



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:21 AM UTC

PDB ID : 9OI3 / pdb_00009oi3
EMDB ID : EMD-70503
Title : Structure of human Fab 604 in complex with influenza H1N1 A/Solomon Island/3/2006 hemagglutinin
Authors : Wu, N.C.; Pholcharee, T.; Lv, H.
Deposited on : 2025-05-06
Resolution : 2.71 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:

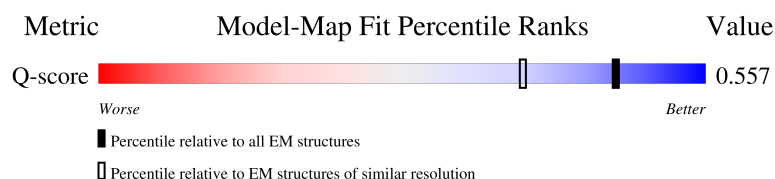
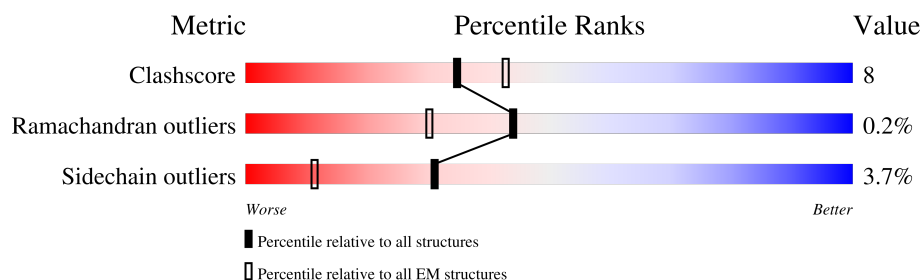
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.71 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10297 (2.21 - 3.21)

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	326	 82% 15% ..
1	C	326	 76% 19% ..
1	E	326	 78% 19% ..
2	B	222	 64% 11% • 24%

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Mol	Chain	Length	Quality of chain
2	D	222	
2	F	222	
3	H	134	
3	I	134	
3	M	134	
4	J	114	
4	L	114	
4	N	114	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16485 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	321	Total	C	N	O	S	0	0
			2428	1538	430	449	11		
1	C	319	Total	C	N	O	S	0	0
			2386	1514	424	437	11		
1	E	320	Total	C	N	O	S	0	0
			2401	1522	425	444	10		

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	169	Total	C	N	O	S	0	0
			1334	838	232	257	7		
2	D	169	Total	C	N	O	S	0	0
			1330	835	230	258	7		
2	F	169	Total	C	N	O	S	0	0
			1338	840	232	259	7		

- Molecule 3 is a protein called Heavy chain of Fab from human antibody 604.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	127	Total	C	N	O	S	0	0
			977	615	167	189	6		
3	I	123	Total	C	N	O	S	0	0
			953	601	163	183	6		
3	M	126	Total	C	N	O	S	0	0
			964	607	164	187	6		

- Molecule 4 is a protein called Light chain of Fab from human antibody 604.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	104	Total	C	N	O	S	0	0
			796	498	131	164	3		

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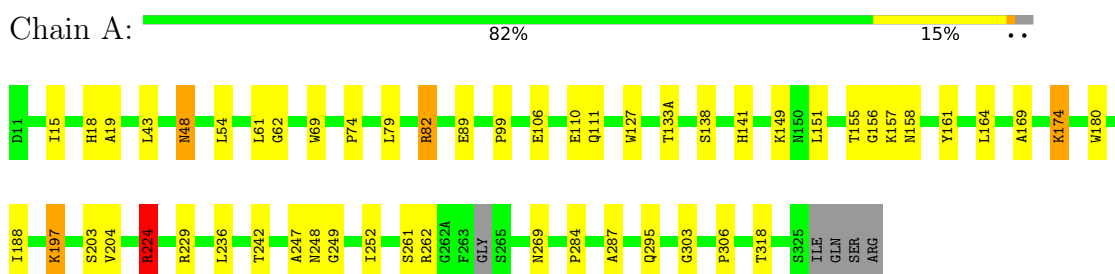
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Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	103	Total	C	N	O	S	0	0
			788	494	130	161	3		
4	N	104	Total	C	N	O	S	0	0
			790	492	131	164	3		

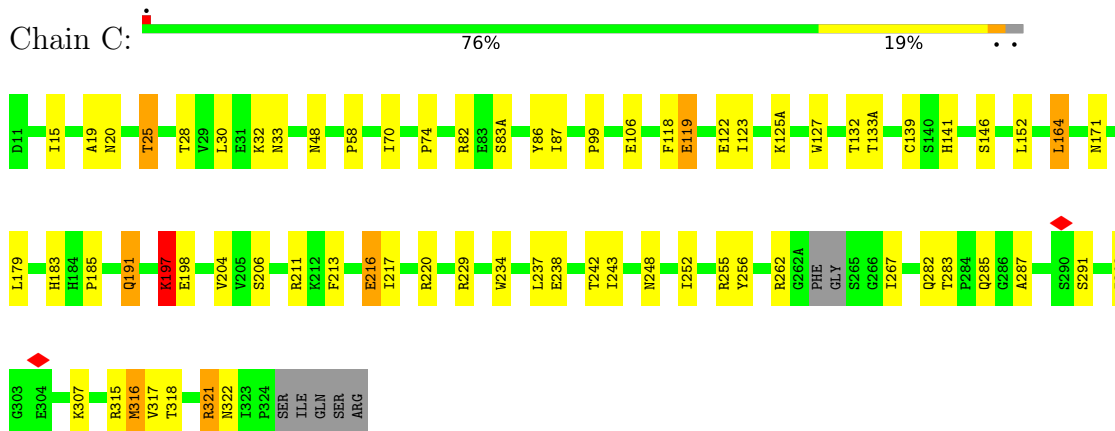
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

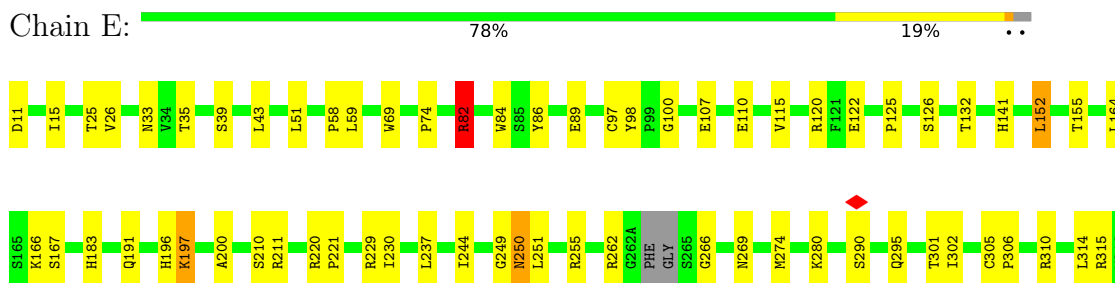
• Molecule 1: Hemagglutinin HA1

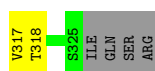


• Molecule 1: Hemagglutinin HA1

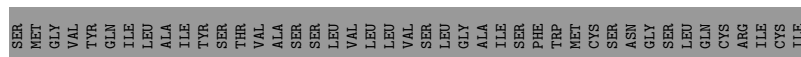
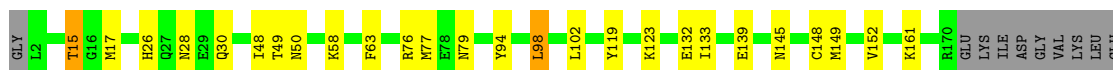


