



wwPDB EM Validation Summary Report ⓘ

Aug 8, 2026 – 10:11 AM EDT

PDB ID : 11MK / pdb_000011mk
EMDB ID : EMD-75836
Title : Bacteriophage Goslar Capsid Asymmetric Unit
Authors : Basu, D.; Gu, Y.; Corbett, K.D.
Deposited on : 2026-03-04
Resolution : 6.28 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:

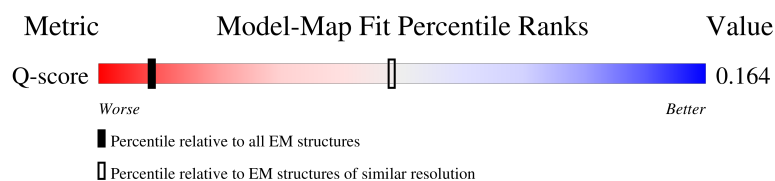
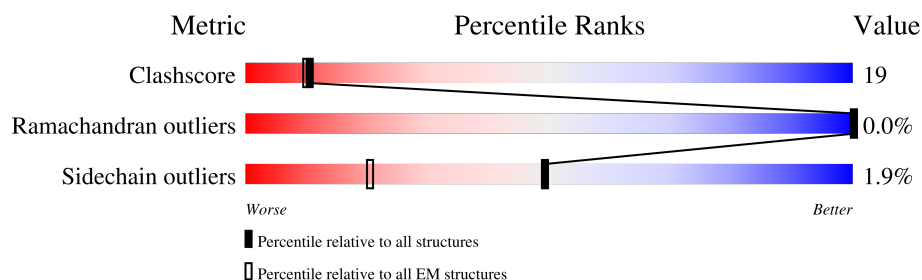
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 6.28 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.



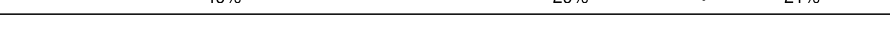
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	509 (5.80 - 6.78)

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	B	104	
2	A0	740	
2	A1	740	
2	A2	740	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	A3	740	
2	A4	740	
2	A5	740	
2	A6	740	
2	A7	740	
2	A8	740	
2	A9	740	
2	Ar	740	
2	As	740	
2	At	740	
2	Au	740	
2	Av	740	
2	Aw	740	
2	Ax	740	
2	Ay	740	
2	Az	740	
2	BA	740	
2	BB	740	
2	BC	740	
2	BD	740	
2	BE	740	
2	BF	740	
2	BG	740	
2	BH	740	
3	Ck	934	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	G	212	
5	O	146	
5	P	146	
6	Q	206	
7	R	176	
8	a	280	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 139724 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 Capsid Latch gp146.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	96	Total	C	N	O	S	0	0
			759	470	137	150	2		

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A0	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A1	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A2	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A3	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A4	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A5	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A6	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A7	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A8	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	A9	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	Ar	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	As	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	At	576	Total	C	N	O	S	0	0
			4593	2902	799	875	17		
2	Au	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Av	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	Aw	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	Ax	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	Ay	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	Az	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BA	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BB	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BC	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BD	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BE	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BF	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BG	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		
2	BH	583	Total	C	N	O	S	0	0
			4651	2939	809	886	17		

- Molecule 3 is a protein called PVC Protein gp65.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ck	662	Total	C	N	O	S	0	0
			5383	3432	930	1003	18		

- Molecule 4 is a protein called Capsid Decorator gp77.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	147	Total	C	N	O	S	0	0
			1198	763	212	216	7		

- Molecule 5 is a protein called PVC Protein gp66.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	O	124	Total	C	N	O	S	0	0
			971	624	166	176	5		
5	P	142	Total	C	N	O	S	0	0
			1079	690	185	199	5		

- Molecule 6 is a protein called PVC Protein gp42.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	206	Total	C	N	O	S	0	0
			1629	1043	286	295	5		

- Molecule 7 is a protein called PVC Protein gp59.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	172	Total	C	N	O	S	0	0
			1400	885	245	264	6		

- Molecule 8 is a protein called PVC Protein gp192.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	227	Total	C	N	O	S	0	0
			1786	1128	301	351	6		

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.

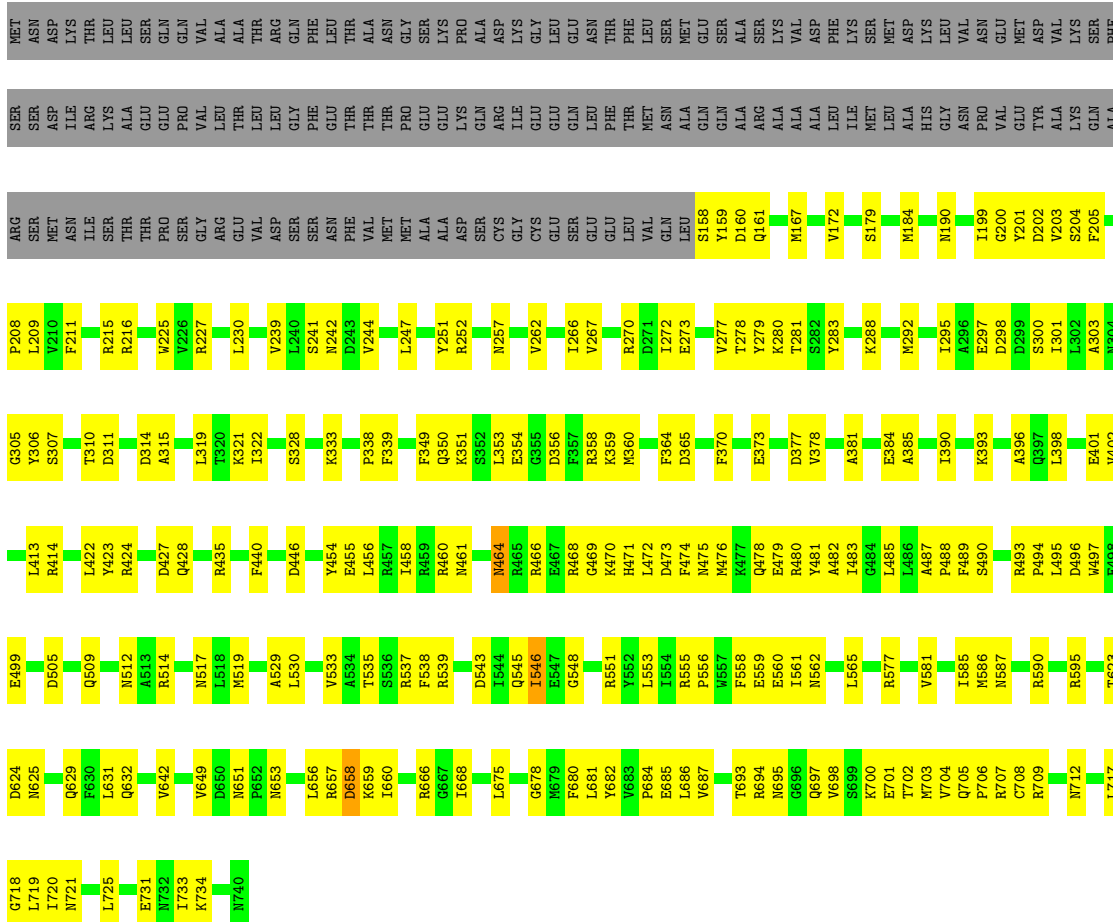
• Molecule 1: Capsid Latch gp146

Chain B: 

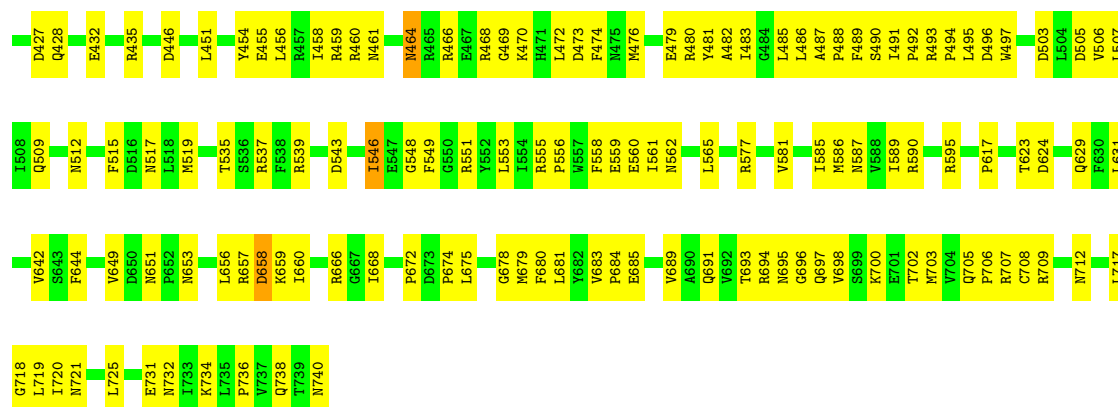


• Molecule 2: Major capsid protein

Chain A0: 

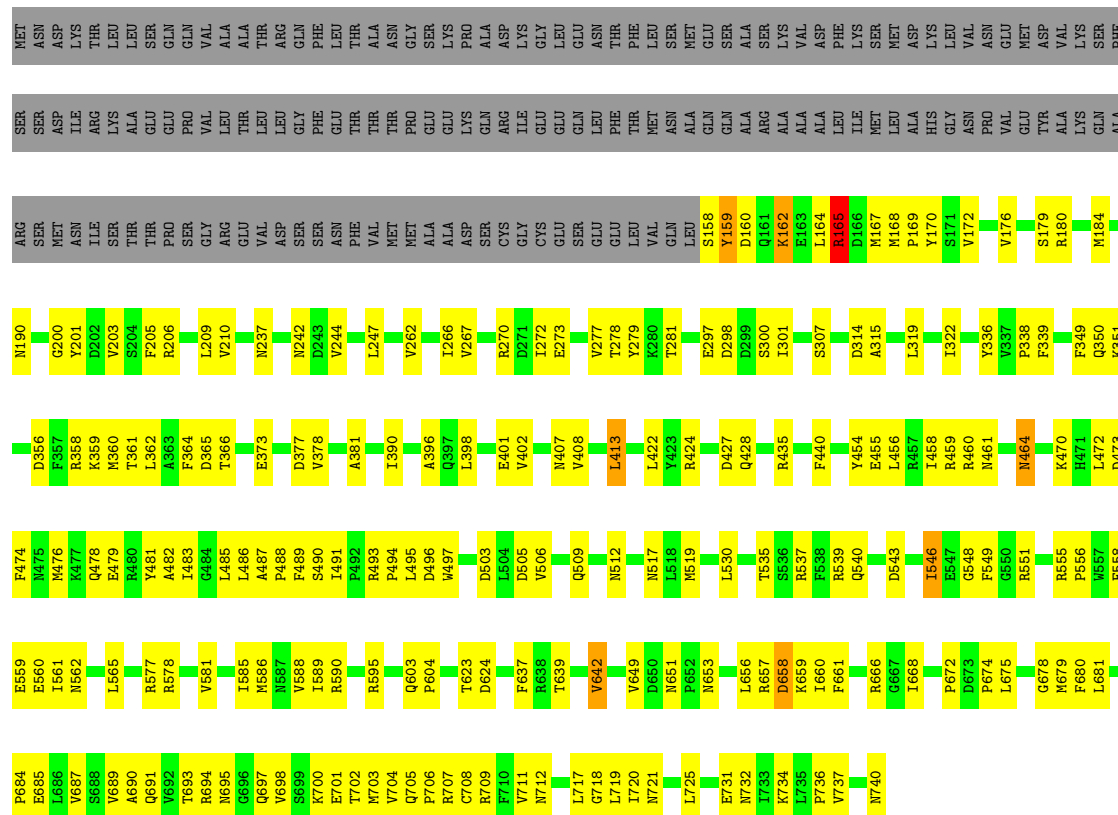


[illegible]



