



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:44 PM UTC

PDB ID : 6H9C / pdb_00006h9c
EMDB ID : EMD-0174
Title : Cryo-EM structure of archaeal extremophilic internal membrane-containing Haloarcula californiae icosahedral virus 1 (HCIV-1) at 3.74 Angstroms resolution.
Authors : Abrescia, N.G.; Santos-Perez, I.; Charro, D.
Deposited on : 2018-08-03
Resolution : 3.74 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

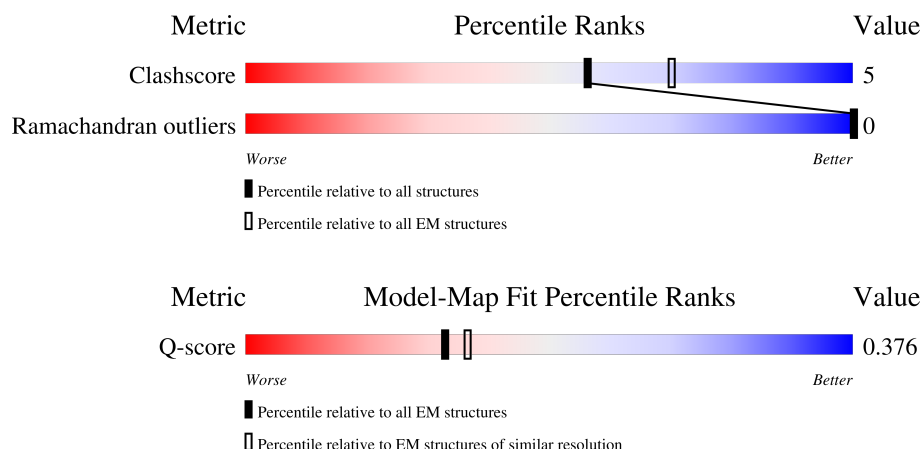
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.74 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	-
Q-score	-	25397	10346 (3.24 - 4.24)

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	D	184	37% 79% 16% 5%
1	E	184	30% 76% 18% 5%
1	F	184	34% 78% 16% 5%
1	I	184	34% 79% 11% 9%
1	J	184	36% 79% 16% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	184	37% 83% 10% 7%
1	L	184	38% 81% 10% 9%
1	M	184	32% 79% 14% 8%
1	N	184	30% 86% 8% 7%
1	R	184	37% 77% 17% 5%
1	S	184	38% 77% 18% 5%
1	T	184	30% 83% 10% 7%
1	W	184	38% 78% 17% 5%
1	Y	184	39% 82% 9% 9%
1	a	184	34% 86% 8% 7%
2	b	146	42% 83% 7% 10%
3	c	108	99% 98% .
4	d	75	100% 99% .
5	e	46	100% 98% .
6	f	18	83% 94% 6%
7	A	232	27% 86% 13% .
7	B	232	33% 85% 13% .
7	C	232	31% 87% 12% .
7	G	232	25% 87% 12% .
7	H	232	31% 88% 11% .
7	O	232	28% 88% 10% .
7	P	232	30% 84% 14% .
7	Q	232	29% 87% 12% .
7	U	232	31% 88% 11% .
7	V	232	30% 86% 13% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	X	232	28% 88% 11%
7	Z	232	31% 84% 14%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 84790 atoms, of which 41099 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 VP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	D	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	F	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	E	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	R	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	T	172	Total	C	H	N	O	S	0	0
			2574	814	1255	224	277	4		
1	S	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	W	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	K	172	Total	C	H	N	O	S	0	0
			2574	814	1255	224	277	4		
1	J	174	Total	C	H	N	O	S	0	0
			2607	823	1273	227	280	4		
1	M	170	Total	C	H	N	O	S	0	0
			2548	806	1241	222	275	4		
1	N	172	Total	C	H	N	O	S	0	0
			2574	814	1255	224	277	4		
1	I	167	Total	C	H	N	O	S	0	0
			2501	792	1218	217	270	4		
1	L	167	Total	C	H	N	O	S	0	0
			2501	792	1218	217	270	4		
1	a	172	Total	C	H	N	O	S	0	0
			2574	814	1255	224	277	4		
1	Y	167	Total	C	H	N	O	S	0	0
			2501	792	1218	217	270	4		

- Molecule 2 is a protein called VP9.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	b	131	Total	C	H	N	O	S	0	0
			1802	587	860	162	192	1		

- Molecule 3 is a protein called GPS-III molecule located underneath the capsomer close to the icosahedral three-fold axis..

Mol	Chain	Residues	Atoms						AltConf	Trace
3	c	108	Total	C	H	N	O		0	0
			970	324	430	108	108			

- Molecule 4 is a protein called GPS-II protein located underneath the two-tower capsomer NOT sitting on the icosahedral 2-fold axis..

Mol	Chain	Residues	Atoms						AltConf	Trace
4	d	75	Total	C	H	N	O		0	0
			671	225	296	75	75			

- Molecule 5 is a protein called (Half) GPS-II protein located underneath the two-tower capsomer sitting ON the icosahedral 2-fold axis..

Mol	Chain	Residues	Atoms						AltConf	Trace
5	e	46	Total	C	H	N	O		0	0
			410	138	180	46	46			

- Molecule 6 is a protein called Peripentonal unknown polypeptide.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	f	18	Total	C	H	N	O		0	0
			161	54	71	18	18			

- Molecule 7 is a protein called VP4.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	Z	229	Total	C	H	N	O	S	0	0
			3515	1134	1703	301	375	2		
7	A	229	Total	C	H	N	O	S	0	0
			3515	1134	1703	301	375	2		
7	B	229	Total	C	H	N	O	S	0	0
			3515	1134	1703	301	375	2		
7	C	229	Total	C	H	N	O	S	0	0
			3515	1134	1703	301	375	2		
7	P	229	Total	C	H	N	O	S	0	0
			3515	1134	1703	301	375	2		

Continued on next page...

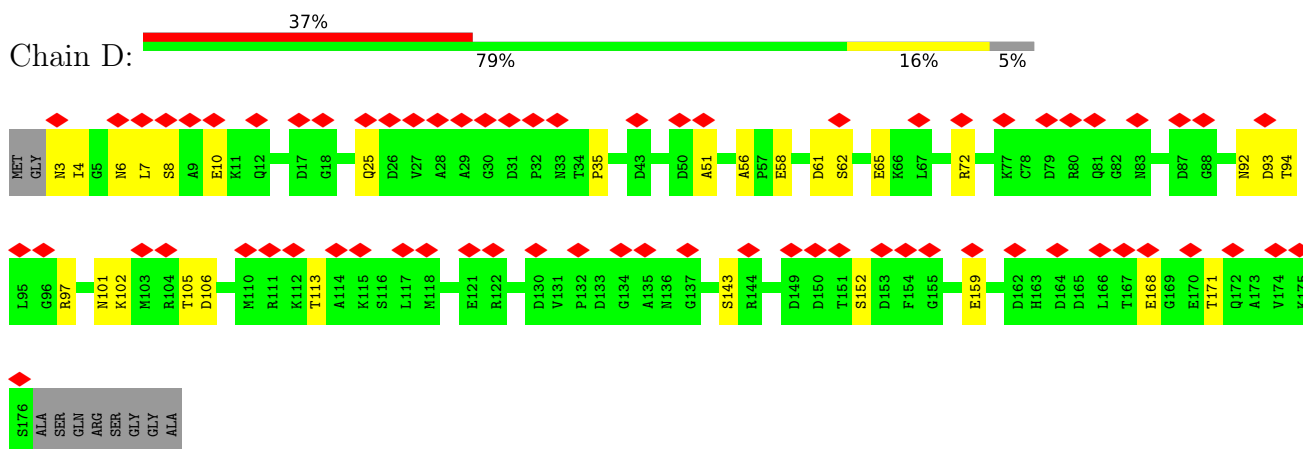
Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf	Trace
7	Q	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	O	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	V	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	U	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	H	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	G	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0
7	X	229	Total 3515	C 1134	H 1703	N 301	O 375	S 2	0	0

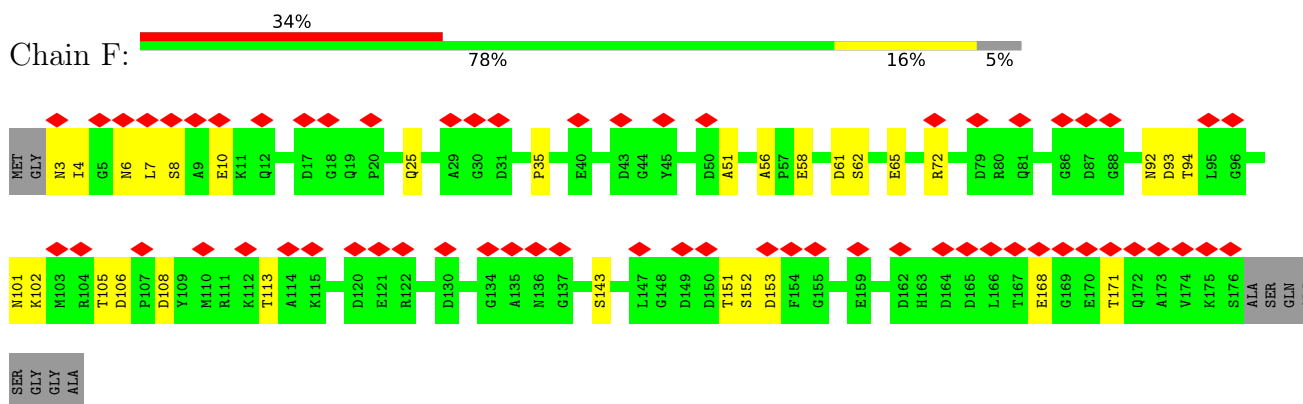
3 Residue-property plots

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.

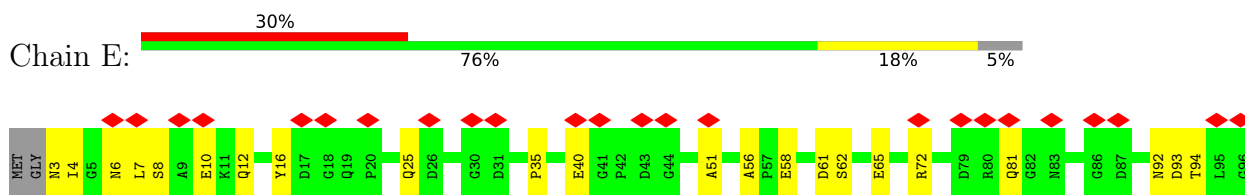
• Molecule 1: VP7

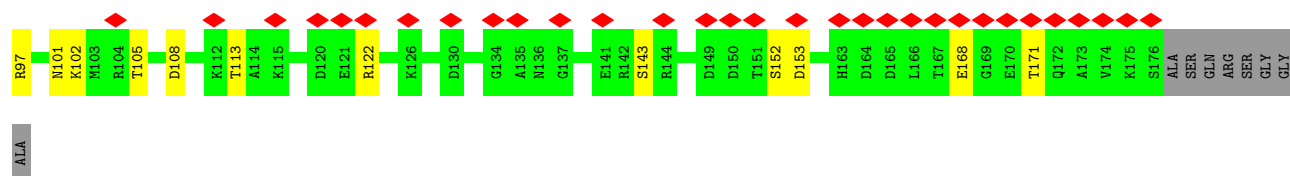


• Molecule 1: VP7

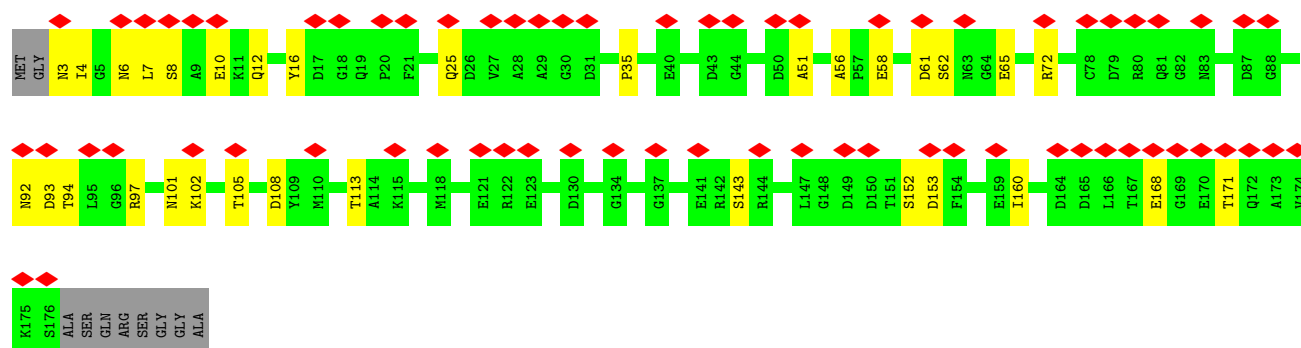
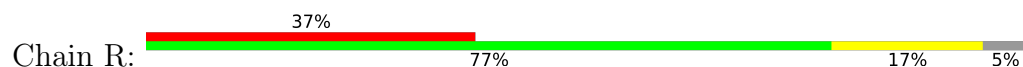


