



wwPDB EM Validation Summary Report ⓘ

Oct 18, 2026 – 04:34 PM EDT

PDB ID : 12TF / pdb_000012tf
EMDB ID : EMD-76740
Title : GII.4 Syd T=4 (raised) VLP
Authors : Anish, R.; Apostol, C.; Pham, S.; Prasad, B.V.V.
Deposited on : 2026-04-17
Resolution : 3.89 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

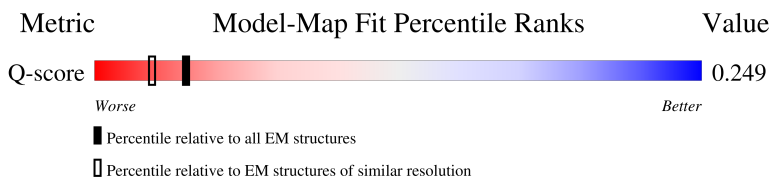
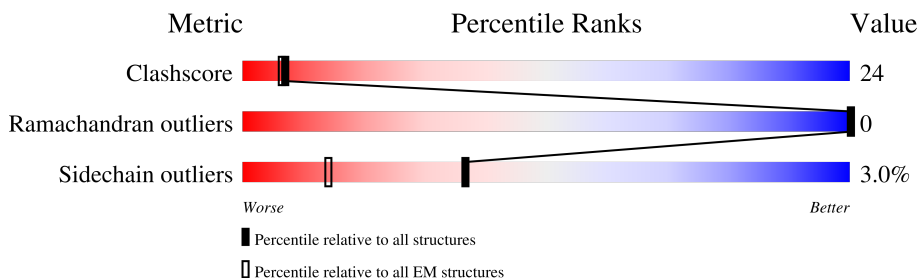
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.89 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	8712 (3.39 - 4.39)

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	540	
1	B	540	
1	C	540	
1	D	540	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15053 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.

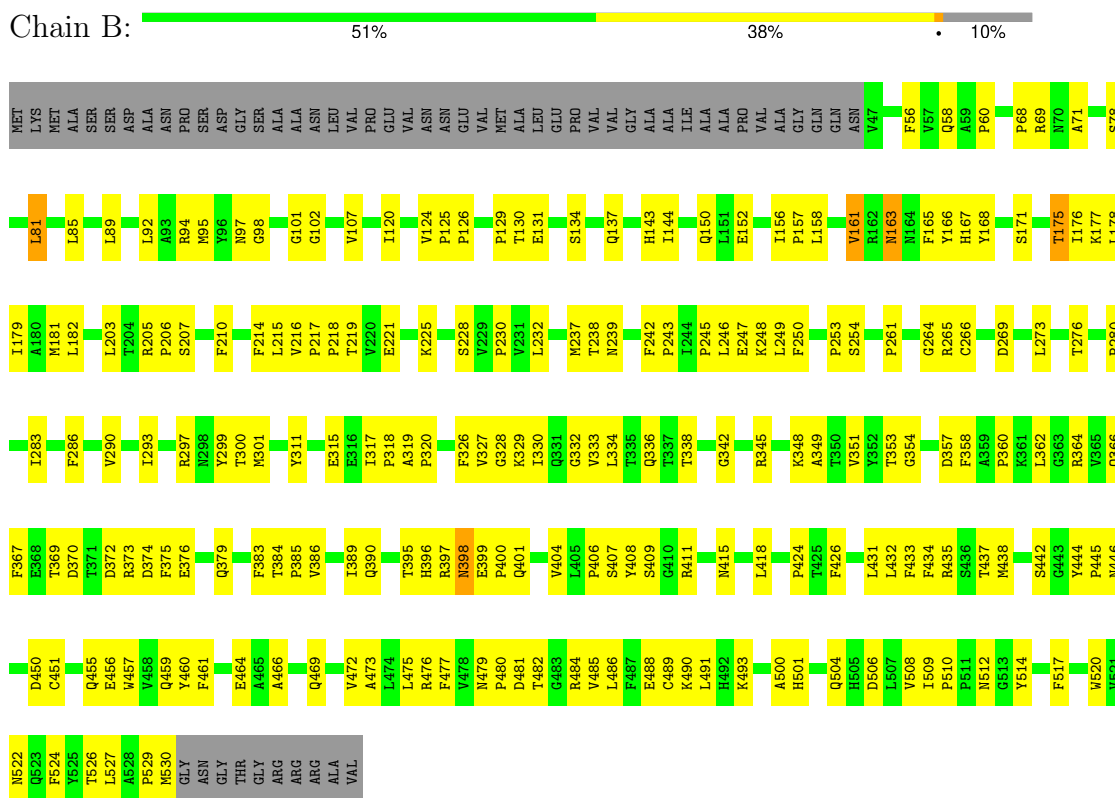
- Molecule 1 is a protein called VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	484	Total	C	N	O	S	0	0
			3767	2413	638	702	14		
1	D	484	Total	C	N	O	S	0	0
			3767	2413	638	702	14		
1	C	484	Total	C	N	O	S	0	0
			3761	2410	635	702	14		
1	A	484	Total	C	N	O	S	0	0
			3758	2409	634	701	14		