• Molecule 1: Hemagglutinin HA1

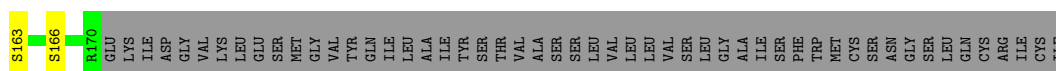
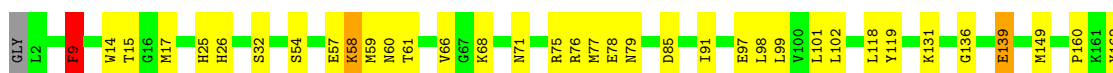




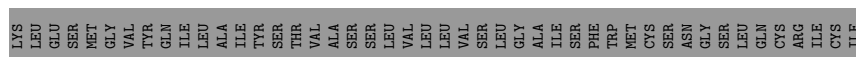
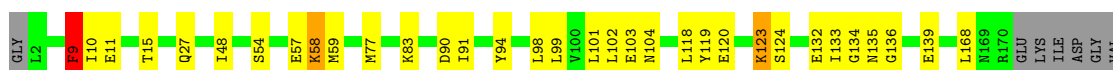
• Molecule 2: Hemagglutinin HA2



• Molecule 2: Hemagglutinin HA2



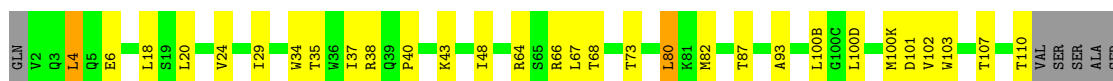
• Molecule 2: Hemagglutinin HA2



• Molecule 3: Heavy chain of Fab from human antibody 604



• Molecule 3: Heavy chain of Fab from human antibody 604



THR
LYS
GLY
PRO
SER

- Molecule 3: Heavy chain of Fab from human antibody 604

Chain M:  72% 21% 6%

GLN V2 E6 S15 E16 T29 S30 T35 V36 I37 W47 I48 Q49 Y50 H51 Y52 D53 T57 H69 S70 L71 V82C T83 A84 Y91 C92 A93 G96 R99 R100E M100K D101 V102 W103 G104 K105 G106 T107 V111 S112 S113 ALA SER THR LYS GLY

PRO
SER

- Molecule 4: Light chain of Fab from human antibody 604

Chain J:  73% 18% 9%

D1 I2 Q3 M4 V15 V19 C23 R24 A25 Q37 Q38 R61 F62 S63 E70 T74 L78 Q79 D82 F83 A84 Y86 Q90 L104 GLN ILE LYS ARG THR VAL ALA PRO SER

- Molecule 4: Light chain of Fab from human antibody 604

Chain L:  67% 24% 10%

ASP I2 Q3 M4 Q6 S7 P8 L11 V19 A25 S31 W32 A35 Q38 R61 F62 S63 S67 T74 I75 S76 Q79 D82 F83 A84 Q89 Q90 S96 T97 F98 G99 Q100 L104 GLN ILE LYS ARG THR VAL ALA PRO SER

- Molecule 4: Light chain of Fab from human antibody 604

Chain N:  79% 12% 9%

D1 I2 Q3 M4 S7 P8 T22 Q38 L78 D81 D82 F83 Q90 T93 Y94 S95 F98 L104 GLN ILE LYS ARG THR VAL ALA PRO SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	286029	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	57.35	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.706	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	380.87997, 380.87997, 380.87997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.058, 1.058, 1.058	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	0.44	0/2492	0.69	0/3403
1	C	0.42	1/2450 (0.0%)	0.65	0/3349
1	E	0.44	1/2465 (0.0%)	0.65	1/3369 (0.0%)
2	B	0.42	0/1361	0.65	0/1833
2	D	0.46	0/1357	0.68	2/1829 (0.1%)
2	F	0.42	0/1365	0.65	2/1838 (0.1%)
3	H	0.46	0/998	0.69	0/1353
3	I	0.35	0/974	0.54	0/1320
3	M	0.49	0/985	0.76	0/1337
4	J	0.22	0/815	0.42	0/1110
4	L	0.19	0/807	0.40	0/1099
4	N	0.37	0/808	0.56	0/1101
All	All	0.42	2/16877 (0.0%)	0.64	5/22941 (0.0%)

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	2
1	C	0	2
1	E	0	4
3	H	0	2
3	I	0	2
3	M	0	1
All	All	0	13

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	210	SER	C-N	-5.78	1.26	1.33
1	C	171	ASN	C-N	5.53	1.41	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	280	LYS	N-CA-C	-6.67	104.85	114.12
2	F	9	PHE	CB-CA-C	6.48	123.31	110.42
2	D	9	PHE	CA-CB-CG	6.47	120.27	113.80
2	D	9	PHE	CB-CA-C	6.18	122.72	110.42
2	F	9	PHE	CA-CB-CG	5.08	118.88	113.80

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	ARG	Sidechain
1	A	82	ARG	Sidechain
1	C	315	ARG	Sidechain
1	C	321	ARG	Sidechain
1	E	82	ARG	Sidechain

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	A	2428	0	2298	35	0
1	C	2386	0	2238	39	0
1	E	2401	0	2256	38	0
2	B	1334	0	1250	22	0
2	D	1330	0	1237	31	0
2	F	1338	0	1254	26	0
3	H	977	0	961	19	0
3	I	953	0	937	15	0
3	M	964	0	939	26	0
4	J	796	0	756	15	0
4	L	788	0	749	16	0
4	N	790	0	749	8	0
All	All	16485	0	15624	257	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 257 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)
3:M:6:GLU:HB2	3:M:107:THR:CG2	1.87	1.05
3:M:6:GLU:HB2	3:M:107:THR:HG21	1.58	0.85
3:M:6:GLU:HB2	3:M:107:THR:HG23	1.57	0.83
1:A:174:LYS:HD2	1:A:261:SER:OG	1.85	0.77
1:C:82:ARG:NH2	1:C:83(A):SER:O	2.20	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	A	317/326 (97%)	296 (93%)	20 (6%)	1 (0%)	36	59
1	C	315/326 (97%)	293 (93%)	20 (6%)	2 (1%)	21	42
1	E	316/326 (97%)	291 (92%)	24 (8%)	1 (0%)	36	59
2	B	167/222 (75%)	161 (96%)	6 (4%)	0	100	100
2	D	167/222 (75%)	162 (97%)	5 (3%)	0	100	100
2	F	167/222 (75%)	157 (94%)	10 (6%)	0	100	100
3	H	125/134 (93%)	118 (94%)	7 (6%)	0	100	100
3	I	121/134 (90%)	118 (98%)	3 (2%)	0	100	100
3	M	124/134 (92%)	116 (94%)	8 (6%)	0	100	100
4	J	102/114 (90%)	97 (95%)	5 (5%)	0	100	100
4	L	101/114 (89%)	94 (93%)	7 (7%)	0	100	100
4	N	102/114 (90%)	94 (92%)	8 (8%)	0	100	100
All	All	2124/2388 (89%)	1997 (94%)	123 (6%)	4 (0%)	44	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	119	GLU
1	C	197	LYS
1	E	290	SER
1	A	82	ARG

