



## wwPDB EM Validation Summary Report ⓘ

Jun 9, 2024 – 09:42 PM EDT

PDB ID : 8FN4  
EMDB ID : EMD-29305  
Title : Cryo-EM structure of RNase-treated RESC-A in trypanosomal RNA editing  
Authors : Liu, S.; Wang, H.; Li, X.; Zhang, F.; Lee, J.K.J.; Li, Z.; Yu, C.; Zhao, X.;  
Hu, J.J.; Suematsu, T.; Alvarez-Cabrera, A.L.; Liu, Q.; Zhang, L.; Huang, L.;  
Aphasizheva, I.; Aphasizhev, R.; Zhou, Z.H.  
Deposited on : 2022-12-26  
Resolution : 3.70 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.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2



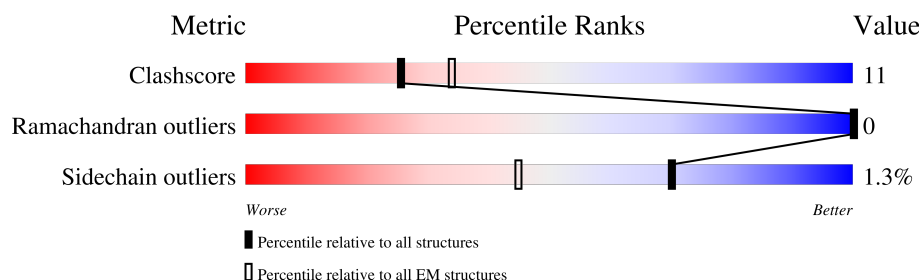
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.70 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1	473	
2	2	492	
3	3	482	
4	4	1087	
5	5	402	
6	6	516	



## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20638 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 RNA-editing substrate-binding complex protein 1 (RESC1).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	319	Total	C	N	O	S	0	0
			2525	1599	447	469	10		

- Molecule 2 is a protein called RNA-editing substrate-binding complex protein 2 (RESC2).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	357	Total	C	N	O	S	0	0
			2876	1837	503	520	16		

- Molecule 3 is a protein called RNA-editing substrate-binding complex protein 3 (RESC3).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	480	Total	C	N	O	S	0	0
			3705	2334	672	676	23		

- Molecule 4 is a protein called RNA-editing substrate-binding complex protein 4 (RESC4).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	741	Total	C	N	O	S	0	0
			5790	3647	1004	1103	36		

- Molecule 5 is a protein called RNA-editing substrate-binding complex protein 5 (RESC5).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	276	Total	C	N	O	S	0	0
			2163	1372	373	402	16		

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	311	GLY	-	expression tag	UNP Q389F5
5	312	SER	-	expression tag	UNP Q389F5

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Chain	Residue	Modelled	Actual	Comment	Reference
5	313	GLY	-	expression tag	UNP Q389F5
5	314	SER	-	expression tag	UNP Q389F5
5	315	GLY	-	expression tag	UNP Q389F5
5	316	SER	-	expression tag	UNP Q389F5
5	317	ALA	-	expression tag	UNP Q389F5
5	318	SER	-	expression tag	UNP Q389F5
5	319	SER	-	expression tag	UNP Q389F5
5	320	GLY	-	expression tag	UNP Q389F5
5	321	ALA	-	expression tag	UNP Q389F5
5	322	SER	-	expression tag	UNP Q389F5
5	323	ALA	-	expression tag	UNP Q389F5
5	324	ALA	-	expression tag	UNP Q389F5
5	325	GLY	-	expression tag	UNP Q389F5
5	326	SER	-	expression tag	UNP Q389F5
5	327	SER	-	expression tag	UNP Q389F5
5	328	GLY	-	expression tag	UNP Q389F5
5	329	ALA	-	expression tag	UNP Q389F5
5	330	SER	-	expression tag	UNP Q389F5
5	331	ALA	-	expression tag	UNP Q389F5
5	332	SER	-	expression tag	UNP Q389F5
5	333	SER	-	expression tag	UNP Q389F5
5	334	GLY	-	expression tag	UNP Q389F5
5	335	ALA	-	expression tag	UNP Q389F5
5	336	SER	-	expression tag	UNP Q389F5
5	337	ALA	-	expression tag	UNP Q389F5
5	338	ALA	-	expression tag	UNP Q389F5
5	339	GLY	-	expression tag	UNP Q389F5
5	340	SER	-	expression tag	UNP Q389F5
5	341	SER	-	expression tag	UNP Q389F5
5	342	GLY	-	expression tag	UNP Q389F5
5	343	ALA	-	expression tag	UNP Q389F5
5	344	SER	-	expression tag	UNP Q389F5
5	345	ALA	-	expression tag	UNP Q389F5
5	346	GLY	-	expression tag	UNP Q389F5
5	347	HIS	-	expression tag	UNP Q389F5
5	348	HIS	-	expression tag	UNP Q389F5
5	349	HIS	-	expression tag	UNP Q389F5
5	350	HIS	-	expression tag	UNP Q389F5
5	351	HIS	-	expression tag	UNP Q389F5
5	352	HIS	-	expression tag	UNP Q389F5
5	353	HIS	-	expression tag	UNP Q389F5
5	354	HIS	-	expression tag	UNP Q389F5

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Chain	Residue	Modelled	Actual	Comment	Reference
5	355	HIS	-	expression tag	UNP Q389F5
5	356	HIS	-	expression tag	UNP Q389F5
5	357	SER	-	expression tag	UNP Q389F5
5	358	GLY	-	expression tag	UNP Q389F5
5	359	SER	-	expression tag	UNP Q389F5
5	360	GLU	-	expression tag	UNP Q389F5
5	361	ASP	-	expression tag	UNP Q389F5
5	362	GLN	-	expression tag	UNP Q389F5
5	363	VAL	-	expression tag	UNP Q389F5
5	364	ASP	-	expression tag	UNP Q389F5
5	365	PRO	-	expression tag	UNP Q389F5
5	366	ARG	-	expression tag	UNP Q389F5
5	367	LEU	-	expression tag	UNP Q389F5
5	368	ILE	-	expression tag	UNP Q389F5
5	369	ASP	-	expression tag	UNP Q389F5
5	370	GLY	-	expression tag	UNP Q389F5
5	371	LYS	-	expression tag	UNP Q389F5
5	372	ALA	-	expression tag	UNP Q389F5
5	373	SER	-	expression tag	UNP Q389F5
5	374	ALA	-	expression tag	UNP Q389F5
5	375	TRP	-	expression tag	UNP Q389F5
5	376	SER	-	expression tag	UNP Q389F5
5	377	HIS	-	expression tag	UNP Q389F5
5	378	PRO	-	expression tag	UNP Q389F5
5	379	GLN	-	expression tag	UNP Q389F5
5	380	PHE	-	expression tag	UNP Q389F5
5	381	GLU	-	expression tag	UNP Q389F5
5	382	LYS	-	expression tag	UNP Q389F5
5	383	GLY	-	expression tag	UNP Q389F5
5	384	GLY	-	expression tag	UNP Q389F5
5	385	GLY	-	expression tag	UNP Q389F5
5	386	SER	-	expression tag	UNP Q389F5
5	387	GLY	-	expression tag	UNP Q389F5
5	388	GLY	-	expression tag	UNP Q389F5
5	389	GLY	-	expression tag	UNP Q389F5
5	390	SER	-	expression tag	UNP Q389F5
5	391	GLY	-	expression tag	UNP Q389F5
5	392	GLY	-	expression tag	UNP Q389F5
5	393	SER	-	expression tag	UNP Q389F5
5	394	ALA	-	expression tag	UNP Q389F5
5	395	TRP	-	expression tag	UNP Q389F5
5	396	SER	-	expression tag	UNP Q389F5

