



wwPDB EM Validation Summary Report ⓘ

Mar 11, 2024 – 01:07 AM EDT

PDB ID : 6OGY
EMDB ID : EMD-20059
Title : In situ structure of Rotavirus RNA-dependent RNA polymerase at duplex-open state
Authors : Ding, K.; Chang, T.; Shen, W.; Roy, P.; Zhou, Z.H.
Deposited on : 2019-04-03
Resolution : 3.40 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:

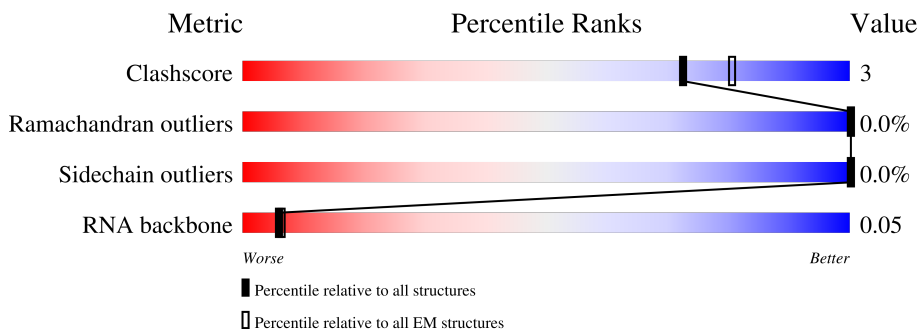
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 3.40 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.




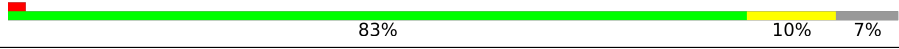
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1088	 7% 88% 9%
2	C	887	 80% 10% 10%
2	D	887	 83% 9% 8%
2	E	887	 78% 10% 12%
2	F	887	 82% 9% 9%
2	G	887	 79% 9% 12%
2	H	887	 84% 7% 9%

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Mol	Chain	Length	Quality of chain
2	I	887	 84% 7% 9%
2	J	887	 83% 7% 9%
2	K	887	 83% 10% 7%
2	L	887	 81% 10% 9%
3	M	3	 33% 67% 100%
4	N	4	 25% 50% 25% 100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 74364 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 RNA-dependent RNA polymerase of rotavirus A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1053	8523	5464	1411	1611	37	0	0

- Molecule 2 is a protein called Inner capsid protein VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	794	6492	4127	1117	1212	36	0	0
2	D	815	6670	4238	1147	1249	36	0	0
2	E	781	6379	4052	1101	1190	36	0	0
2	F	805	6587	4186	1134	1231	36	0	0
2	G	781	6379	4052	1101	1190	36	0	0
2	H	805	6587	4186	1134	1231	36	0	0
2	I	810	6628	4213	1140	1239	36	0	0
2	J	805	6587	4186	1134	1231	36	0	0
2	K	827	6765	4297	1163	1269	36	0	0
2	L	805	6587	4186	1134	1231	36	0	0

- Molecule 3 is DNA/RNA hybrid called DNA/RNA (5'-D*(GTG))-R(P*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	M	3	95	40	18	32	5	0	0

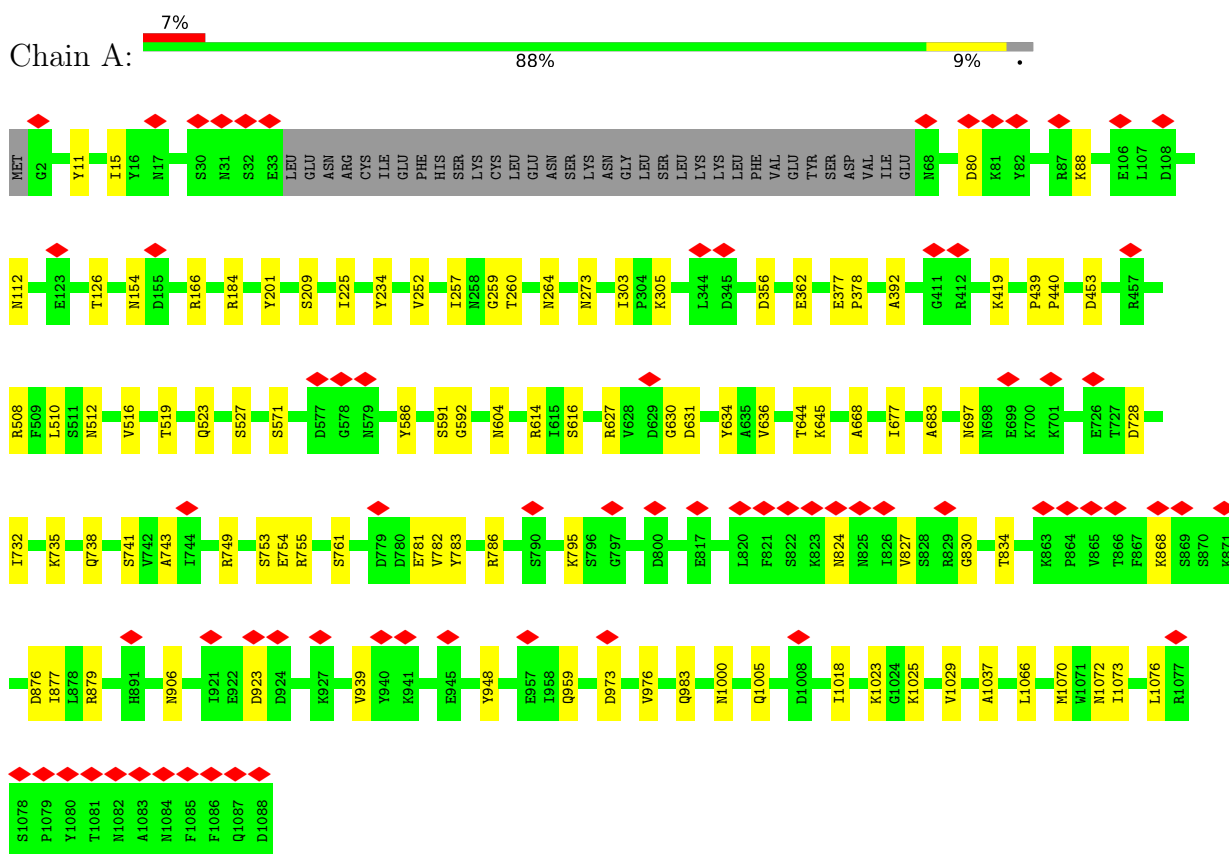
- Molecule 4 is a RNA chain called RNA (5'-R(P*AP*GP*CP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	N	4	85	38	16	27	4	0	0

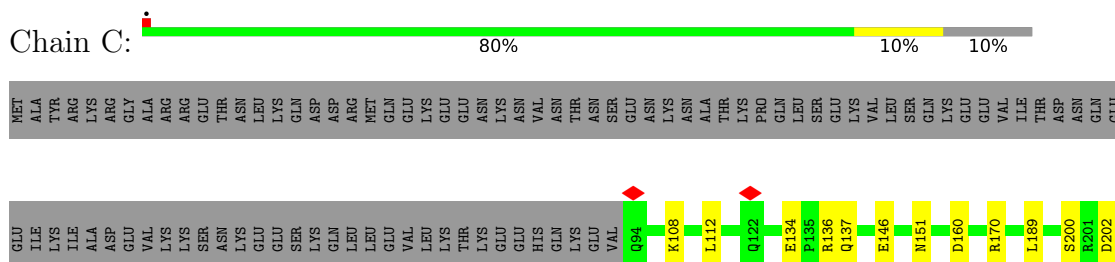
3 Residue-property plots [i](#)