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	256/286 (90%)	248 (97%)	8 (3%)	35	63
1	C	246/286 (86%)	231 (94%)	15 (6%)	17	38
1	E	250/286 (87%)	243 (97%)	7 (3%)	38	67
2	B	138/191 (72%)	136 (99%)	2 (1%)	59	80
2	D	137/191 (72%)	131 (96%)	6 (4%)	25	51
2	F	139/191 (73%)	130 (94%)	9 (6%)	15	35
3	H	108/114 (95%)	103 (95%)	5 (5%)	24	50
3	I	105/114 (92%)	101 (96%)	4 (4%)	29	56
3	M	106/114 (93%)	104 (98%)	2 (2%)	50	75
4	J	90/98 (92%)	88 (98%)	2 (2%)	45	72
4	L	89/98 (91%)	87 (98%)	2 (2%)	45	72
4	N	89/98 (91%)	86 (97%)	3 (3%)	32	60
All	All	1753/2067 (85%)	1688 (96%)	65 (4%)	31	57

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	104	LEU
4	L	79	GLN
1	C	321	ARG
1	C	318	THR
3	M	99	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18

such sidechains are listed below:

Mol	Chain	Res	Type
4	J	90	GLN
4	L	92	ASN
4	L	90	GLN
2	D	129	ASN
4	J	50	GLN

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.

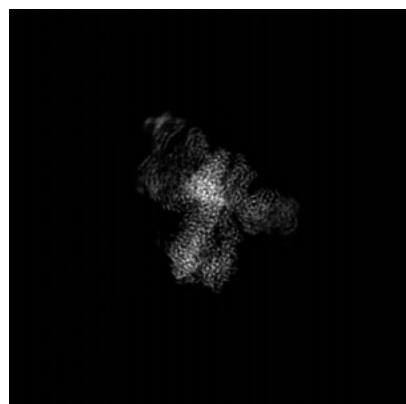
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70503. These allow visual inspection of the internal detail of the map and identification of artifacts.

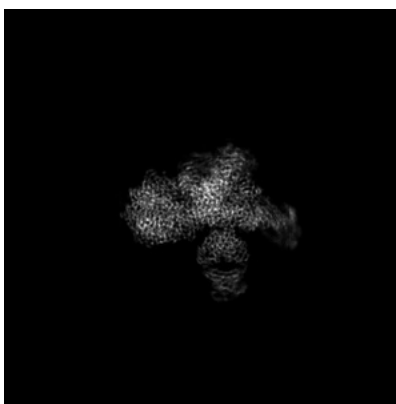
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

