



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:33 PM UTC

PDB ID : 3IZX / pdb_00003izx
EMDB ID : EMD-5256
Title : 3.1 Angstrom cryoEM structure of cytoplasmic polyhedrosis virus
Authors : Yu, X.; Ge, P.; Jiang, J.; Atanasov, I.; Zhou, Z.H.
Deposited on : 2011-01-15
Resolution : 3.10 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

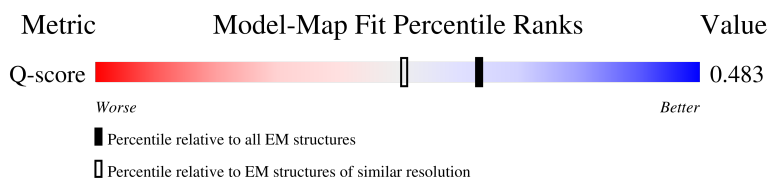
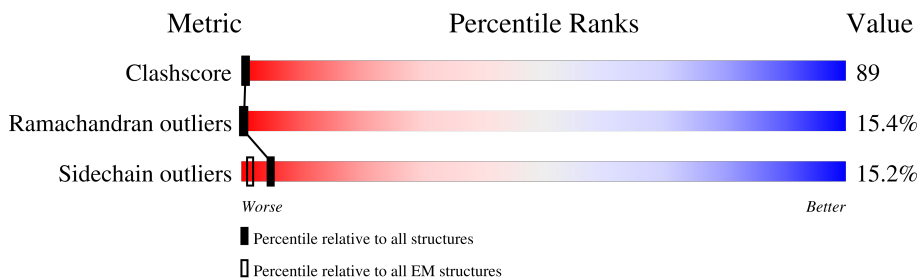
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	1058	
2	B	1333	
2	C	1333	
3	D	448	

Continued on next page...

Mol	Chain	Length	Quality of chain
3	E	448	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32209 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 Structural protein VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1057	Total	C	N	O	S	0	0
			8434	5345	1457	1587	45		

- Molecule 2 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1191	Total	C	N	O	S	0	0
			9397	5937	1634	1789	37		
2	C	1249	Total	C	N	O	S	0	0
			9844	6213	1712	1882	37		

- Molecule 3 is a protein called Viral structural protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	290	Total	C	N	O	S	0	0
			2267	1440	398	422	7		
3	E	290	Total	C	N	O	S	0	0
			2267	1440	398	422	7		

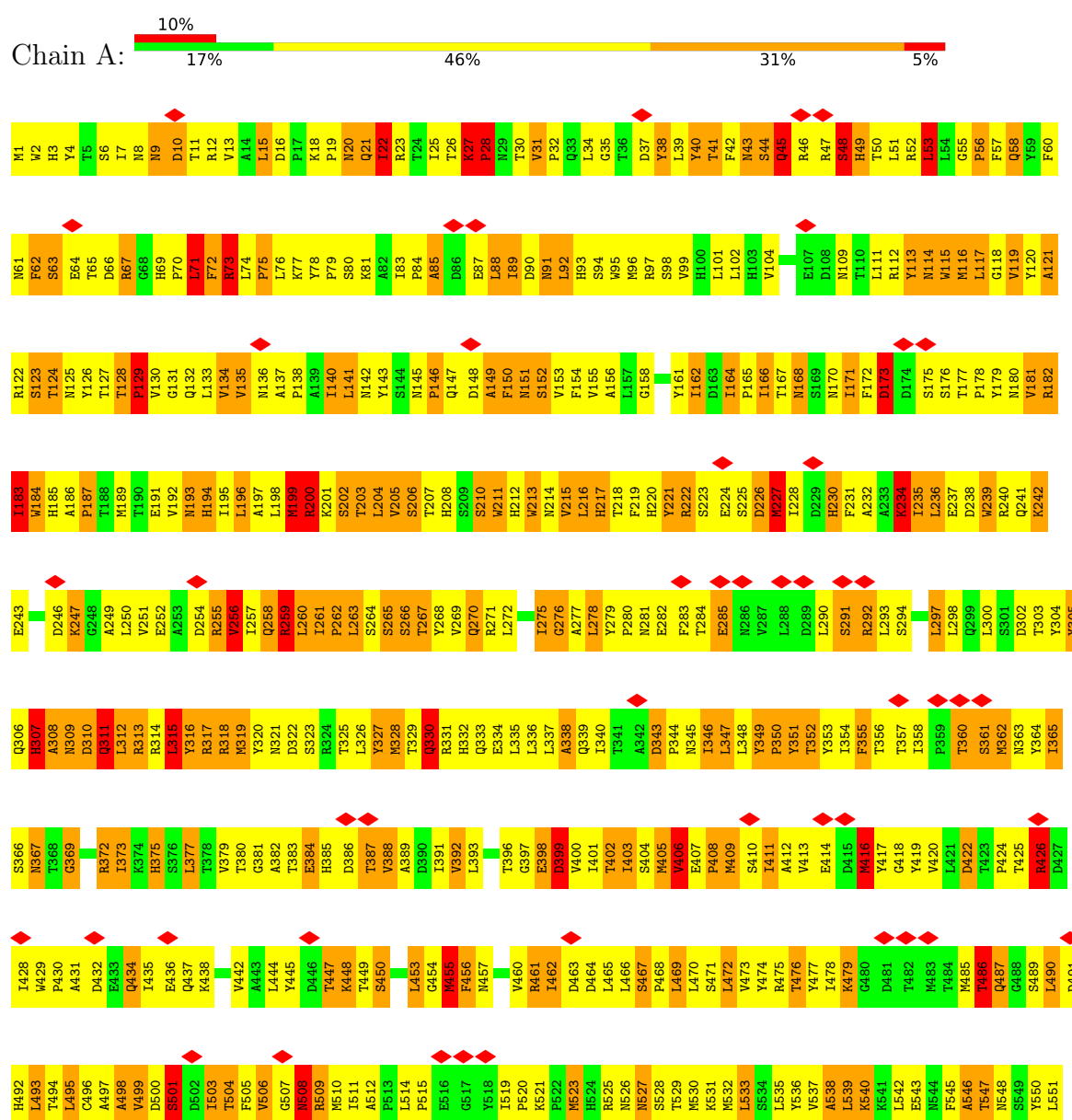
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	37	TRP	TYR	conflict	UNP C6K2M8
E	37	TRP	TYR	conflict	UNP C6K2M8

