



## wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 01:06 pm BST

PDB ID : 7Z4J / pdb\_00007z4j  
EMDB ID : EMD-14499  
Title : SpCas9 bound to 18-nucleotide complementary DNA substrate in the catalytic state  
Authors : Pacesa, M.; Jinek, M.  
Deposited on : 2022-03-03  
Resolution : 2.99 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>.

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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

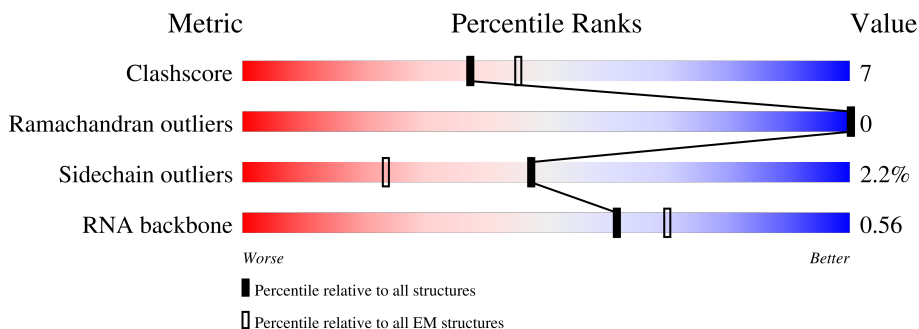
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.99 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
RNA backbone	6643	2191

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	A	102	
2	c	13	
3	C	32	
4	D	44	
5	B	1368	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13948 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 RNA chain called sgRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	98	Total	C	N	O	P	0	1
			2081	931	384	669	97		

- Molecule 2 is a DNA chain called Target strand of 18-nucleotide complementary DNA substrate, PAM-proximal end.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	13	Total	C	N	O	P	0	0
			263	126	48	77	12		

- Molecule 3 is a DNA chain called Target strand of 18-nucleotide complementary DNA substrate, PAM-distal end.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	17	Total	C	N	O	P	0	1
			324	156	51	101	16		

- Molecule 4 is a DNA chain called Non-target strand of 18-nucleotide complementary DNA substrate.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	14	Total	C	N	O	P	0	1
			269	128	49	79	13		

- Molecule 5 is a protein called CRISPR-associated endonuclease Cas9/Csn1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	1345	Total	C	N	O	S	0	0
			10999	7003	1911	2063	22		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total 1	Mg 1	0
6	B	3	Total 3	Mg 3	0

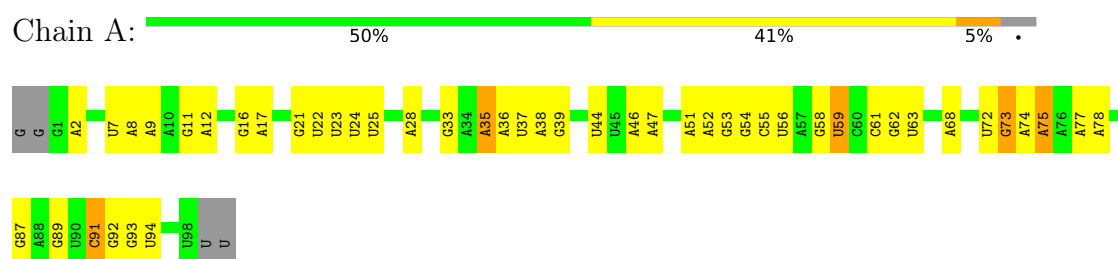
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		AltConf
7	A	6	Total 6	O 6	0
7	C	1	Total 1	O 1	0
7	B	1	Total 1	O 1	0

### 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.

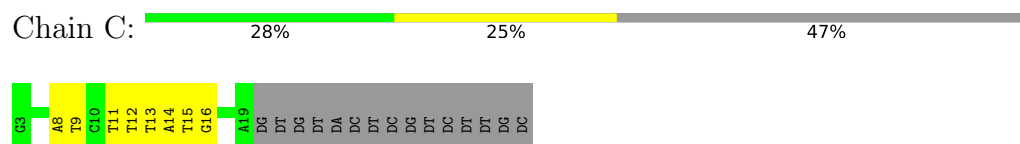
#### • Molecule 1: sgRNA



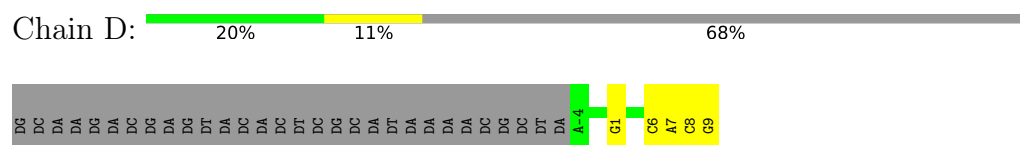
#### • Molecule 2: Target strand of 18-nucleotide complementary DNA substrate, PAM-proximal end



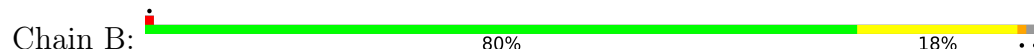
#### • Molecule 3: Target strand of 18-nucleotide complementary DNA substrate, PAM-distal end