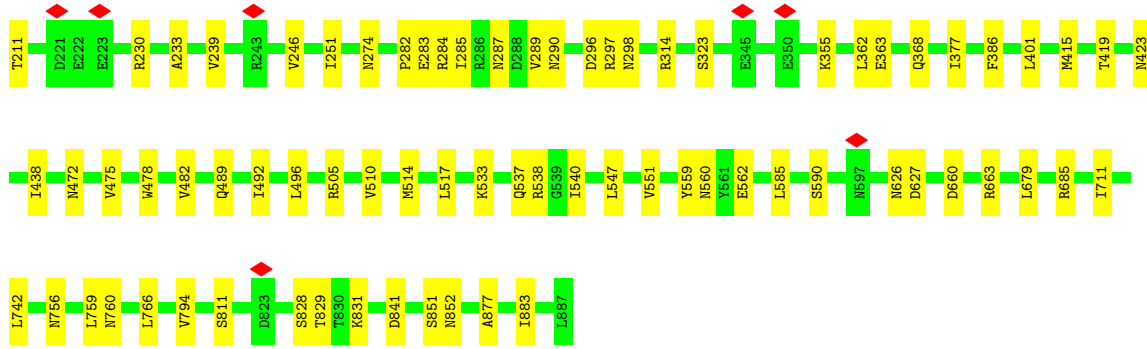
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA-dependent RNA polymerase of rotavirus A

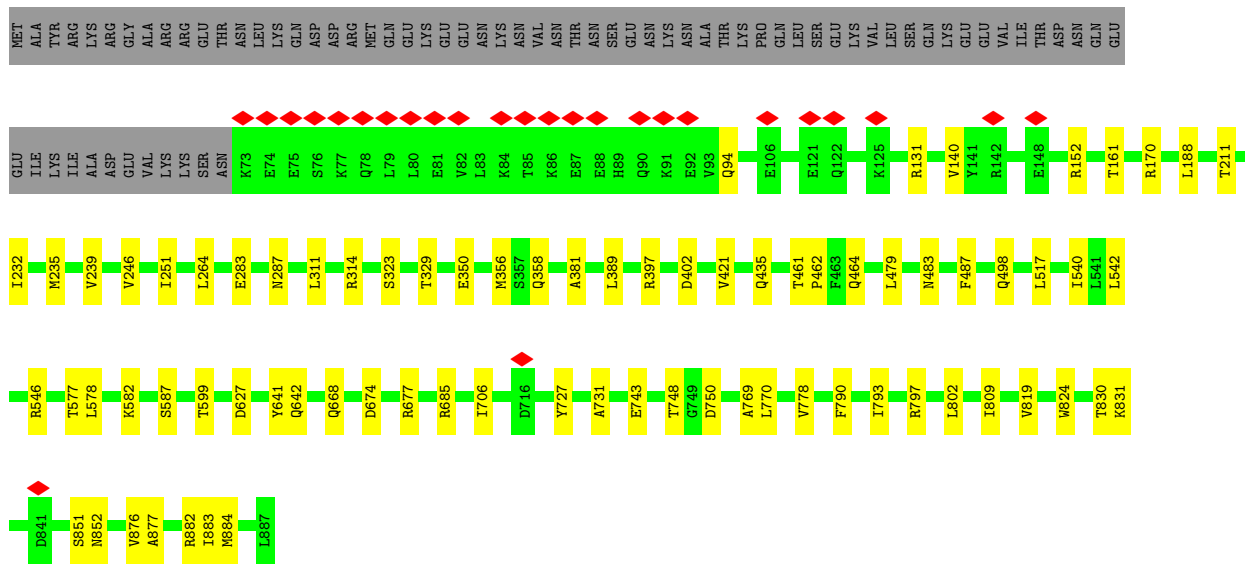
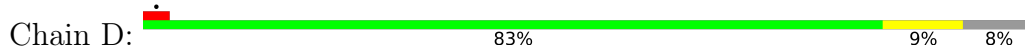


- Molecule 2: Inner capsid protein VP2

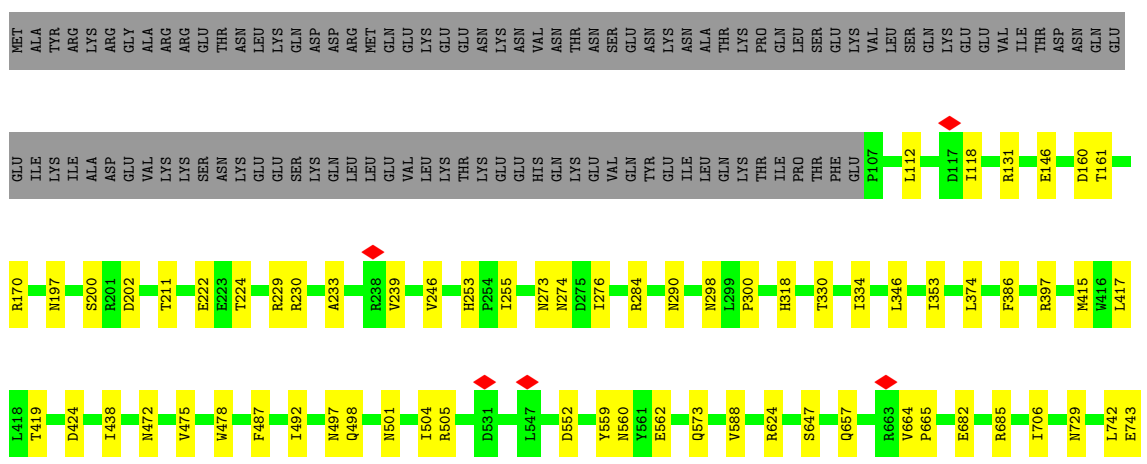
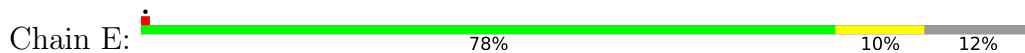


