



wwPDB EM Validation Summary Report ⓘ

Apr 21, 2025 – 02:36 PM JST

PDB ID : 8XA1 / pdb_00008xa1
EMDB ID : EMD-38191
Title : Portal vertex capsomer of VZV B-capsid
Authors : Nan, W.; Lei, C.; Xiangxi, W.
Deposited on : 2023-12-01
Resolution : 4.80 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

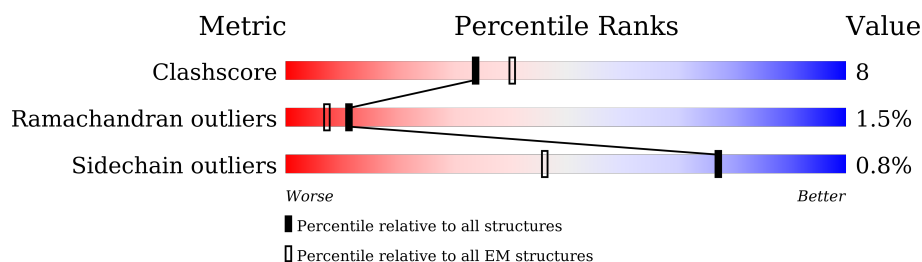
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1345	 7% 80% 19%
2	C	1297	 7% 81% 19%
3	G	297	 45% 73% 25% .
3	I	297	 34% 77% 22% .
4	P	307	 61% 69% 28% .
4	R	307	 40% 74% 23% .
5	Y	357	 27% 59% 22% . 19%
5	d	357	 34% 92% 8% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 33981 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1345	Total	C	N	O	S	0	0
			10340	6543	1816	1917	64		

- Molecule 2 is a protein called major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1297	Total	C	N	O	S	0	0
			10033	6354	1760	1856	63		

- Molecule 3 is a protein called Tri2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	297	Total	C	N	O	S	0	0
			2124	1367	365	383	9		
3	I	297	Total	C	N	O	S	0	0
			2124	1367	365	383	9		

- Molecule 4 is a protein called Tri2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	307	Total	C	N	O	S	0	0
			2279	1456	399	413	11		
4	R	307	Total	C	N	O	S	0	0
			2279	1456	399	413	11		

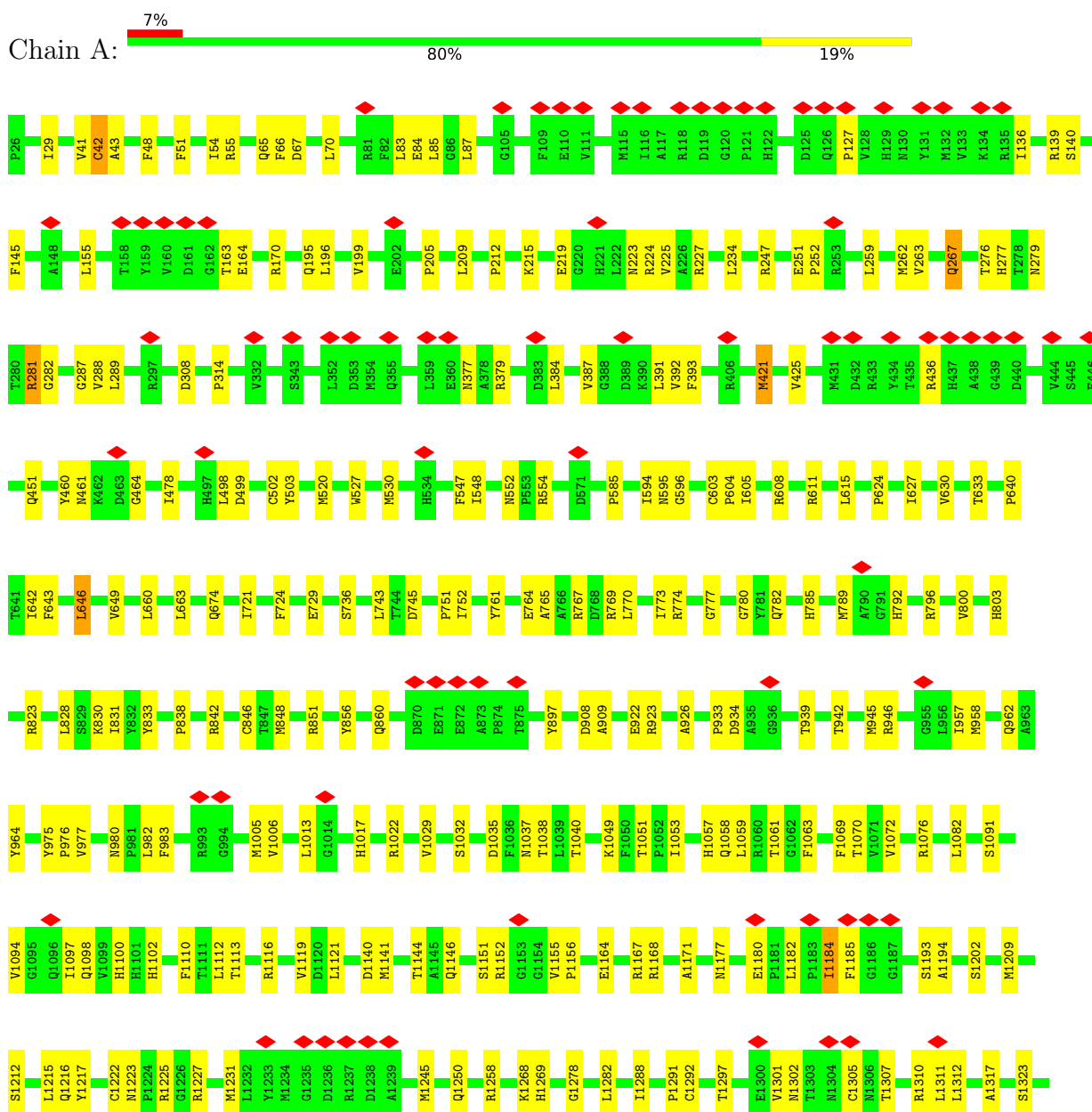
- Molecule 5 is a protein called Tri1.

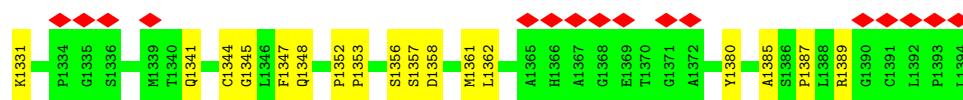
Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	289	Total	C	N	O	S	0	0
			2198	1392	397	395	14		
5	d	357	Total	C	N	O	S	0	0
			2604	1640	475	474	15		