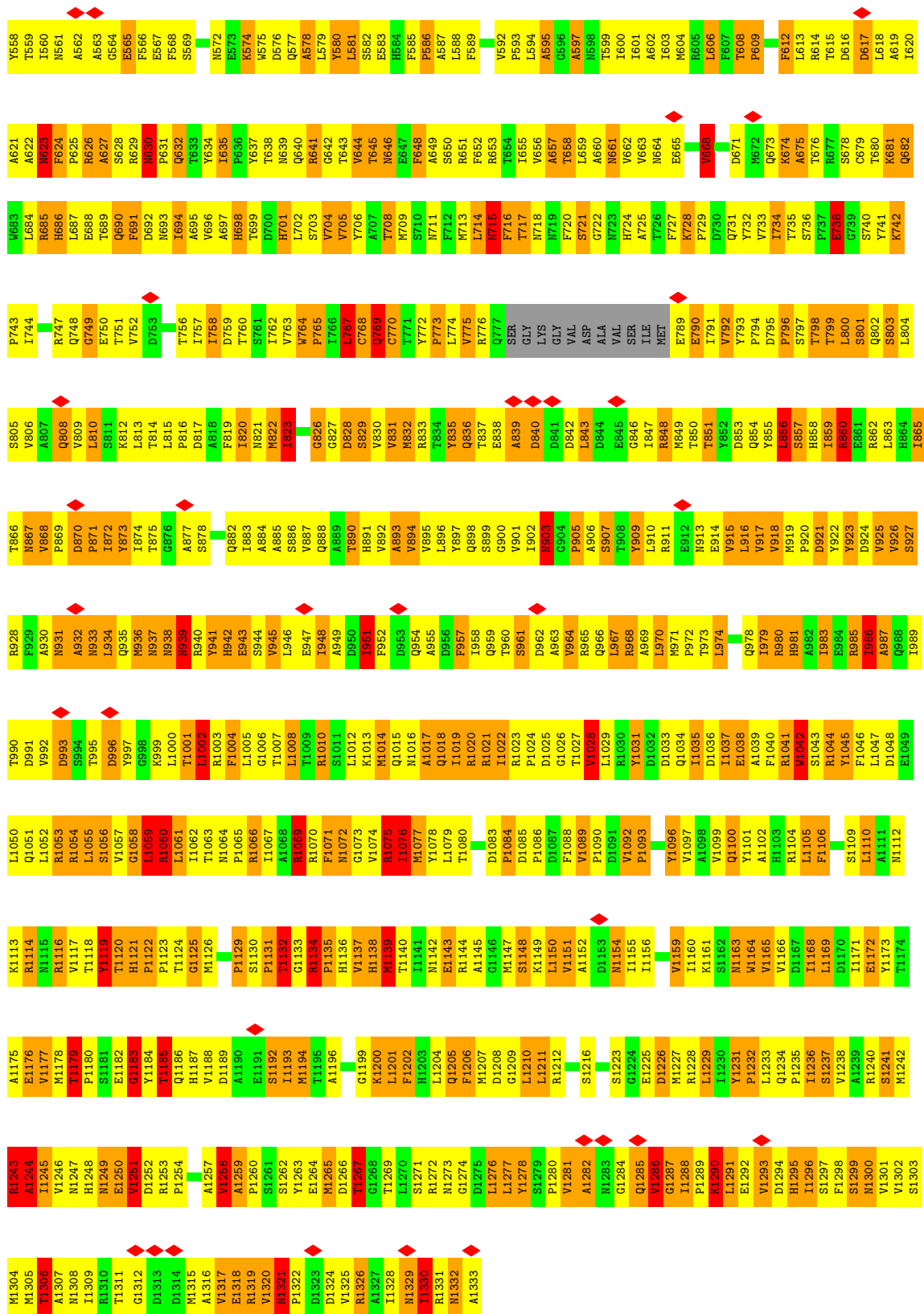
3 Residue-property plots

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: Structural protein VP3

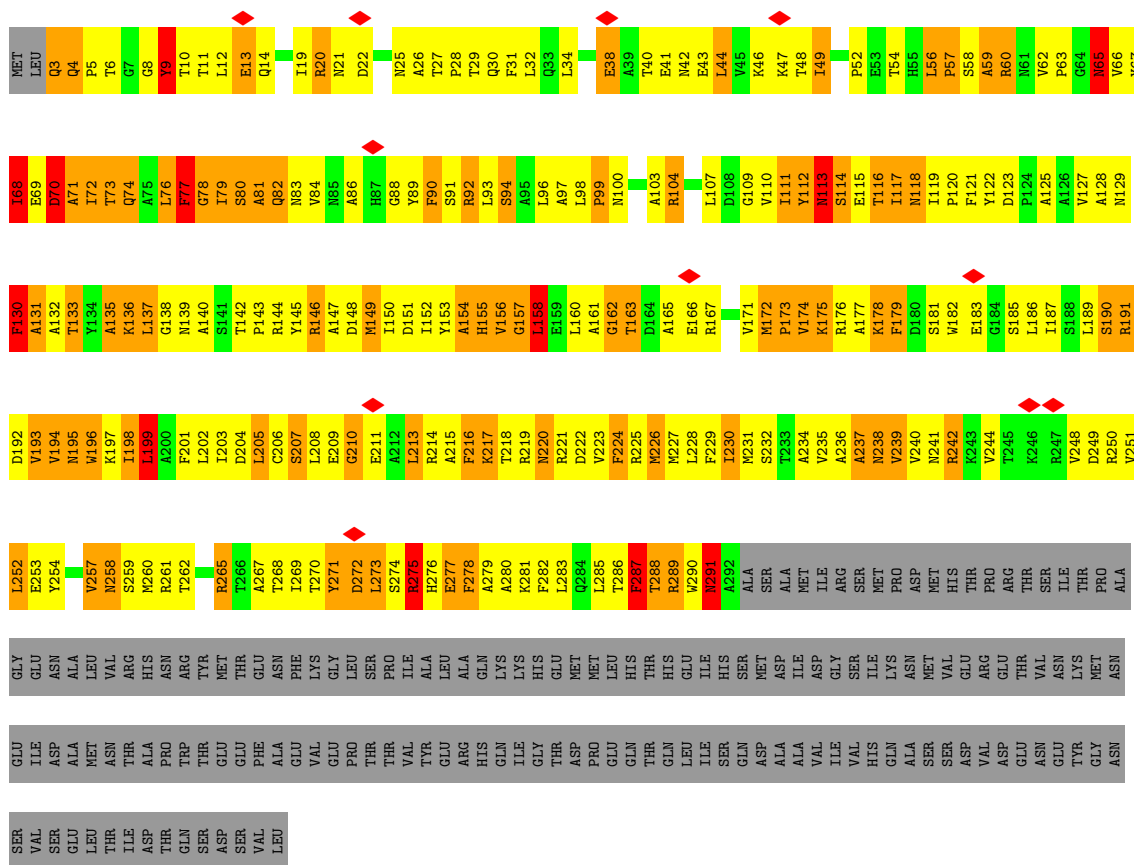




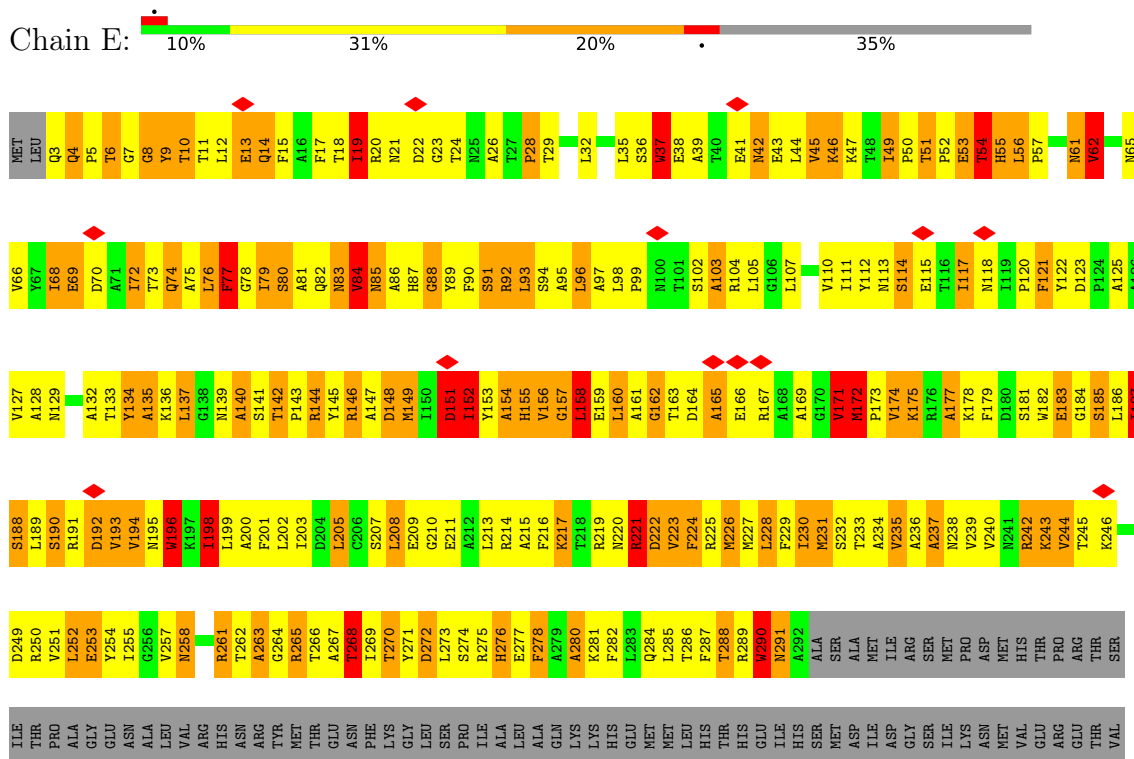


• Molecule 3: Viral structural protein 5





• Molecule 3: Viral structural protein 5



ASN	GLU
LYS	TYR
MET	GLY
ASN	ASN
GLU	SER
ILE	VAL
ASP	SER
ALA	GLU
MET	LEU
ASN	THR
THR	ILE
ALA	ASP
PRO	THR
TRP	GLN
THR	SER
GLU	ASP
GLU	SER
PHE	VAL
ALA	LEU
GLU	
VAL	
GLU	
PRO	
THR	
THR	
VAL	
TYR	
GLU	
ARG	
HIS	
GLN	
ILE	
GLY	
THR	
ASP	
PRO	
GLU	
GLN	
THR	
GLN	
LEU	
ILE	
SER	
GLN	
ASP	
ALA	
ALA	
VAL	
ILE	
VAL	
HIS	
GLN	
ALA	
SER	
SER	
ASP	
VAL	
ASP	
GLU	
ASN	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	28993	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	87.348	Depositor
Minimum map value	-47.523	Depositor
Average map value	0.800	Depositor
Map value standard deviation	5.885	Depositor
Recommended contour level	16	Depositor
Map size ($\text{\AA}$)	728.63995, 728.63995, 728.63995	wwPDB
