



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2025 – 10:14 AM JST

PDB ID : 9K2X / pdb_00009k2x
EMDB ID : EMD-62000
Title : Cryo-EM structure of USP7:DNMT1 complex; open conformation
Authors : Nakamura, N.; Arita, K.
Deposited on : 2024-10-18
Resolution : 3.75 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

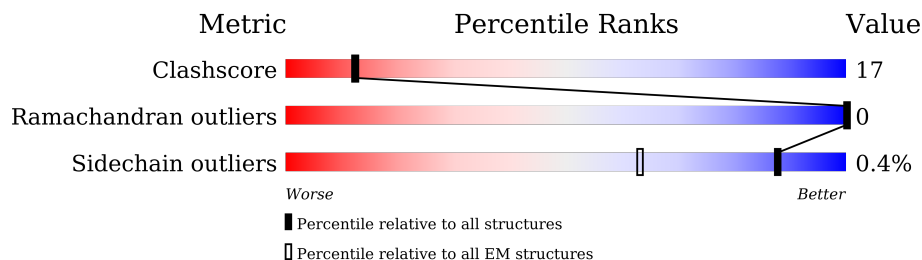
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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	1107	<div> <div>9%</div> <div>29%</div> <div>19%</div> <div>53%</div> </div>
2	B	1271	<div> <div>55%</div> <div>26%</div> <div>19%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12376 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 Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	524	Total	C	N	O	S	0	0
			4311	2744	728	812	27		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q93009
A	-3	PRO	-	expression tag	UNP Q93009
A	-2	LEU	-	expression tag	UNP Q93009
A	-1	GLY	-	expression tag	UNP Q93009
A	0	SER	-	expression tag	UNP Q93009

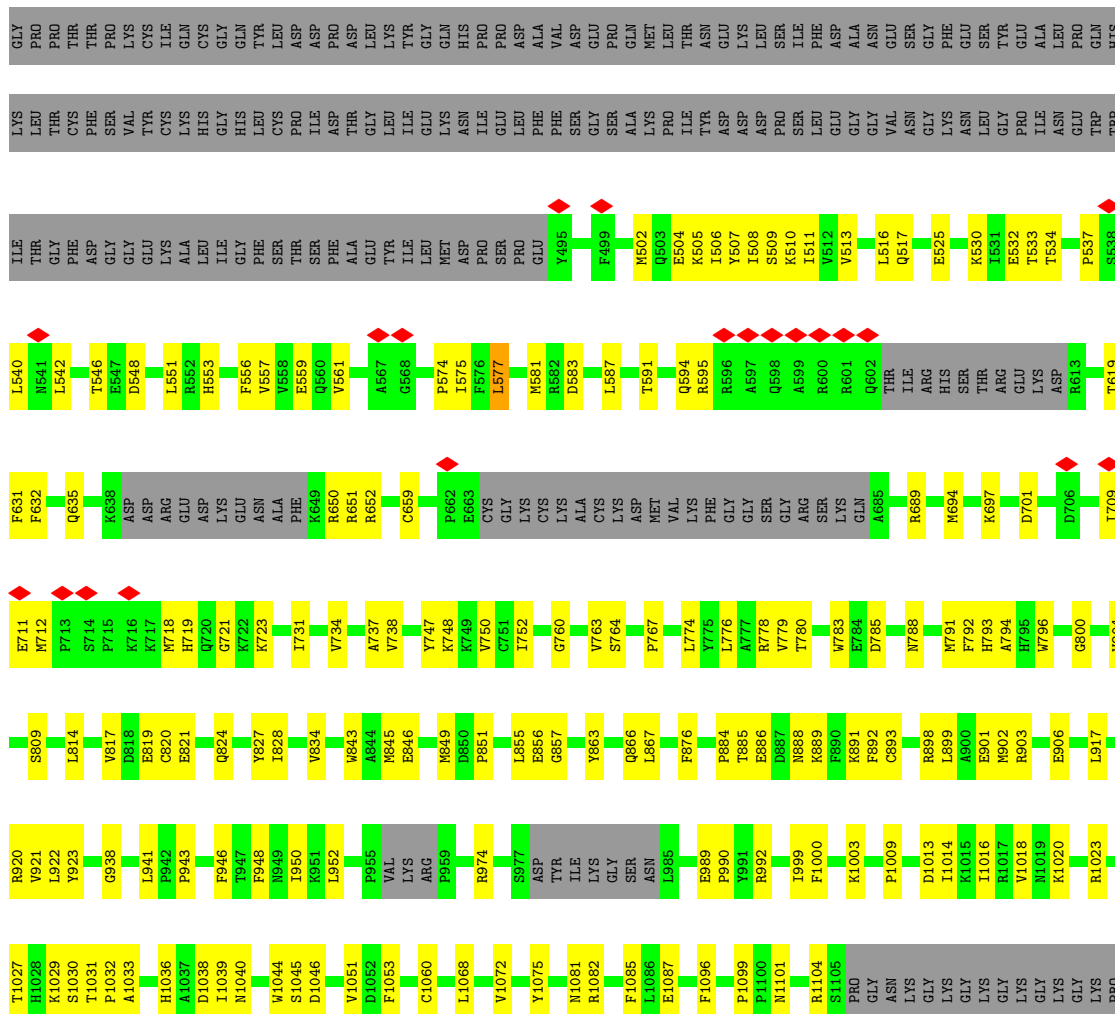
- Molecule 2 is a protein called DNA (cytosine-5)-methyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1027	Total	C	N	O	S	0	0
			8065	5106	1412	1493	54		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	346	GLY	-	expression tag	UNP P26358
B	347	PRO	-	expression tag	UNP P26358
B	348	PRO	-	expression tag	UNP P26358
B	349	THR	-	expression tag	UNP P26358
B	350	THR	-	expression tag	UNP P26358