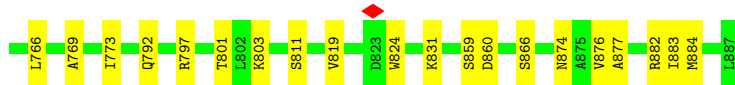


• Molecule 2: Inner capsid protein VP2

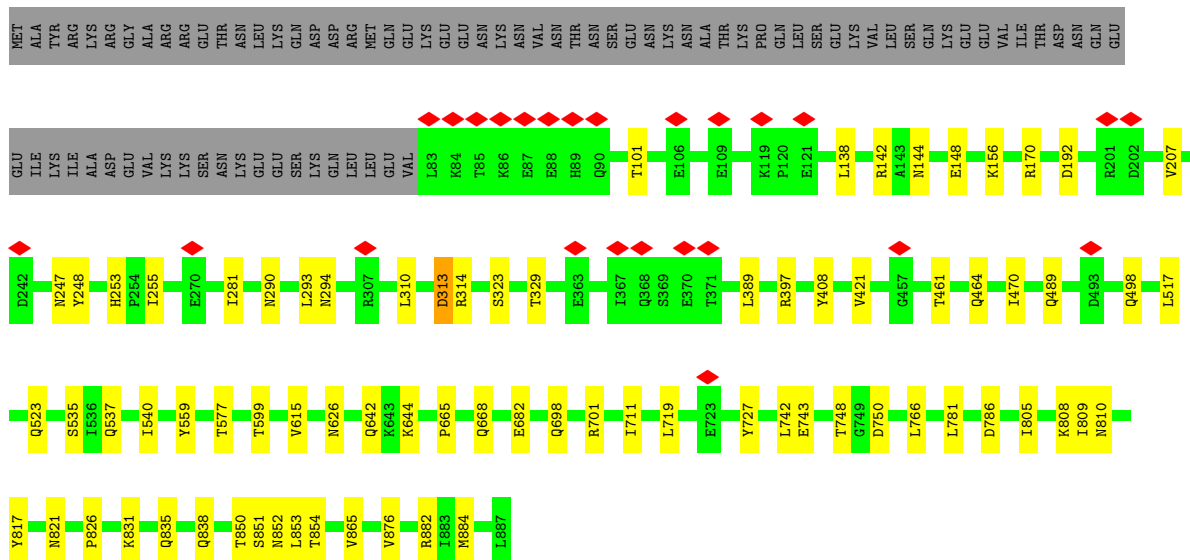
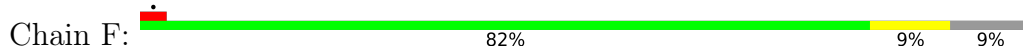


• Molecule 2: Inner capsid protein VP2

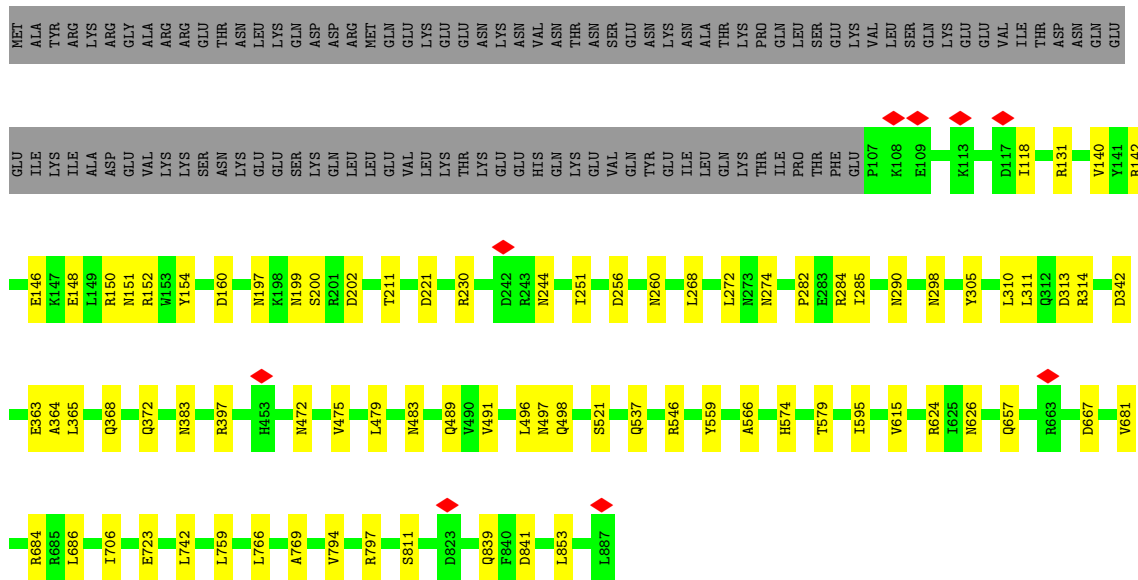
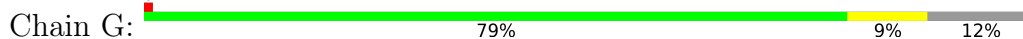




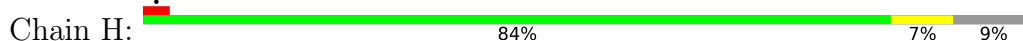
• Molecule 2: Inner capsid protein VP2




• Molecule 2: Inner capsid protein VP2

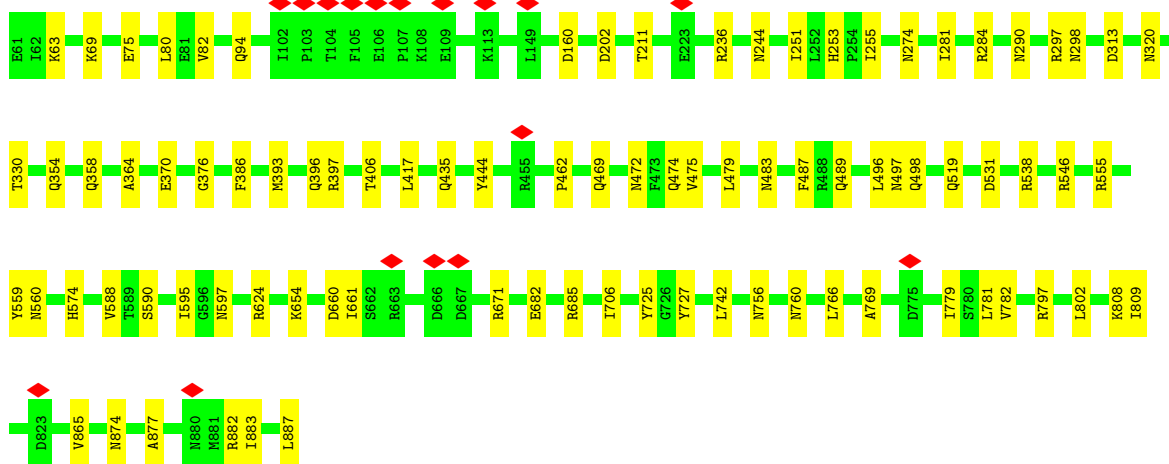


• Molecule 2: Inner capsid protein VP2




Chain K: 

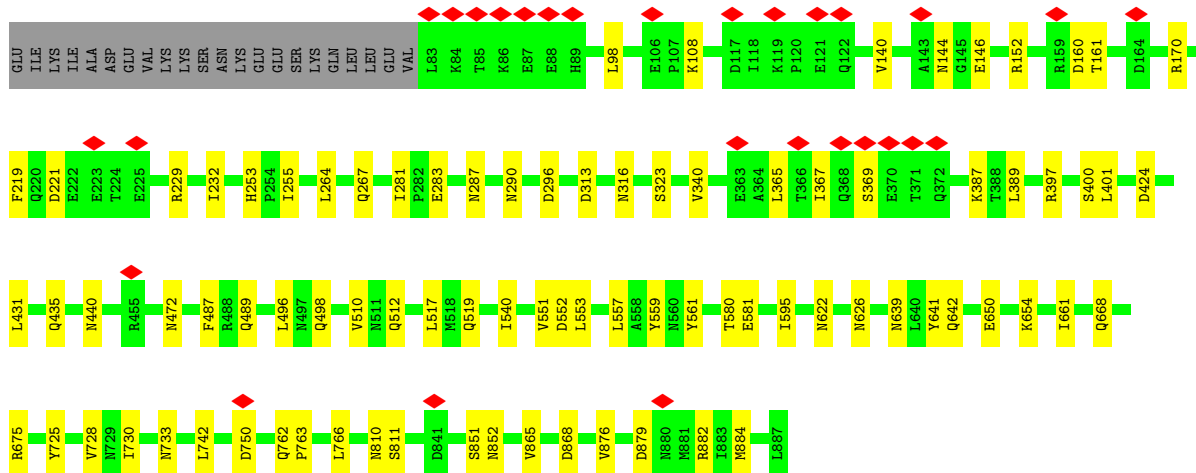
MET ALA TYR ARG LYS ARG GLY ALA ARG ARG GLU THR ASN LEU LYS GLN ASP ASP ARG MET GLU GLU GLU ASN LYS ASN VAL ASN THR ASN SER SER GLU ASN LYS THR PRO GLN LEU SER GLU VAL LYS THR