#### • Molecule 4: Non-target strand of 18-nucleotide complementary DNA substrate



#### • Molecule 5: CRISPR-associated endonuclease Cas9/Csn1



N1308	N1309	L1312	K1325	I1331	D1332	R1333	I1352	T1353	G1354	E1357	T1358	R1359	G1366	GLY	ASP	K1155	K1156	G1165	T1166	T1167	N1177	D1180	K1191	L1194	T1195	I1196	K1197	L1198	F1204	R1212	A1215	Q1221	N1224	E1225	Y1232	H1241	Y1242	E1243	K1244	L1245	H1262	Y1265	L1266	D1267	E1268	E1275	V1280	K1289	V1290	K1296	H1297	R1298	D1299	R1303	E1304	N1308	I1309	L1312	K1325	I1331	D1332	R1333	I1352	T1353	G1354	E1357	T1358	R1359	G1366	GLY	ASP	L1502	L508	L512	S513	L514	T525	T531	M534	F539	R557	M588	A589	S590	I600	E617	E627	L636	M648	K649	Q650	R655	R661	R664	K665	L666	I667	M668	G669	L680	L683	K684	M690	M694	D699	I700	S701	V713	K735	Q739	K742	V748	H754	K755	P756	V760	A764	T769	T770	S777	R778	E779	R780	I784	H799	K810	Y815	D821	M822	Y823	V824	D837	V838	D839	K848	D849	D850	N854	S860	D861	K862	M863	R864	V870	E874	M883	L886	I917	R918	R919	Q920	L921	V922	R925	Q926	H930	T934	M939	R951	K954	V955	T956	R957	L958	L962	V963	F966	R967	K974	E977	N980	A984	H985	D986	N990	A991	T998	K999	E1005	Y1013	LYS	VAL	TYR	ASP	VAL	ARG	LYS	MET	ILE	ALA	L173	L174	P176	S179	T191	E197	E198	N199	G205	V206	D207	A208	K209	L212	S213	R220	R221	L222	E223	N224	L225	P230	N240	I242	A243	L244	S245	L246	G247	L248	K253	S254	N255	F256	D257	L258	A259	E260	D261	Q265	L266	S267	Y271	L275	D276	MET	D2	Y5	G8	L9	D10	I11	N14	T22	K44	K45	I48	F53	D54	S55	K65	R74	N77	R78	L82	E89	D95	L101	S104	D110	K111	R115	M121	D124	H137	L138	R139	D150	L151	R152	H160	M161	I162
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68772	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	64.2	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.295	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0445	Depositor
Map size ( $\text{\AA}$ )	249.59999, 249.59999, 249.59999	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.65, 0.65, 0.65	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.36	0/2332	0.30	0/3635
2	c	0.40	0/294	0.39	0/452
3	C	0.54	0/360	0.45	0/554
4	D	0.38	0/301	0.40	0/464
5	B	0.14	0/11194	0.24	0/15041
All	All	0.22	0/14481	0.27	0/20146

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	2081	0	1045	39	0
2	c	263	0	148	8	0
3	C	324	0	184	7	0
4	D	269	0	148	3	0
5	B	10999	0	11167	159	0
6	A	1	0	0	0	0
6	B	3	0	0	0	0
7	A	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	1	0	0	0	0
7	C	1	0	0	0	0
All	All	13948	0	12692	193	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 7.

The worst 5 of 193 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)
5:B:419:LEU:HD13	5:B:444:LEU:HD12	1.73	0.70
5:B:1212:ARG:NH2	5:B:1280:VAL:O	2.28	0.67
5:B:1050:ILE:HB	5:B:1058:ARG:HB3	1.78	0.65
5:B:435:ASP:OD1	5:B:436:ASN:ND2	2.30	0.65
5:B:860:SER:OG	5:B:864:ARG:NH1	2.30	0.65

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	
5	B	1339/1368 (98%)	1310 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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
5	B	1208/1227 (98%)	1182 (98%)	26 (2%)	47 76

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	839	ASP
5	B	951	ARG
5	B	1290	VAL
5	B	874	GLU
5	B	1033	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	826	GLN
5	B	946	ASN
5	B	885	GLN
5	B	1177	ASN
5	B	544	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	96/102 (94%)	15 (15%)	0

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	G
1	A	17	A
1	A	28	A
1	A	33	G
1	A	35	A

There are no RNA pucker outliers to report.

## 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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

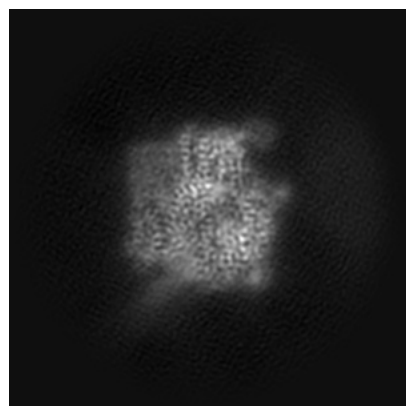
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14499. These allow visual inspection of the internal detail of the map and identification of artifacts.

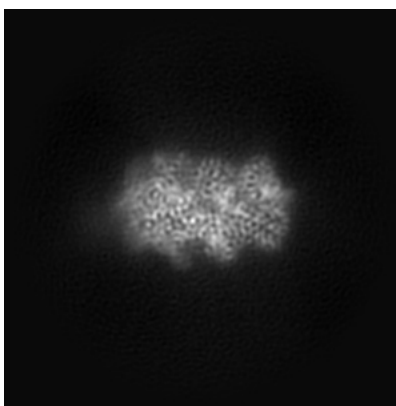
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

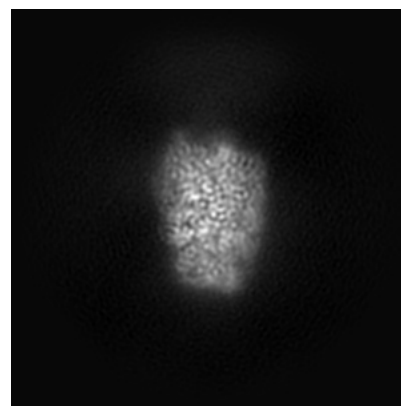
#### 6.1.1 Primary map



X

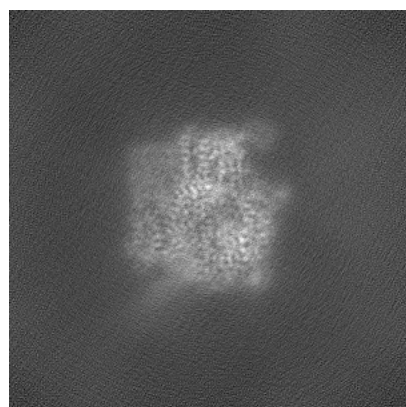


Y

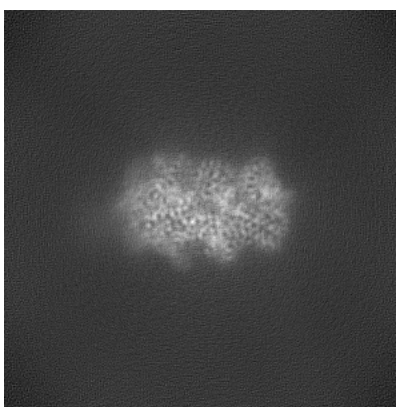


Z

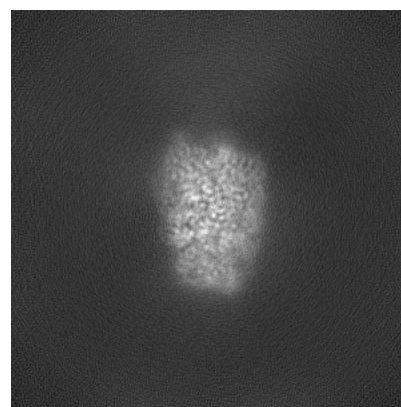
#### 6.1.2 Raw map



X



Y

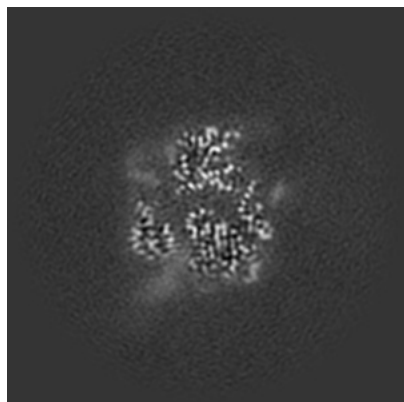


Z

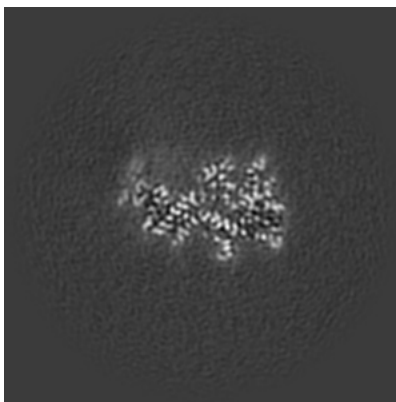
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

