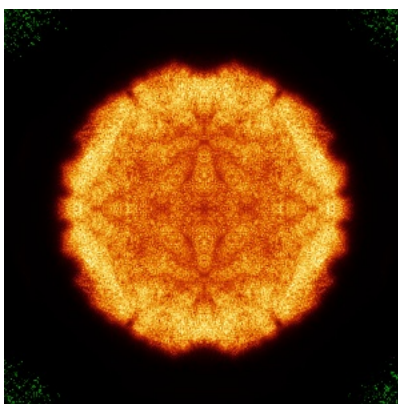
The images above show the largest variance slices of the map in three orthogonal directions.

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

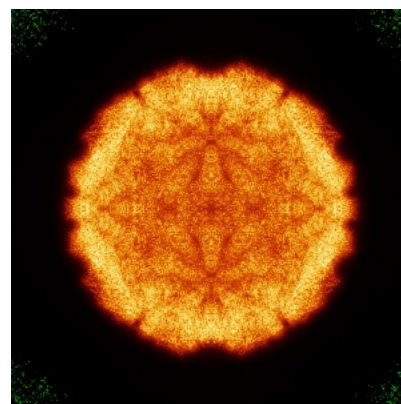
6.4.1 Primary map



X

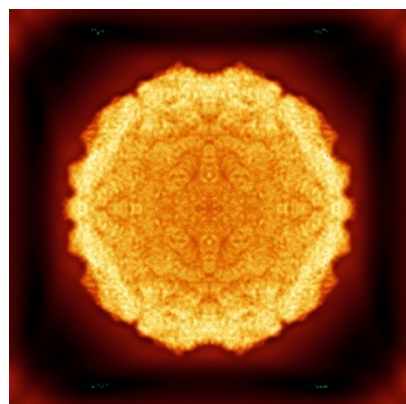


Y

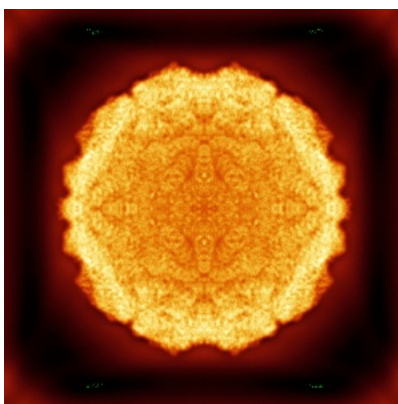