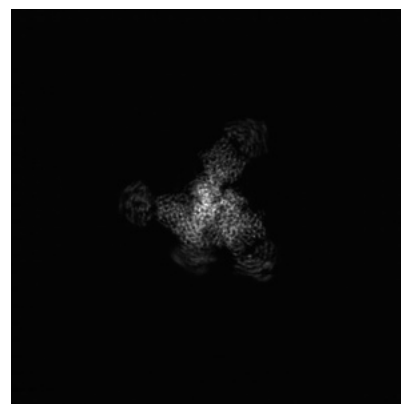
6.1.1 Primary map



X

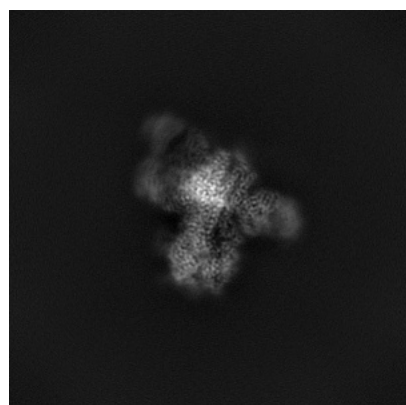


Y

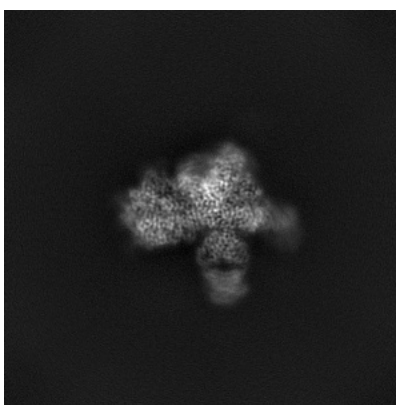


Z

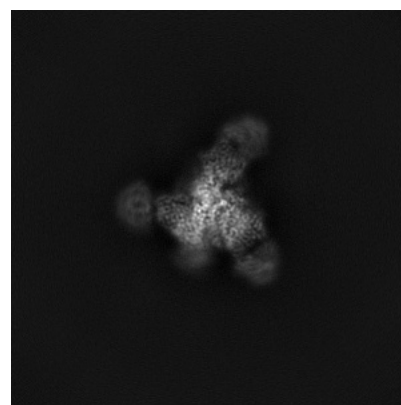
6.1.2 Raw map



X



Y

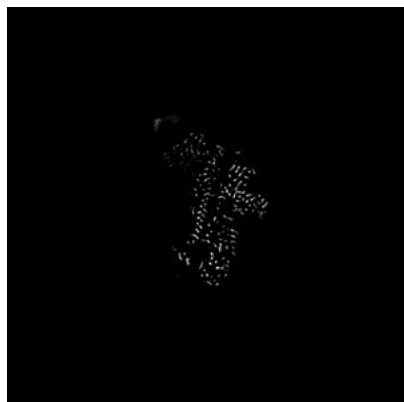


Z

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

6.2 Central slices [i](#)

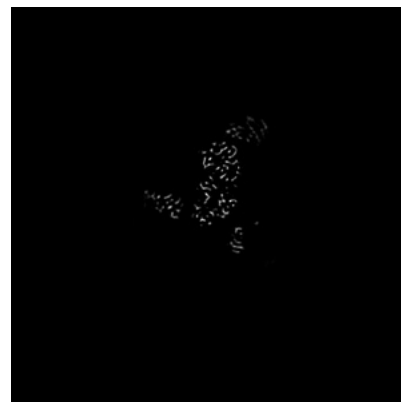
6.2.1 Primary map



X Index: 180

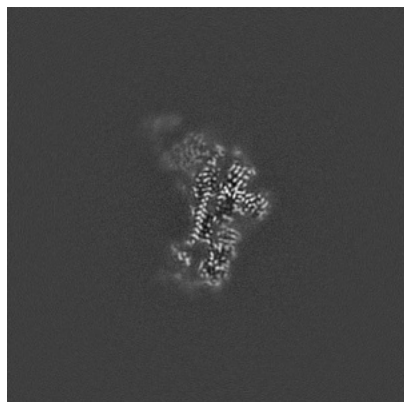


Y Index: 180

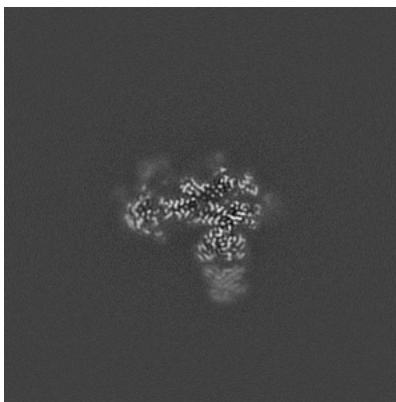


Z Index: 180

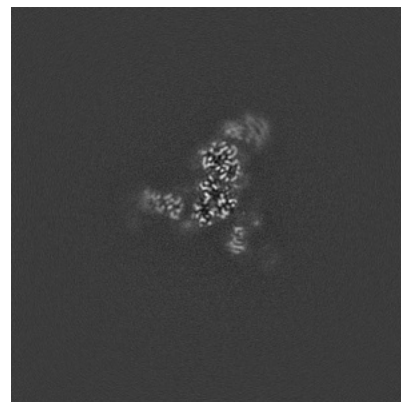
6.2.2 Raw map



X Index: 180



Y Index: 180



Z Index: 180

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: 174

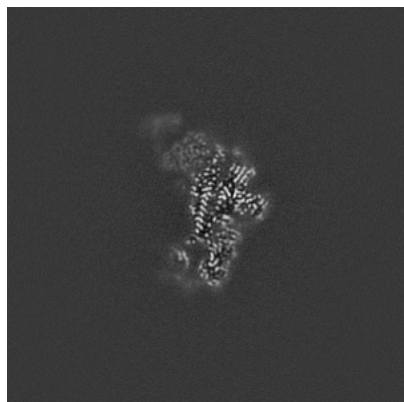


Y Index: 175

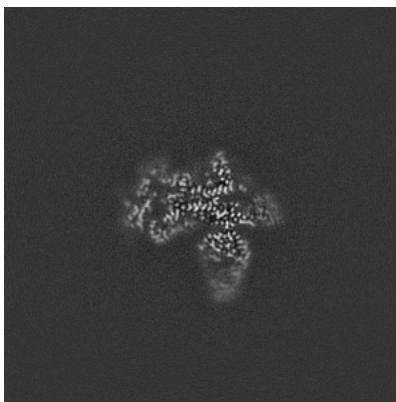


Z Index: 191

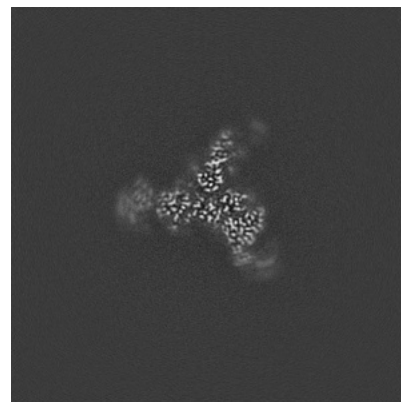
6.3.2 Raw map



X Index: 179



Y Index: 175

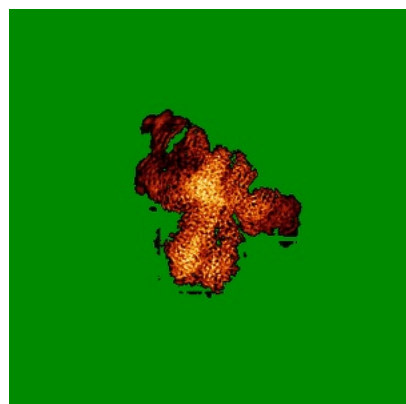


Z Index: 191

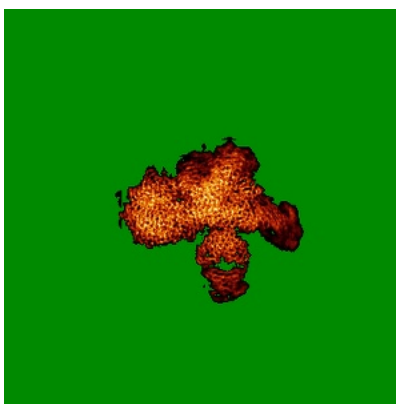
The images above show the largest variance slices of the map in three orthogonal directions.