- Molecule 2: DNA (cytosine-5)-methyltransferase 1



L1525	L1409	T1309	R1210	LYS
T1526	R1410	R1310	L1211	SER
	D1411		P1212	GLN
M1529	H1412	T1315	Q1213	ALA
		L1316	K1214	CYS
L1540	M1417	A1317	G1215	GLU
H1541			D1216	PRO
P1542	V1421	P1325		SER
		L1326	M1219	GLU
H1545	R1424	F1327		PRO
R1546	M1425	P1328	G1228	GLU
		E1329	F1229	ILE
Q1553	I1428	P1330	S1230	GLU
A1554				T1134
R1555	L1439	V1333	N1236	K1135
S1556	P1440	F1334	S1237	L1136
Q1557	N1441			P1137
G1558	I1442	A1338	Y1240	K1138
F1559			S1241	L1139
F1560	R1445	D1346	K1242	R1140
D1561	L1446	D1347	F1243	T1141
	S1447	K1348	K1244	L1142
		K1349		D1143
D1571	T1450	F1350	V1249	V1144
K1572	M1451			
	A1452	N1353	L1252	L1151
V1576	R1453			S1152
		R1356	Y1257	E1153
A1585	H1460		Y1258	G1154
	D1461	P1361	R1259	
I1588	R1462	F1362	P1260	Q1157
		R1363		
T1592	R1466	T1364	F1263	T1160
K1593		I1365	L1264	S1161
	G1470	T1366	L1265	D1162
		V1367		T1163
	V1475	R1368	V1268	L1164
A1600	C1476	D1369	R1269	W1165
ARG	S1477	T1370	N1270	A1166
GLU		M1371	F1271	I1167
SER	E1480	S1372		
ALA		D1373	F1274	W1170
SER	K1483			D1171
ALA		N1379	K1281	P1172
LYS	R1490		L1282	
ILE	Q1491	E1385	T1283	A1176
LYS	F1492			
GLU	N1493	Y1388	L1287	N1180
GLU	T1494		W1288	
GLU	L1495	Q1393	R1289	S1184
ALA	I1496	S1394	M1290	
ALA	P1497	W1395	G1291	L1195
LYS		F1396	Y1292	
ASP	L1500	Q1397	M1199	
	P1501	R1398		E1202
		Q1399	Q1300	
	R1516	L1400	Y1304	N1205
	F1522		A1307	Q1209
		Q1406		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73679	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62.918	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.031	Depositor
Minimum map value	-0.616	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.0565	Depositor
Map size (Å)	248.54999, 248.54999, 248.54999	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3808333, 1.3808333, 1.3808333	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	0.21	0/4410	0.67	4/5954 (0.1%)
2	B	0.14	0/8256	0.38	3/11177 (0.0%)
All	All	0.17	0/12666	0.50	7/17131 (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	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1260	PRO	CA-N-CD	-10.01	97.98	112.00
2	B	711	GLU	CA-C-N	8.74	137.43	121.70
2	B	711	GLU	C-N-CA	8.74	137.43	121.70
1	A	871	ARG	CA-CB-CG	6.49	127.08	114.10
1	A	1045	MET	CA-CB-CG	5.24	124.57	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1033	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4311	0	4223	174	0
2	B	8065	0	7833	240	0
All	All	12376	0	12056	408	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 408 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:625:MET:SD	1:A:633:LYS:HG3	2.14	0.88
2:B:950:ILE:HG22	2:B:952:LEU:H	1.37	0.87
2:B:551:LEU:HB3	2:B:1490:ARG:HH22	1.43	0.83
1:A:779:GLU:HG3	1:A:780:LEU:HD22	1.62	0.81
2:B:763:VAL:HG11	2:B:828:ILE:HD12	1.62	0.81

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	522/1107 (47%)	494 (95%)	28 (5%)	0	100	100
2	B	1013/1271 (80%)	972 (96%)	41 (4%)	0	100	100
All	All	1535/2378 (65%)	1466 (96%)	69 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	481/1007 (48%)	479 (100%)	2 (0%)	89	93
2	B	859/1100 (78%)	856 (100%)	3 (0%)	91	94
All	All	1340/2107 (64%)	1335 (100%)	5 (0%)	88	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	835	MET
1	A	988	MET
2	B	561	VAL
2	B	577	LEU
2	B	999	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	626	GLN
2	B	829	HIS
2	B	824	GLN
2	B	1026	ASN
1	A	855	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

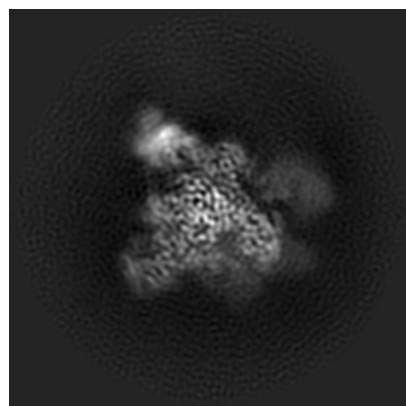
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62000. These allow visual inspection of the internal detail of the map and identification of artifacts.

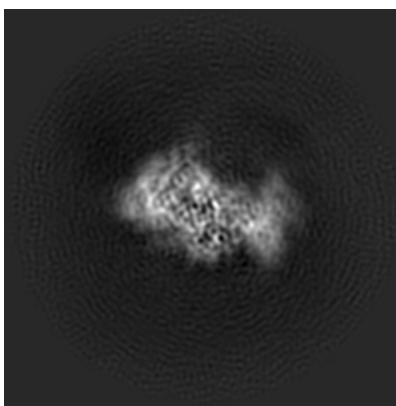
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