3 Residue-property plots

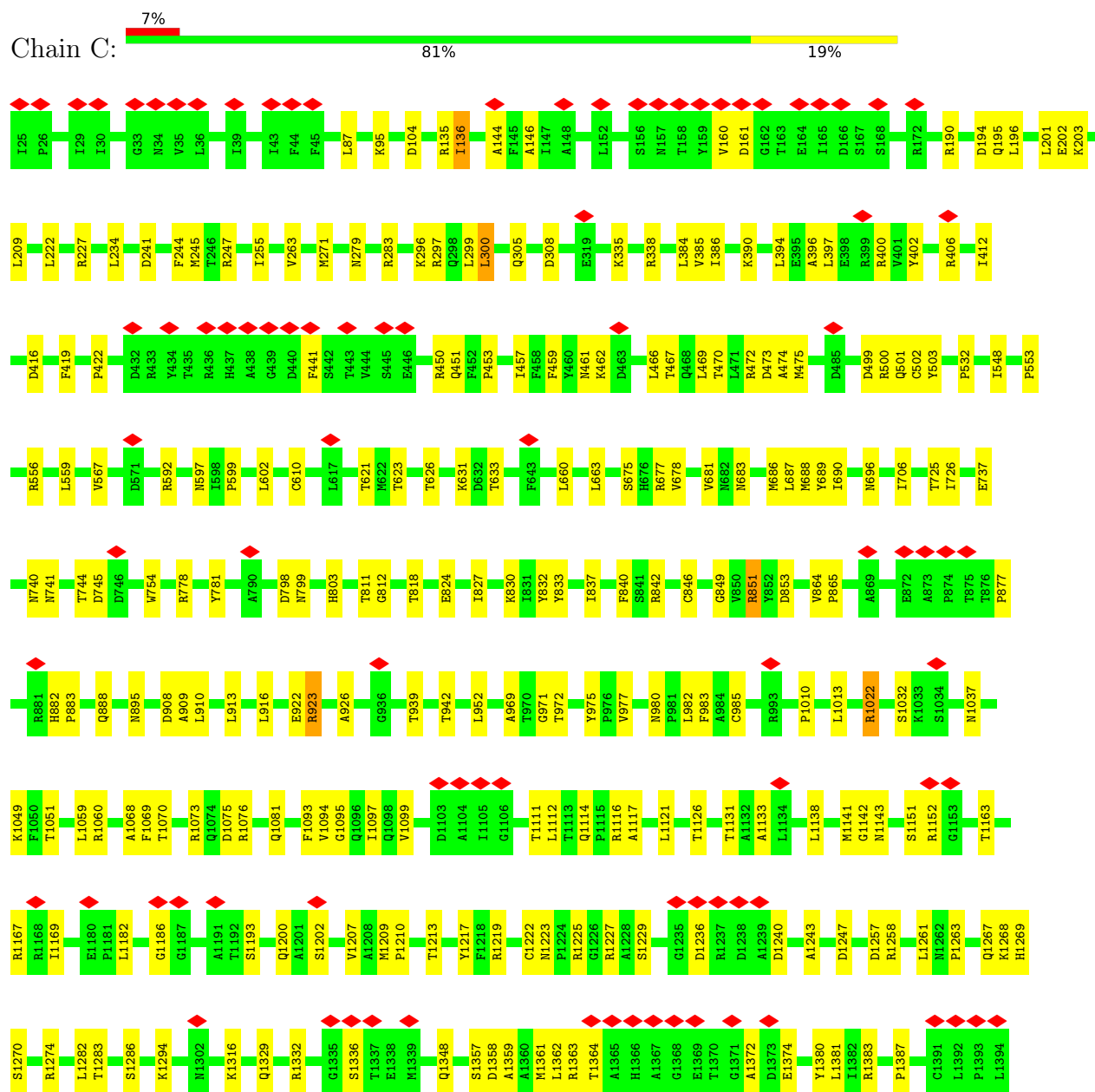
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

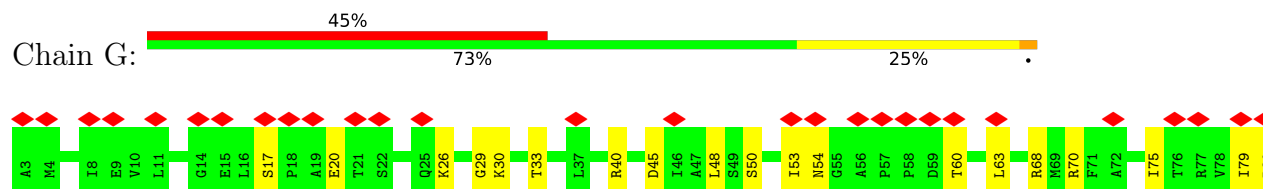


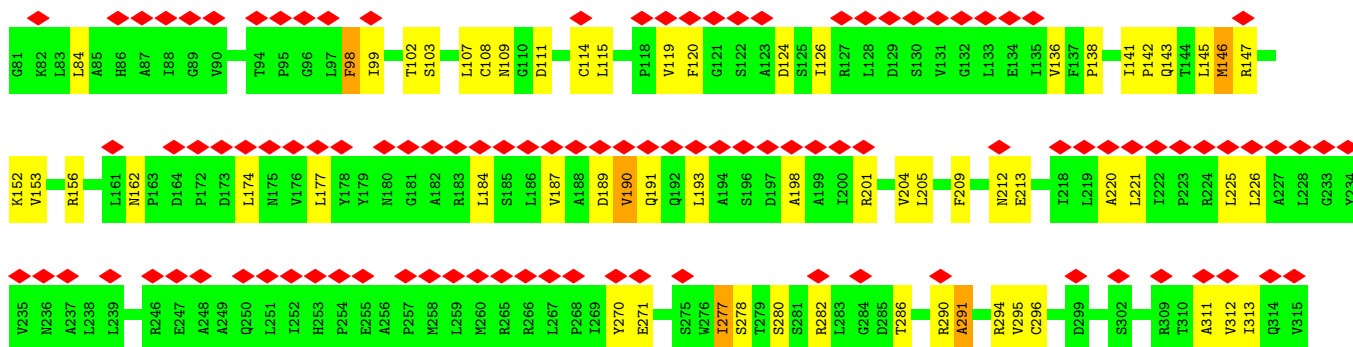


• Molecule 2: major capsid protein

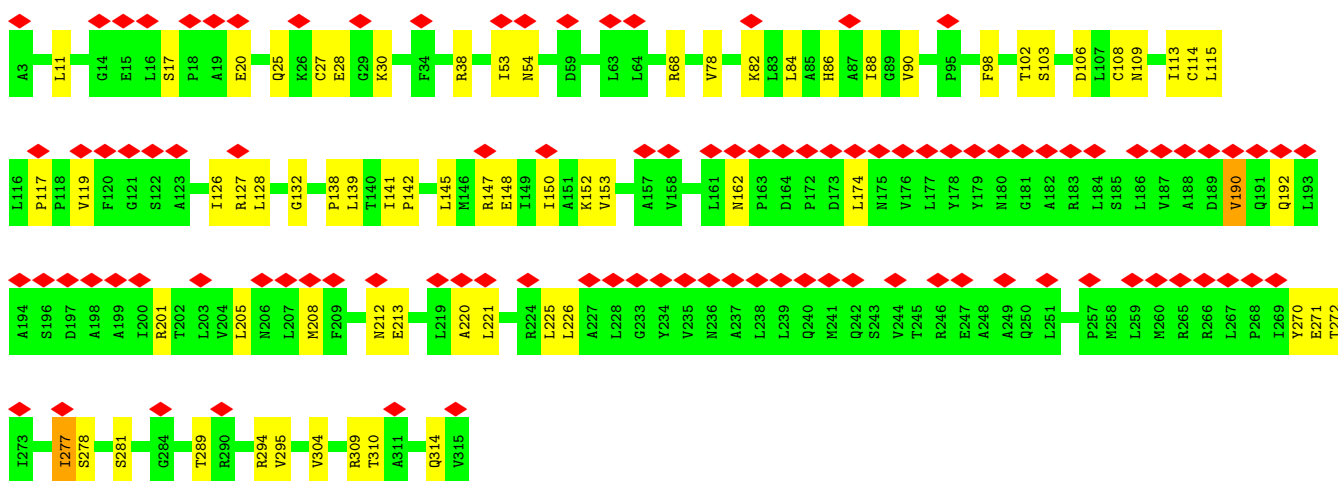
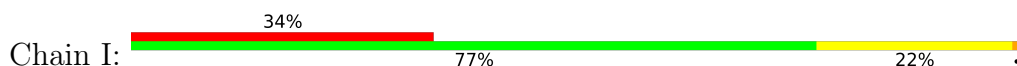


