



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:46 PM UTC

PDB ID : 8FN4 / pdb_00008fn4
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)

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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

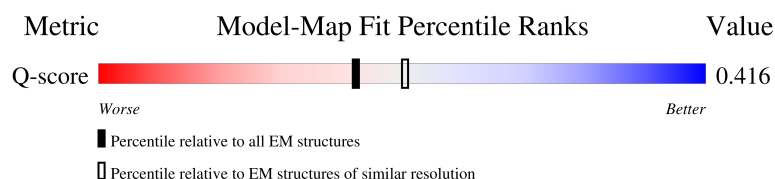
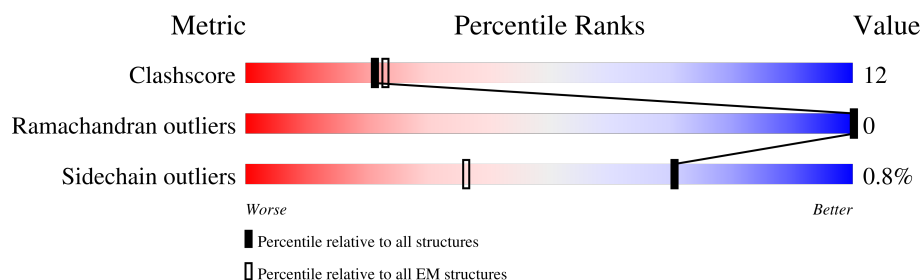
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	1	473	
2	2	492	
3	3	482	
4	4	1087	

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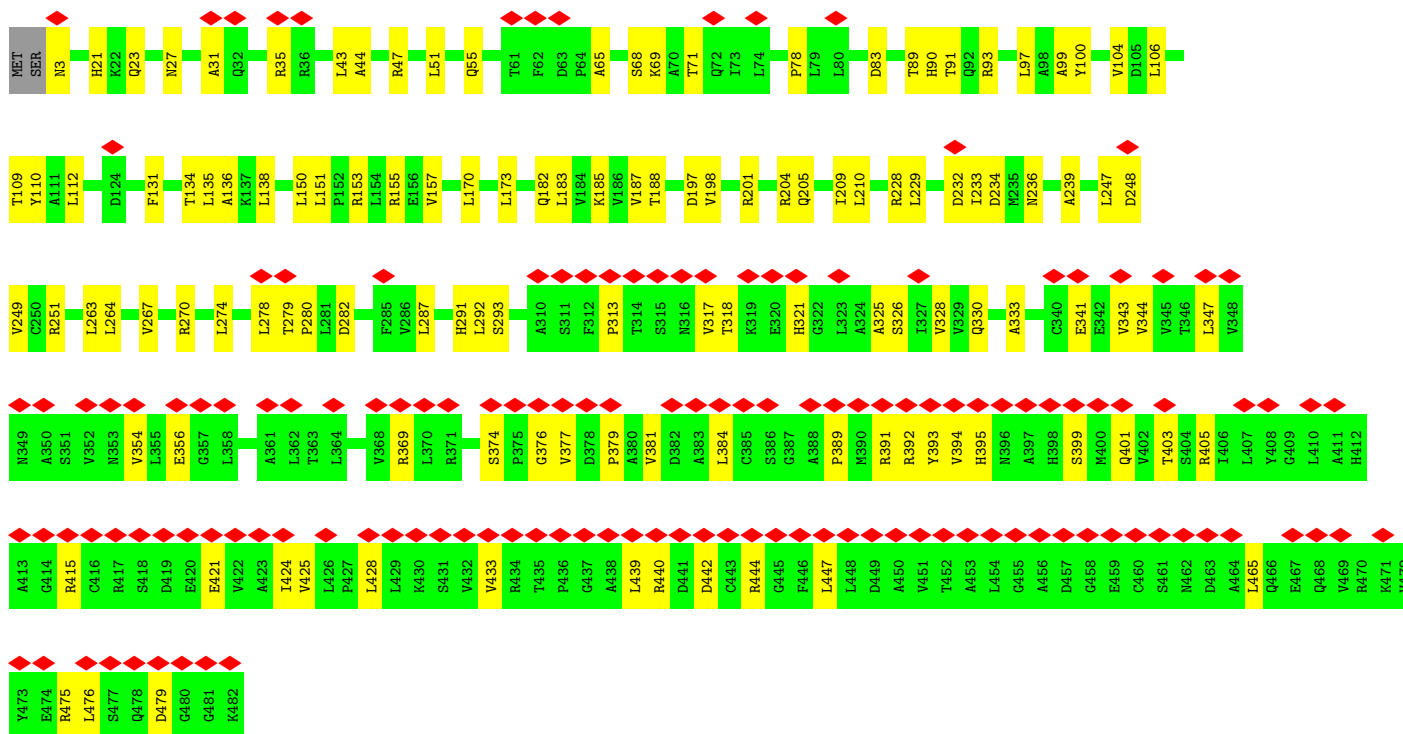
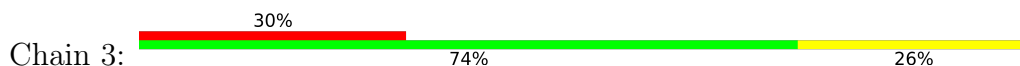
Chain	Residue	Modelled	Actual	Comment	Reference
5	397	HIS	-	expression tag	UNP Q389F5
5	398	PRO	-	expression tag	UNP Q389F5
5	399	GLN	-	expression tag	UNP Q389F5
5	400	PHE	-	expression tag	UNP Q389F5
5	401	GLU	-	expression tag	UNP Q389F5
5	402	LYS	-	expression tag	UNP Q389F5