- Molecule 2: Inner capsid protein VP2

Chain L: 

MET ALA TYR ARG LYS ARG GLY ALA ARG ARG GLU THR ASN LEU LYS GLN ASP ASP ARG MET GLN LYS GLU GLU ASN LYS ASN VAL ASN THR ASN SER SER GLU VAL SER LEU SER GLN LYS VAL VAL THR ASP ASN GLU



- Molecule 3: DNA/RNA (5'-D*(GTG)-R(P*GP*C)-3')

Chain M: 



- Molecule 4: RNA (5'-R(P*AP*GP*CP*C)-3')



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	798260	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	22	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.231	Depositor
Minimum map value	-0.164	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.0311	Depositor
Map size (\AA)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTG

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	0/8692	0.50	0/11755
2	C	0.31	0/6611	0.53	0/8969
2	D	0.30	0/6790	0.52	0/9206
2	E	0.31	0/6495	0.53	0/8810
2	F	0.30	0/6707	0.52	0/9096
2	G	0.31	0/6495	0.53	0/8810
2	H	0.30	0/6707	0.52	0/9096
2	I	0.31	0/6748	0.53	0/9152
2	J	0.30	0/6707	0.51	0/9096
2	K	0.31	0/6885	0.51	0/9332
2	L	0.30	0/6707	0.51	0/9096
3	M	0.17	0/47	0.70	0/71
4	N	0.23	0/94	1.09	1/144 (0.7%)
All	All	0.31	0/75685	0.52	1/102633 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	2	C	N1-C2-O2	5.47	122.18	118.90

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	8523	0	8596	63	0
2	C	6492	0	6520	52	0
2	D	6670	0	6707	47	0
2	E	6379	0	6408	56	0
2	F	6587	0	6619	48	0
2	G	6379	0	6408	52	0
2	H	6587	0	6619	36	0
2	I	6628	0	6664	41	0
2	J	6587	0	6619	39	0
2	K	6765	0	6809	56	0
2	L	6587	0	6619	56	0
3	M	95	0	49	3	0
4	N	85	0	45	1	0
All	All	74364	0	74682	505	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 3.

The worst 5 of 505 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:D:94:GLN:HE22	2:E:860:ASP:H	1.40	0.68
2:F:642:GLN:HG2	2:G:202:ASP:HA	1.79	0.65
2:I:150:ARG:HH22	2:I:152:ARG:HH11	1.46	0.64
2:G:498:GLN:HE22	2:G:574:HIS:HB2	1.62	0.63
1:A:377:GLU:HG2	1:A:378:PRO:HD3	1.81	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	1049/1088 (96%)	1007 (96%)	42 (4%)	0	100	100
2	C	792/887 (89%)	759 (96%)	33 (4%)	0	100	100
2	D	813/887 (92%)	786 (97%)	27 (3%)	0	100	100
2	E	779/887 (88%)	749 (96%)	30 (4%)	0	100	100
2	F	803/887 (90%)	769 (96%)	34 (4%)	0	100	100
2	G	779/887 (88%)	751 (96%)	28 (4%)	0	100	100
2	H	803/887 (90%)	773 (96%)	30 (4%)	0	100	100
2	I	808/887 (91%)	774 (96%)	34 (4%)	0	100	100
2	J	803/887 (90%)	781 (97%)	21 (3%)	1 (0%)	51	82
2	K	825/887 (93%)	792 (96%)	33 (4%)	0	100	100
2	L	803/887 (90%)	767 (96%)	36 (4%)	0	100	100
All	All	9057/9958 (91%)	8708 (96%)	348 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	J	120	PRO

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	955/989 (97%)	954 (100%)	1 (0%)	93	98
2	C	730/818 (89%)	729 (100%)	1 (0%)	93	98
2	D	751/818 (92%)	751 (100%)	0	100	100
2	E	717/818 (88%)	717 (100%)	0	100	100
2	F	741/818 (91%)	740 (100%)	1 (0%)	93	98
2	G	717/818 (88%)	716 (100%)	1 (0%)	93	98
2	H	741/818 (91%)	741 (100%)	0	100	100
2	I	746/818 (91%)	746 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	741/818 (91%)	741 (100%)	0	100	100
2	K	762/818 (93%)	762 (100%)	0	100	100
2	L	741/818 (91%)	741 (100%)	0	100	100
All	All	8342/9169 (91%)	8338 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1072	ASN
2	C	170	ARG
2	F	313	ASP
2	G	221	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	511	ASN
2	L	257	HIS
2	H	698	GLN
2	L	247	ASN
2	K	354	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	M	1/3 (33%)	0	0
4	N	3/4 (75%)	2 (66%)	0
All	All	4/7 (57%)	2 (50%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	N	1	G
4	N	3	C

There are no RNA pucker outliers to report.

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 monosaccharides 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.

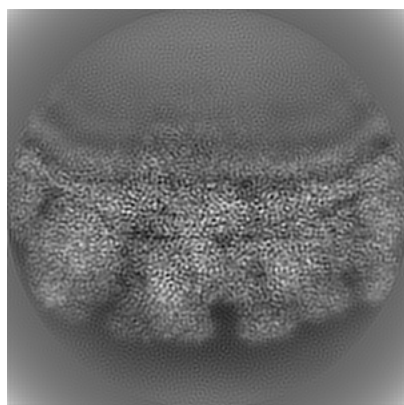
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20059. These allow visual inspection of the internal detail of the map and identification of artifacts.