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

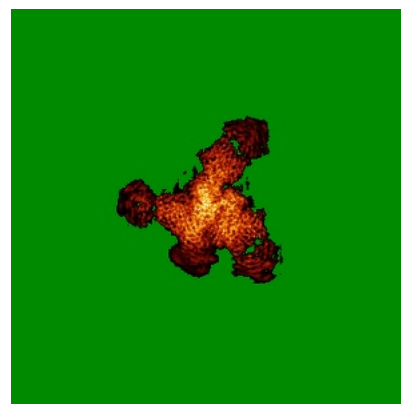
6.4.1 Primary map



X

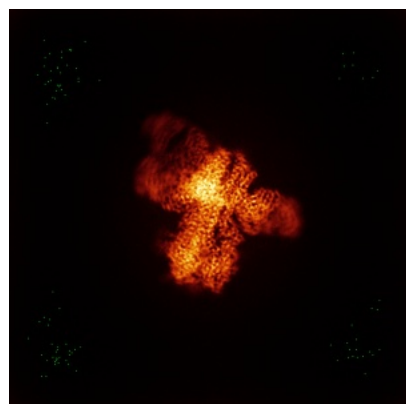


Y

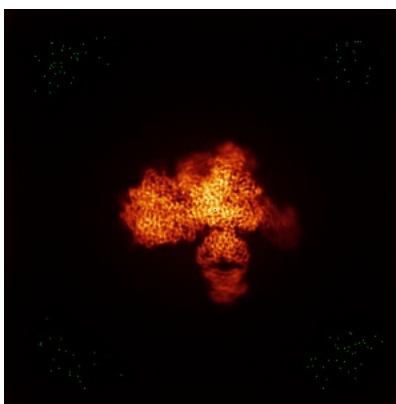


Z

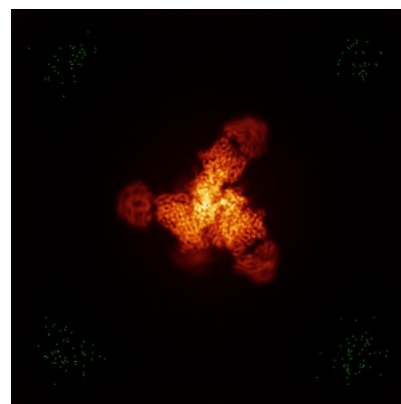
6.4.2 Raw map



X



Y

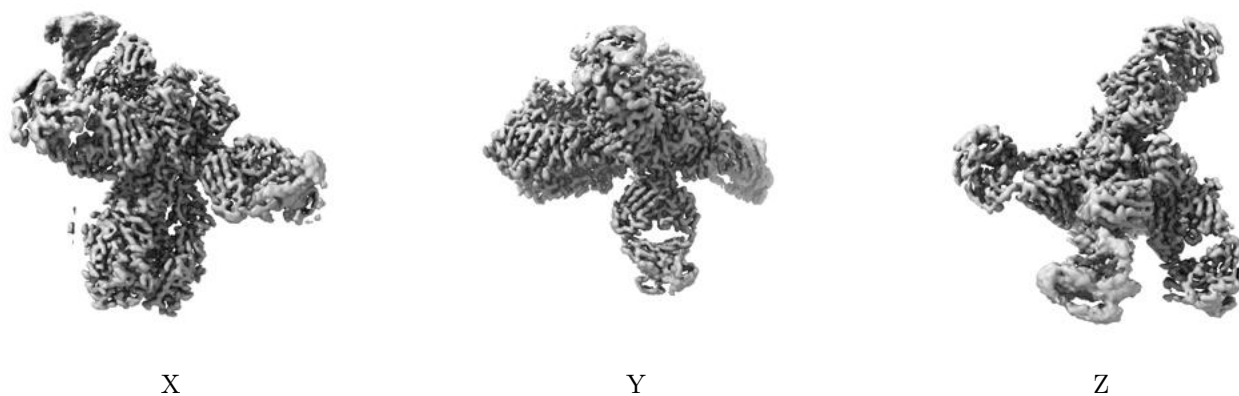


Z

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.

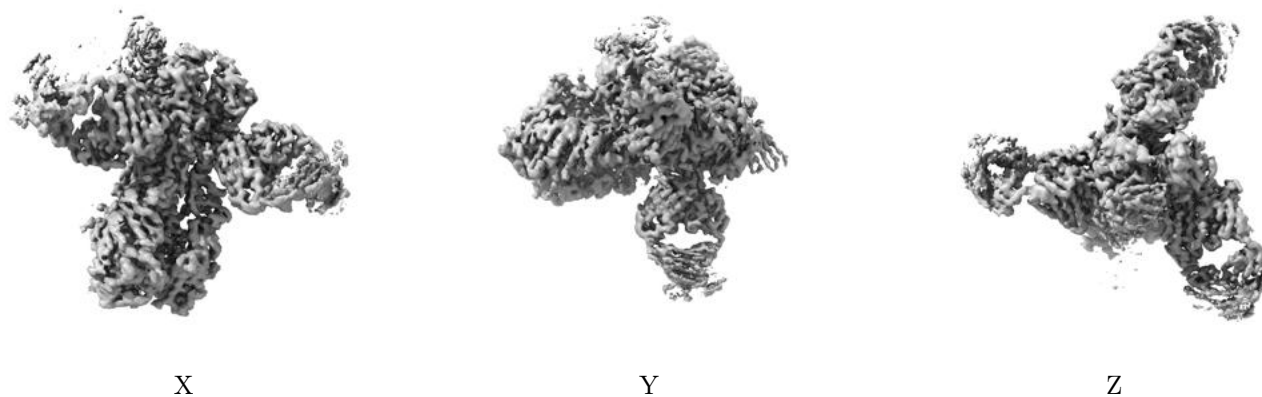
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

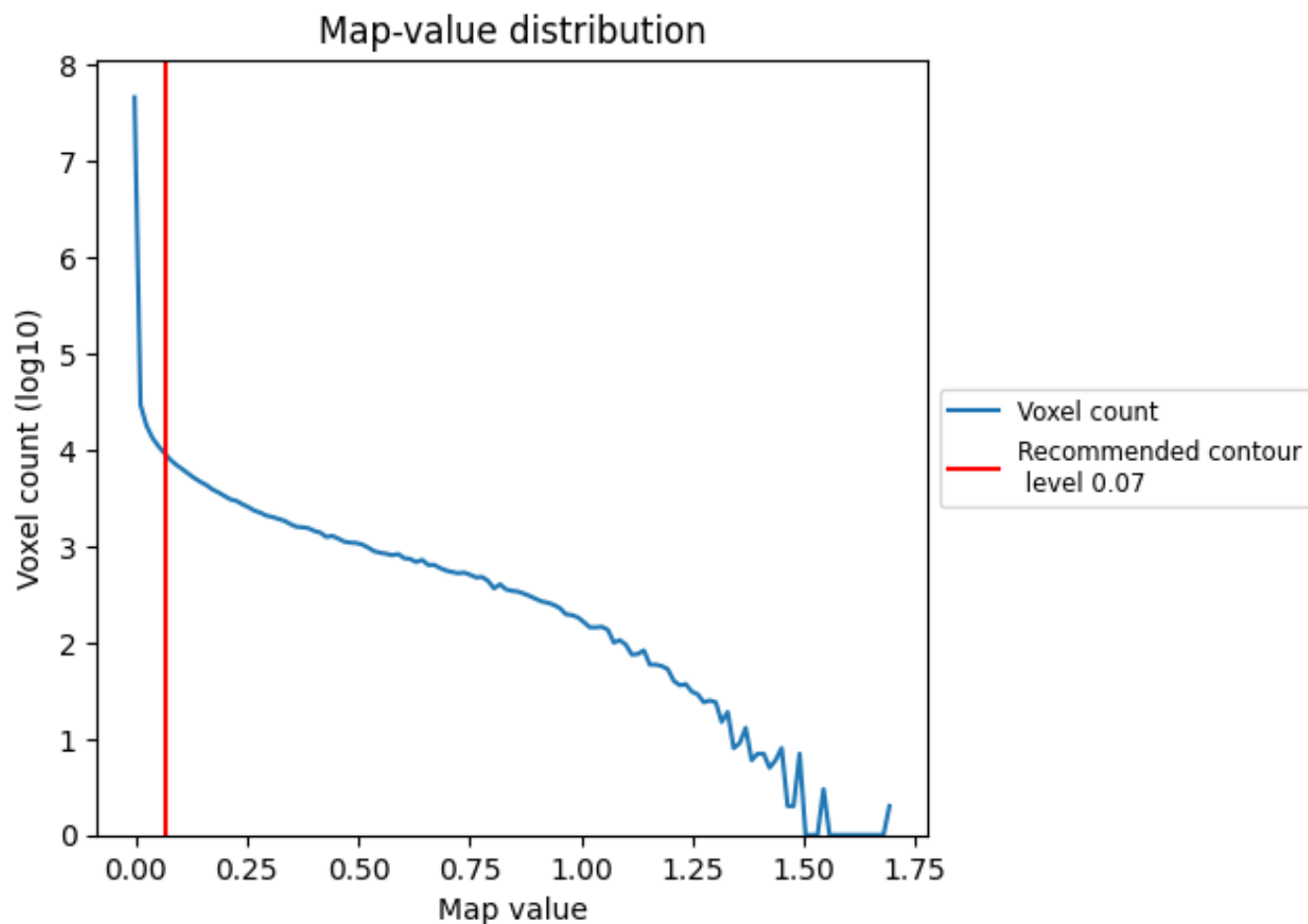
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