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Chain	Residue	Modelled	Actual	Comment	Reference
5	397	HIS	-	expression tag	UNP Q389F5
5	398	PRO	-	expression tag	UNP Q389F5
5	399	GLN	-	expression tag	UNP Q389F5
5	400	PHE	-	expression tag	UNP Q389F5
5	401	GLU	-	expression tag	UNP Q389F5
5	402	LYS	-	expression tag	UNP Q389F5

- Molecule 6 is a protein called RNA-editing substrate-binding complex protein 6 (RESC6).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	452	Total	C	N	O	S	0	0
			3579	2282	631	649	17		

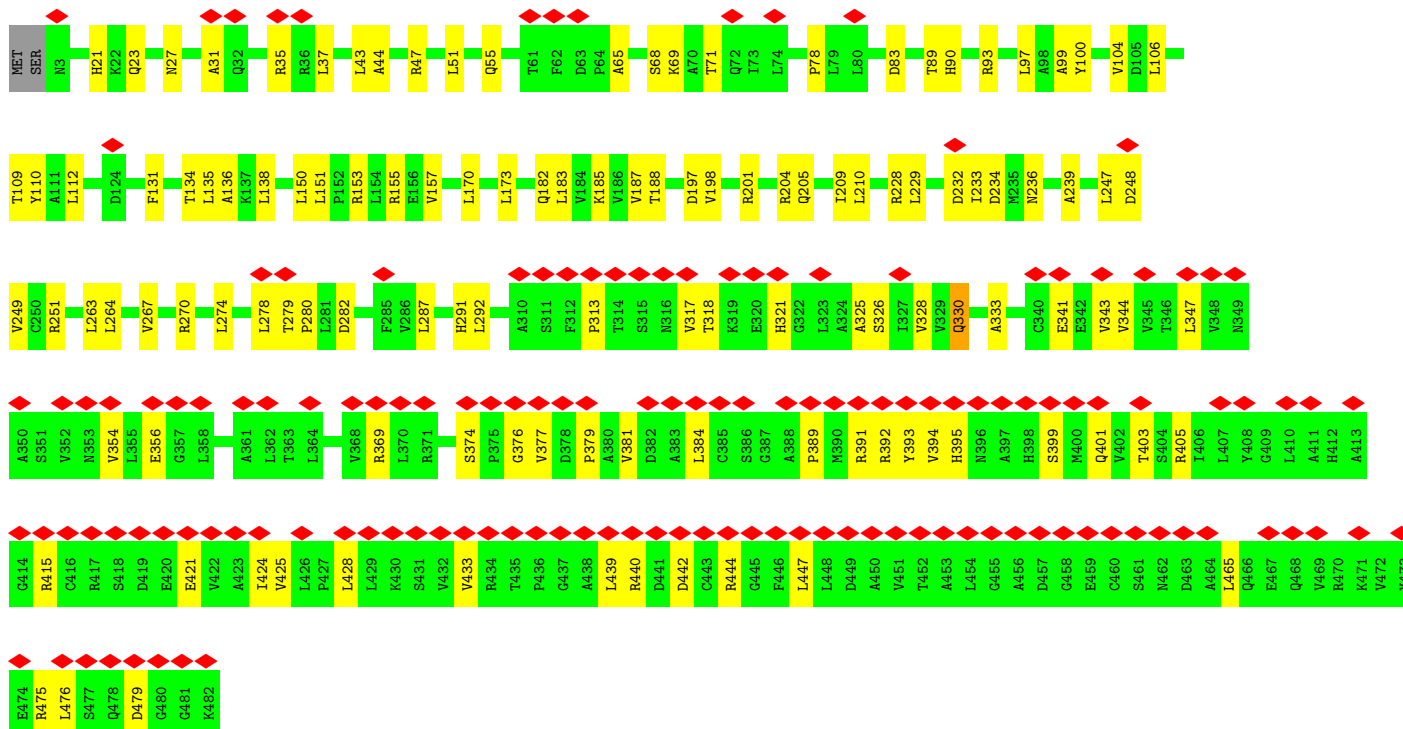
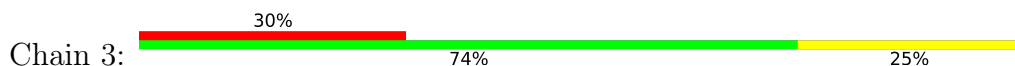




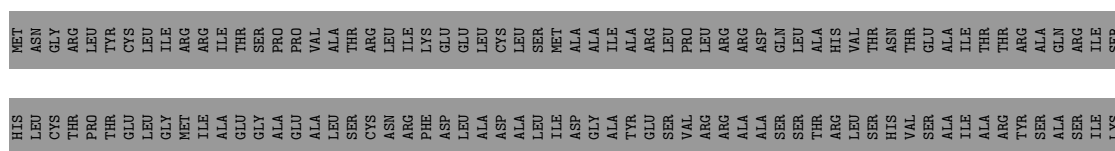




• Molecule 3: RNA-editing substrate-binding complex protein 3 (RESC3)



• Molecule 4: RNA-editing substrate-binding complex protein 4 (RESC4)









PRO  
GLN  
PHE  
GLU  
ALA  
LYS  
GLY  
GLY  
GLY  
SER  
GLY  
GLY  
GLY  
GLY  
GLY  
GLY  
SER  
GLN  
GLY  
GLY  
GLY  
SER  
PHE  
GLU  
LYS

● Molecule 6: RNA-editing substrate-binding complex protein 6 (RESC6)



MET  
ARG  
SER  
ALA  
LEU  
ARG  
ARG  
CYS  
ILE  
LEU  
ARG  
HIS  
GLN  
GLY  
CYS  
LEU  
SER  
ARG  
MET  
LYS  
GLN  
SER  
LEU  
PHE  
ALA  
PRO  
THR  
VAL  
VAL  
THR  
GLY  
MET  
THR  
ARG  
HIS  
D133  
GLN  
GLY  
ASN  
SER  
LEU  
ILE  
GLY  
THR  
THR  
HIS  
GLY  
ALA  
GLU  
LEU  
SER  
LEU  
ALA  
GLY  
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PRO  
GLN  
SER  
V58  
S59  
H60

L61  
S62  
A63  
I66  
L71  
Q72  
M73  
R80  
L86  
A87  
Q88  
R92  
I99  
L104  
D105  
S108  
L111  
L112  
E122  
S123  
D124  
A125  
I132  
D133  
Y134  
D139  
C154  
L157  
R160  
V165  
I166  
E167  
M168  
Q169  
A170  
Q171  
F179  
L180  
D181  
T186  
I189

T195  
F203  
H223  
L227  
S232  
R233  
L234  
L241  
E254  
R255  
V256  
T257  
V258  
N259  
E260  
I271  
G272  
L273  
V290  
M293  
M301  
F302  
F308  
F316  
G317  
V318  
L319  
T320  
A332  
I335  
S336  
T337  
T338  
F342  
I345  
G346  
I347  
P350  
F351  
L352  
F353

L361  
A362  
V363  
V364  
Q365  
D366  
H367  
D371  
I372  
F382  
G383  
L384  
K385  
F390  
K391  
R392  
A397  
A398  
S399  
I400  
A401  
D402  
D405  
A406  
M407  
G408  
L409  
V410  
N411  
T412  
A413  
H414  
N420  
F421  
D425  
M426  
A429  
L430  
R433  
L440  
E445  
R448  
W451  
R459  
L464

V467  
R470  
C471  
L474  
D477  
A480  
T483  
E490  
D493  
M498  
F499  
L503  
Y504  
Q505  
L506  
S509  
ARG  
GLY  
SER  
THR  
PRO  
GLN  
ALA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	290408	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	271.872, 271.872, 271.872	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.062, 1.062, 1.062	Depositor



## 5 Model quality [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	1	0.26	0/2574	0.52	0/3491
2	2	0.25	0/2944	0.48	0/3990
3	3	0.25	0/3764	0.49	0/5106
4	4	0.27	0/5879	0.48	0/7961
5	5	0.27	0/2217	0.48	0/3007
6	6	0.27	0/3643	0.48	0/4923
All	All	0.26	0/21021	0.49	0/28478

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	1	2525	0	2549	106	0
2	2	2876	0	2837	75	0
3	3	3705	0	3819	86	0
4	4	5790	0	5831	107	0
5	5	2163	0	2103	55	0
6	6	3579	0	3610	76	0
All	All	20638	0	20749	472	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 11.