• Molecule 3: Tri2A

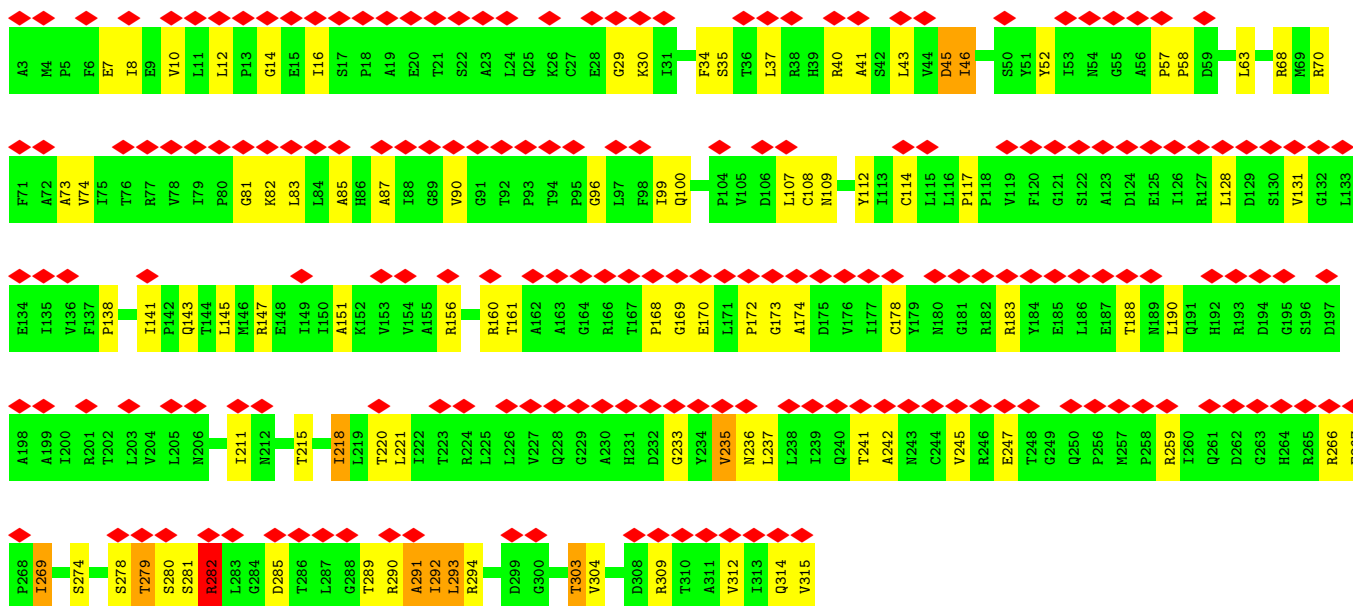




• Molecule 3: Tri2A



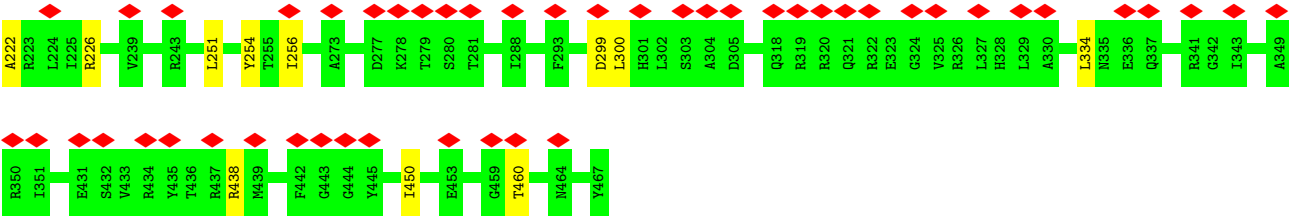
• Molecule 4: Tri2B



- Molecule 5: Tri1

- Molecule 5: Tri1

L194	R135	T138	D139	L140	P141	H142	L143	A144	R145	H146	R147	A148	P149	P150	G151	R152	Q153	T154	E155																													
L158	E159	A160	G162	Q163	L164	L165	E166	A167	S168	E176	S177	G178	C179	A182	S188	E196	E197	Y198	T199	D200	K201	E208	S213	A214	Y215	G216	C217	S218	R219	M220	C221																	
A8	A9	A10	A11	A12	A13	A19	A20	A21	A25	A29	A30	A36	A44	A45	A46	A47	A48	A49	V77	I78	N82	N83	N87	P88	I91	L99	P100	L101	N102	N103	F104	K105	S106	T107	L108	Q109	T117	F118	F119	F120	R121	P122	D123	I124	E125	H126	A127	I133



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25531	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.032	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	418.5, 418.5, 418.5	wwPDB
Map dimensions	310, 310, 310	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	A	0.31	0/10588	0.68	9/14438 (0.1%)
2	C	0.30	0/10275	0.67	5/14009 (0.0%)
3	G	0.33	0/2158	0.84	4/2951 (0.1%)
3	I	0.33	0/2158	0.80	3/2951 (0.1%)
4	P	0.33	0/2320	0.88	11/3165 (0.3%)
4	R	0.32	0/2320	0.88	12/3165 (0.4%)
5	Y	0.34	0/2244	0.82	5/3050 (0.2%)
5	d	0.38	0/2651	0.93	9/3612 (0.2%)
All	All	0.32	0/34714	0.76	58/47341 (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
1	A	0	1
2	C	0	2
3	G	0	3
3	I	0	3
4	P	0	4
4	R	0	3
5	d	0	4
All	All	0	20

There are no bond length outliers.

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	421	MET	CG-SD-CE	8.55	113.89	100.20
4	P	291	ALA	C-N-CA	8.19	142.18	121.70
5	d	101	LEU	CA-CB-CG	7.60	132.78	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	277	ILE	C-N-CA	7.40	140.20	121.70
1	A	1184	ILE	CG1-CB-CG2	-7.31	95.31	111.40

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	LEU	Peptide
2	C	136	ILE	Peptide
2	C	202	GLU	Peptide
3	G	146	MET	Peptide
3	G	209	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10340	0	10012	149	0
2	C	10033	0	9816	148	0
3	G	2124	0	2111	46	0
3	I	2124	0	2111	34	0
4	P	2279	0	2316	59	0
4	R	2279	0	2316	42	0
5	Y	2198	0	2124	47	0
5	d	2604	0	2521	0	0
All	All	33981	0	33327	492	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 8.

The worst 5 of 492 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:C:592:ARG:HH22	2:C:599:PRO:HD3	1.54	0.72
4:P:74:VAL:HG21	4:P:99:ILE:HG22	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:63:LEU:HD23	4:R:117:PRO:HB3	1.72	0.70
1:A:848:MET:HG3	1:A:976:PRO:HA	1.74	0.69
4:P:63:LEU:HD23	4:P:117:PRO:HB3	1.75	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1339/1345 (100%)	1181 (88%)	152 (11%)	6 (0%)	30	68
2	C	1291/1297 (100%)	1180 (91%)	110 (8%)	1 (0%)	48	83
3	G	287/297 (97%)	230 (80%)	49 (17%)	8 (3%)	4	24
3	I	287/297 (97%)	229 (80%)	49 (17%)	9 (3%)	3	22
4	P	299/307 (97%)	248 (83%)	42 (14%)	9 (3%)	3	22
4	R	299/307 (97%)	254 (85%)	36 (12%)	9 (3%)	3	22
5	Y	283/357 (79%)	238 (84%)	38 (13%)	7 (2%)	4	26
5	d	347/357 (97%)	278 (80%)	53 (15%)	16 (5%)	2	17
All	All	4432/4564 (97%)	3838 (87%)	529 (12%)	65 (2%)	11	39

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	84	GLU
3	G	40	ARG
3	G	98	PHE
3	G	103	SER

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	A	1089/1137 (96%)	1082 (99%)	7 (1%)	84	88
2	C	1072/1093 (98%)	1064 (99%)	8 (1%)	81	87
3	G	212/252 (84%)	208 (98%)	4 (2%)	52	70
3	I	212/252 (84%)	208 (98%)	4 (2%)	52	70
4	P	242/258 (94%)	240 (99%)	2 (1%)	79	85
4	R	242/258 (94%)	241 (100%)	1 (0%)	89	91
5	Y	220/270 (82%)	218 (99%)	2 (1%)	75	83
5	d	244/270 (90%)	242 (99%)	2 (1%)	79	85
All	All	3533/3790 (93%)	3503 (99%)	30 (1%)	77	85

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1294	LYS
5	Y	219	ARG
3	G	162	ASN
5	d	226	ARG
4	P	282	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	799	ASN
2	C	1143	ASN
5	d	83	ASN
5	Y	236	GLN
5	Y	321	GLN

5.3.3 RNA ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	d	4
3	I	4
3	G	4
4	R	3
4	P	3
2	C	2
1	A	2
5	Y	2

The worst 5 of 24 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	45:PHE	C	81:ARG	N	44.28
1	d	36:ALA	C	44:ALA	N	41.89
1	A	360:GLU	C	377:ASN	N	31.99
1	C	338:ARG	C	377:ASN	N	25.70
1	d	51:ALA	C	76:ILE	N	23.55

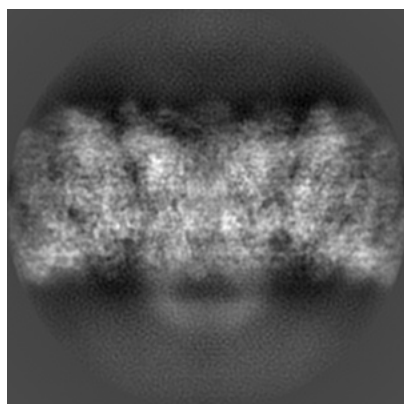
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38191. These allow visual inspection of the internal detail of the map and identification of artifacts.

