



## wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 11:39 PM UTC

PDB ID : 7RD1 / pdb\_00007rd1  
EMDB ID : EMD-24408  
Title : The Capsid Structure of the ChAdOx1 viral vector/chimpanzee adenovirus Y25  
Authors : Baker, A.T.; Boyd, R.J.; Sarkar, D.; Vermaas, J.V.; Williams, D.; Singharoy, A.  
Deposited on : 2021-07-08  
Resolution : 3.07 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](mailto: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:

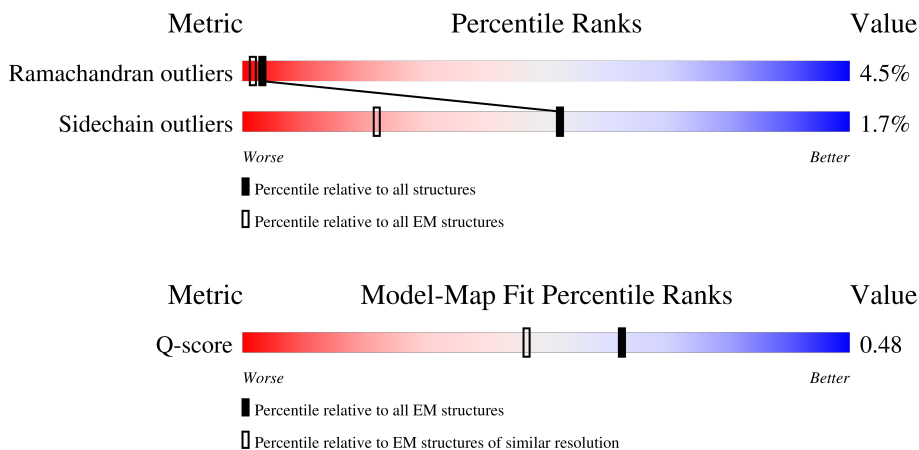
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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*




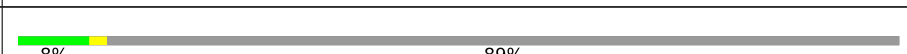

The reported resolution of this entry is 3.07 Å.

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))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13977 ( 2.57 - 3.57 )

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  $\geq 3$ , 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	0	243	 97%
1	1	243	 6% 93%
1	2	243	 8% 91%
1	3	243	 8% 89%
1	4	243	 8% 91%



*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	8	243	7% 90%
1	U	243	95%
1	V	243	7% 92%
1	W	243	9% 90%
1	X	243	8% 89%
1	Y	243	5% 10% 89%
1	Z	243	97%
2	A	942	89% 10%
2	B	942	83% 15%
2	C	942	91% 9%
2	D	942	88% 11%
2	E	942	90% 10%
2	F	942	89% 10%
2	G	942	90% 10%
2	H	942	88% 11%
2	I	942	90% 9%
2	J	942	90% 10%
2	K	942	91% 8%
2	L	942	91% 8%
3	M	532	24% 75% 6% 18%
4	N	142	47% 12% 37%
4	O	142	42% 6% 44%
4	P	142	47% 11% 32%
4	Q	142	35% 7% 49%
5	R	589	5% 16% 81%

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
6	S	227	 <p>5% 69% 7% 23%</p>
6	T	227	 <p>5% 67% 11% 22%</p>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 197782 atoms, of which 96589 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 Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
1	0	7	Total	C	H	N	O	0	0	
			106	35	51	8	12			
1	U	11	Total	C	H	N	O	0	0	
			171	55	83	17	16			
1	1	17	Total	C	H	N	O	0	0	
			245	77	118	23	27			
1	V	20	Total	C	H	N	O	S	0	0
			286	96	136	22	31	1		
1	2	21	Total	C	H	N	O	S	0	0
			323	106	156	31	29	1		
1	W	24	Total	C	H	N	O	S	0	0
			361	118	174	34	34	1		
1	3	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	X	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	4	22	Total	C	H	N	O	S	0	0
			335	110	160	32	32	1		
1	Y	26	Total	C	H	N	O	S	0	0
			386	125	186	36	38	1		
1	8	24	Total	C	H	N	O	S	0	0
			363	118	177	34	33	1		
1	Z	7	Total	C	H	N	O	0	0	
			106	35	51	8	12			

- Molecule 2 is a protein called Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
2	A	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	B	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	C	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	E	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	F	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	G	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	H	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	I	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	J	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	K	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		
2	L	942	Total	C	H	N	O	S	0	0
			14601	4743	7121	1259	1442	36		

- Molecule 3 is a protein called Penton protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	M	435	Total	C	H	N	O	S	0	0
			6923	2219	3423	596	672	13		

- Molecule 4 is a protein called Hexon-interlacing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	N	89	Total	C	H	N	O	S	0	0
			1328	412	664	114	135	3		
4	O	79	Total	C	H	N	O	S	0	0
			1187	368	595	102	119	3		
4	P	96	Total	C	H	N	O	S	0	0
			1435	443	720	125	144	3		
4	Q	73	Total	C	H	N	O	S	0	0
			1108	342	560	99	104	3		

- Molecule 5 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	R	114	Total	C	H	N	O	S	0	0
			1767	539	885	167	173	3		

- Molecule 6 is a protein called Pre-hexon-linking protein VIII.

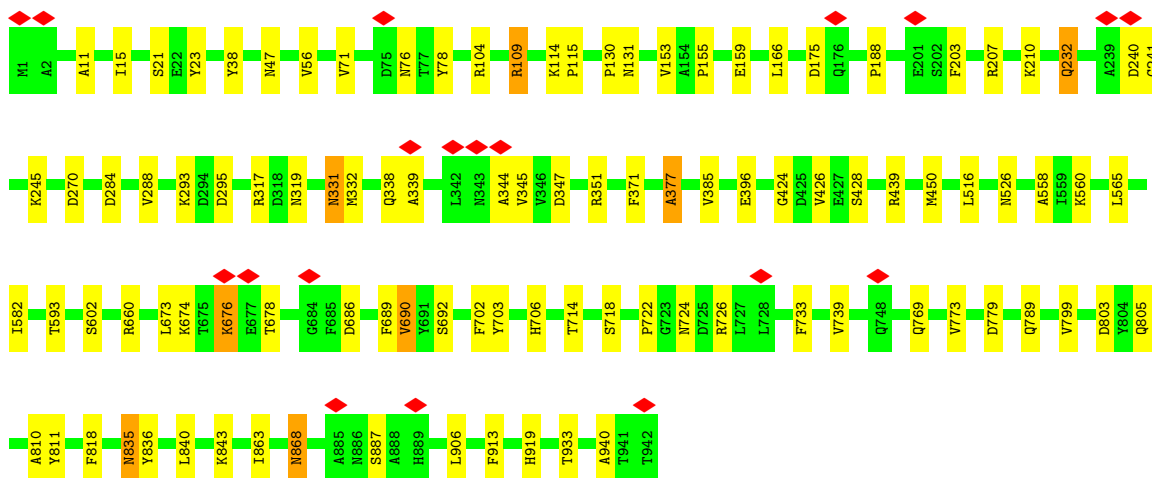
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	S	175	Total	C	H	N	O	S	0	0
			2673	861	1308	234	265	5		
6	T	177	Total	C	H	N	O	S	0	0
			2695	867	1318	236	269	5		



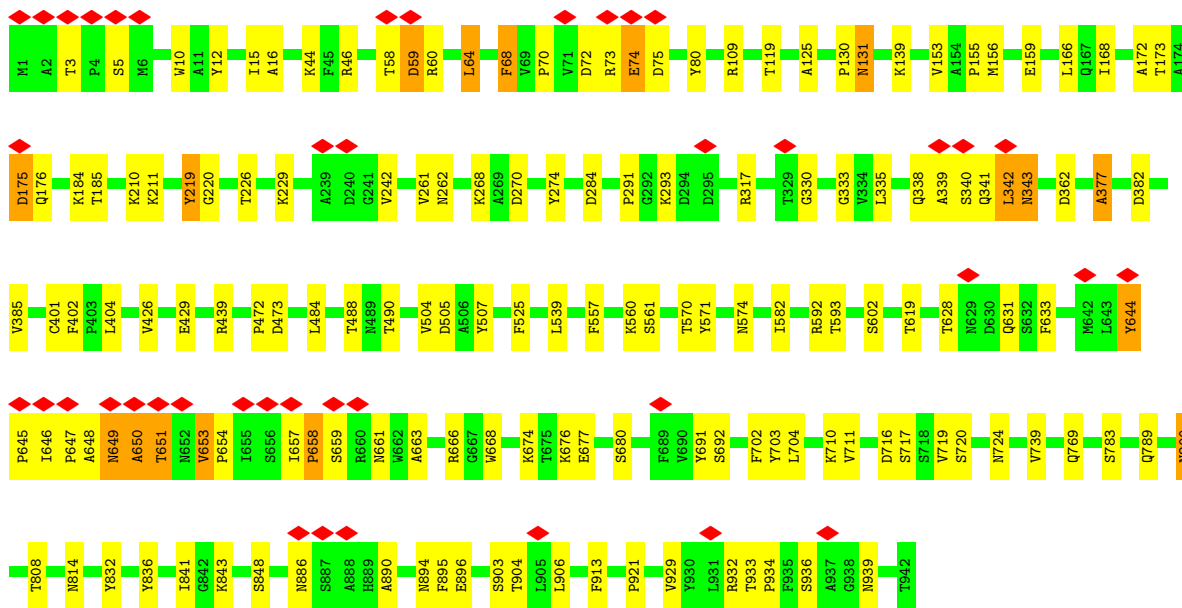
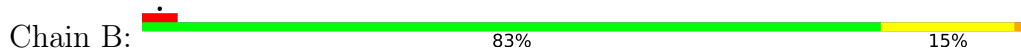




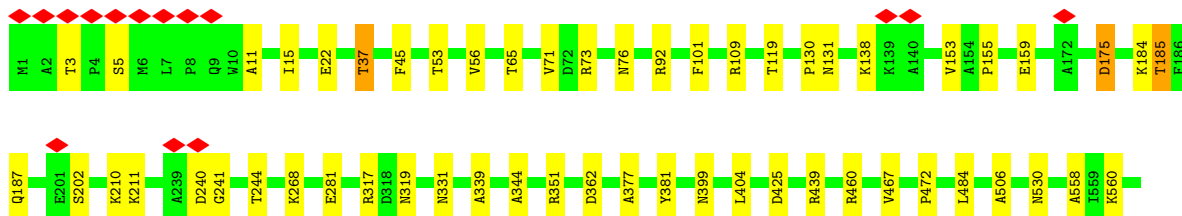


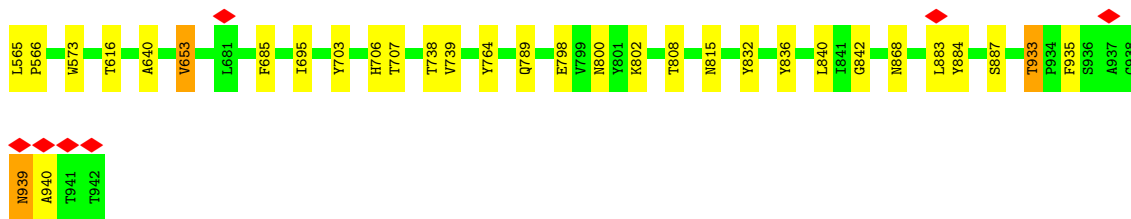


• Molecule 2: Hexon protein

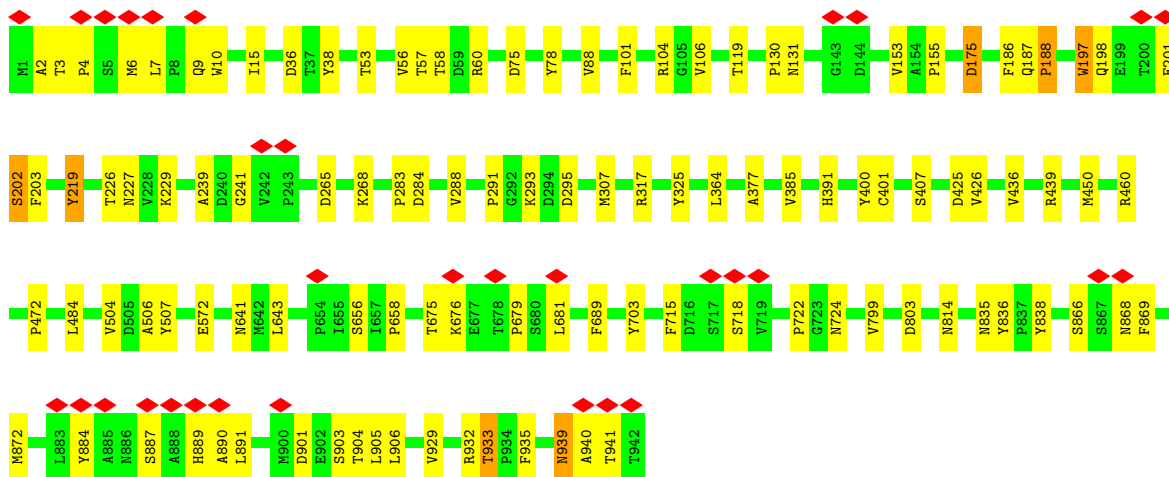
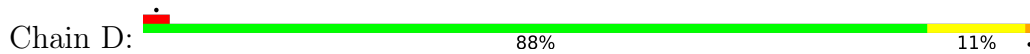