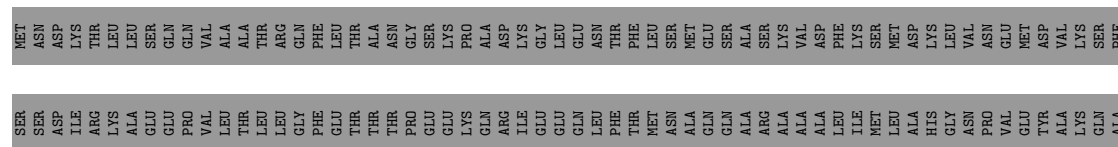
• Molecule 2: Major capsid protein

Chain A3: 51% 26% 21%

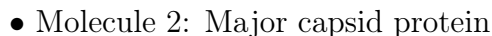


• Molecule 2: Major capsid protein

Chain A4: 49% 29% 21%

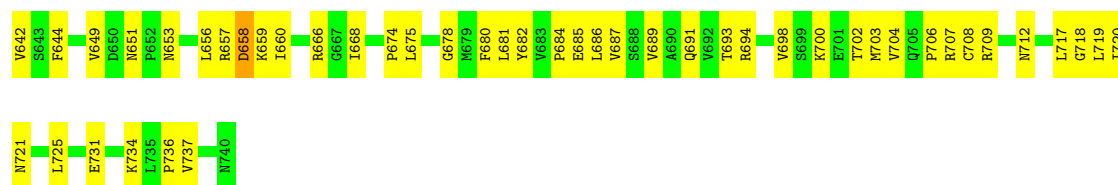


Response	Percentage
Yes	53%
No	25%
Don't know	21%



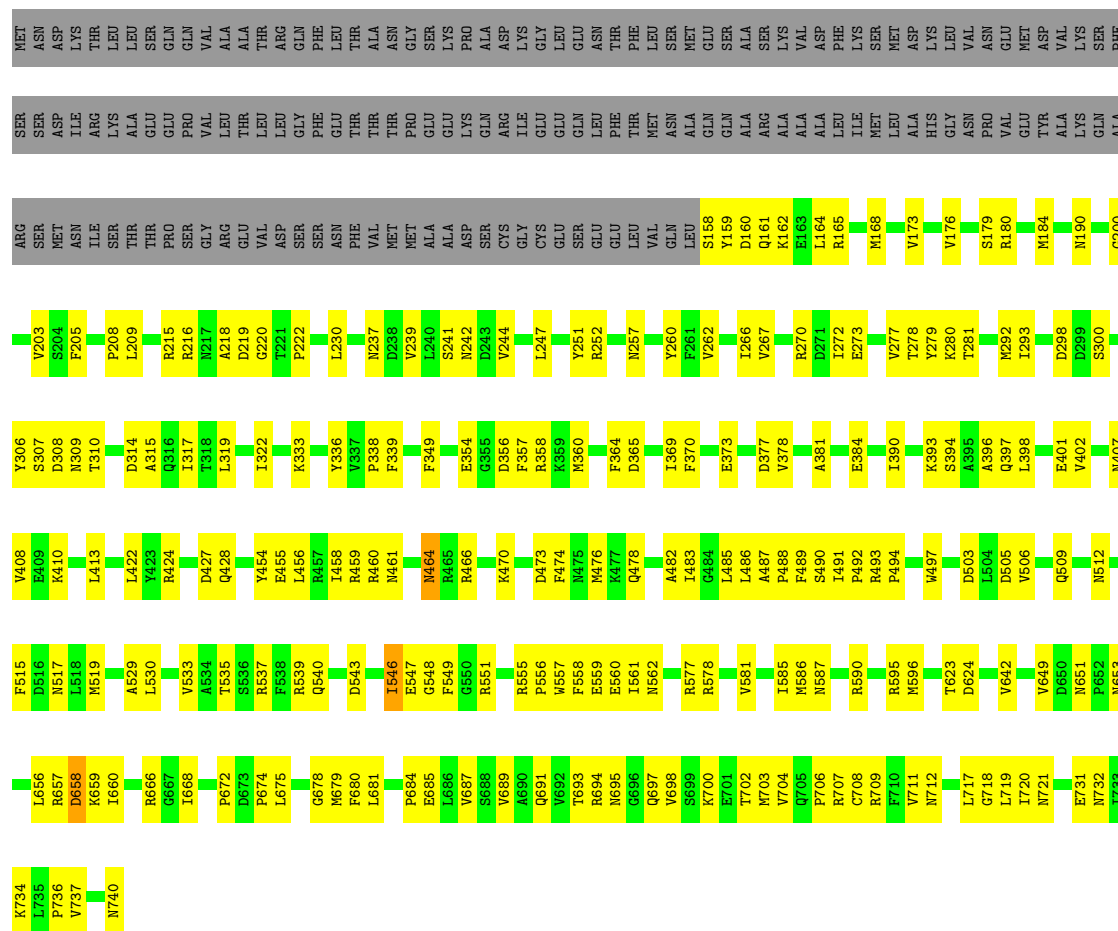
Response	Percentage
Yes	51%
No	28%
Don't know	21%





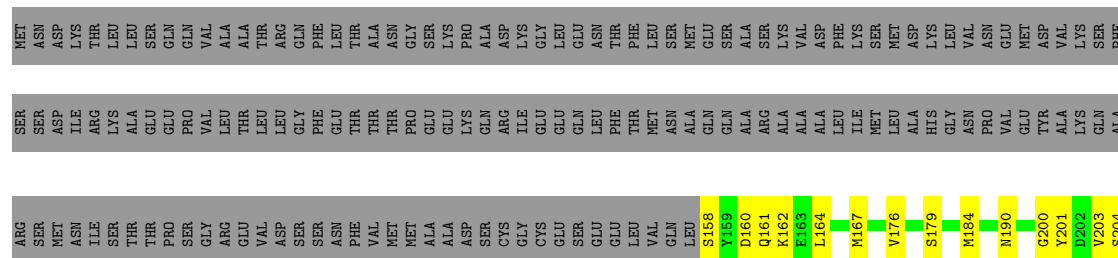
• Molecule 2: Major capsid protein

Chain A8:



• Molecule 2: Major capsid protein

Chain A9:

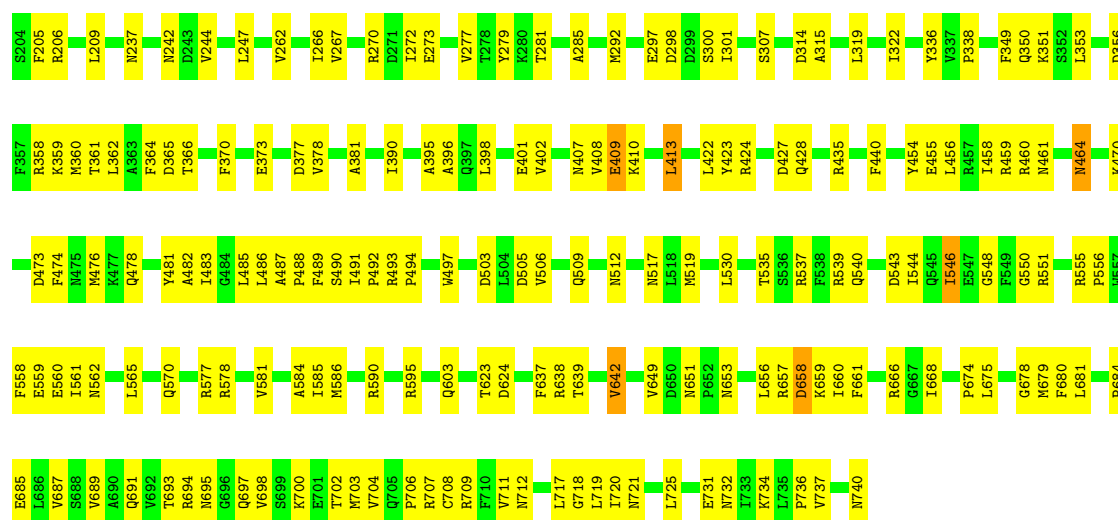


Response	Percentage
Yes	49%
No	29%
Don't know	21%

- Molecule 2: Major capsid protein

Frequency	Percentage
Daily	50%
Weekly	25%
Monthly	2%
Never	22%





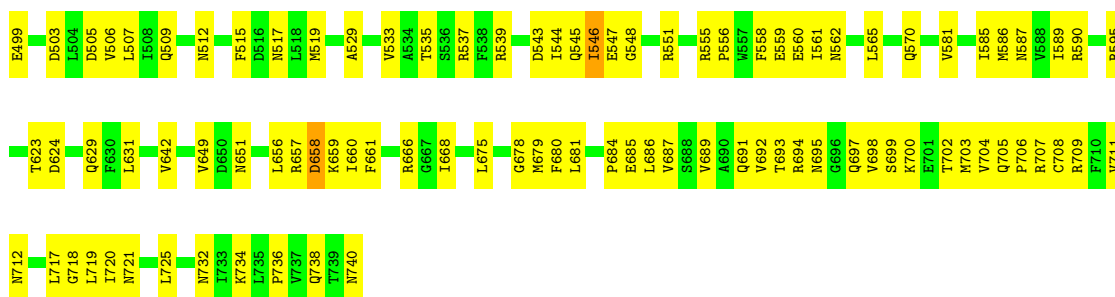
- Molecule 2: Major capsid protein



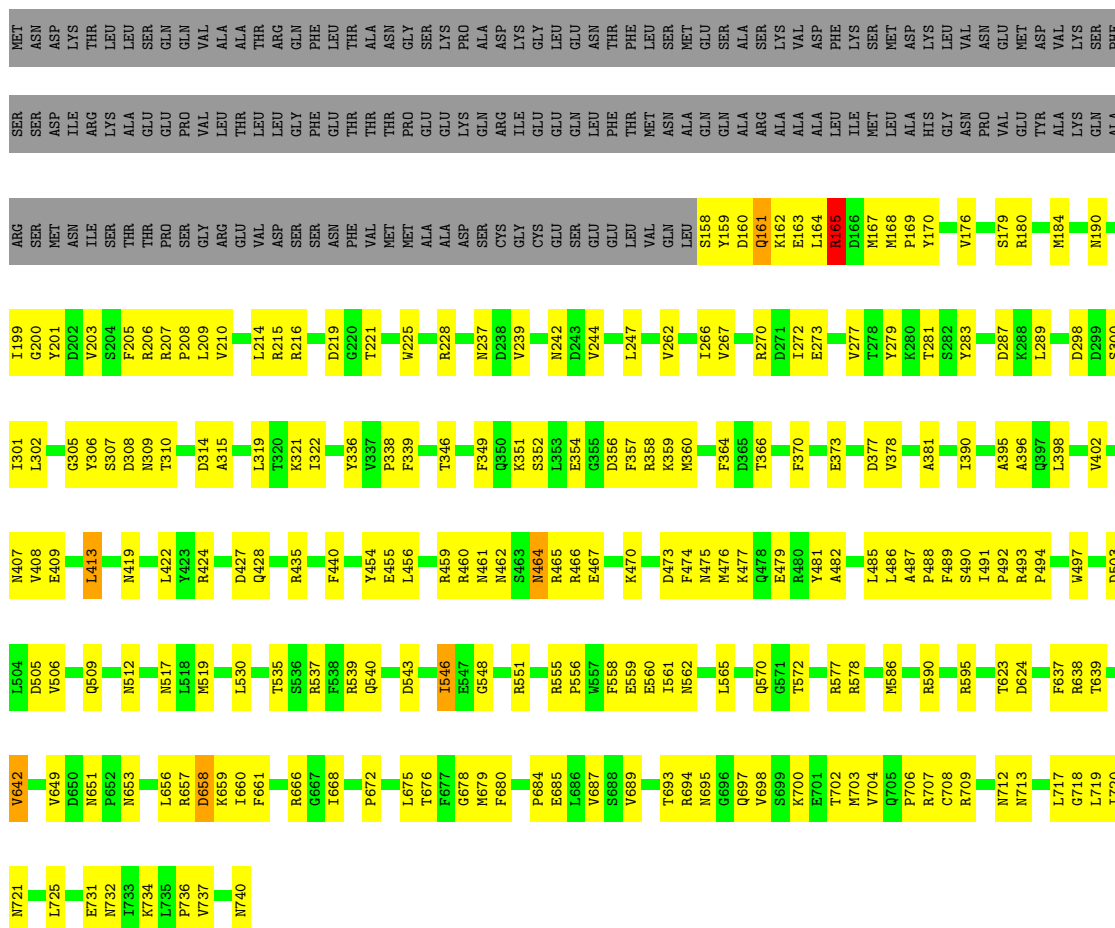
- Molecule 2: Major capsid protein



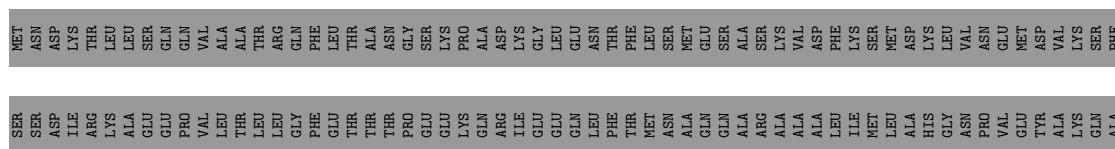


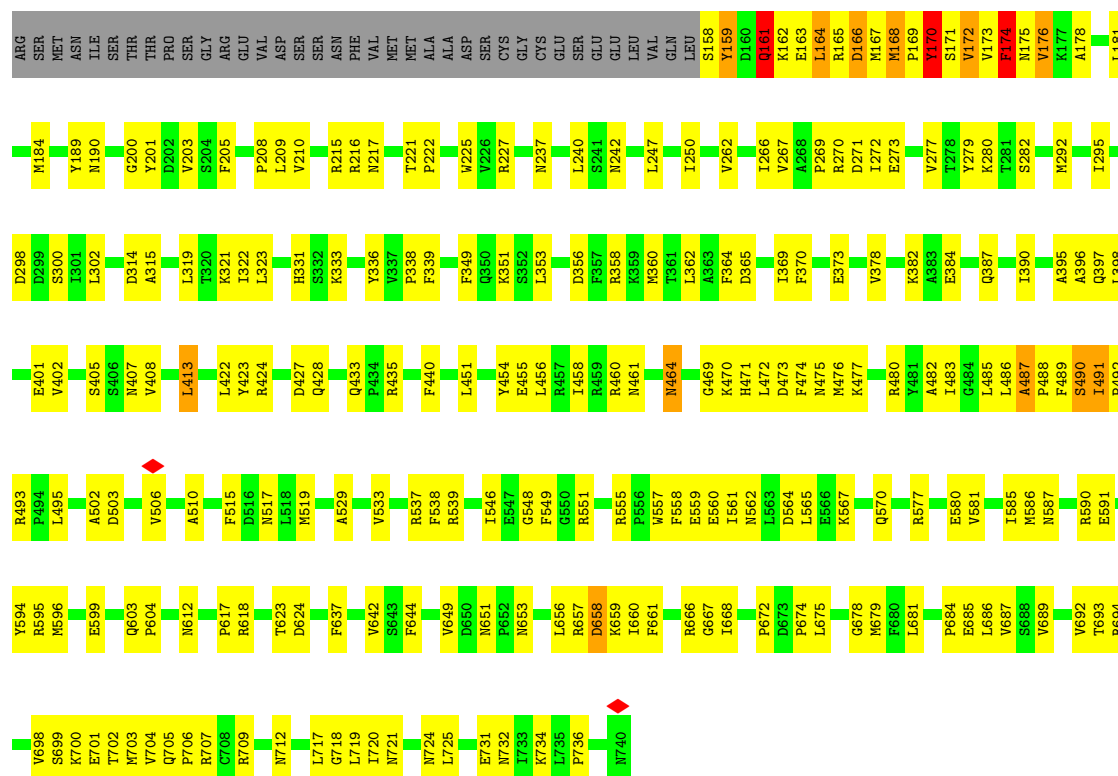


- Molecule 2: Major capsid protein



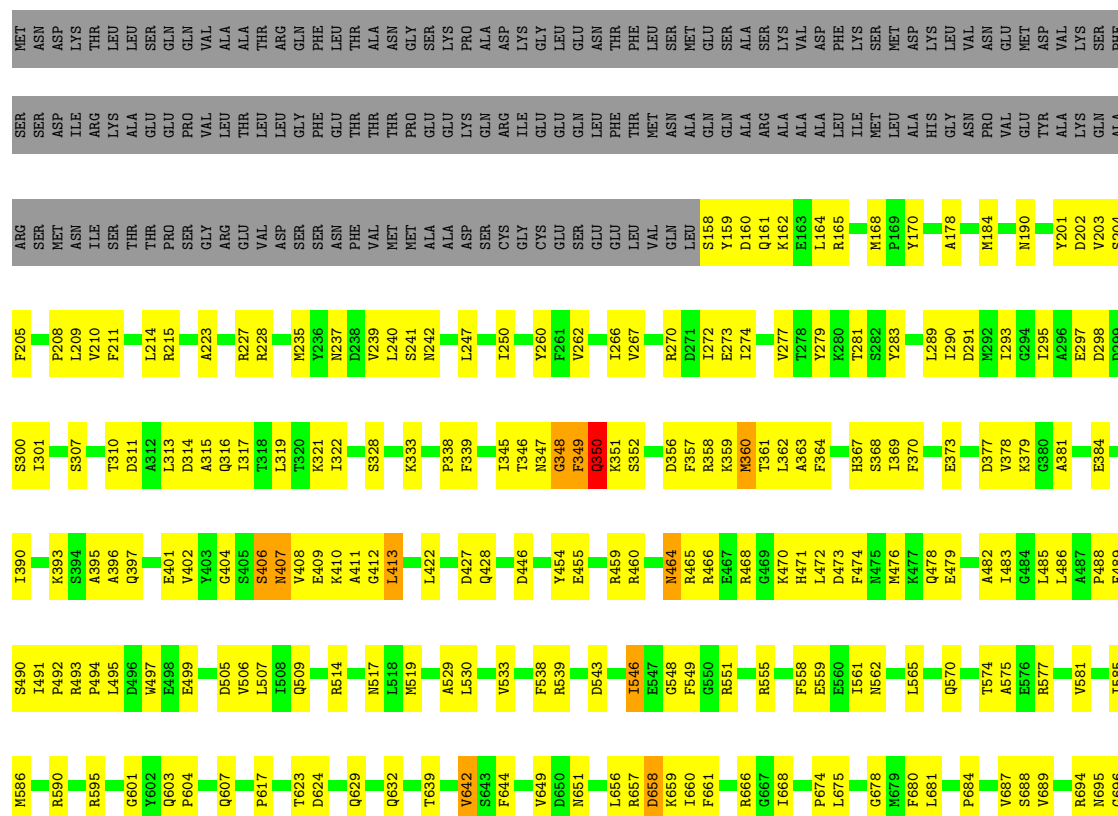
- Molecule 2: Major capsid protein





• Molecule 2: Major capsid protein

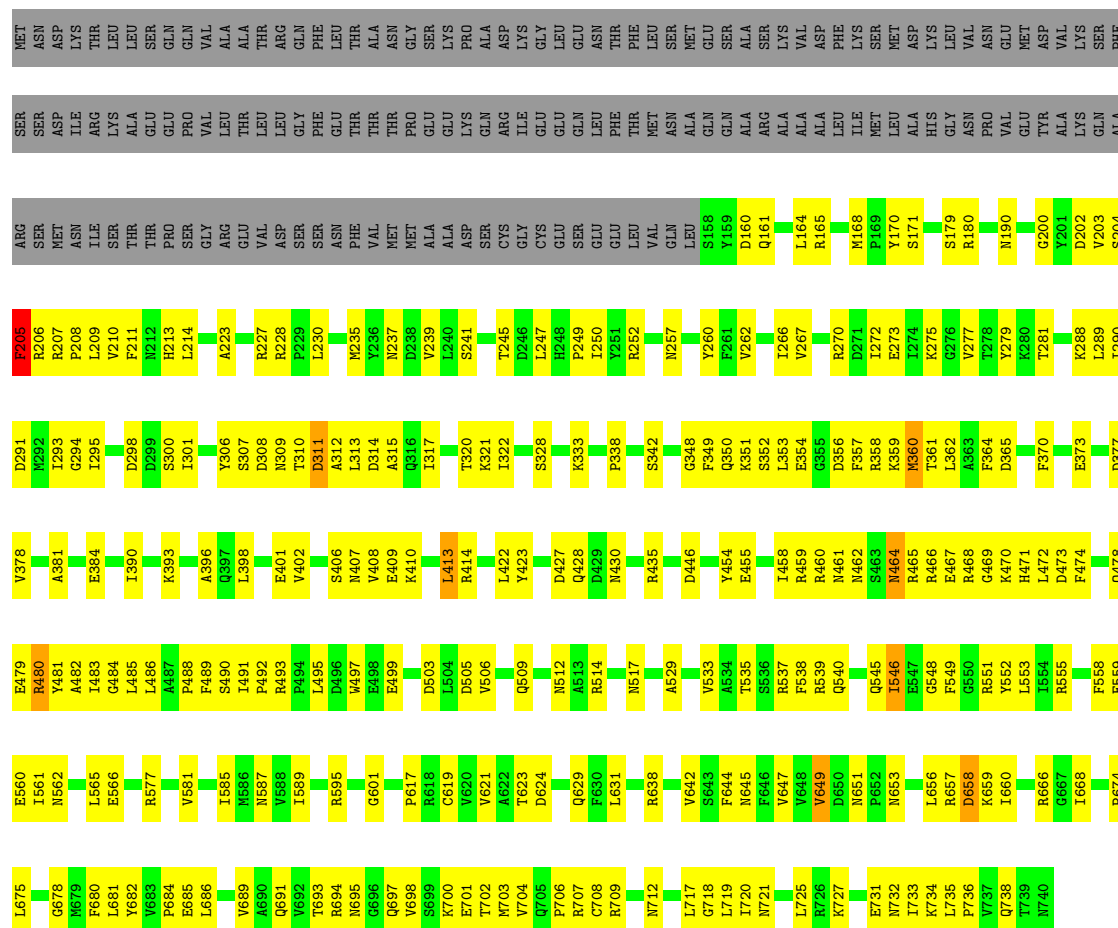
Chain BB:





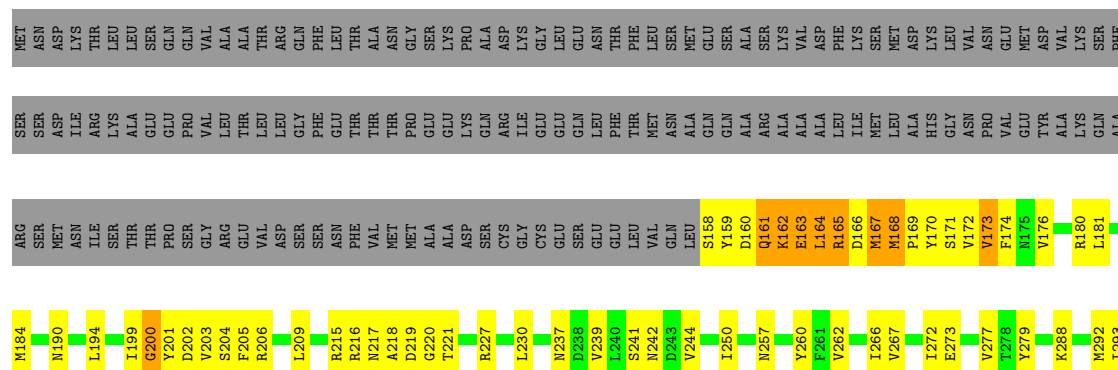
• Molecule 2: Major capsid protein

Chain BC: 45% 33% 21%

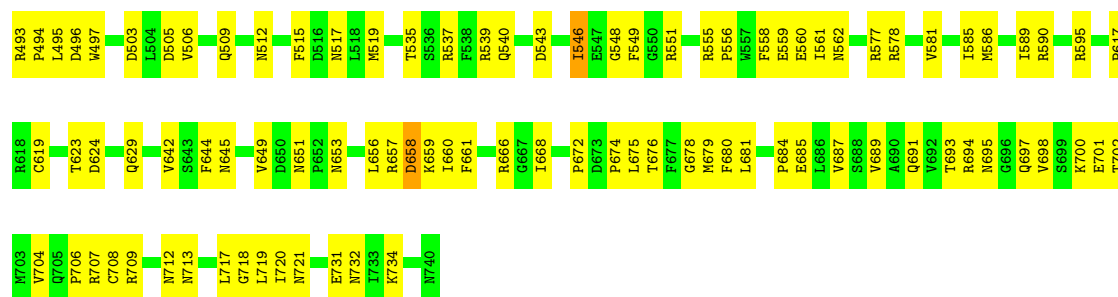


• Molecule 2: Major capsid protein

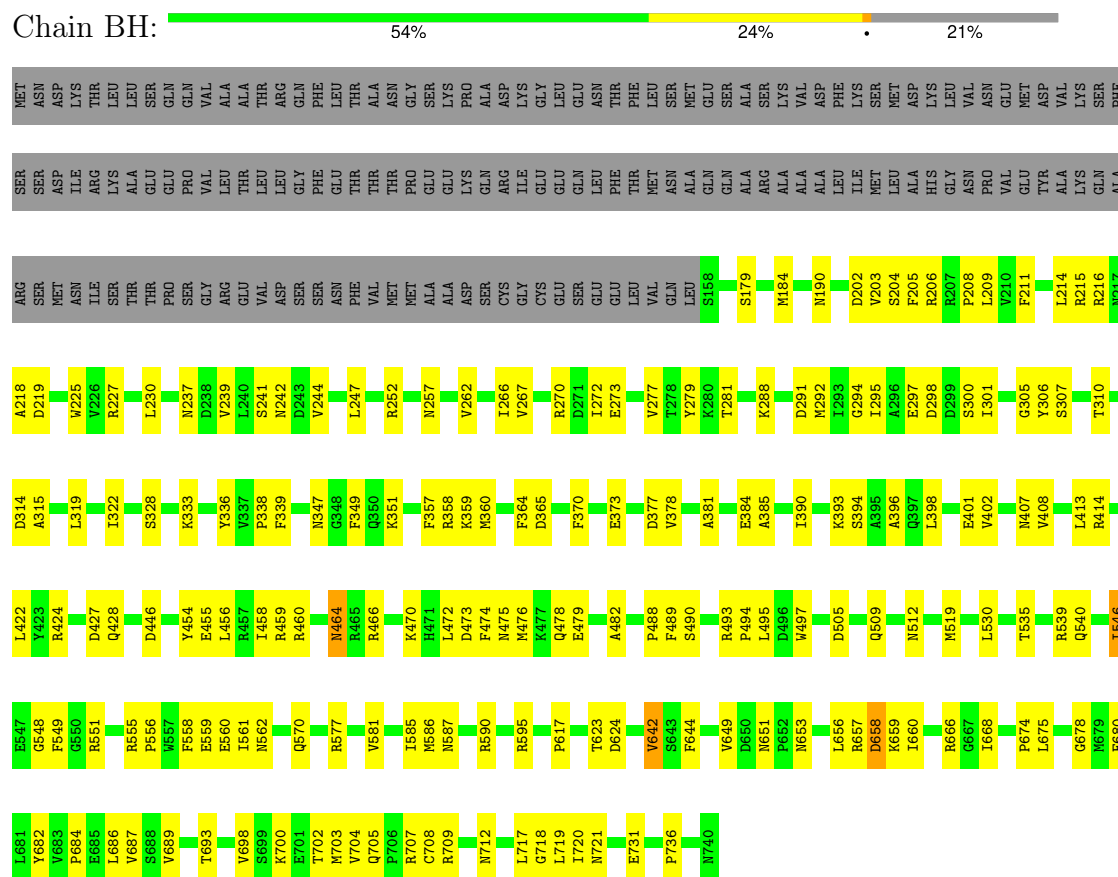
Chain BD: 46% 31% 21%



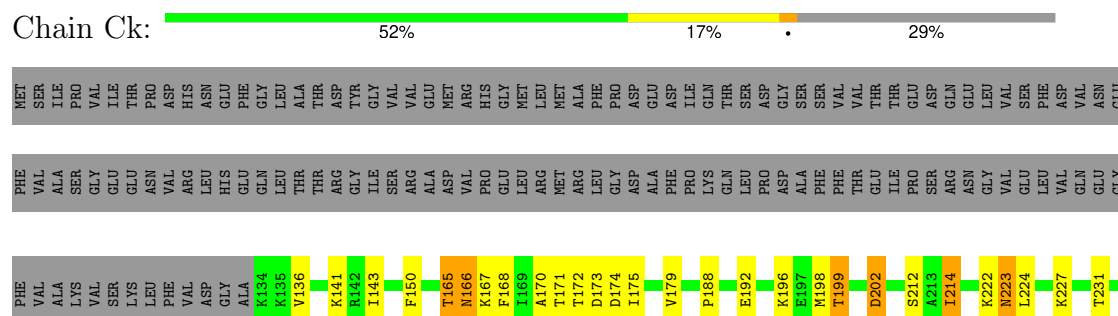


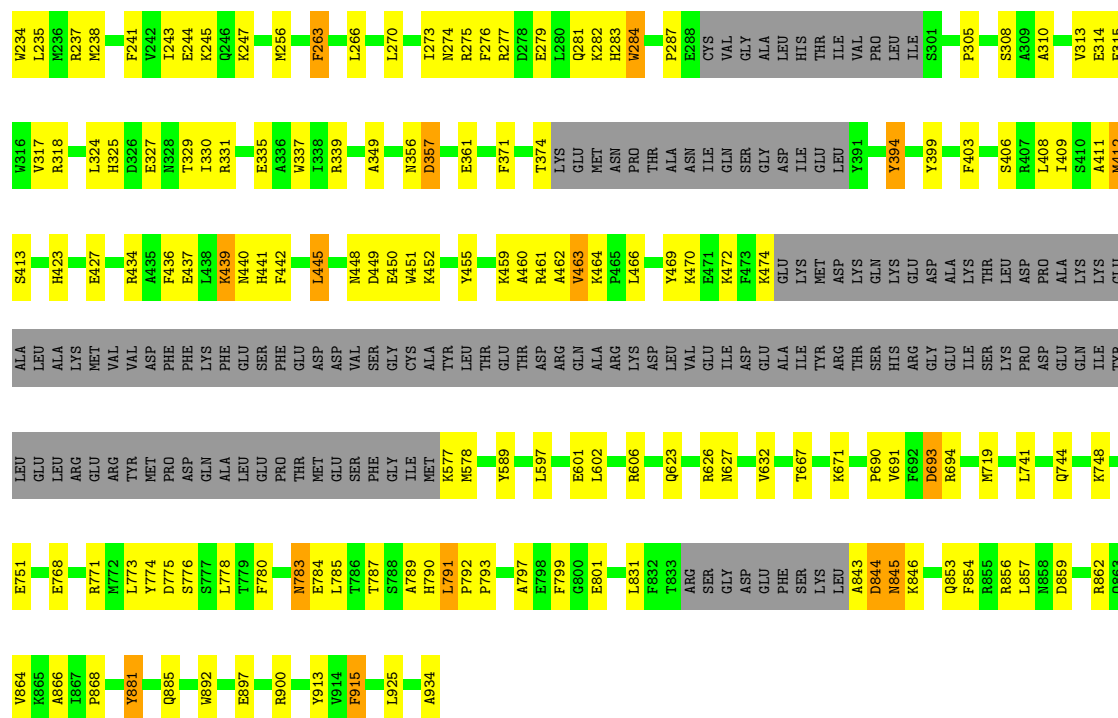


• Molecule 2: Major capsid protein



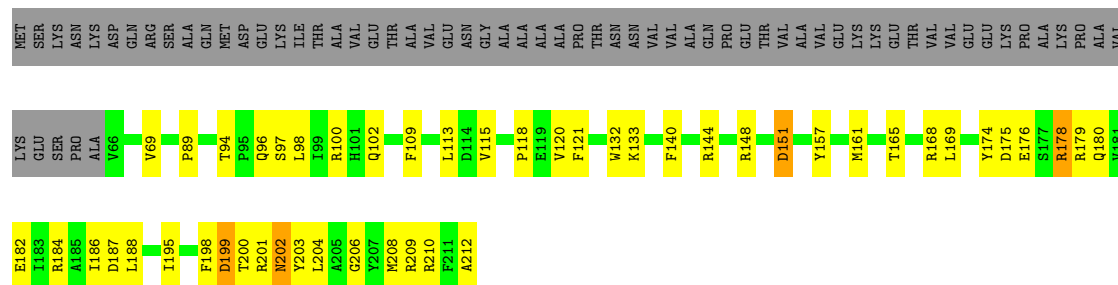
• Molecule 3: PVC Protein gp65





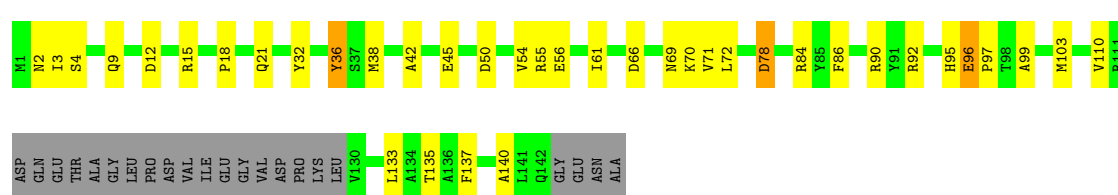
• Molecule 4: Capsid Decorator gp77

Chain G:



• Molecule 5: PVC Protein gp66

Chain O:



• Molecule 5: PVC Protein gp66

Chain P:

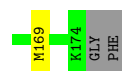
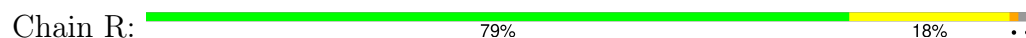




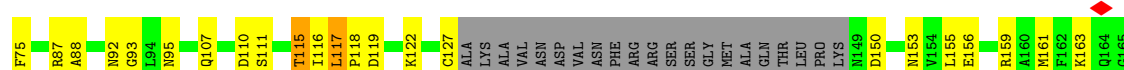
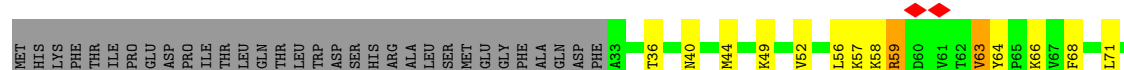
• Molecule 6: PVC Protein gp42



• Molecule 7: PVC Protein gp59



• Molecule 8: PVC Protein gp192



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	5214	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.748	Depositor
Minimum map value	-0.531	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	2380.0, 2380.0, 2380.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.975, 2.975, 2.975	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	B	0.21	0/766	0.41	0/1027
2	A0	0.21	0/4735	0.45	0/6411
2	A1	0.25	0/4735	0.55	2/6411 (0.0%)
2	A2	0.22	0/4735	0.50	0/6411
2	A3	0.23	0/4735	0.56	4/6411 (0.1%)
2	A4	0.24	0/4735	0.52	2/6411 (0.0%)
2	A5	0.23	0/4735	0.60	5/6411 (0.1%)
2	A6	0.21	0/4735	0.46	0/6411
2	A7	0.19	0/4735	0.43	0/6411
2	A8	0.20	0/4735	0.44	0/6411
2	A9	0.23	0/4735	0.54	1/6411 (0.0%)
2	Ar	0.20	0/4735	0.44	0/6411
2	As	0.22	0/4735	0.46	0/6411
2	At	0.18	0/4676	0.43	0/6330
2	Au	0.20	0/4735	0.42	0/6411
2	Av	0.22	0/4735	0.49	3/6411 (0.0%)
2	Aw	0.22	0/4735	0.47	1/6411 (0.0%)
2	Ax	0.22	0/4735	0.49	4/6411 (0.1%)
2	Ay	0.26	0/4735	0.57	6/6411 (0.1%)
2	Az	0.29	1/4735 (0.0%)	0.59	6/6411 (0.1%)
2	BA	0.34	1/4735 (0.0%)	0.72	13/6411 (0.2%)
2	BB	0.30	0/4735	0.71	17/6411 (0.3%)
2	BC	0.29	0/4735	0.67	10/6411 (0.2%)
2	BD	0.31	0/4735	0.75	21/6411 (0.3%)
2	BE	0.32	0/4735	0.77	18/6411 (0.3%)
2	BF	0.36	0/4735	0.78	14/6411 (0.2%)
2	BG	0.18	0/4735	0.40	0/6411
2	BH	0.18	0/4735	0.40	0/6411
3	Ck	0.15	0/5481	0.31	0/7397
4	G	0.14	0/1224	0.33	0/1656
5	O	0.18	0/988	0.35	0/1339
5	P	0.16	0/1098	0.35	0/1492
6	Q	0.19	0/1669	0.41	0/2277
7	R	0.18	0/1433	0.36	0/1947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	a	0.19	0/1811	0.49	0/2454
All	All	0.24	2/142256 (0.0%)	0.54	127/192605 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A3	0	1
2	BA	0	3
2	BB	0	2
2	BC	0	1
8	a	0	3
All	All	0	10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Az	161	GLN	CA-C	6.24	1.62	1.52
2	BA	161	GLN	CB-CG	-5.54	1.35	1.52