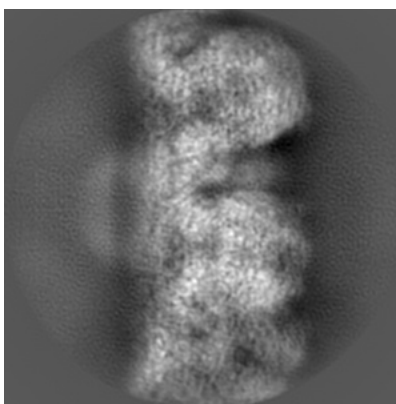
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

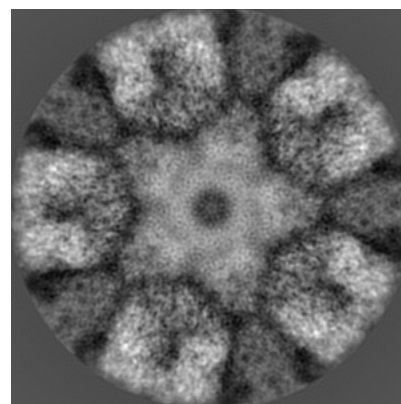
6.1.1 Primary map



X

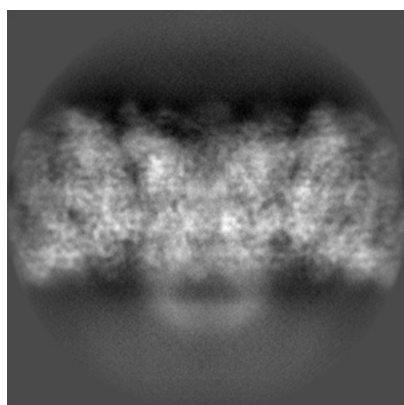


Y

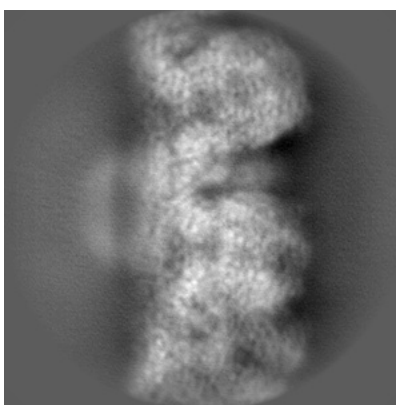


Z

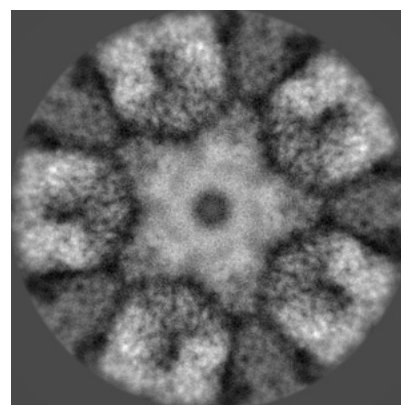
6.1.2 Raw map



X



Y

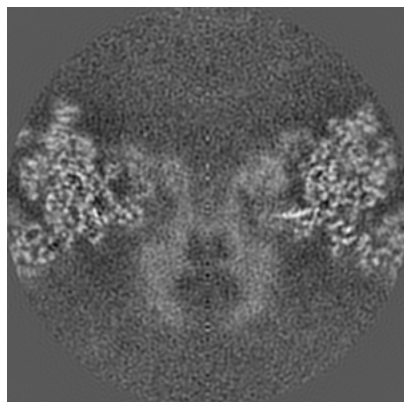


Z

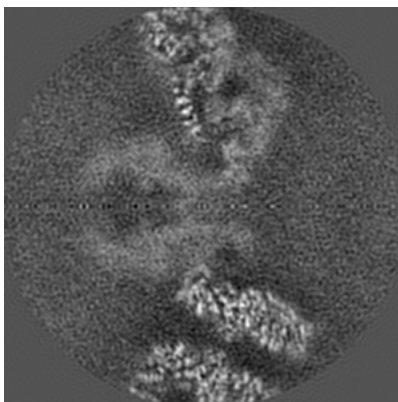
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

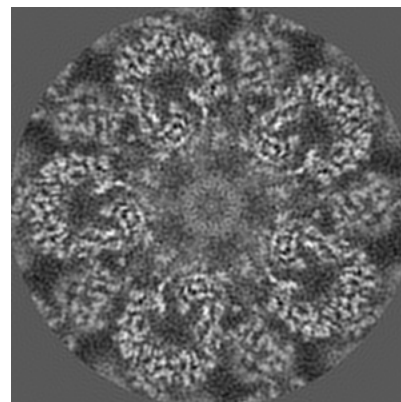
6.2.1 Primary map



X Index: 155

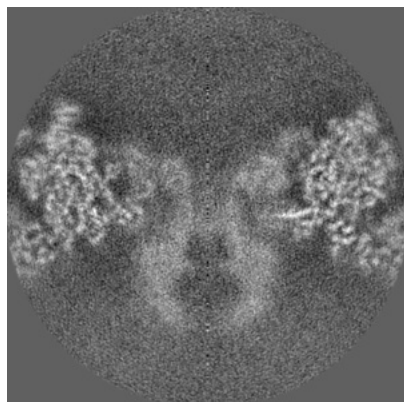


Y Index: 155

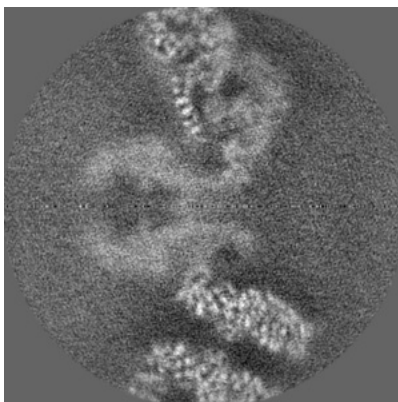


Z Index: 155

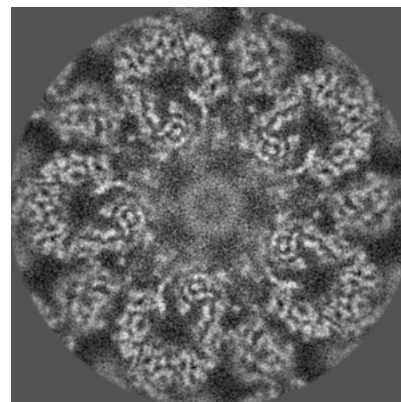
6.2.2 Raw map



X Index: 155



Y Index: 155

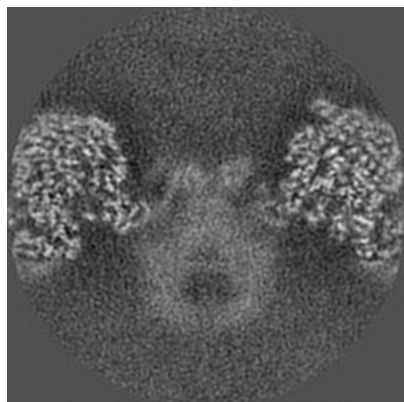


Z Index: 155

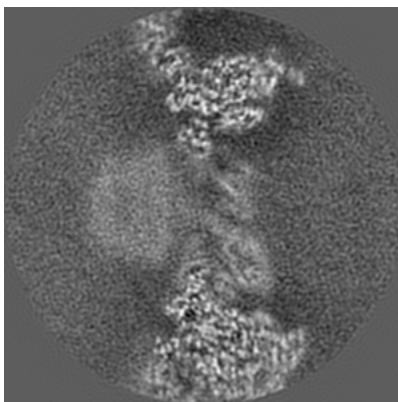
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

