



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2024 – 12:45 PM EST

PDB ID : 6DZU
EMDB ID : EMD-8939
Title : Mechanism of cellular recognition by PCV2
Authors : Khayat, R.; Dhindwal, S.
Deposited on : 2018-07-05
Resolution : 3.30 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:

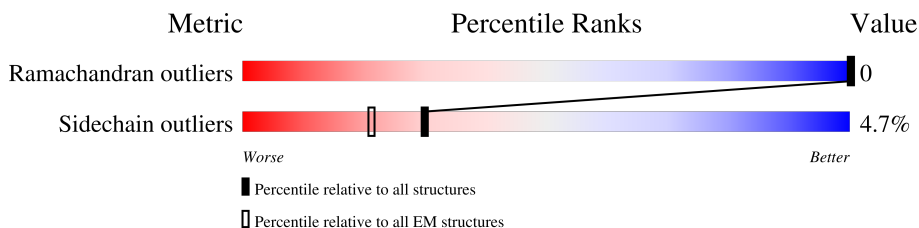
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



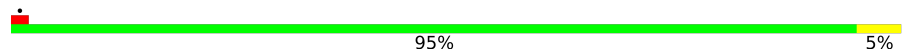
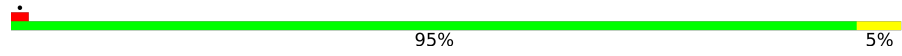
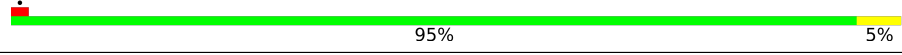
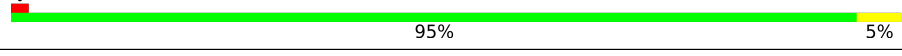
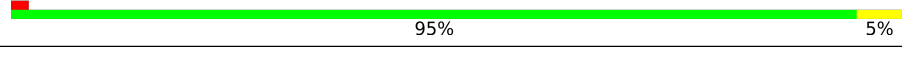
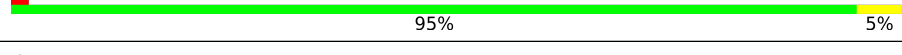
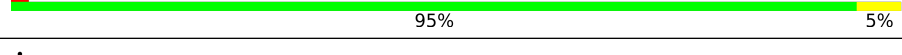
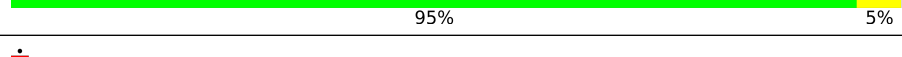
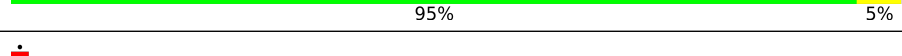
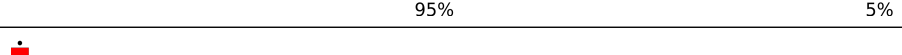
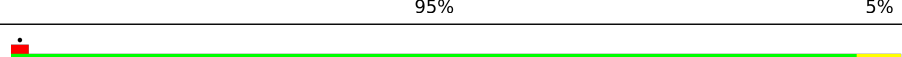
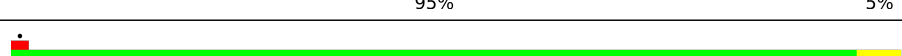
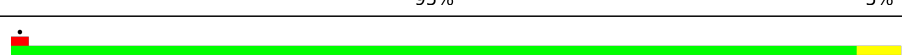
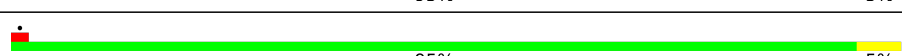
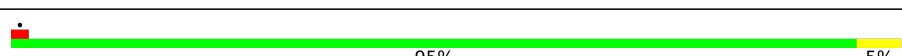
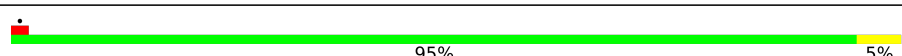
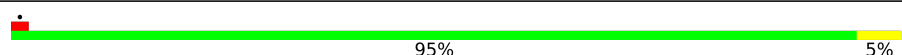
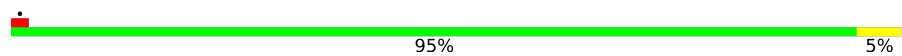
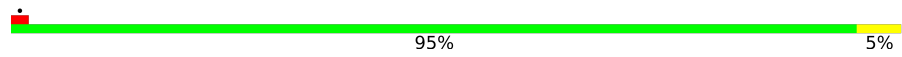
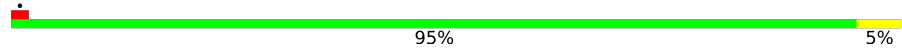
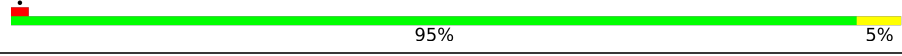
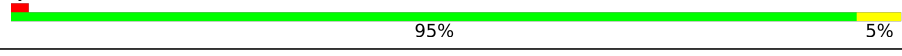
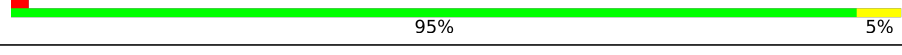
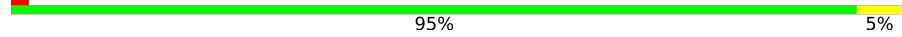

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A1	189	95% 5%
1	A2	189	95% 5%
1	A3	189	95% 5%
1	A4	189	95% 5%
1	A5	189	95% 5%
1	A6	189	95% 5%
1	A7	189	95% 5%
1	A8	189	95% 5%
1	A9	189	95% 5%