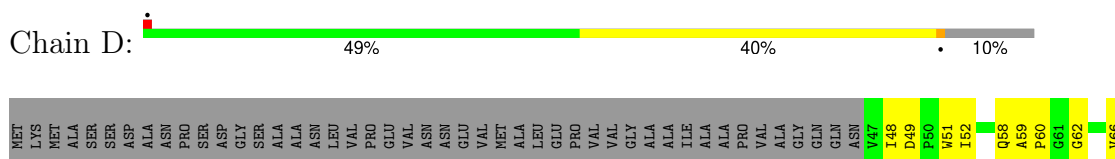
3 Residue-property plots

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: VP1



• Molecule 1: VP1





F515	F516	S442	A359	P261	M163	G73
		G443	P360		N164	E74
W520		Y444	K361	R265	F165	I75
W521		P445	L362	C266	Y166	L76
N522		M446	G363		H167	W77
Q523		M447	R364	L273	Y168	
F524		D448	V365	G274	N169	L81
W525		L449	Q366	T275	Q170	G82
T526		D450		T276	T175	P83
L527			D370	Q277		D84
A528		P454	T371		I179	
P529		Q455	D372	P280	A180	S90
W530		E456	R373	I283	M181	H91
GLY		W457	D374	C284	L182	L92
ASN		V458	F375	T285	Y183	A93
GLY		Q459	E376	T286	T184	R94
THR		Y460		F287		
GLY			Q379	R287	R187	N97
ARG		A465			A188	G98
ARG			F383	R297		Y99
ARG		Q469			S199	A100
ALA		S470	V386	L303	C200	G101
VAL		D471	G387		R201	
		V472	V388	W308	V202	Q106
			I389			V107
		R476	Q390	Y311	F210	I108
		F477				L109
		V478	T395	E315	I213	
		M479	R396	E316	F214	N112
		P480	R397	L317	L215	A113
		D481	N398	P318	V216	F114
		T482	E399	A319		T115
		G483	P400	P320	V220	A116
		R484	Q401	L321		G117
		V485			R223	K118
		L486	V404	P324	T224	V119
		F487			K225	I120
		E488	S407	V327	P226	F121
		C489	Y408	G328		
		K490	S409	K329	P230	L133
		L491	G410		V234	S134
		H492	R411	G332		P135
		K493		V333		S136
			M415		W237	Q137
		V497		Q336	T238	V138
		T498	L418	T337	N239	T139
		V499		S240	S240	
		A500	P424		R241	H143
			T425	G342	F242	I144
			F426		P243	V145
				R345	I244	D146
		Q504	L431	G346	P245	V146
		H505	L432	H347	E247	D147
			F433		K248	P153
		I509	F343	T353	L249	
			P511	G354	F250	I156
		N512	S436	S355		P157
		G513	T437	A356	P253	L158
		Y514	M438	D357		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16898	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.550	Depositor
Minimum map value	-0.162	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.076	Depositor
Map size ($\text{\AA}$)	1058.4, 1058.4, 1058.4	wwPDB
Map dimensions	980, 980, 980	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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	0.31	0/3874	0.45	0/5314
1	B	0.32	0/3883	0.42	0/5325
1	C	0.28	0/3877	0.42	0/5318
1	D	0.24	0/3883	0.39	0/5325
All	All	0.29	0/15517	0.42	0/21282

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3758	0	3619	178	0
1	B	3767	0	3634	180	0
1	C	3761	0	3623	205	0
1	D	3767	0	3634	175	0
All	All	15053	0	14510	710	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 24.

The worst 5 of 710 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:165:PHE:HB3	1:B:167:HIS:CE1	1.75	1.20
1:A:135:PRO:HB3	1:A:183:TYR:CD1	2.00	0.97
1:B:165:PHE:CB	1:B:167:HIS:CE1	2.52	0.93
1:B:165:PHE:HB3	1:B:167:HIS:HE1	1.37	0.86
1:B:490:LYS:HG3	1:B:527:LEU:HD21	1.57	0.86

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	482/540 (89%)	436 (90%)	46 (10%)	0	100	100
1	B	482/540 (89%)	438 (91%)	44 (9%)	0	100	100
1	C	482/540 (89%)	445 (92%)	37 (8%)	0	100	100
1	D	482/540 (89%)	445 (92%)	37 (8%)	0	100	100
All	All	1928/2160 (89%)	1764 (92%)	164 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	413/459 (90%)	399 (97%)	14 (3%)	32	55
1	B	415/459 (90%)	404 (97%)	11 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	414/459 (90%)	398 (96%)	16 (4%)	28	52
1	D	415/459 (90%)	406 (98%)	9 (2%)	45	64
All	All	1657/1836 (90%)	1607 (97%)	50 (3%)	37	57

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	178	LEU
1	C	530	MET
1	A	411	ARG
1	C	219	THR
1	C	395	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	302	ASN
1	A	417	HIS
1	C	347	HIS
1	A	366	GLN
1	C	336	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.

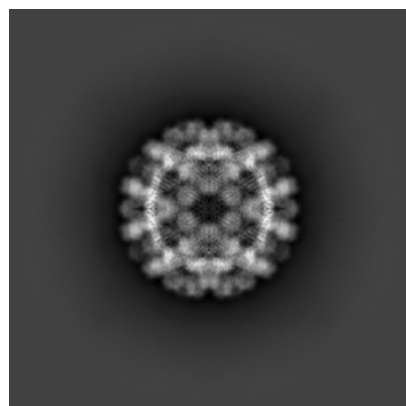
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76740. These allow visual inspection of the internal detail of the map and identification of artifacts.

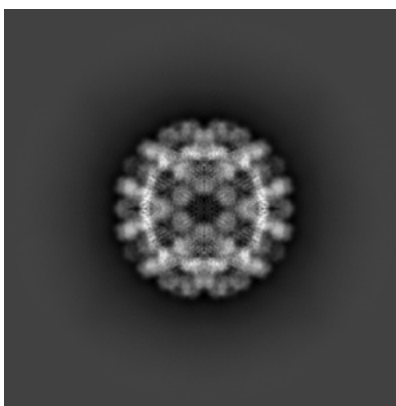
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