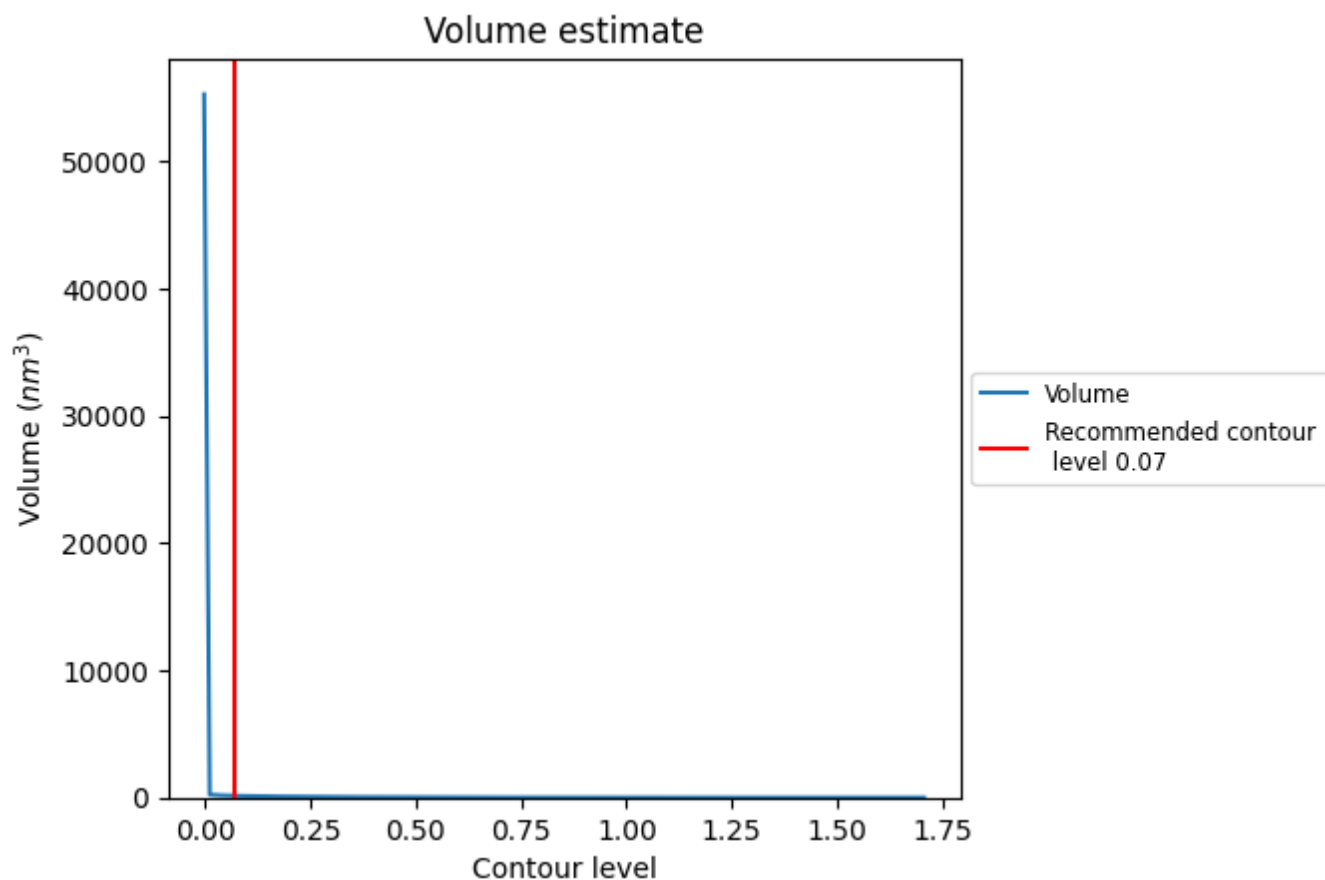
This section contains the results of statistical analysis of the map.

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.

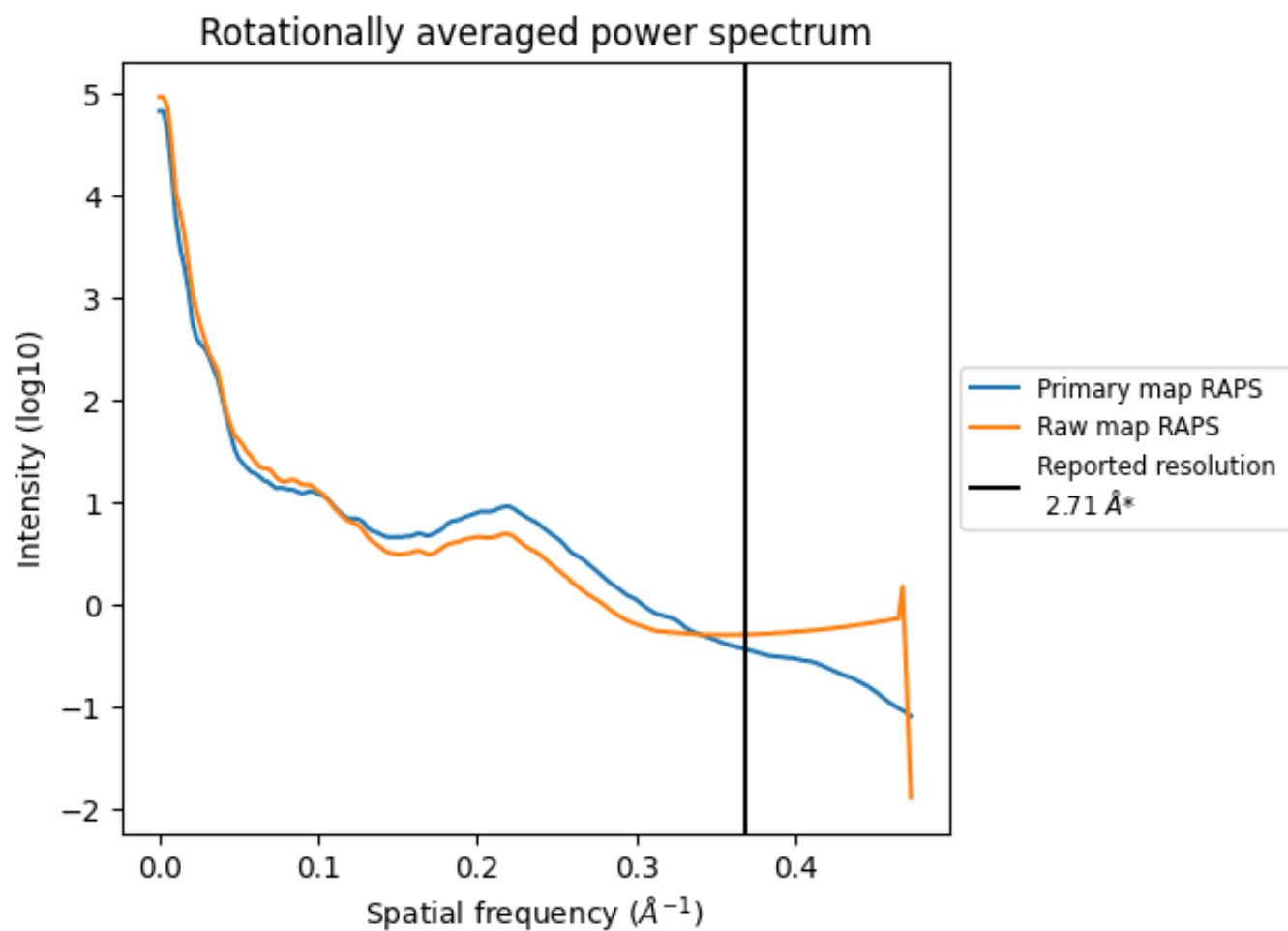
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 141 nm^3 ; this corresponds to an approximate mass of 128 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 ⓘ