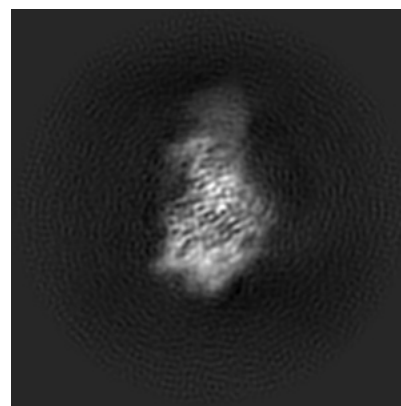
6.1.1 Primary map



X

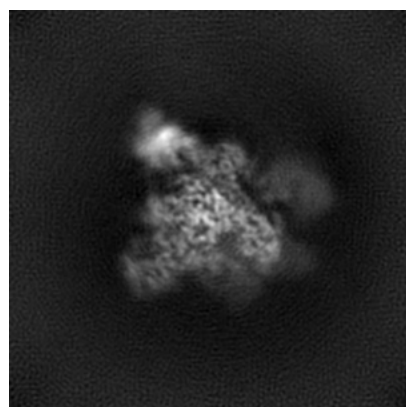


Y

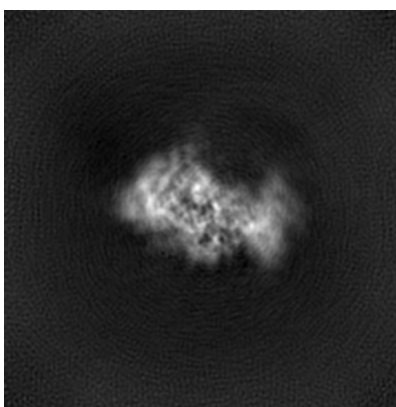


Z

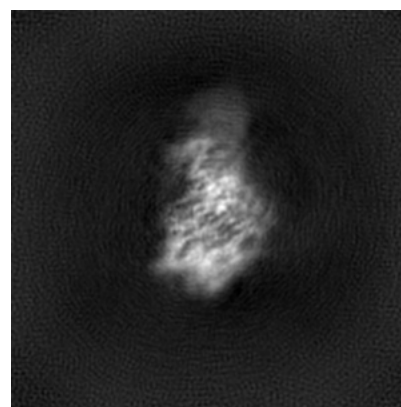
6.1.2 Raw map



X



Y

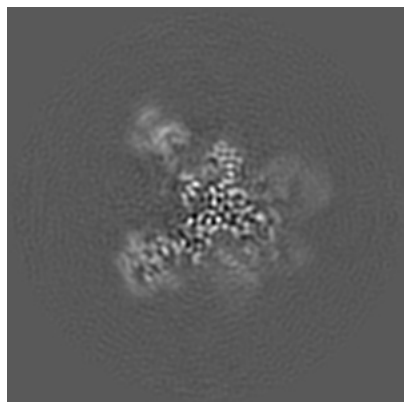


Z

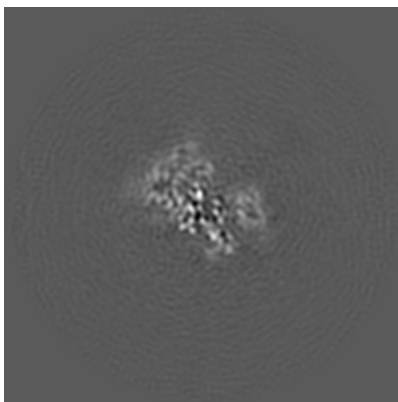
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

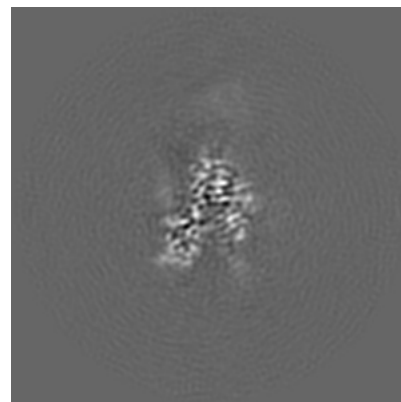
6.2.1 Primary map



X Index: 90

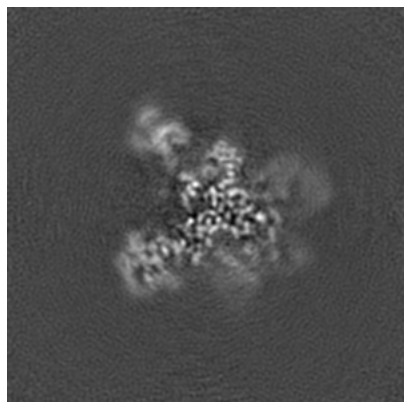


Y Index: 90

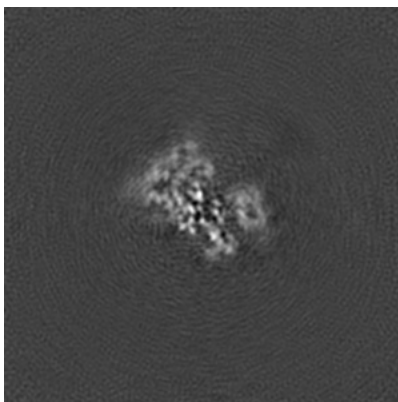


Z Index: 90

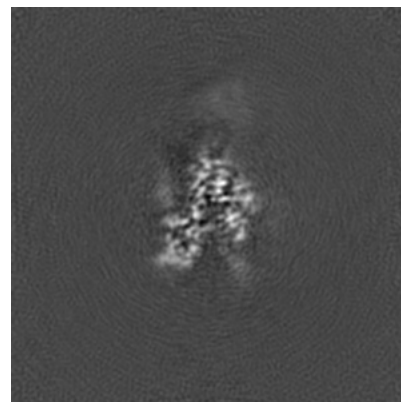
6.2.2 Raw map



X Index: 90



Y Index: 90

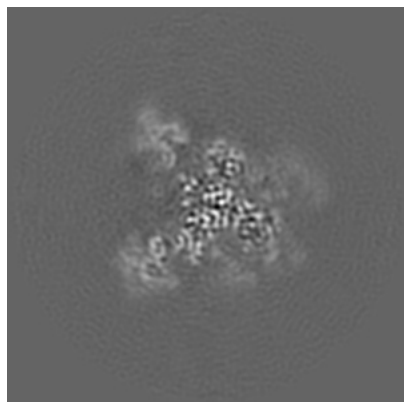


Z Index: 90

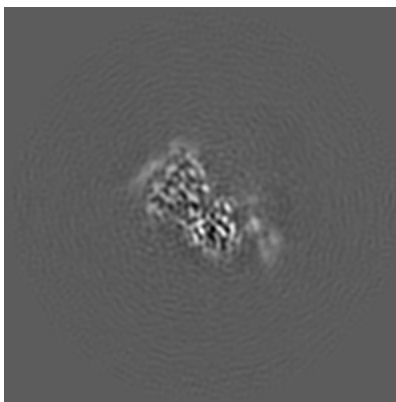
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