Map dimensions	660, 660, 660	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.104, 1.104, 1.104	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	0.93	30/8619 (0.3%)	1.56	245/11737 (2.1%)
2	B	1.09	63/9590 (0.7%)	1.71	337/13056 (2.6%)
2	C	1.01	47/10045 (0.5%)	1.68	318/13678 (2.3%)
3	D	0.88	5/2314 (0.2%)	1.61	72/3147 (2.3%)
3	E	0.91	11/2314 (0.5%)	1.61	74/3147 (2.4%)
All	All	1.00	156/32882 (0.5%)	1.65	1046/44765 (2.3%)

The worst 5 of 156 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	114	VAL	CA-CB	14.99	1.72	1.54
2	C	1320	VAL	CA-CB	13.90	1.70	1.54
2	B	202	ALA	CA-CB	13.71	1.77	1.53
2	B	1098	ALA	CA-CB	13.19	1.69	1.53
2	C	1193	ILE	CA-CB	11.41	1.67	1.54

The worst 5 of 1046 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	149	MET	N-CA-C	16.90	129.70	111.28
2	C	533	GLN	N-CA-C	-15.69	93.67	111.71
3	E	157	GLY	N-CA-C	14.94	130.57	112.49
2	B	408	ILE	N-CA-C	14.64	124.48	110.42
2	C	1258	VAL	N-CA-C	14.57	125.51	111.67

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	8434	0	8395	1578	0
2	B	9397	0	9313	1647	0
2	C	9844	0	9749	1755	0
3	D	2267	0	2260	359	0
3	E	2267	0	2260	361	0
All	All	32209	0	31977	5611	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 89.