• Molecule 2: Hexon protein

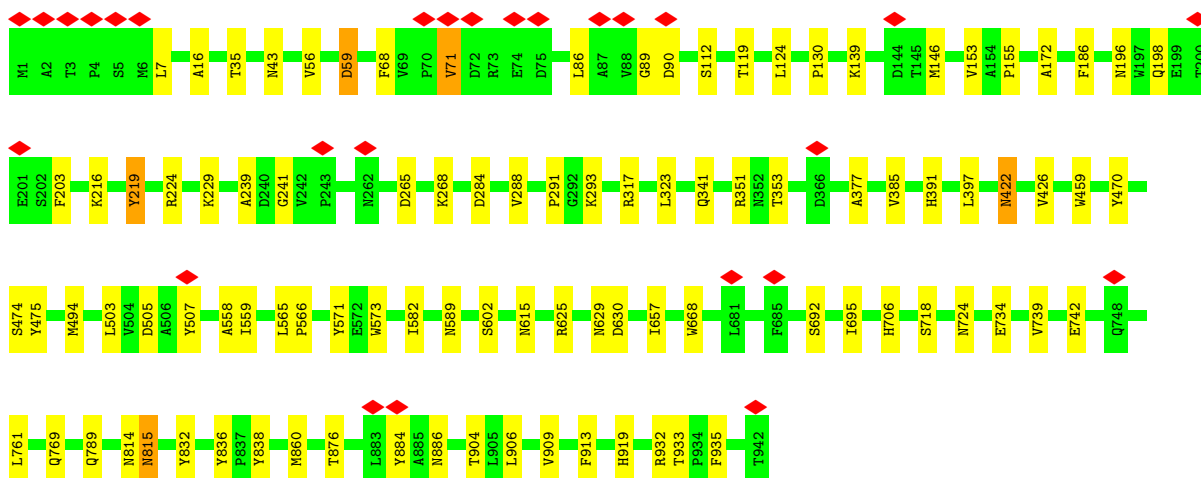
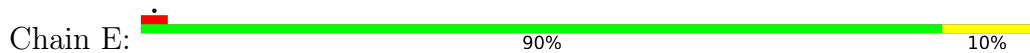




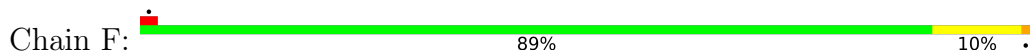
• Molecule 2: Hexon protein

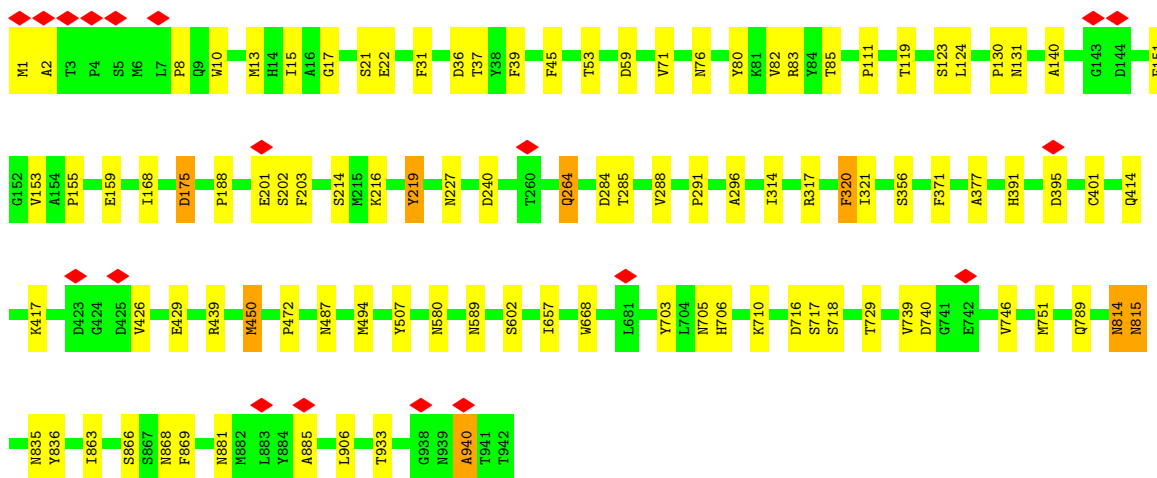


• Molecule 2: Hexon protein

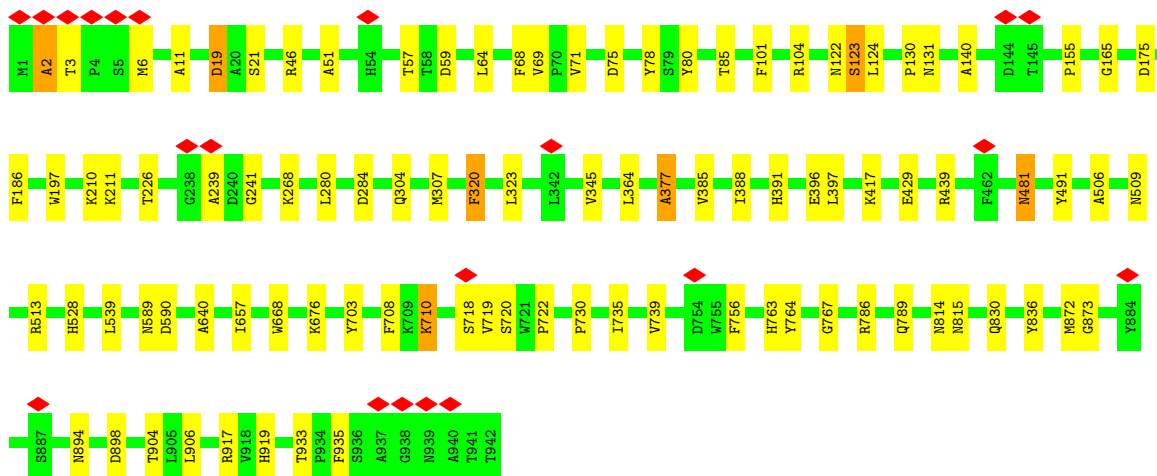
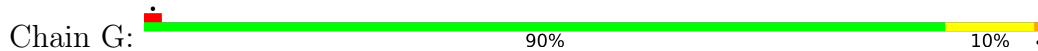


• Molecule 2: Hexon protein

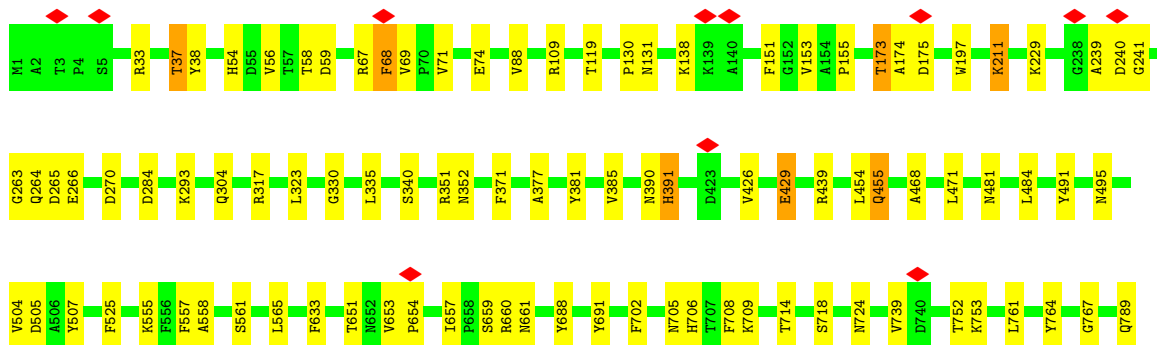
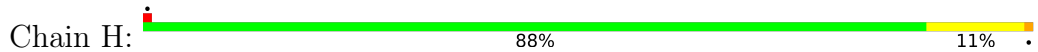


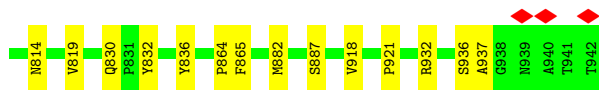


• Molecule 2: Hexon protein

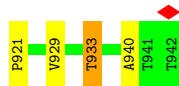
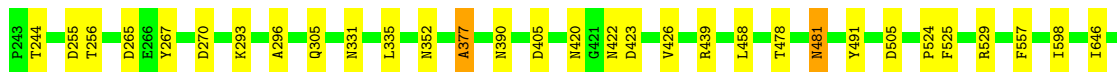
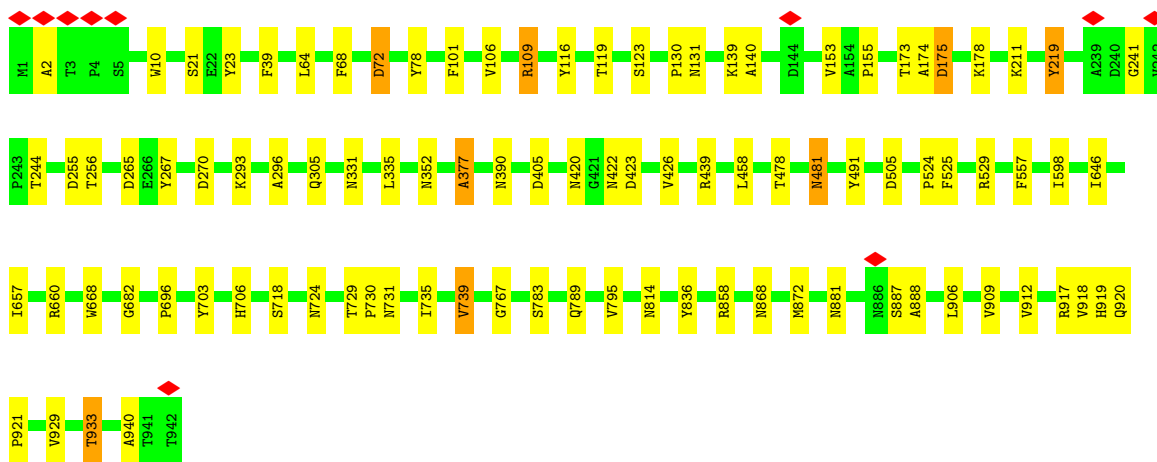
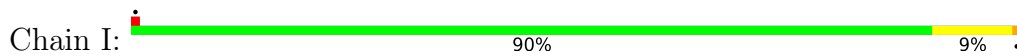