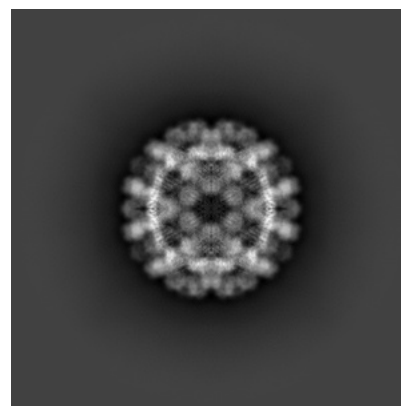
6.1.1 Primary map



X

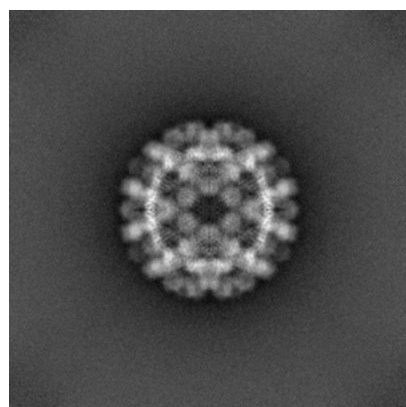


Y

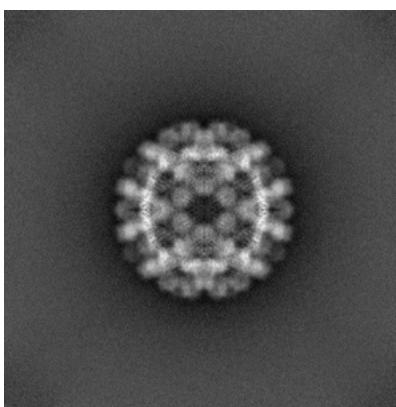


Z

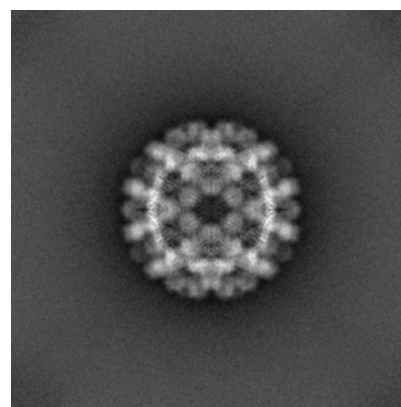
6.1.2 Raw map



X



Y

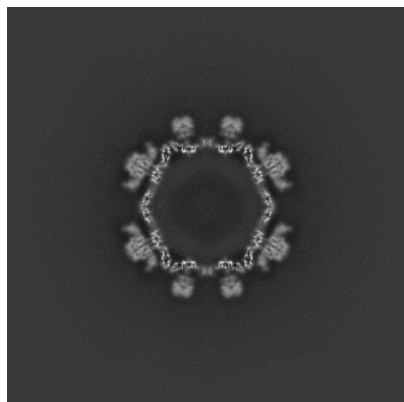


Z

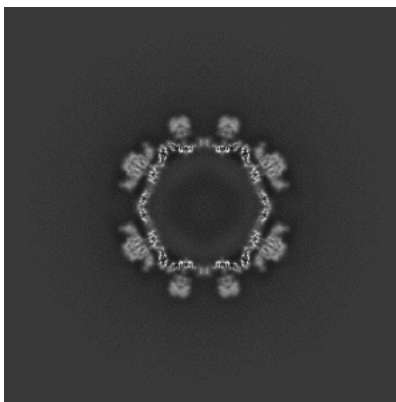
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

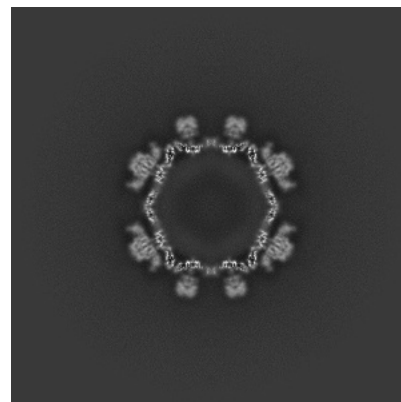
6.2.1 Primary map



X Index: 490

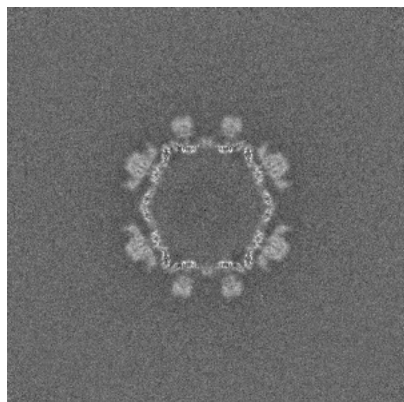


Y Index: 490

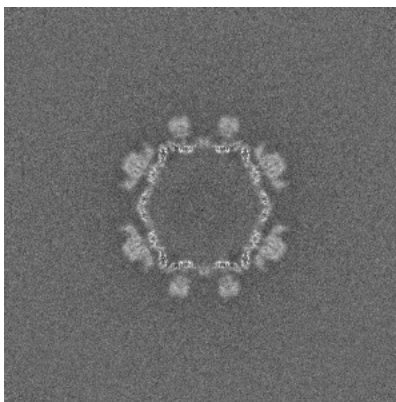


Z Index: 490

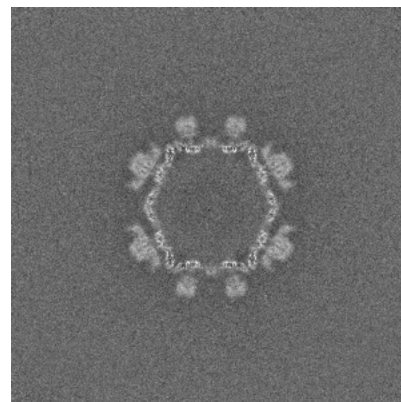
6.2.2 Raw map



X Index: 490



Y Index: 490

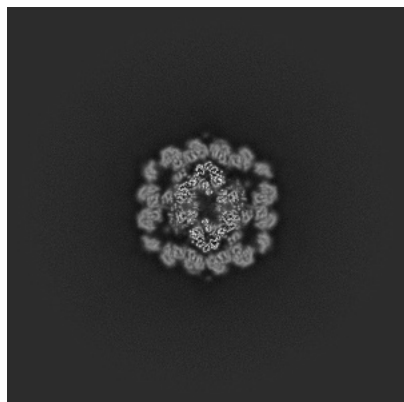


Z Index: 490

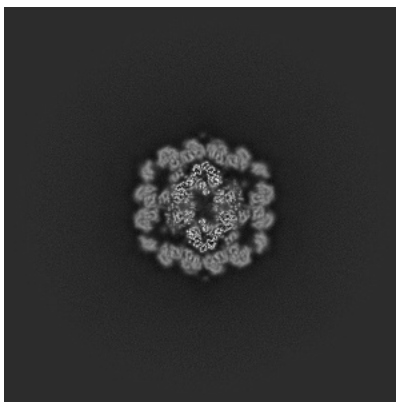
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