Z

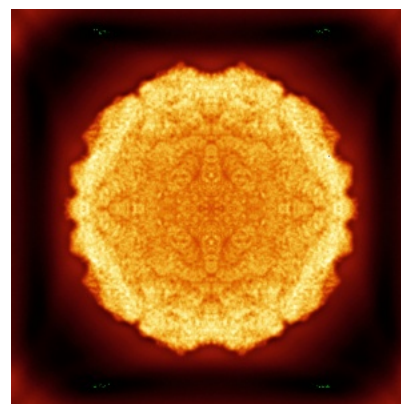
6.4.2 Raw map



X



Y

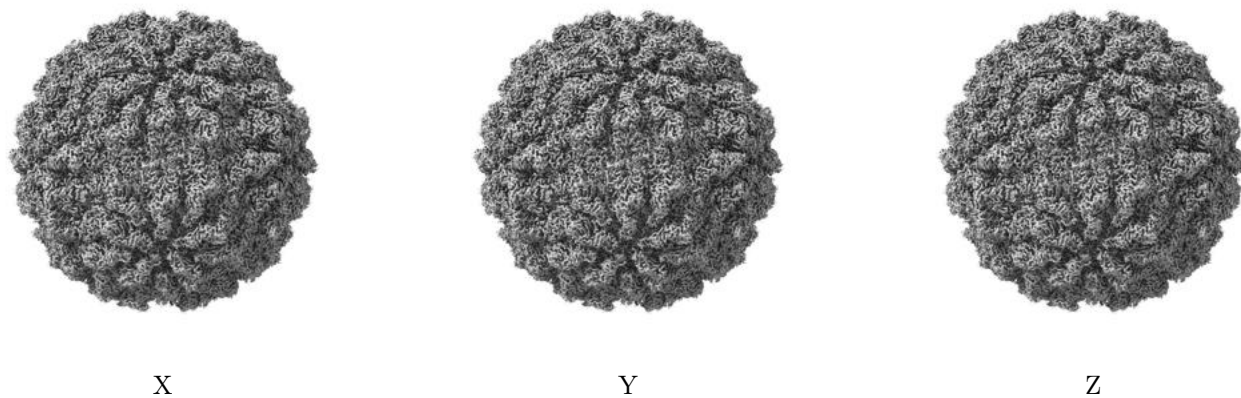


Z

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.

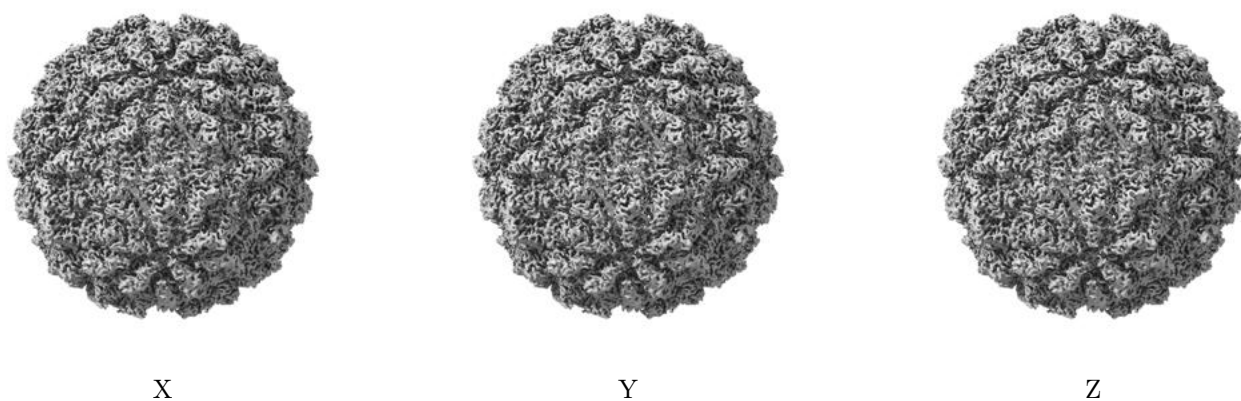
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.774. 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.