• Molecule 2: Hexon protein

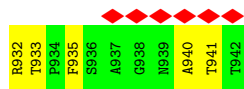
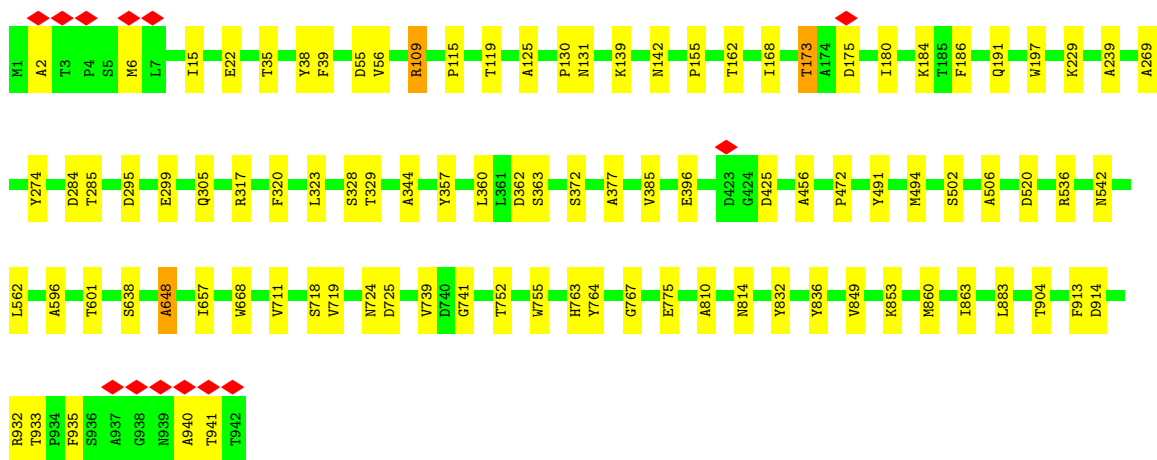
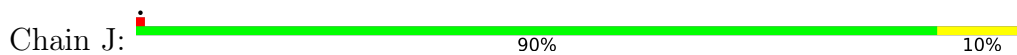




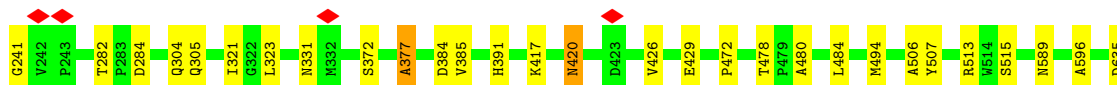
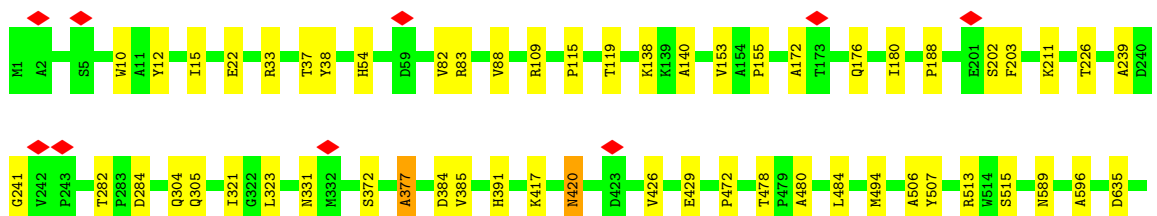
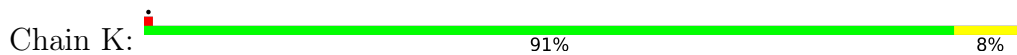
• Molecule 2: Hexon protein

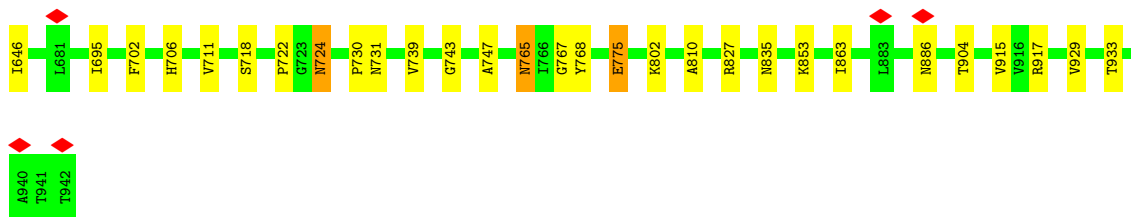


• Molecule 2: Hexon protein

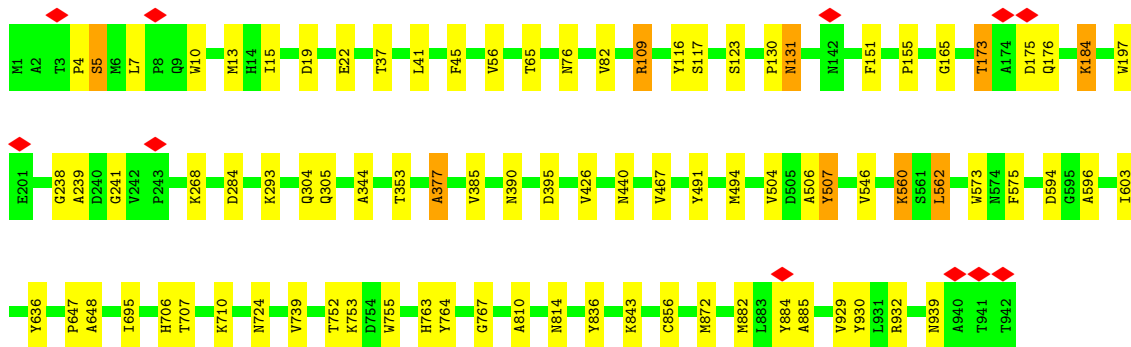
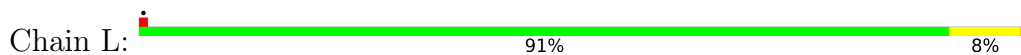


• Molecule 2: Hexon protein

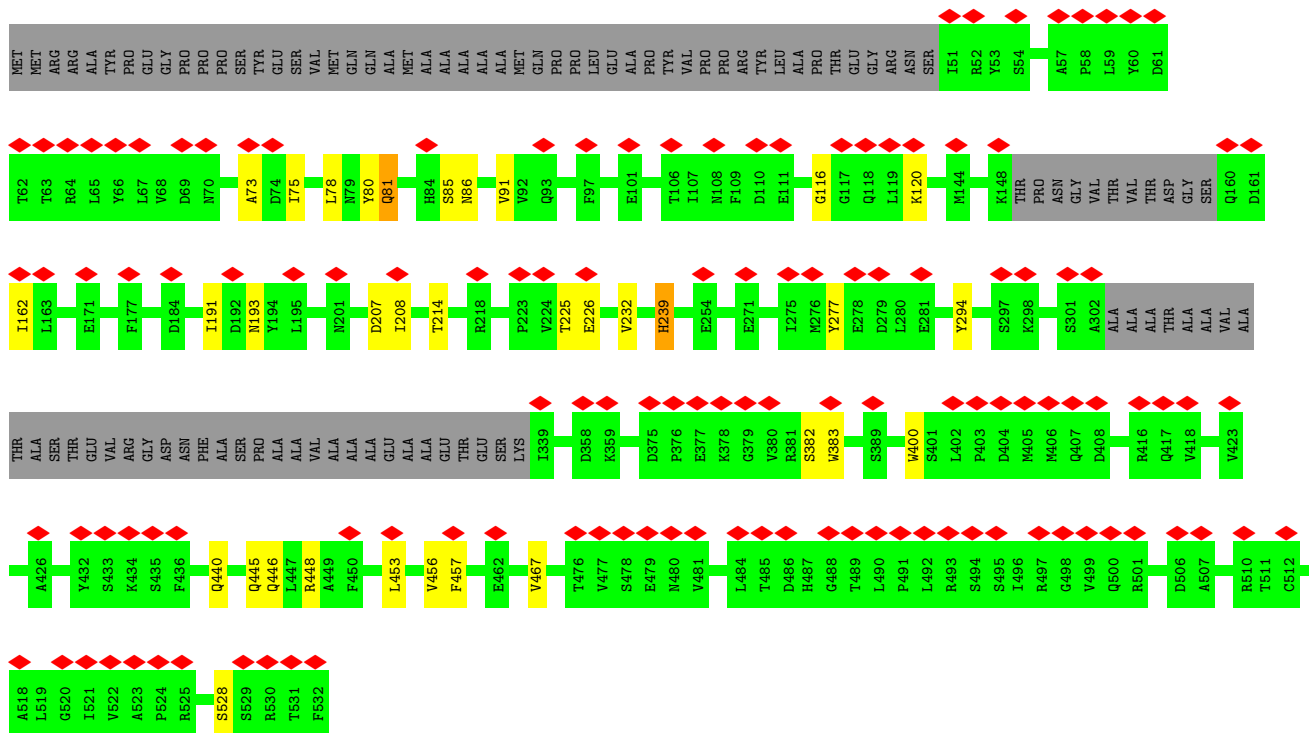
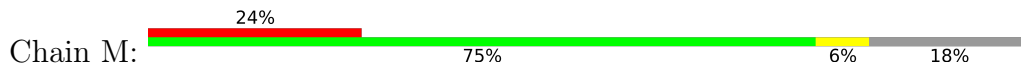




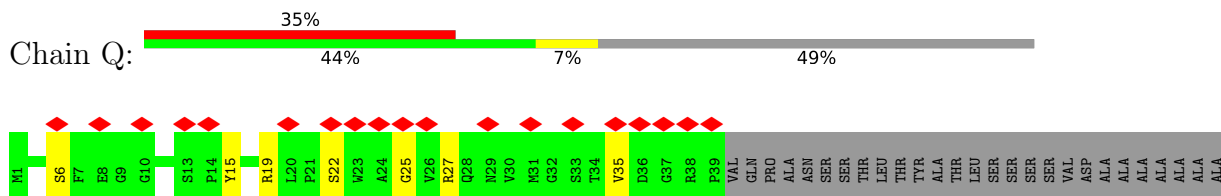
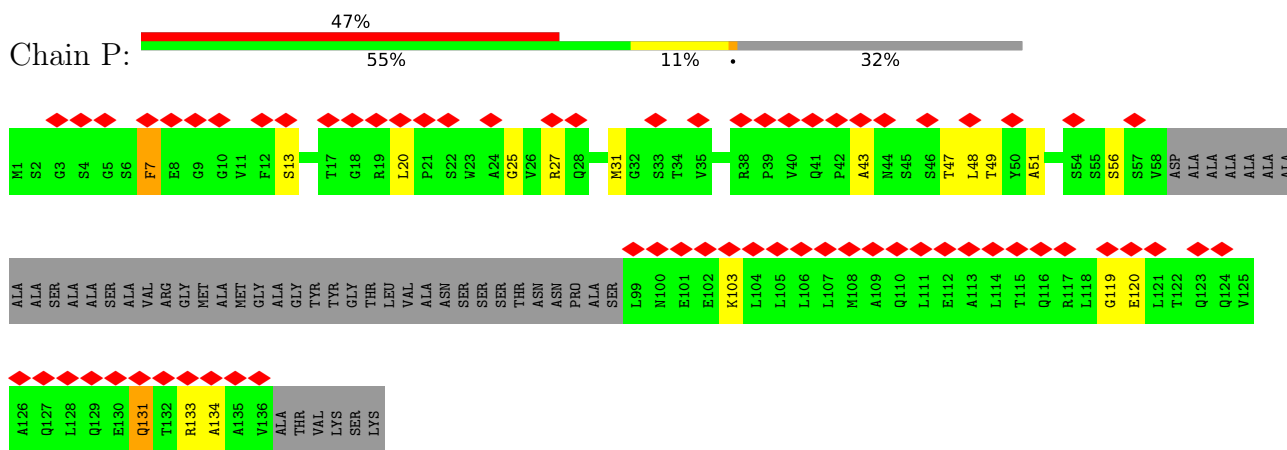
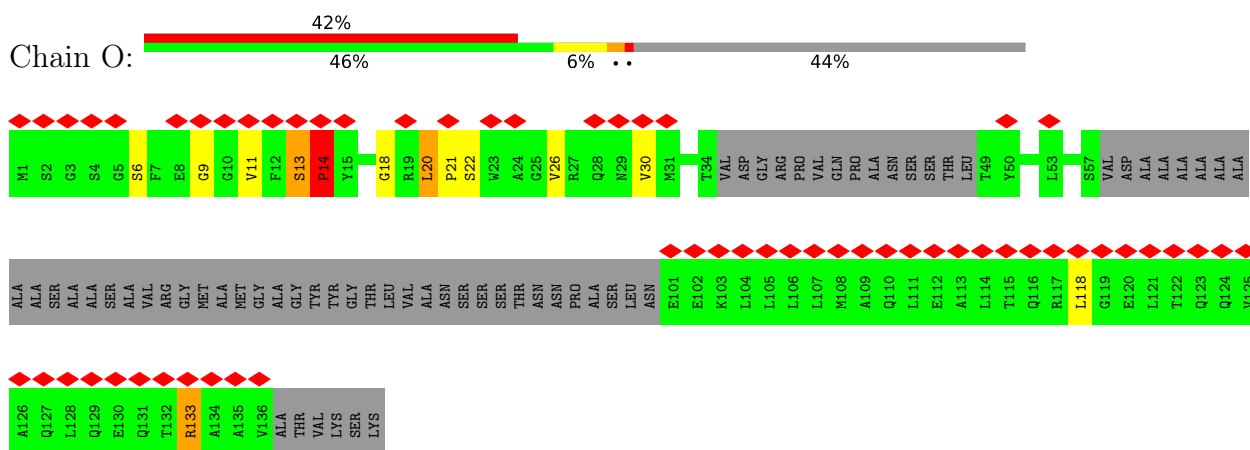
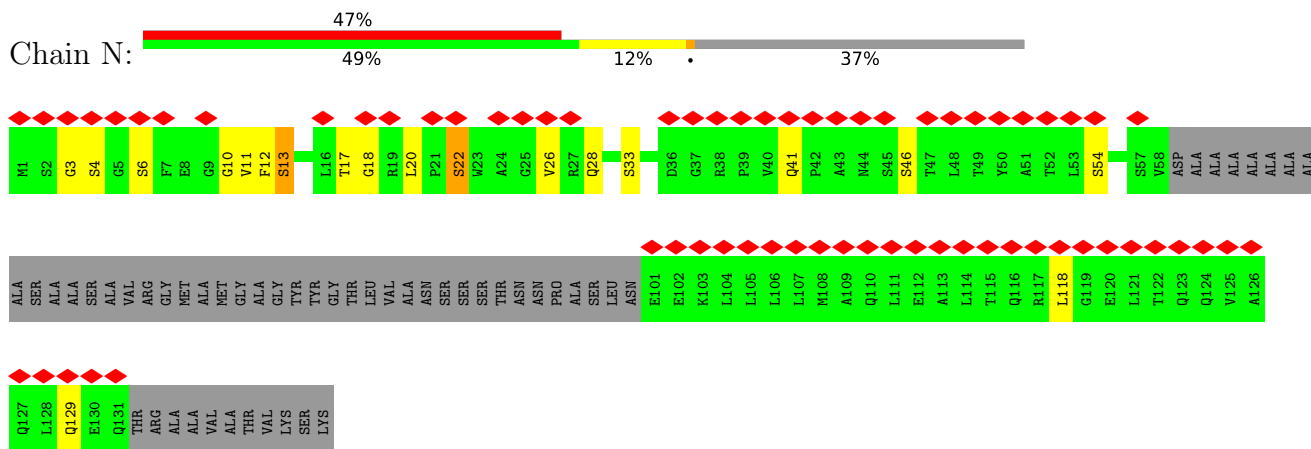
• Molecule 2: Hexon protein