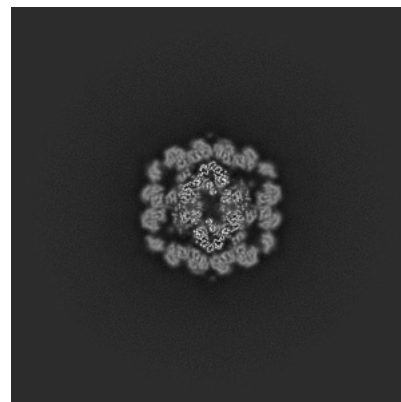
6.3.1 Primary map



X Index: 355

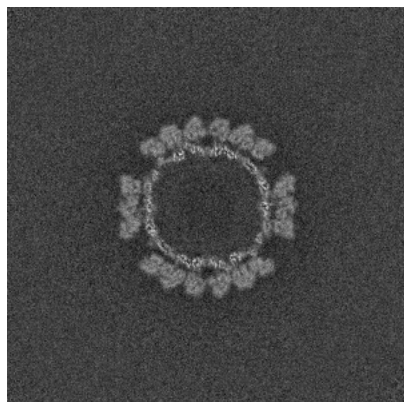


Y Index: 355

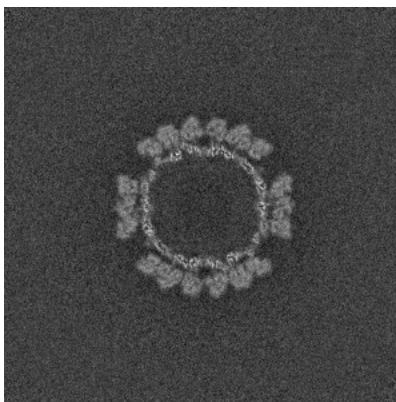


Z Index: 355

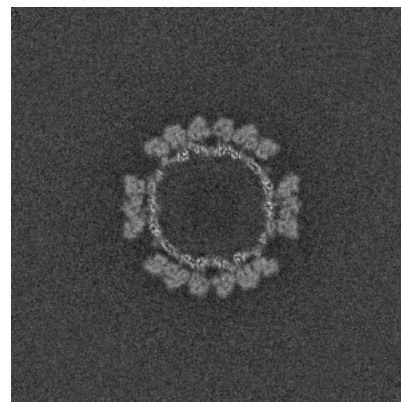
6.3.2 Raw map



X Index: 533



Y Index: 533

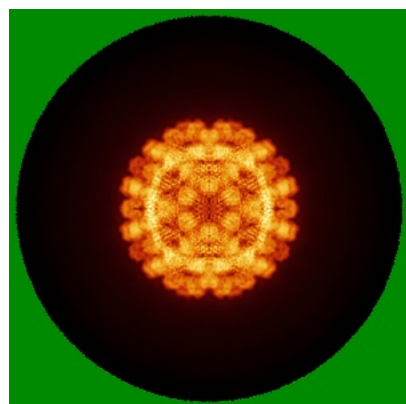


Z Index: 533

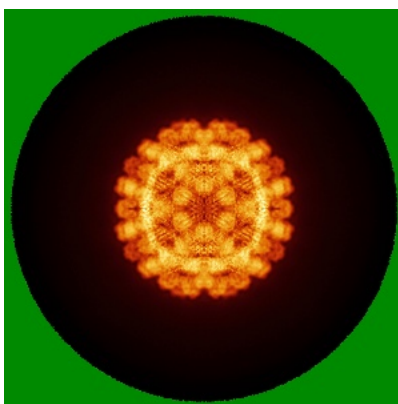
The images above show the largest variance slices of the map in three orthogonal directions.

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

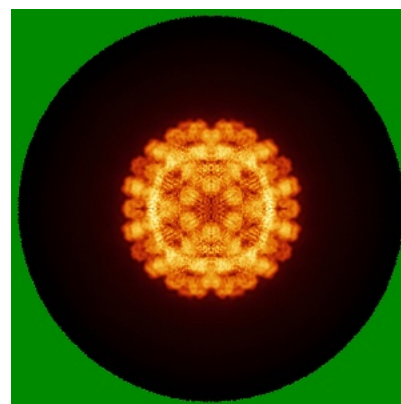
6.4.1 Primary map



X

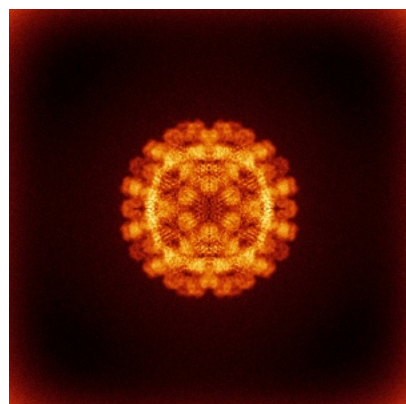


Y

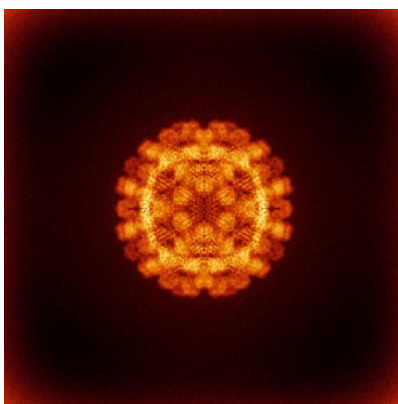


Z

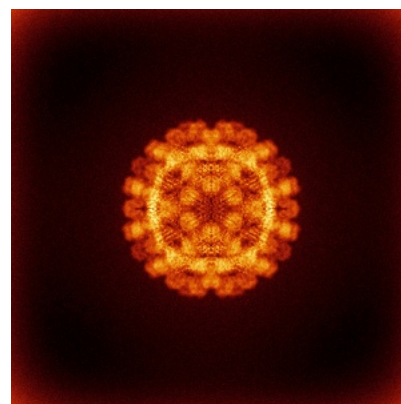
6.4.2 Raw map



X



Y

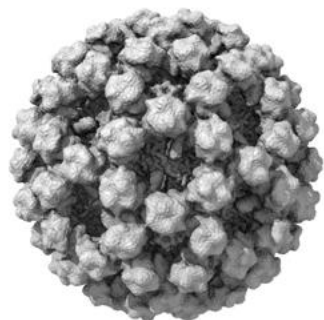


Z

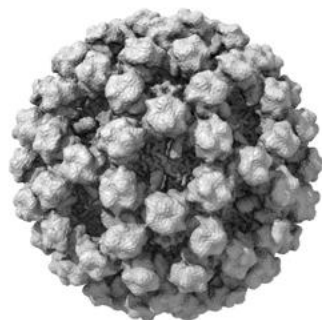
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

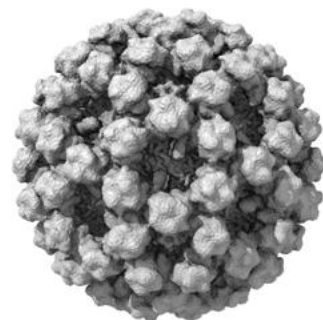
6.5.1 Primary map



X



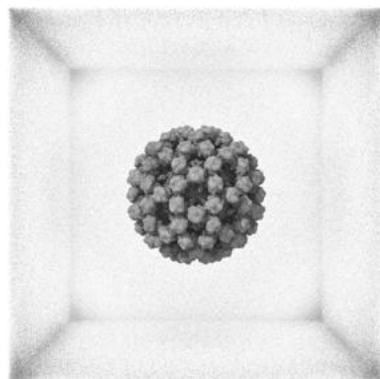
Y



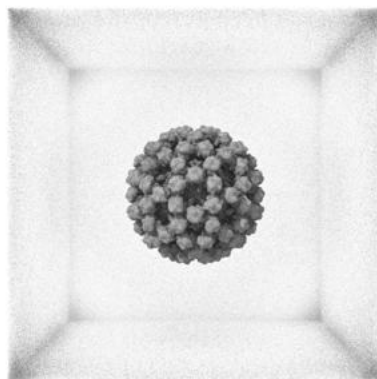
Z

The images above show the 3D surface view of the map at the recommended contour level 0.076. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

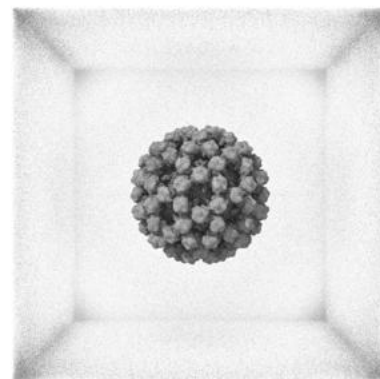
6.5.2 Raw map



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.