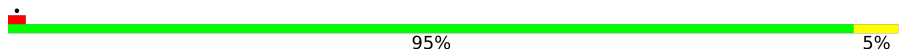
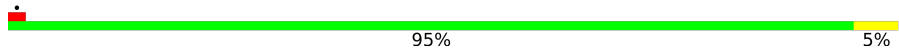
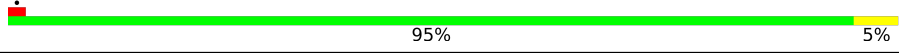
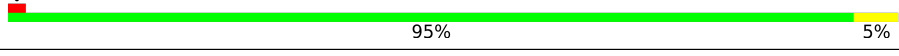
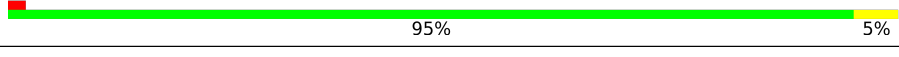
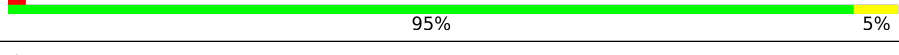
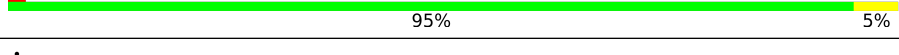
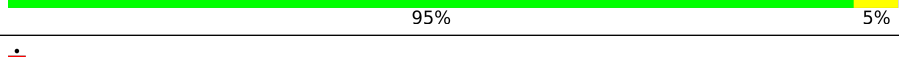
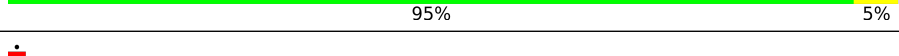
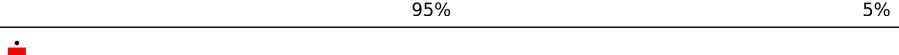
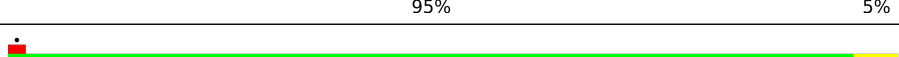
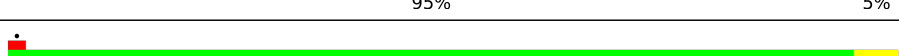
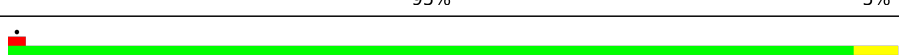
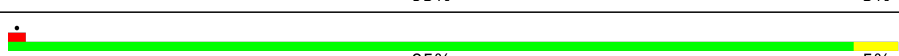
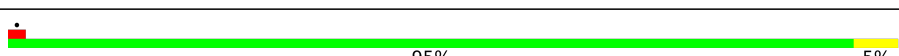
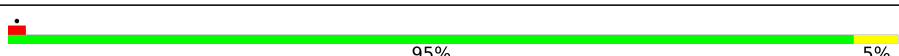
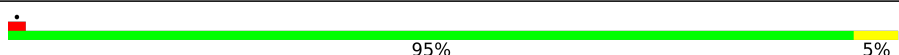
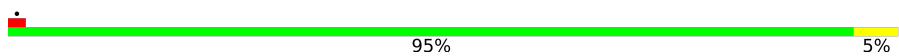
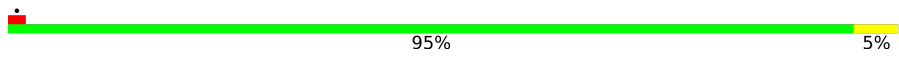
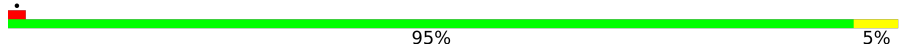
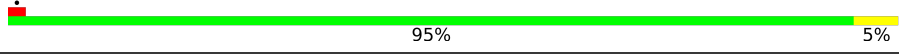
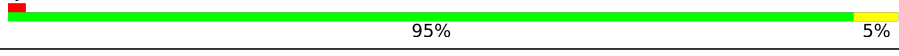
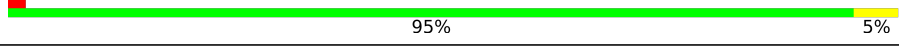
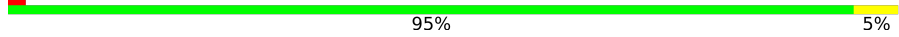

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Mol	Chain	Length	Quality of chain
1	AA	189	
1	AB	189	
1	AC	189	
1	AD	189	
1	AE	189	
1	AF	189	
1	AG	189	
1	AH	189	
1	AI	189	
1	AJ	189	
1	AK	189	
1	AL	189	
1	AM	189	
1	AN	189	
1	AO	189	
1	AP	189	
1	AQ	189	
1	AR	189	
1	AS	189	
1	AT	189	
1	AU	189	
1	AV	189	
1	AW	189	
1	AX	189	
1	AY	189	

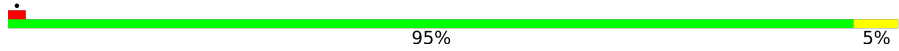
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Mol	Chain	Length	Quality of chain
1	AZ	189	
1	Aa	189	
1	Ab	189	
1	Ac	189	
1	Ad	189	
1	Ae	189	
1	Af	189	
1	Ag	189	
1	Ah	189	
1	Ai	189	
1	Aj	189	
1	Ak	189	
1	Al	189	
1	Am	189	
1	An	189	
1	Ao	189	
1	Ap	189	
1	Aq	189	
1	Ar	189	
1	As	189	
1	At	189	
1	Au	189	
1	Av	189	
1	Aw	189	
1	Ax	189	

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Mol	Chain	Length	Quality of chain
1	Ay	189	 A horizontal bar chart representing the quality of the chain. The bar is primarily green, indicating a high quality score of 95%. A small yellow segment at the far right indicates a lower quality score of 5%. A small red square is visible at the beginning of the bar.

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 182100 atoms, of which 89040 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 Putative capsid protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A1	189	3035	995	1484	268	284	4	0	0
1	A2	189	3035	995	1484	268	284	4	0	0
1	A3	189	3035	995	1484	268	284	4	0	0
1	A4	189	3035	995	1484	268	284	4	0	0
1	A5	189	3035	995	1484	268	284	4	0	0
1	A6	189	3035	995	1484	268	284	4	0	0
1	A7	189	3035	995	1484	268	284	4	0	0
1	A8	189	3035	995	1484	268	284	4	0	0
1	A9	189	3035	995	1484	268	284	4	0	0
1	AA	189	3035	995	1484	268	284	4	0	0
1	AB	189	3035	995	1484	268	284	4	0	0
1	AC	189	3035	995	1484	268	284	4	0	0
1	AD	189	3035	995	1484	268	284	4	0	0
1	AE	189	3035	995	1484	268	284	4	0	0
1	AF	189	3035	995	1484	268	284	4	0	0
1	AG	189	3035	995	1484	268	284	4	0	0
1	AH	189	3035	995	1484	268	284	4	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	AI	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AJ	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AK	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AL	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AM	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AN	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AO	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AP	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AQ	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AR	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AS	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AT	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AU	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AV	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AW	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AX	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AY	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	AZ	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Aa	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ab	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ac	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace	
1	Ad	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ae	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Af	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ag	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ah	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ai	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Aj	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ak	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Al	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Am	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	An	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ao	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ap	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Aq	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ar	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	As	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	At	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Au	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Av	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Aw	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		
1	Ax	189	Total	C	H	N	O	S	0	0
			3035	995	1484	268	284	4		

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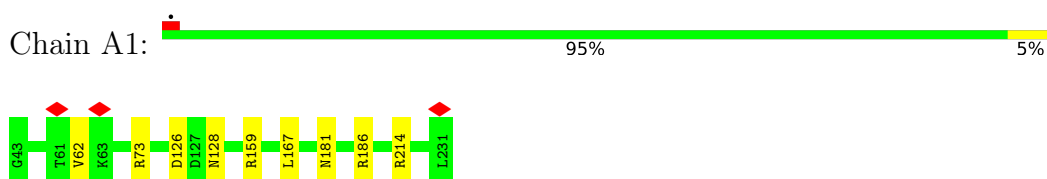
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Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	Ay	189	3035	995	1484	268	284	4	0	0

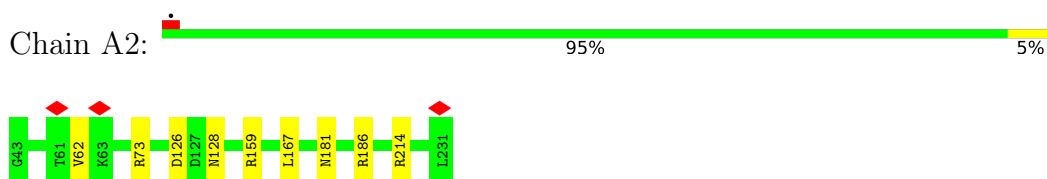
3 Residue-property plots [i](#)

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.