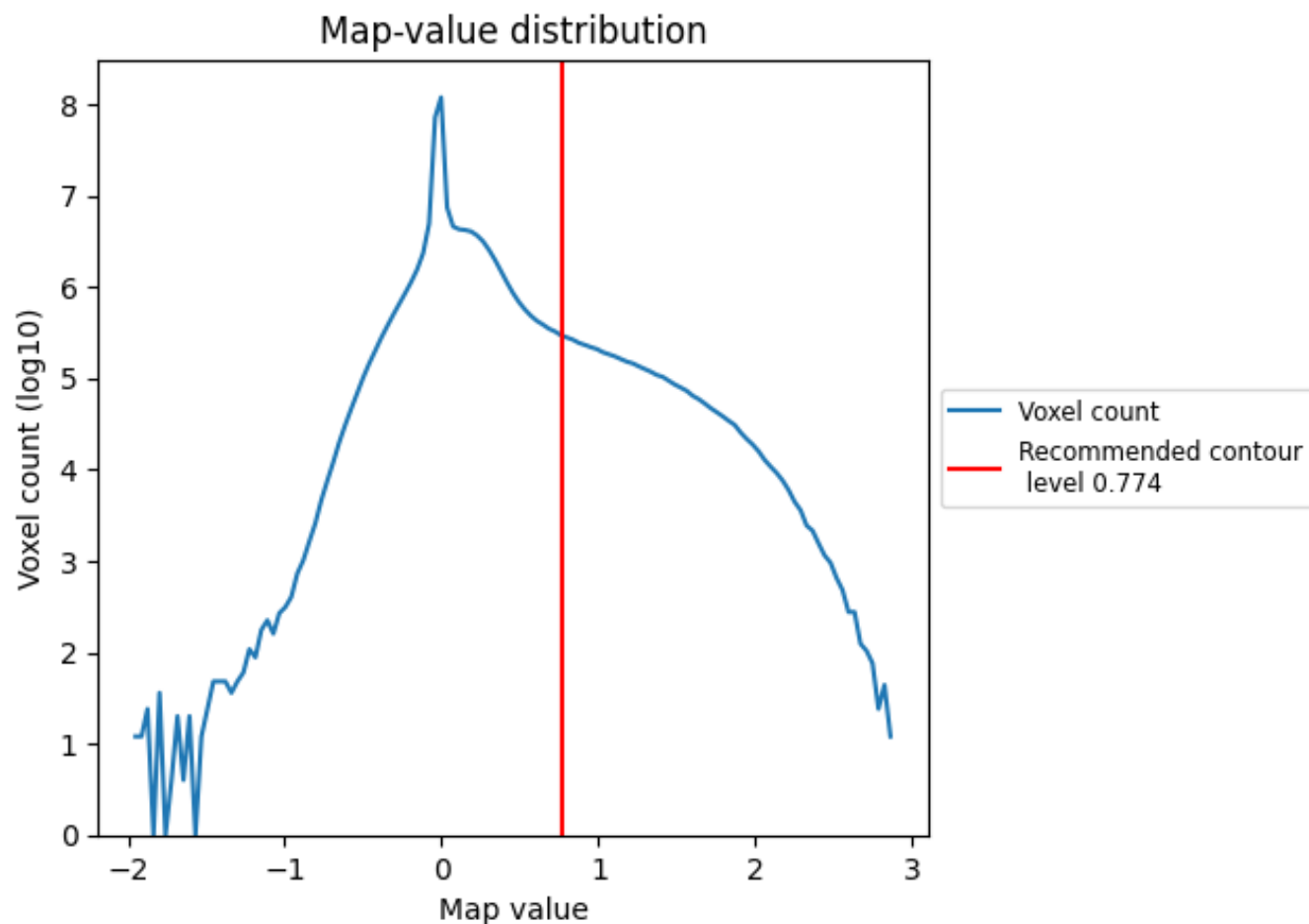
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