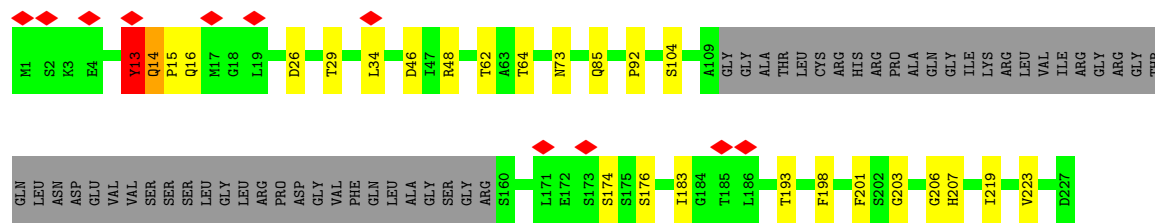
• Molecule 3: Penton protein



• Molecule 4: Hexon-interlacing protein







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5748	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.1802	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.095	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ( $\text{\AA}$ )	1929.6006, 1929.6006, 1929.6006	wwPDB
Map dimensions	1260, 1260, 1260	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.531429, 1.531429, 1.531429	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	0	1.10	0/55	1.26	0/73
1	1	1.07	0/128	1.65	1/171 (0.6%)
1	2	1.04	0/173	1.51	0/234
1	3	0.98	0/206	1.72	4/279 (1.4%)
1	4	0.93	0/181	1.57	0/245
1	8	1.20	0/192	1.68	2/260 (0.8%)
1	U	1.09	0/90	1.44	0/121
1	V	1.05	0/153	1.54	0/206
1	W	1.02	0/193	1.53	0/261
1	X	1.20	0/206	1.63	2/279 (0.7%)
1	Y	0.96	0/206	1.64	0/279
1	Z	1.08	0/55	0.90	0/73
2	A	1.21	1/7683 (0.0%)	1.51	66/10460 (0.6%)
2	B	1.23	0/7683	1.53	97/10460 (0.9%)
2	C	1.22	0/7683	1.49	58/10460 (0.6%)
2	D	1.19	0/7683	1.51	63/10460 (0.6%)
2	E	1.21	0/7683	1.48	63/10460 (0.6%)
2	F	1.23	0/7683	1.48	69/10460 (0.7%)
2	G	1.23	0/7683	1.49	78/10460 (0.7%)
2	H	1.23	0/7683	1.51	81/10460 (0.8%)
2	I	1.22	0/7683	1.49	59/10460 (0.6%)
2	J	1.22	0/7683	1.48	70/10460 (0.7%)
2	K	1.23	0/7683	1.46	53/10460 (0.5%)
2	L	1.23	0/7683	1.47	53/10460 (0.5%)
3	M	1.15	0/3580	1.45	24/4872 (0.5%)
4	N	1.14	0/672	1.63	12/909 (1.3%)
4	O	1.05	0/597	1.60	8/803 (1.0%)
4	P	1.15	0/723	1.56	8/979 (0.8%)
4	Q	1.12	0/554	1.52	6/746 (0.8%)
5	R	1.23	0/892	1.56	14/1213 (1.2%)
6	S	1.16	0/1403	1.54	10/1917 (0.5%)
6	T	1.20	0/1415	1.60	16/1933 (0.8%)
All	All	1.21	1/103870 (0.0%)	1.50	917/141373 (0.6%)

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	A	0	2
2	B	0	5
2	D	0	6
2	E	0	4
2	F	0	2
2	G	0	1
2	H	0	3
2	I	0	6
2	J	0	2
2	K	0	1
2	L	0	5
3	M	0	1
4	O	0	1
4	Q	0	1
5	R	0	1
6	T	0	2
All	All	0	43

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	673	LEU	CA-C	-5.45	1.50	1.53

The worst 5 of 917 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	15	ILE	N-CA-C	-11.37	102.57	112.12
2	E	385	VAL	N-CA-C	-11.17	102.85	111.90
2	K	385	VAL	N-CA-C	-10.88	103.02	111.62
2	I	72	ASP	CA-CB-CG	10.15	122.75	112.60
2	G	756	PHE	N-CA-C	-9.98	100.98	113.55

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	109	ARG	Sidechain
2	A	207	ARG	Sidechain

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
2	B	219	TYR	Sidechain
2	B	507	TYR	Sidechain
2	B	571	TYR	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	55	51	50	0	0
1	1	127	118	116	0	0
1	2	167	156	155	0	0
1	3	200	186	185	0	0
1	4	175	160	159	0	0
1	8	186	177	176	0	0
1	U	88	83	82	0	0
1	V	150	136	134	0	0
1	W	187	174	173	0	0
1	X	200	186	185	0	0
1	Y	200	186	185	0	0
1	Z	55	51	50	0	0
2	A	7480	7121	7121	0	0
2	B	7480	7121	7121	0	0
2	C	7480	7121	7121	0	0
2	D	7480	7121	7121	0	0
2	E	7480	7121	7121	0	0
2	F	7480	7121	7121	0	0
2	G	7480	7121	7121	0	0
2	H	7480	7121	7121	0	0
2	I	7480	7121	7121	0	0
2	J	7480	7121	7121	0	0
2	K	7480	7121	7121	0	0
2	L	7480	7121	7121	0	0
3	M	3500	3423	3420	0	0
4	N	664	664	663	0	0
4	O	592	595	593	0	0
4	P	715	720	719	0	0
4	Q	548	560	559	0	0
5	R	882	885	884	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	S	1365	1308	1307	0	0
6	T	1377	1318	1317	0	0
All	All	101193	96589	96564	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	0	5/243 (2%)	4 (80%)	0	1 (20%)	0	0
1	1	13/243 (5%)	9 (69%)	3 (23%)	1 (8%)	1	4
1	2	19/243 (8%)	15 (79%)	2 (10%)	2 (10%)	0	2
1	3	24/243 (10%)	16 (67%)	7 (29%)	1 (4%)	2	11
1	4	20/243 (8%)	14 (70%)	3 (15%)	3 (15%)	0	0
1	8	22/243 (9%)	13 (59%)	5 (23%)	4 (18%)	0	0
1	U	9/243 (4%)	7 (78%)	2 (22%)	0	100	100
1	V	16/243 (7%)	13 (81%)	2 (12%)	1 (6%)	1	6
1	W	22/243 (9%)	12 (54%)	8 (36%)	2 (9%)	0	3
1	X	24/243 (10%)	16 (67%)	3 (12%)	5 (21%)	0	0
1	Y	24/243 (10%)	18 (75%)	5 (21%)	1 (4%)	2	11
1	Z	5/243 (2%)	5 (100%)	0	0	100	100
2	A	940/942 (100%)	822 (87%)	80 (8%)	38 (4%)	2	12
2	B	940/942 (100%)	771 (82%)	99 (10%)	70 (7%)	1	4
2	C	940/942 (100%)	824 (88%)	85 (9%)	31 (3%)	3	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	940/942 (100%)	819 (87%)	75 (8%)	46 (5%)	1	9
2	E	940/942 (100%)	826 (88%)	79 (8%)	35 (4%)	2	13
2	F	940/942 (100%)	834 (89%)	67 (7%)	39 (4%)	2	12
2	G	940/942 (100%)	824 (88%)	82 (9%)	34 (4%)	2	14
2	H	940/942 (100%)	811 (86%)	89 (10%)	40 (4%)	2	11
2	I	940/942 (100%)	827 (88%)	79 (8%)	34 (4%)	2	14
2	J	940/942 (100%)	829 (88%)	75 (8%)	36 (4%)	2	13
2	K	940/942 (100%)	816 (87%)	95 (10%)	29 (3%)	3	16
2	L	940/942 (100%)	827 (88%)	75 (8%)	38 (4%)	2	12
3	M	429/532 (81%)	390 (91%)	28 (6%)	11 (3%)	4	19
4	N	85/142 (60%)	65 (76%)	9 (11%)	11 (13%)	0	1
4	O	73/142 (51%)	54 (74%)	9 (12%)	10 (14%)	0	1
4	P	92/142 (65%)	69 (75%)	11 (12%)	12 (13%)	0	1
4	Q	69/142 (49%)	57 (83%)	9 (13%)	3 (4%)	2	11
5	R	112/589 (19%)	94 (84%)	13 (12%)	5 (4%)	2	10
6	S	171/227 (75%)	141 (82%)	20 (12%)	10 (6%)	1	7
6	T	173/227 (76%)	143 (83%)	18 (10%)	12 (7%)	1	5
All	All	12687/16363 (78%)	10985 (87%)	1137 (9%)	565 (4%)	3	10

5 of 565 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	6	PHE
1	W	10	ALA
1	8	25	ILE
2	A	21	SER
2	A	76	ASN