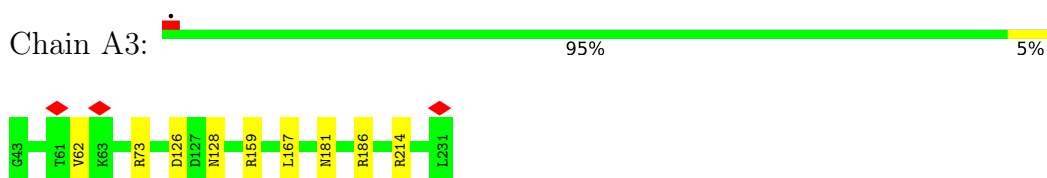
- Molecule 1: Putative capsid protein



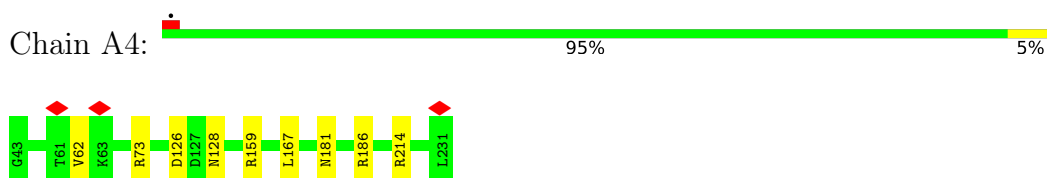
- Molecule 1: Putative capsid protein



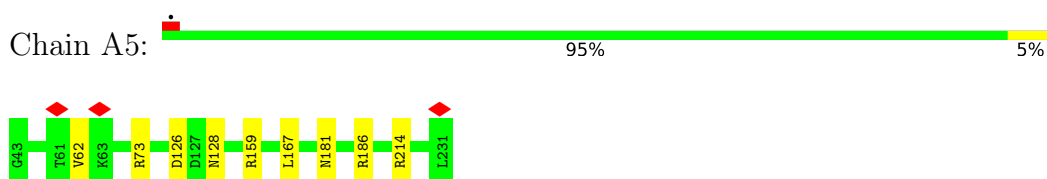
- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



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• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein





• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein

Chain AJ:  95% 5%



- Molecule 1: Putative capsid protein

Chain AK:  95% 5%



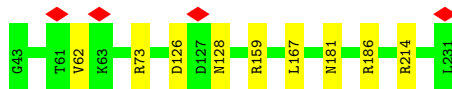
- Molecule 1: Putative capsid protein

Chain AL:  95% 5%



- Molecule 1: Putative capsid protein

Chain AM:  95% 5%



- Molecule 1: Putative capsid protein

Chain AN:  95% 5%



- Molecule 1: Putative capsid protein

Chain AO:  95% 5%

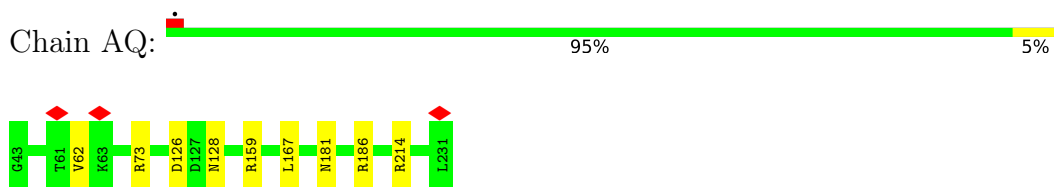


- Molecule 1: Putative capsid protein

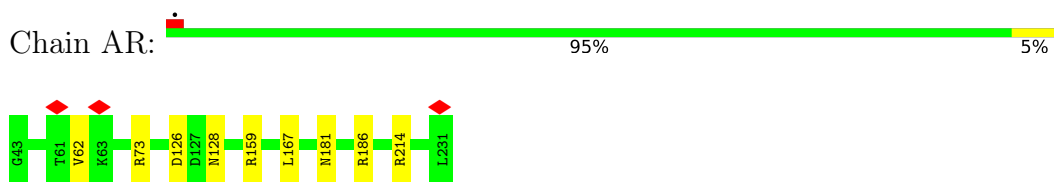
Chain AP:  95% 5%



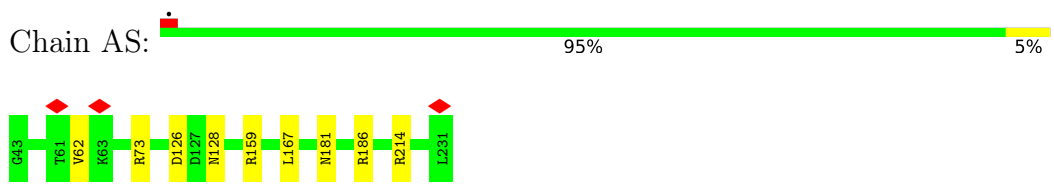
- Molecule 1: Putative capsid protein



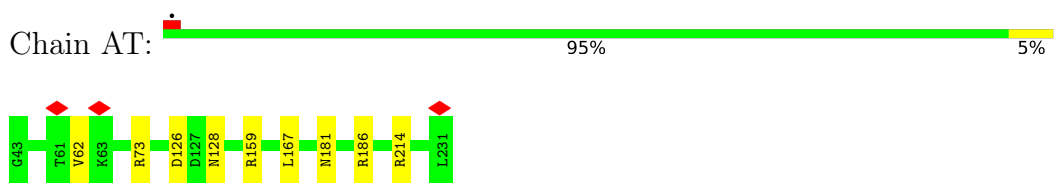
- Molecule 1: Putative capsid protein



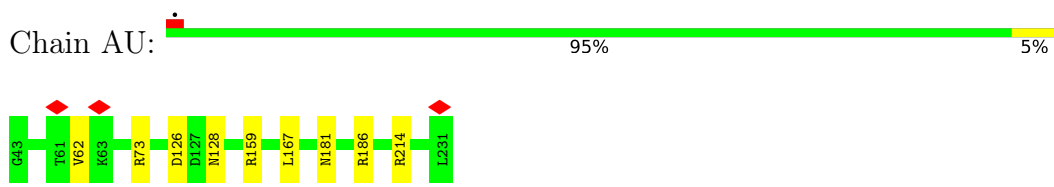
- Molecule 1: Putative capsid protein



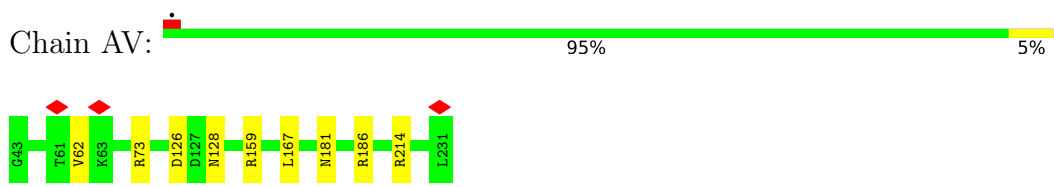
- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein

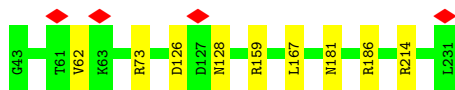


- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein





- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



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- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



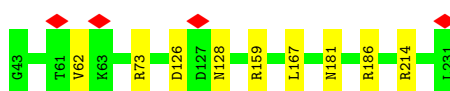
- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein



- Molecule 1: Putative capsid protein





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• Molecule 1: Putative capsid protein



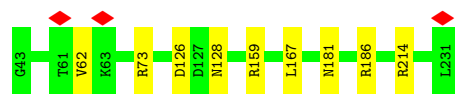
• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