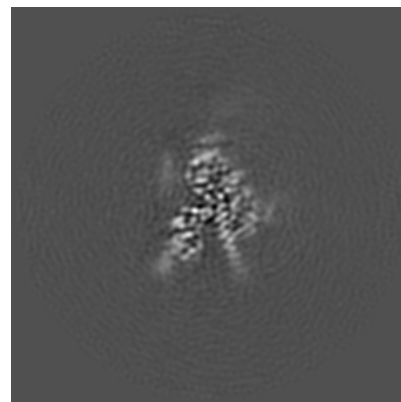
6.3.1 Primary map



X Index: 88

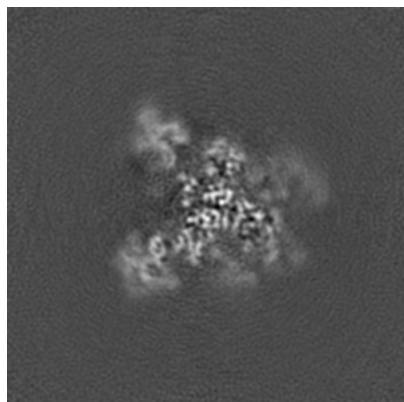


Y Index: 84

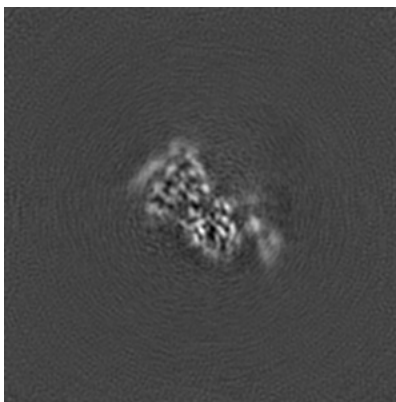


Z Index: 86

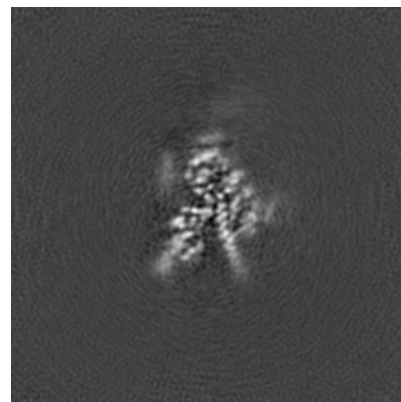
6.3.2 Raw map



X Index: 88



Y Index: 84

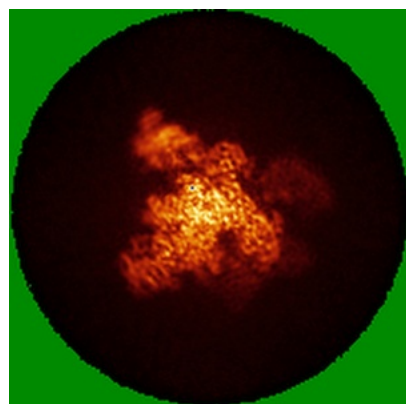


Z Index: 86

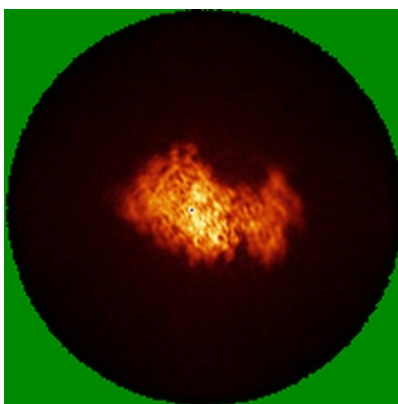
The images above show the largest variance slices of the map in three orthogonal directions.

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

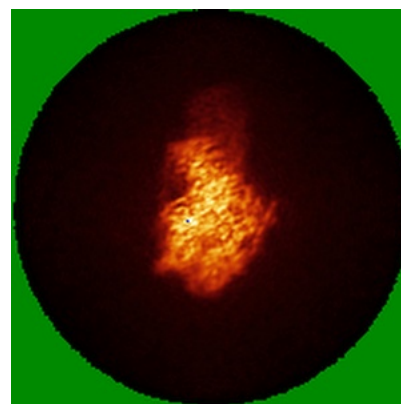
6.4.1 Primary map



X

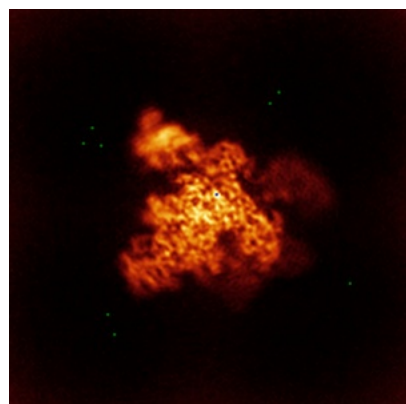


Y

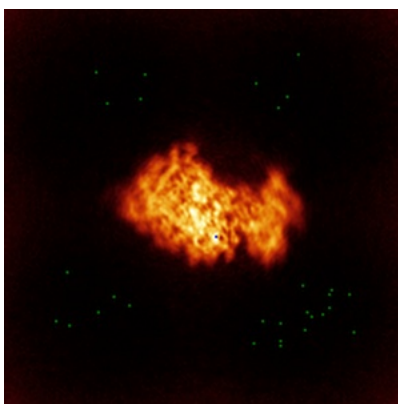


Z

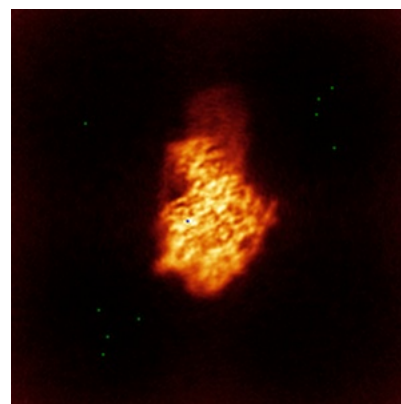
6.4.2 Raw map



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.

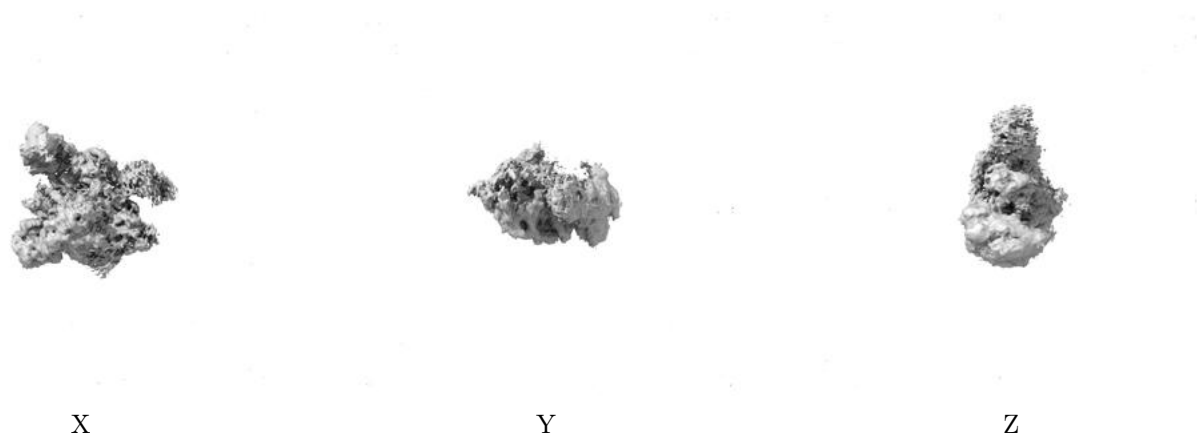
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0565. 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.