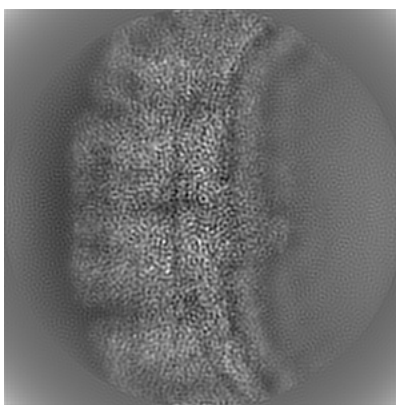
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

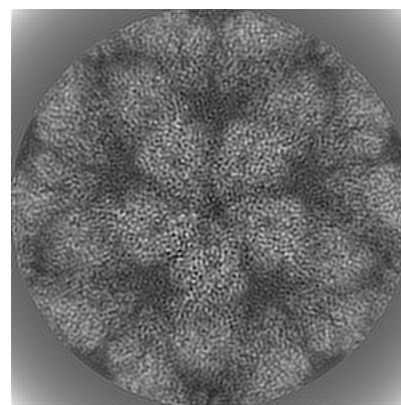
6.1.1 Primary map



X



Y

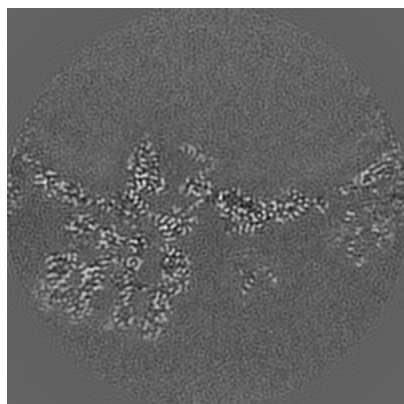


Z

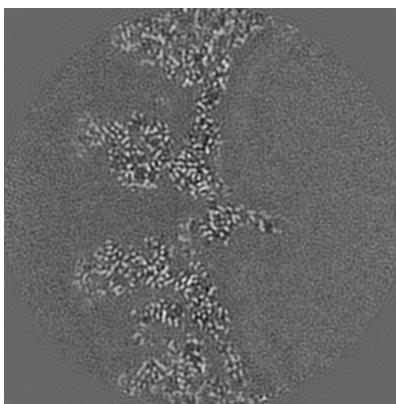
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

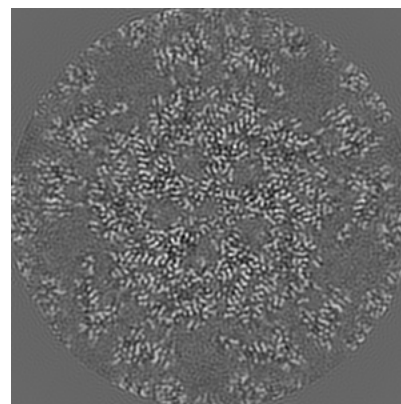
6.2.1 Primary map



X Index: 160



Y Index: 160

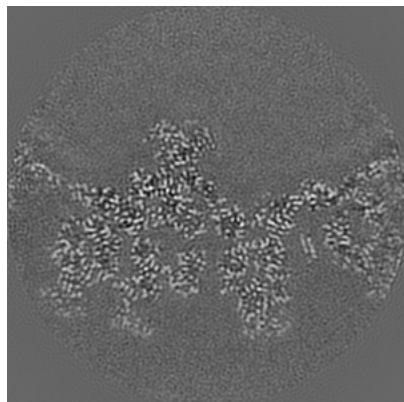


Z Index: 160

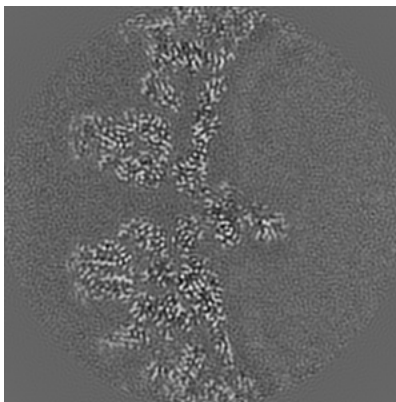
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

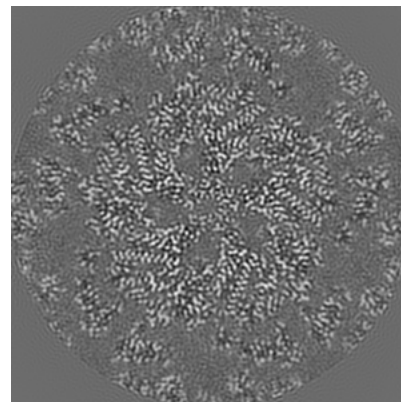
6.3.1 Primary map



X Index: 141



Y Index: 153

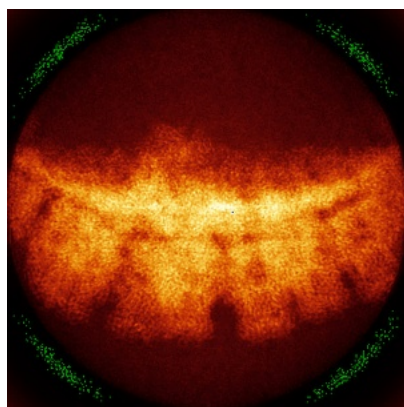


Z Index: 161

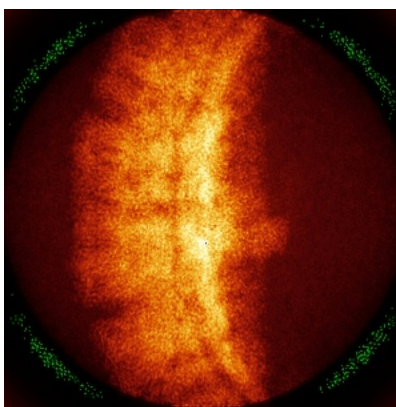
The images above show the largest variance slices of the map in three orthogonal directions.

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

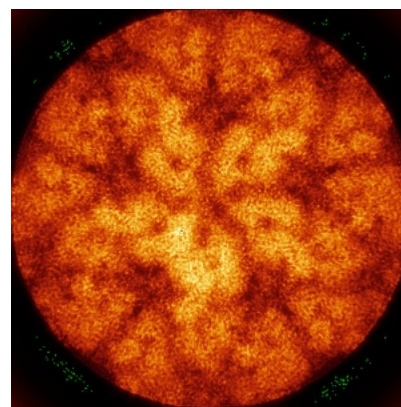
6.4.1 Primary map



X



Y

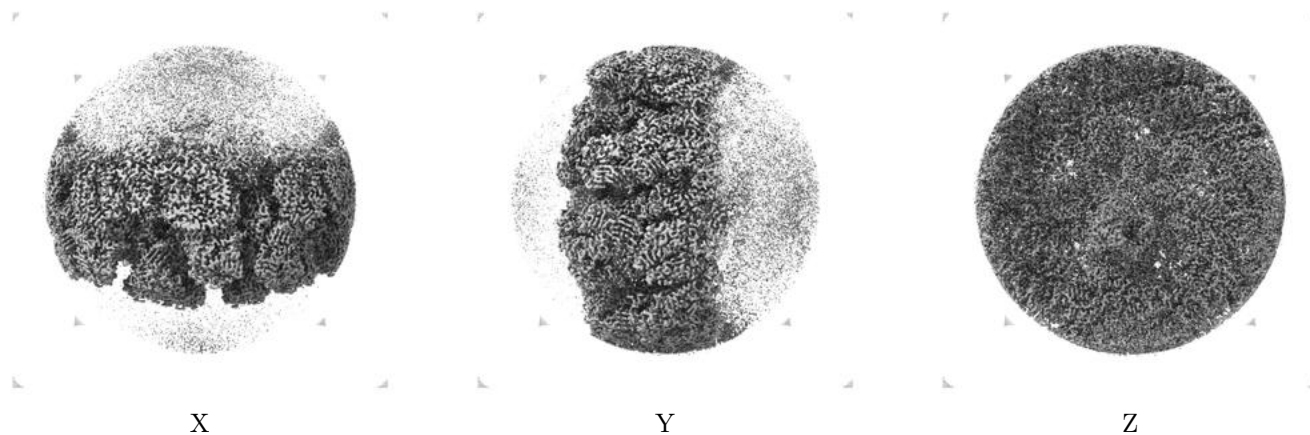


Z

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 0.0311. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