The worst 5 of 127 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A5	165	ARG	CA-CB-CG	16.43	146.96	114.10
2	A5	165	ARG	CB-CG-CD	15.40	146.72	111.30
2	BD	163	GLU	CA-CB-CG	13.59	141.28	114.10
2	Az	165	ARG	CB-CG-CD	13.46	142.26	111.30
2	A3	165	ARG	CB-CG-CD	13.39	142.10	111.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A3	162	LYS	Peptide
2	BA	161	GLN	Mainchain
2	BA	170	TYR	Peptide
2	BA	174	PHE	Sidechain
2	BB	350	GLN	Peptide

5.2 Too-close contacts ⓘ

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	B	759	0	770	13	0
2	A0	4651	0	4633	223	0
2	A1	4651	0	4633	269	0
2	A2	4651	0	4633	224	0
2	A3	4651	0	4633	221	0
2	A4	4651	0	4633	219	0
2	A5	4651	0	4633	246	0
2	A6	4651	0	4633	179	0
2	A7	4651	0	4633	176	0
2	A8	4651	0	4633	207	0
2	A9	4651	0	4633	239	0
2	Ar	4651	0	4633	208	0
2	As	4651	0	4633	232	0
2	At	4593	0	4562	150	0
2	Au	4651	0	4633	172	0
2	Av	4651	0	4633	180	0
2	Aw	4651	0	4633	200	0
2	Ax	4651	0	4633	192	0
2	Ay	4651	0	4633	266	0
2	Az	4651	0	4633	252	0
2	BA	4651	0	4633	364	0
2	BB	4651	0	4633	302	0
2	BC	4651	0	4633	319	0
2	BD	4651	0	4633	363	0
2	BE	4651	0	4633	406	0
2	BF	4651	0	4633	392	0
2	BG	4651	0	4633	145	0
2	BH	4651	0	4633	141	0
3	Ck	5383	0	5418	119	0
4	G	1198	0	1190	30	0
5	O	971	0	989	33	0
5	P	1079	0	1073	37	0
6	Q	1629	0	1559	38	0
7	R	1400	0	1347	18	0
8	a	1786	0	1795	64	0
All	All	139724	0	139161	5228	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 19.

The worst 5 of 5228 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:A1:350:GLN:O	2:A3:165:ARG:NE	1.79	1.12
2:BC:480:ARG:HG2	2:BD:167:MET:HB2	1.28	1.12
2:A4:350:GLN:O	2:Az:165:ARG:NE	1.86	1.08
2:BA:163:GLU:HB2	2:BE:317:ILE:HG22	1.37	1.04
2:A2:202:ASP:HB3	2:A3:169:PRO:HA	1.39	1.04

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	B	94/104 (90%)	93 (99%)	1 (1%)	0	100	100
2	A0	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	A1	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	A2	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	A3	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	A4	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	A5	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	A6	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	A7	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	A8	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
2	A9	581/740 (78%)	565 (97%)	16 (3%)	0	100	100
2	Ar	581/740 (78%)	567 (98%)	14 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	As	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
2	At	574/740 (78%)	532 (93%)	41 (7%)	1 (0%)	43	77
2	Au	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	Av	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
2	Aw	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	Ax	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	Ay	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	Az	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	BA	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	BB	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	BC	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	BD	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	BE	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
2	BF	581/740 (78%)	568 (98%)	13 (2%)	0	100	100
2	BG	581/740 (78%)	567 (98%)	14 (2%)	0	100	100
2	BH	581/740 (78%)	566 (97%)	15 (3%)	0	100	100
3	Ck	652/934 (70%)	630 (97%)	21 (3%)	1 (0%)	43	77
4	G	145/212 (68%)	142 (98%)	3 (2%)	0	100	100
5	O	120/146 (82%)	116 (97%)	4 (3%)	0	100	100
5	P	140/146 (96%)	137 (98%)	3 (2%)	0	100	100
6	Q	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
7	R	170/176 (97%)	160 (94%)	10 (6%)	0	100	100
8	a	223/280 (80%)	219 (98%)	4 (2%)	0	100	100
All	All	17428/22184 (79%)	16949 (97%)	477 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	At	642	VAL
3	Ck	327	GLU

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	B	83/91 (91%)	83 (100%)	0	100	100
2	A0	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A1	509/644 (79%)	501 (98%)	8 (2%)	55	70
2	A2	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A3	509/644 (79%)	499 (98%)	10 (2%)	48	66
2	A4	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A5	509/644 (79%)	501 (98%)	8 (2%)	55	70
2	A6	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A7	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A8	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	A9	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	Ar	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	As	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	At	500/644 (78%)	472 (94%)	28 (6%)	19	40
2	Au	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	Av	509/644 (79%)	501 (98%)	8 (2%)	55	70
2	Aw	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	Ax	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	Ay	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	Az	509/644 (79%)	501 (98%)	8 (2%)	55	70
2	BA	509/644 (79%)	500 (98%)	9 (2%)	51	68
2	BB	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	BC	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	BD	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	BE	509/644 (79%)	500 (98%)	9 (2%)	51	68
2	BF	509/644 (79%)	501 (98%)	8 (2%)	55	70

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	BG	509/644 (79%)	502 (99%)	7 (1%)	59	72
2	BH	509/644 (79%)	502 (99%)	7 (1%)	59	72
3	Ck	573/811 (71%)	536 (94%)	37 (6%)	15	37
4	G	125/177 (71%)	119 (95%)	6 (5%)	23	44
5	O	101/118 (86%)	98 (97%)	3 (3%)	36	57
5	P	108/118 (92%)	103 (95%)	5 (5%)	24	45
6	Q	168/186 (90%)	158 (94%)	10 (6%)	17	39
7	R	155/160 (97%)	150 (97%)	5 (3%)	34	55
8	a	195/241 (81%)	190 (97%)	5 (3%)	40	61
All	All	15242/19290 (79%)	14949 (98%)	293 (2%)	49	67

5 of 293 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Ck	276	PHE
7	R	104	VAL
3	Ck	394	TYR
4	G	115	VAL
2	At	413	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
2	BE	540	GLN
7	R	29	ASN
2	BF	213	HIS
2	BH	651	ASN
8	a	227	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

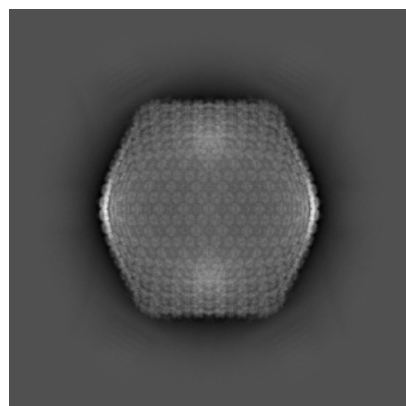
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75836. These allow visual inspection of the internal detail of the map and identification of artifacts.

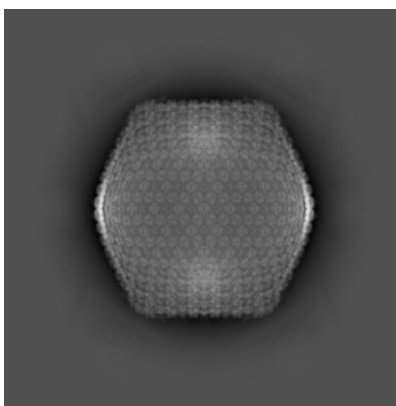
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

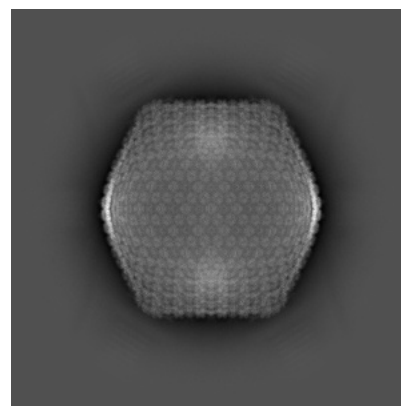
6.1.1 Primary map



X

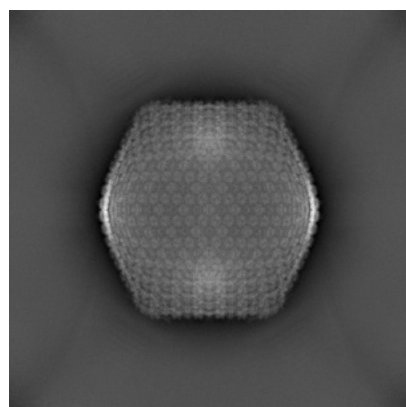


Y

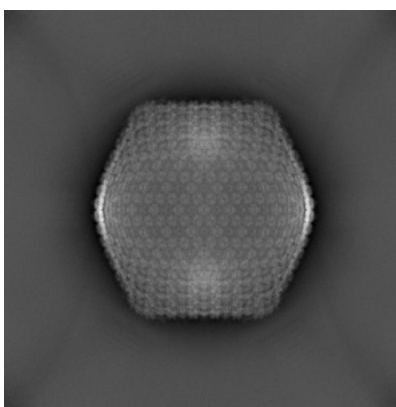


Z

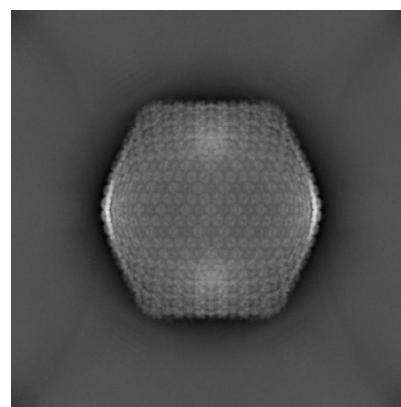
6.1.2 Raw map



X



Y

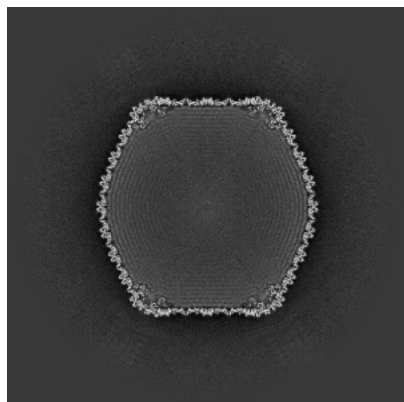


Z

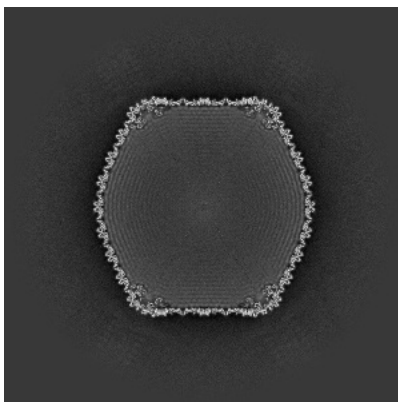
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