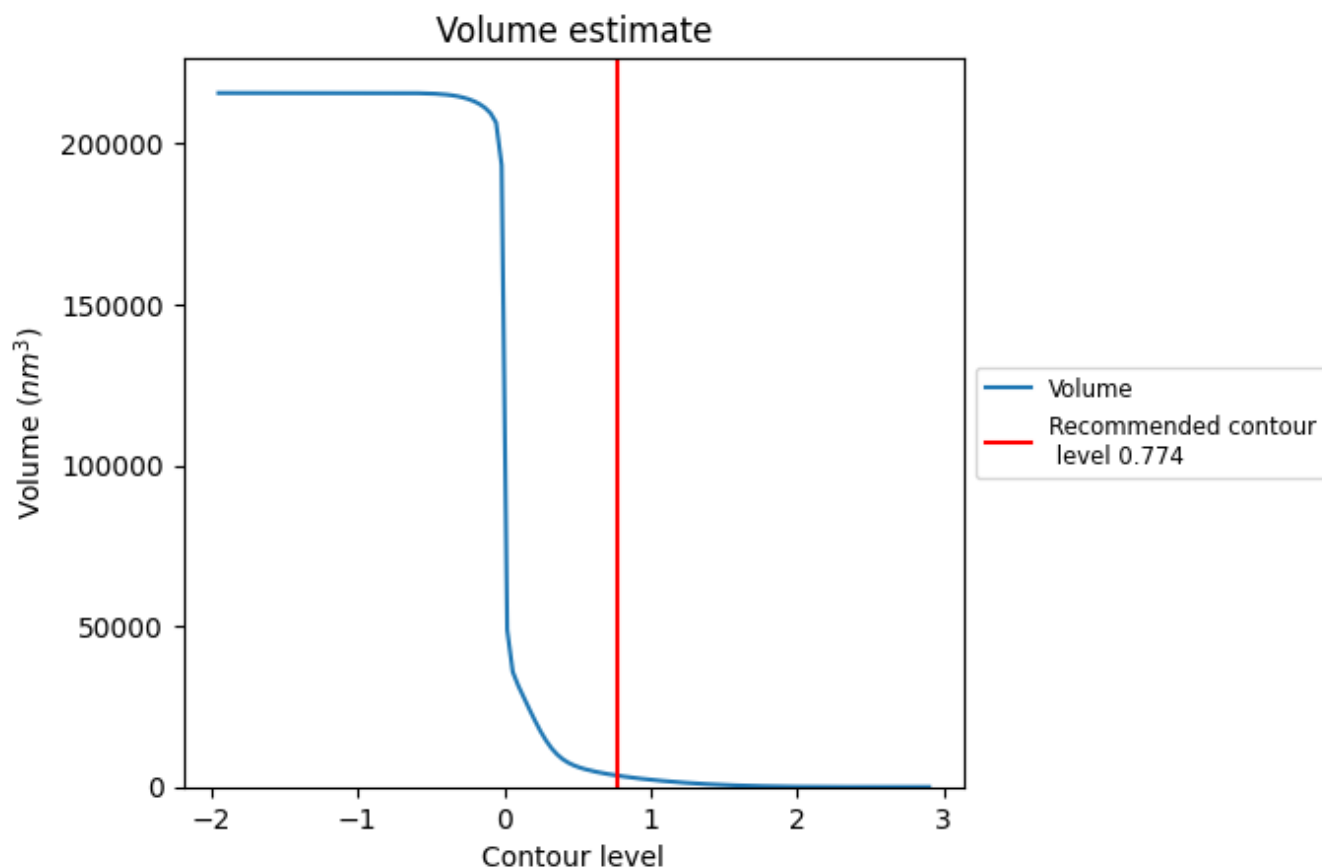
This section contains the results of statistical analysis of the map.

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.