The worst 5 of 5611 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)
2:C:615:THR:CG2	2:C:632:GLN:HB3	1.26	1.60
3:D:26:ALA:CB	3:D:30:GLN:HE21	1.13	1.60
2:C:832:MET:CE	2:C:946:LEU:HD12	1.34	1.56
2:B:202:ALA:CA	2:B:202:ALA:CB	1.77	1.56
2:C:1242:MET:CE	2:C:1260:PRO:HD3	1.36	1.56

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	1055/1058 (100%)	659 (62%)	233 (22%)	163 (16%)	0	0
2	B	1187/1333 (89%)	800 (67%)	183 (15%)	204 (17%)	0	0
2	C	1245/1333 (93%)	861 (69%)	207 (17%)	177 (14%)	0	1
3	D	288/448 (64%)	203 (70%)	46 (16%)	39 (14%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	288/448 (64%)	191 (66%)	55 (19%)	42 (15%)	0	0
All	All	4063/4620 (88%)	2714 (67%)	724 (18%)	625 (15%)	0	0

5 of 625 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	SER
1	A	63	SER
1	A	123	SER
1	A	135	VAL
1	A	202	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	942/943 (100%)	797 (85%)	145 (15%)	2	12
2	B	1038/1153 (90%)	881 (85%)	157 (15%)	3	13
2	C	1088/1153 (94%)	924 (85%)	164 (15%)	3	13
3	D	238/379 (63%)	206 (87%)	32 (13%)	4	17
3	E	238/379 (63%)	196 (82%)	42 (18%)	2	9
All	All	3544/4007 (88%)	3004 (85%)	540 (15%)	5	13

5 of 540 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1321	ASN
3	D	113	ASN
2	C	1290	LYS
3	E	152	ILE
2	B	527	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 151 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	724	HIS
3	D	276	HIS
2	C	858	HIS
2	C	1187	HIS
3	E	276	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

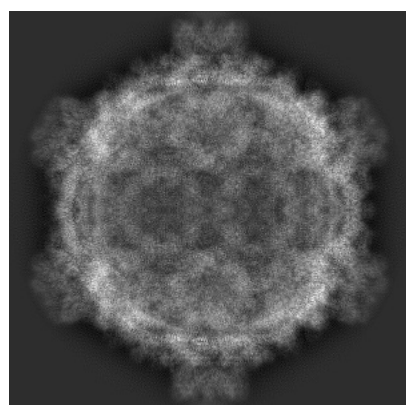
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5256. These allow visual inspection of the internal detail of the map and identification of artifacts.

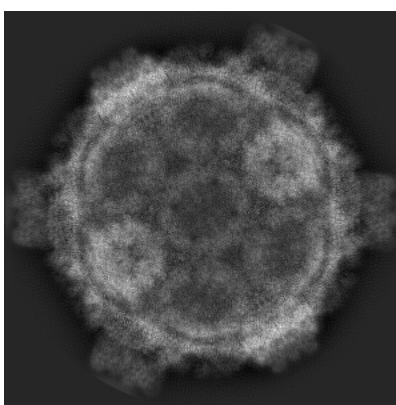
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

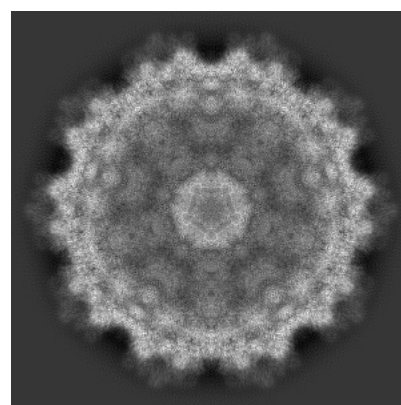
6.1.1 Primary map



X



Y

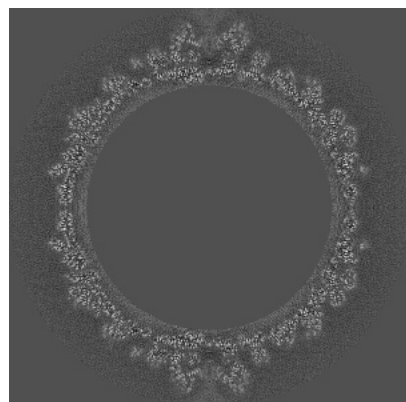


Z

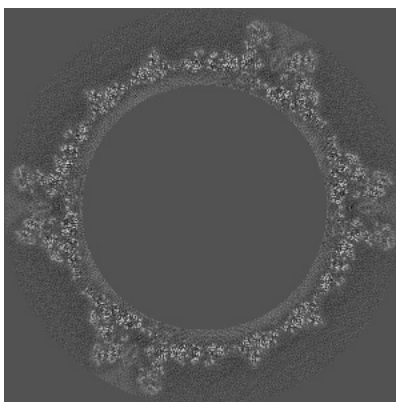
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

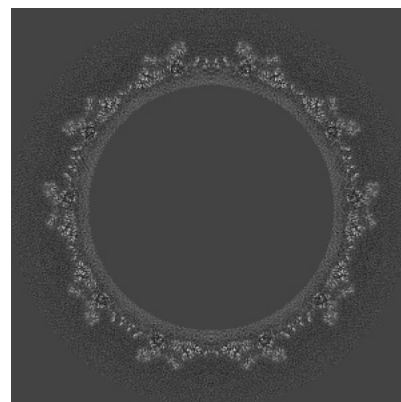
6.2.1 Primary map



X Index: 330



Y Index: 330

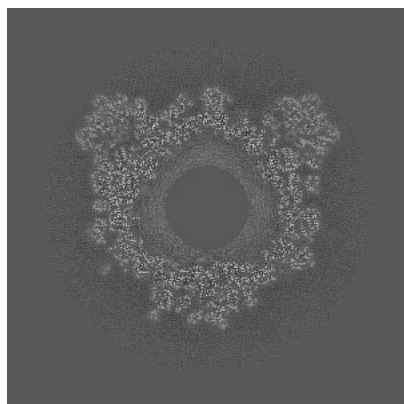


Z Index: 330

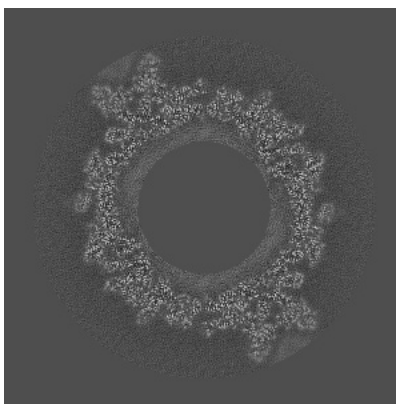
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