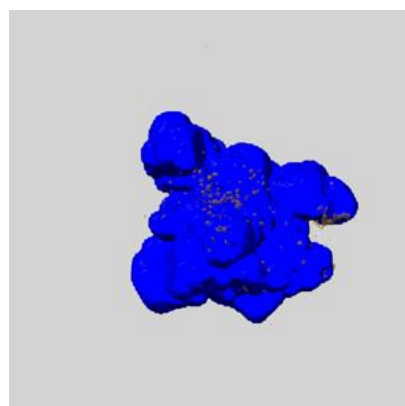
6.6 Mask visualisation [i](#)

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

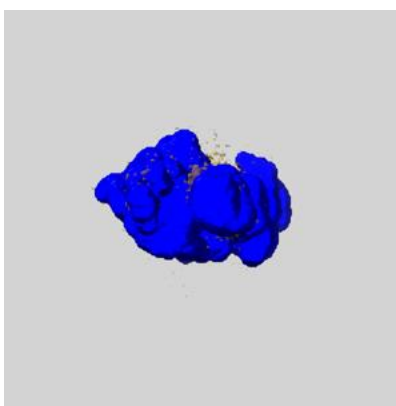
A mask typically either:

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

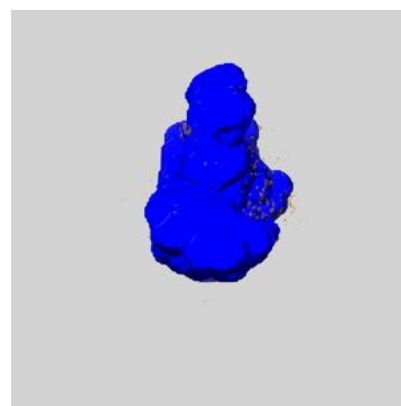
6.6.1 emd_62000_msk_1.map [i](#)