The worst 5 of 472 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)
2:2:404:VAL:HG22	2:2:422:THR:HG23	1.29	1.12
1:1:278:LEU:HD11	1:1:458:LEU:HD22	1.40	1.00
6:6:189:ILE:HG21	6:6:227:LEU:HD12	1.44	0.99
1:1:278:LEU:HD11	1:1:458:LEU:CD2	1.93	0.98
6:6:189:ILE:HG21	6:6:227:LEU:CD1	1.93	0.98

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	1	315/473 (67%)	294 (93%)	21 (7%)	0	100	100
2	2	343/492 (70%)	329 (96%)	14 (4%)	0	100	100
3	3	478/482 (99%)	454 (95%)	24 (5%)	0	100	100
4	4	737/1087 (68%)	675 (92%)	62 (8%)	0	100	100
5	5	274/402 (68%)	254 (93%)	20 (7%)	0	100	100
6	6	450/516 (87%)	428 (95%)	22 (5%)	0	100	100
All	All	2597/3452 (75%)	2434 (94%)	163 (6%)	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	
1	1	276/400 (69%)	271 (98%)	5 (2%)	59	77
2	2	304/410 (74%)	300 (99%)	4 (1%)	69	83
3	3	405/407 (100%)	403 (100%)	2 (0%)	88	94
4	4	643/933 (69%)	637 (99%)	6 (1%)	78	88
5	5	236/322 (73%)	231 (98%)	5 (2%)	53	74
6	6	375/428 (88%)	367 (98%)	8 (2%)	53	74
All	All	2239/2900 (77%)	2209 (99%)	30 (1%)	70	83

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

Mol	Chain	Res	Type
4	4	603	HIS
6	6	352	LEU
5	5	83	PHE
6	6	390	PHE
6	6	302	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	291	GLN
3	3	21	HIS
4	4	845	GLN
4	4	899	ASN

### 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 ⓘ

There are no monosaccharides 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.



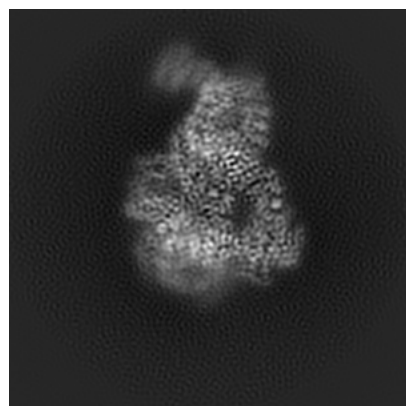
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29305. These allow visual inspection of the internal detail of the map and identification of artifacts.

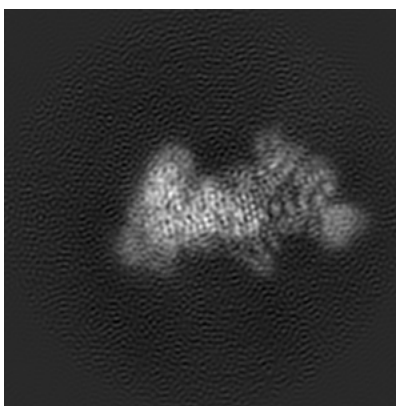
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