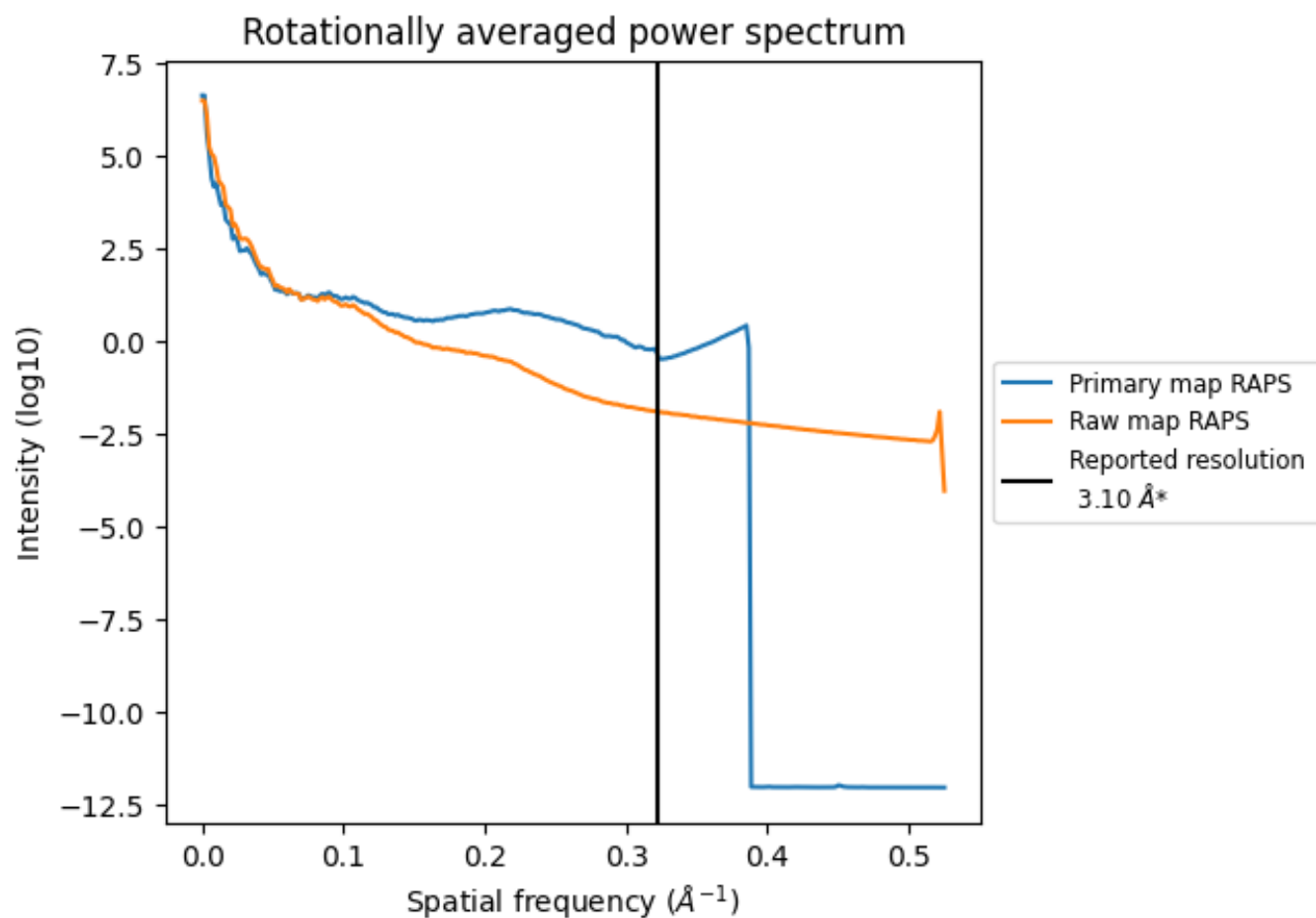
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3518 nm³; this corresponds to an approximate mass of 3178 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 ⓘ