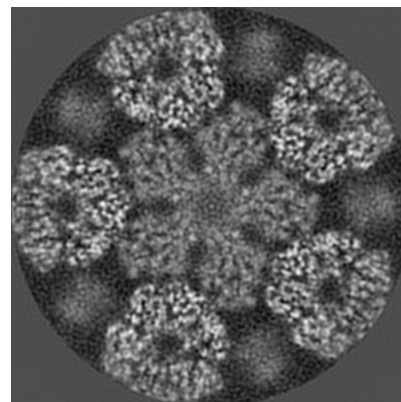
6.3.1 Primary map



X Index: 138

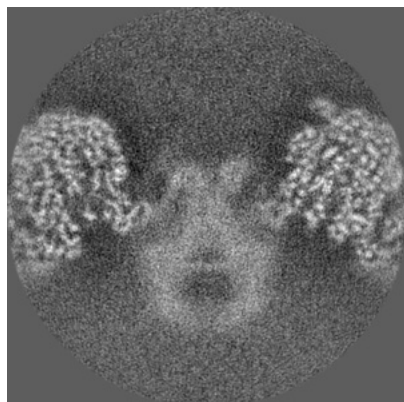


Y Index: 126

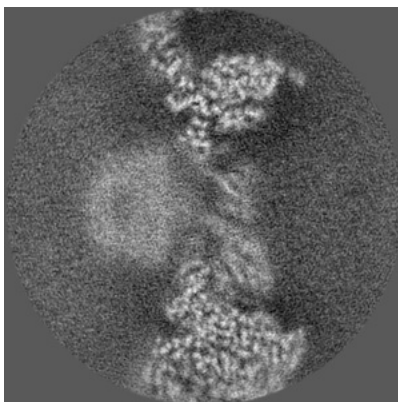


Z Index: 176

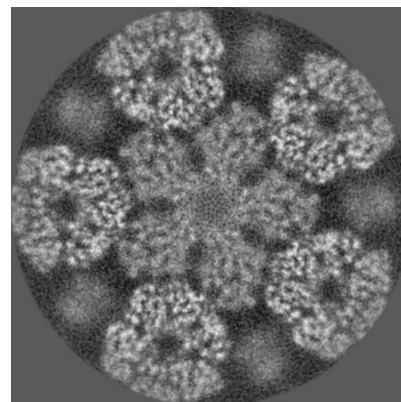
6.3.2 Raw map



X Index: 139



Y Index: 127

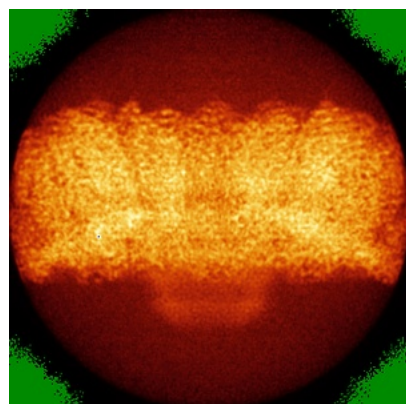


Z Index: 176

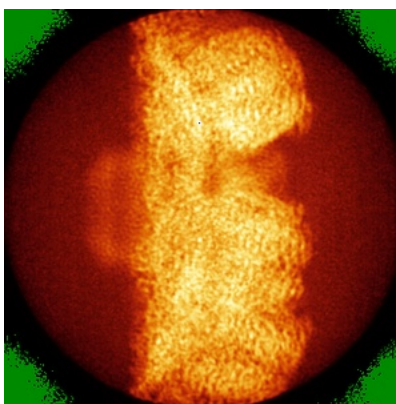
The images above show the largest variance slices of the map in three orthogonal directions.

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

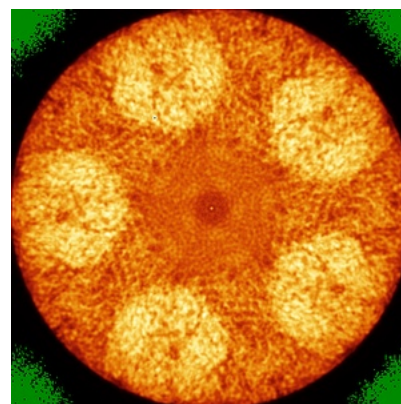
6.4.1 Primary map



X

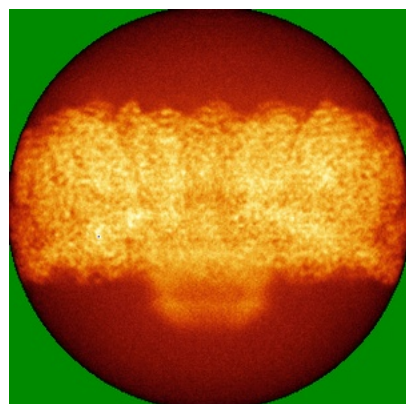


Y

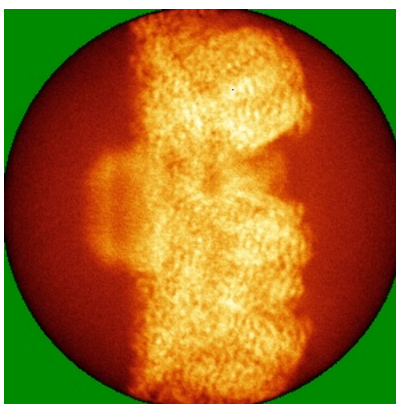


Z

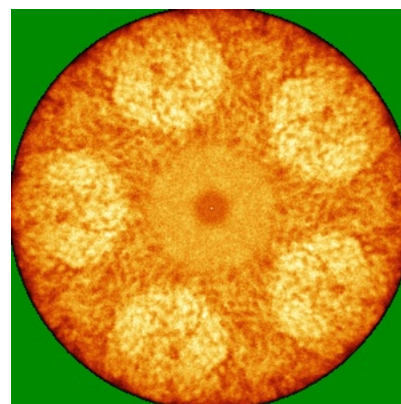
6.4.2 Raw map



X



Y

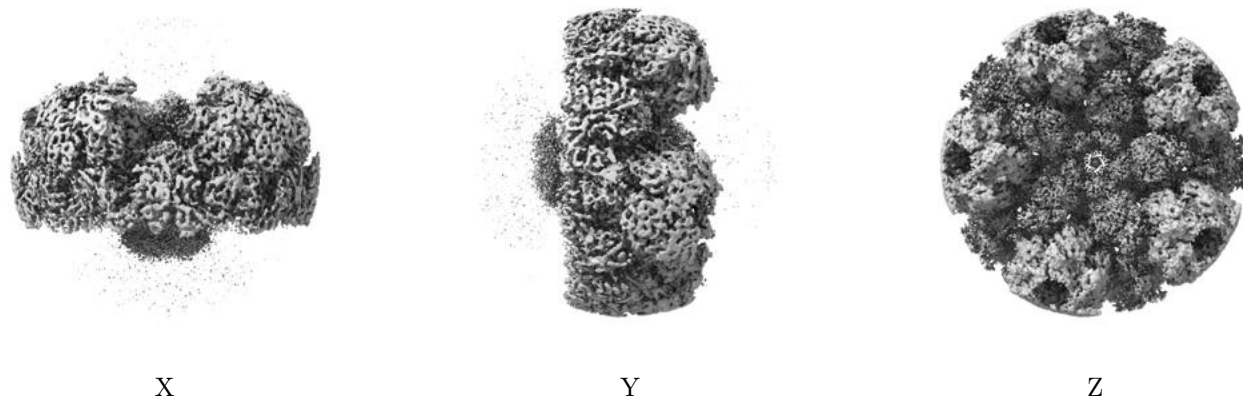


Z

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.

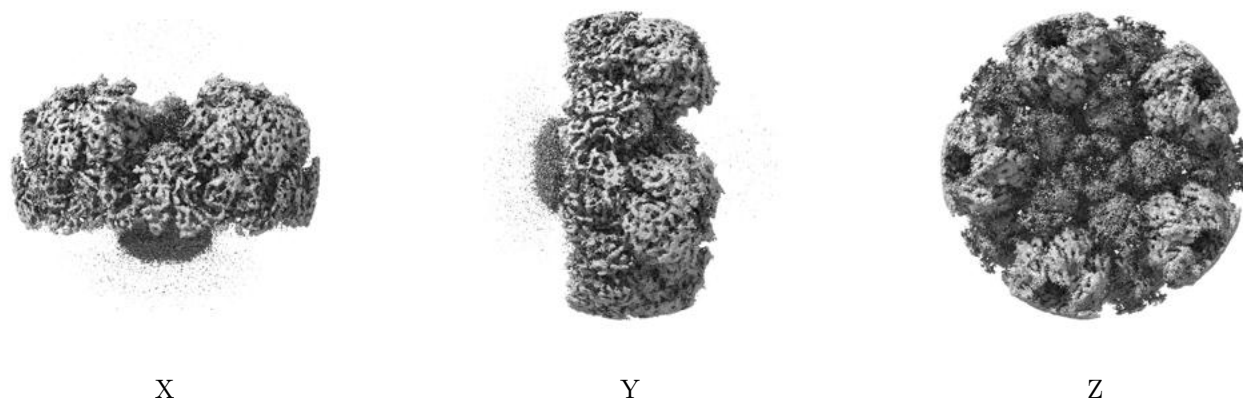
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. 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.