• Molecule 1: Putative capsid protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	28938	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Per particle estimation	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	280	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.219	Depositor
Minimum map value	-0.137	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	279.04, 279.04, 279.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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	A1	0.55	0/1598	0.63	1/2175 (0.0%)
1	A2	0.55	0/1598	0.63	1/2175 (0.0%)
1	A3	0.55	0/1598	0.63	1/2175 (0.0%)
1	A4	0.55	0/1598	0.63	1/2175 (0.0%)
1	A5	0.55	0/1598	0.63	1/2175 (0.0%)
1	A6	0.55	0/1598	0.63	1/2175 (0.0%)
1	A7	0.55	0/1598	0.63	1/2175 (0.0%)
1	A8	0.55	0/1598	0.63	1/2175 (0.0%)
1	A9	0.55	0/1598	0.63	1/2175 (0.0%)
1	AA	0.55	0/1598	0.63	1/2175 (0.0%)
1	AB	0.55	0/1598	0.63	1/2175 (0.0%)
1	AC	0.55	0/1598	0.63	1/2175 (0.0%)
1	AD	0.55	0/1598	0.63	1/2175 (0.0%)
1	AE	0.55	0/1598	0.63	1/2175 (0.0%)
1	AF	0.55	0/1598	0.63	1/2175 (0.0%)
1	AG	0.55	0/1598	0.63	1/2175 (0.0%)
1	AH	0.55	0/1598	0.63	1/2175 (0.0%)
1	AI	0.55	0/1598	0.63	1/2175 (0.0%)
1	AJ	0.55	0/1598	0.63	1/2175 (0.0%)
1	AK	0.55	0/1598	0.63	1/2175 (0.0%)
1	AL	0.55	0/1598	0.63	1/2175 (0.0%)
1	AM	0.55	0/1598	0.63	1/2175 (0.0%)
1	AN	0.55	0/1598	0.63	1/2175 (0.0%)
1	AO	0.55	0/1598	0.63	1/2175 (0.0%)
1	AP	0.55	0/1598	0.63	1/2175 (0.0%)
1	AQ	0.55	0/1598	0.63	1/2175 (0.0%)
1	AR	0.55	0/1598	0.63	1/2175 (0.0%)
1	AS	0.55	0/1598	0.63	1/2175 (0.0%)
1	AT	0.55	0/1598	0.63	1/2175 (0.0%)
1	AU	0.55	0/1598	0.63	1/2175 (0.0%)
1	AV	0.55	0/1598	0.63	1/2175 (0.0%)
1	AW	0.55	0/1598	0.63	1/2175 (0.0%)
1	AX	0.55	0/1598	0.63	1/2175 (0.0%)
1	AY	0.55	0/1598	0.63	1/2175 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AZ	0.55	0/1598	0.63	1/2175 (0.0%)
1	Aa	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ab	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ac	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ad	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ae	0.55	0/1598	0.63	1/2175 (0.0%)
1	Af	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ag	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ah	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ai	0.55	0/1598	0.63	1/2175 (0.0%)
1	Aj	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ak	0.55	0/1598	0.63	1/2175 (0.0%)
1	Al	0.55	0/1598	0.63	1/2175 (0.0%)
1	Am	0.55	0/1598	0.63	1/2175 (0.0%)
1	An	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ao	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ap	0.55	0/1598	0.63	1/2175 (0.0%)
1	Aq	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ar	0.55	0/1598	0.63	1/2175 (0.0%)
1	As	0.55	0/1598	0.63	1/2175 (0.0%)
1	At	0.55	0/1598	0.63	1/2175 (0.0%)
1	Au	0.55	0/1598	0.63	1/2175 (0.0%)
1	Av	0.55	0/1598	0.63	1/2175 (0.0%)
1	Aw	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ax	0.55	0/1598	0.63	1/2175 (0.0%)
1	Ay	0.55	0/1598	0.63	1/2175 (0.0%)
All	All	0.55	0/95880	0.63	60/130500 (0.0%)

There are no bond length outliers.

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ag	62	VAL	CG1-CB-CG2	6.74	121.68	110.90
1	Au	62	VAL	CG1-CB-CG2	6.72	121.66	110.90
1	AA	62	VAL	CG1-CB-CG2	6.72	121.65	110.90
1	AE	62	VAL	CG1-CB-CG2	6.72	121.65	110.90
1	Ac	62	VAL	CG1-CB-CG2	6.71	121.64	110.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A1	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A2	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A3	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A4	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A5	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A6	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A7	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A8	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	A9	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	AA	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	AB	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AC	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AD	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AE	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AF	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	AG	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AH	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AI	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	AJ	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AK	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AL	187/189 (99%)	176 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AM	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AN	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AO	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AP	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AQ	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AR	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AS	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AT	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	AU	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AV	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AW	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AX	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AY	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	AZ	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Aa	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	Ab	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ac	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	Ad	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ae	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Af	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	Ag	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ah	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ai	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	Aj	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ak	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Al	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Am	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	An	187/189 (99%)	175 (94%)	12 (6%)	0	100	100
1	Ao	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ap	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Aq	187/189 (99%)	176 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ar	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	As	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	At	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Au	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Av	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Aw	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ax	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
1	Ay	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
All	All	11220/11340 (99%)	10550 (94%)	670 (6%)	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	A1	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A2	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A3	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A4	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A5	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A6	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A7	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A8	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	A9	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AA	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AB	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AC	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AD	172/172 (100%)	164 (95%)	8 (5%)	26	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AE	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AF	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AG	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AH	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AI	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AJ	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AK	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AL	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AM	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AN	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AO	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AP	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AQ	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AR	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AS	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AT	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AU	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AV	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AW	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AX	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AY	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	AZ	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Aa	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ab	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ac	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ad	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ae	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Af	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ag	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ah	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ai	172/172 (100%)	164 (95%)	8 (5%)	26	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Aj	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ak	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Al	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Am	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	An	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ao	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ap	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Aq	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ar	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	As	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	At	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Au	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Av	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Aw	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ax	172/172 (100%)	164 (95%)	8 (5%)	26	57
1	Ay	172/172 (100%)	164 (95%)	8 (5%)	26	57
All	All	10320/10320 (100%)	9840 (95%)	480 (5%)	30	57

5 of 480 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AT	214	ARG
1	Au	159	ARG
1	Aa	186	ARG
1	At	186	ARG
1	Ay	126	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 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.