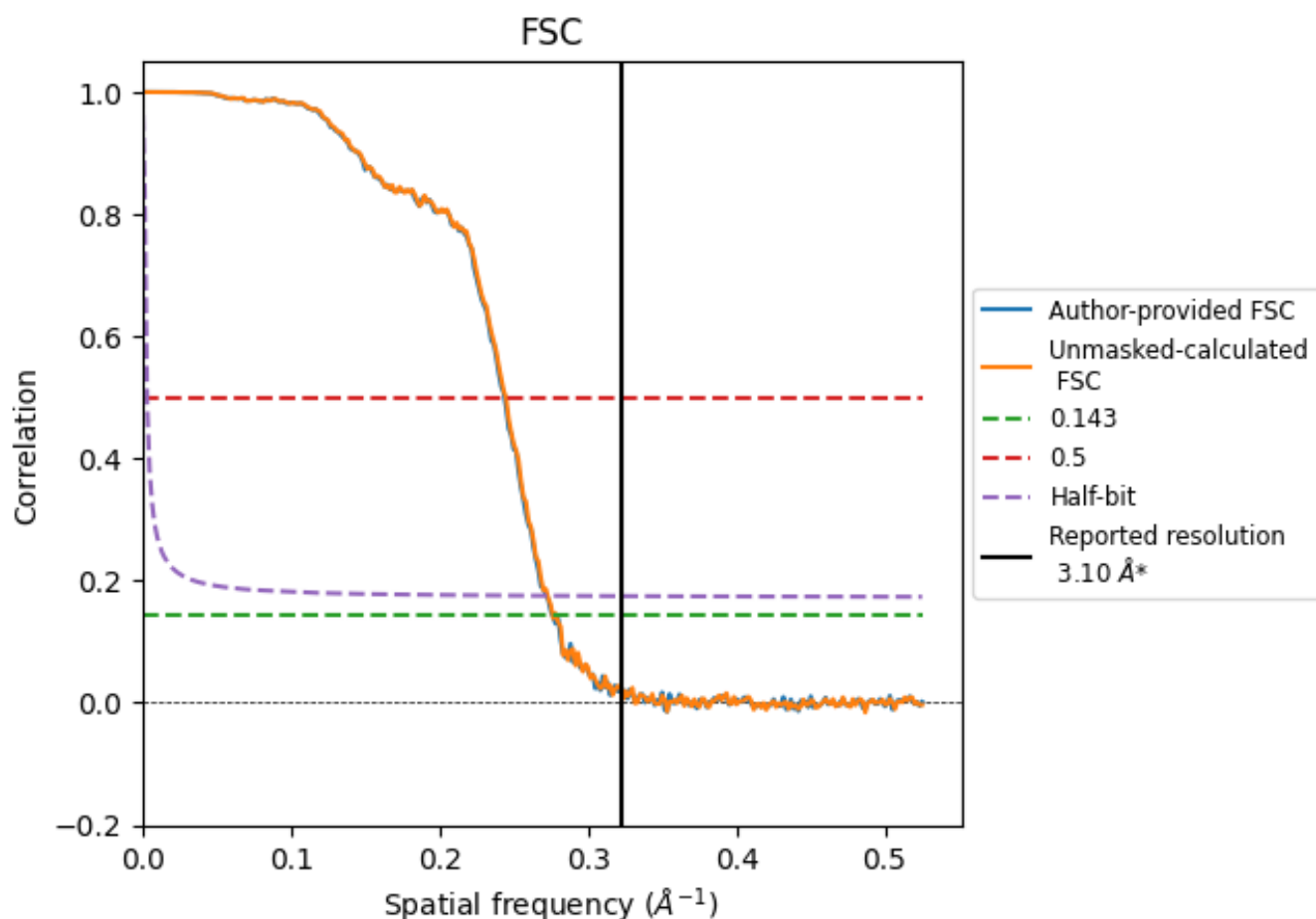


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.62	4.10	3.67
Unmasked-calculated*	3.62	4.08	3.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.62 differs from the reported value 3.1 by more than 10 %

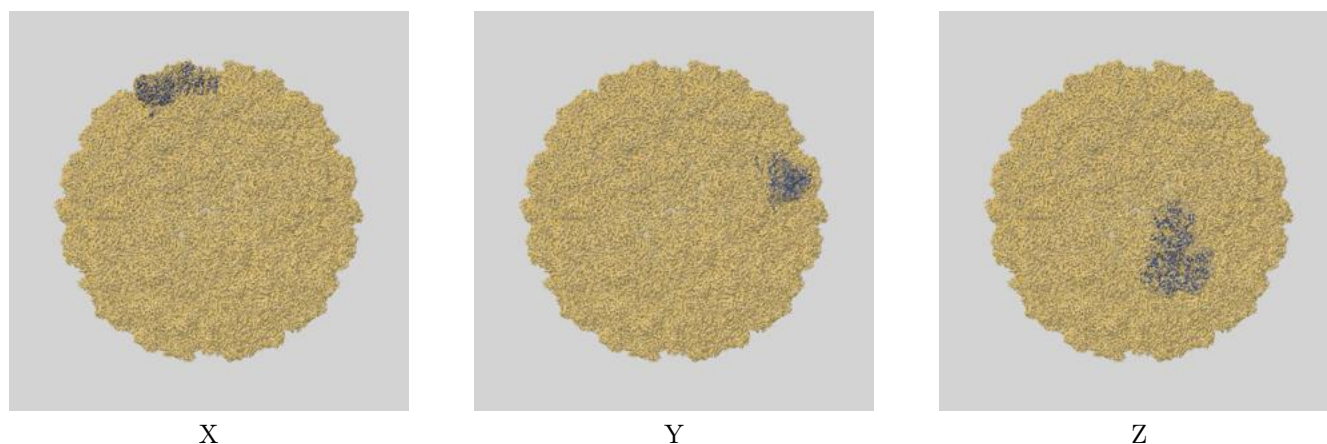
The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.62 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