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

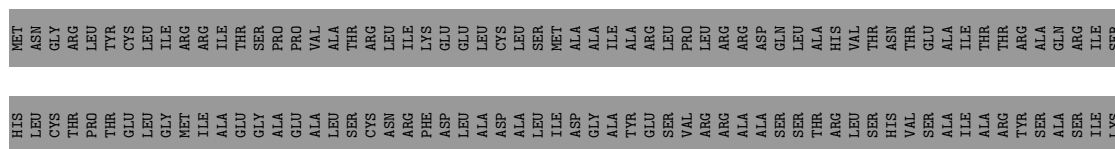
Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	452	Total	C	N	O	S	0	0
			3579	2282	631	649	17		



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



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



TRP
SER
HIS
PRO
ALA
LEU
GLN
PHE
GLU
LYS
GLY
LEU
GLY
GLY
SER
GLN
GLY
GLY
GLY
SER
GLY
GLY
MET
GLY
SER
ALA
TRP
SER
HIS
PRO
GLN
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
GLY
CYS
LEU
SER
ARG
MET
LYS
GLN
SER
LEU
SER
ALA
PHE
PRO
THR
VAL
VAL
THR
GLY
MET
THR
D124
ARG
HIS
GLN
GLY
ASN
SER
LEU
ILE
GLY
THR
THR
HIS
GLY
ALA
GLU
LEU
SER
LEU
ALA
ASP
PRO
GLN
SER
V58
S59
H60

L61
S62
A63
I66
L71
Q72
M73
R80
L86
A87
Q88
R92
Y93
L94
I99
L104
D105
S108
L111
L112
E122
S123
D124
A125
I132
D133
Y134
C135
D139
C154
L157
R160
V165
I166
E167
M168
Q169
A170
Q171
F179
L180
D181

T186
T189
T195
F203
H223
L227
S232
R235
L234
L241
E254
R255
V256
T257
V258
N259
E260
I271
G272
L273
V290
M293
M301
F302
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
R392
A397
A398
S399
I400
A401
D402
D405
A406
M407
G408
L409
V410
M411
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
N498
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	0.17	0/2574	0.36	0/3491
2	2	0.12	0/2944	0.30	0/3990
3	3	0.13	0/3764	0.30	0/5106
4	4	0.16	0/5879	0.31	0/7961
5	5	0.14	0/2217	0.31	0/3007
6	6	0.16	0/3643	0.31	0/4923
All	All	0.15	0/21021	0.31	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	107	0
2	2	2876	0	2837	76	0
3	3	3705	0	3819	90	0
4	4	5790	0	5831	110	0
5	5	2163	0	2103	59	0
6	6	3579	0	3610	80	0
All	All	20638	0	20749	488	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 12.