• Molecule 1: VP7

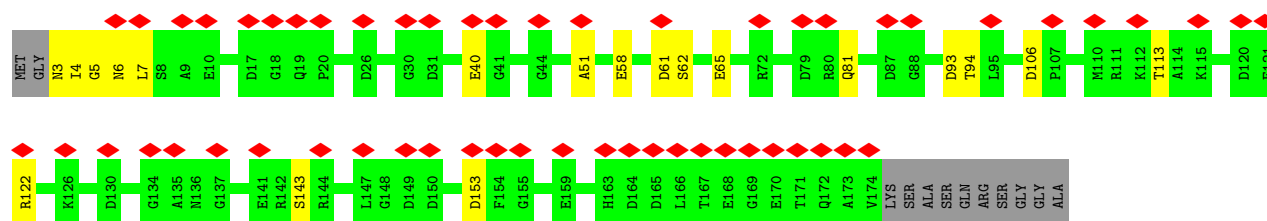
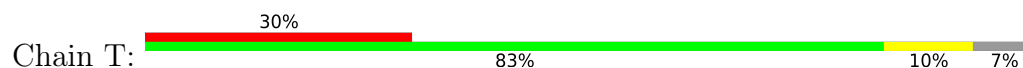




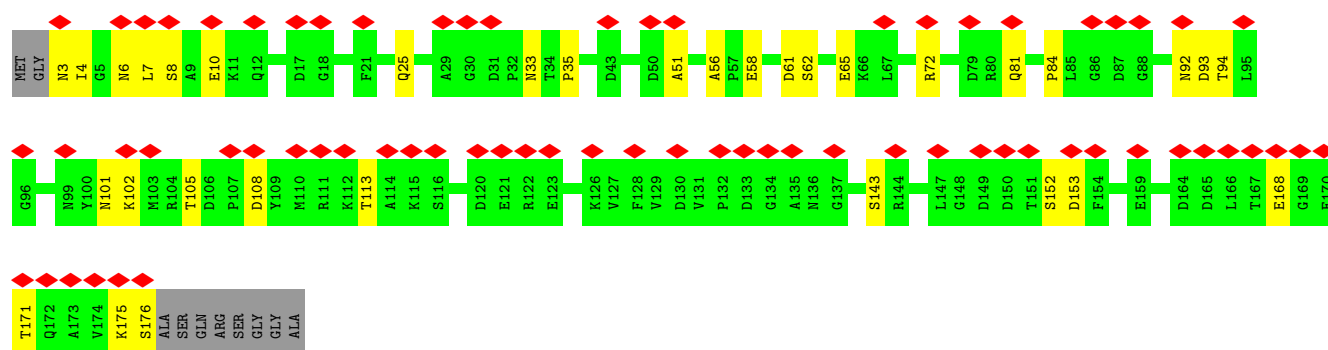
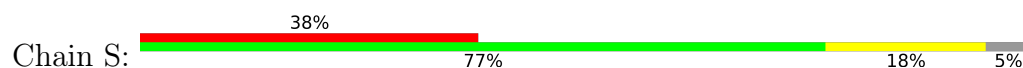
- Molecule 1: VP7



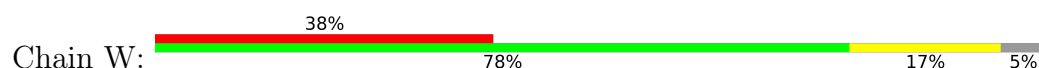
- Molecule 1: VP7

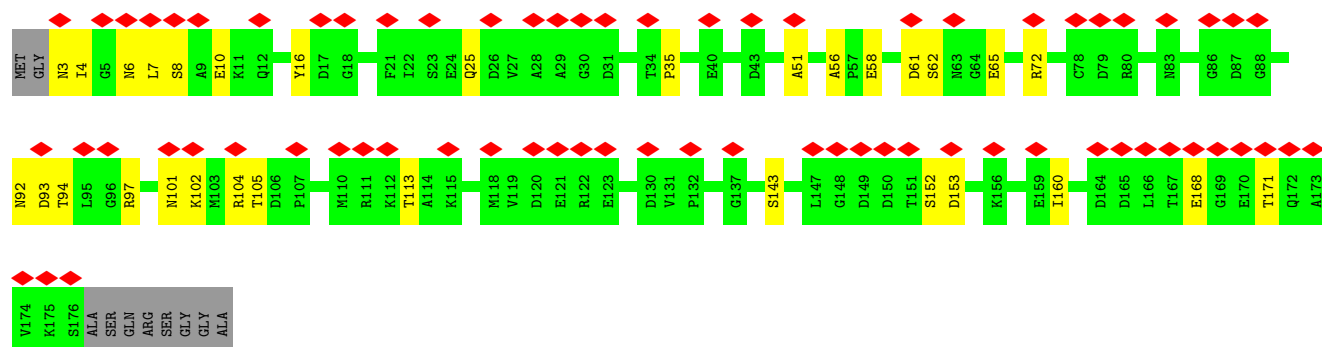


- Molecule 1: VP7

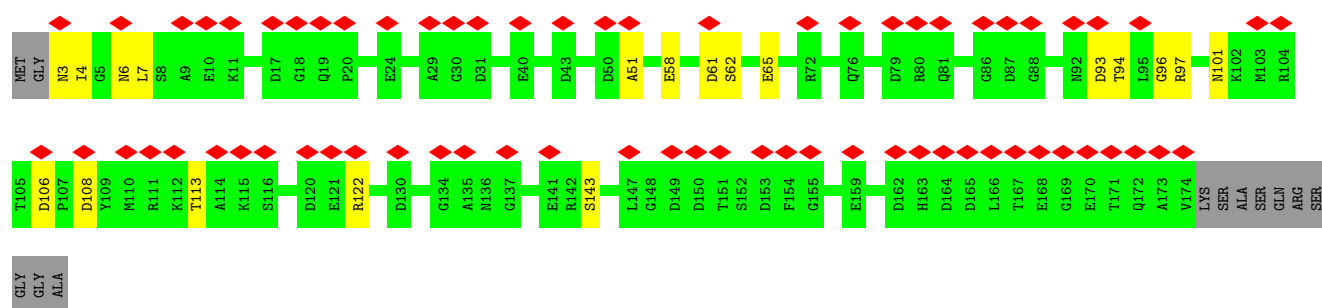
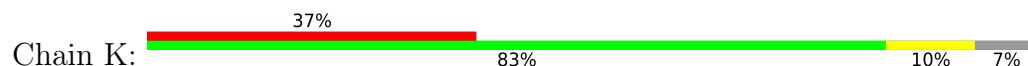


- Molecule 1: VP7

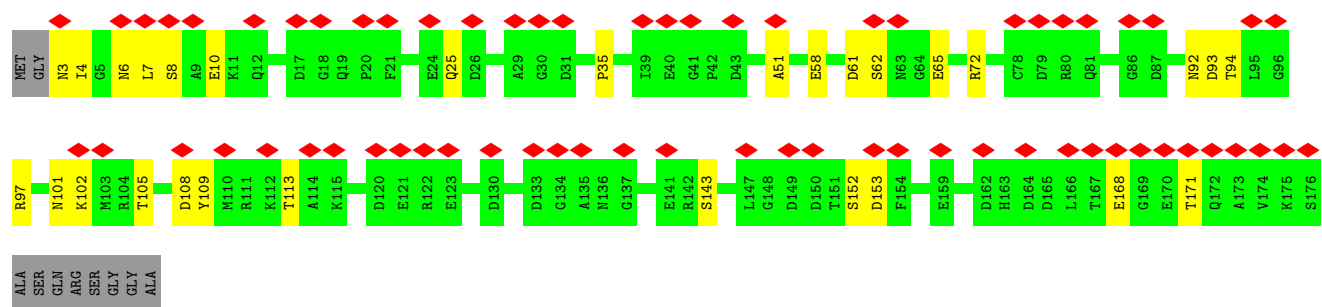
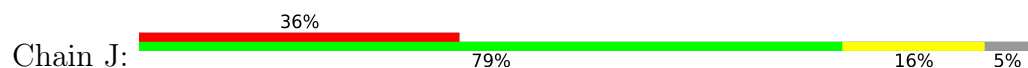




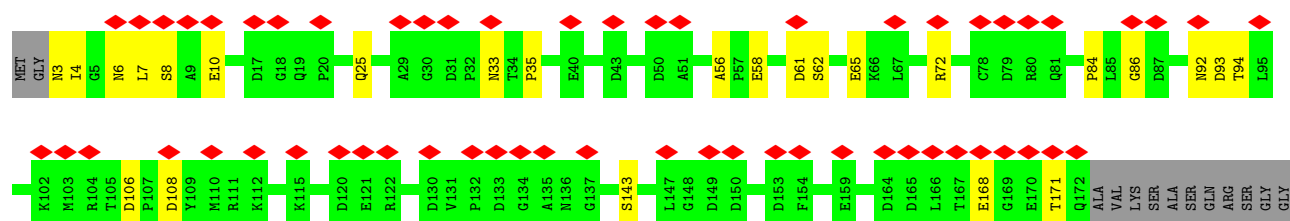
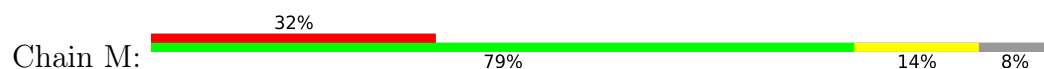
• Molecule 1: VP7



• Molecule 1: VP7



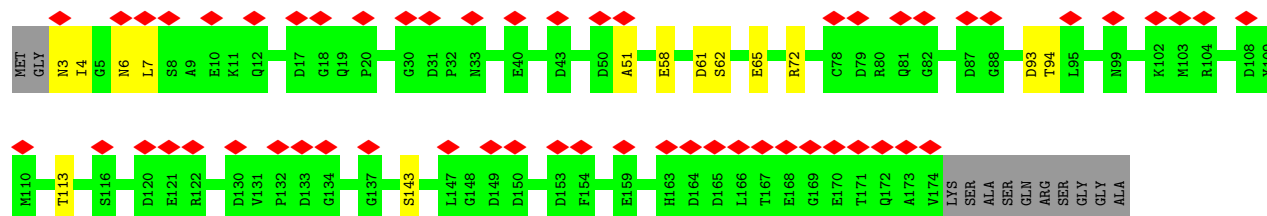
• Molecule 1: VP7



ALA

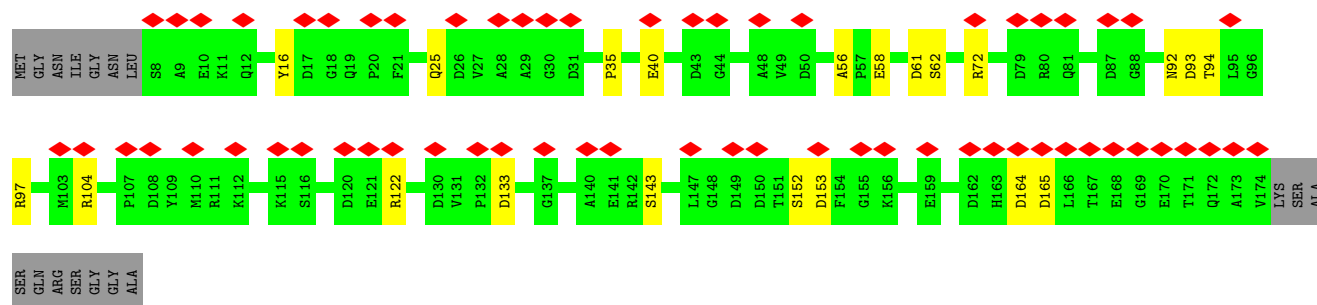
- Molecule 1: VP7

Chain N: 



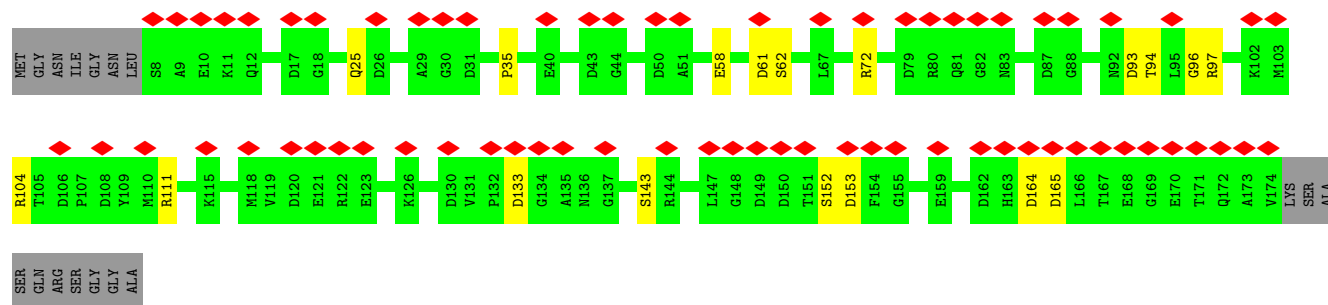
- Molecule 1: VP7

Chain I: 