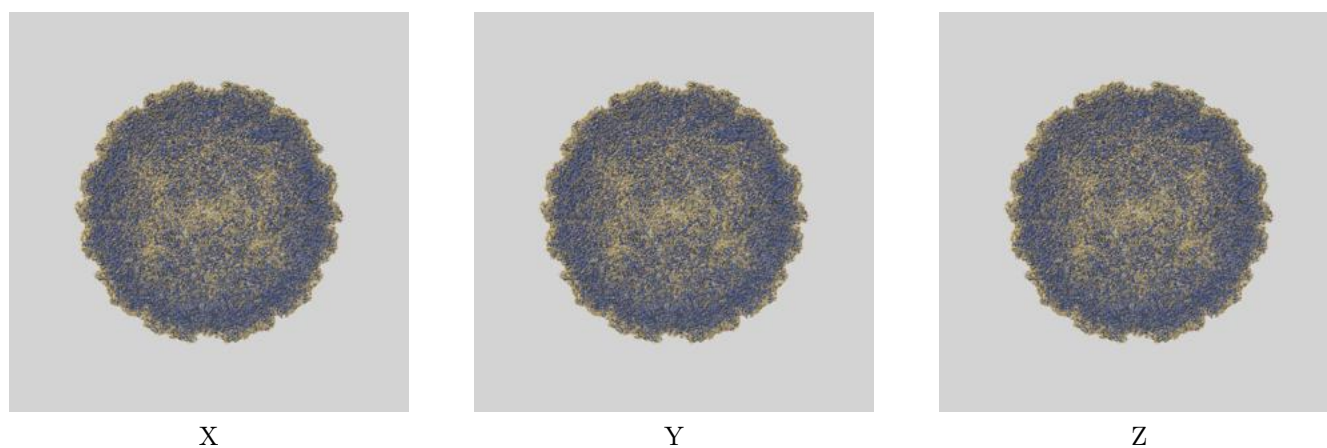
This section contains information regarding the fit between EMDB map EMD-55927 and PDB model 9THH. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



9.1.2 Map-model assembly overlay [i](#)



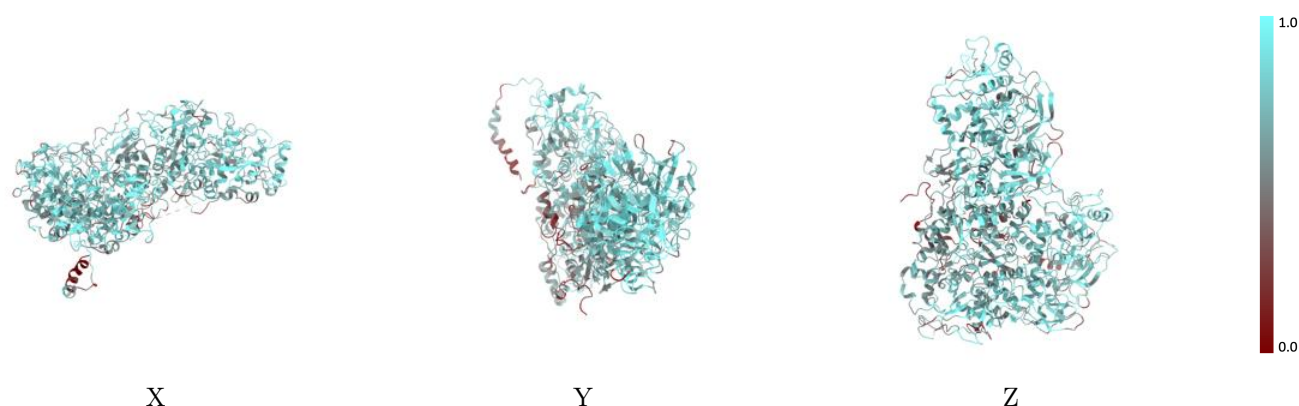
The images above show the 3D surface view of the map at the recommended contour level 0.774 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