The worst 5 of 488 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%)	272 (99%)	4 (1%)	59	70
2	2	304/410 (74%)	303 (100%)	1 (0%)	86	83
3	3	405/407 (100%)	405 (100%)	0	100	100
4	4	643/933 (69%)	638 (99%)	5 (1%)	73	76
5	5	236/322 (73%)	234 (99%)	2 (1%)	73	76
6	6	375/428 (88%)	369 (98%)	6 (2%)	55	68
All	All	2239/2900 (77%)	2221 (99%)	18 (1%)	70	76

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	301	MET
6	6	367	HIS
6	6	352	LEU
4	4	603	HIS
6	6	241	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
4	4	899	ASN
6	6	423	GLN
6	6	475	HIS
6	6	102	GLN
3	3	177	GLN

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.

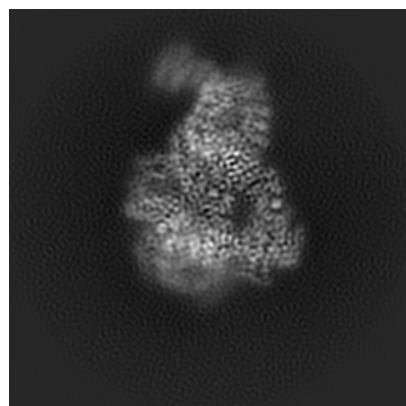
6 Map visualisation [i](#)

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

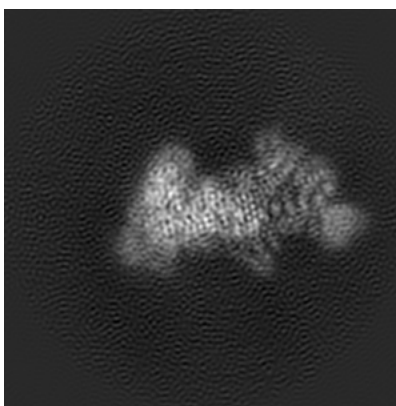
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