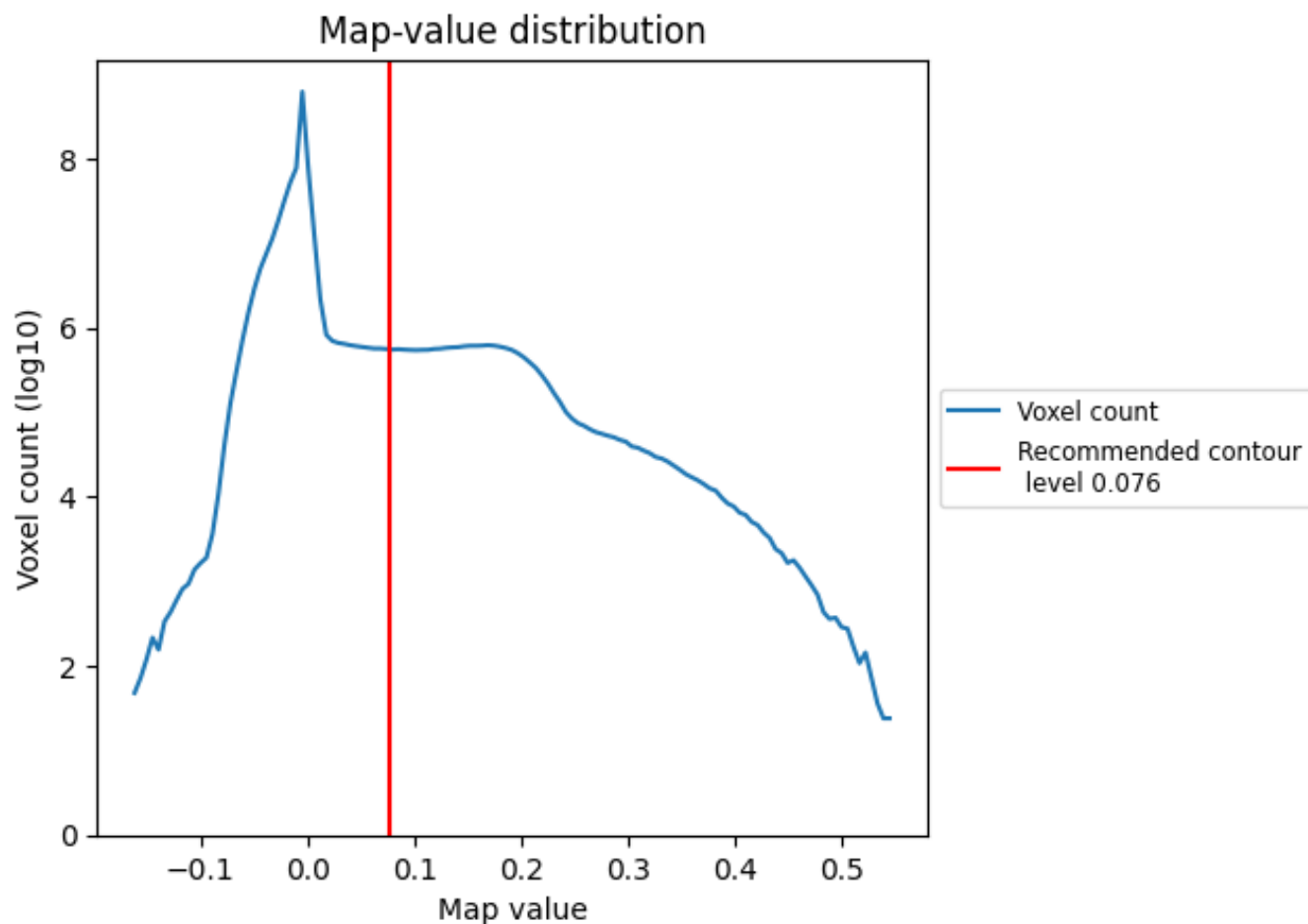
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

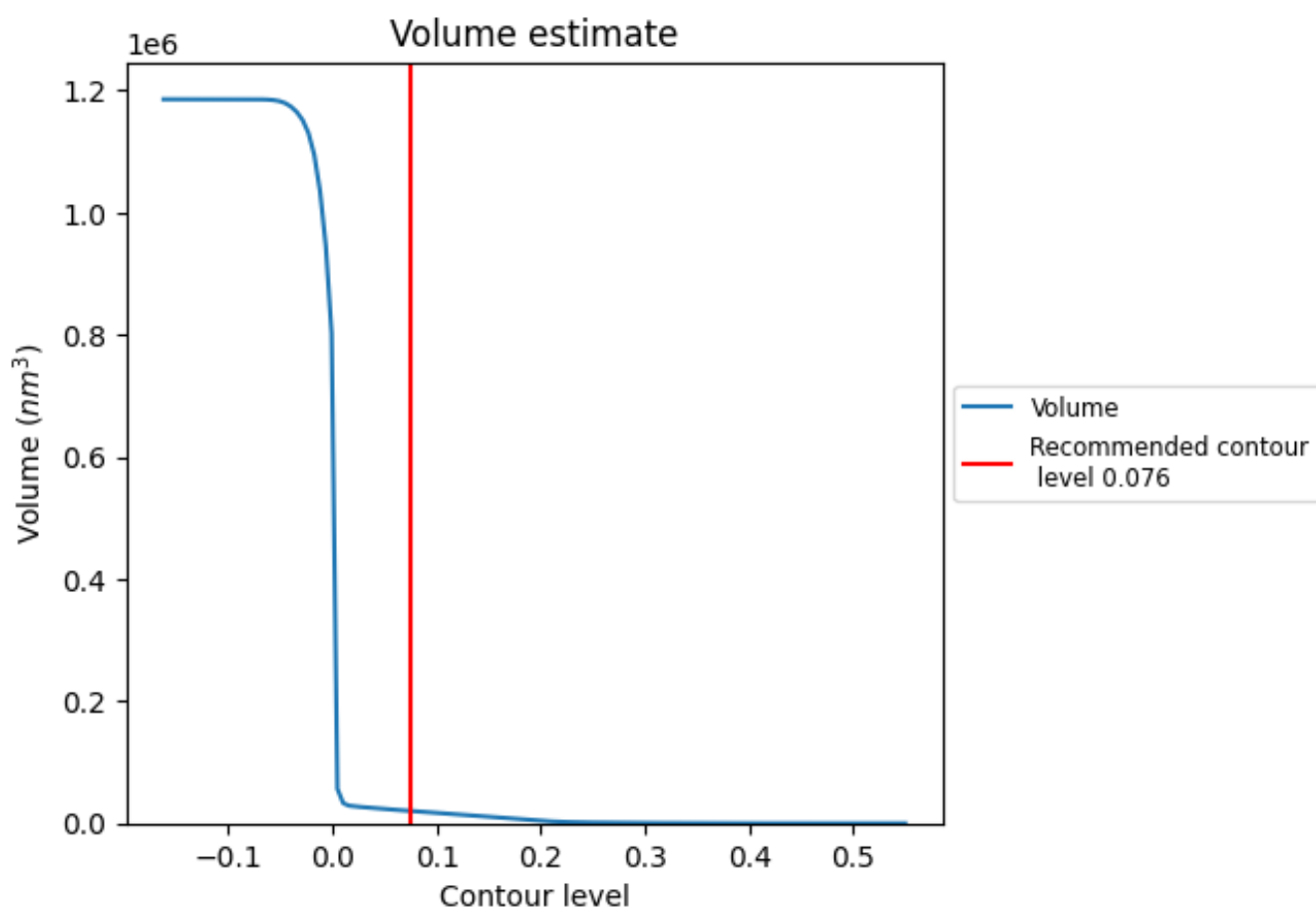
This section contains the results of statistical analysis of the map.