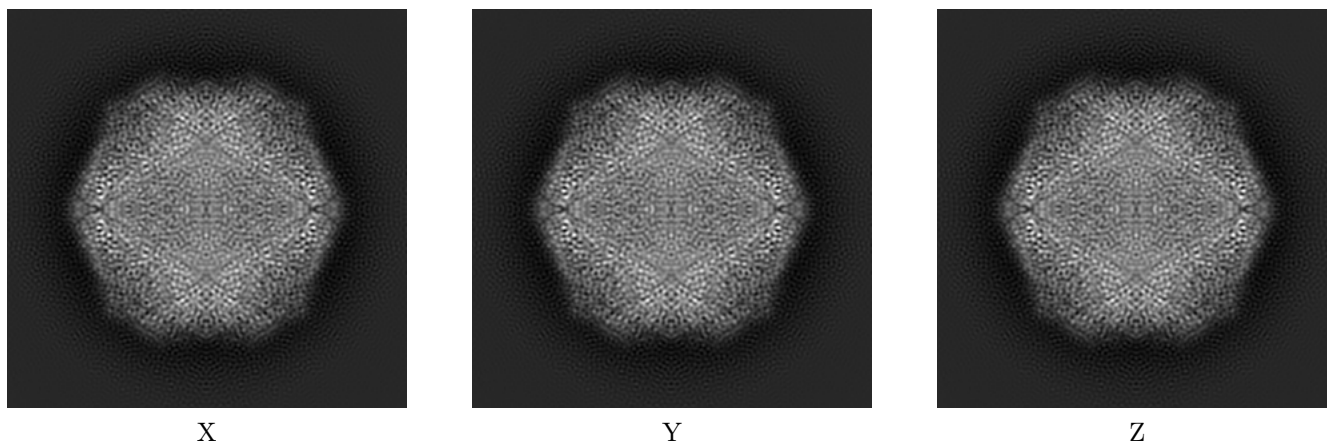
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8939. 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](#)

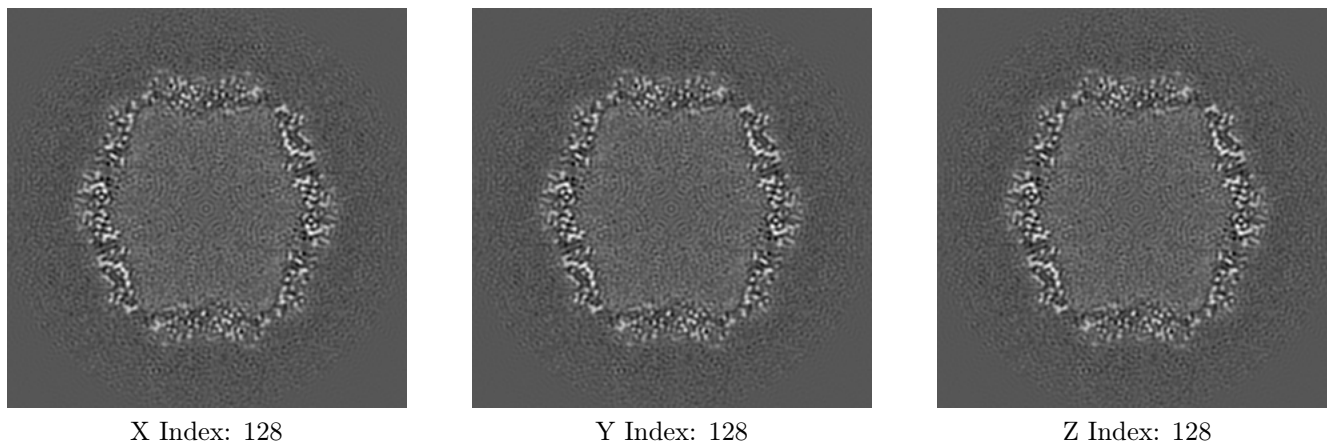
6.1.1 Primary map



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

6.2 Central slices [i](#)

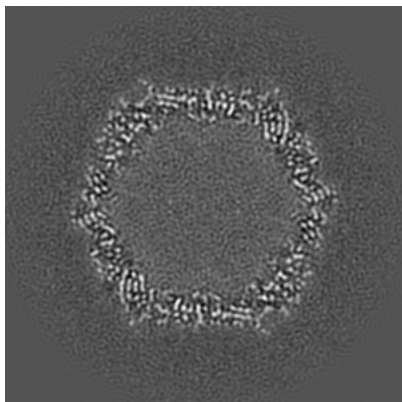
6.2.1 Primary map



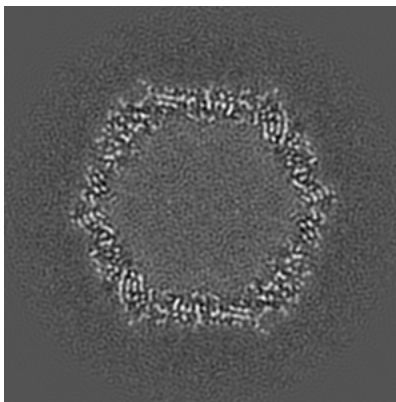
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

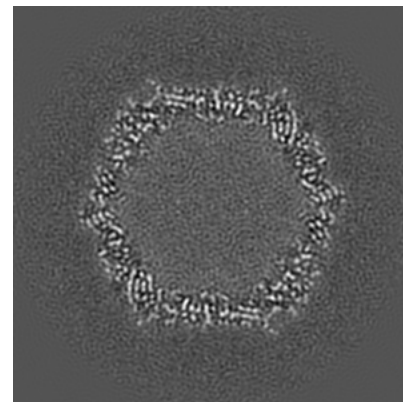
6.3.1 Primary map



X Index: 108



Y Index: 108

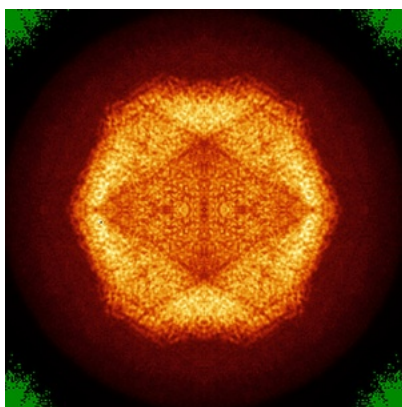


Z Index: 108

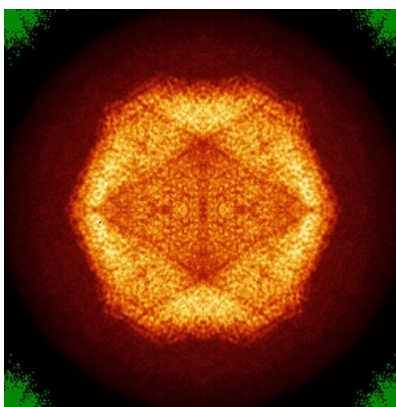
The images above show the largest variance slices of the map in three orthogonal directions.

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

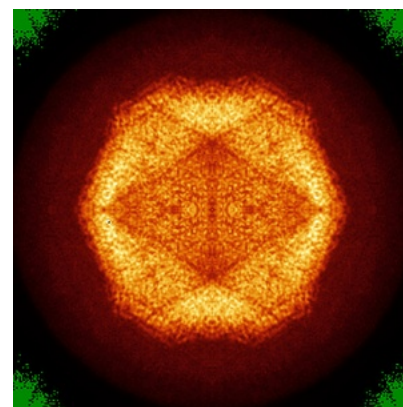
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