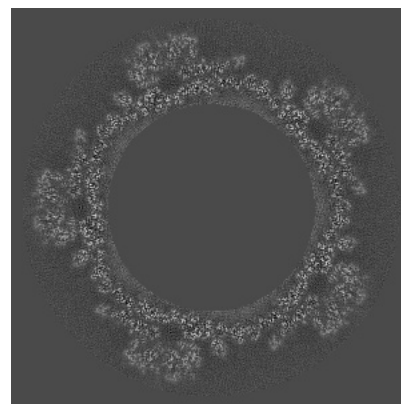
6.3.1 Primary map



X Index: 140



Y Index: 160

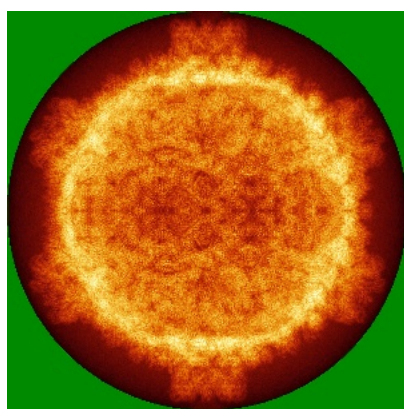


Z Index: 222

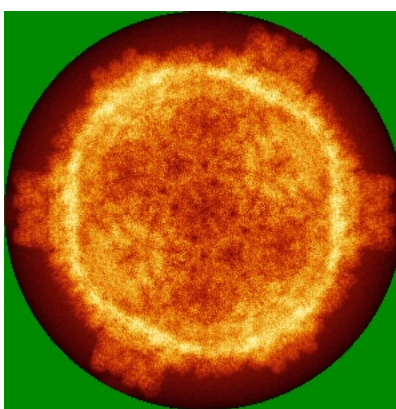
The images above show the largest variance slices of the map in three orthogonal directions.

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

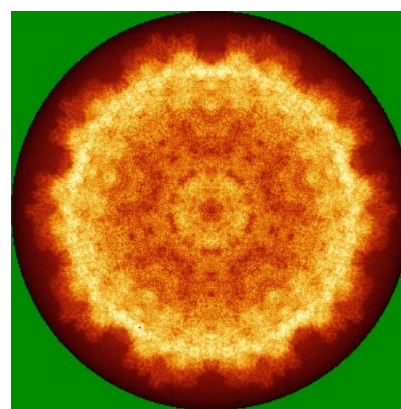
6.4.1 Primary map



X



Y

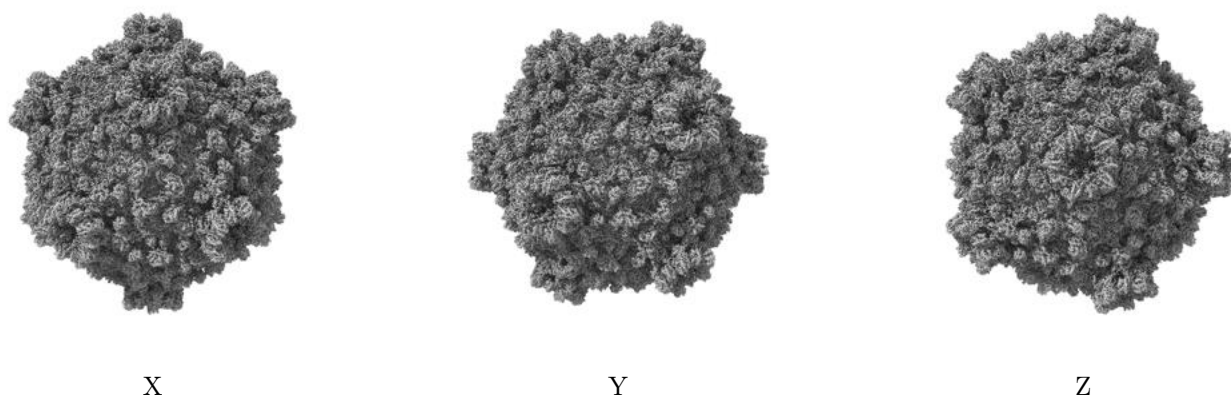


Z

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 16.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

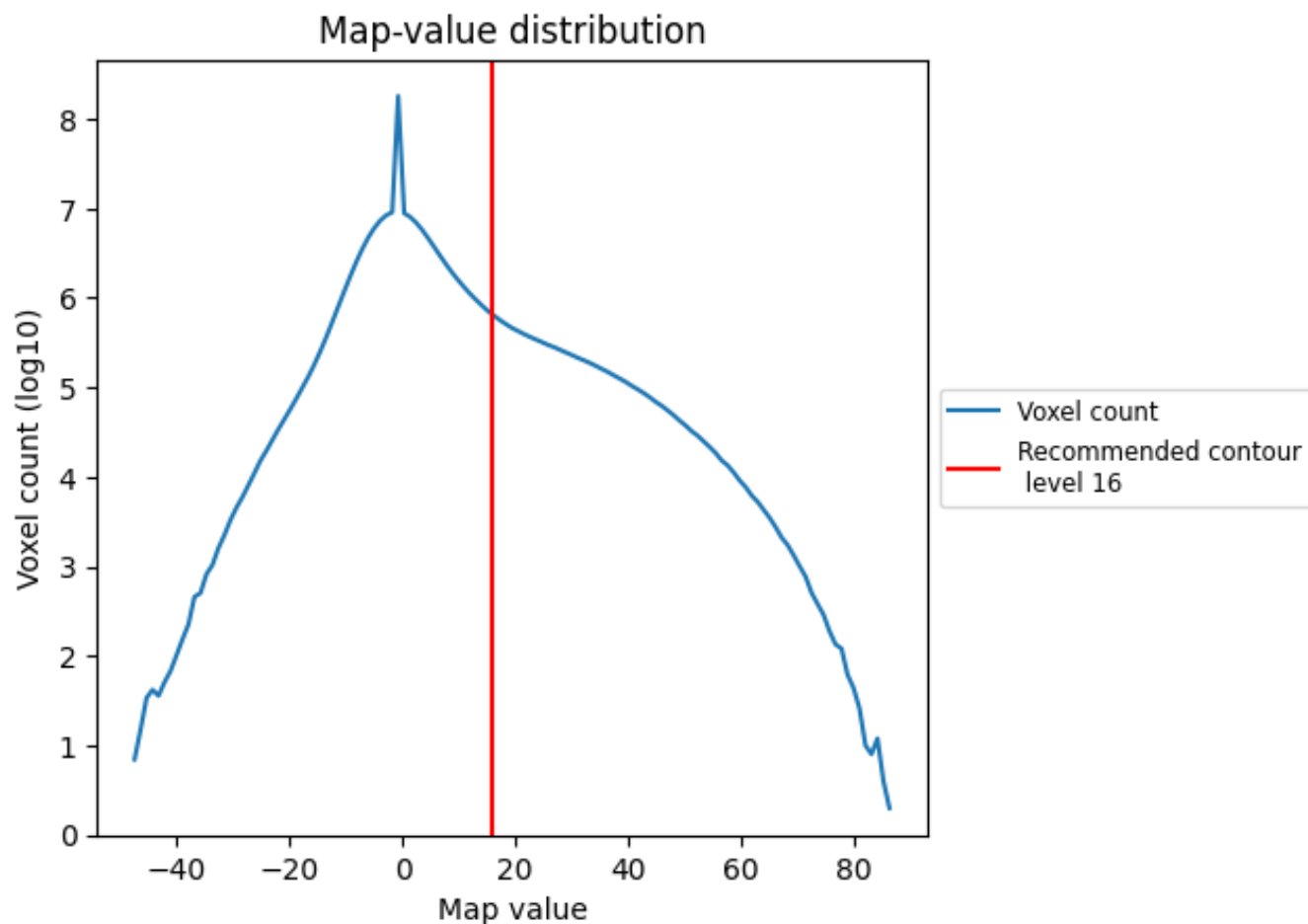
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