X



Y

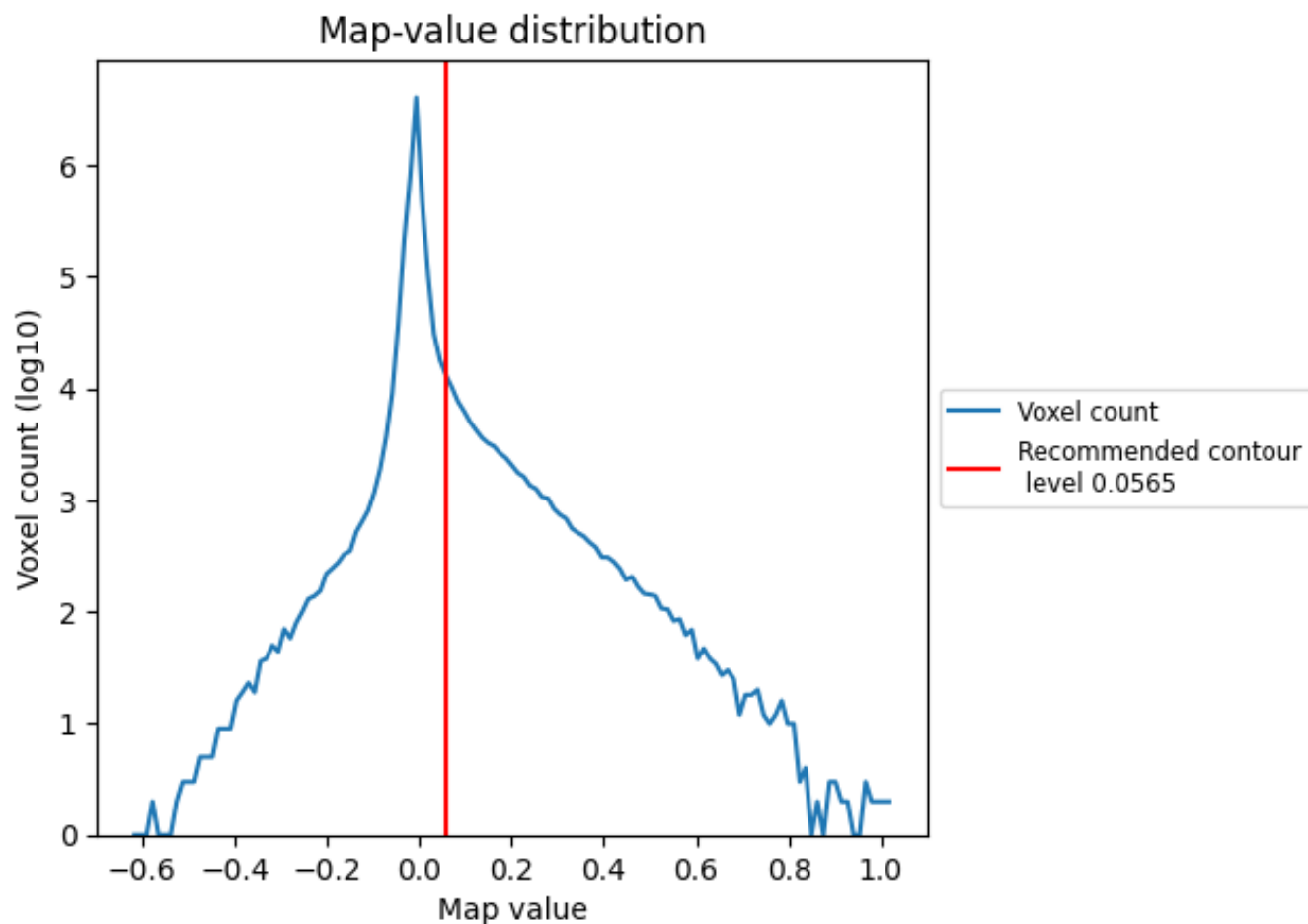


Z

7 Map analysis [i](#)

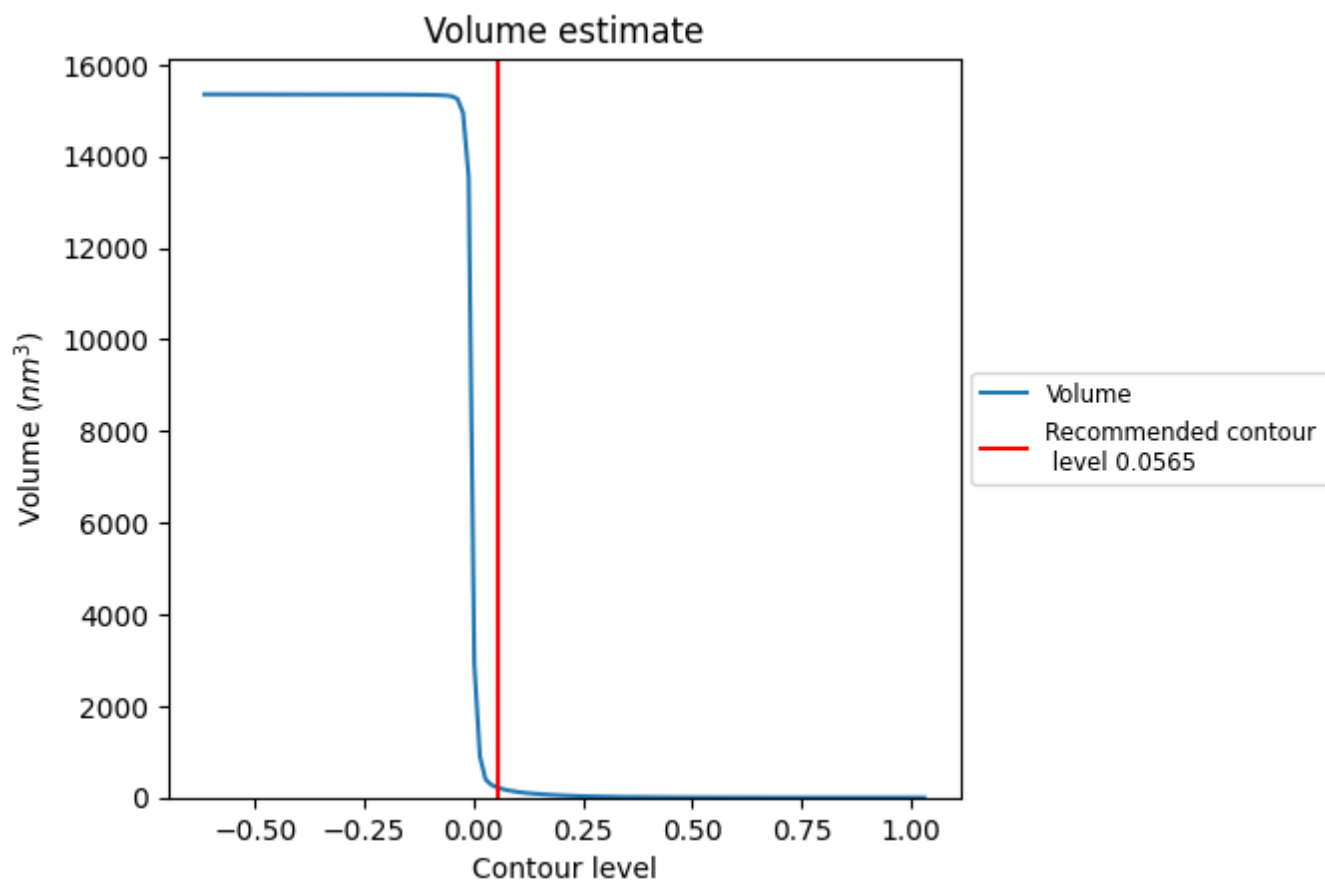
This section contains the results of statistical analysis of the map.

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.

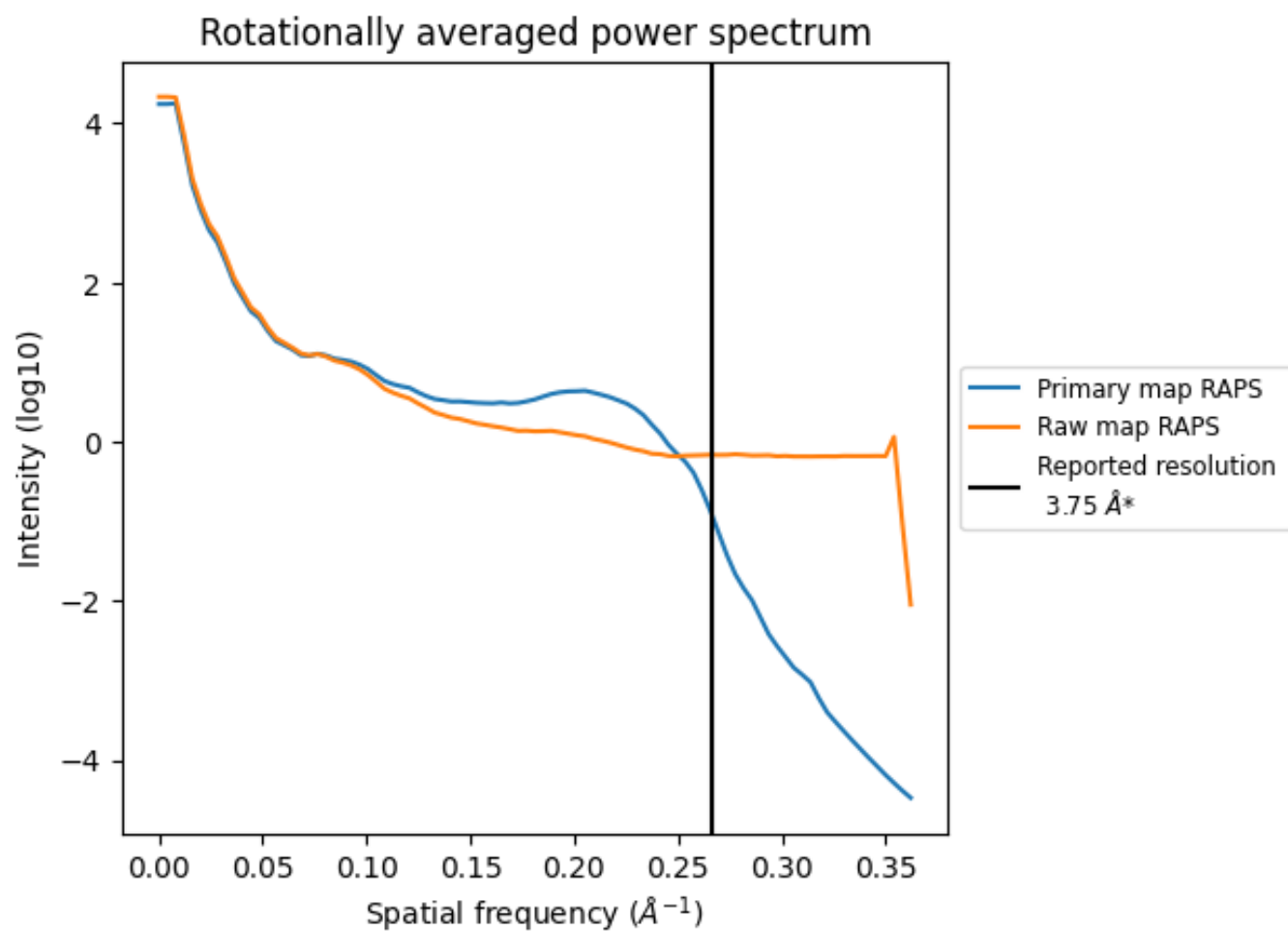
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 216 nm³; this corresponds to an approximate mass of 195 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