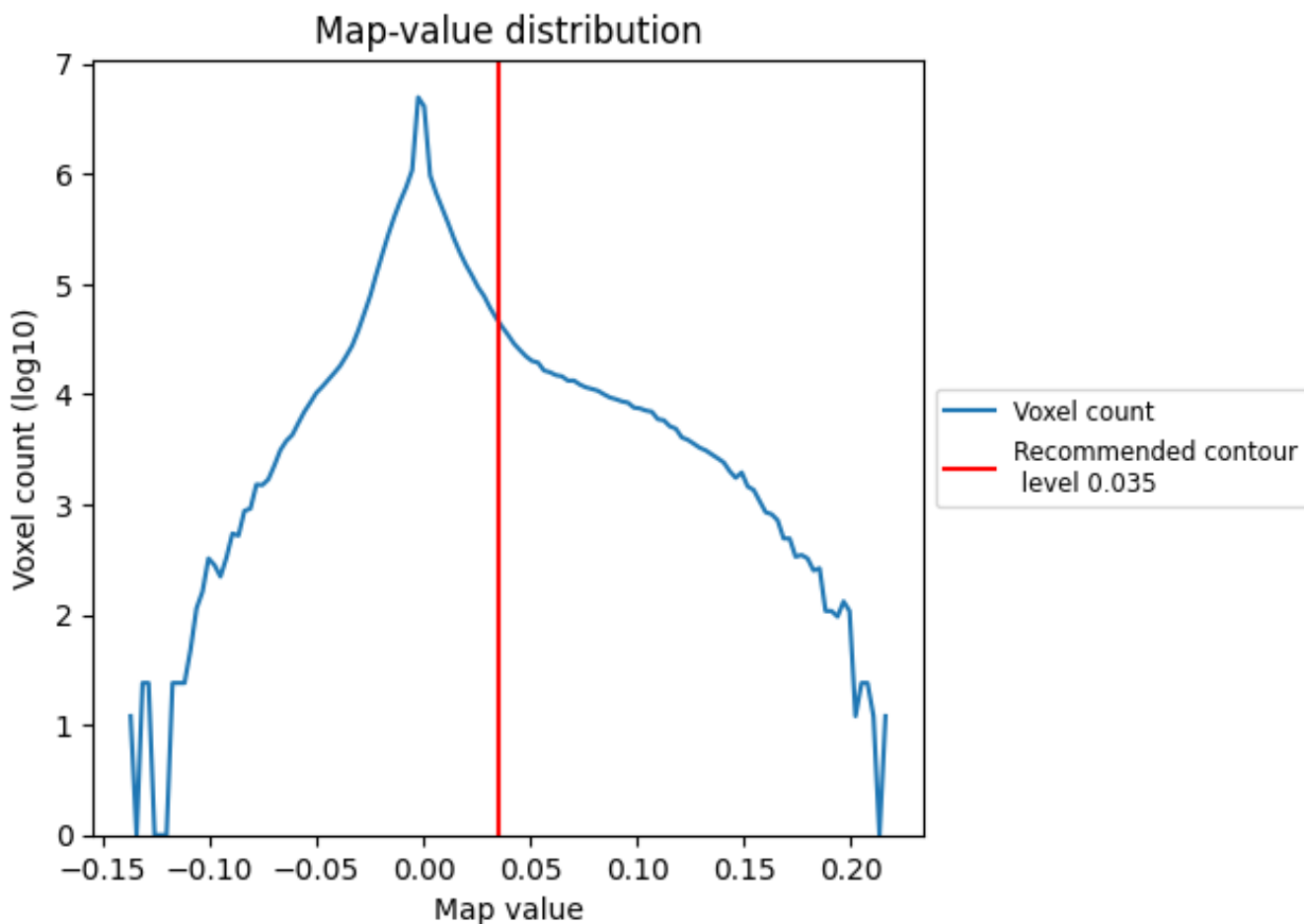
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

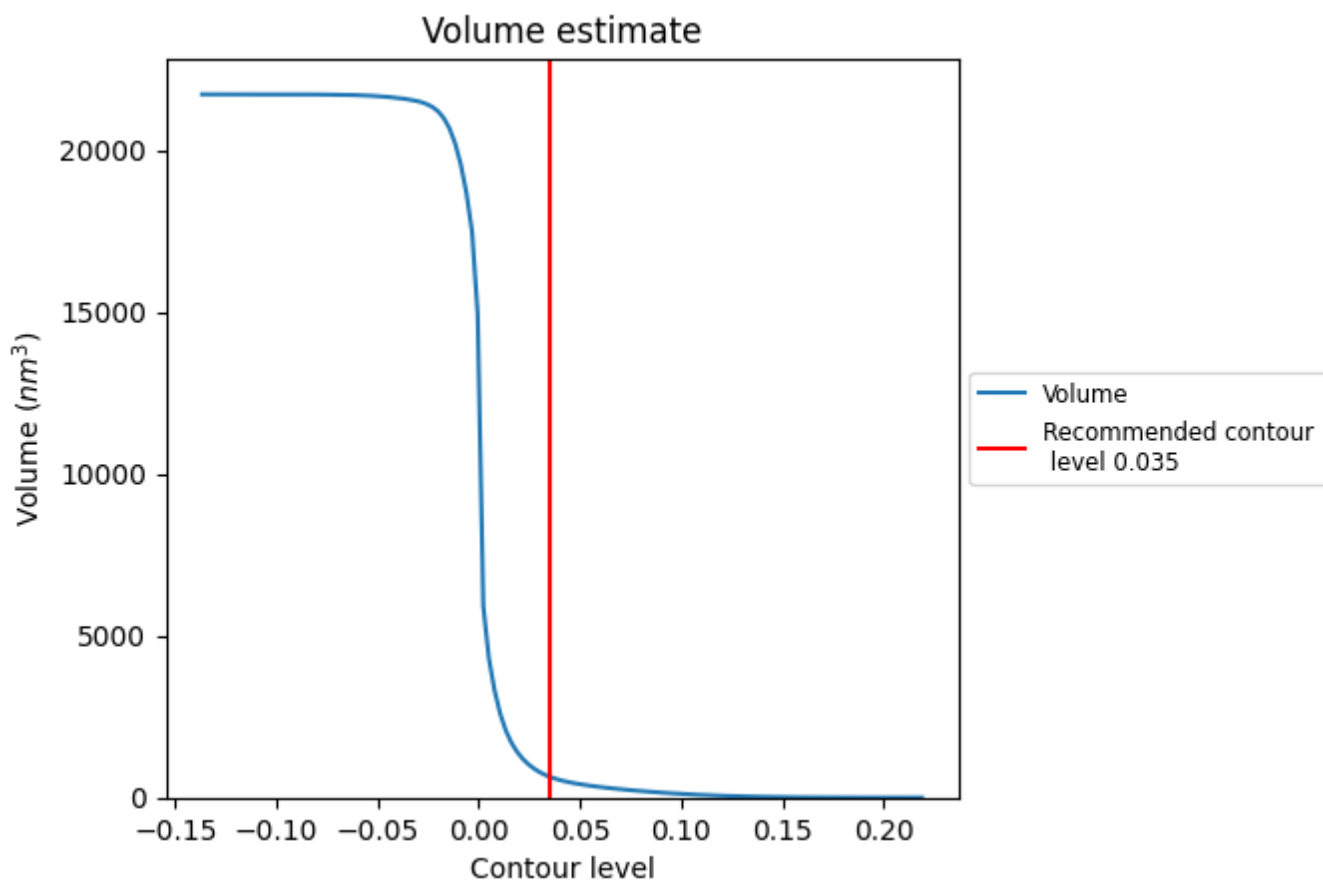
This section contains the results of statistical analysis of the map.

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.