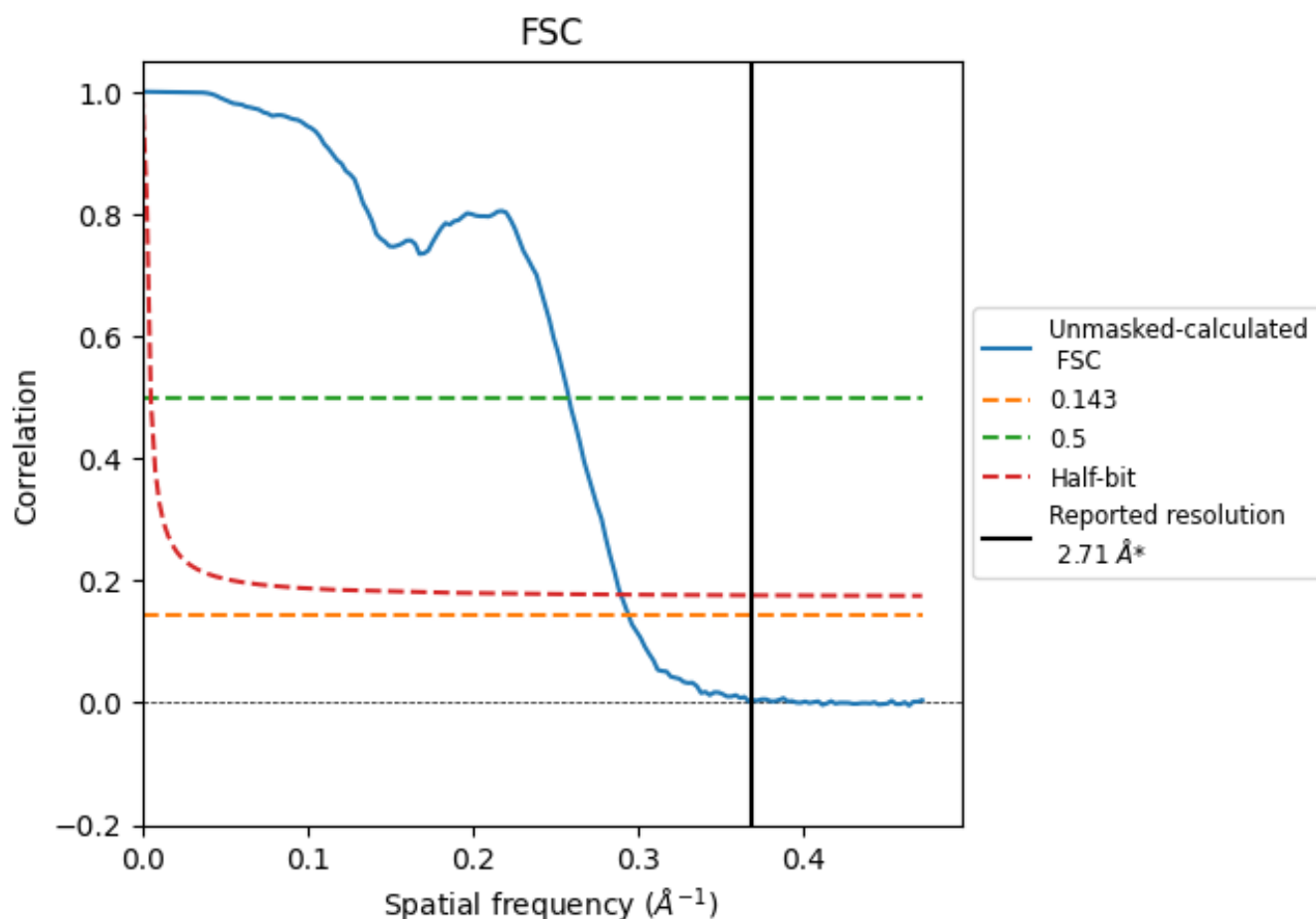


*Reported resolution corresponds to spatial frequency of 0.369 $\text{\AA}^{-1}$

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 0.369 Å⁻¹

8.2 Resolution estimates [i](#)

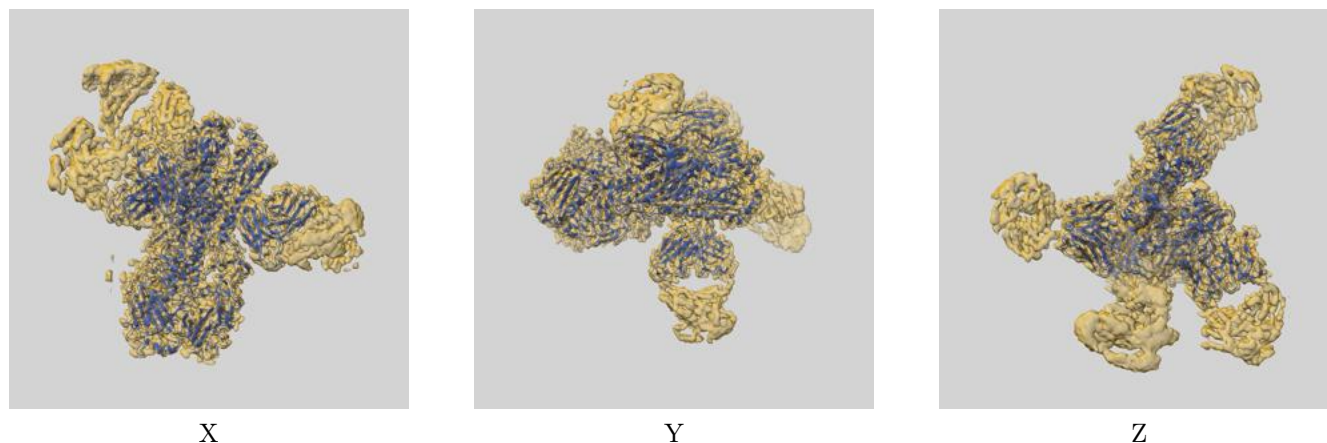
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.71	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.39	3.87	3.45

*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 3.39 differs from the reported value 2.71 by more than 10 %