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.

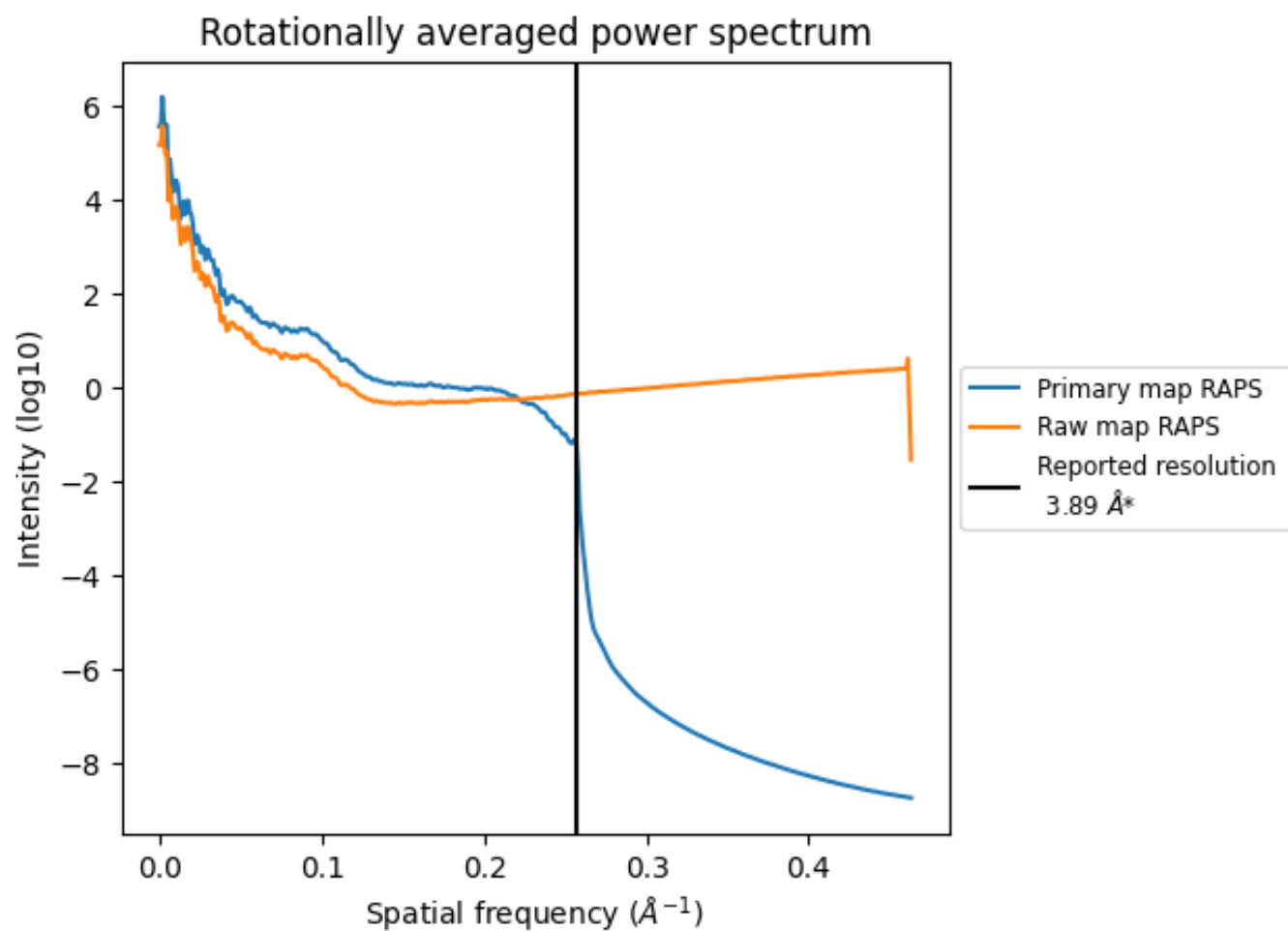
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 20172 nm³; this corresponds to an approximate mass of 18222 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 ⓘ