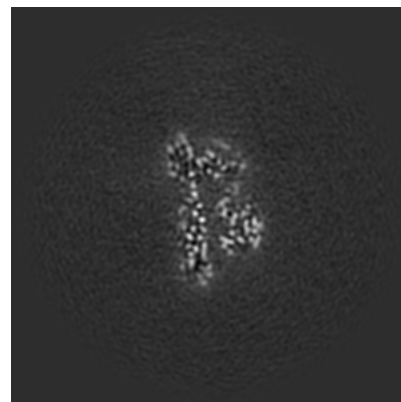
### 6.2.1 Primary map



X Index: 192

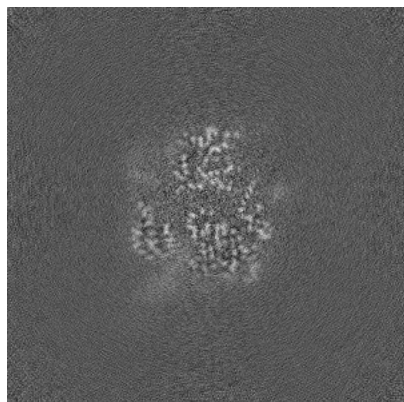


Y Index: 192

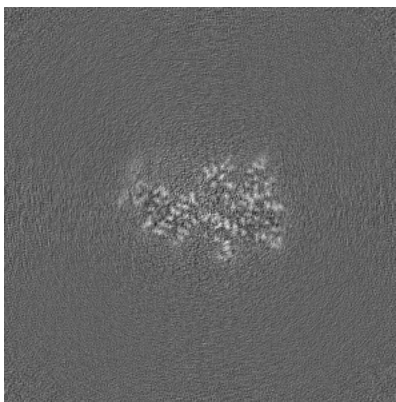


Z Index: 192

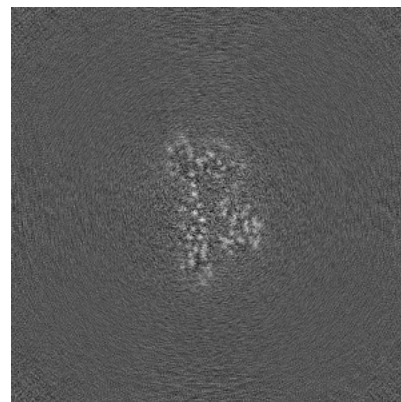
### 6.2.2 Raw map



X Index: 192



Y Index: 192

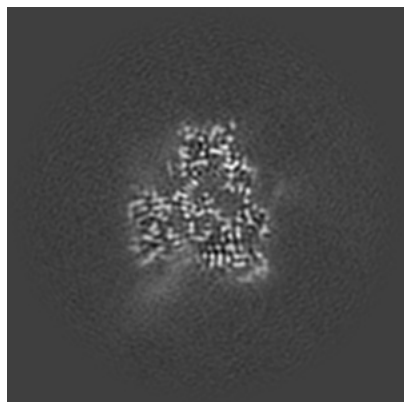


Z Index: 192

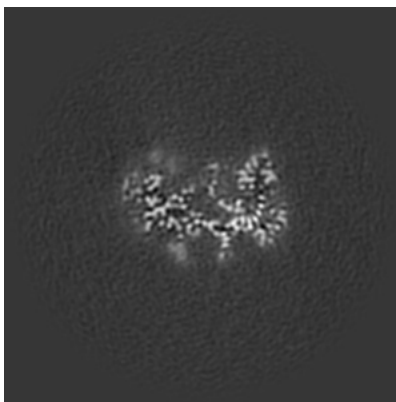
The images above show central slices of the map in three orthogonal directions.