### 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	0	7/203 (3%)	7 (100%)	0	100	100
1	1	15/203 (7%)	14 (93%)	1 (7%)	15	41
1	2	18/203 (9%)	17 (94%)	1 (6%)	19	46
1	3	22/203 (11%)	19 (86%)	3 (14%)	3	14
1	4	19/203 (9%)	18 (95%)	1 (5%)	20	48
1	8	20/203 (10%)	19 (95%)	1 (5%)	22	50
1	U	10/203 (5%)	9 (90%)	1 (10%)	7	26
1	V	17/203 (8%)	15 (88%)	2 (12%)	5	20
1	W	20/203 (10%)	19 (95%)	1 (5%)	22	50
1	X	22/203 (11%)	22 (100%)	0	100	100
1	Y	22/203 (11%)	21 (96%)	1 (4%)	24	53
1	Z	7/203 (3%)	7 (100%)	0	100	100
2	A	810/810 (100%)	799 (99%)	11 (1%)	59	73
2	B	810/810 (100%)	787 (97%)	23 (3%)	38	63
2	C	810/810 (100%)	794 (98%)	16 (2%)	48	69
2	D	810/810 (100%)	796 (98%)	14 (2%)	53	71
2	E	810/810 (100%)	797 (98%)	13 (2%)	55	72
2	F	810/810 (100%)	797 (98%)	13 (2%)	55	72
2	G	810/810 (100%)	801 (99%)	9 (1%)	65	76
2	H	810/810 (100%)	799 (99%)	11 (1%)	59	73
2	I	810/810 (100%)	796 (98%)	14 (2%)	53	71
2	J	810/810 (100%)	802 (99%)	8 (1%)	68	77
2	K	810/810 (100%)	795 (98%)	15 (2%)	50	70
2	L	810/810 (100%)	801 (99%)	9 (1%)	65	76
3	M	393/461 (85%)	389 (99%)	4 (1%)	68	77
4	N	74/105 (70%)	72 (97%)	2 (3%)	39	64
4	O	64/105 (61%)	62 (97%)	2 (3%)	35	61
4	P	79/105 (75%)	77 (98%)	2 (2%)	42	66
4	Q	58/105 (55%)	57 (98%)	1 (2%)	53	71
5	R	96/502 (19%)	93 (97%)	3 (3%)	35	61
6	S	149/189 (79%)	146 (98%)	3 (2%)	48	69
6	T	151/189 (80%)	148 (98%)	3 (2%)	48	69

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10983/13917 (79%)	10795 (98%)	188 (2%)	52 71

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	153	VAL
2	J	933	THR
2	H	633	PHE
2	I	795	VAL
2	K	417	LYS

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 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.

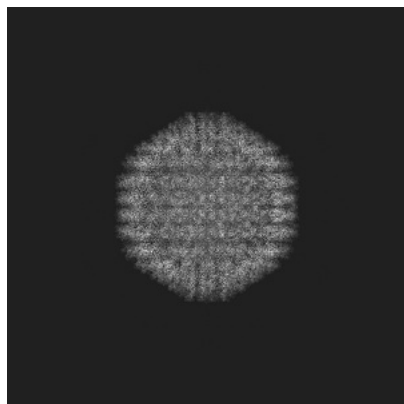
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24408. These allow visual inspection of the internal detail of the map and identification of artifacts.

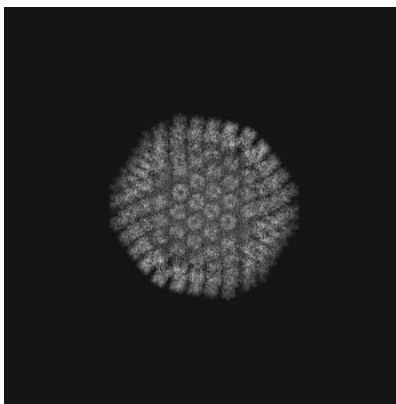
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

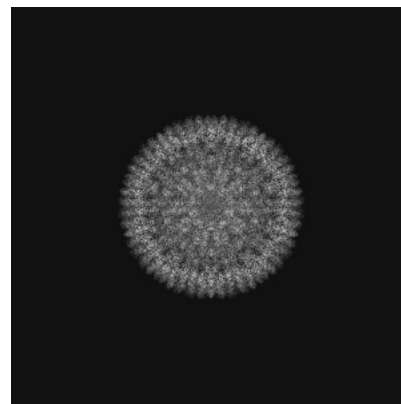
#### 6.1.1 Primary map



X

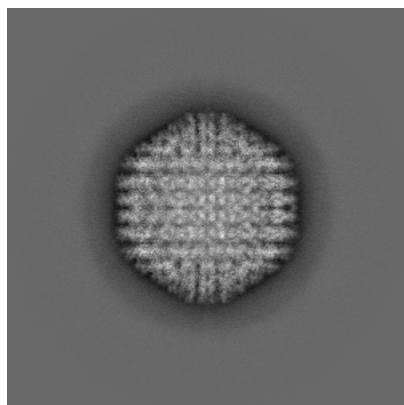


Y

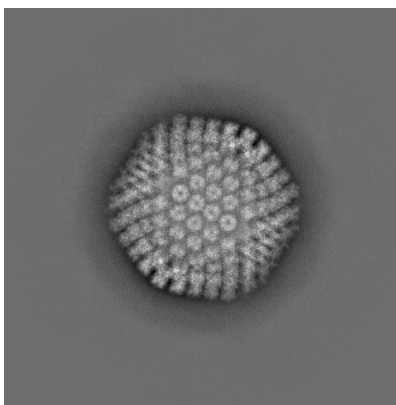


Z

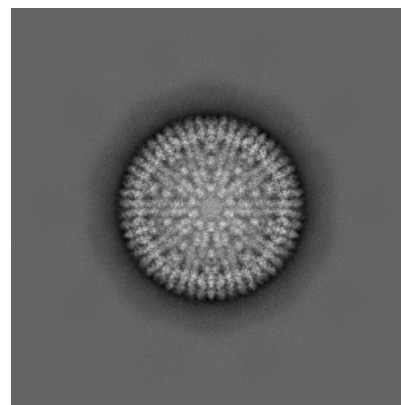
#### 6.1.2 Raw map



X



Y

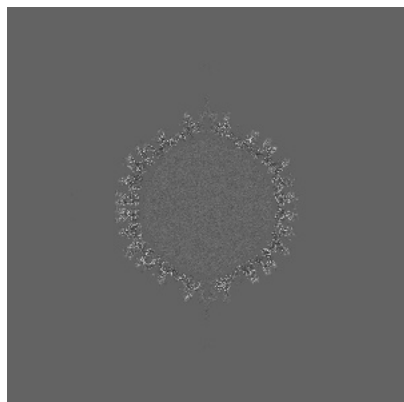


Z

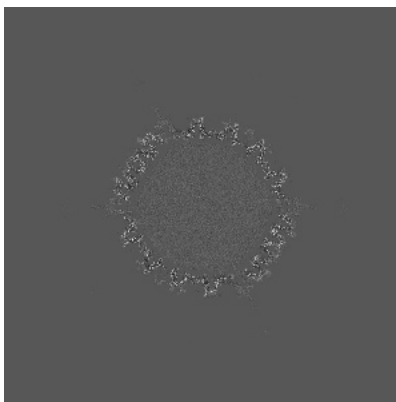
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

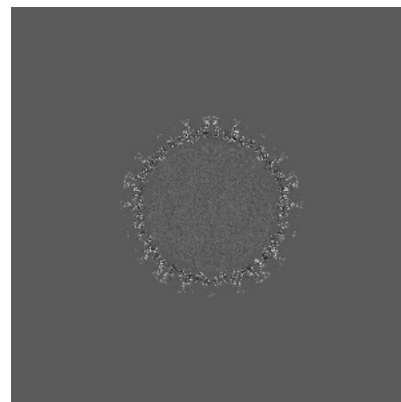
### 6.2.1 Primary map



X Index: 630

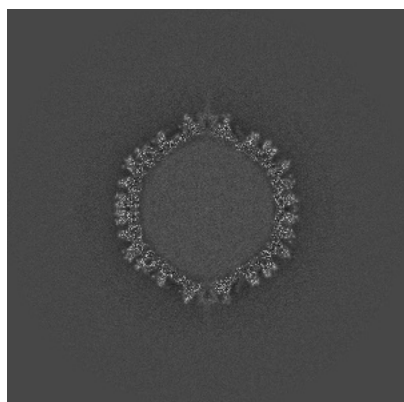


Y Index: 630

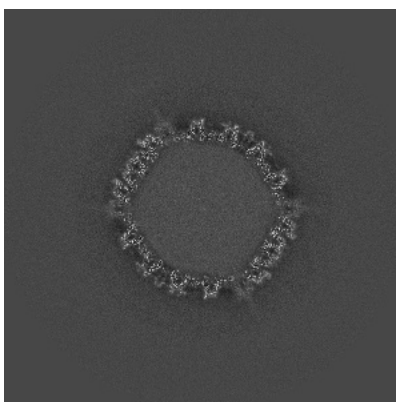


Z Index: 630

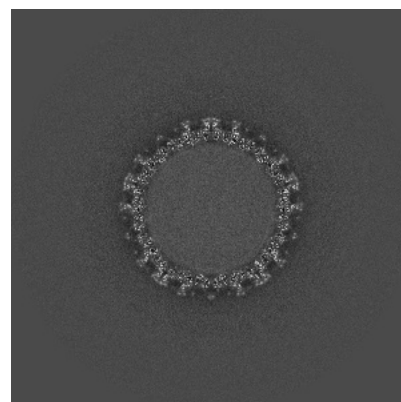
### 6.2.2 Raw map



X Index: 630



Y Index: 630

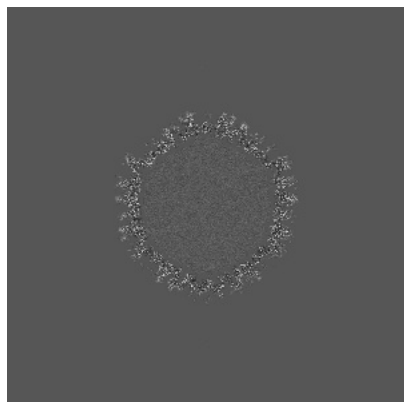


Z Index: 630

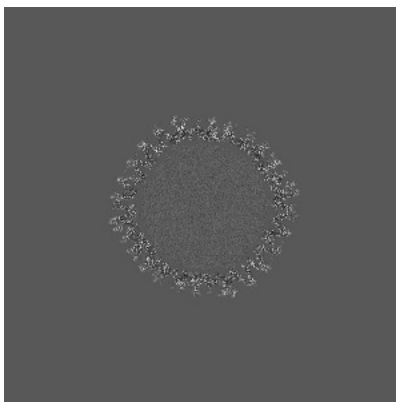
The images above show central slices of the map in three orthogonal directions.

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

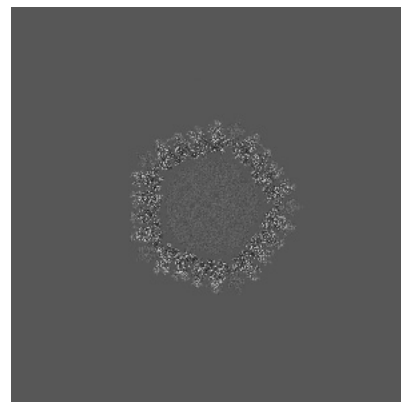
### 6.3.1 Primary map



X Index: 601

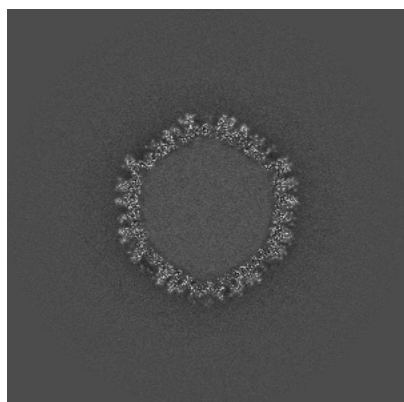


Y Index: 583

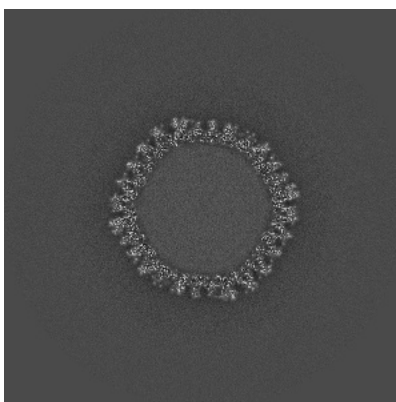


Z Index: 492

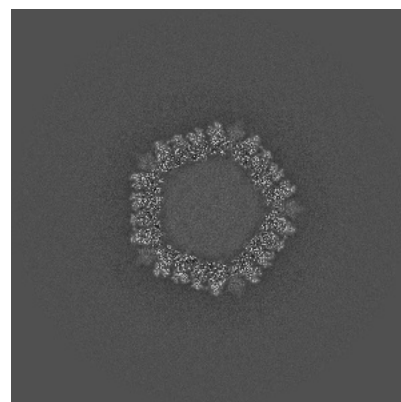
### 6.3.2 Raw map



X Index: 601



Y Index: 581

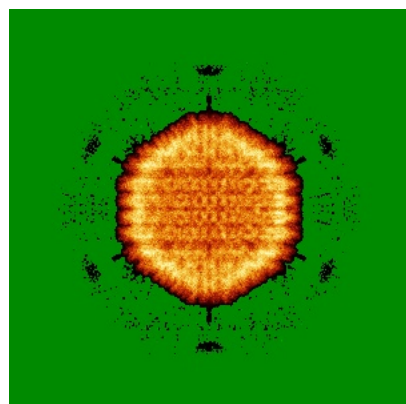


Z Index: 492

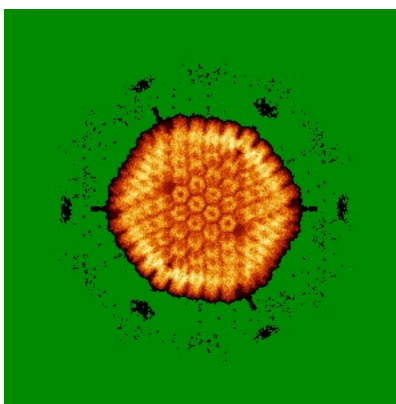
The images above show the largest variance slices of the map in three orthogonal directions.