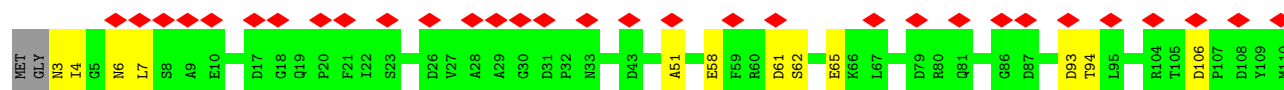
- Molecule 1: VP7

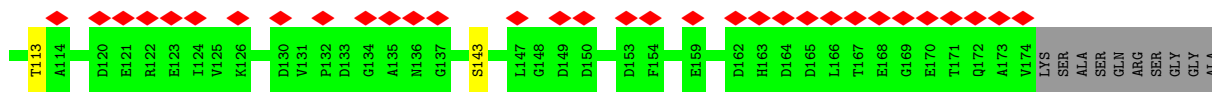
Chain L: 



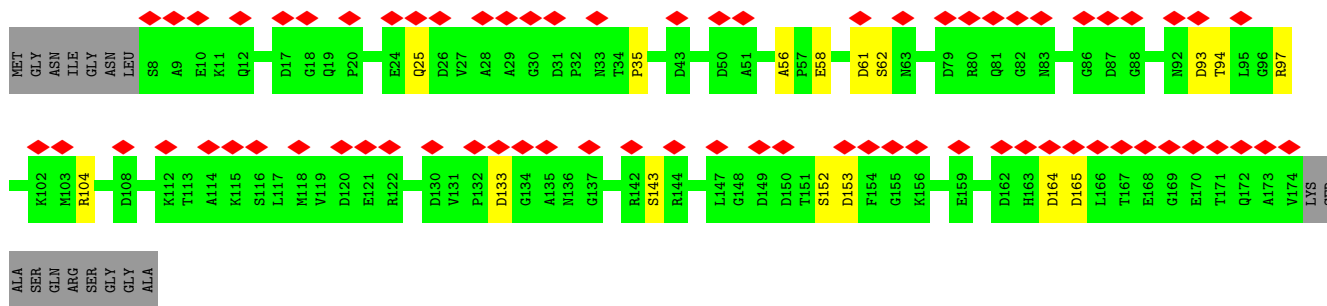
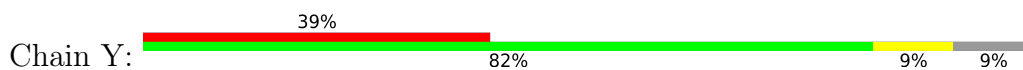
- Molecule 1: VP7

Chain a: 

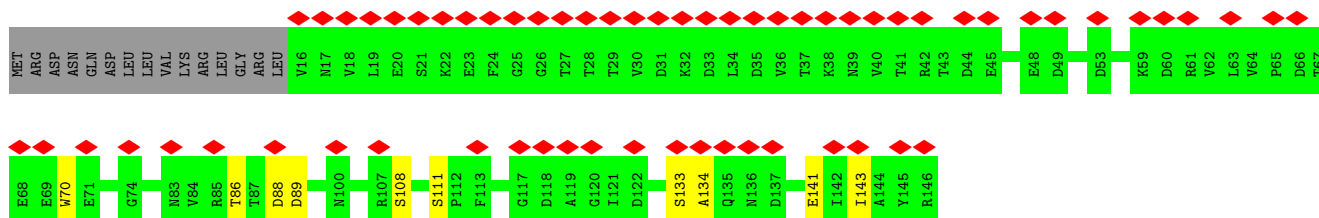
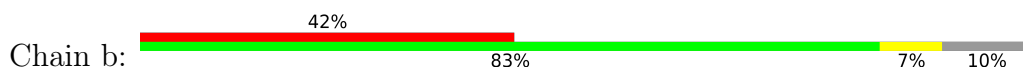




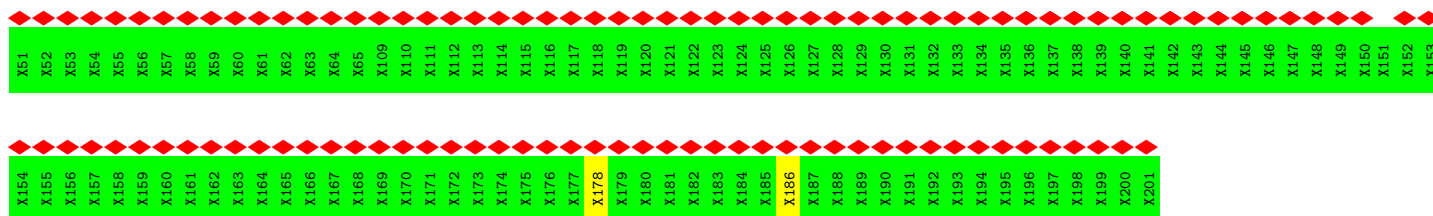
- Molecule 1: VP7



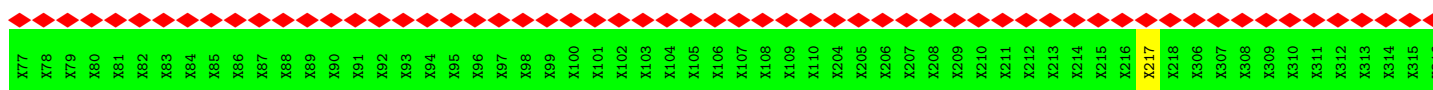
- Molecule 2: VP9

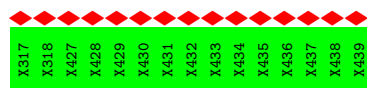


- Molecule 3: GPS-III molecule located underneath the capsomer close to the icosahedral three-fold axis.

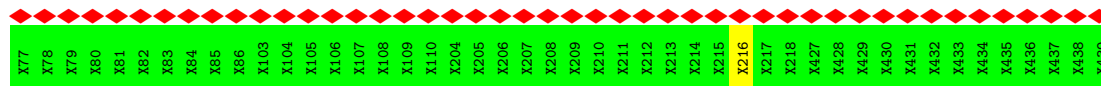


- Molecule 4: GPS-II protein located underneath the two-tower capsomer NOT sitting on the icosahedral 2-fold axis.

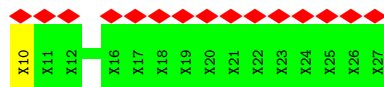
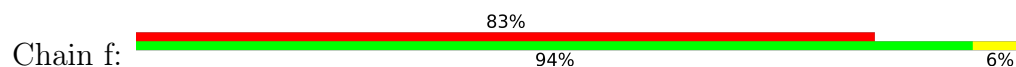




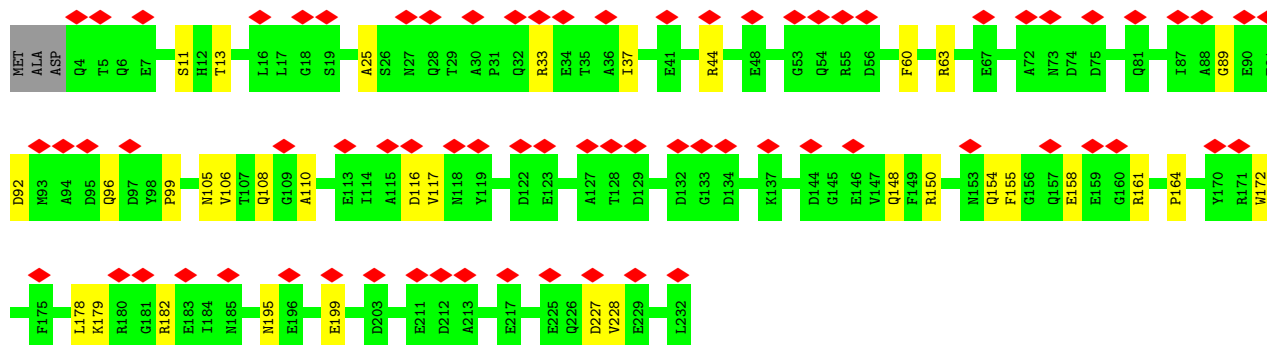
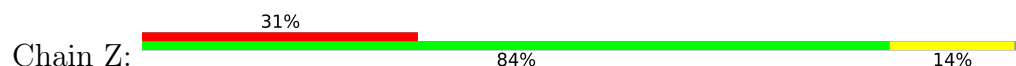
- Molecule 5: (Half) GPS-II protein located underneath the two-tower capsomer sitting ON the icosahedral 2-fold axis.



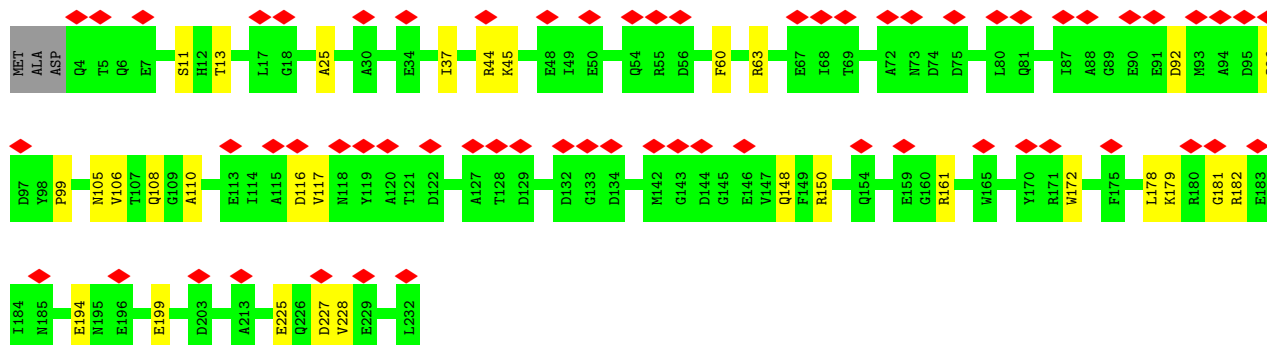
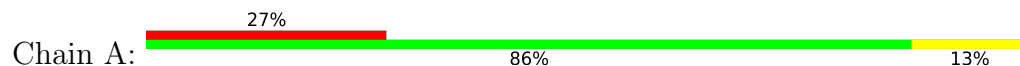
- Molecule 6: Peripentonal unknown polypeptide



- Molecule 7: VP4

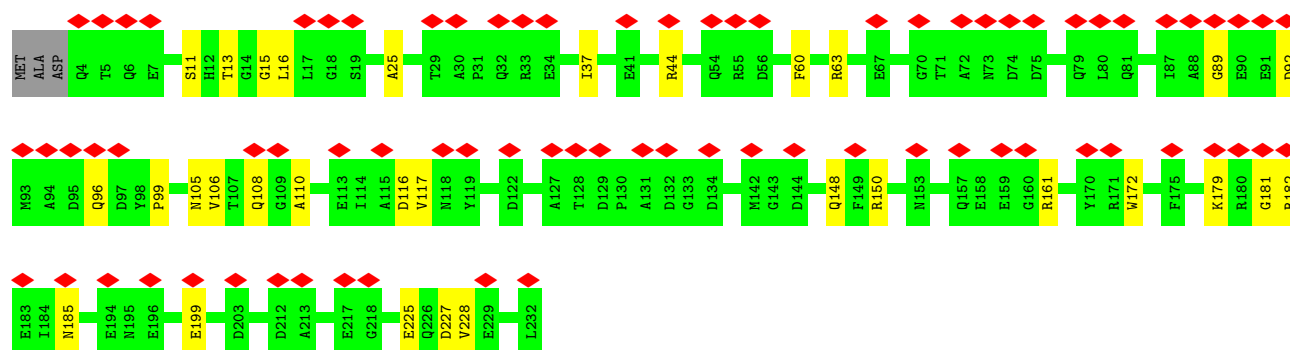


- Molecule 7: VP4



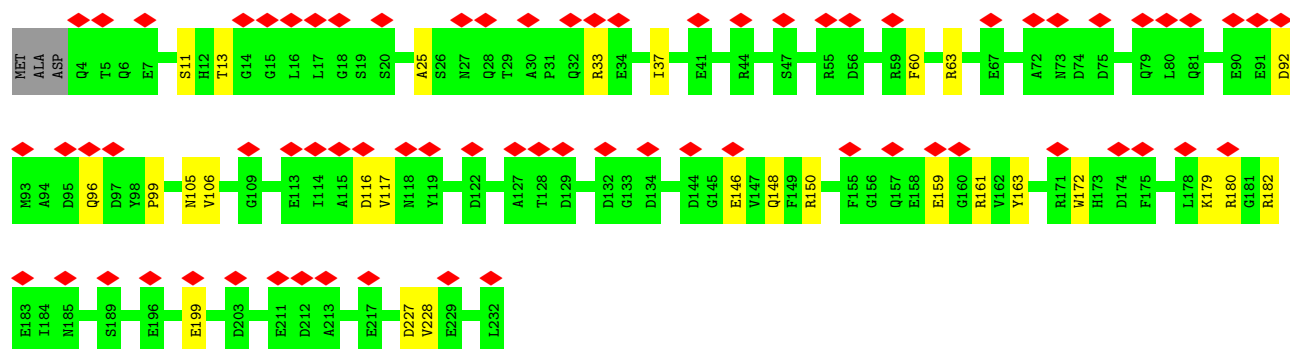
- Molecule 7: VP4

Chain B: 