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

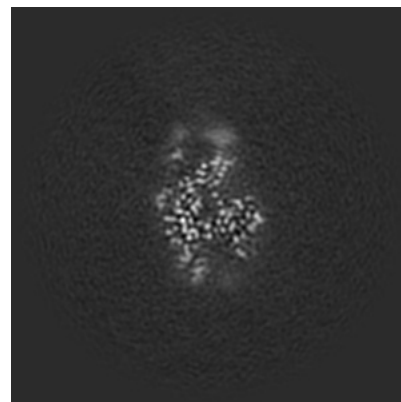
### 6.3.1 Primary map



X Index: 185

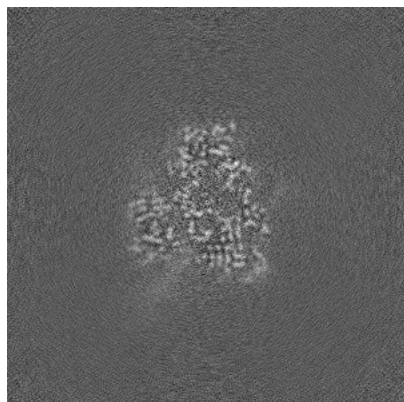


Y Index: 203

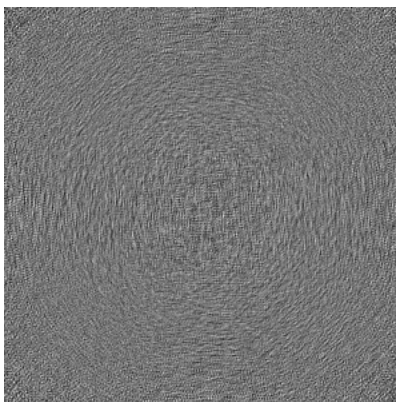


Z Index: 207

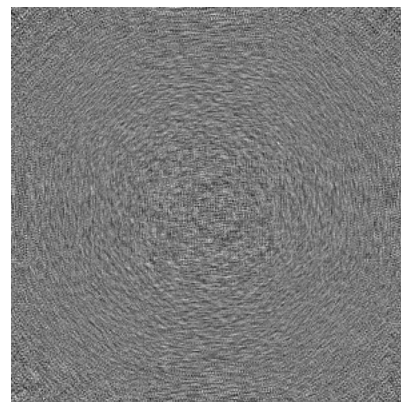
### 6.3.2 Raw map



X Index: 186



Y Index: 0

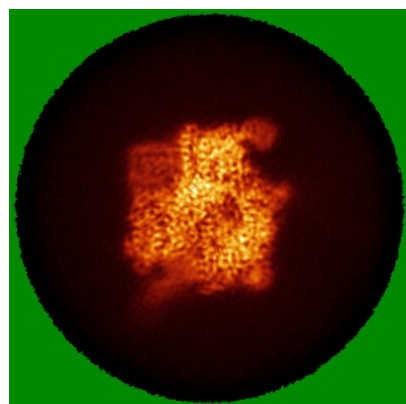


Z Index: 0

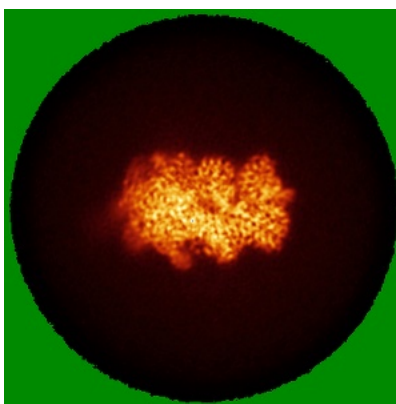
The images above show the largest variance slices of the map in three orthogonal directions.

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

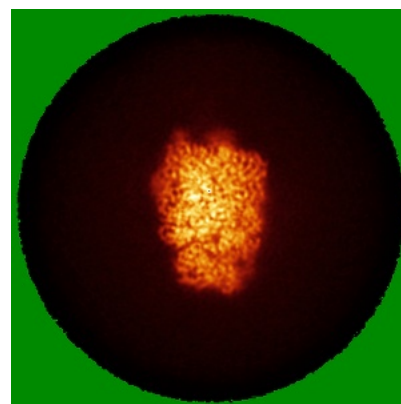
### 6.4.1 Primary map



X

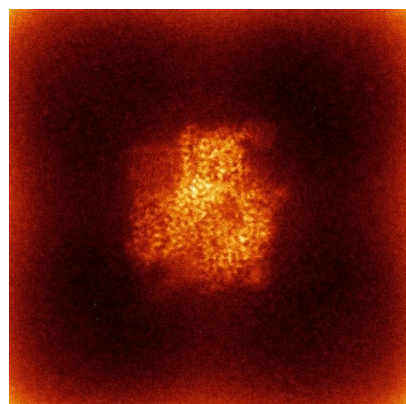


Y

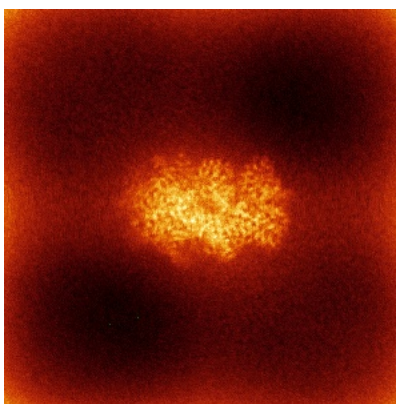


Z

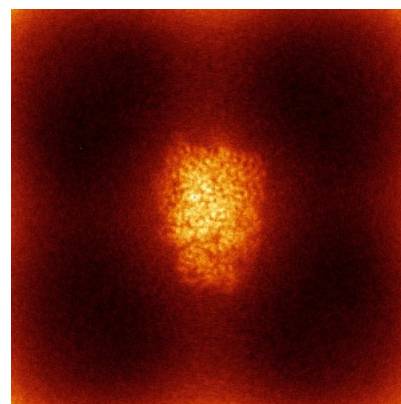
### 6.4.2 Raw map



X



Y

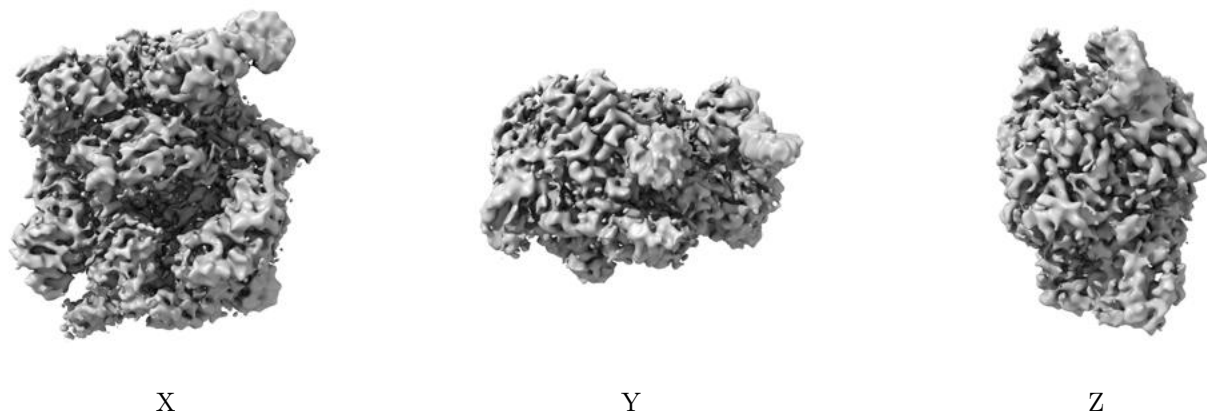


Z

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.

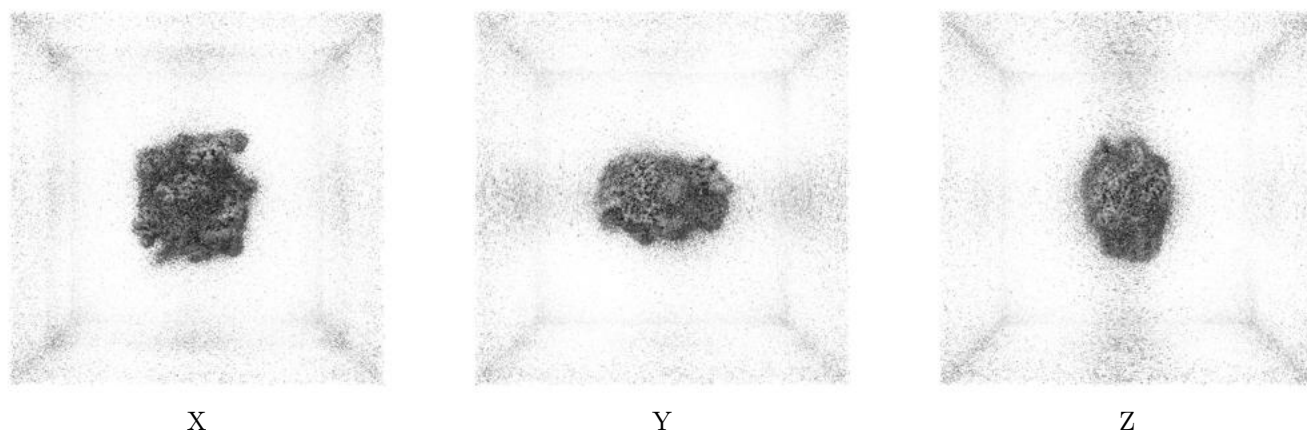
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0445. 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.