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

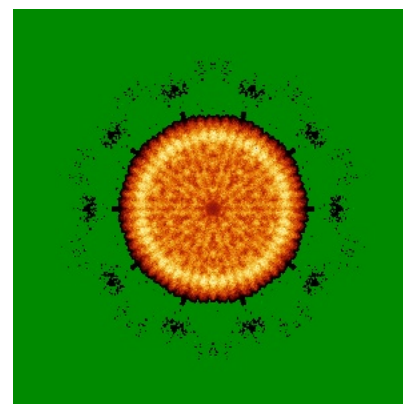
### 6.4.1 Primary map



X

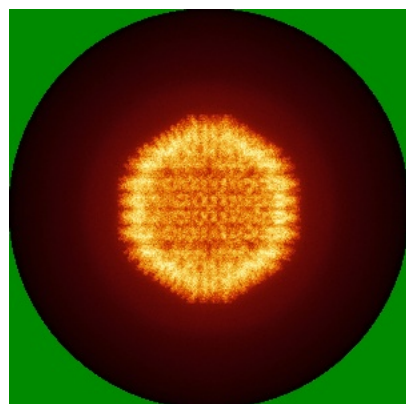


Y

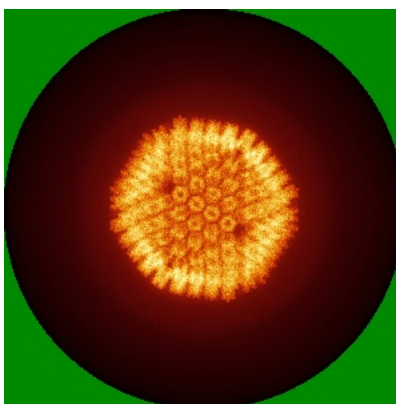


Z

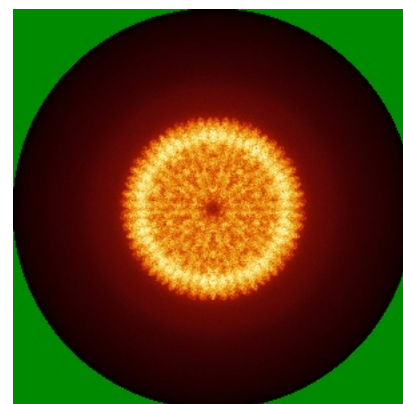
### 6.4.2 Raw map



X



Y

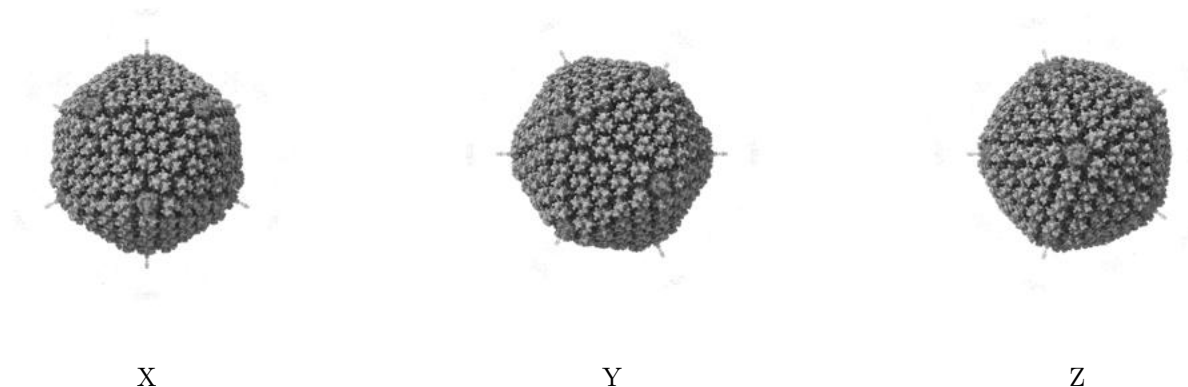


Z

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.

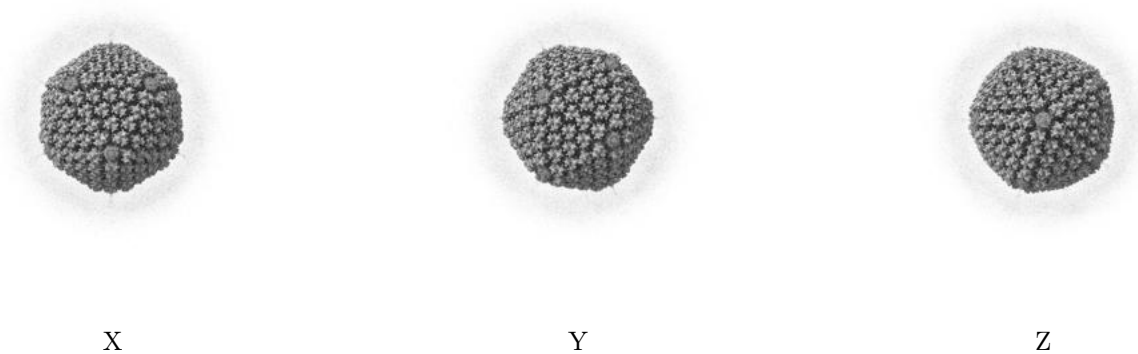
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

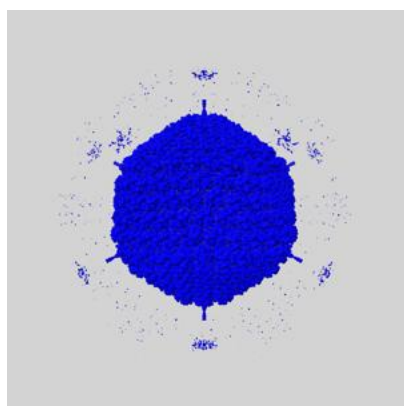
## 6.6 Mask visualisation [i](#)

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

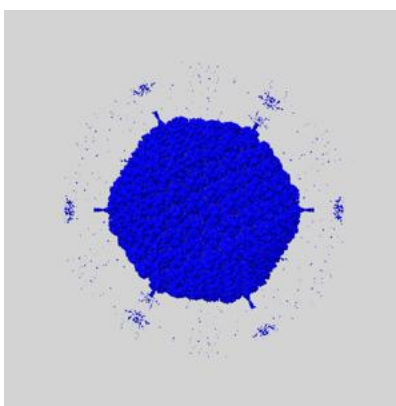
A mask typically either:

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

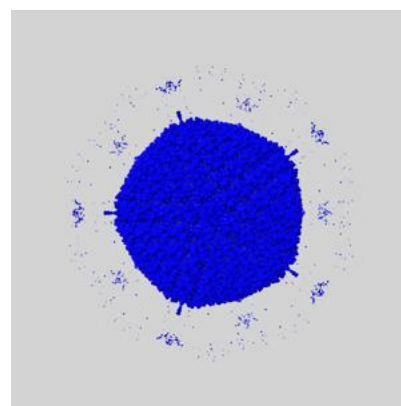
### 6.6.1 emd\_24408\_msk\_1.map [i](#)