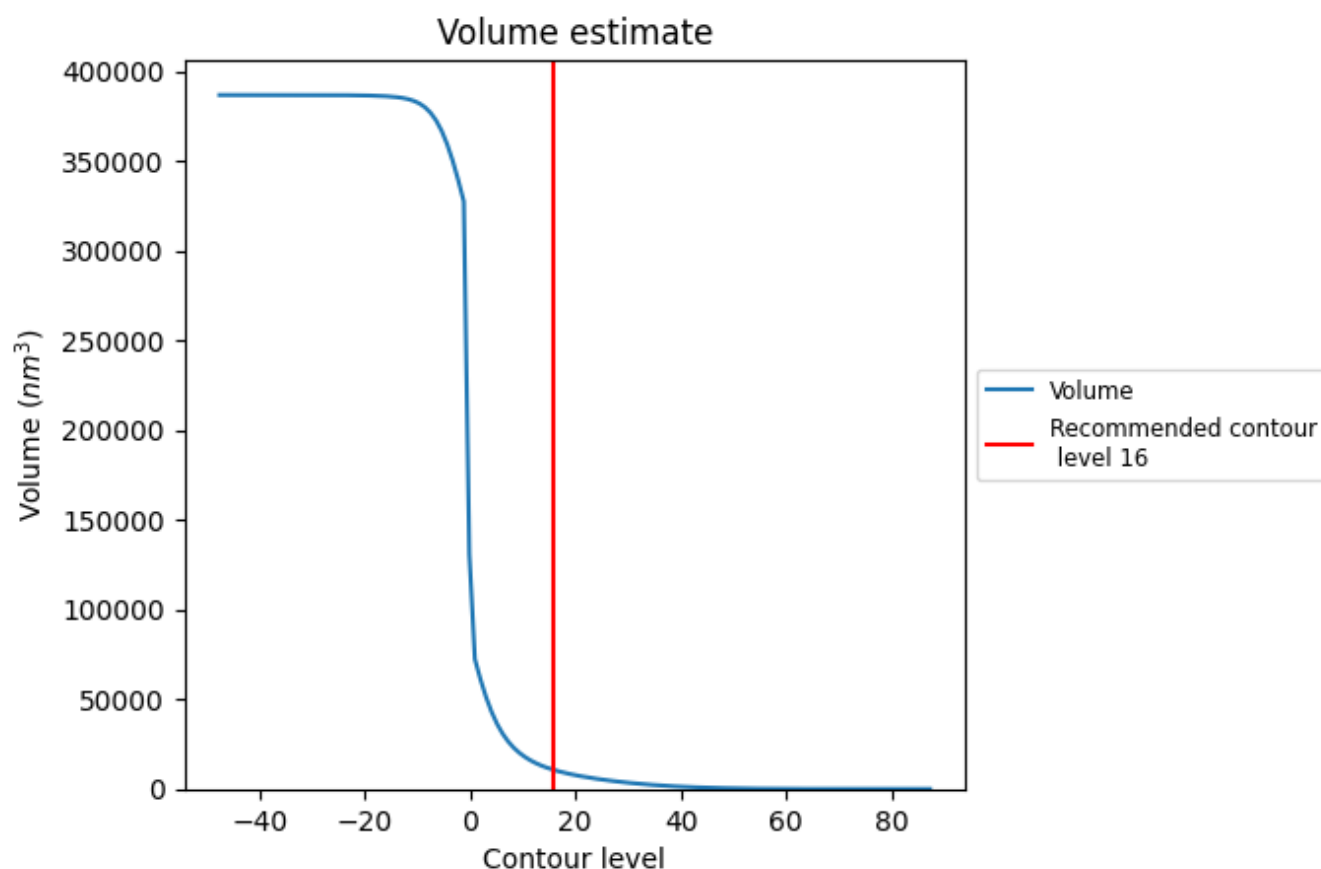
This section contains the results of statistical analysis of the map.

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.

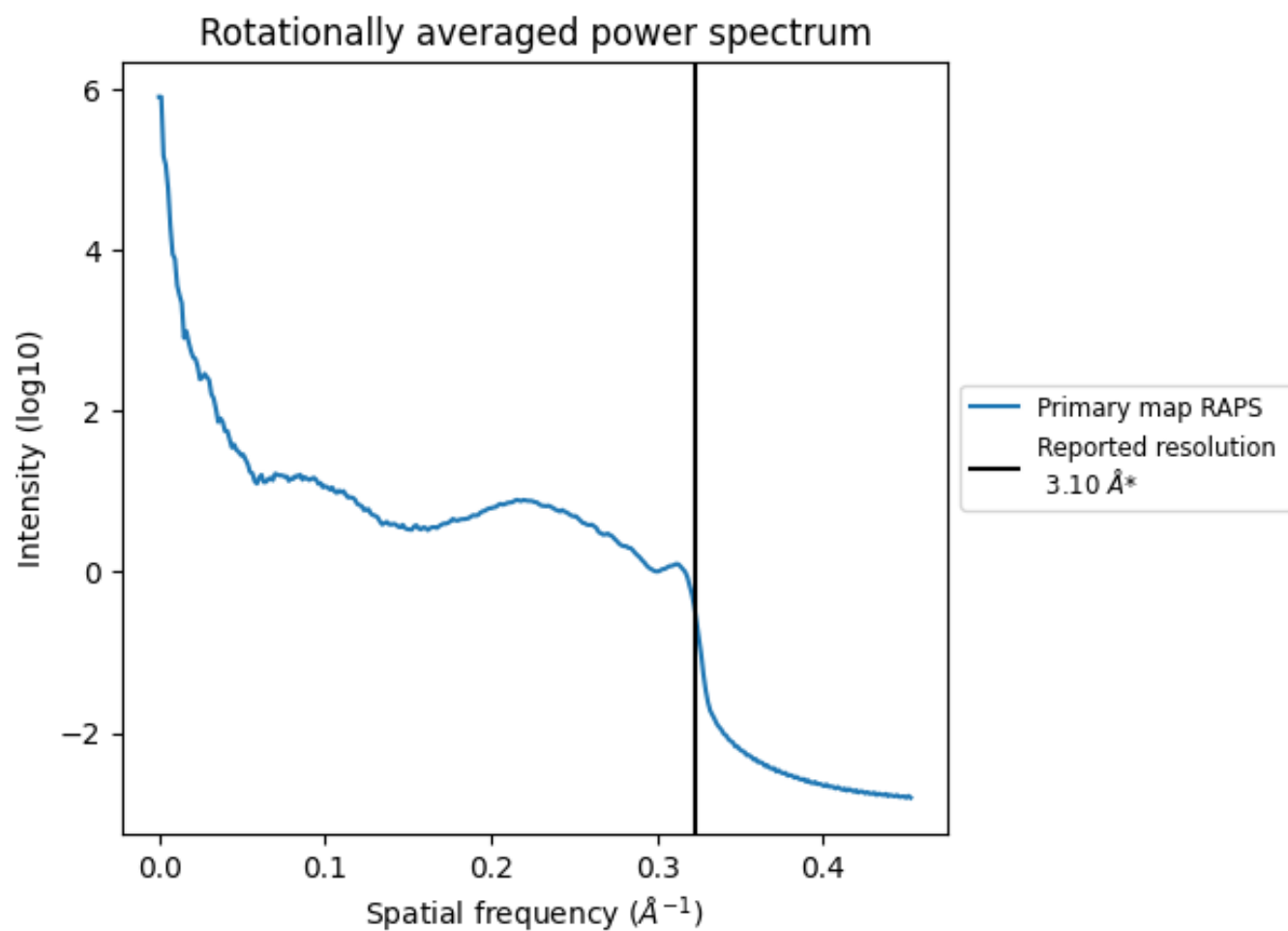
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105533 nm^3 ; this corresponds to an approximate mass of 9533 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