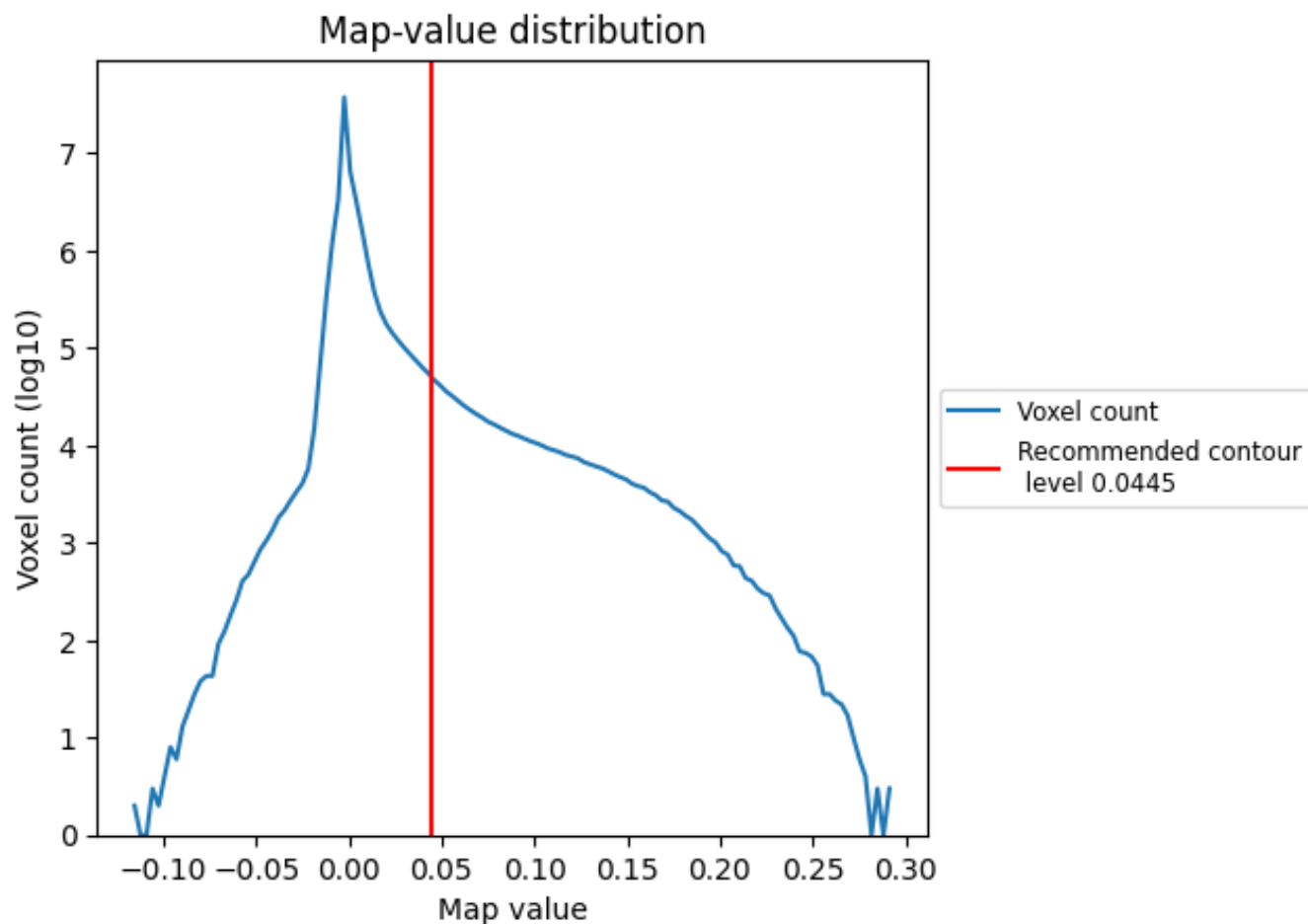
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