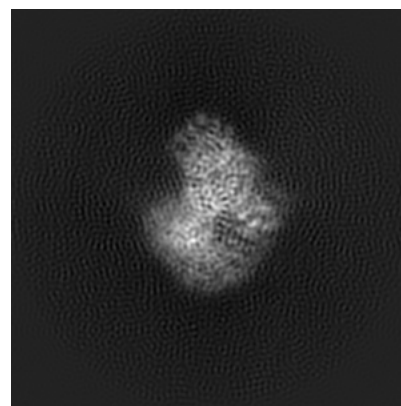
#### 6.1.1 Primary map



X

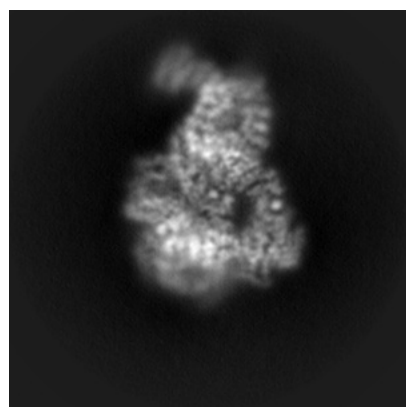


Y

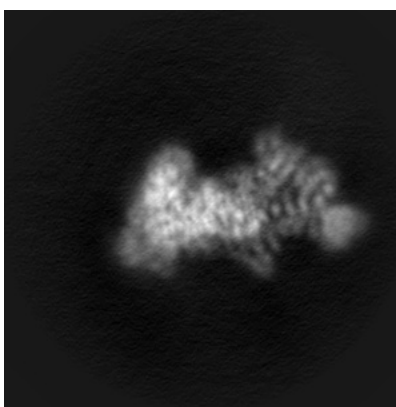


Z

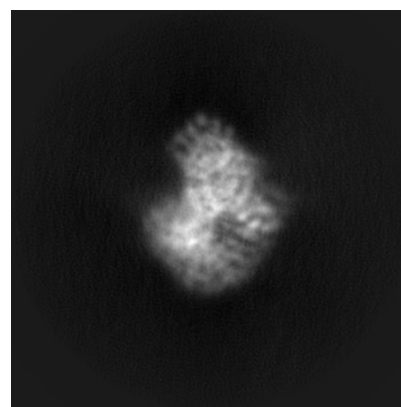
#### 6.1.2 Raw map



X



Y



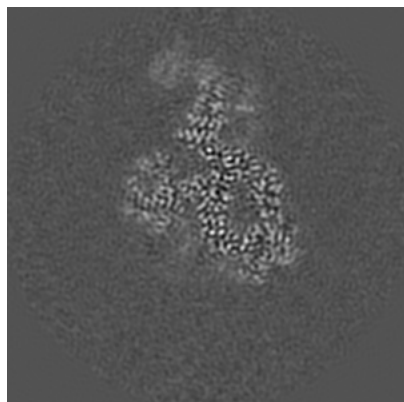
Z

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

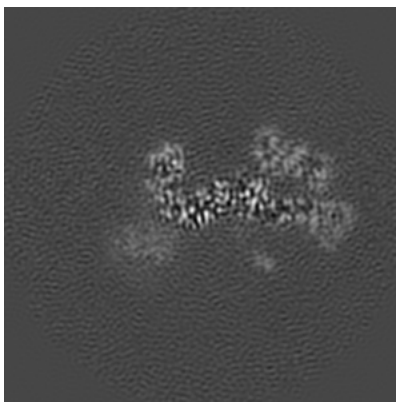


## 6.2 Central slices [i](#)

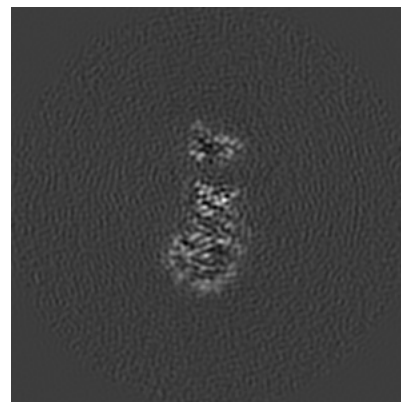
### 6.2.1 Primary map



X Index: 128

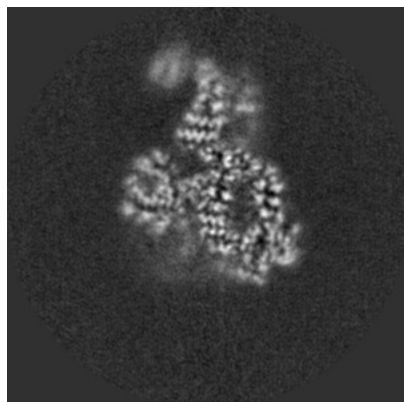


Y Index: 128

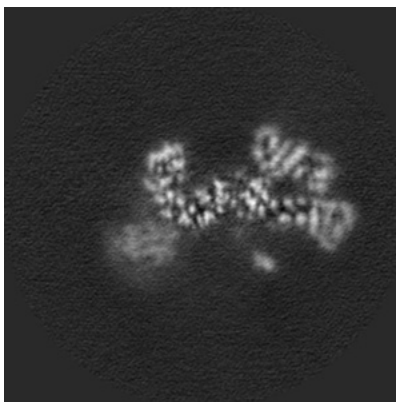


Z Index: 128

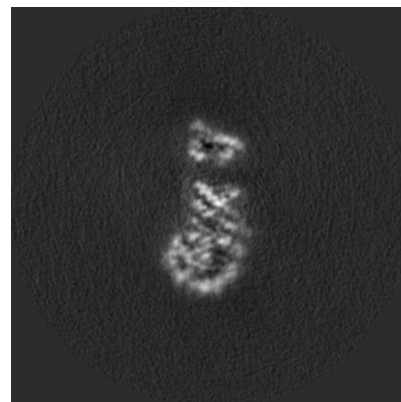
### 6.2.2 Raw map



X Index: 128



Y Index: 128



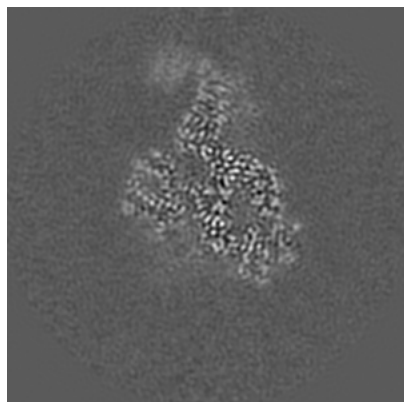
Z Index: 128

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

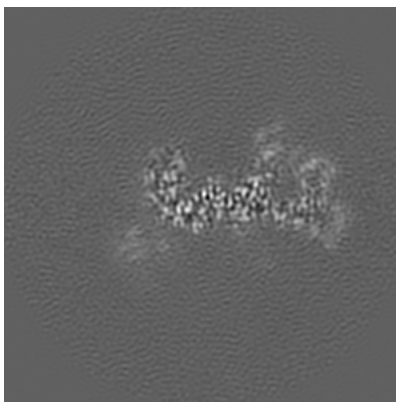


## 6.3 Largest variance slices [i](#)

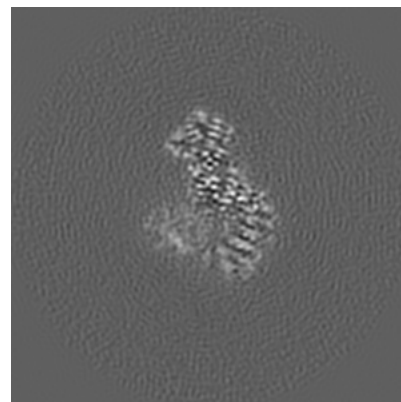
### 6.3.1 Primary map



X Index: 126