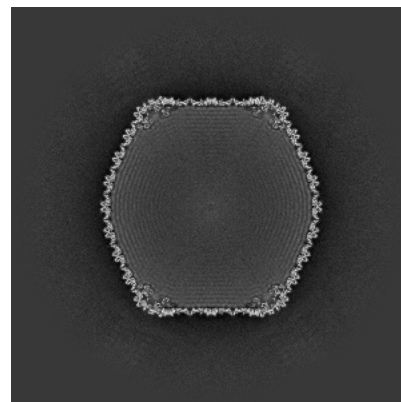
6.2.1 Primary map



X Index: 400

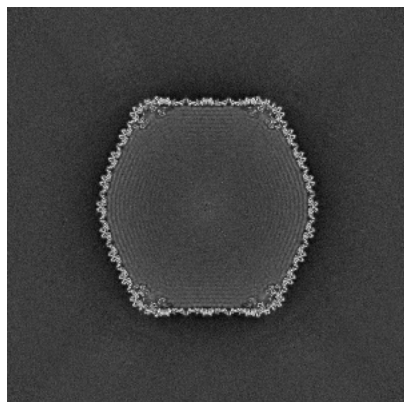


Y Index: 400

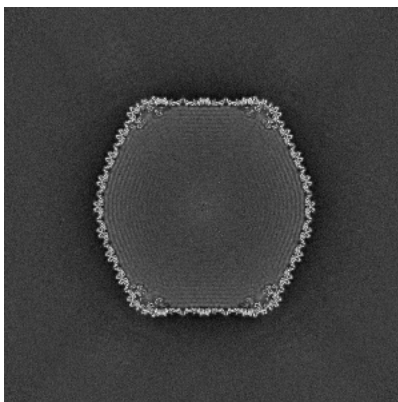


Z Index: 400

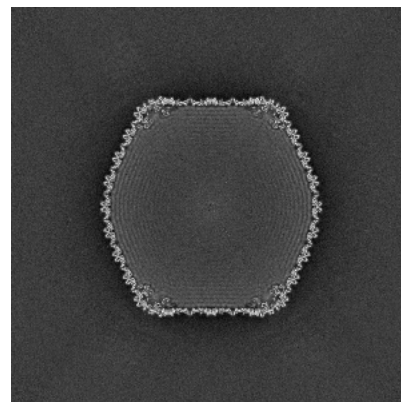
6.2.2 Raw map



X Index: 400



Y Index: 400

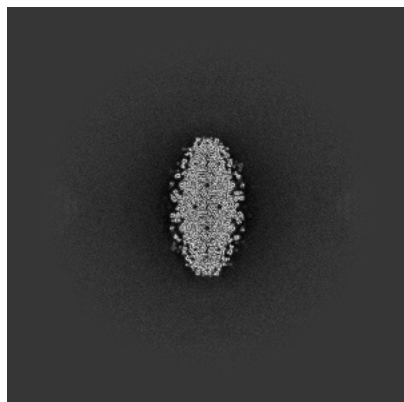


Z Index: 400

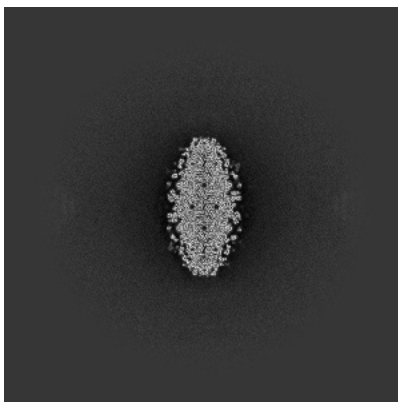
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

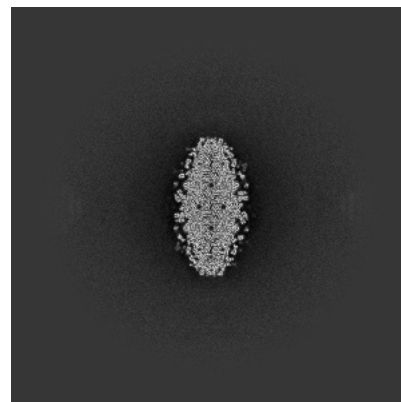
6.3.1 Primary map



X Index: 196

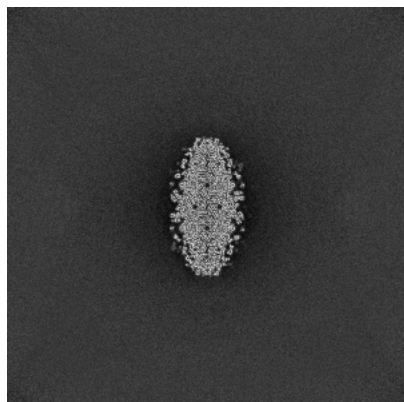


Y Index: 196

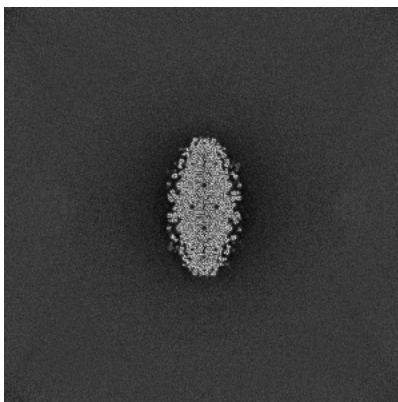


Z Index: 196

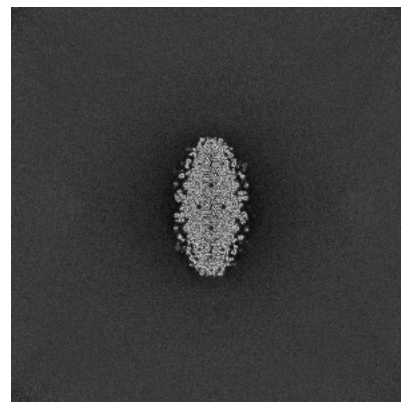
6.3.2 Raw map



X Index: 196



Y Index: 196

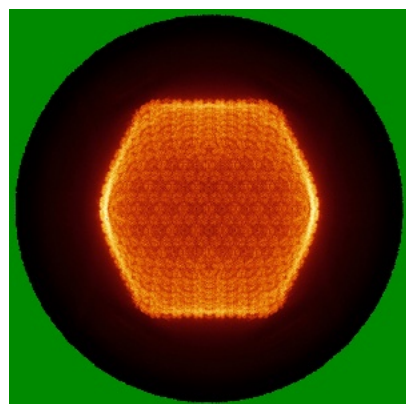


Z Index: 196

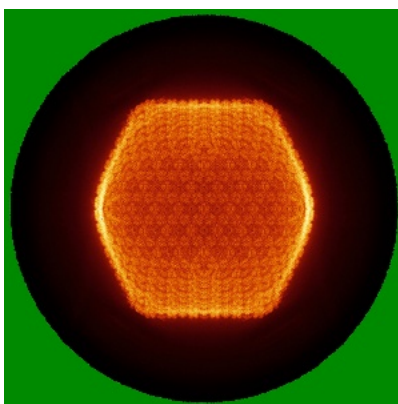
The images above show the largest variance slices of the map in three orthogonal directions.

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

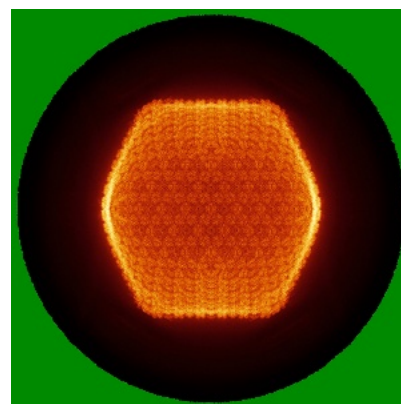
6.4.1 Primary map



X

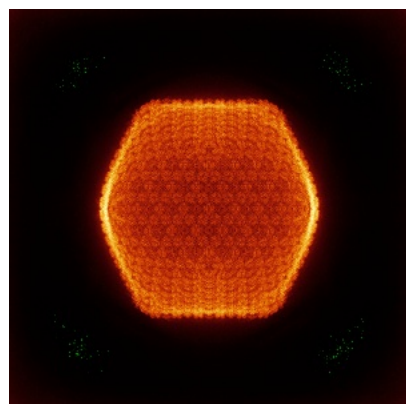


Y

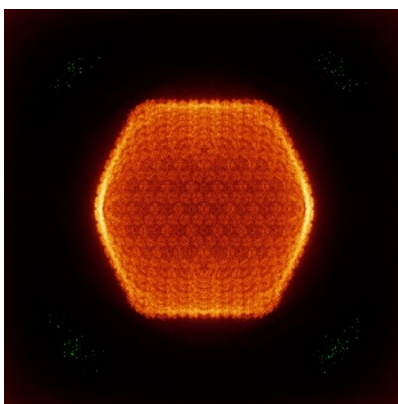


Z

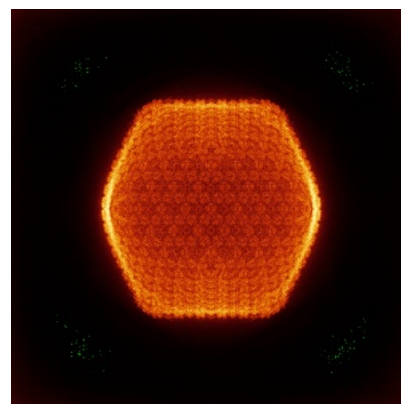
6.4.2 Raw map



X



Y

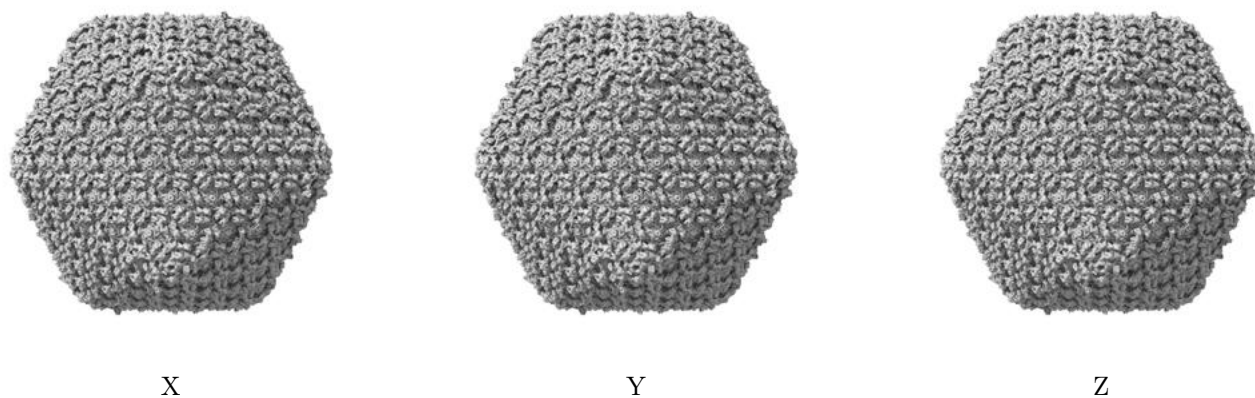


Z

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

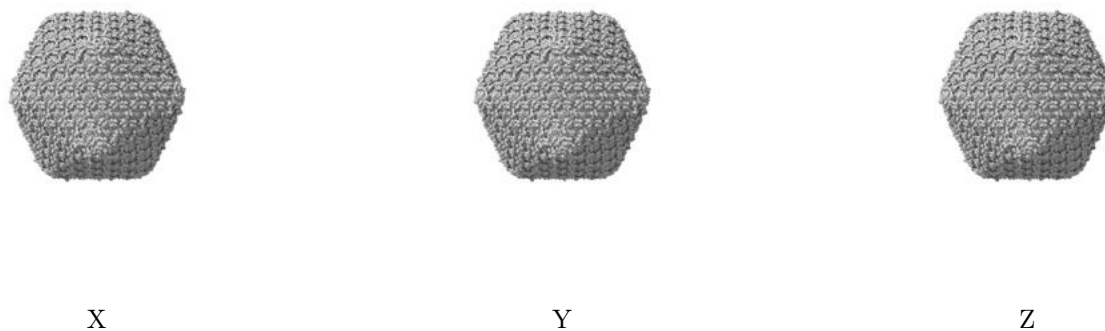
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