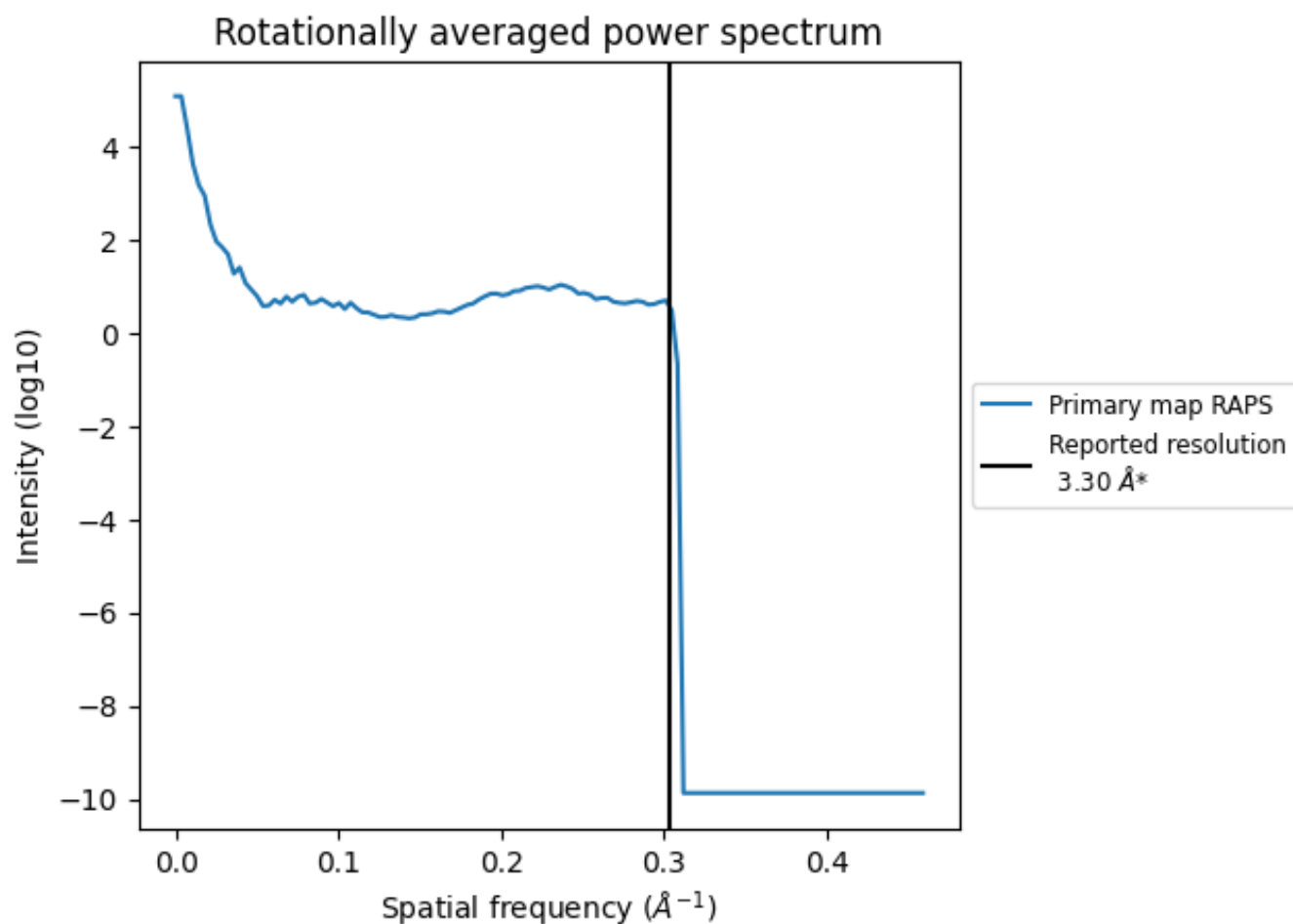
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 643 nm³; this corresponds to an approximate mass of 581 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 0.303 Å⁻¹

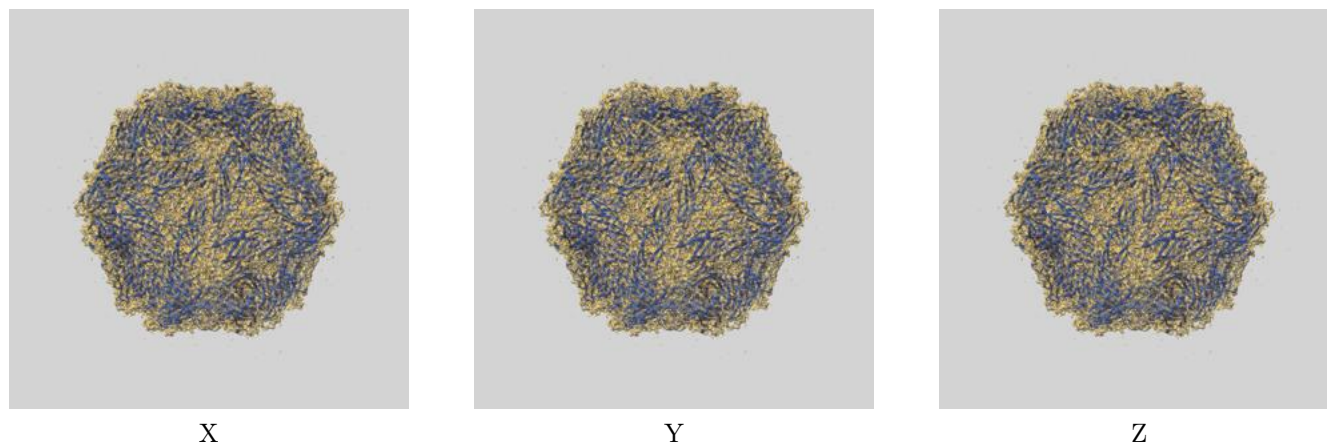
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

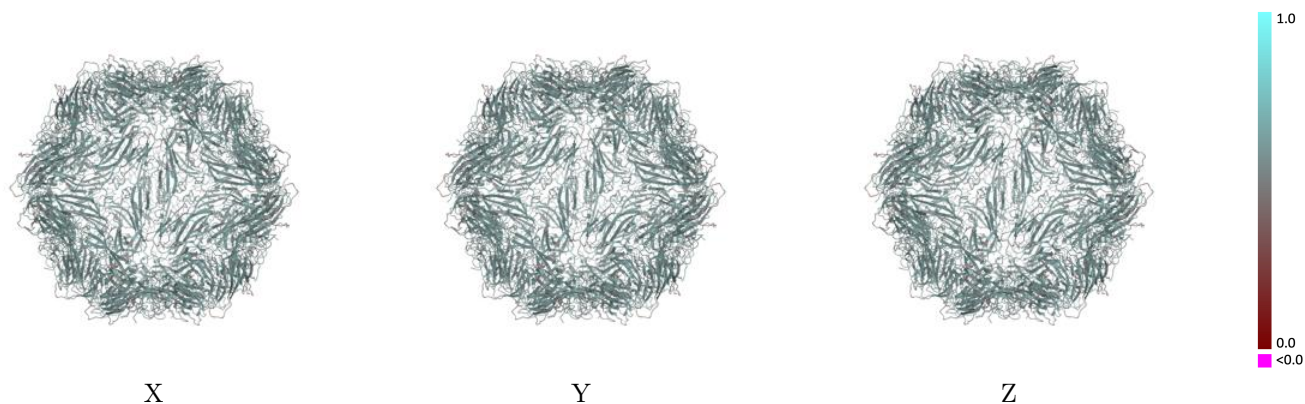
This section contains information regarding the fit between EMDB map EMD-8939 and PDB model 6DZU. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