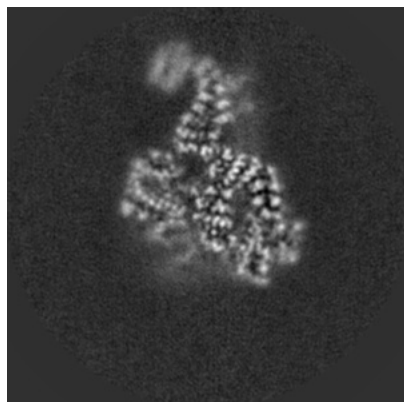


Y Index: 132

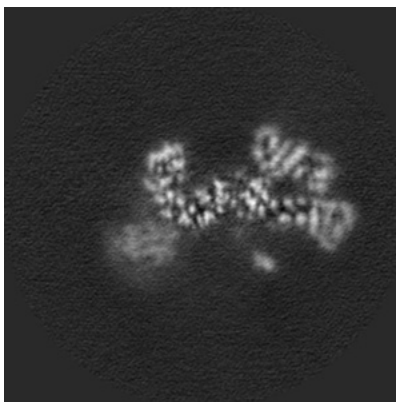


Z Index: 108

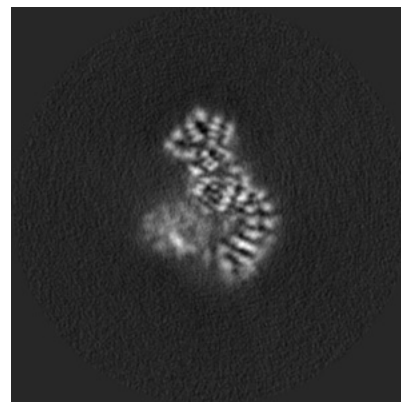
### 6.3.2 Raw map



X Index: 125



Y Index: 128



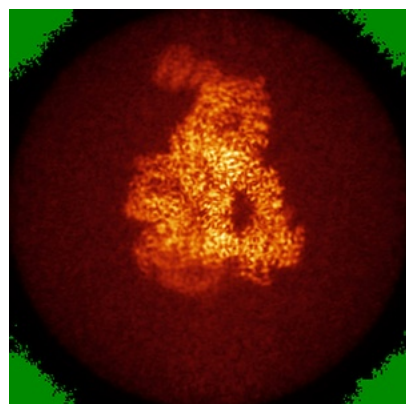
Z Index: 107

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

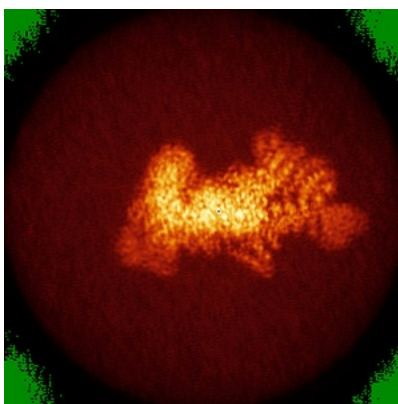


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

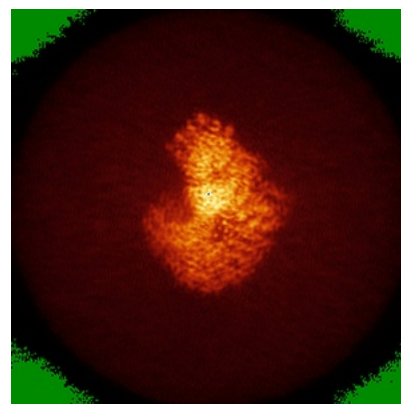
### 6.4.1 Primary map



X

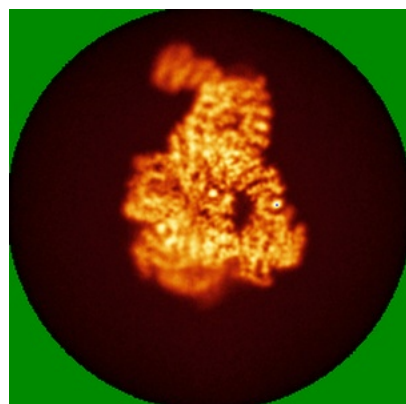


Y

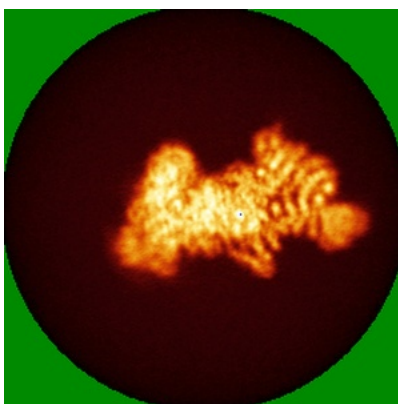


Z

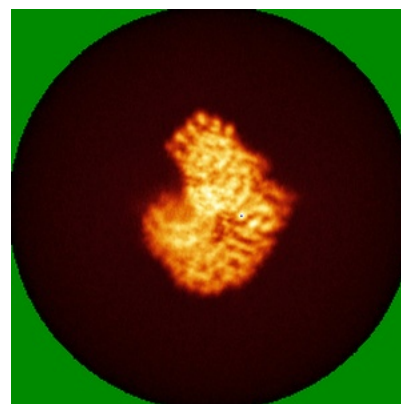
### 6.4.2 Raw map



X



Y



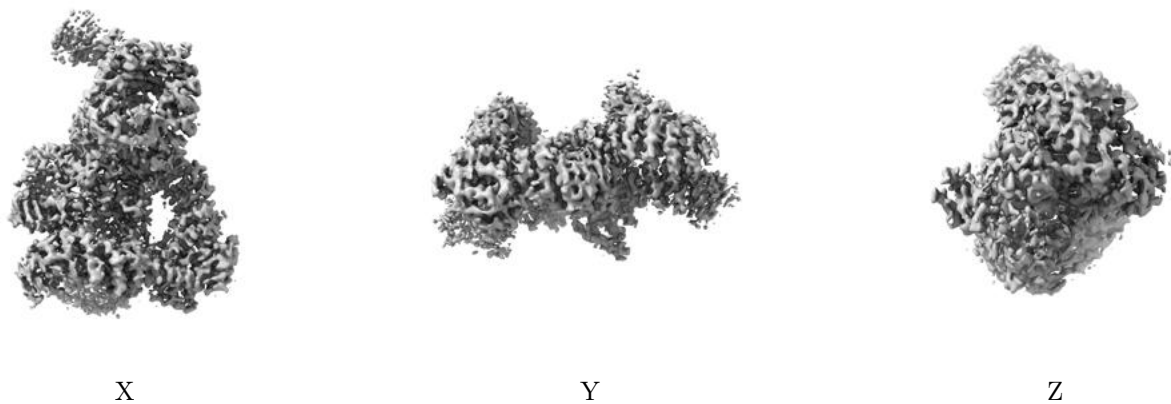
Z

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.



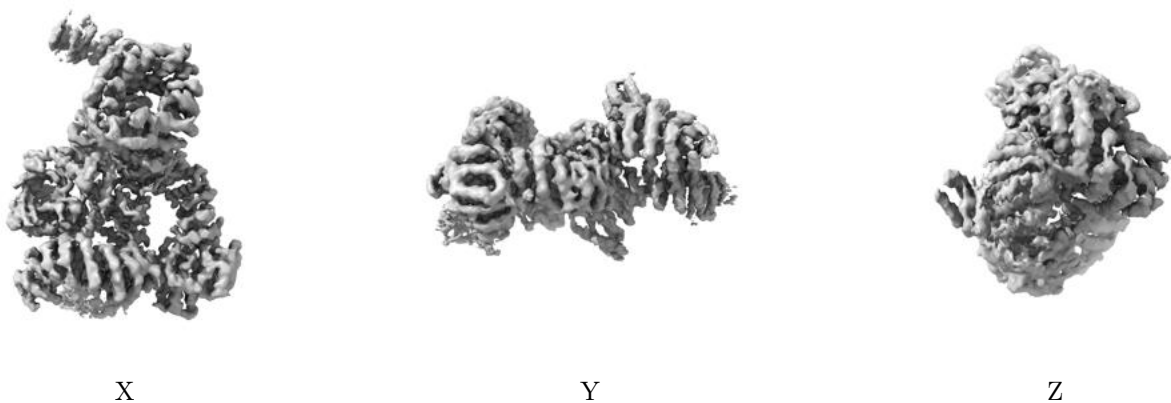
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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](#)

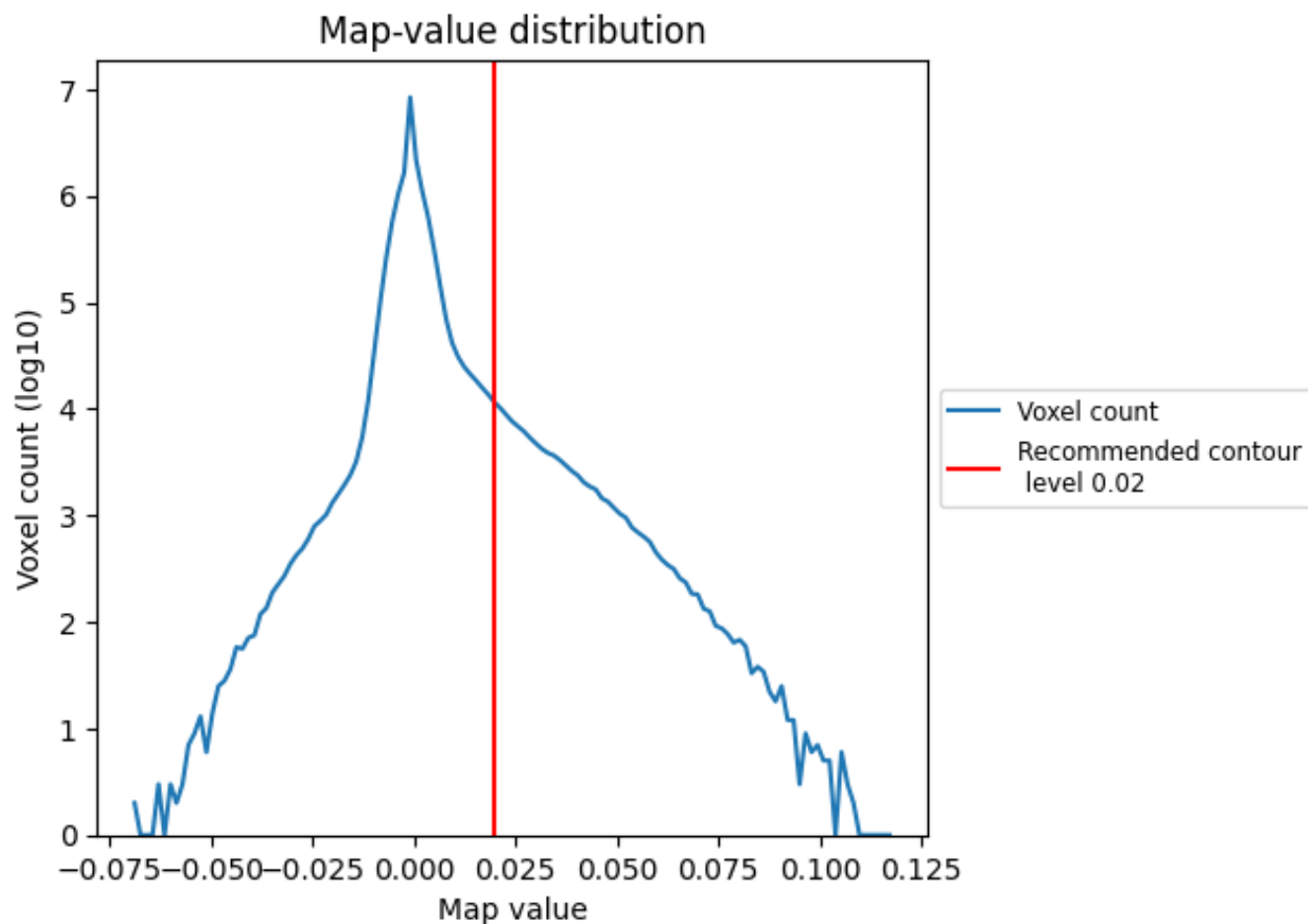
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