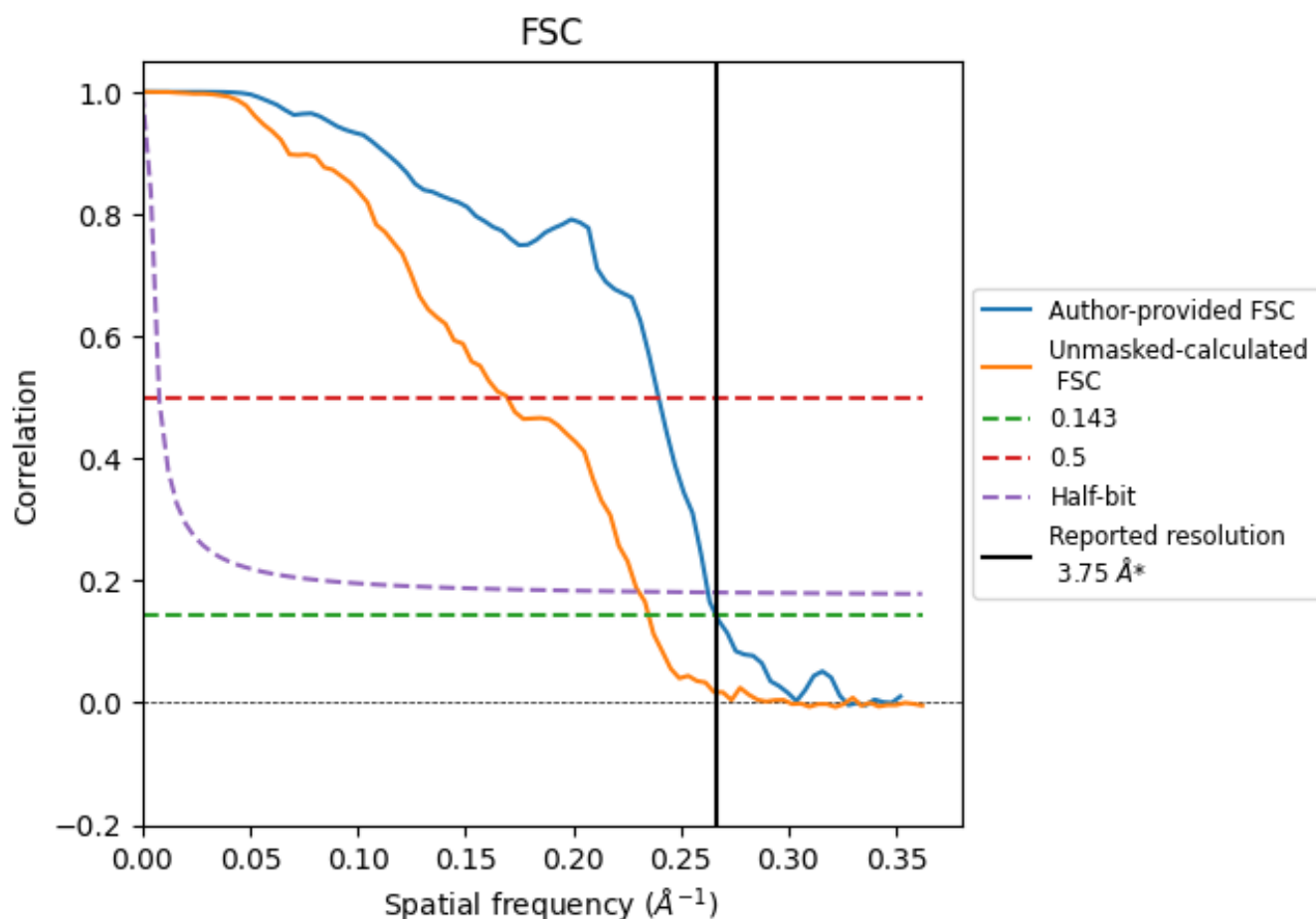


*Reported resolution corresponds to spatial frequency of 0.267 \AA^{-1}

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 0.267 Å⁻¹

8.2 Resolution estimates [i](#)

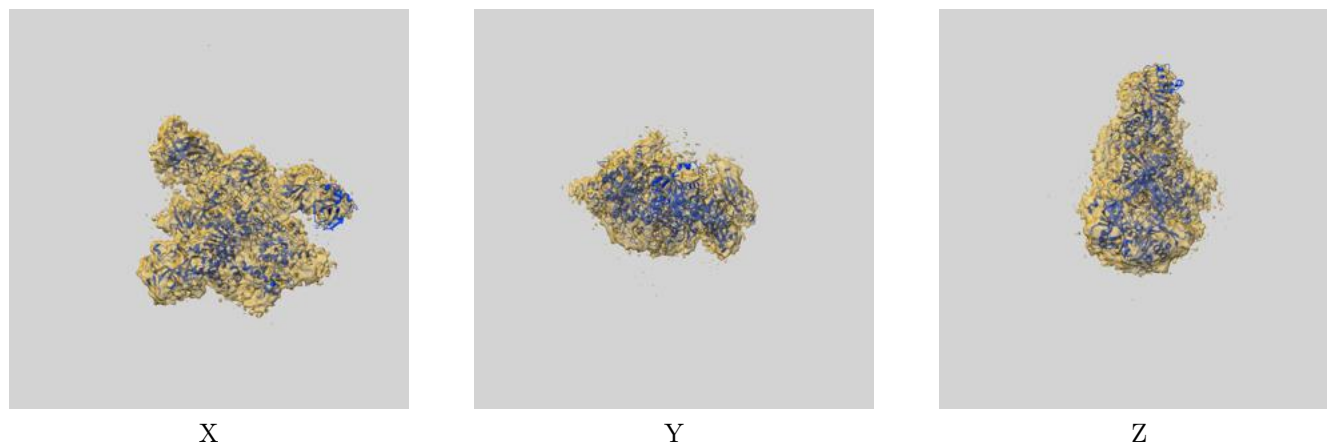
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.75	-	-
Author-provided FSC curve	3.75	4.17	3.81
Unmasked-calculated*	4.25	5.91	4.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.25 differs from the reported value 3.75 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62000 and PDB model 9K2X. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