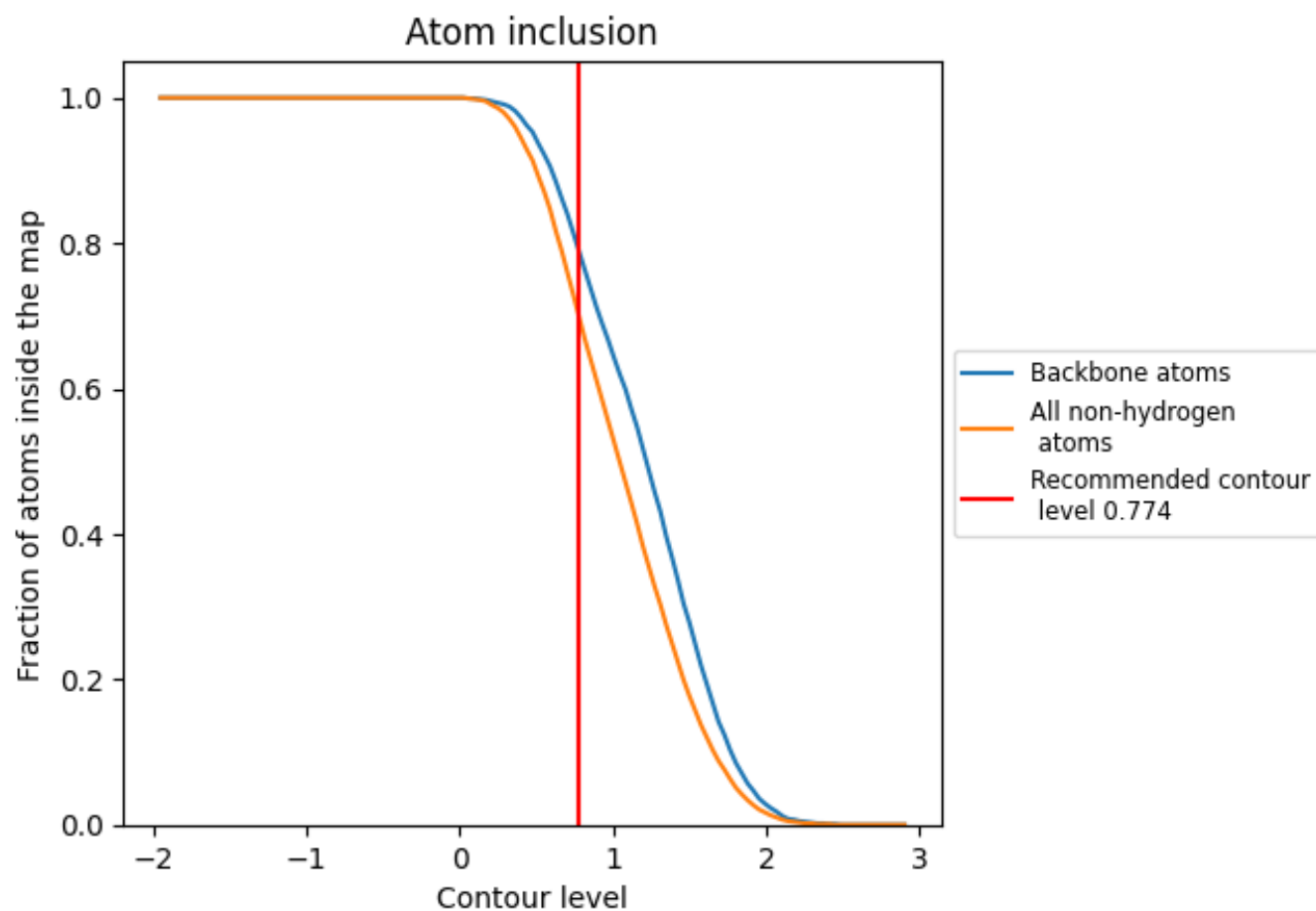
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.774).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 70% 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 (0.774) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7020	<div></div> 0.5450
A	<div></div> 0.7080	<div></div> 0.5460
B	<div></div> 0.6960	<div></div> 0.5440