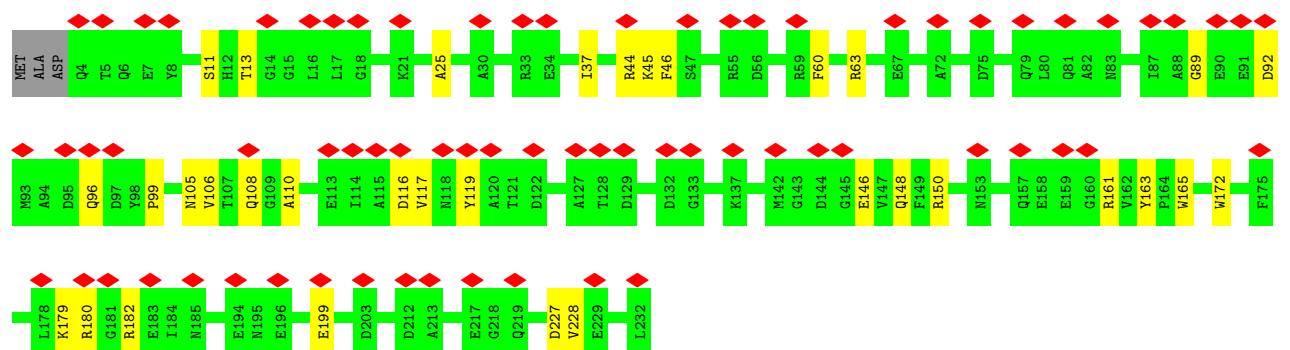
• Molecule 7: VP4

Chain C: 



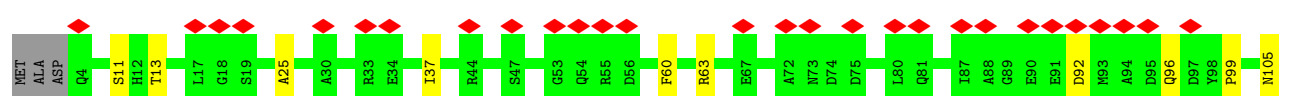
• Molecule 7: VP4

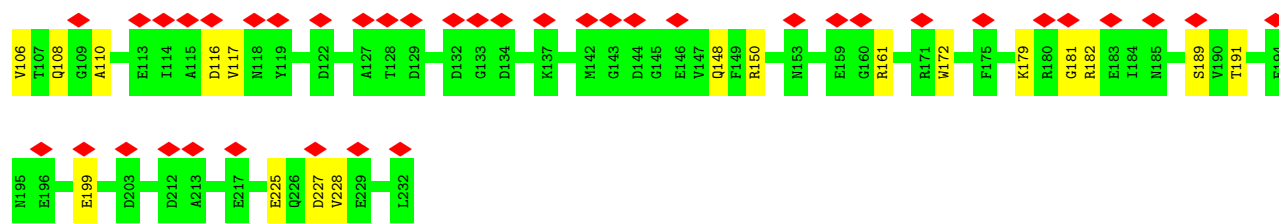
Chain P: 



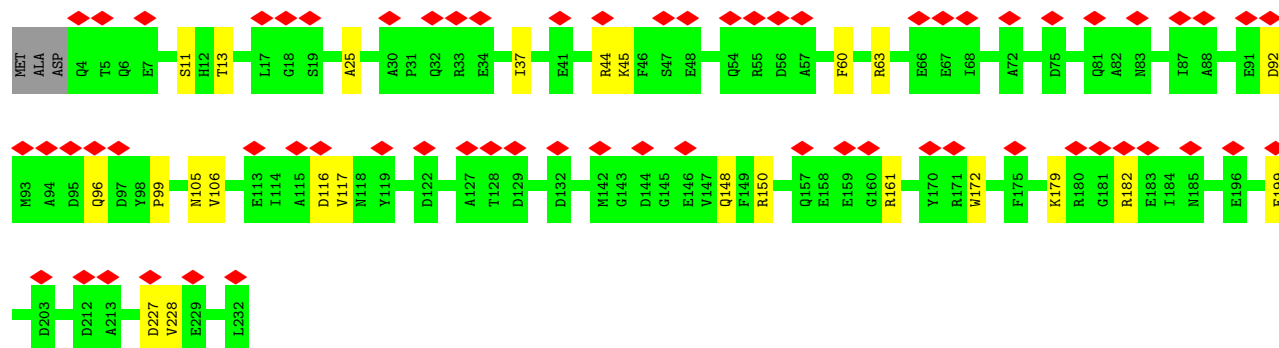
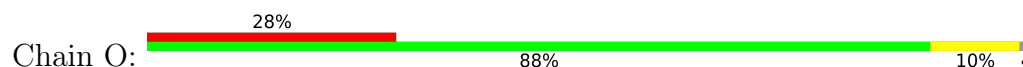
• Molecule 7: VP4

Chain Q: 

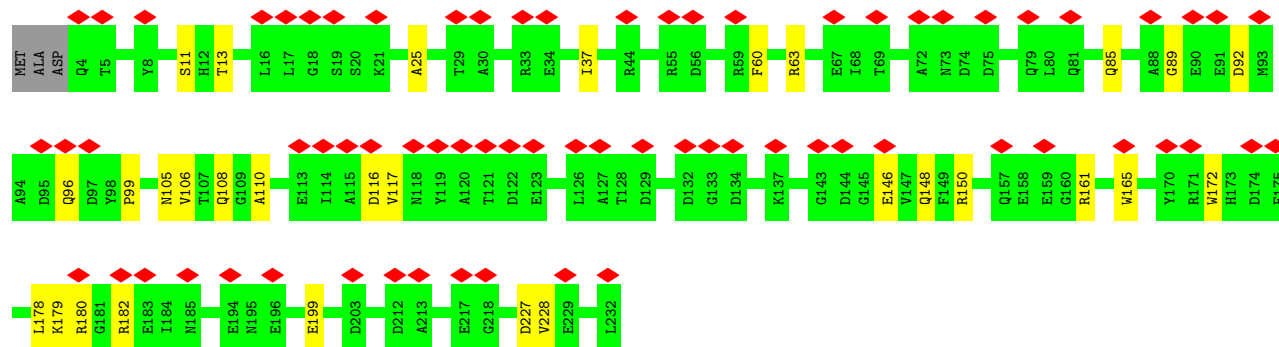
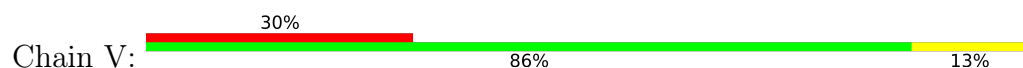