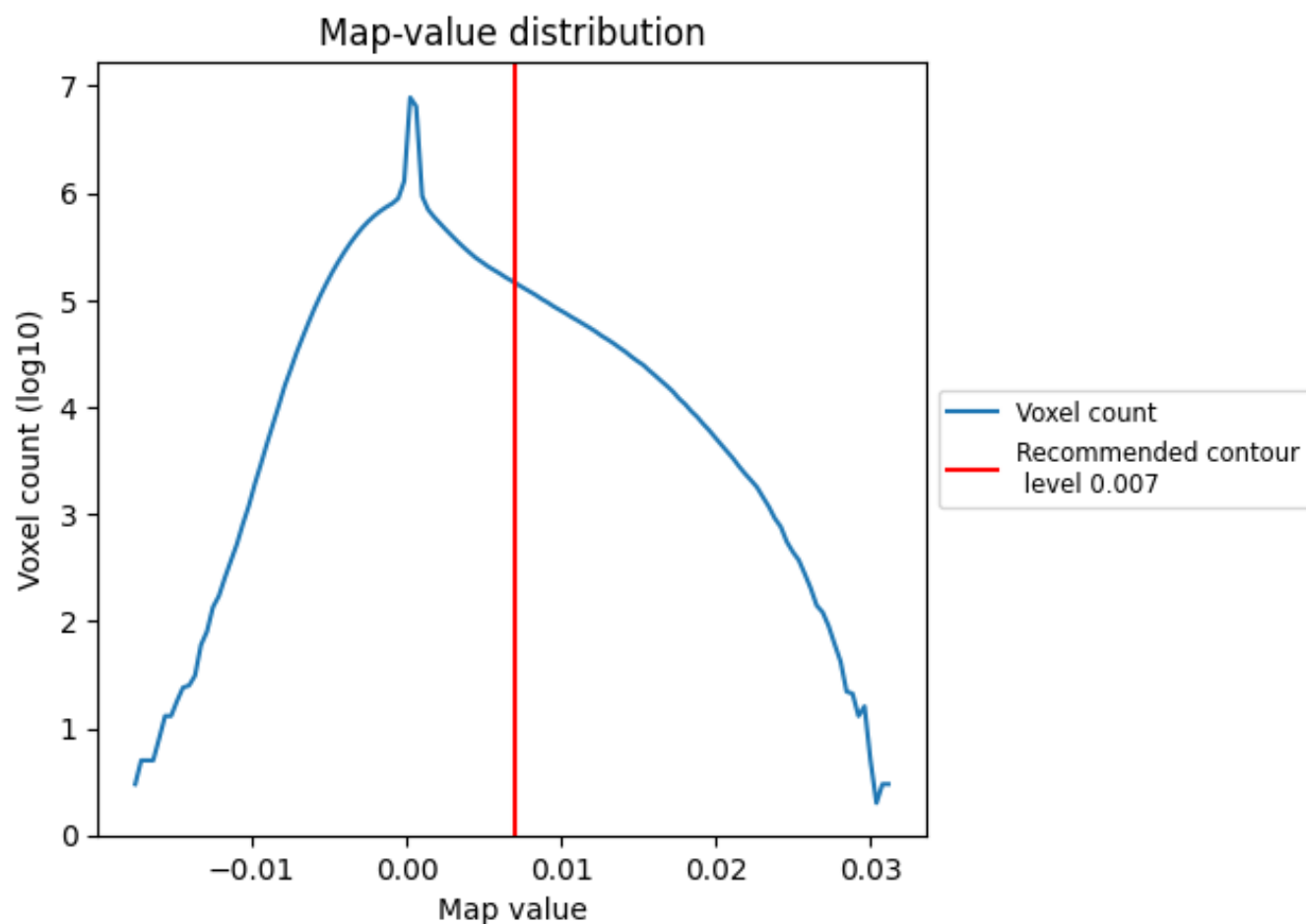
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

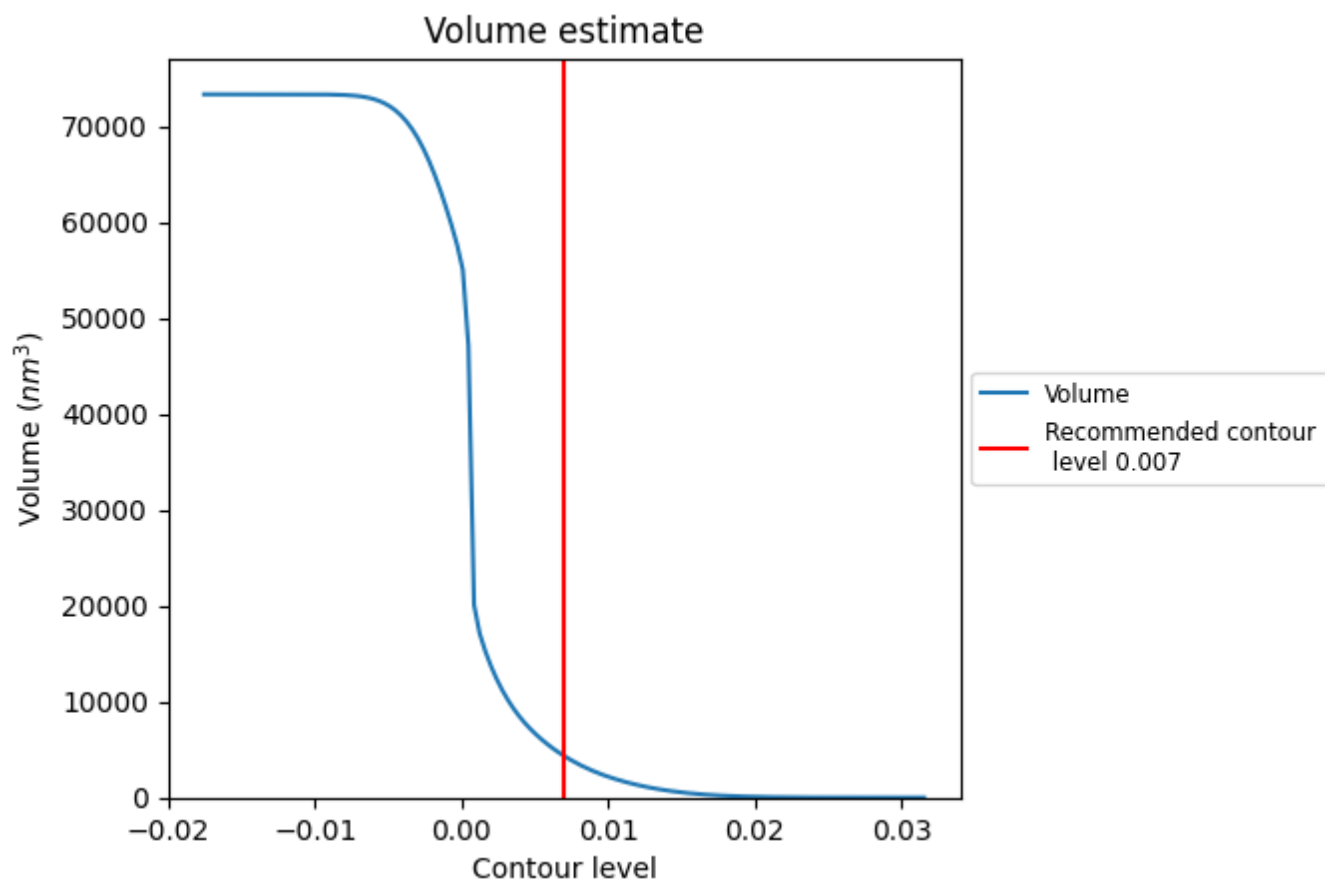
This section contains the results of statistical analysis of the map.

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.