9 Map-model fit [i](#)

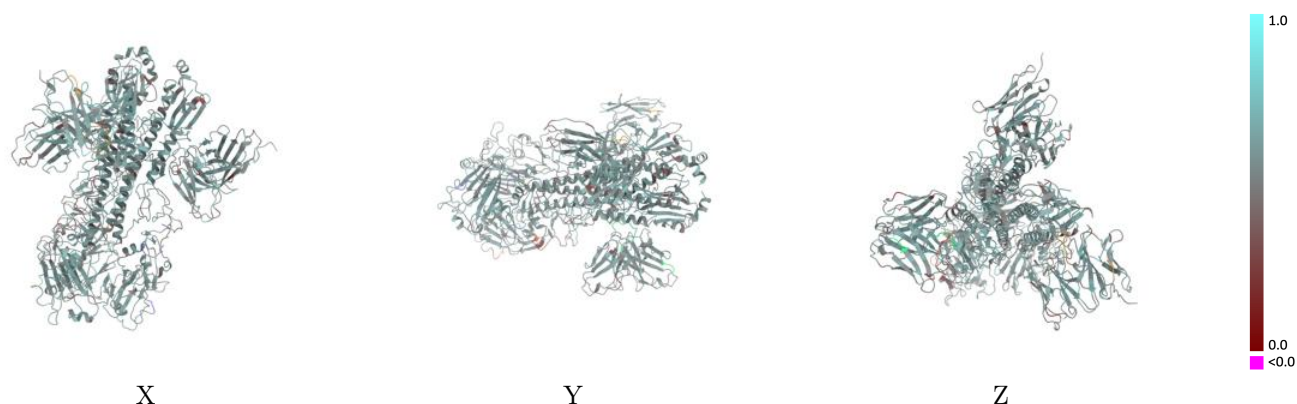
This section contains information regarding the fit between EMDB map EMD-70503 and PDB model 9OI3. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



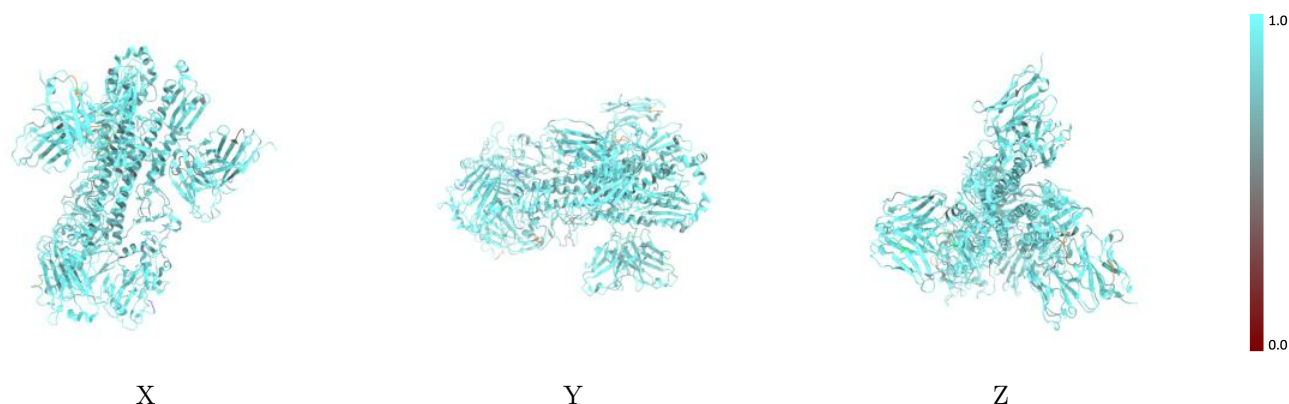
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



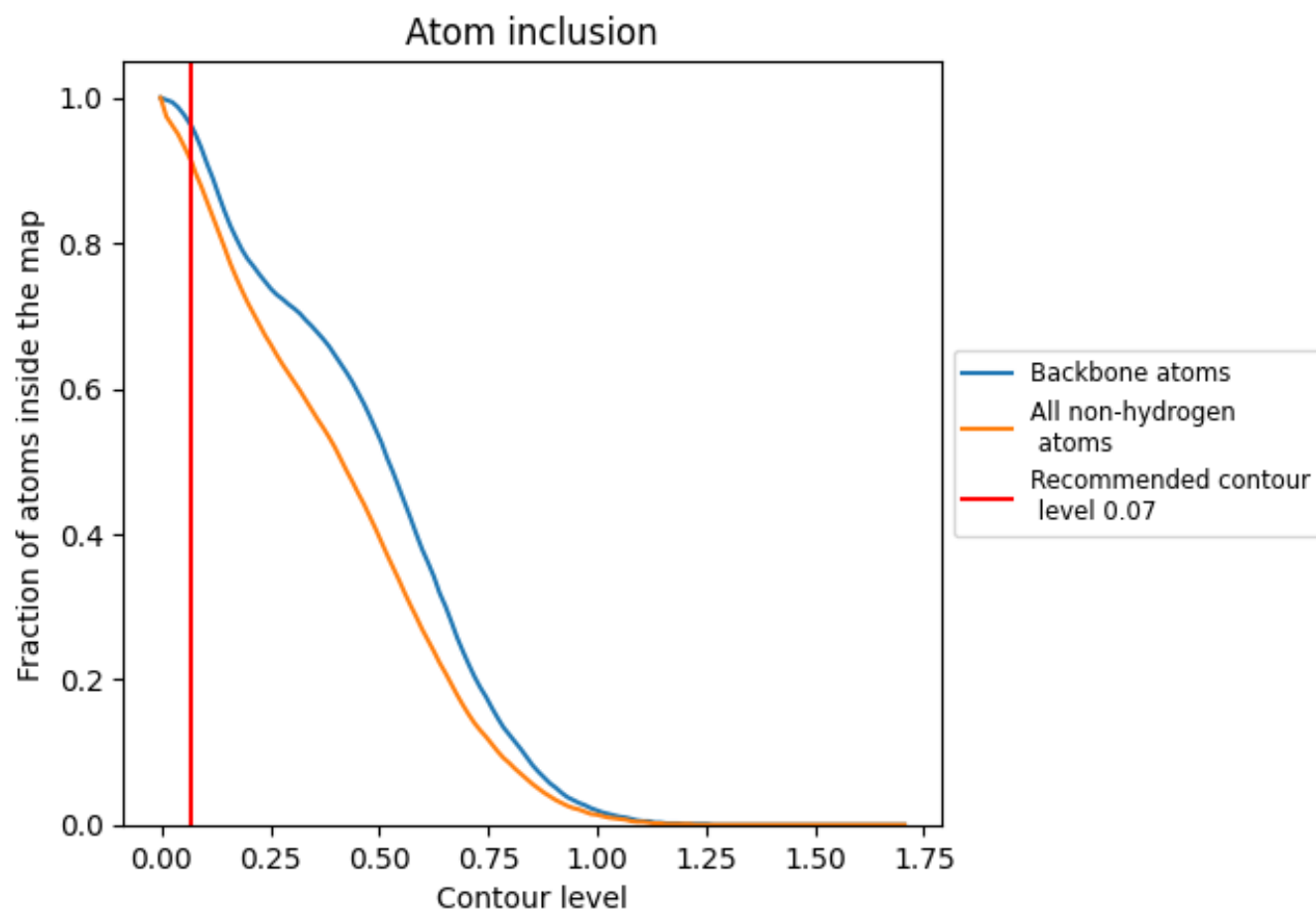
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 91% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9110	0.5570
A	0.9300	0.5630
B	0.8990	0.5630
C	0.9240	0.5540
D	0.8950	0.5620
E	0.9190	0.5550
F	0.8990	0.5630
H	0.9050	0.5530
I	0.9080	0.5620
J	0.8940	0.5400
L	0.8900	0.5470
M	0.9150	0.5670
N	0.8870	0.5380