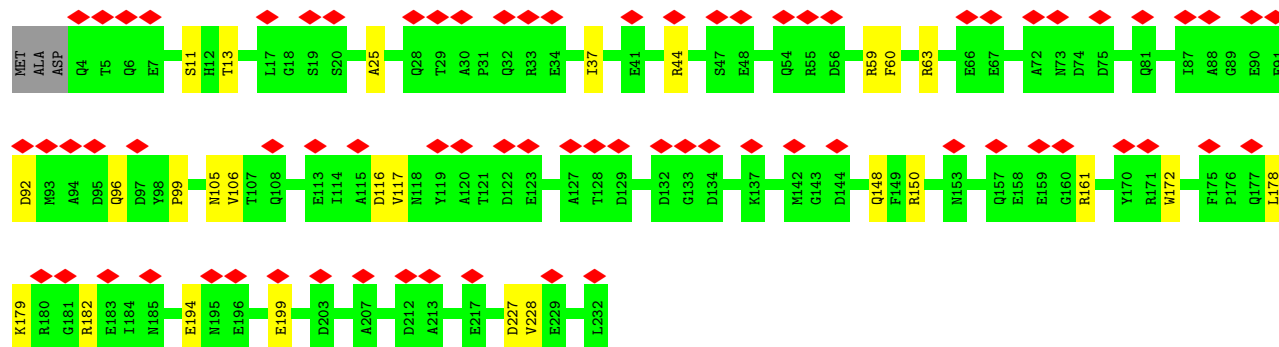
• Molecule 7: VP4



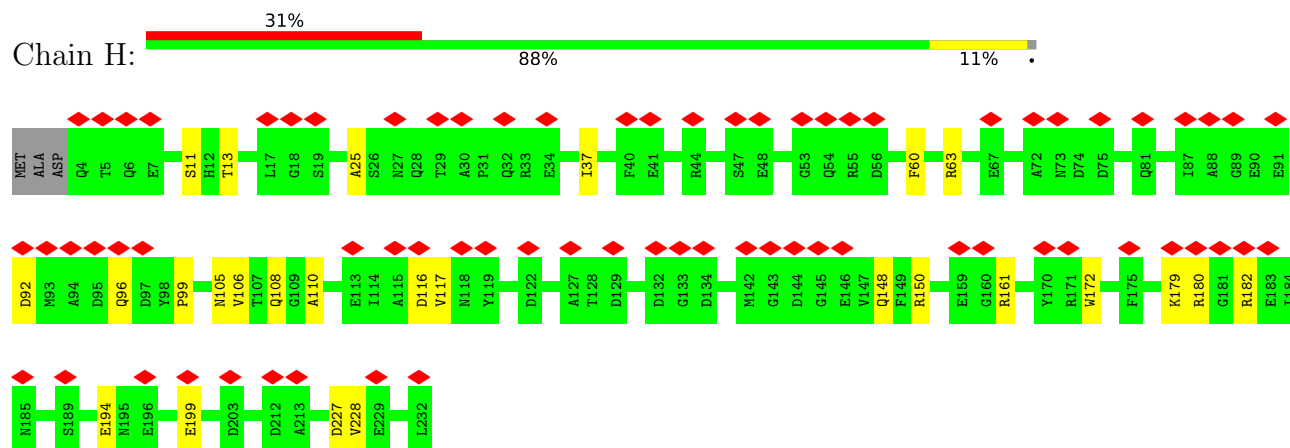
• Molecule 7: VP4



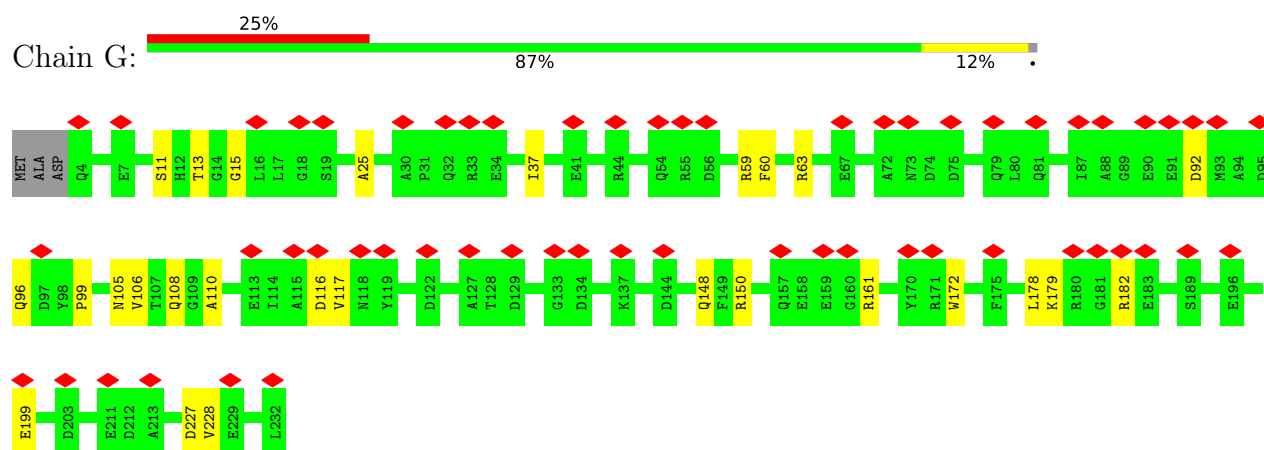
• Molecule 7: VP4



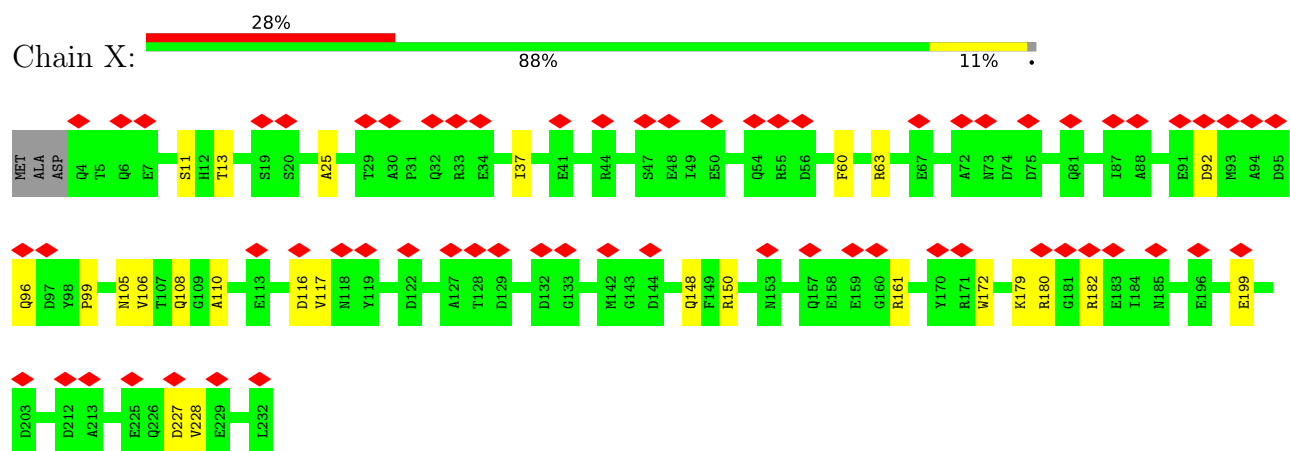
- Molecule 7: VP4



- Molecule 7: VP4



- Molecule 7: VP4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	3414	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.131	Depositor
Minimum map value	-0.060	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	1075.2, 1075.2, 1075.2	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	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	D	0.40	0/1356	0.52	0/1838
1	E	0.40	0/1356	0.52	0/1838
1	F	0.40	0/1356	0.52	0/1838
1	I	0.41	0/1305	0.50	0/1770
1	J	0.40	0/1356	0.52	0/1838
1	K	0.40	0/1341	0.50	0/1819
1	L	0.41	0/1305	0.50	0/1770
1	M	0.39	0/1329	0.50	0/1802
1	N	0.39	0/1341	0.50	0/1819
1	R	0.40	0/1356	0.52	0/1838
1	S	0.40	0/1356	0.52	0/1838
1	T	0.39	0/1341	0.50	0/1819
1	W	0.40	0/1356	0.52	0/1838
1	Y	0.41	0/1305	0.50	0/1770
1	a	0.40	0/1341	0.50	0/1819
2	b	0.39	0/960	0.51	0/1313
7	A	0.42	0/1852	0.53	0/2535
7	B	0.42	0/1852	0.53	0/2535
7	C	0.42	0/1852	0.53	0/2535
7	G	0.42	0/1852	0.53	0/2535
7	H	0.42	0/1852	0.53	0/2535
7	O	0.42	0/1852	0.53	0/2535
7	P	0.42	0/1852	0.53	0/2535
7	Q	0.42	0/1852	0.53	0/2535
7	U	0.42	0/1852	0.53	0/2535
7	V	0.42	0/1852	0.53	0/2535
7	X	0.42	0/1852	0.53	0/2535
7	Z	0.42	0/1852	0.53	0/2535
All	All	0.41	0/43284	0.52	0/58987

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	D	1334	1273	1273	20	0
1	E	1334	1273	1273	26	0
1	F	1334	1273	1273	20	0
1	I	1283	1218	1218	14	0
1	J	1334	1273	1273	19	0
1	K	1319	1255	1255	13	0
1	L	1283	1218	1218	12	0
1	M	1307	1241	1241	15	0
1	N	1319	1255	1255	8	0
1	R	1334	1273	1273	22	0
1	S	1334	1273	1273	25	0
1	T	1319	1255	1255	16	0
1	W	1334	1273	1273	21	0
1	Y	1283	1218	1218	10	0
1	a	1319	1255	1255	8	0
2	b	942	860	821	6	0
3	c	540	430	129	2	0
4	d	375	296	88	1	0
5	e	230	180	58	1	0
6	f	90	71	20	1	0
7	A	1812	1703	1703	24	0
7	B	1812	1703	1703	20	0
7	C	1812	1703	1703	17	0
7	G	1812	1703	1703	15	0
7	H	1812	1703	1703	14	0
7	O	1812	1703	1703	16	0
7	P	1812	1703	1703	27	0
7	Q	1812	1703	1703	18	0
7	U	1812	1703	1703	16	0
7	V	1812	1703	1703	22	0
7	X	1812	1703	1703	14	0
7	Z	1812	1703	1703	31	0
All	All	43691	41099	40378	408	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 5.

The worst 5 of 408 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)
7:B:182:ARG:NH2	1:F:106:ASP:OD1	2.05	0.88
7:O:45:LYS:HD2	1:E:81:GLN:HA	1.59	0.83
7:Z:33:ARG:NH2	1:S:33:ASN:O	2.13	0.81
1:D:97:ARG:NH2	7:B:225:GLU:OE1	2.19	0.76
5:e:216:UNK:O	7:X:180:ARG:NH1	2.19	0.75

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	D	172/184 (94%)	152 (88%)	20 (12%)	0	100	100
1	E	4/184 (2%)	4 (100%)	0	0	100	100
1	F	32/184 (17%)	29 (91%)	3 (9%)	0	100	100
1	I	165/184 (90%)	148 (90%)	17 (10%)	0	100	100
1	J	172/184 (94%)	153 (89%)	19 (11%)	0	100	100
1	K	170/184 (92%)	154 (91%)	16 (9%)	0	100	100
1	L	165/184 (90%)	148 (90%)	17 (10%)	0	100	100
1	M	168/184 (91%)	148 (88%)	20 (12%)	0	100	100
1	N	170/184 (92%)	154 (91%)	16 (9%)	0	100	100
1	R	62/184 (34%)	54 (87%)	8 (13%)	0	100	100
1	S	172/184 (94%)	152 (88%)	20 (12%)	0	100	100
1	T	170/184 (92%)	154 (91%)	16 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	172/184 (94%)	153 (89%)	19 (11%)	0	100	100
1	Y	165/184 (90%)	148 (90%)	17 (10%)	0	100	100
1	a	170/184 (92%)	154 (91%)	16 (9%)	0	100	100
2	b	129/146 (88%)	117 (91%)	12 (9%)	0	100	100
7	A	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	B	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	C	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	G	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	H	166/232 (72%)	136 (82%)	30 (18%)	0	100	100
7	O	227/232 (98%)	186 (82%)	41 (18%)	0	100	100
7	P	211/232 (91%)	171 (81%)	40 (19%)	0	100	100
7	Q	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	U	164/232 (71%)	133 (81%)	31 (19%)	0	100	100
7	V	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
7	X	146/232 (63%)	119 (82%)	27 (18%)	0	100	100
7	Z	227/232 (98%)	187 (82%)	40 (18%)	0	100	100
All	All	4761/5690 (84%)	4076 (86%)	685 (14%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	d	3
5	e	3
3	c	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	218:UNK	C	306:UNK	N	26.44
1	d	110:UNK	C	204:UNK	N	25.26
1	e	110:UNK	C	204:UNK	N	24.97
1	d	318:UNK	C	427:UNK	N	24.96
1	c	65:UNK	C	109:UNK	N	24.83

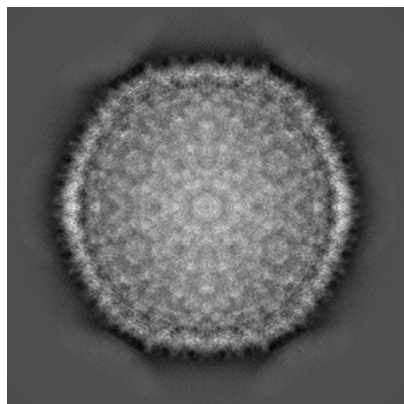
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0174. These allow visual inspection of the internal detail of the map and identification of artifacts.

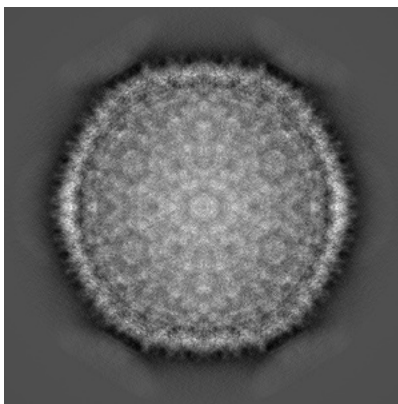
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

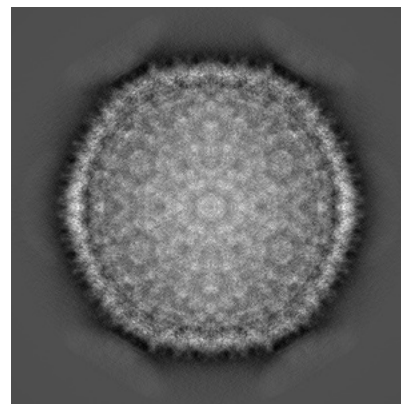
6.1.1 Primary map



X

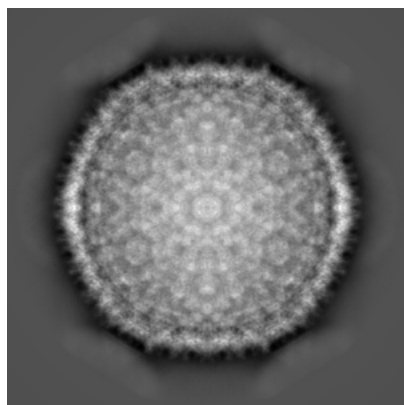


Y

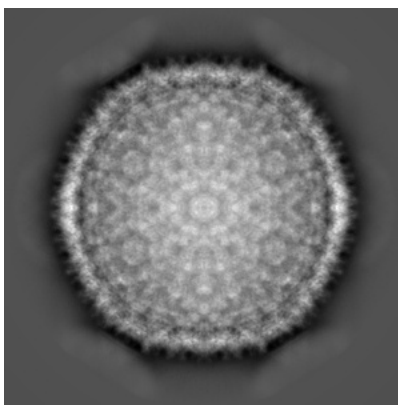


Z

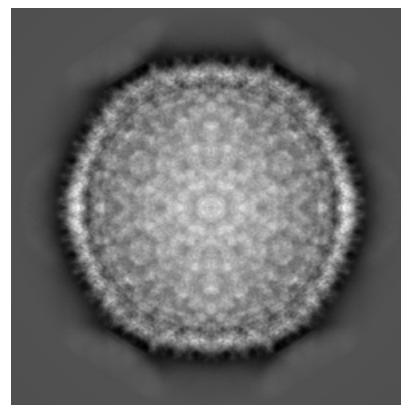
6.1.2 Raw map



X



Y

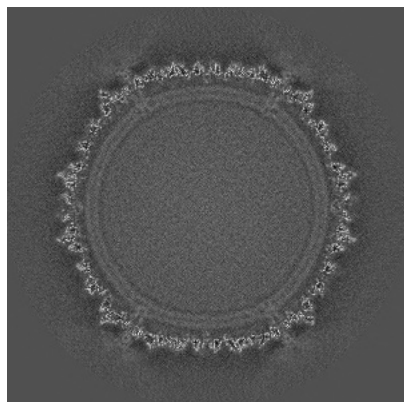


Z

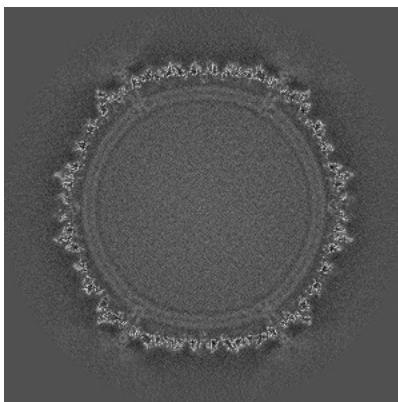
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

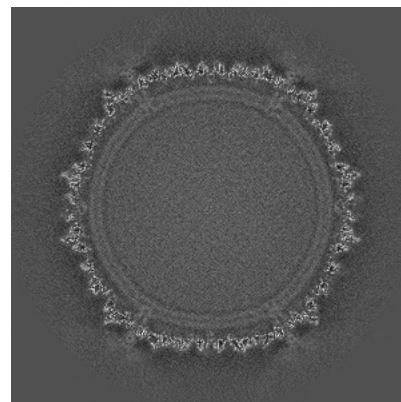
6.2.1 Primary map



X Index: 384

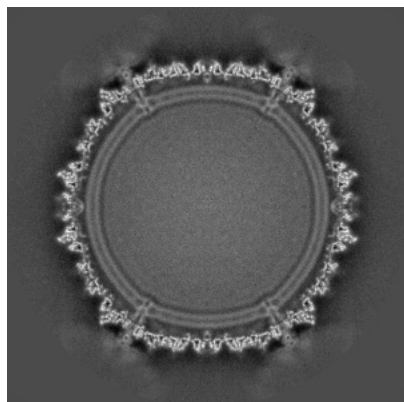


Y Index: 384

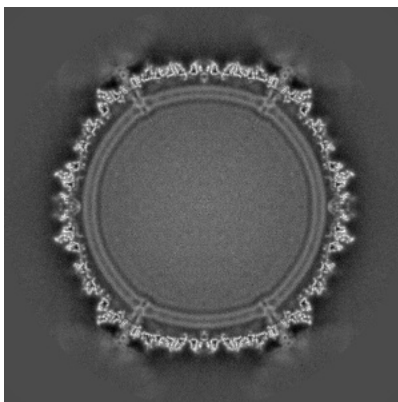


Z Index: 384

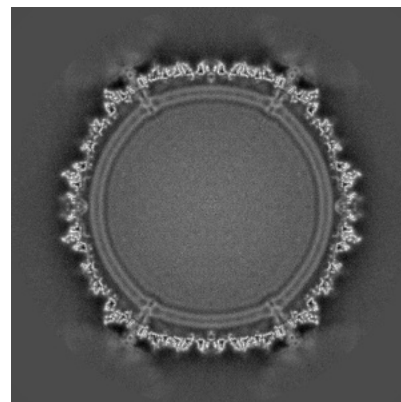
6.2.2 Raw map



X Index: 384



Y Index: 384

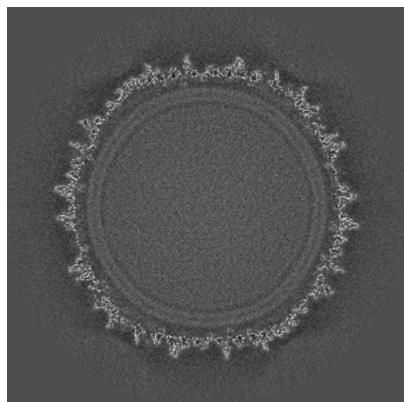


Z Index: 384

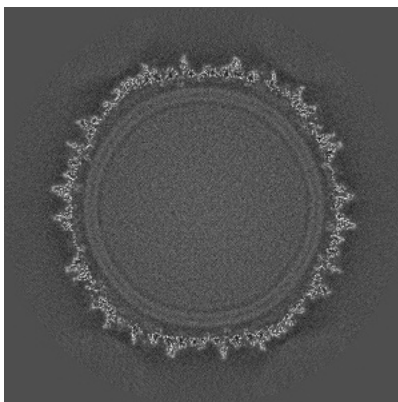
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