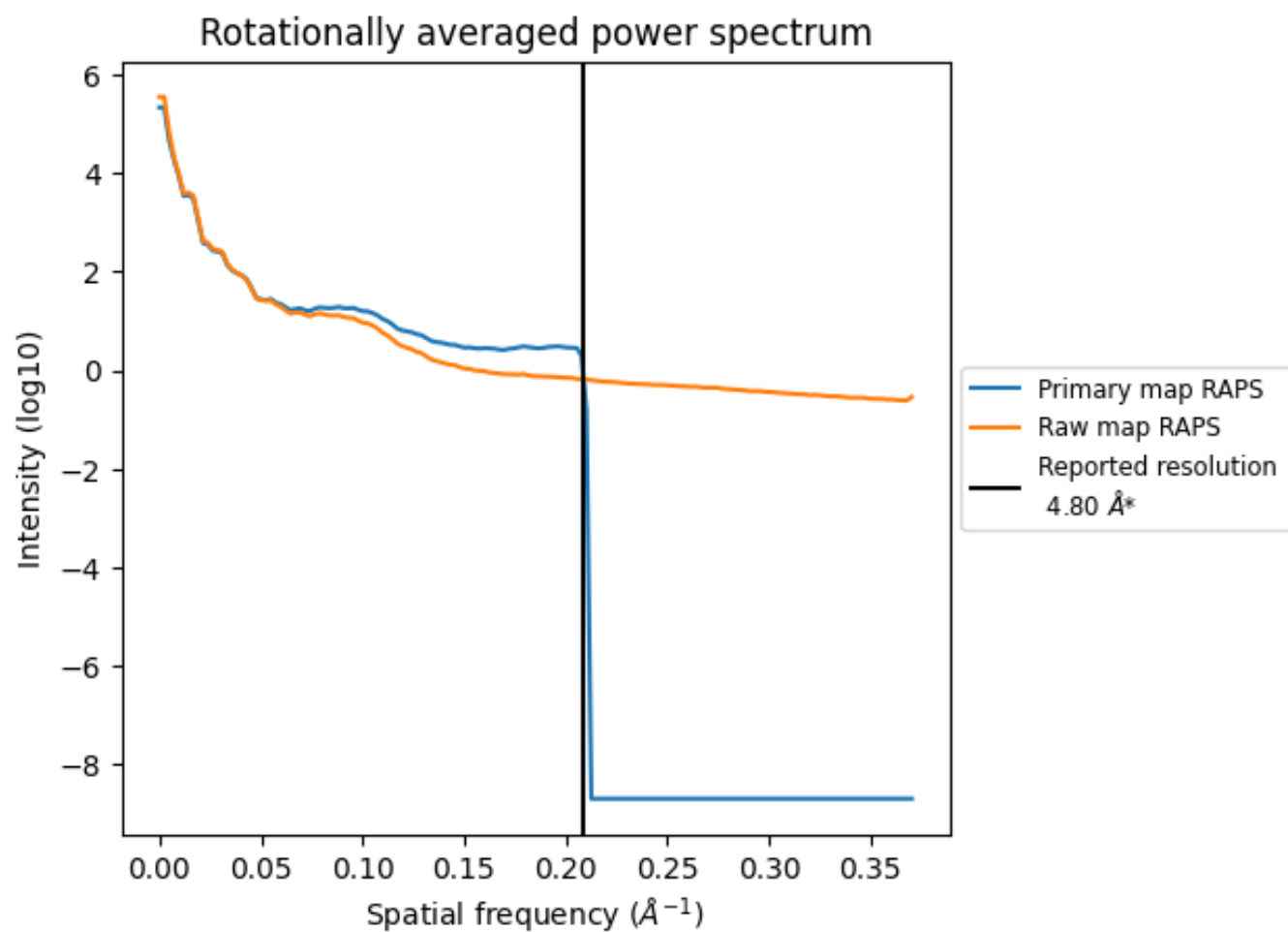
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4343 nm³; this corresponds to an approximate mass of 3924 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 ⓘ

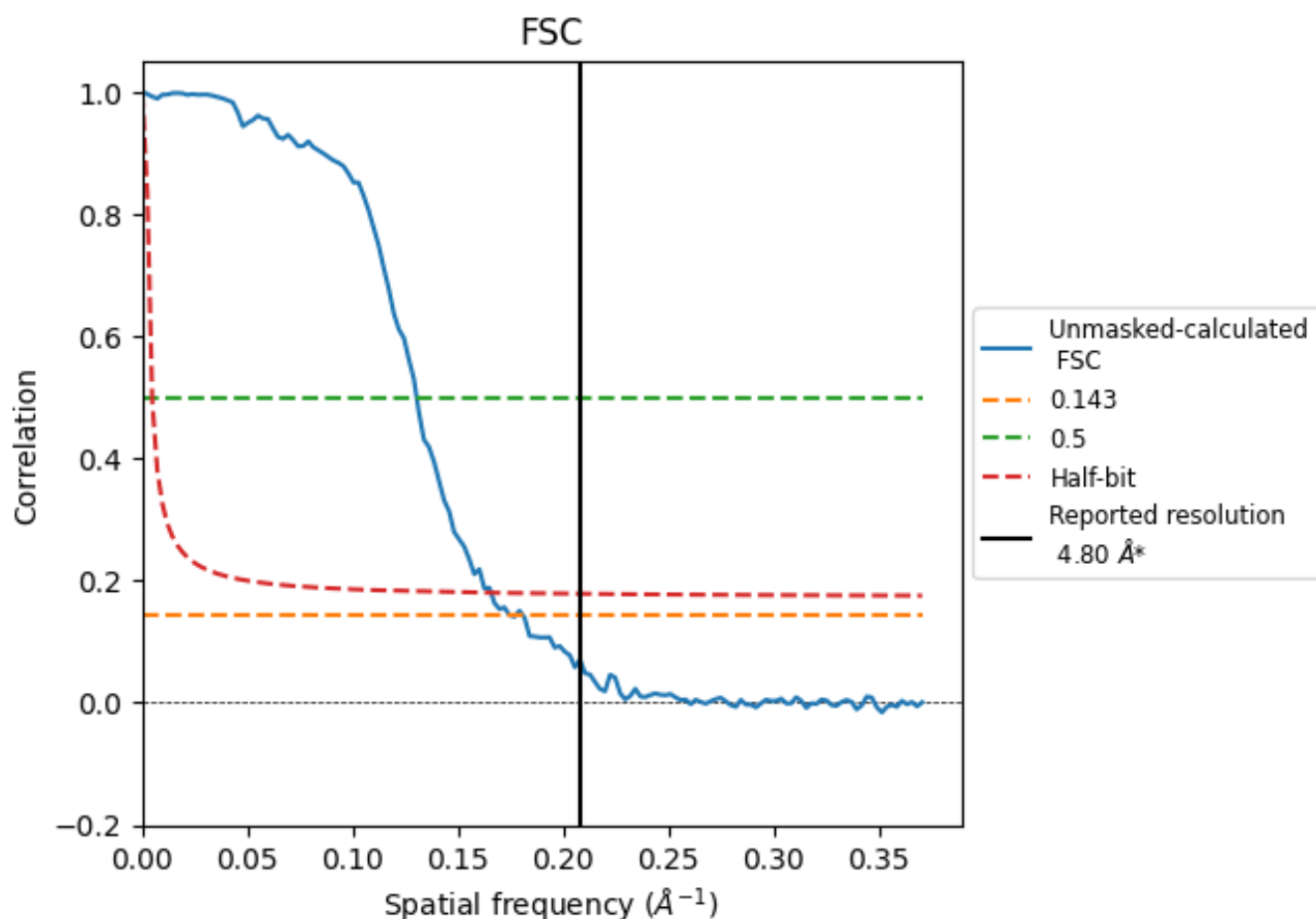


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

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 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

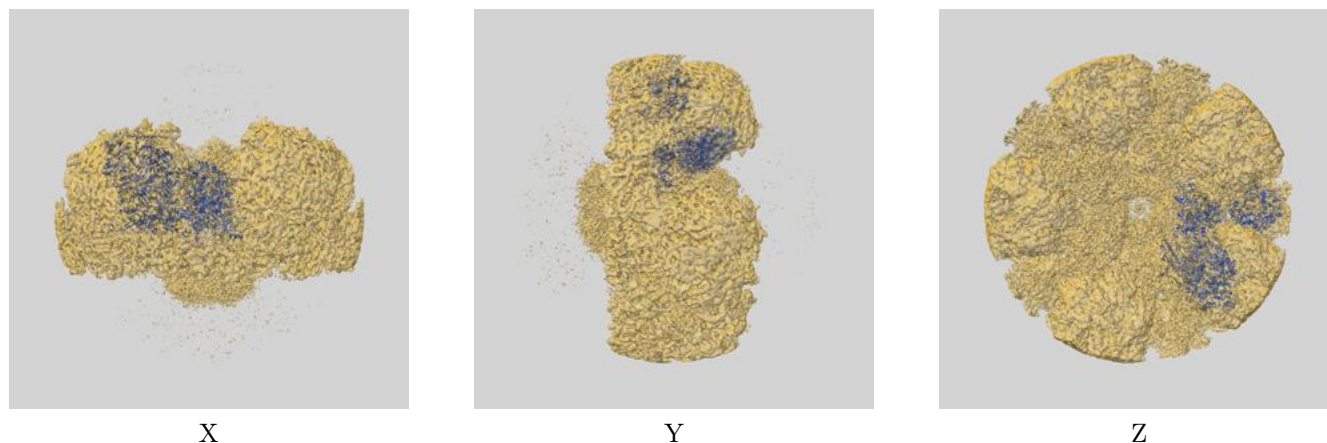
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.72	7.67	6.04