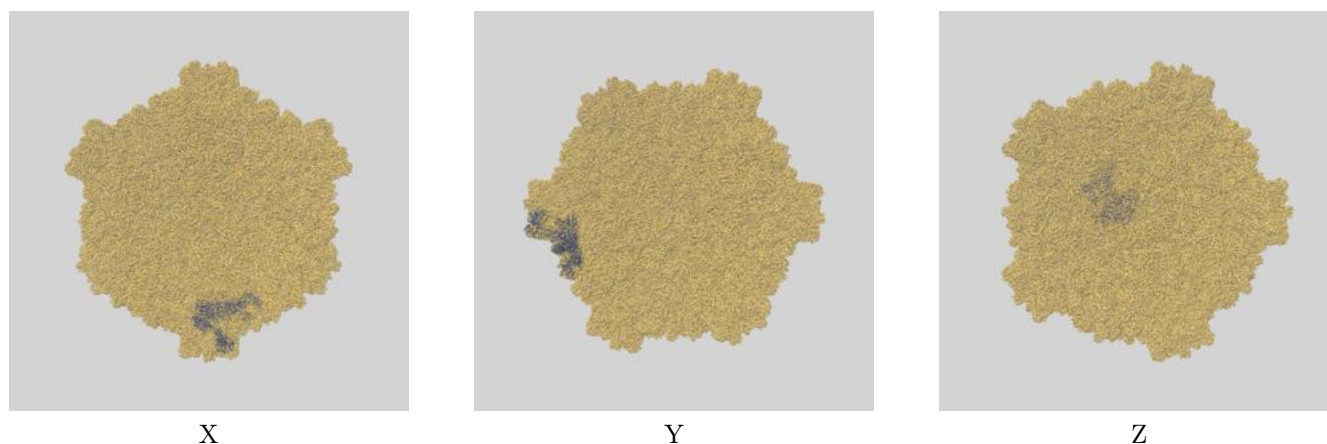
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

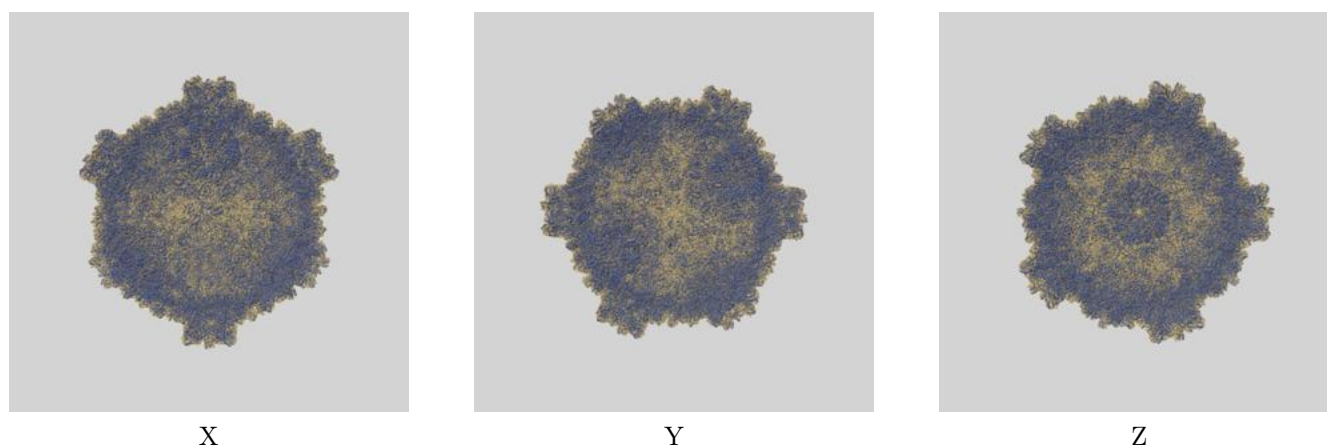
This section contains information regarding the fit between EMDB map EMD-5256 and PDB model 3IZX. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