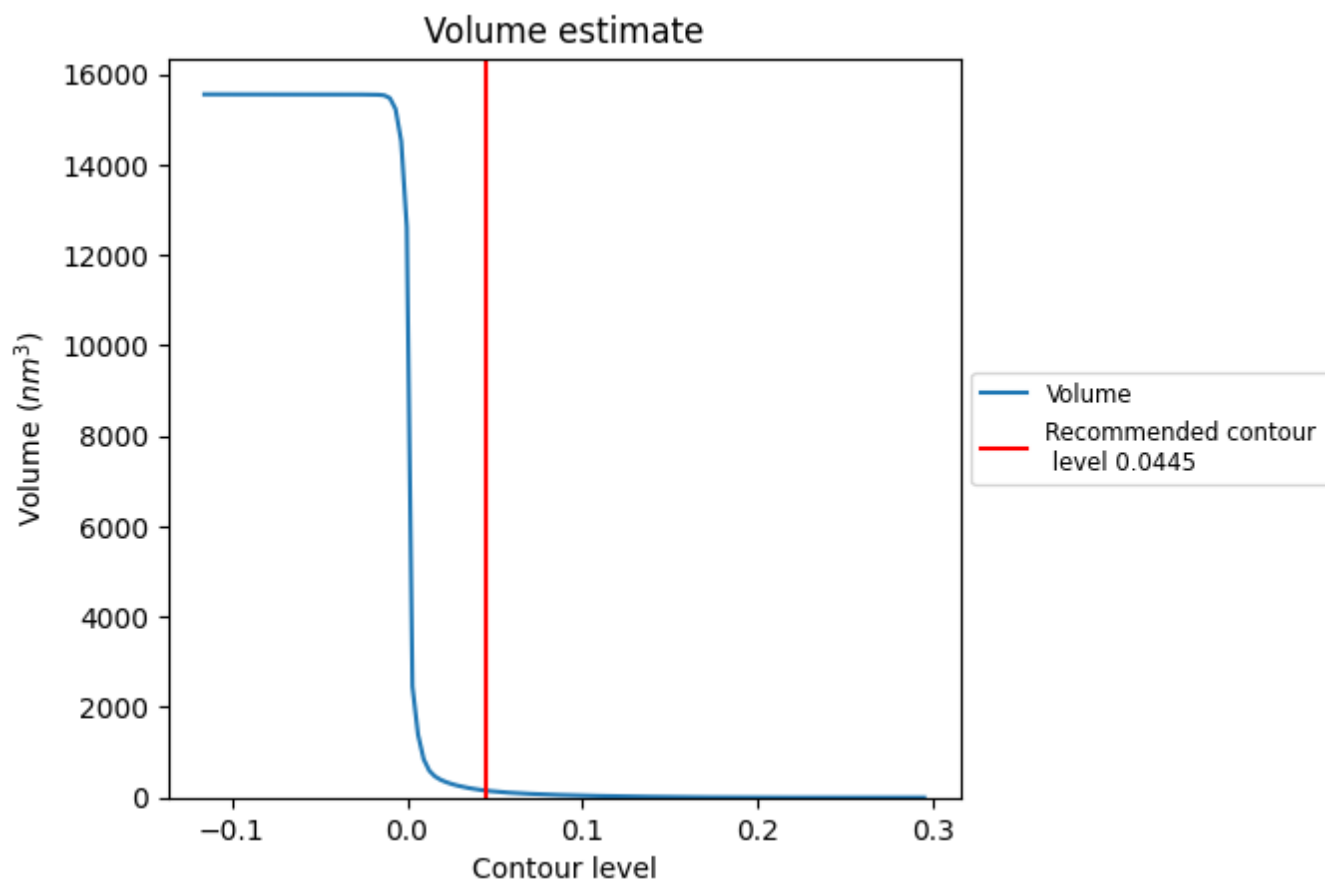
This section contains the results of statistical analysis of the map.

### 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.

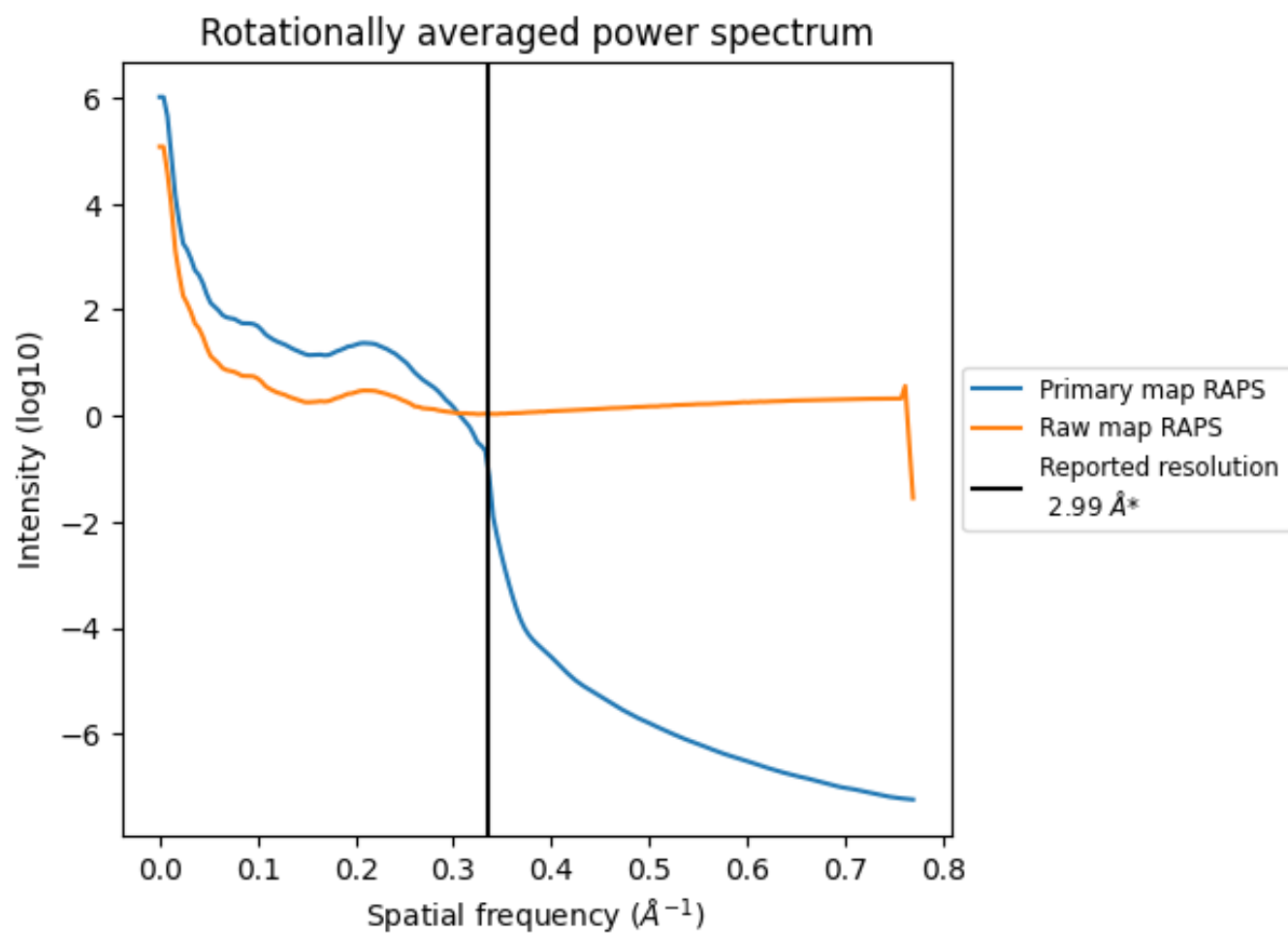
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 156 nm<sup>3</sup>; this corresponds to an approximate mass of 141 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 ⓘ