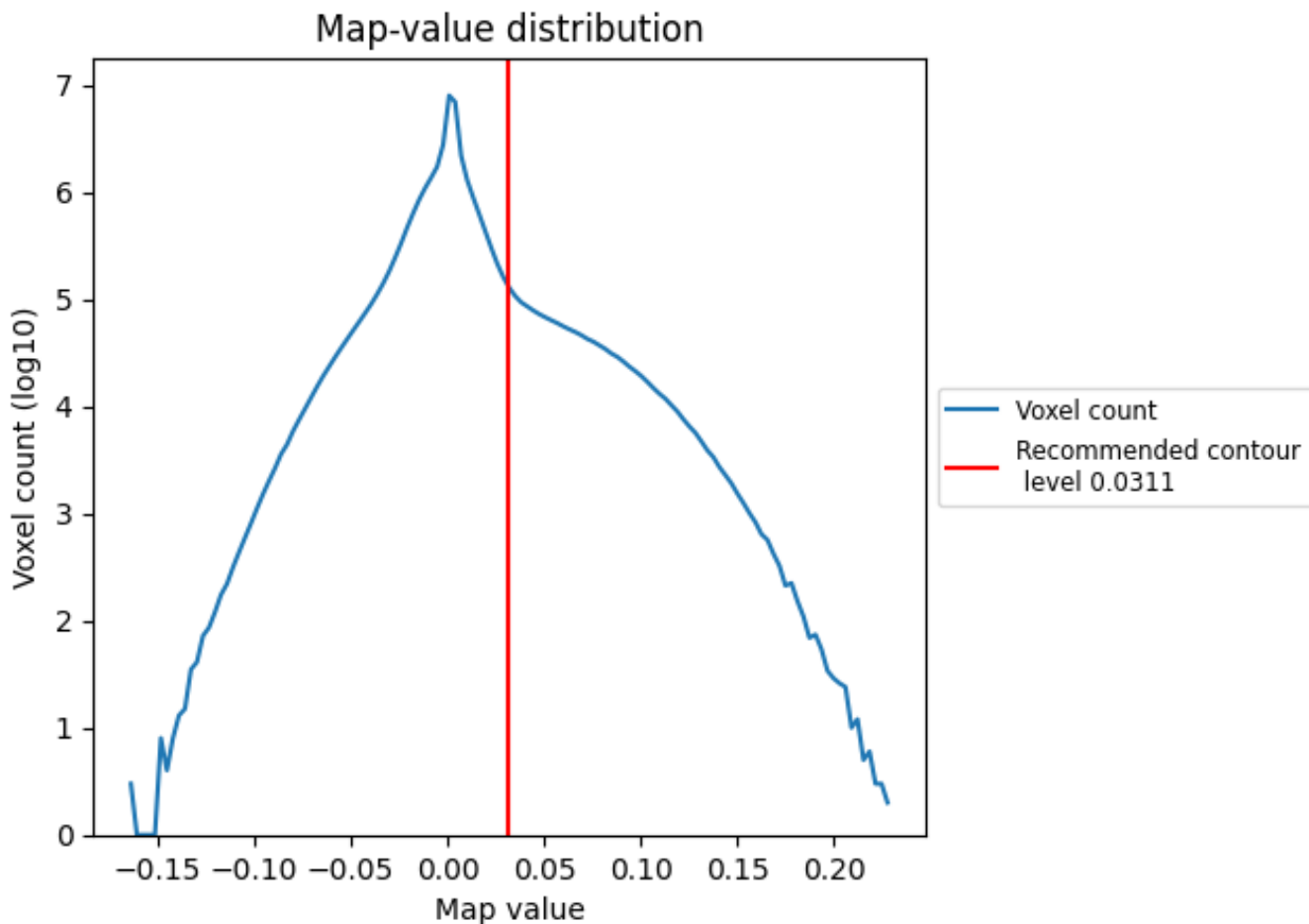
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

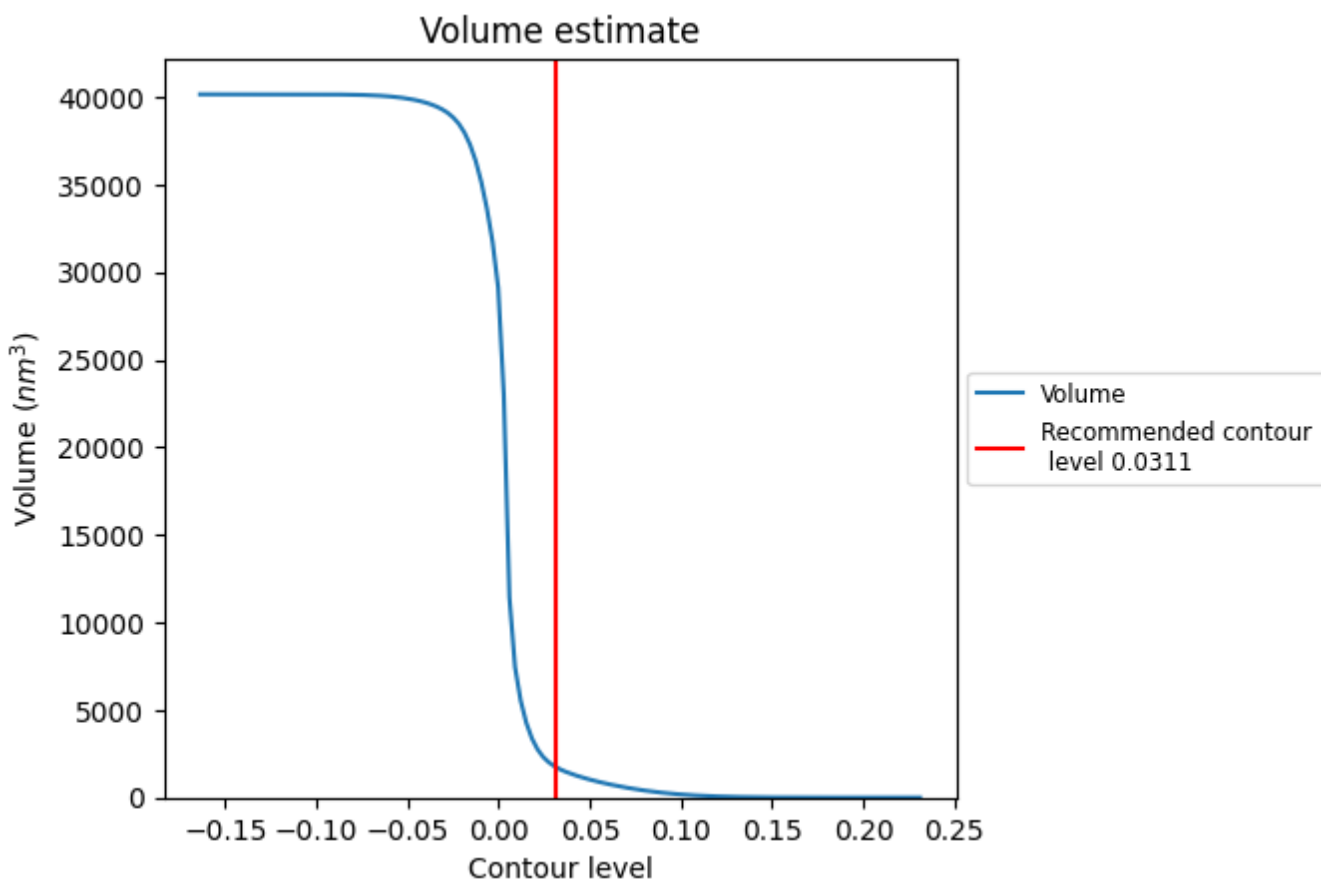
This section contains the results of statistical analysis of the map.