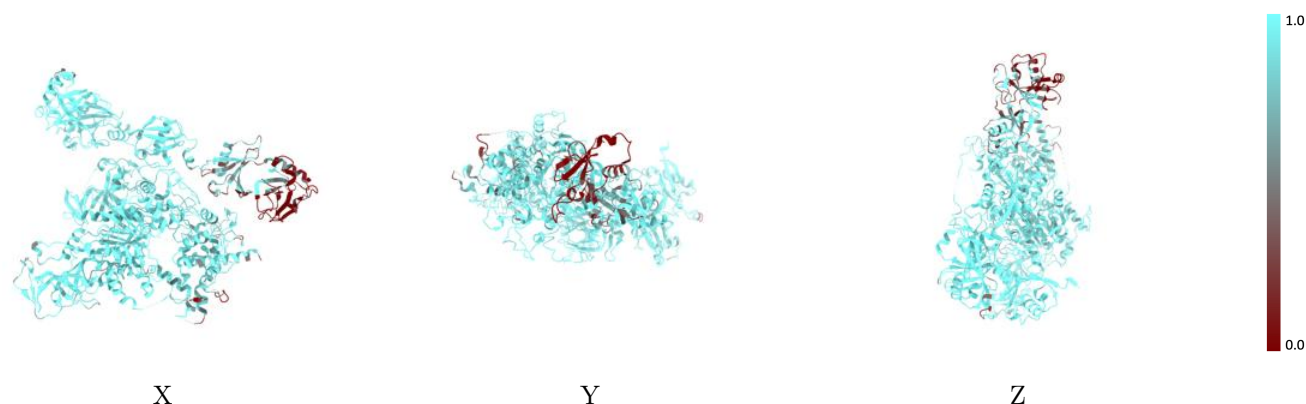
The images above show the 3D surface view of the map at the recommended contour level 0.0565 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



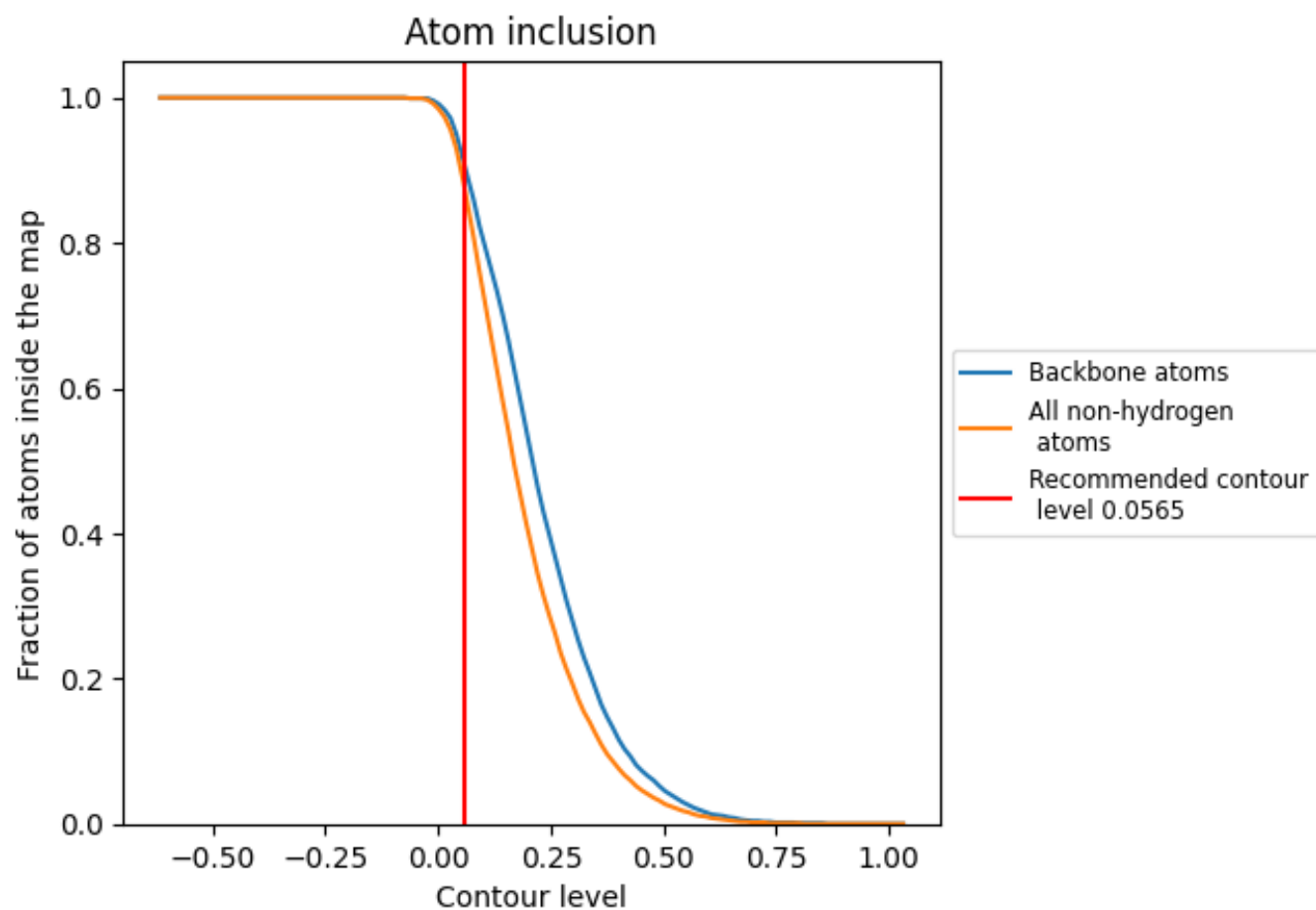
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0565).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.0565) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8830	<div></div> 0.3030
A	<div></div> 0.7660	<div></div> 0.1860
B	<div></div> 0.9470	<div></div> 0.3650