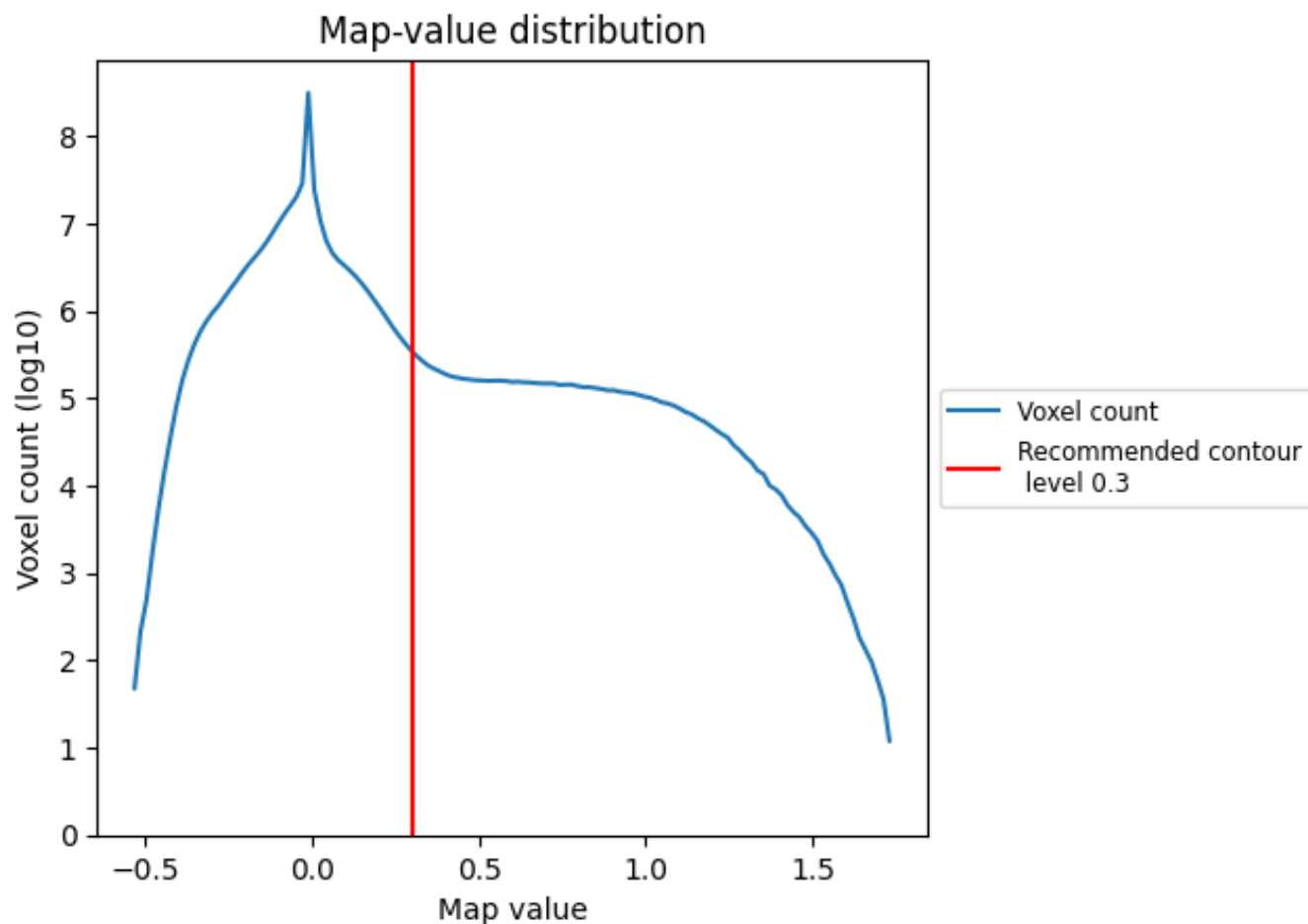
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

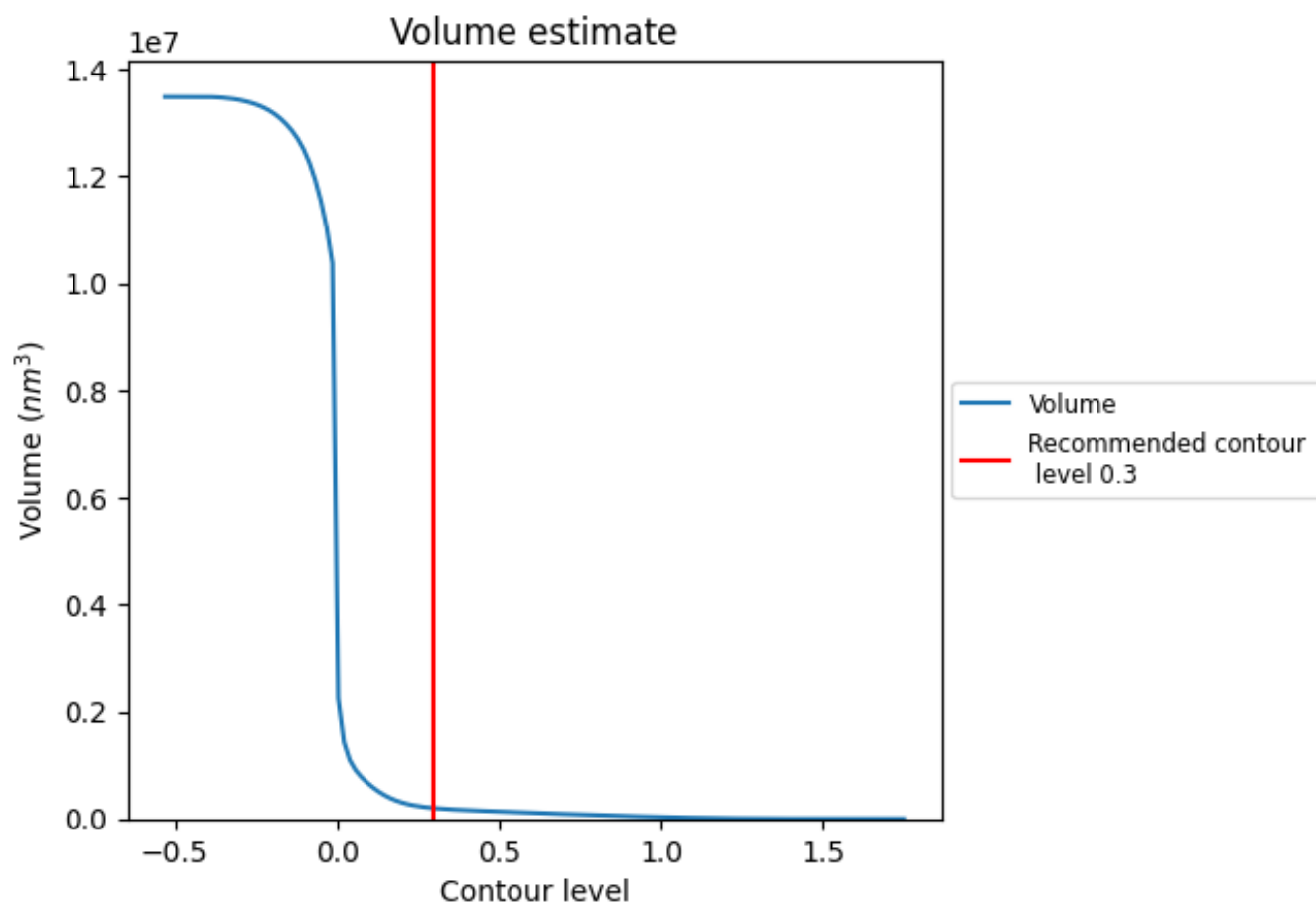
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

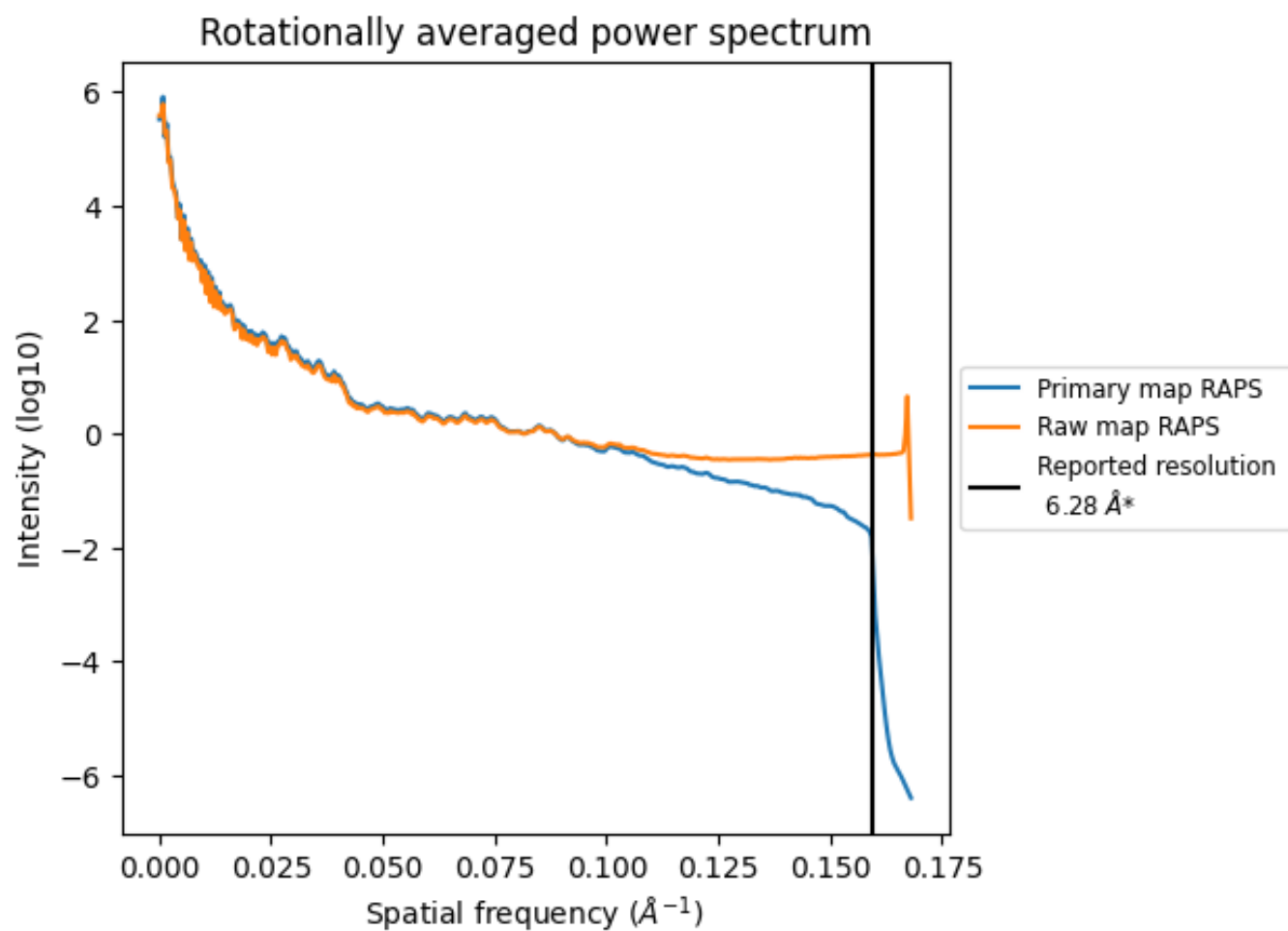
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 197779 nm³; this corresponds to an approximate mass of 178659 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](#)

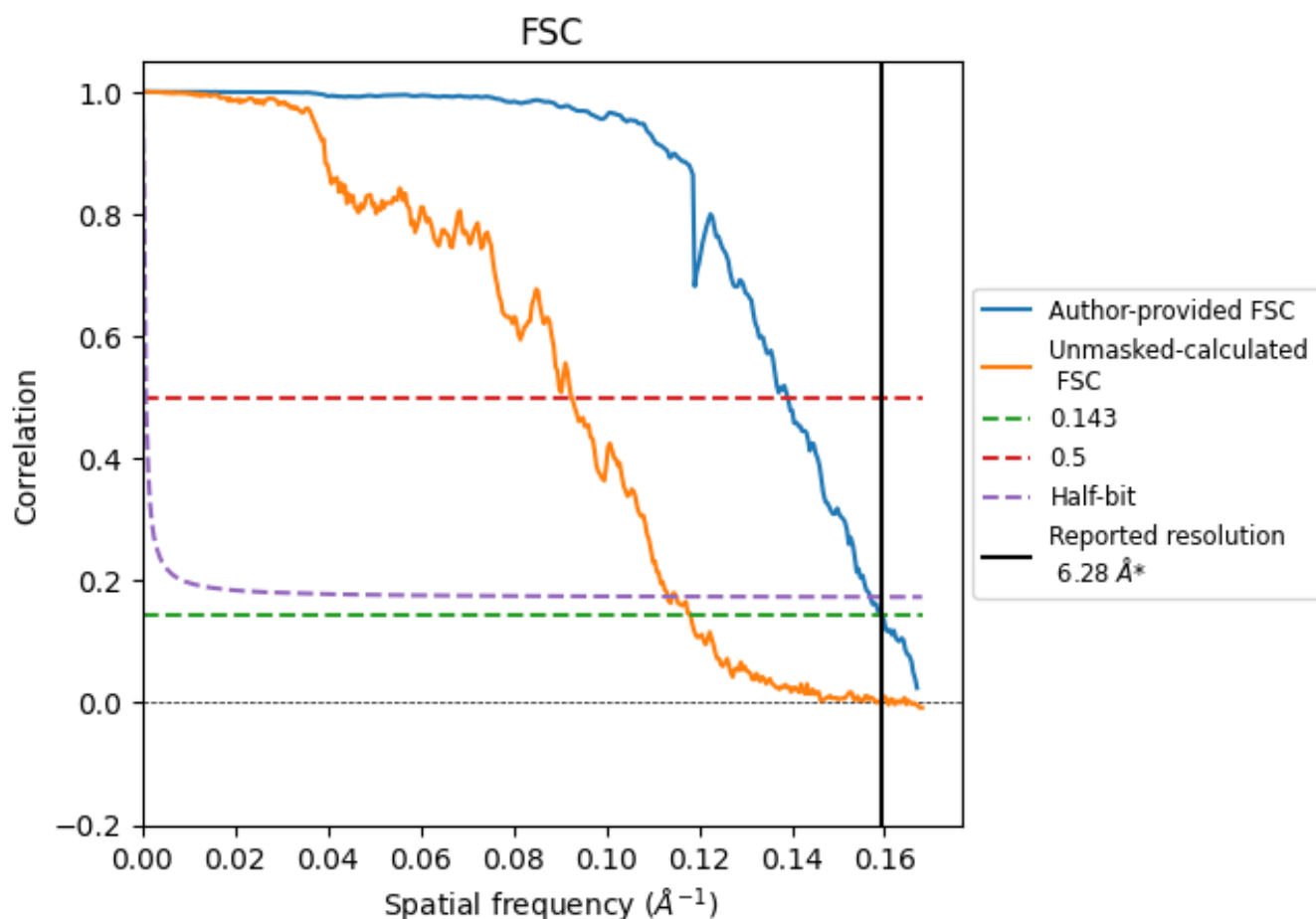


*Reported resolution corresponds to spatial frequency of 0.159 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.159 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