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.

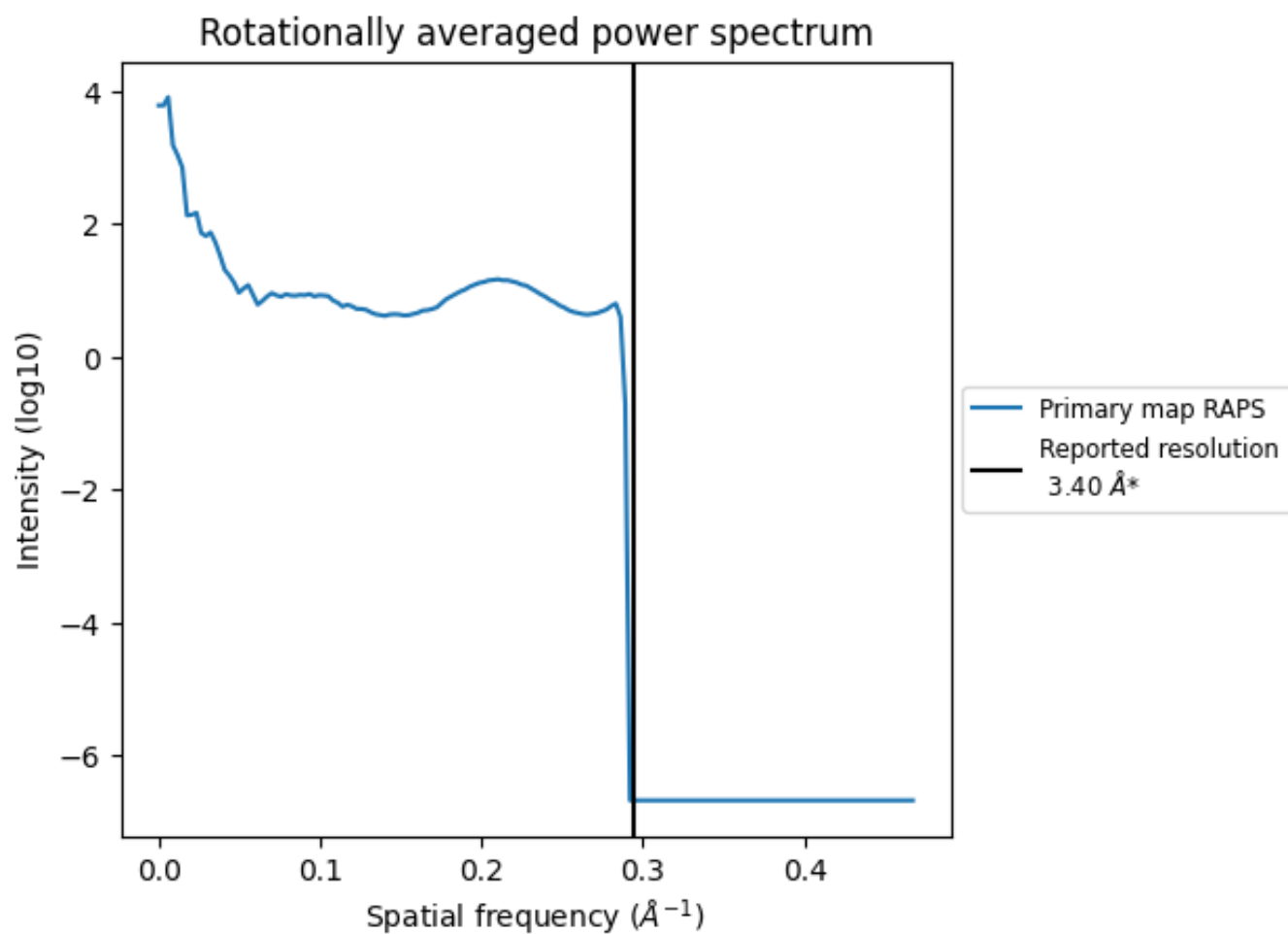
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1759 nm³; this corresponds to an approximate mass of 1589 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 i



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

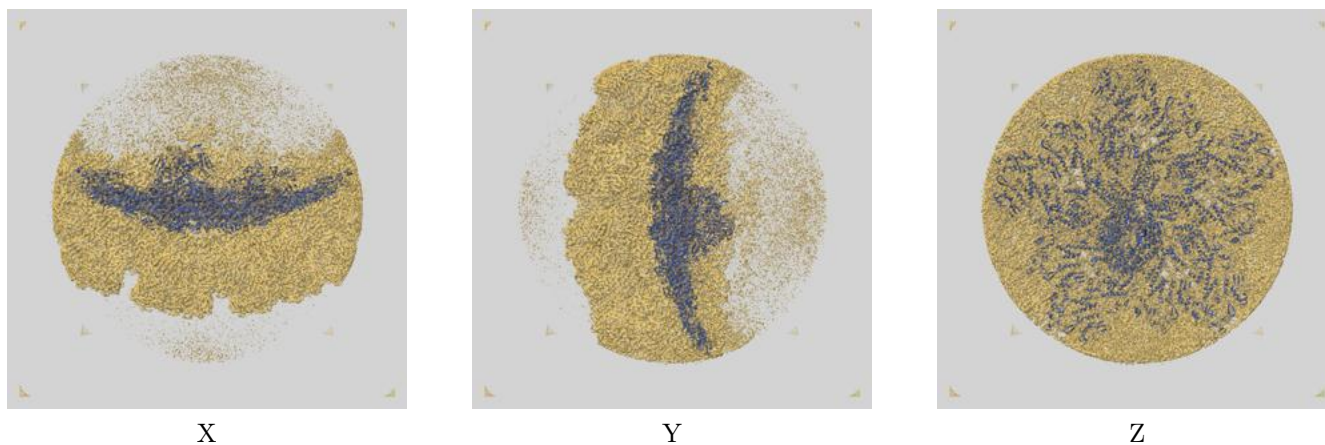
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