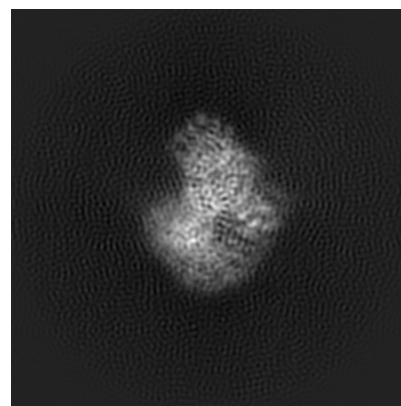
6.1.1 Primary map



X

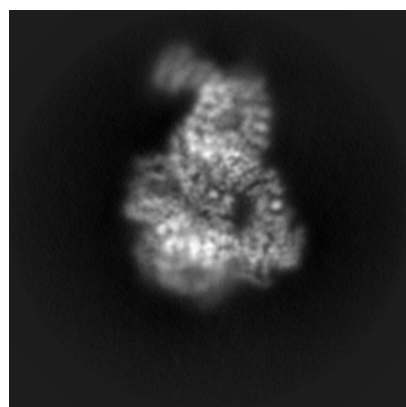


Y

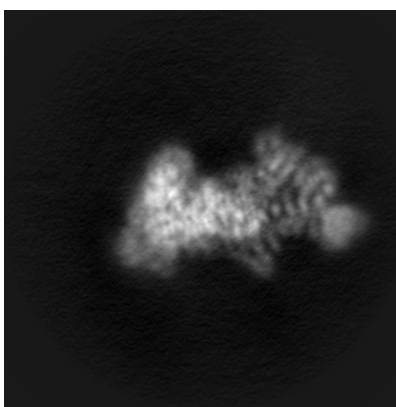


Z

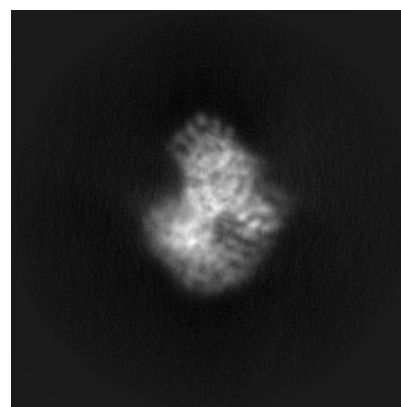
6.1.2 Raw map



X



Y

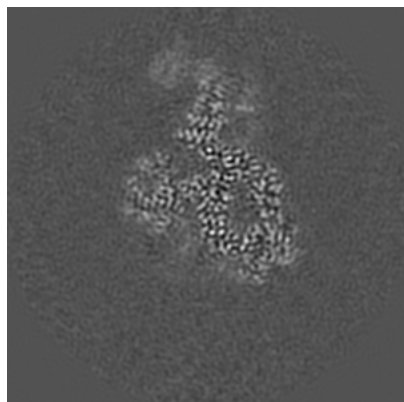


Z

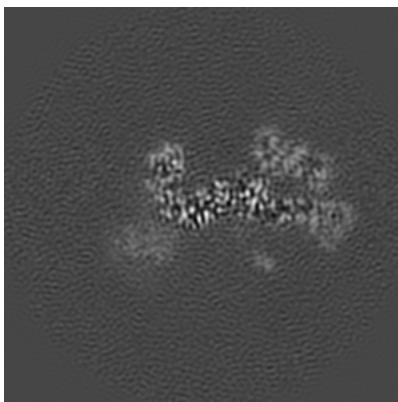
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