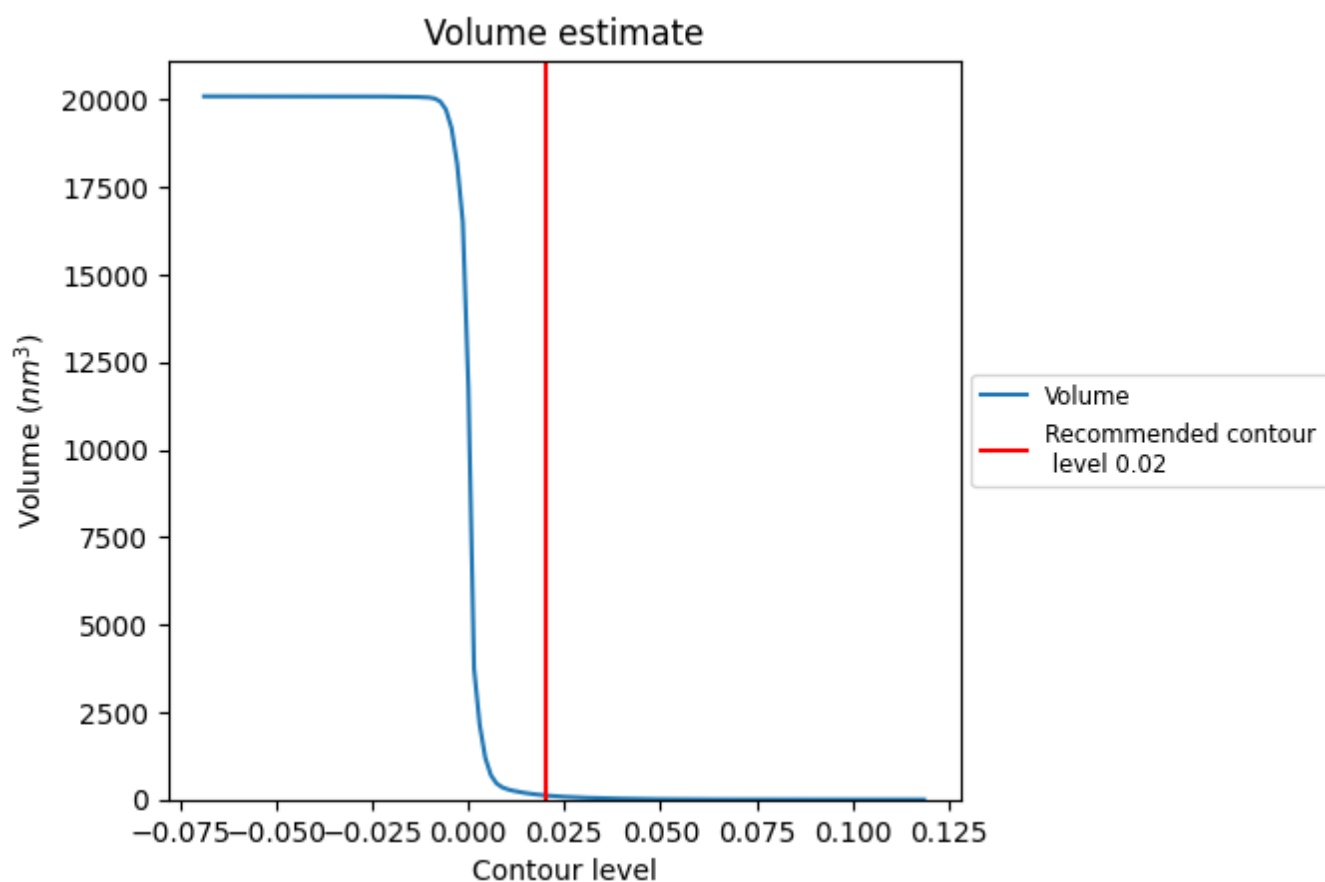
### 7.1 Map-value distribution [i](#)



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](#)