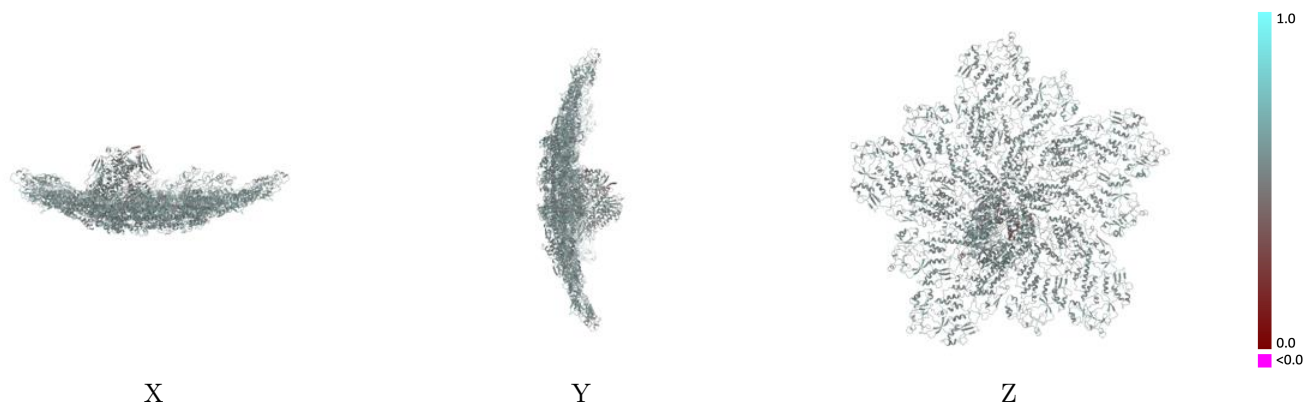
This section contains information regarding the fit between EMDB map EMD-20059 and PDB model 6OGY. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



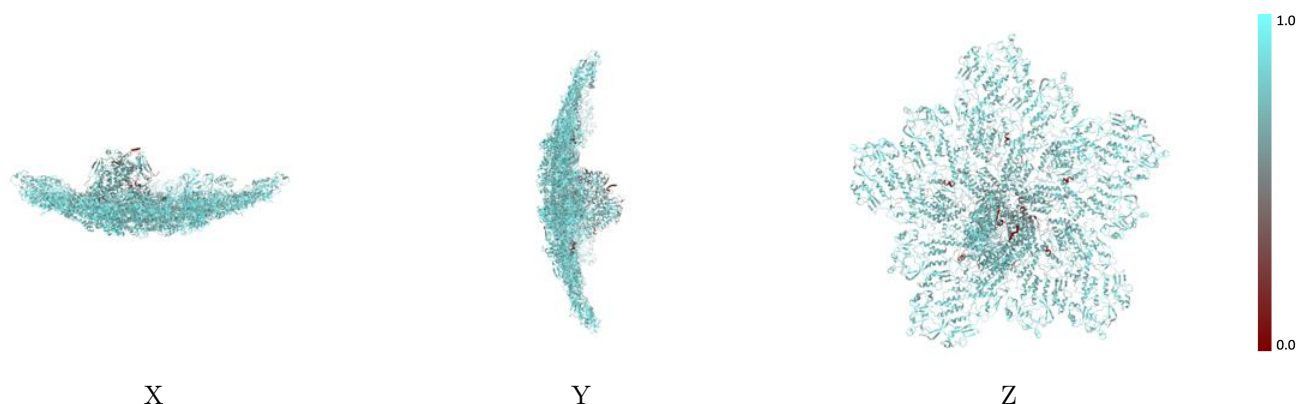
The images above show the 3D surface view of the map at the recommended contour level 0.0311 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



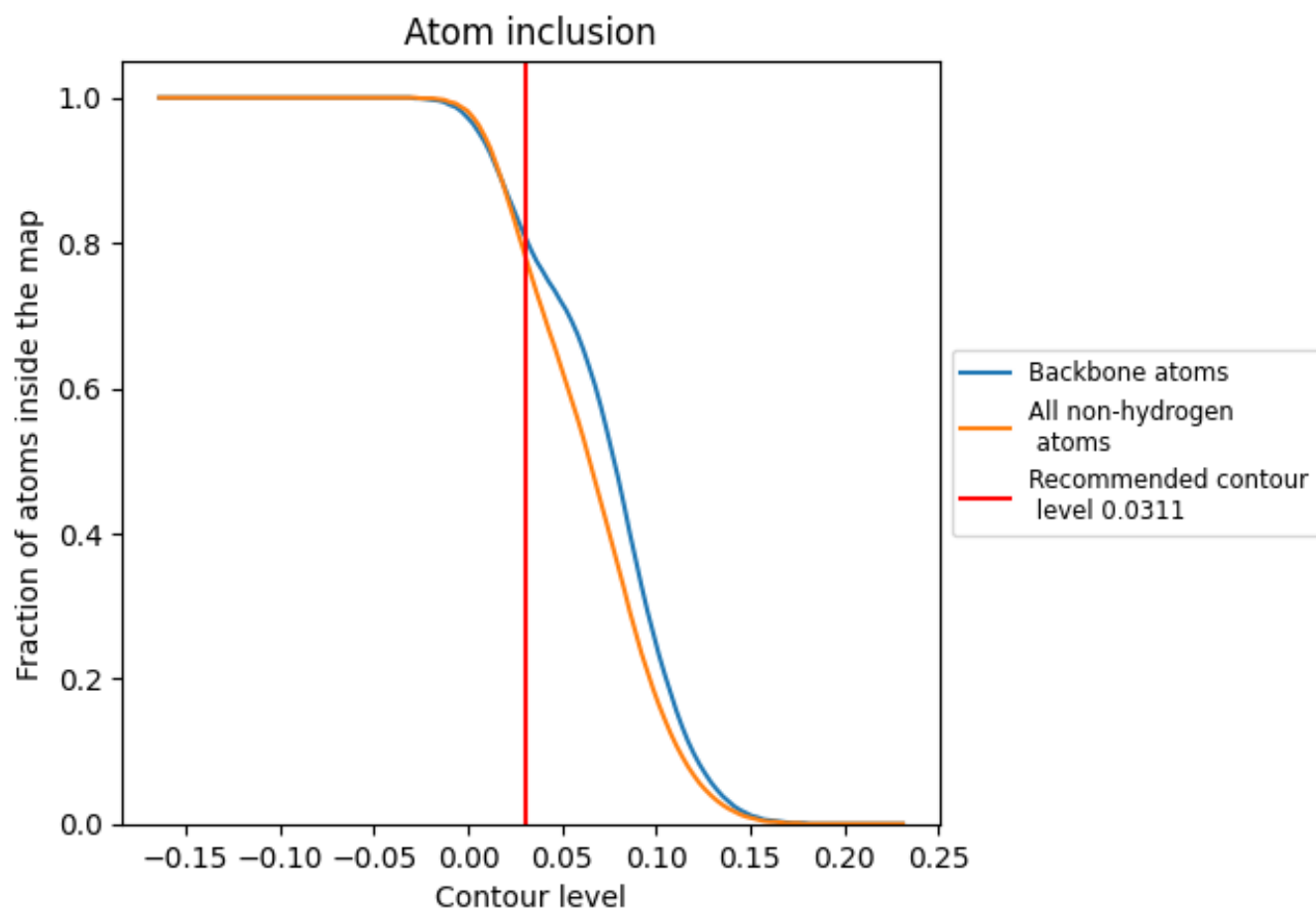
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0311).





























9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 78% 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 (0.0311) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7770	 0.5370
A	 0.7370	 0.5330
C	 0.7950	 0.5430
D	 0.7770	 0.5360
E	 0.8010	 0.5430
F	 0.7820	 0.5360
G	 0.7920	 0.5420
H	 0.7750	 0.5300
I	 0.7800	 0.5410
J	 0.7790	 0.5360
K	 0.7890	 0.5420
L	 0.7740	 0.5370
M	 0.1470	 0.3470
N	 0.0000	 0.2730