X



Y

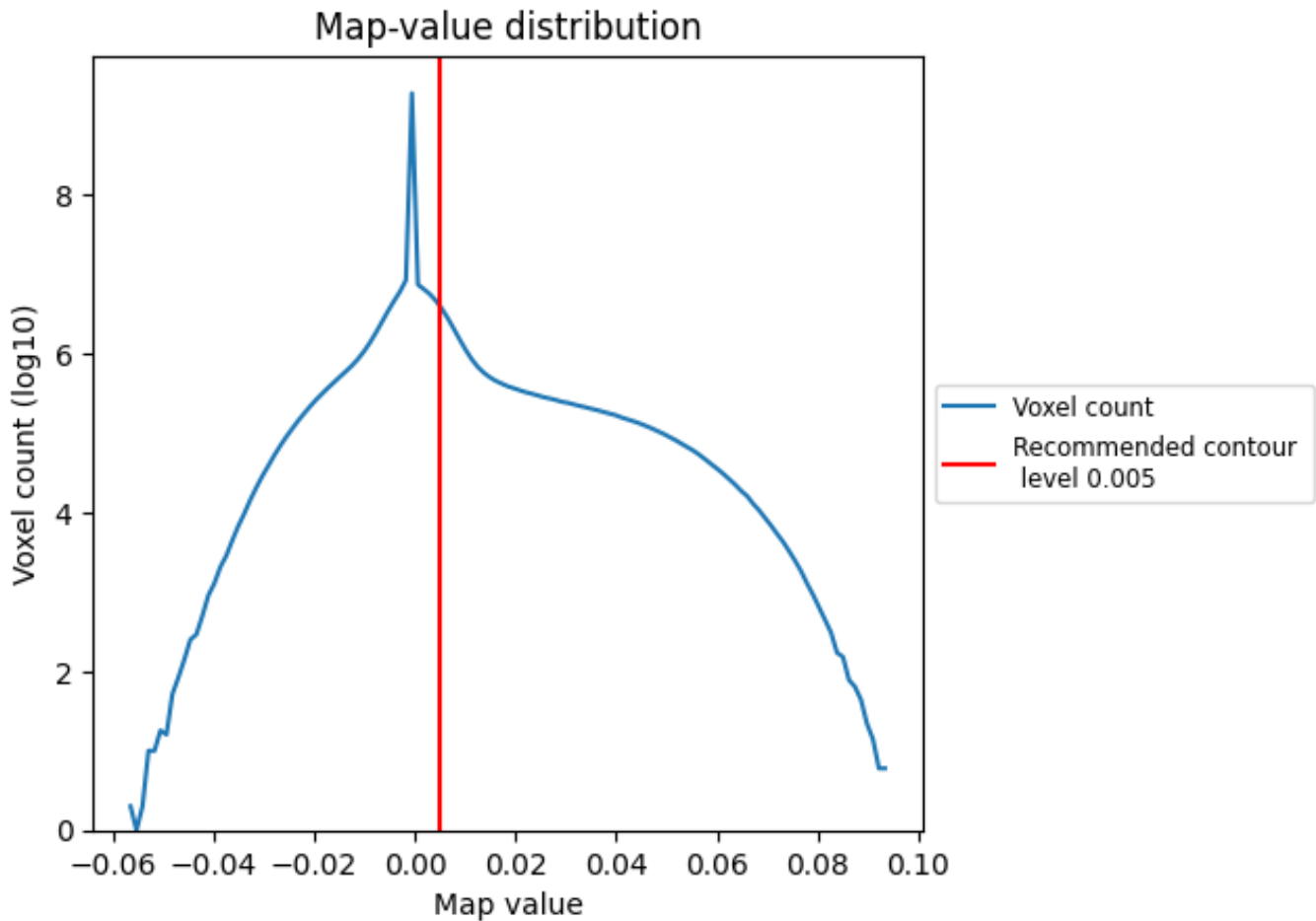


Z

## 7 Map analysis [i](#)

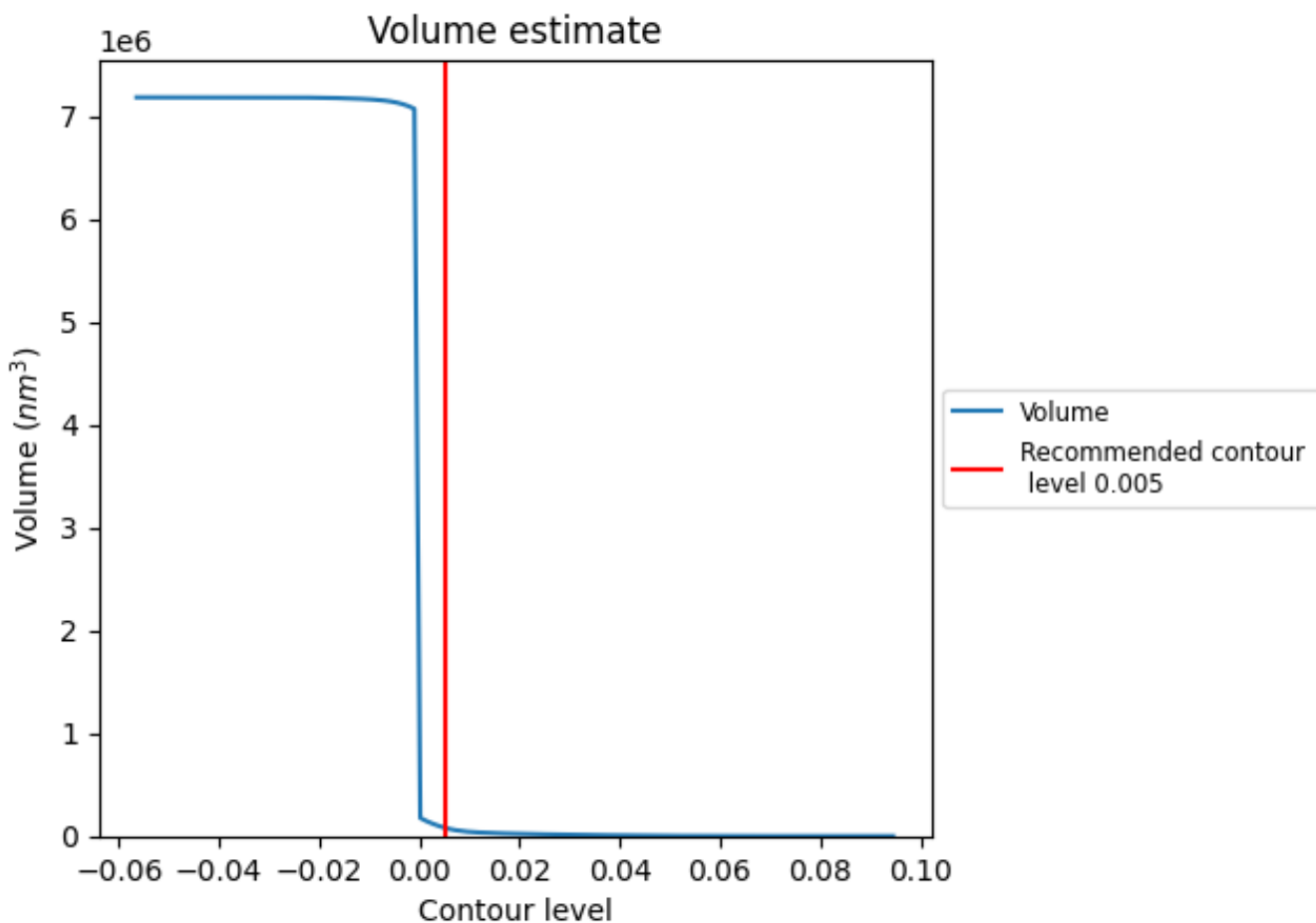
This section contains the results of statistical analysis of the map.

### 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.

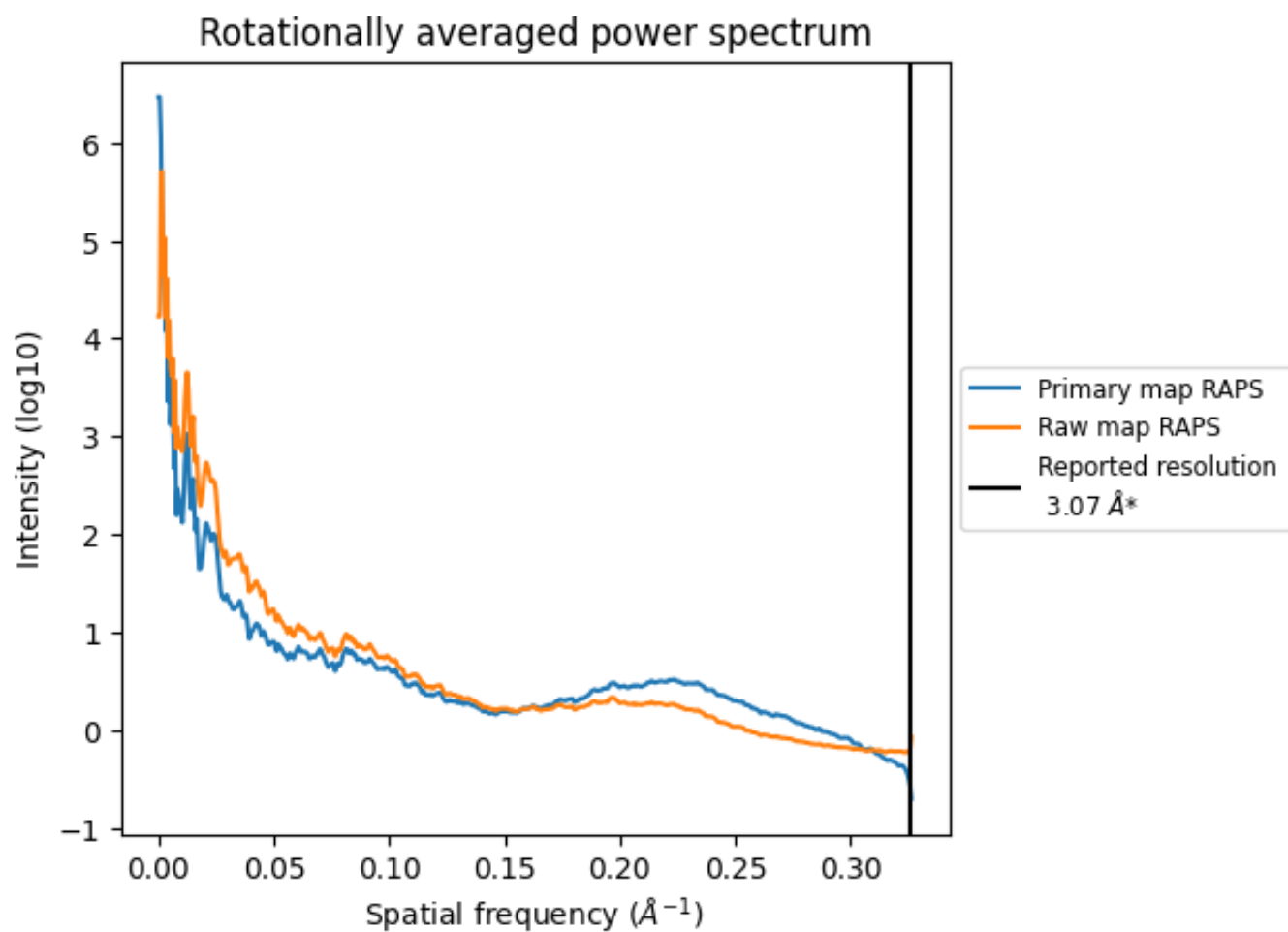
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $82016 \text{ nm}^3$ ; this corresponds to an approximate mass of  $74087 \text{ kDa}$ .

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

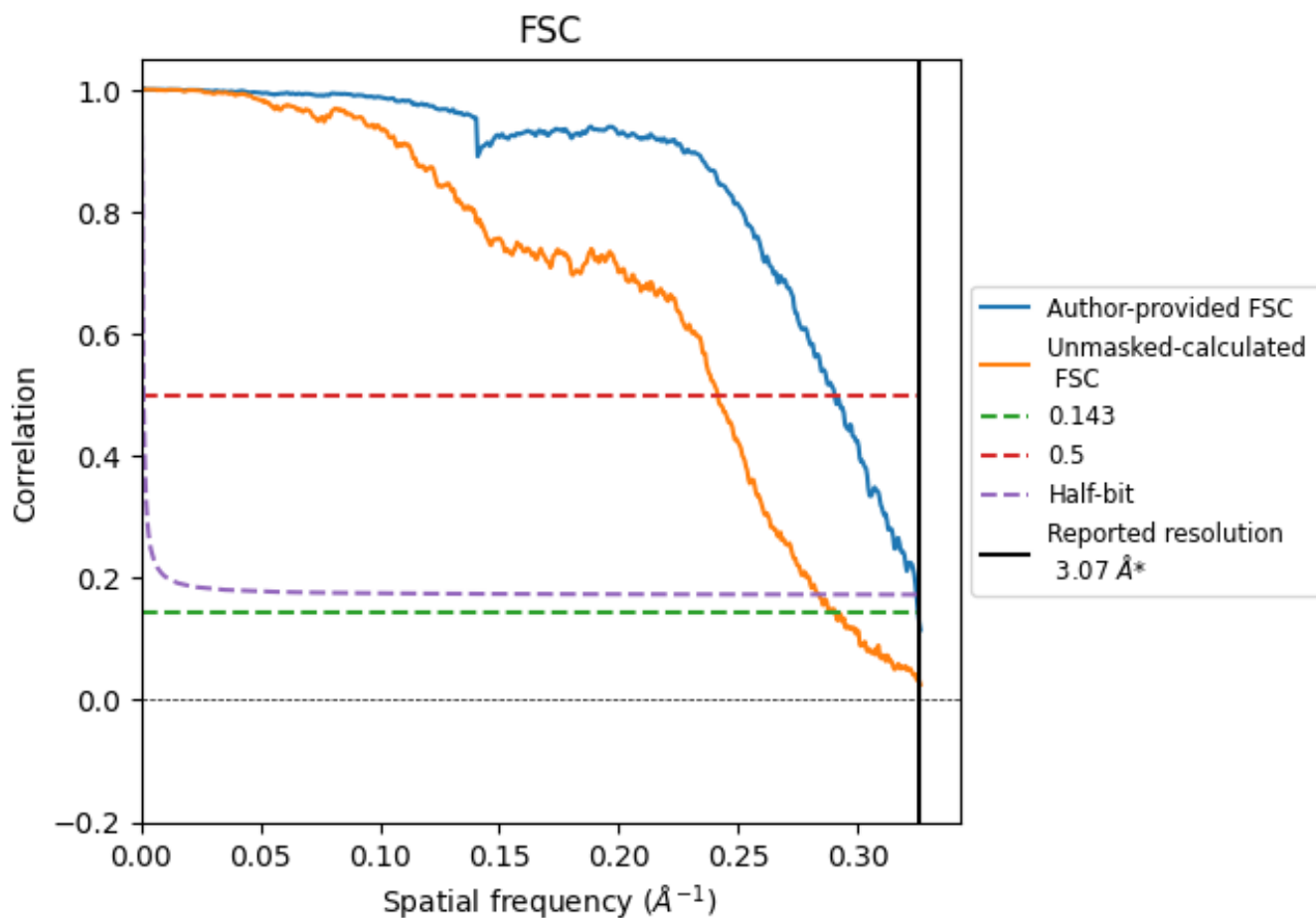


\*Reported resolution corresponds to spatial frequency of 0.326 Å<sup>-1</sup>

## 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  $0.326 \text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.07	-	-
Author-provided FSC curve	3.07	3.44	3.08
Unmasked-calculated*	3.44	4.14	3.52