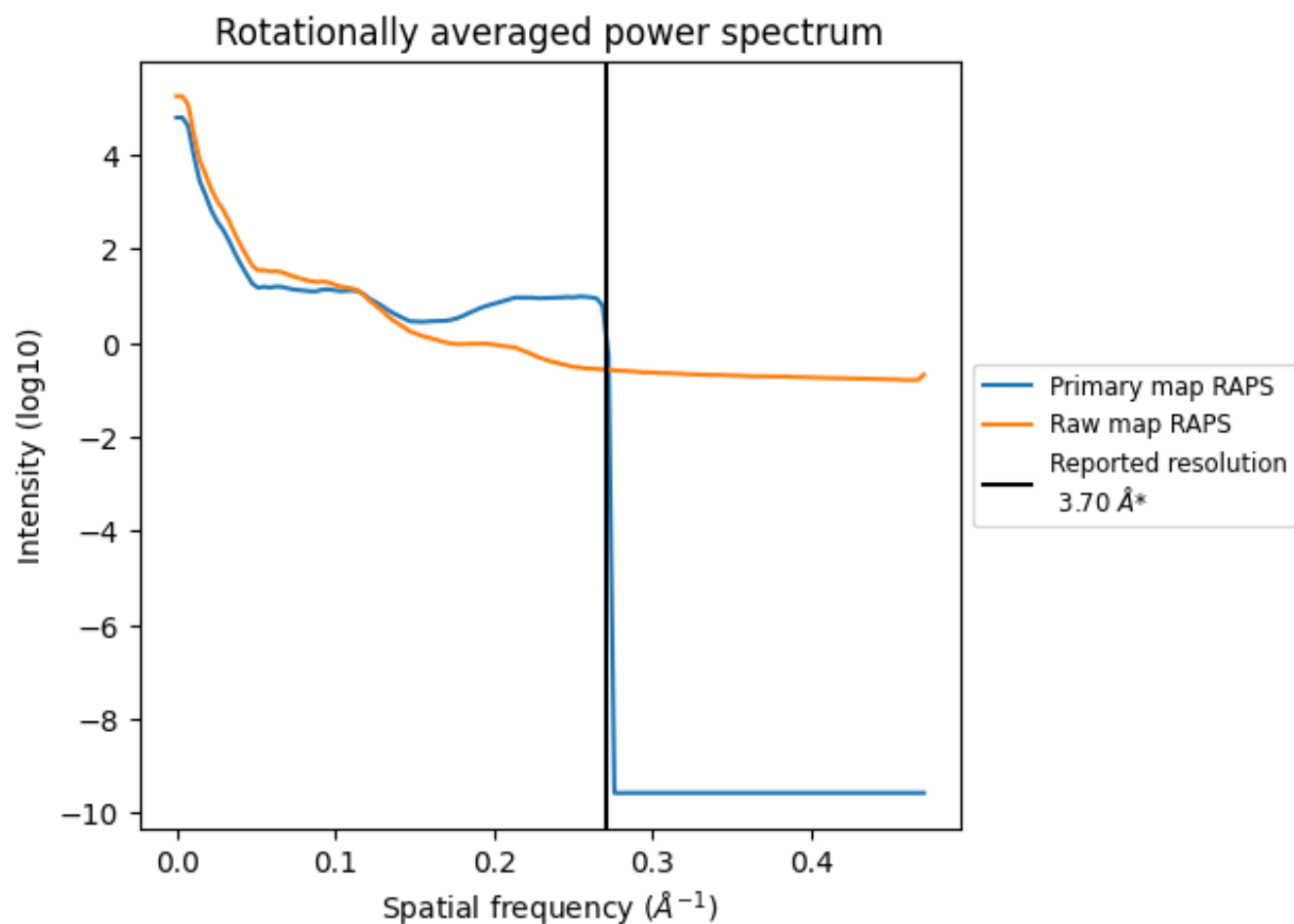


The volume at the recommended contour level is 120 nm<sup>3</sup>; this corresponds to an approximate mass of 108 kDa.

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 ⓘ



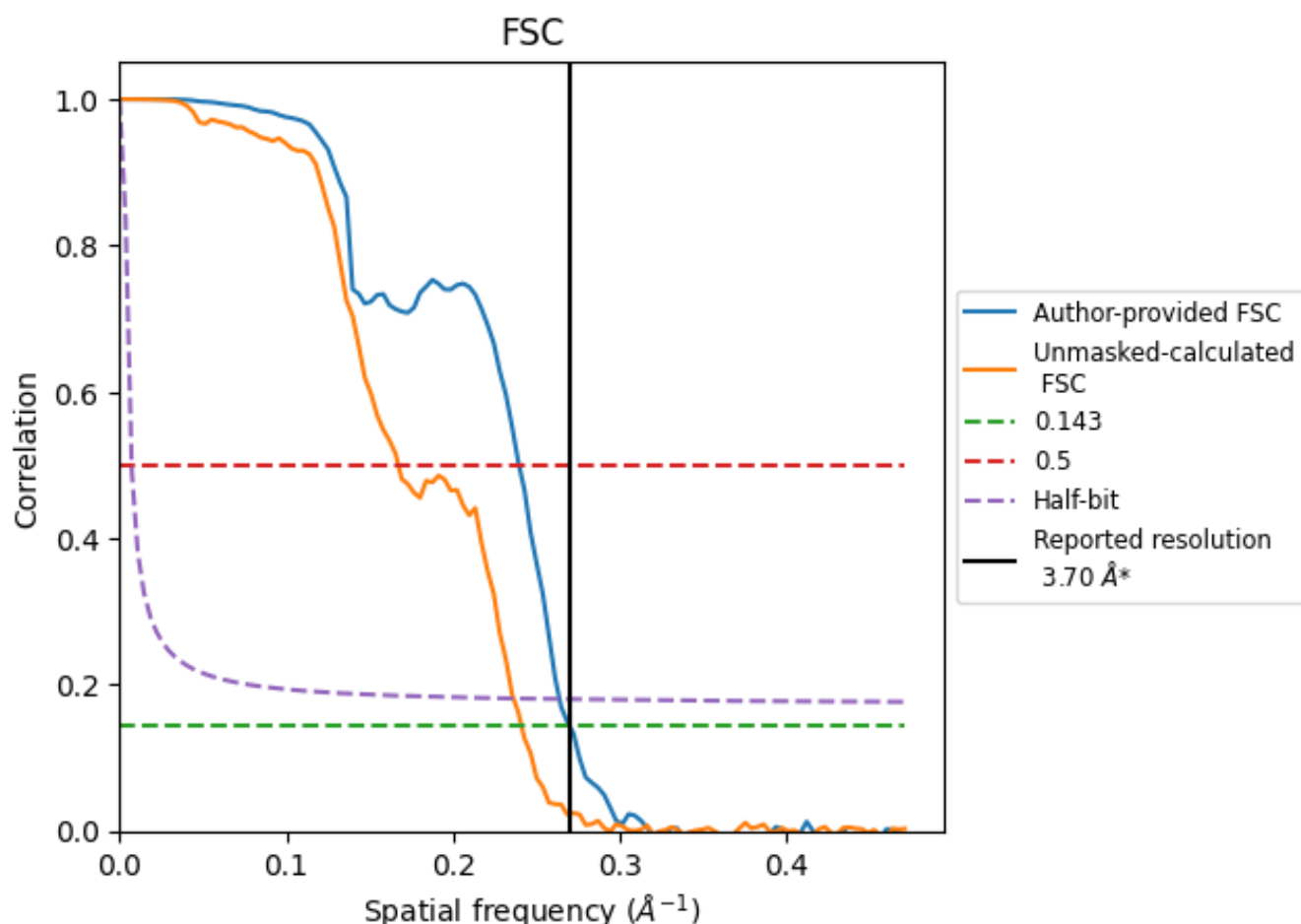
\*Reported resolution corresponds to spatial frequency of 0.270  $\text{\AA}^{-1}$



## 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 0.270 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.71	4.18	3.79
Unmasked-calculated*	4.15	5.98	4.23

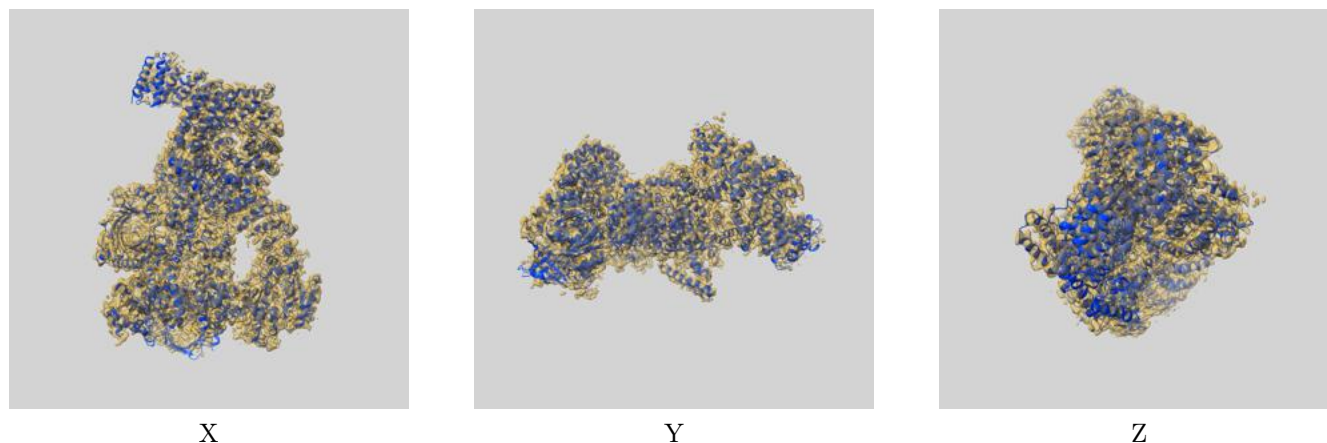
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.15 differs from the reported value 3.7 by more than 10 %



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

This section contains information regarding the fit between EMDB map EMD-29305 and PDB model 8FN4. Per-residue inclusion information can be found in section [3](#) on page [7](#).