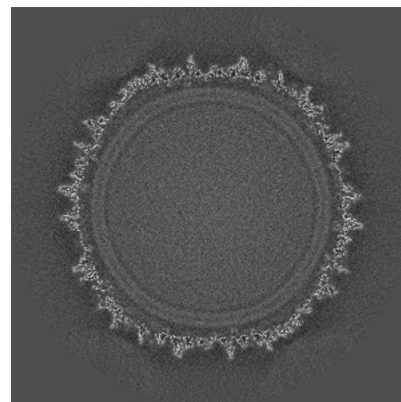
6.3.1 Primary map



X Index: 344

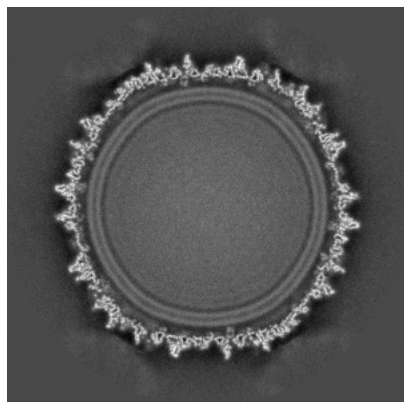


Y Index: 344

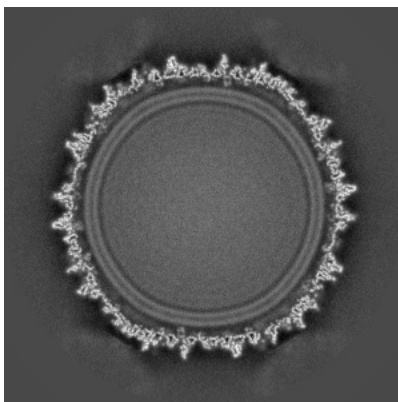


Z Index: 344

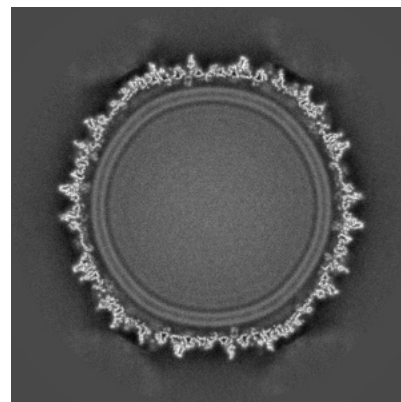
6.3.2 Raw map



X Index: 345



Y Index: 423

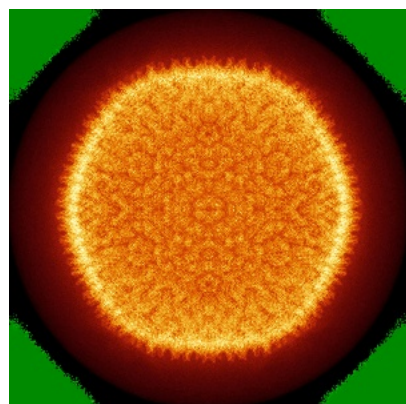


Z Index: 345

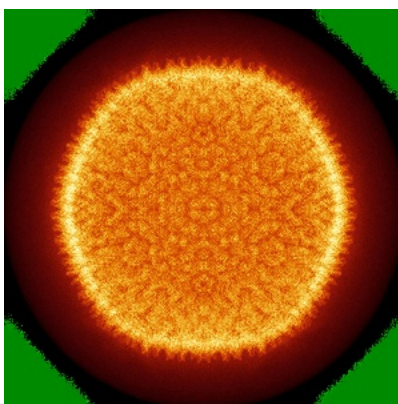
The images above show the largest variance slices of the map in three orthogonal directions.

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

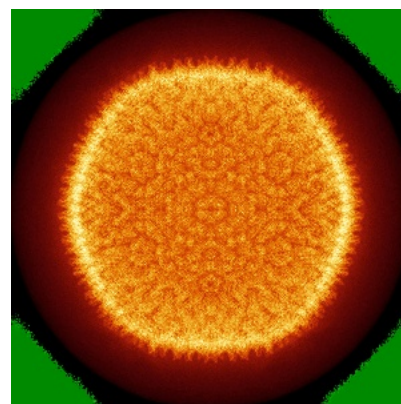
6.4.1 Primary map



X

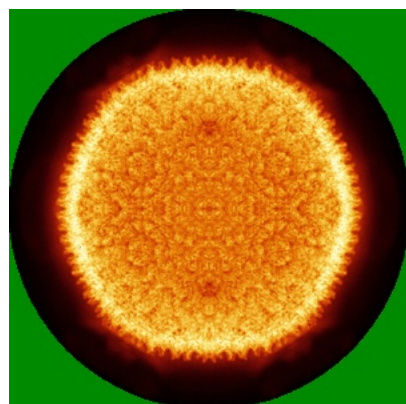


Y

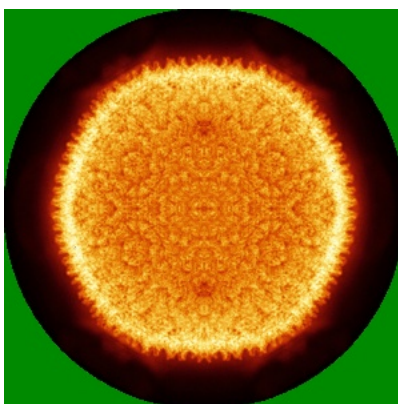


Z

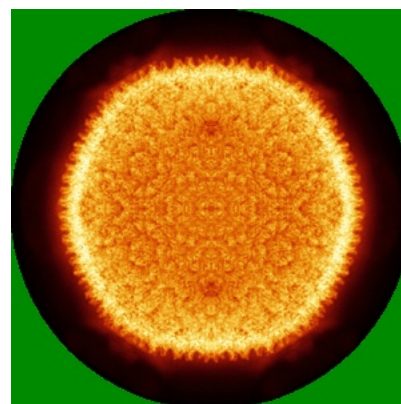
6.4.2 Raw map



X



Y

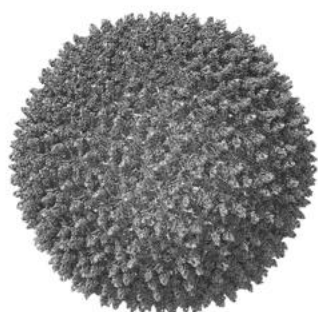


Z

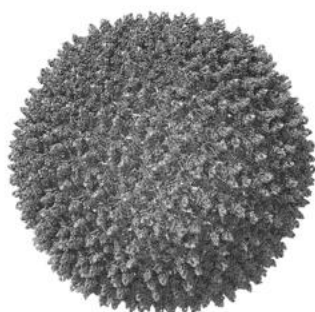
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

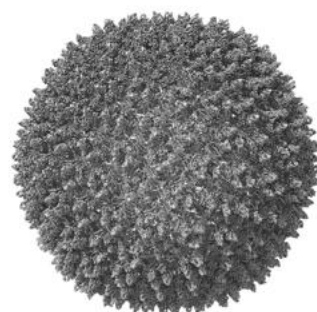
6.5.1 Primary map



X



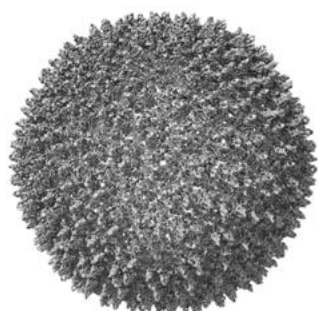
Y



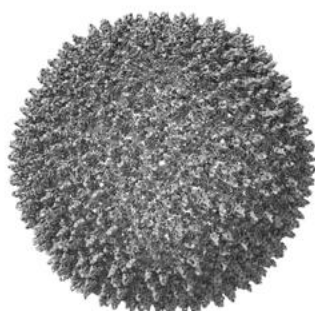
Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

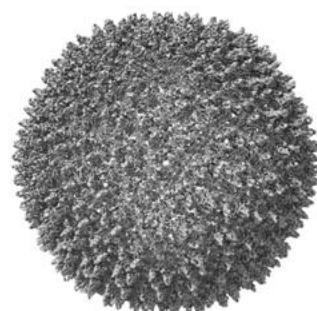
6.5.2 Raw map



X



Y



Z

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

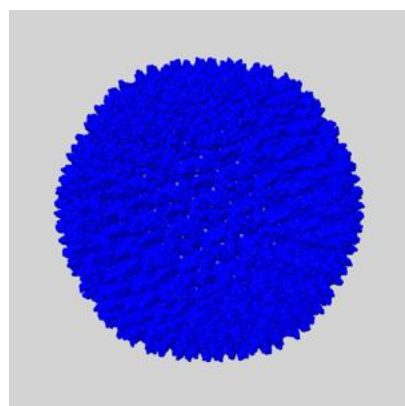
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

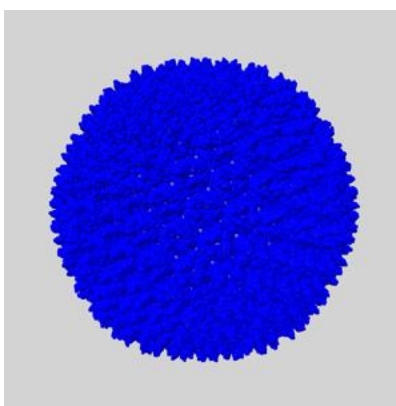
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

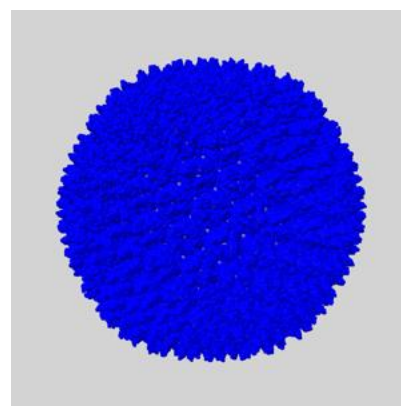
6.6.1 emd_0174_msk_1.map [i](#)