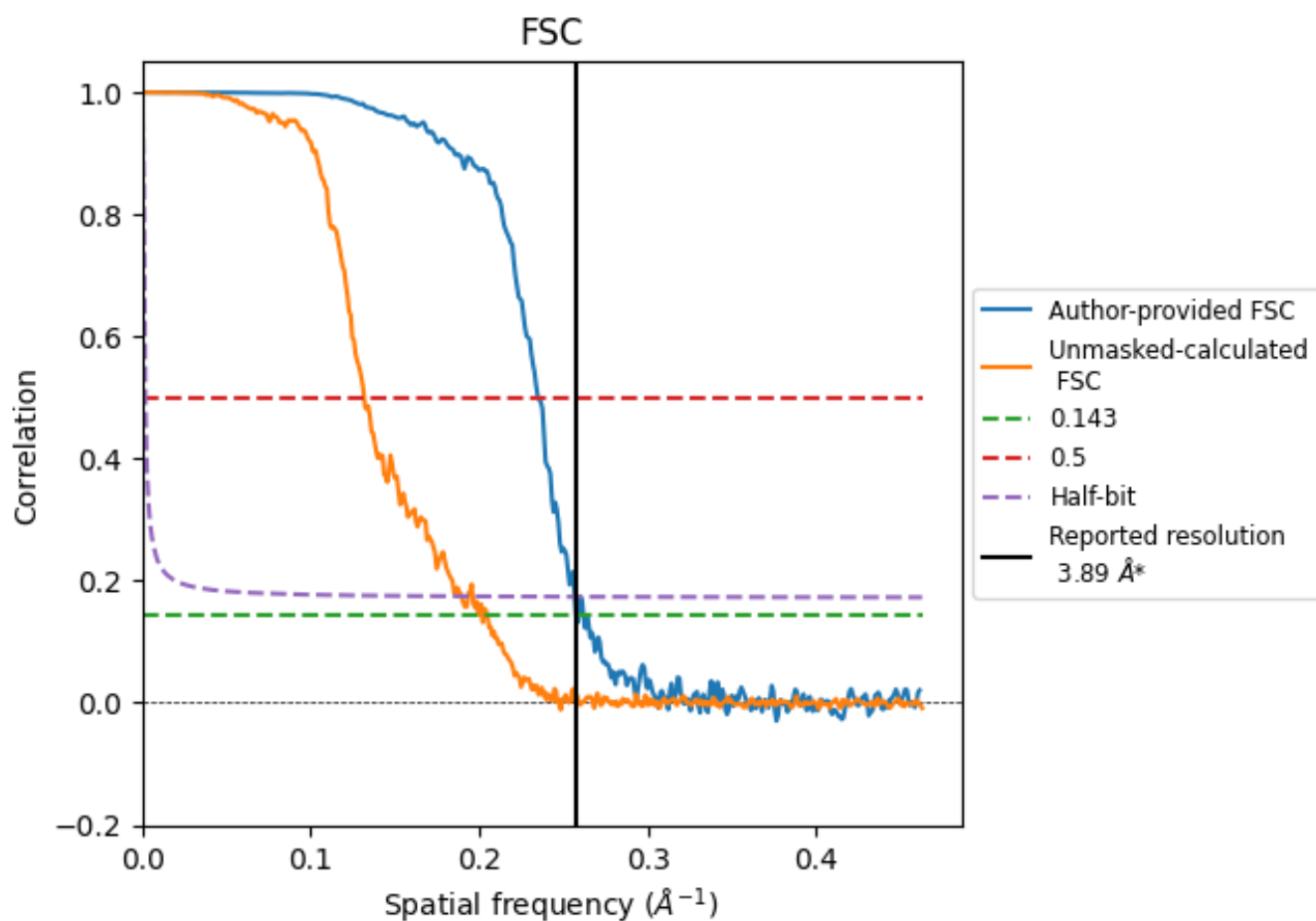


*Reported resolution corresponds to spatial frequency of 0.257 $\text{\AA}^{-1}$

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 0.257 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.89	-	-
Author-provided FSC curve	3.88	4.25	3.89
Unmasked-calculated*	4.96	7.59	5.28

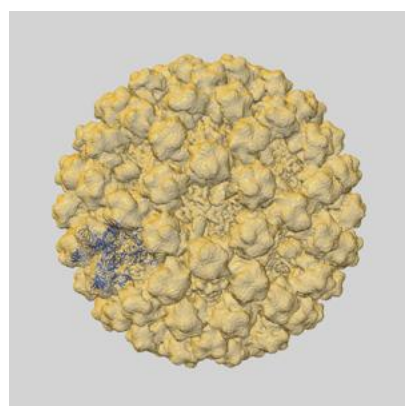
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.96 differs from the reported value 3.89 by more than 10 %

9 Map-model fit [i](#)

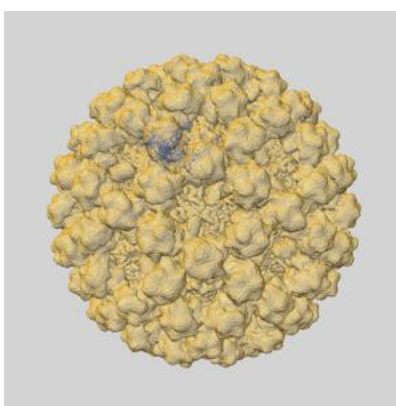
This section contains information regarding the fit between EMDB map EMD-76740 and PDB model 12TF. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlays

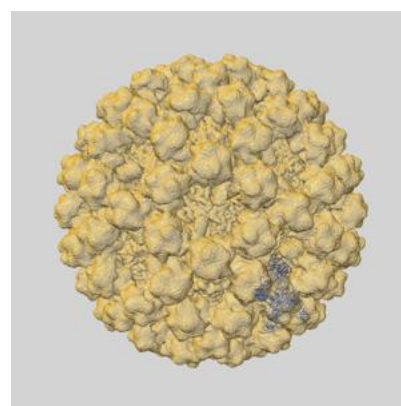
9.1.1 Map-model overlay [i](#)



X

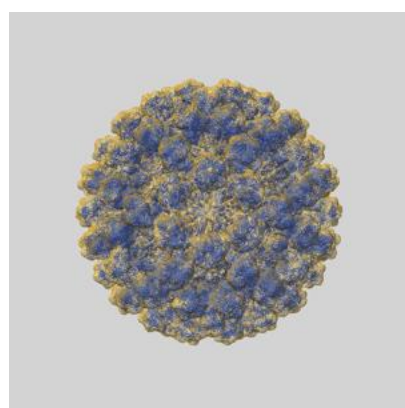


Y

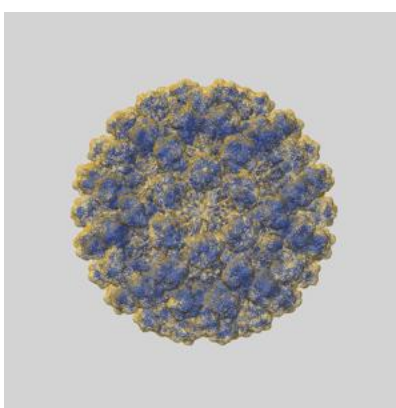


Z

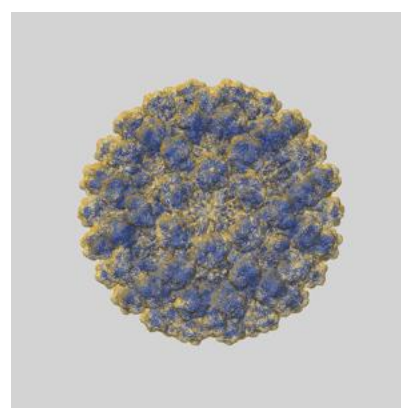
9.1.2 Map-model assembly overlay [i](#)