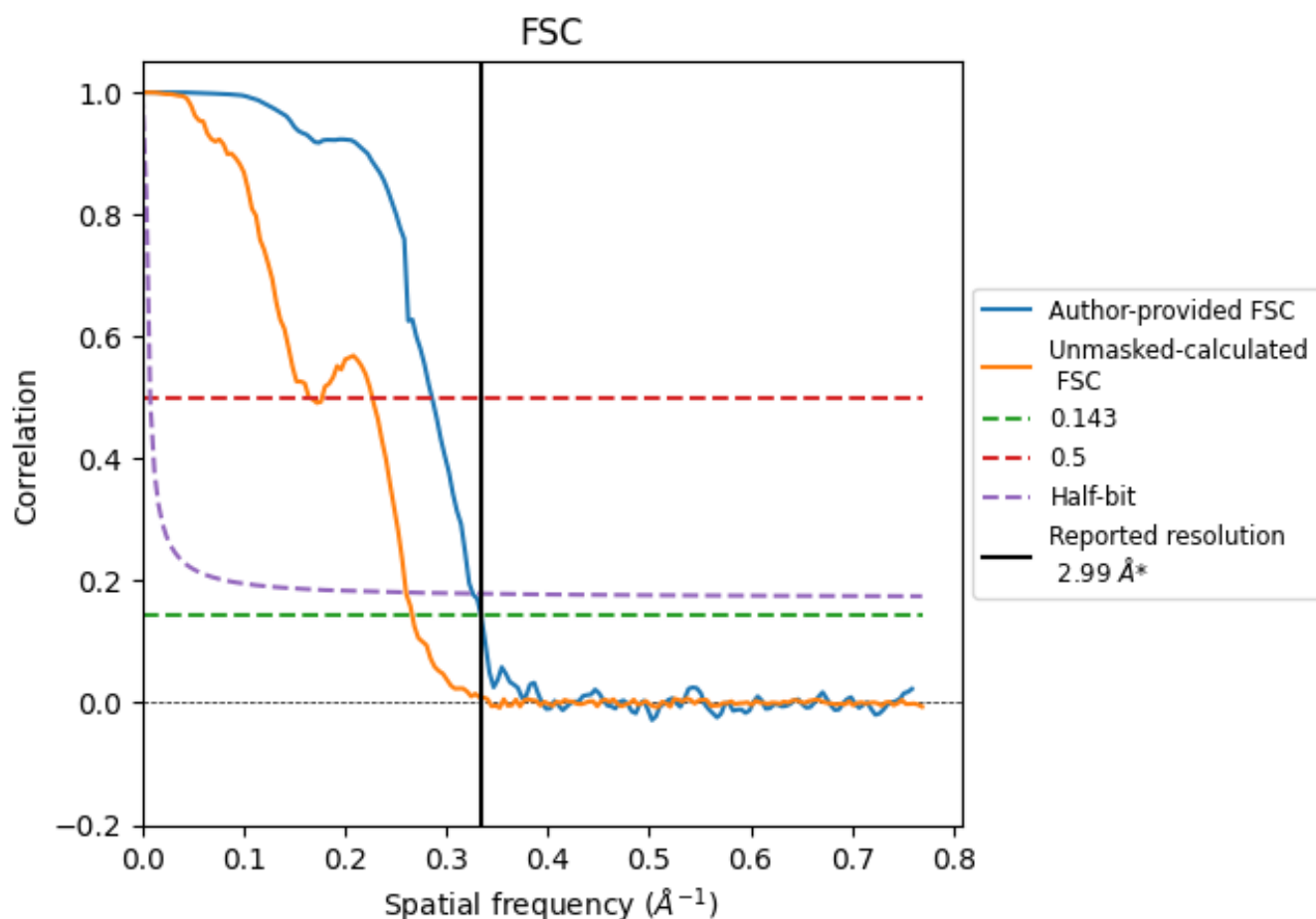


\*Reported resolution corresponds to spatial frequency of 0.334  $\text{\AA}^{-1}$

## 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  $0.334 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

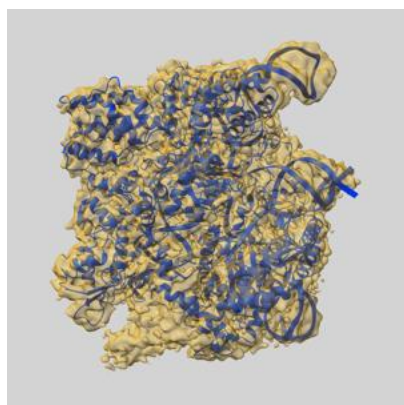
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.99	-	-
Author-provided FSC curve	2.99	3.50	3.07
Unmasked-calculated*	3.76	6.05	3.84

\*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 3.76 differs from the reported value 2.99 by more than 10 %

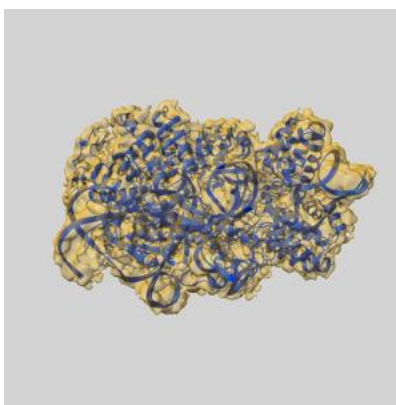
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14499 and PDB model 7Z4J. Per-residue inclusion information can be found in section 3 on page 5.

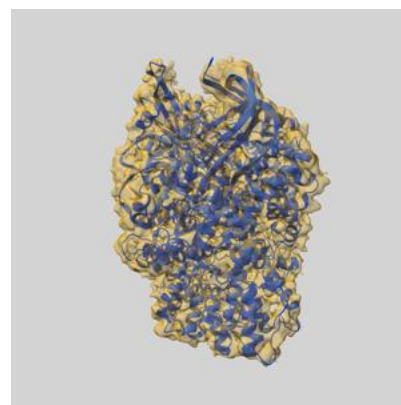
### 9.1 Map-model overlay [i](#)