X



Y

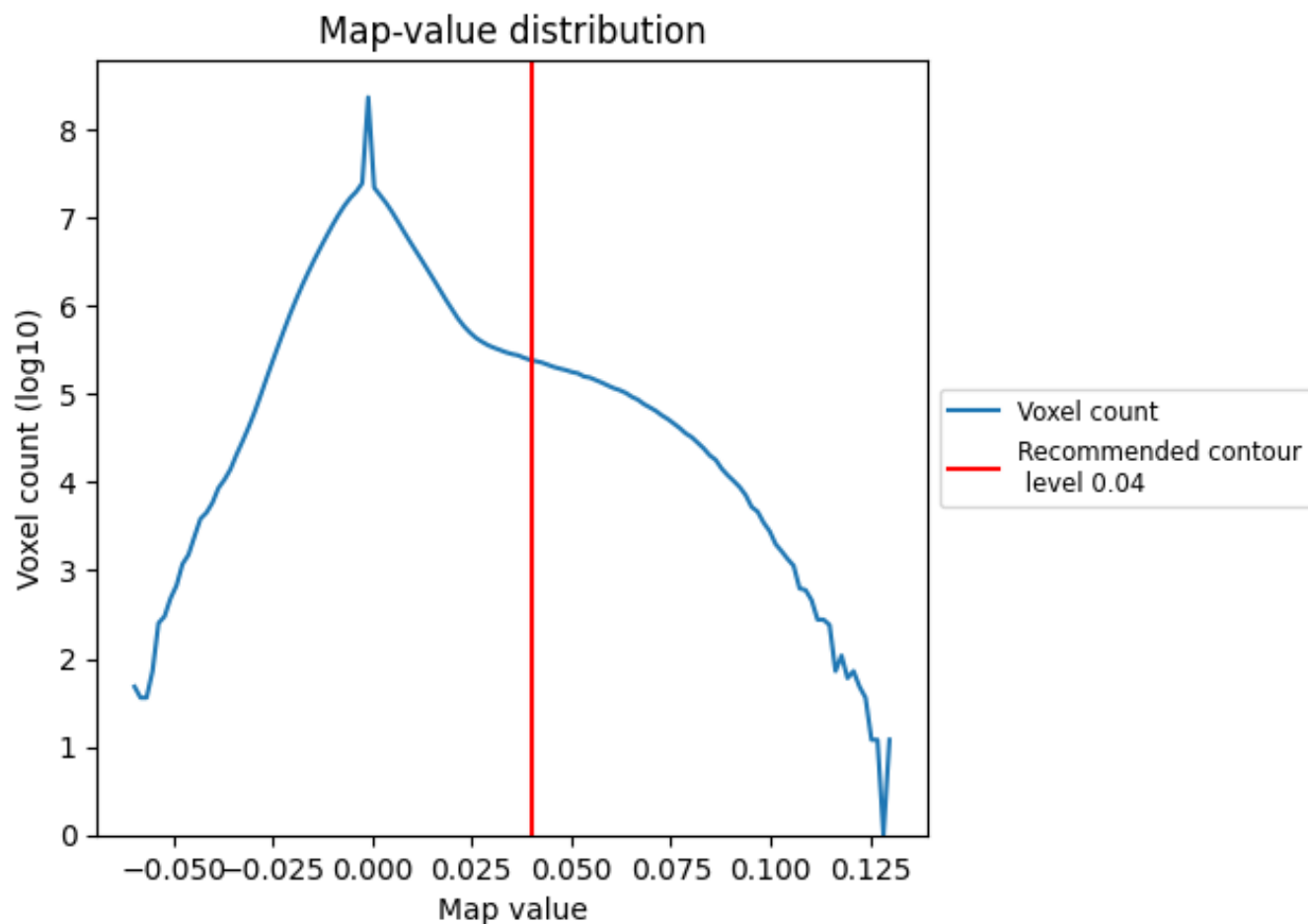


Z

7 Map analysis [i](#)

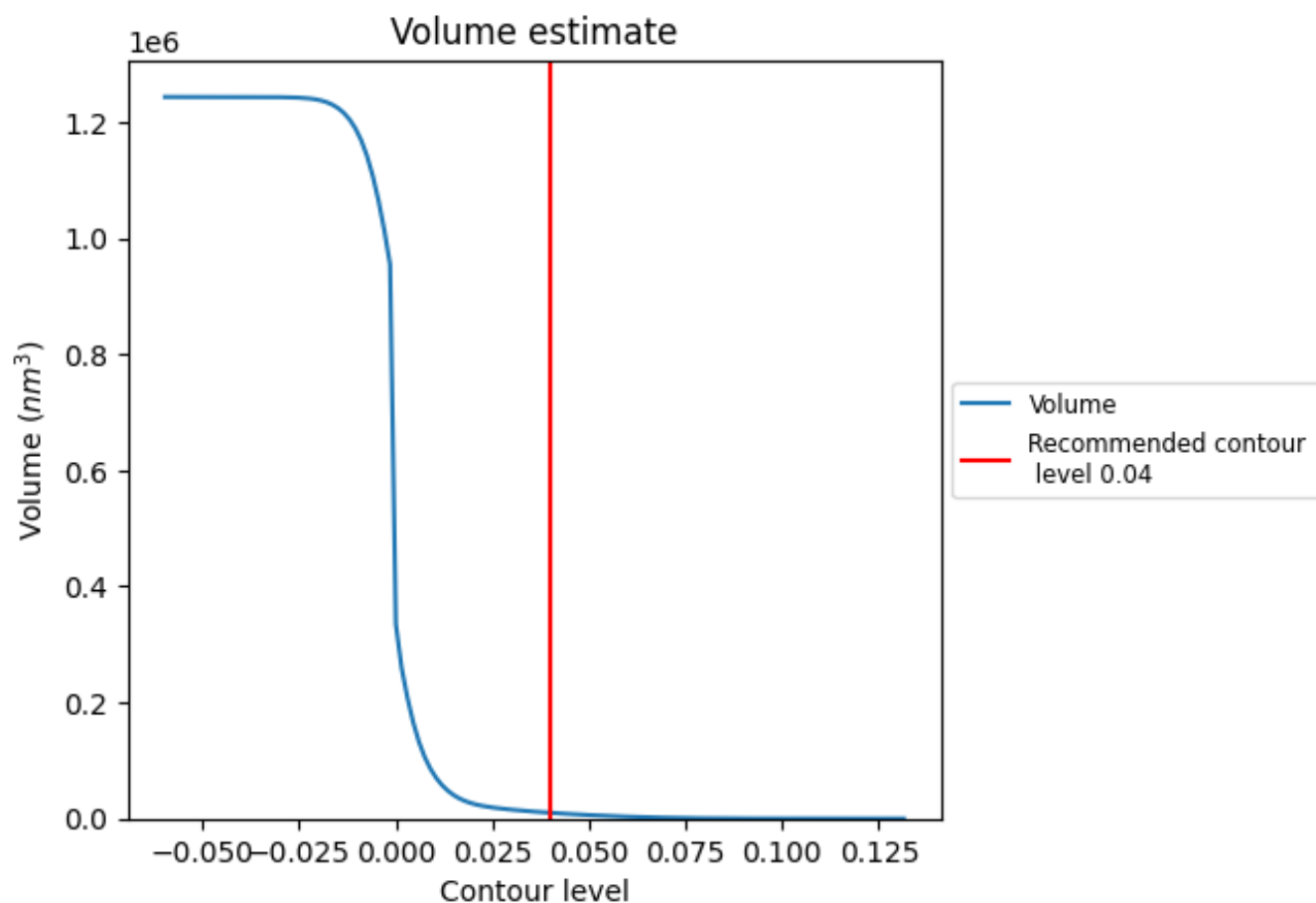
This section contains the results of statistical analysis of the map.

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.

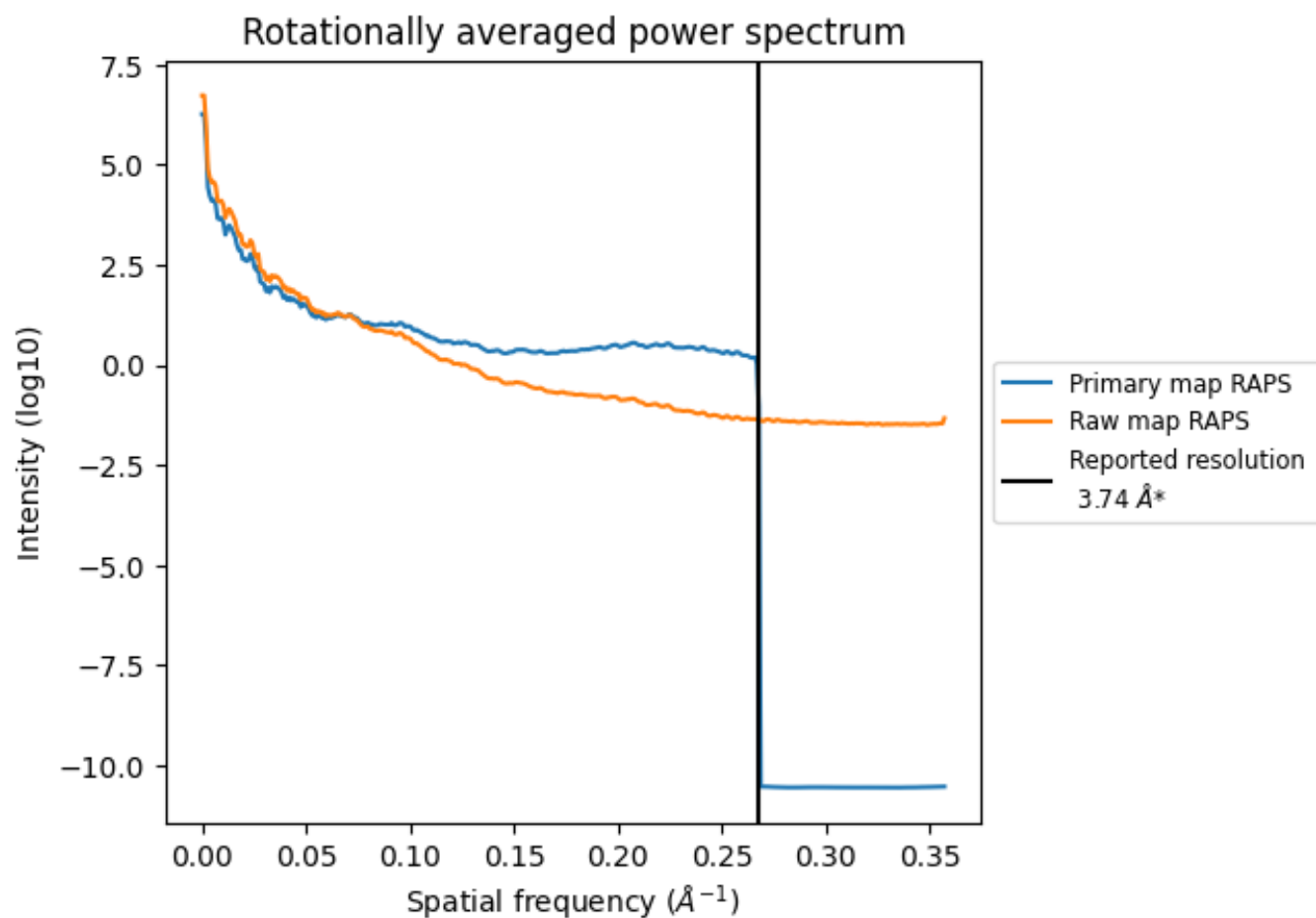
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 9996 nm³; this corresponds to an approximate mass of 9030 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

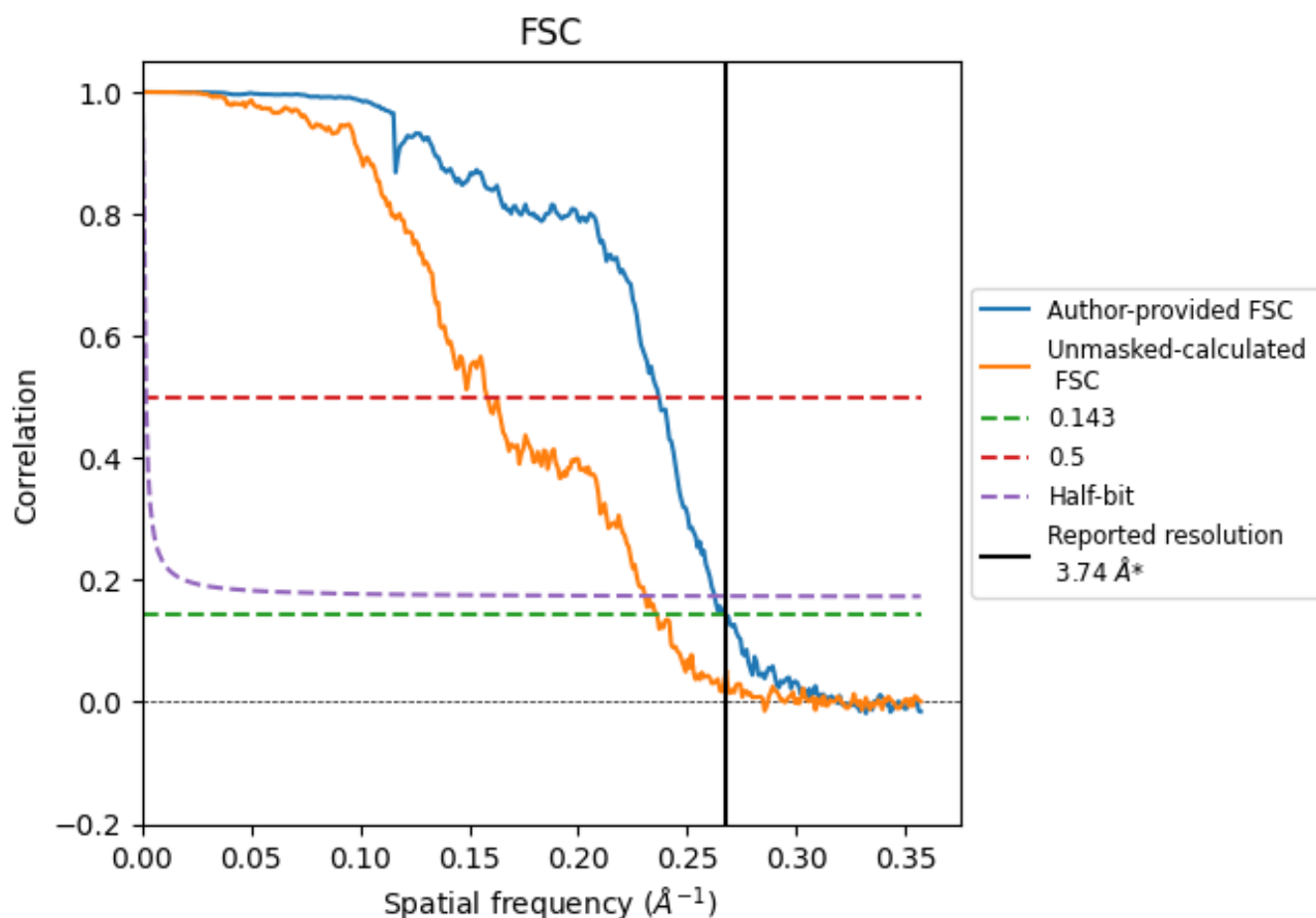


*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

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 $0.267 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.74	-	-
Author-provided FSC curve	3.74	4.22	3.81
Unmasked-calculated*	4.23	6.32	4.34