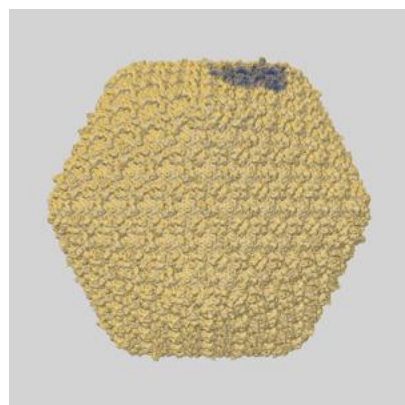
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.28	-	-
Author-provided FSC curve	6.28	7.19	6.37
Unmasked-calculated*	8.47	10.81	8.83

*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 8.47 differs from the reported value 6.28 by more than 10 %

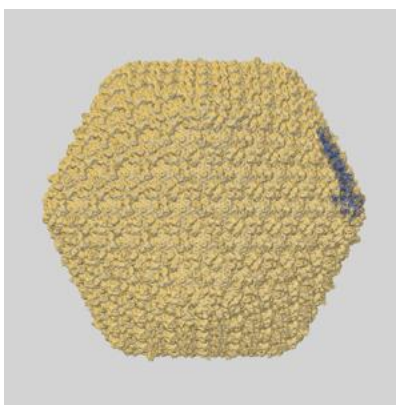
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75836 and PDB model 11MK. Per-residue inclusion information can be found in section [3](#) on page [8](#).

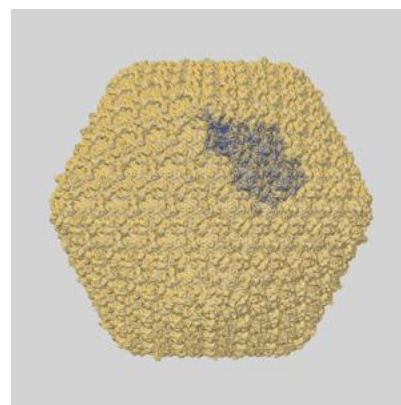
9.1 Map-model overlay [i](#)



X



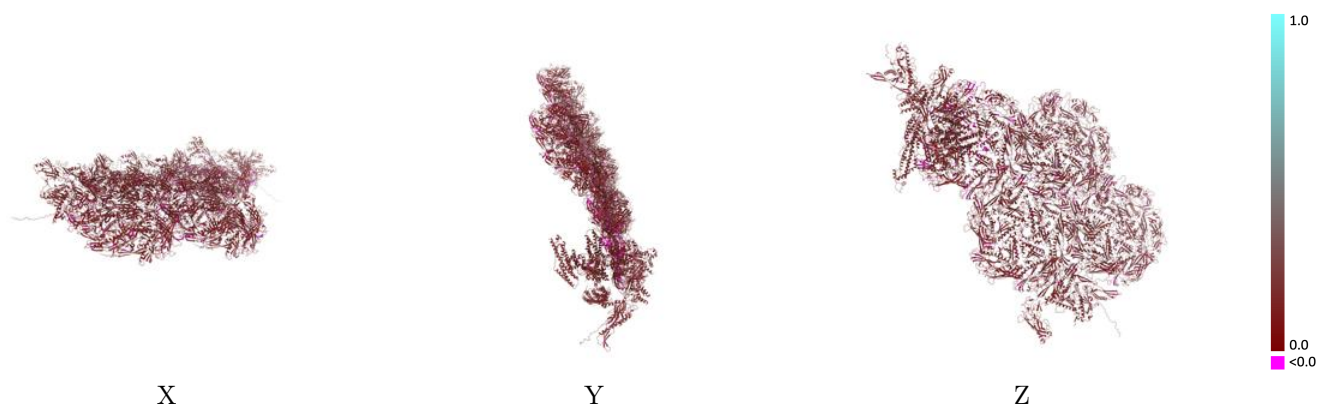
Y



Z

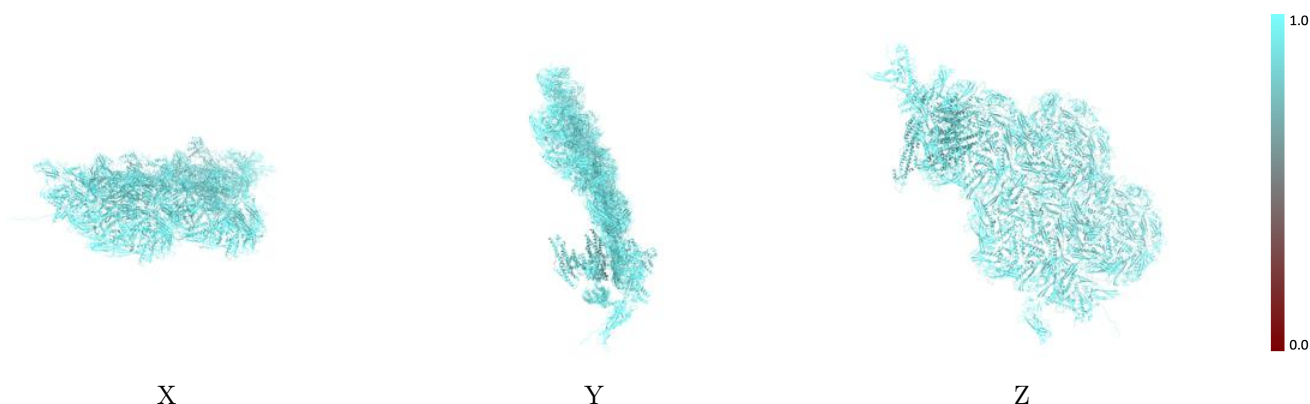
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



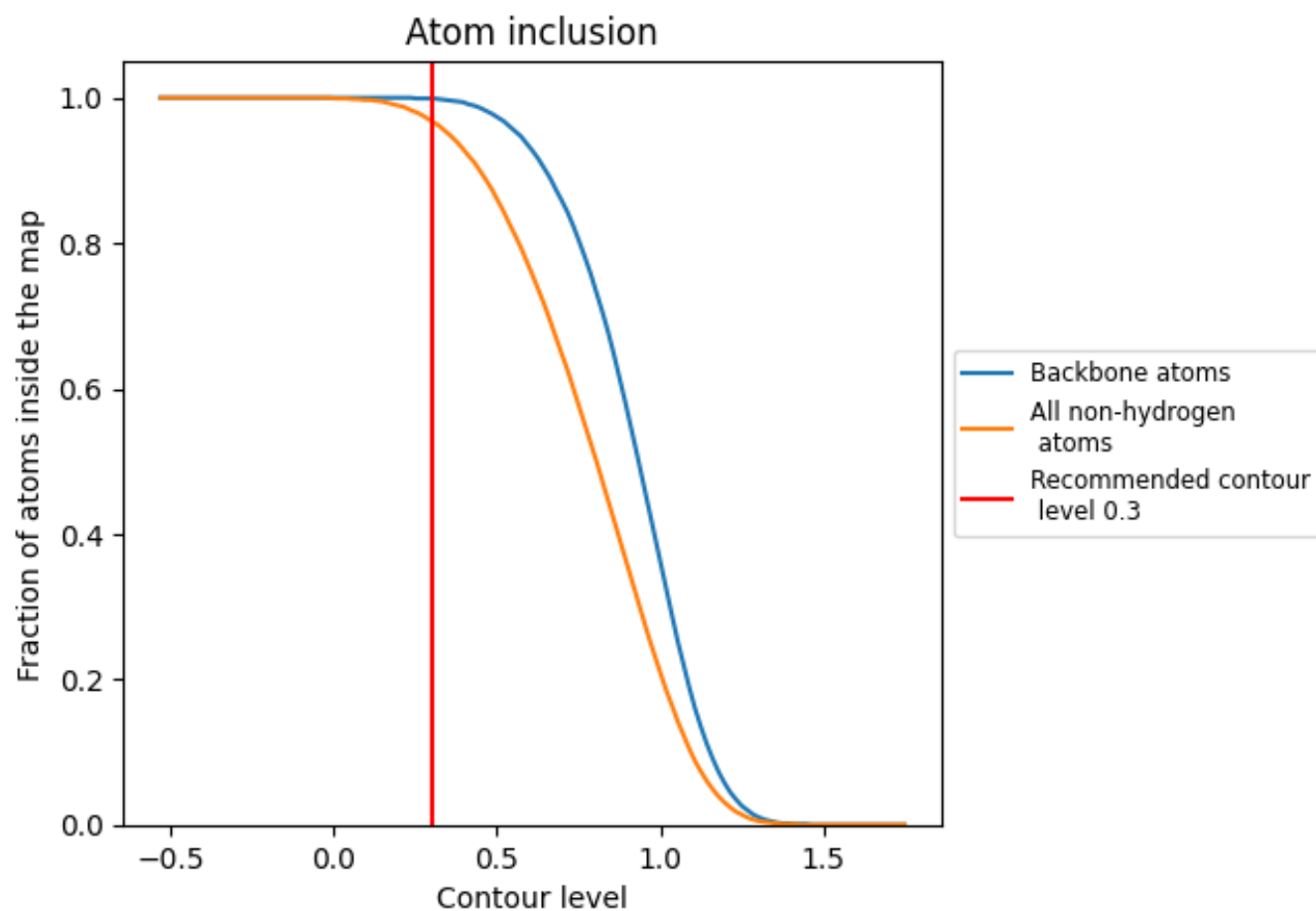
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 97% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.1640
A0	 0.9760	 0.1660
A1	 0.9760	 0.1650
A2	 0.9800	 0.1580
A3	 0.9730	 0.1600
A4	 0.9750	 0.1650
A5	 0.9760	 0.1610
A6	 0.9770	 0.1680
A7	 0.9790	 0.1700
A8	 0.9780	 0.1640
A9	 0.9750	 0.1630
Ar	 0.9780	 0.1630
As	 0.9730	 0.1610
At	 0.9910	 0.1830
Au	 0.9790	 0.1620
Av	 0.9710	 0.1600
Aw	 0.9730	 0.1650
Ax	 0.9730	 0.1700
Ay	 0.9830	 0.1560
Az	 0.9770	 0.1560
B	 0.9850	 0.1840
BA	 0.9670	 0.1290
BB	 0.9790	 0.1650
BC	 0.9810	 0.1630
BD	 0.9800	 0.1550
BE	 0.9700	 0.1430
BF	 0.9770	 0.1580
BG	 0.9780	 0.1700
BH	 0.9770	 0.1690
Ck	 0.8590	 0.1820
G	 0.8600	 0.1840
O	 0.9250	 0.1740
P	 0.9280	 0.1930
Q	 0.9440	 0.1920
R	 0.9590	 0.1920
a	 0.8410	 0.1900