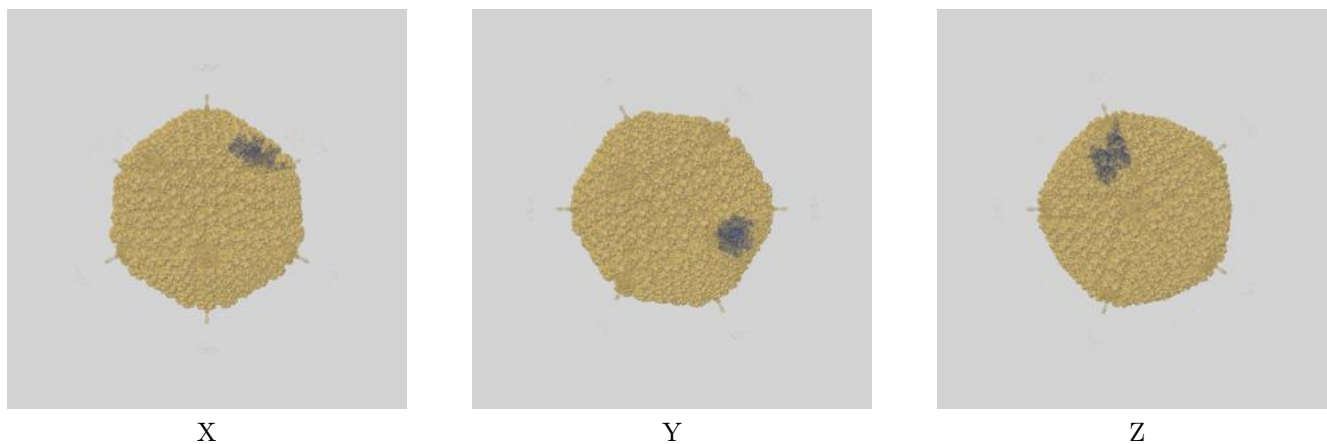
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.44 differs from the reported value 3.07 by more than 10 %

## 9 Map-model fit [i](#)

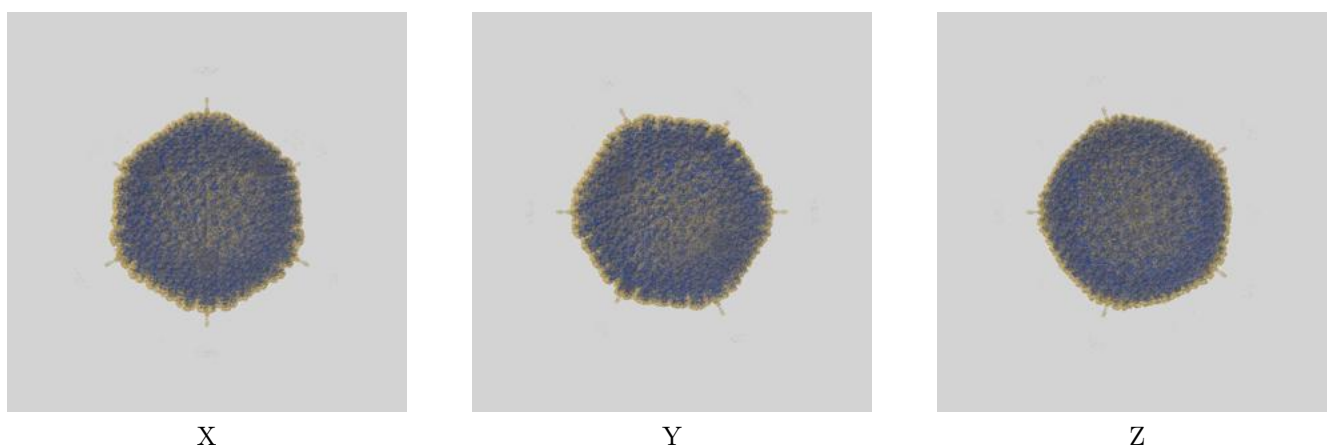
This section contains information regarding the fit between EMDB map EMD-24408 and PDB model 7RD1. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlays

#### 9.1.1 Map-model overlay [i](#)

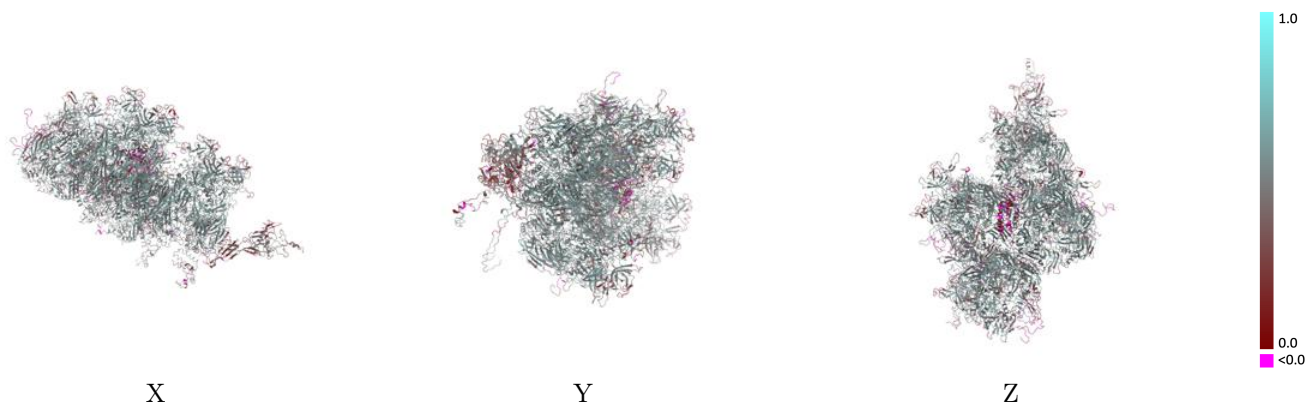


#### 9.1.2 Map-model assembly overlay [i](#)



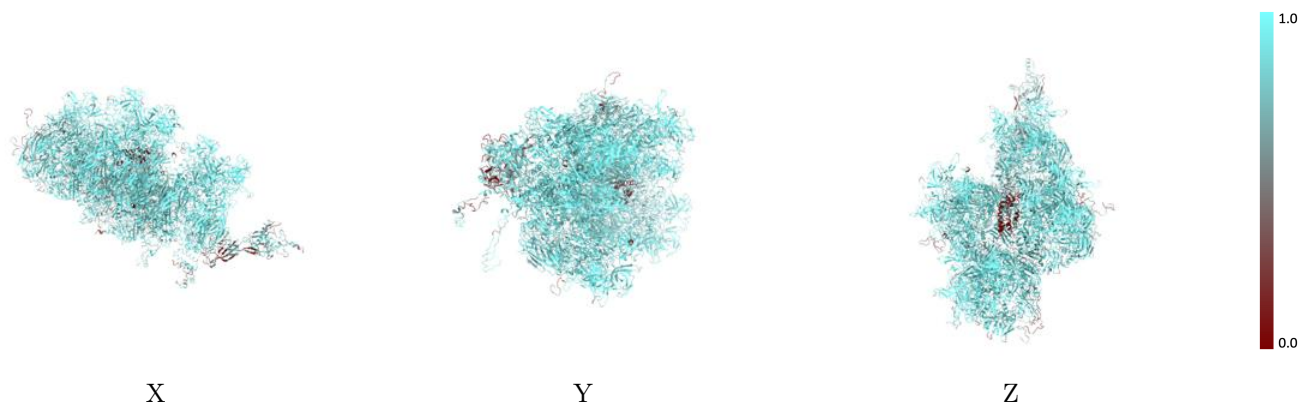
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



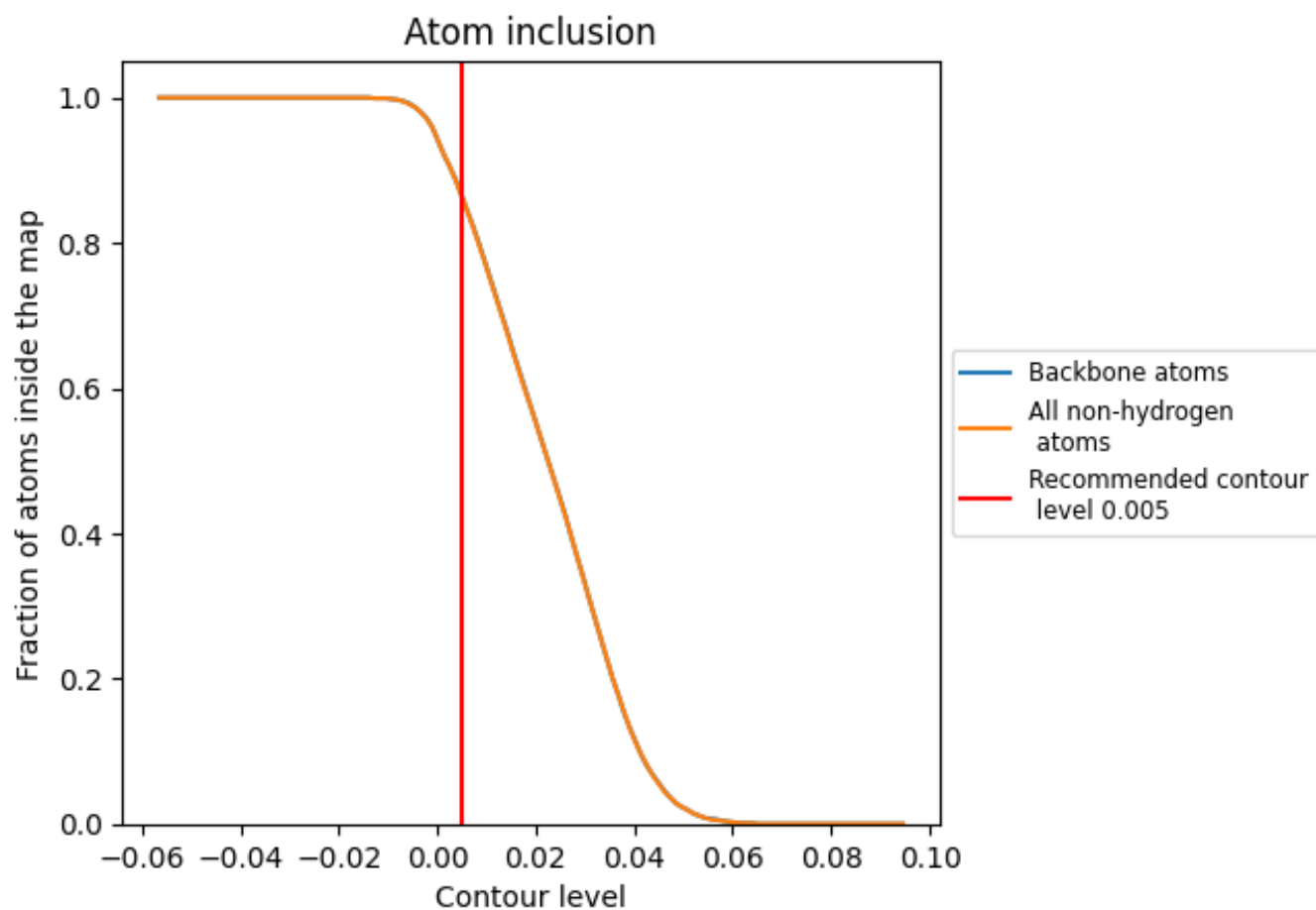
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).



































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.4800
0	 0.2550	 0.1320
1	 0.5040	 0.2770
2	 0.6850	 0.3000
3	 0.7790	 0.4030
4	 0.5880	 0.3410
8	 0.7680	 0.3730
A	 0.9030	 0.4950
B	 0.8720	 0.4690
C	 0.9010	 0.5030
D	 0.8990	 0.5020
E	 0.9060	 0.5030
F	 0.9130	 0.5090
G	 0.9080	 0.5070
H	 0.9040	 0.5030
I	 0.9140	 0.5120
J	 0.9180	 0.5090
K	 0.9200	 0.5100
L	 0.9220	 0.5070
M	 0.5530	 0.3240
N	 0.2530	 0.1310
O	 0.1960	 0.0970
P	 0.2490	 0.0980
Q	 0.3000	 0.1510
R	 0.6450	 0.3480
S	 0.8390	 0.4490
T	 0.7980	 0.4300
U	 0.3370	 0.1390
V	 0.4830	 0.2980
W	 0.6210	 0.3490
X	 0.7030	 0.3460
Y	 0.5080	 0.2970
Z	 0.4360	 0.2690