X



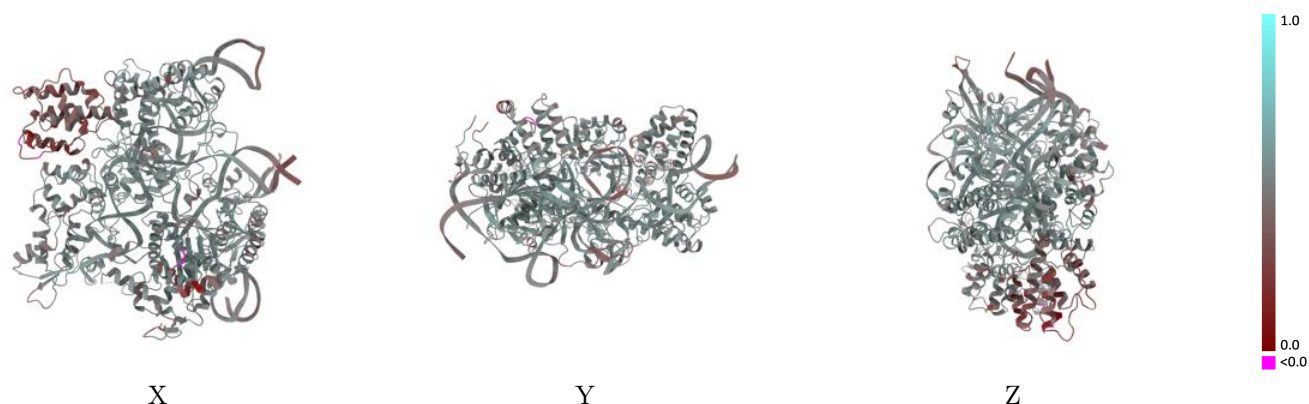
Y



Z

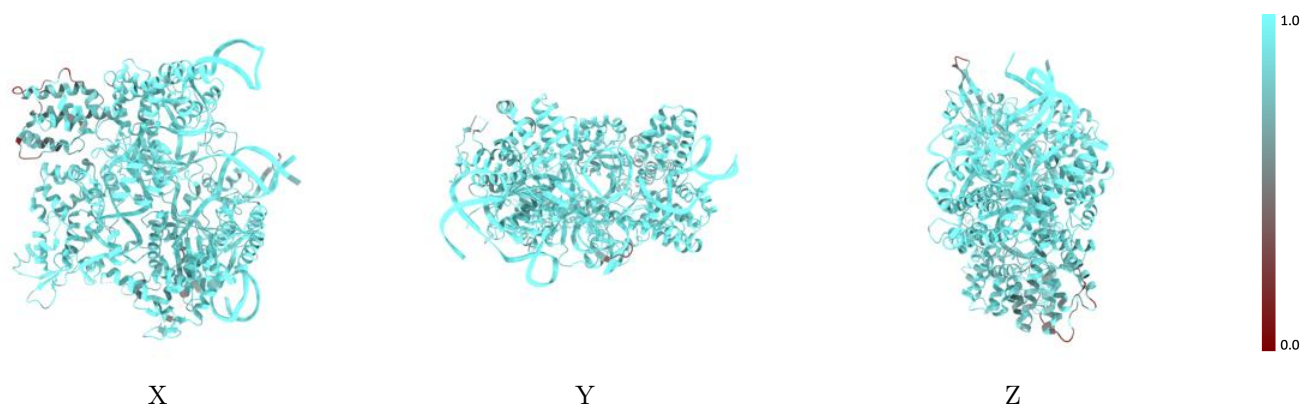
The images above show the 3D surface view of the map at the recommended contour level 0.0445 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



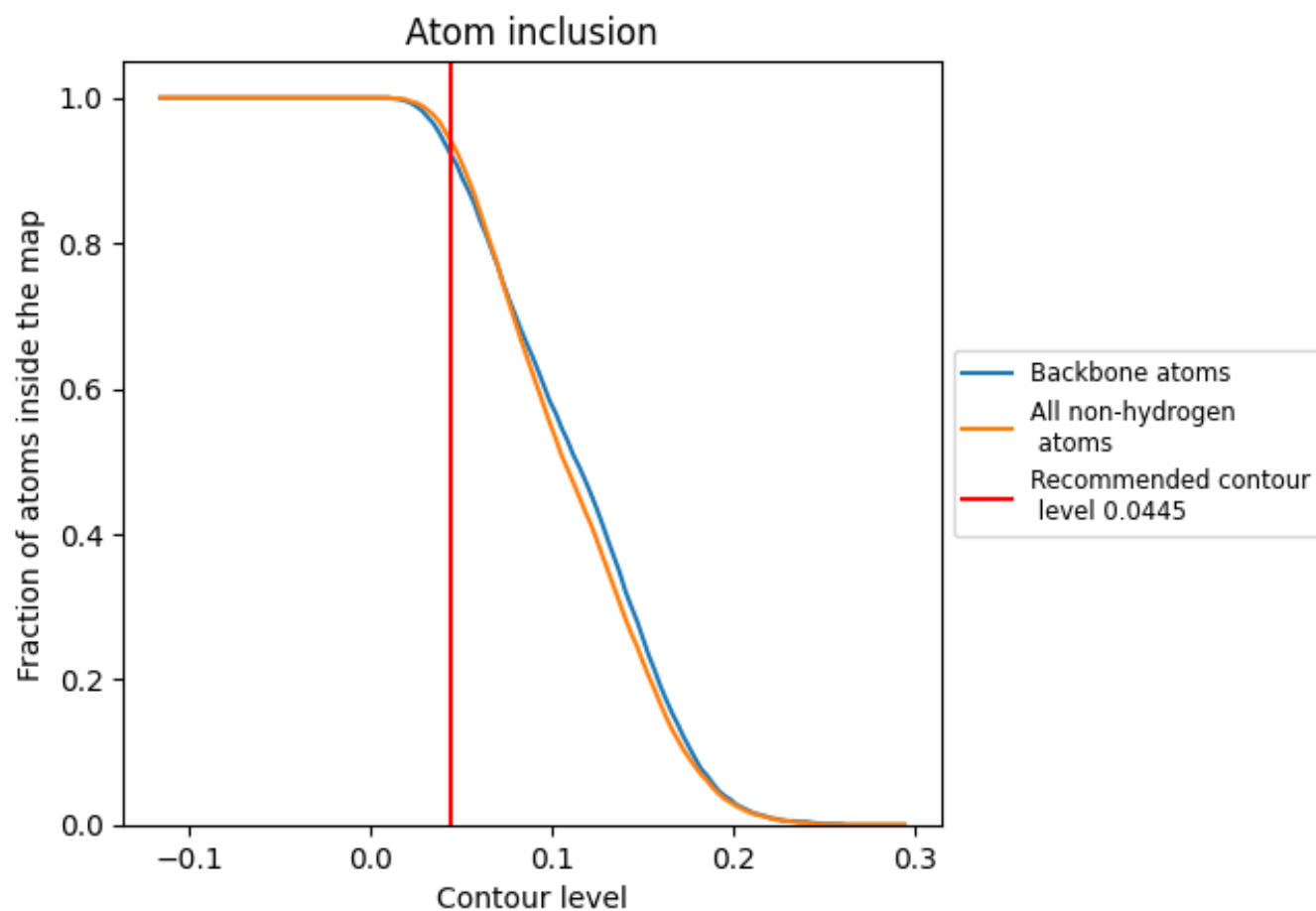
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0445).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 94% 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 (0.0445) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9410	<div></div> 0.4980
A	<div></div> 0.9950	<div></div> 0.5040
B	<div></div> 0.9290	<div></div> 0.4960
C	<div></div> 0.9970	<div></div> 0.5530
D	<div></div> 0.9590	<div></div> 0.4830
c	<div></div> 0.9890	<div></div> 0.4840