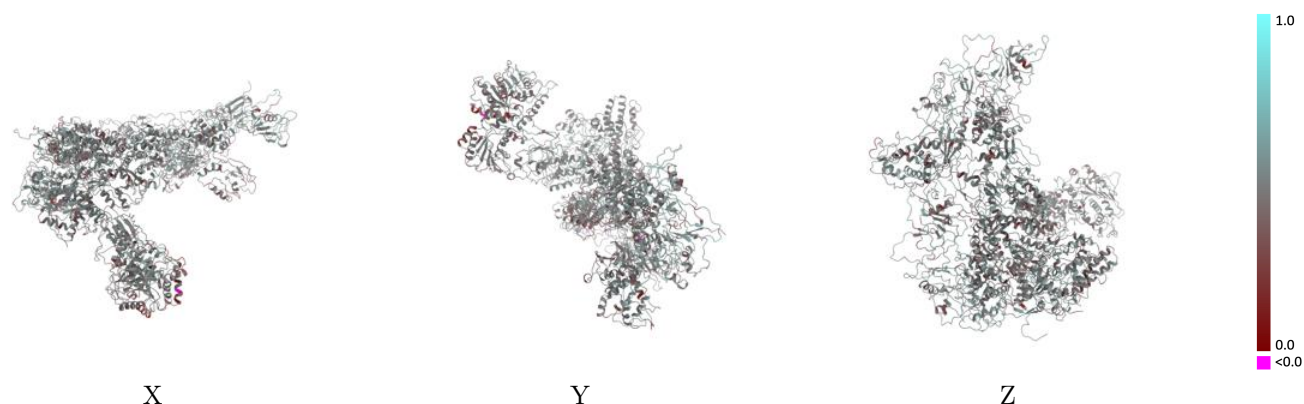


9.1.2 Map-model assembly overlay [i](#)



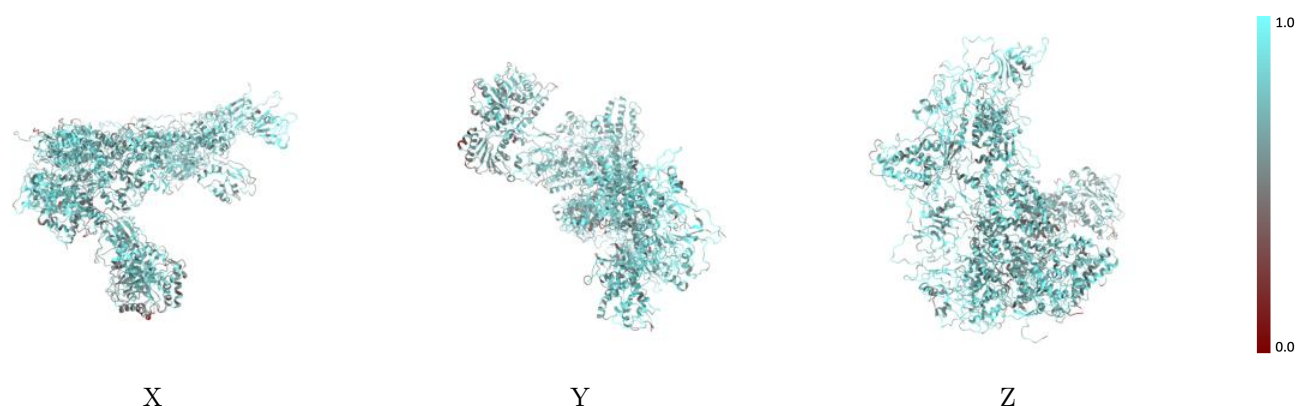
The images above show the 3D surface view of the map at the recommended contour level 16.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



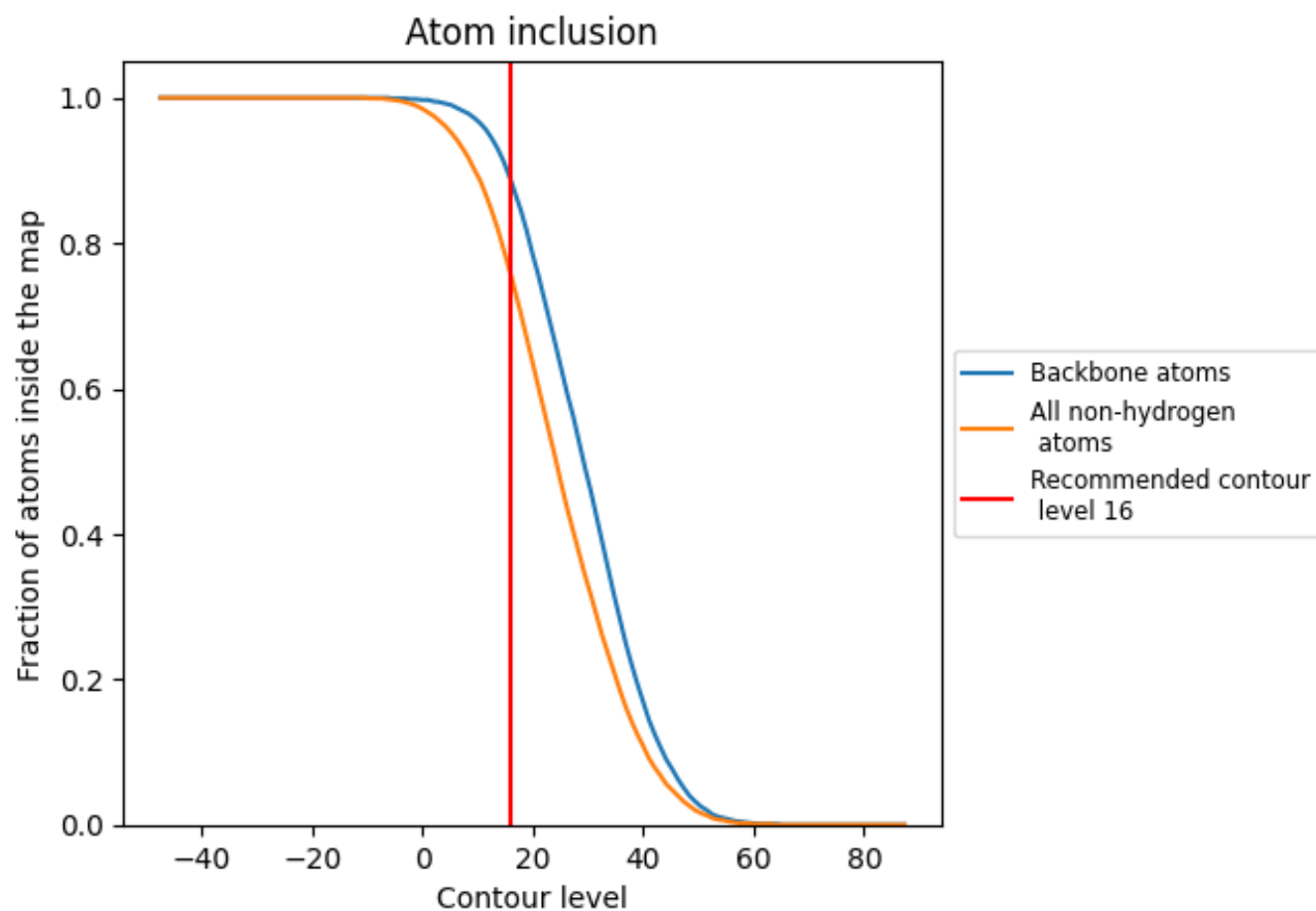
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 76% 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 (16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7560	0.4830
A	0.7050	0.4710
B	0.7720	0.4870
C	0.7710	0.4870
D	0.7930	0.4950
E	0.7760	0.4810