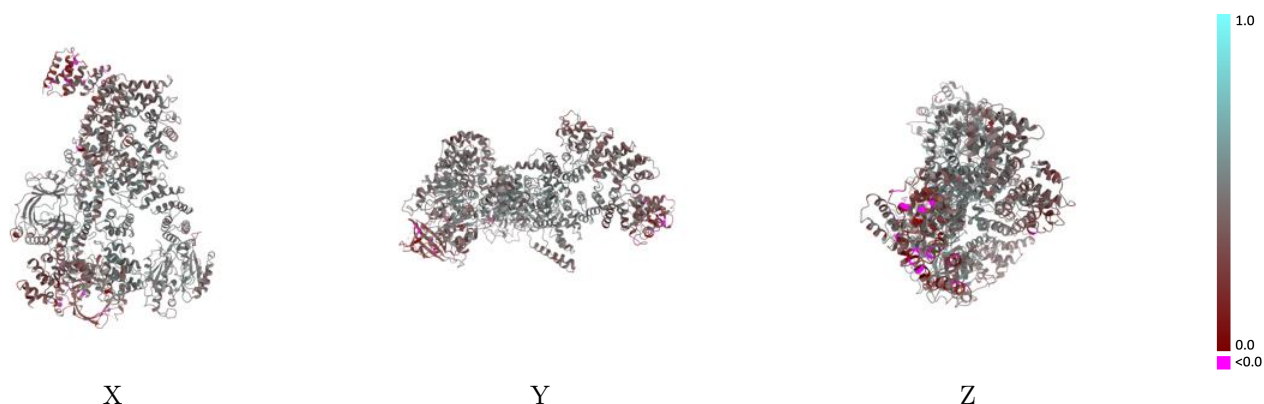
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.02 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.

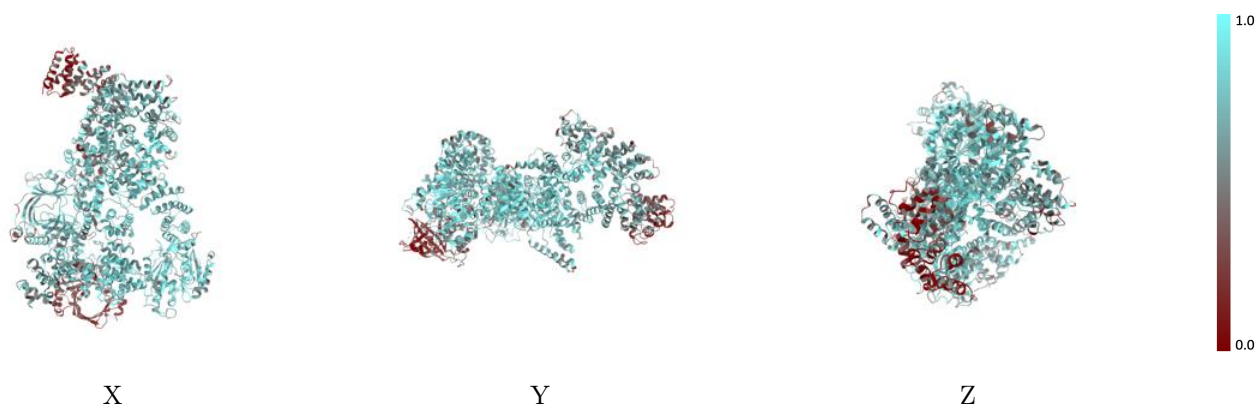


## 9.2 Q-score mapped to coordinate model [i](#)



The images above show the model with each residue coloured according 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.

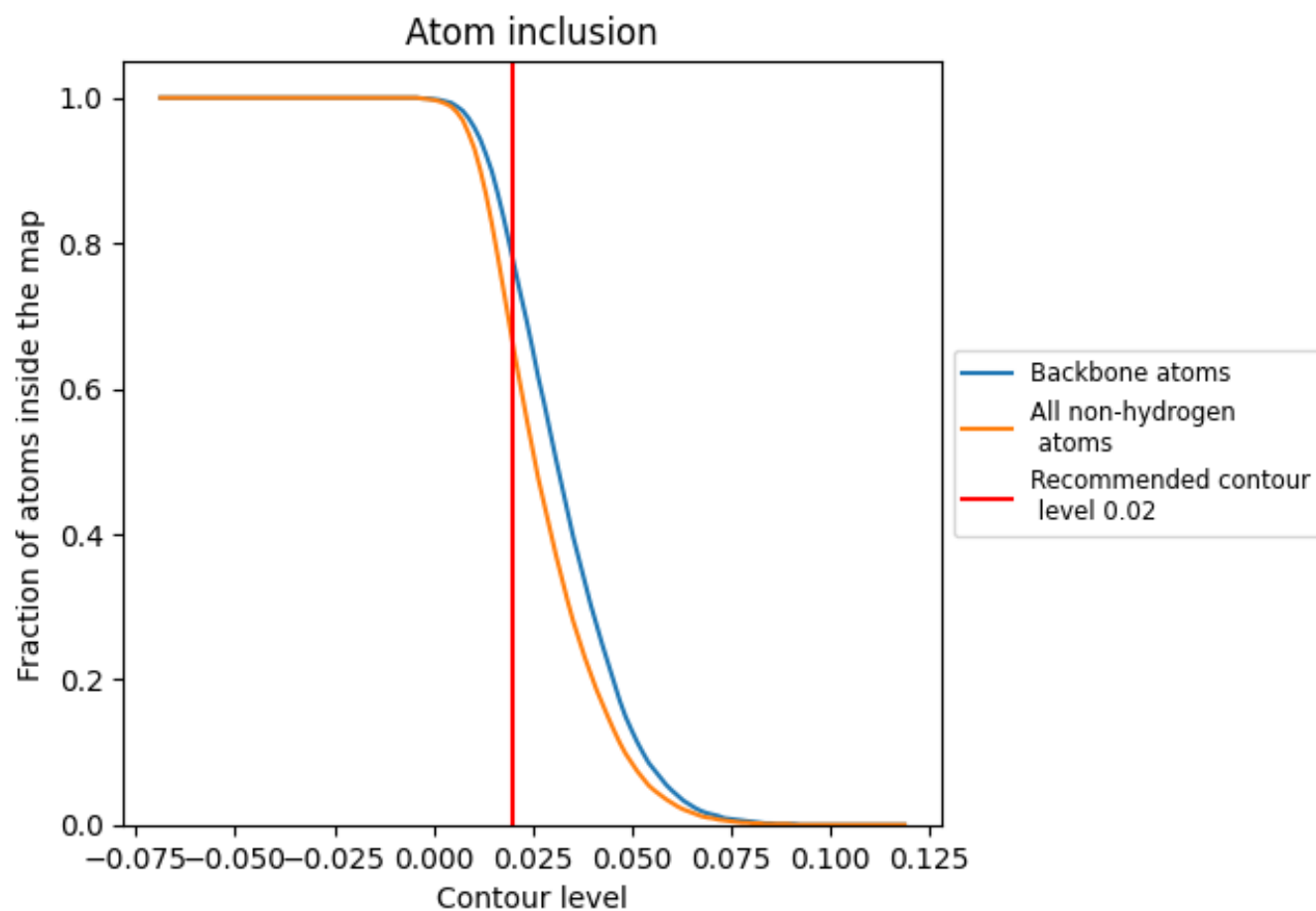
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.02).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 66% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.6610</div>	<div><div></div>0.4160</div>
1	<div><div></div>0.7270</div>	<div><div></div>0.4560</div>
2	<div><div></div>0.4140</div>	<div><div></div>0.3150</div>
3	<div><div></div>0.5540</div>	<div><div></div>0.3770</div>
4	<div><div></div>0.7310</div>	<div><div></div>0.4470</div>
5	<div><div></div>0.7540</div>	<div><div></div>0.4550</div>
6	<div><div></div>0.7550</div>	<div><div></div>0.4370</div>

1.0

0.0

<0.0