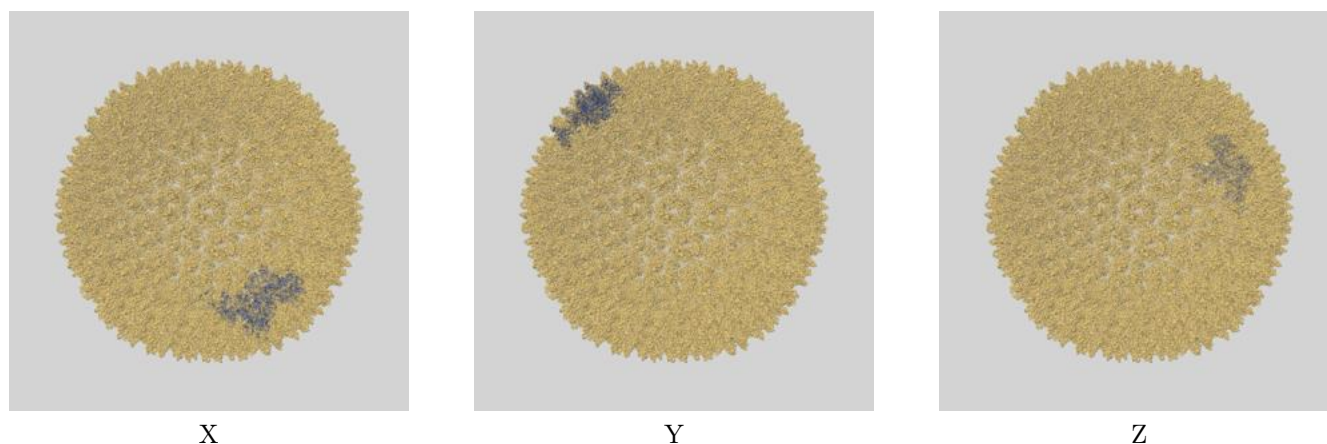
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.23 differs from the reported value 3.74 by more than 10 %

9 Map-model fit [i](#)

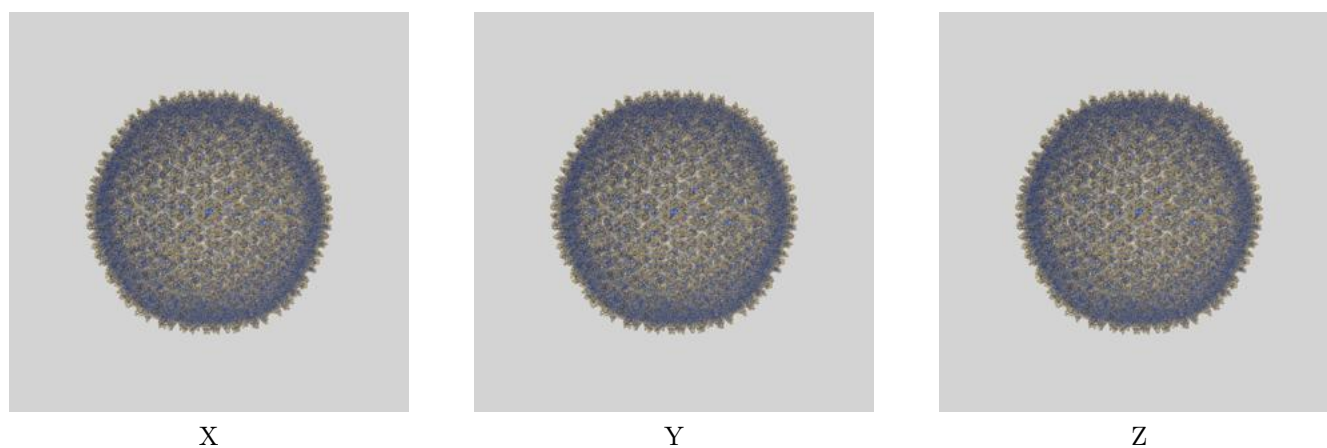
This section contains information regarding the fit between EMDB map EMD-0174 and PDB model 6H9C. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

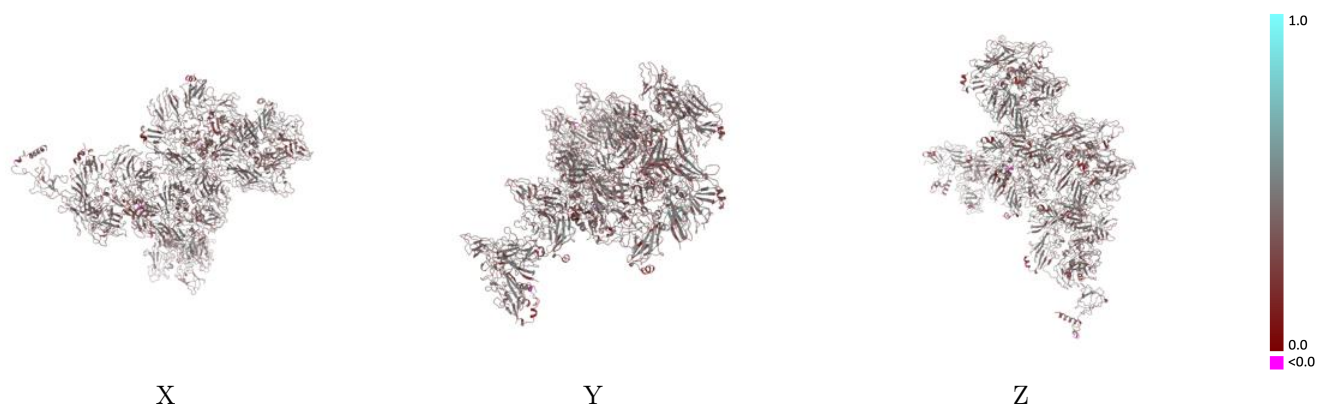


9.1.2 Map-model assembly overlay [i](#)



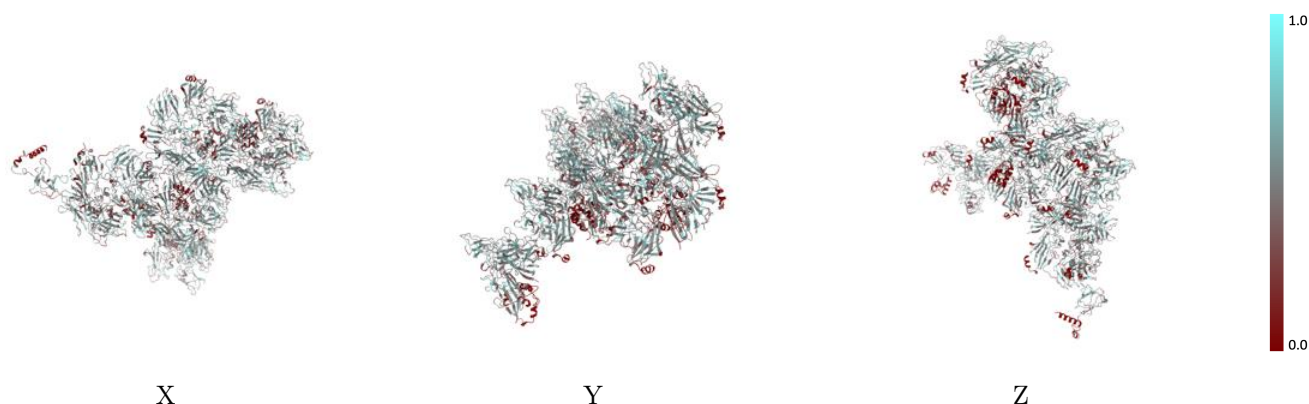
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



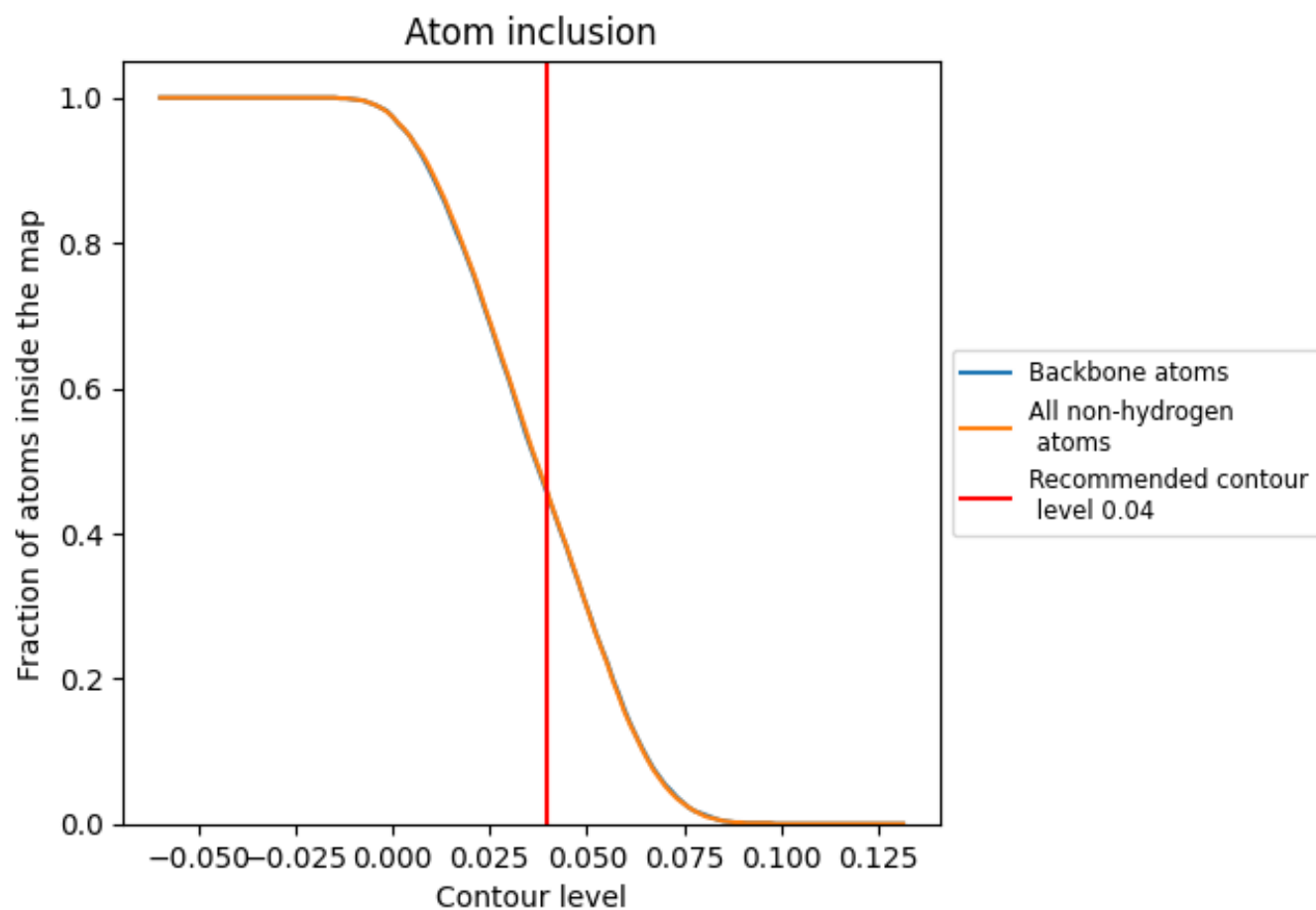
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 46% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4560	 0.3760
A	 0.5030	 0.3800
B	 0.4850	 0.3760
C	 0.5060	 0.3610
D	 0.4350	 0.3710
E	 0.4580	 0.3780
F	 0.4480	 0.3690
G	 0.5220	 0.3720
H	 0.5220	 0.3820
I	 0.4480	 0.3780
J	 0.4310	 0.3670
K	 0.4470	 0.3830
L	 0.4400	 0.3740
M	 0.4670	 0.3980
N	 0.4690	 0.3900
O	 0.5190	 0.3750
P	 0.5040	 0.3690
Q	 0.5150	 0.3750
R	 0.4450	 0.3820
S	 0.4390	 0.3680
T	 0.4630	 0.3920
U	 0.5040	 0.3790
V	 0.5060	 0.3670
W	 0.4390	 0.3800
X	 0.5210	 0.3820
Y	 0.4390	 0.3760
Z	 0.5120	 0.3700
a	 0.4650	 0.3770
b	 0.3930	 0.3690
c	 0.0440	 0.4590
d	 0.0050	 0.3360
e	 0.0130	 0.3010
f	 0.1440	 0.3220