*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 5.72 differs from the reported value 4.8 by more than 10 %

9 Map-model fit [i](#)

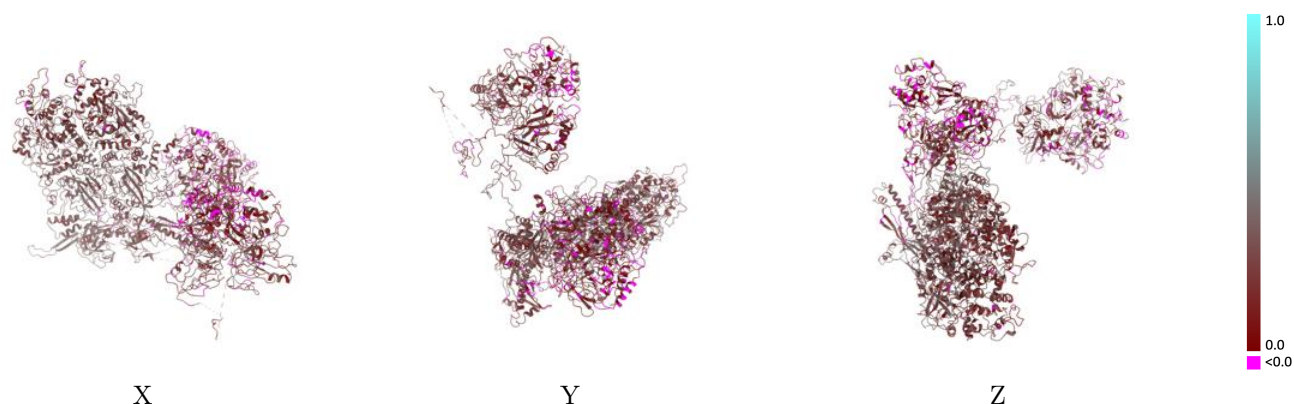
This section contains information regarding the fit between EMDB map EMD-38191 and PDB model 8XA1. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



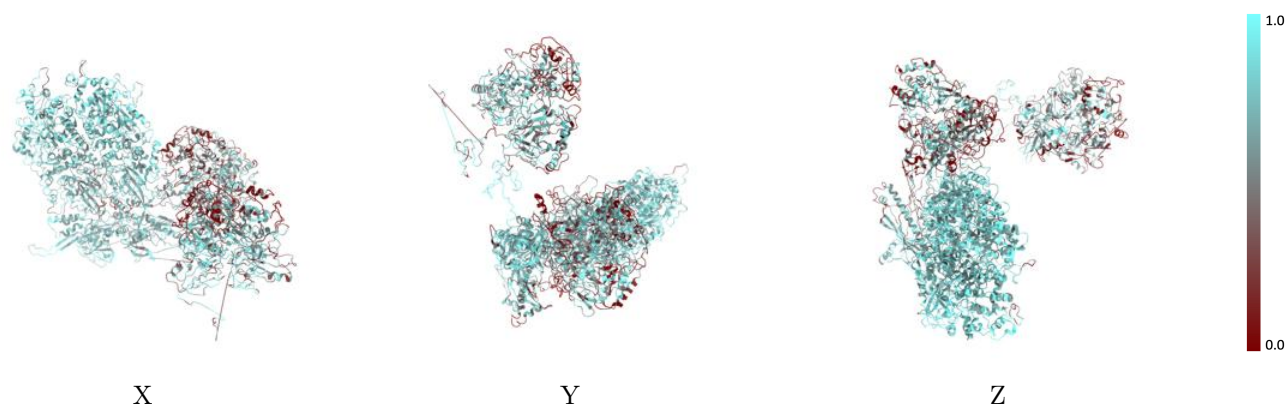
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



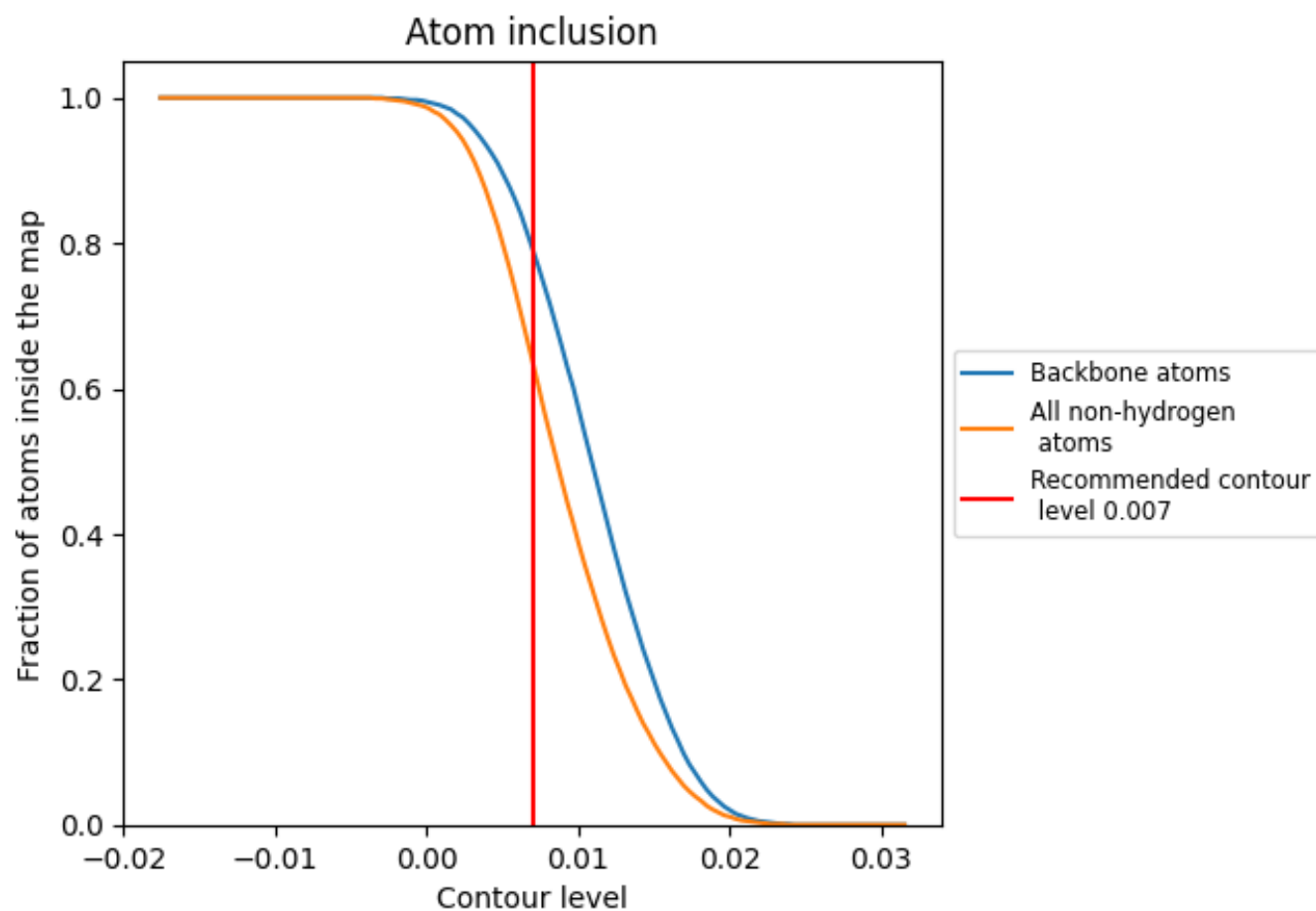
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 64% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6360	<div></div> 0.2430
A	<div></div> 0.7390	<div></div> 0.2770
C	<div></div> 0.7440	<div></div> 0.2850
G	<div></div> 0.4630	<div></div> 0.1760
I	<div></div> 0.5380	<div></div> 0.2210
P	<div></div> 0.3390	<div></div> 0.1450
R	<div></div> 0.4610	<div></div> 0.2130
Y	<div></div> 0.5270	<div></div> 0.1500
d	<div></div> 0.5440	<div></div> 0.2070