X



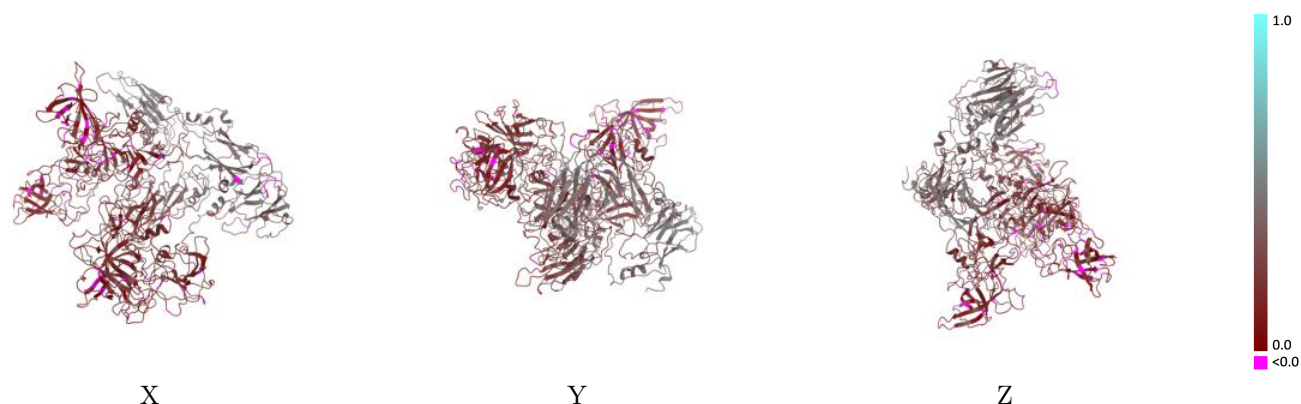
Y



Z

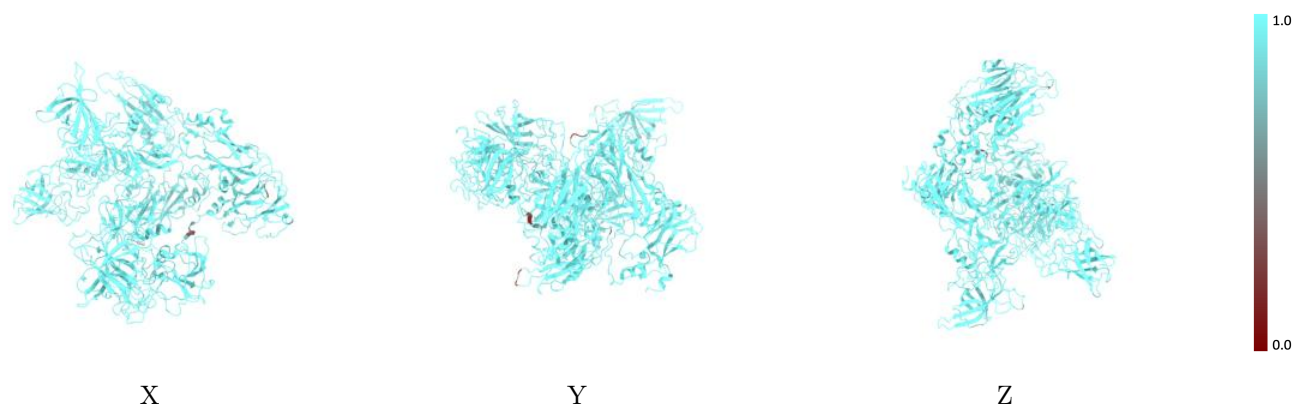
The images above show the 3D surface view of the map at the recommended contour level 0.076 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



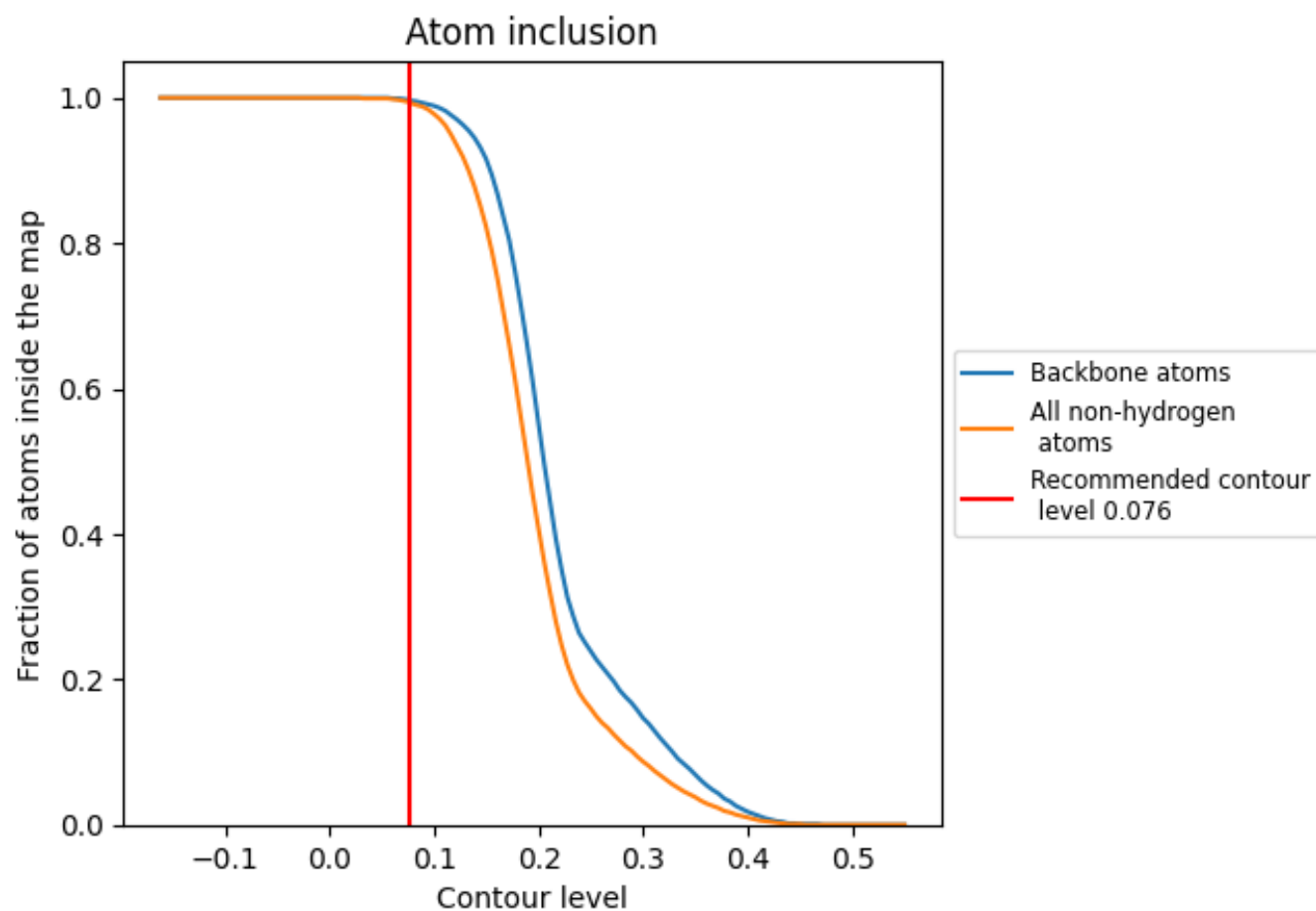
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.076).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.076) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9940	0.2490
A	0.9950	0.2470
B	0.9970	0.2680
C	0.9910	0.2470
D	0.9910	0.2340