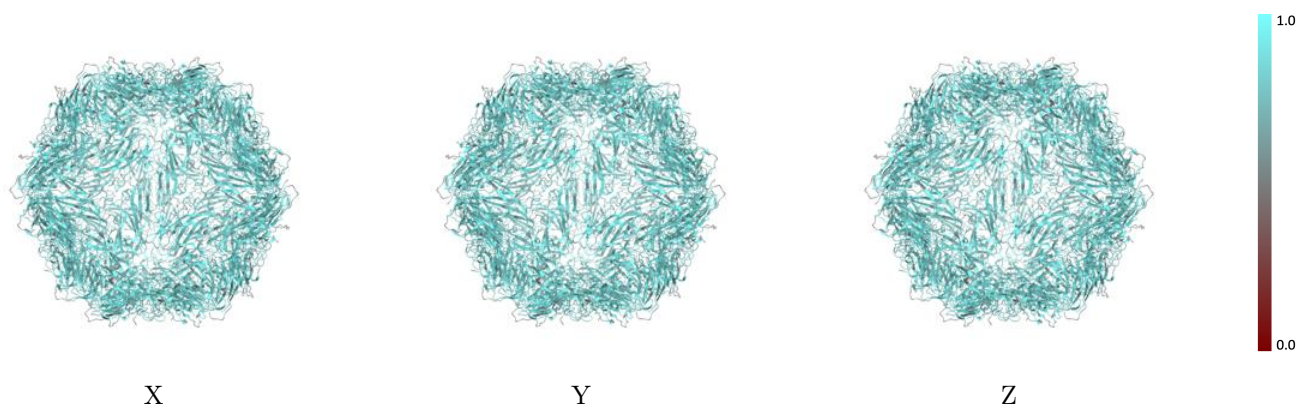
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



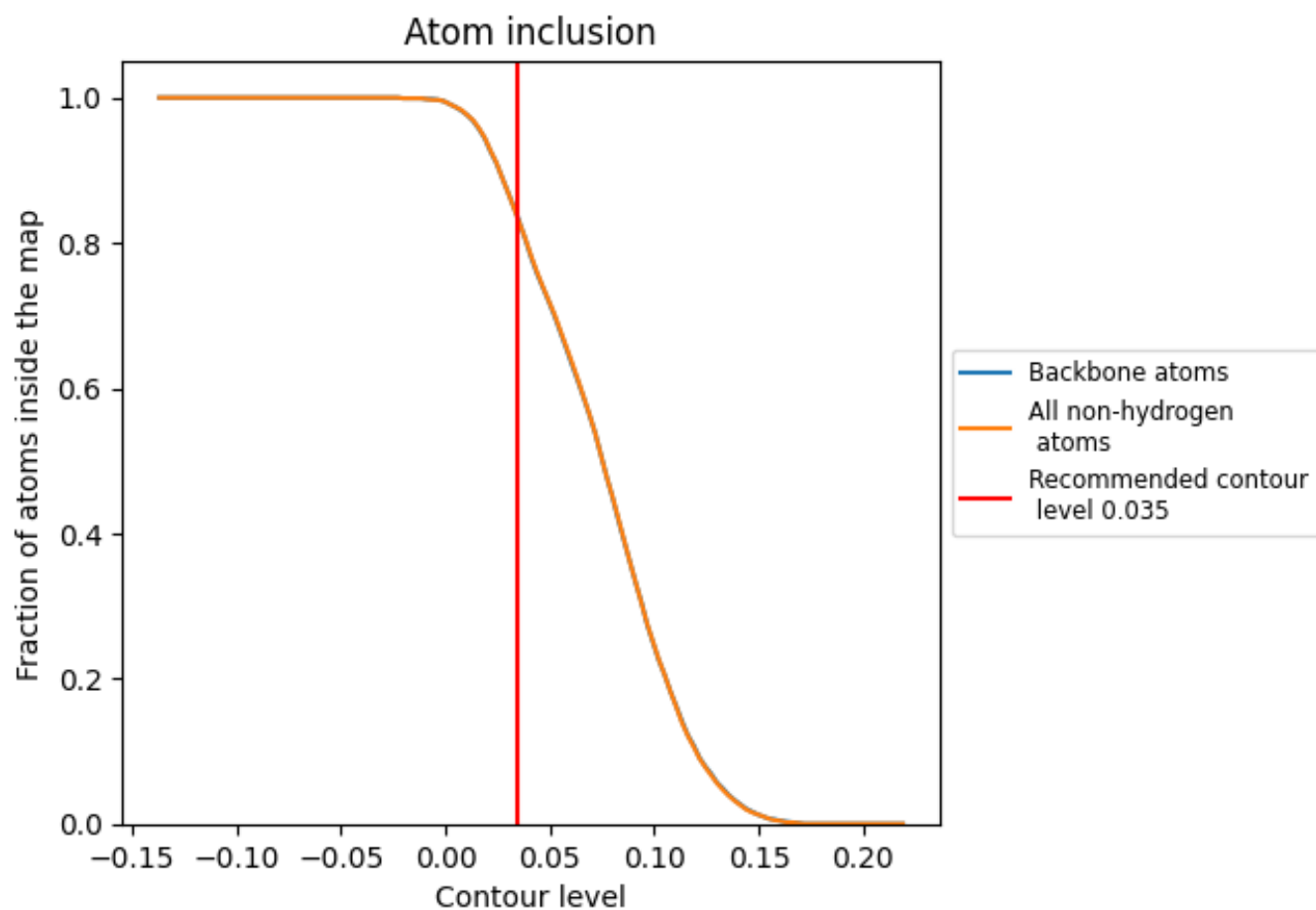
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.5610
A1	 0.8330	 0.5600
A2	 0.8370	 0.5620
A3	 0.8340	 0.5600
A4	 0.8390	 0.5590
A5	 0.8340	 0.5620
A6	 0.8280	 0.5600
A7	 0.8360	 0.5620
A8	 0.8370	 0.5590
A9	 0.8370	 0.5600
AA	 0.8340	 0.5610
AB	 0.8300	 0.5590
AC	 0.8370	 0.5610
AD	 0.8360	 0.5600
AE	 0.8360	 0.5580
AF	 0.8350	 0.5600
AG	 0.8340	 0.5610
AH	 0.8380	 0.5610
AI	 0.8380	 0.5590
AJ	 0.8360	 0.5600
AK	 0.8340	 0.5610
AL	 0.8300	 0.5580
AM	 0.8360	 0.5610
AN	 0.8340	 0.5590
AO	 0.8380	 0.5600
AP	 0.8340	 0.5610
AQ	 0.8300	 0.5600
AR	 0.8370	 0.5620
AS	 0.8360	 0.5590
AT	 0.8350	 0.5610
AU	 0.8360	 0.5600
AV	 0.8300	 0.5610
AW	 0.8350	 0.5630
AX	 0.8340	 0.5620
AY	 0.8370	 0.5630



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Chain	Atom inclusion	Q-score
AZ	 0.8340	 0.5610
Aa	 0.8300	 0.5590
Ab	 0.8370	 0.5610
Ac	 0.8350	 0.5600
Ad	 0.8380	 0.5600
Ae	 0.8340	 0.5610
Af	 0.8360	 0.5620
Ag	 0.8380	 0.5600
Ah	 0.8340	 0.5600
Ai	 0.8360	 0.5610
Aj	 0.8330	 0.5610
Ak	 0.8320	 0.5610
Al	 0.8370	 0.5620
Am	 0.8340	 0.5610
An	 0.8380	 0.5600
Ao	 0.8340	 0.5610
Ap	 0.8270	 0.5610
Aq	 0.8360	 0.5610
Ar	 0.8360	 0.5610
As	 0.8380	 0.5620
At	 0.8340	 0.5620
Au	 0.8340	 0.5620
Av	 0.8370	 0.5620
Aw	 0.8360	 0.5640
Ax	 0.8380	 0.5600
Ay	 0.8340	 0.5600