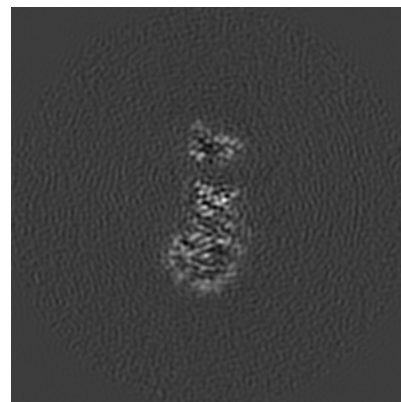
6.2.1 Primary map



X Index: 128

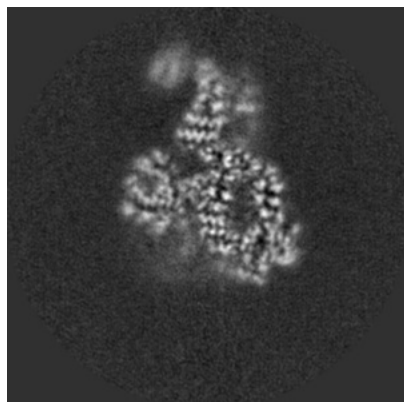


Y Index: 128

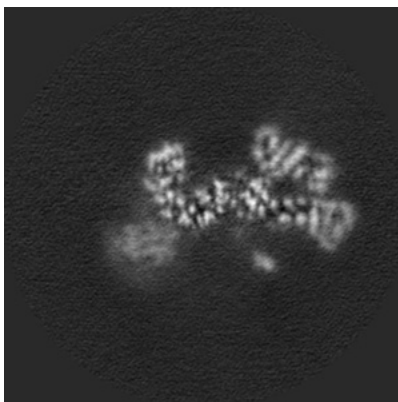


Z Index: 128

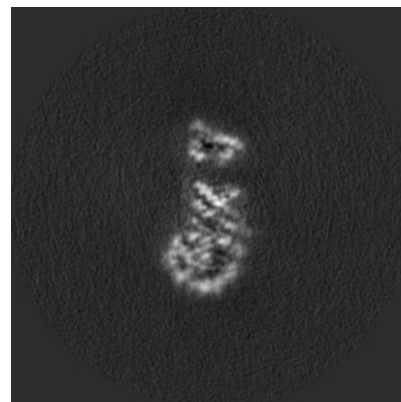
6.2.2 Raw map



X Index: 128



Y Index: 128

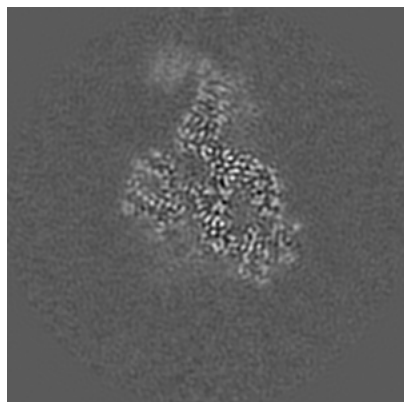


Z Index: 128

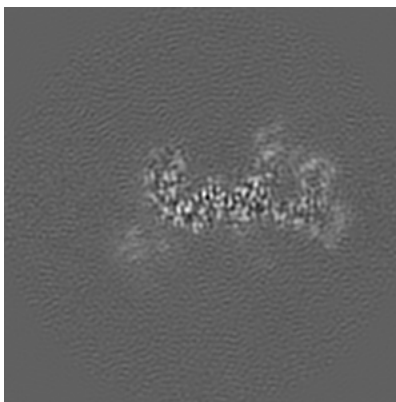
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

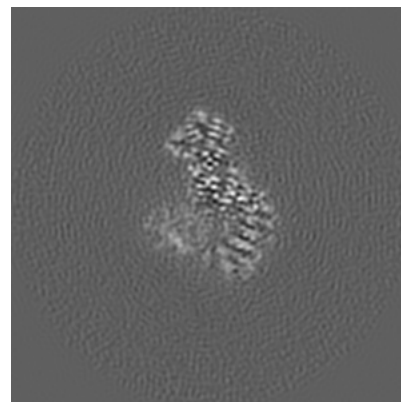
6.3.1 Primary map



X Index: 126

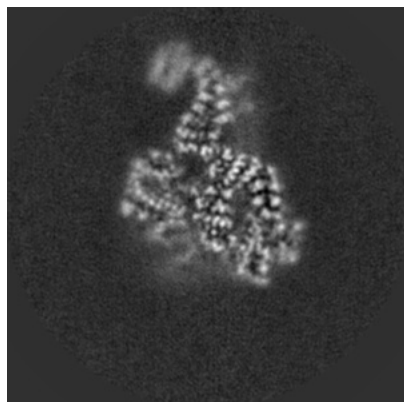


Y Index: 132

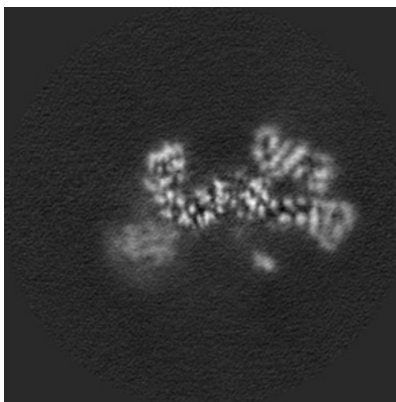


Z Index: 108

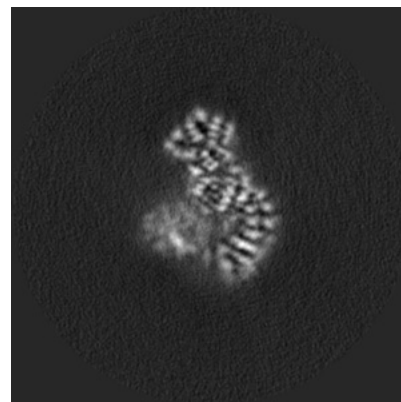
6.3.2 Raw map



X Index: 125



Y Index: 128

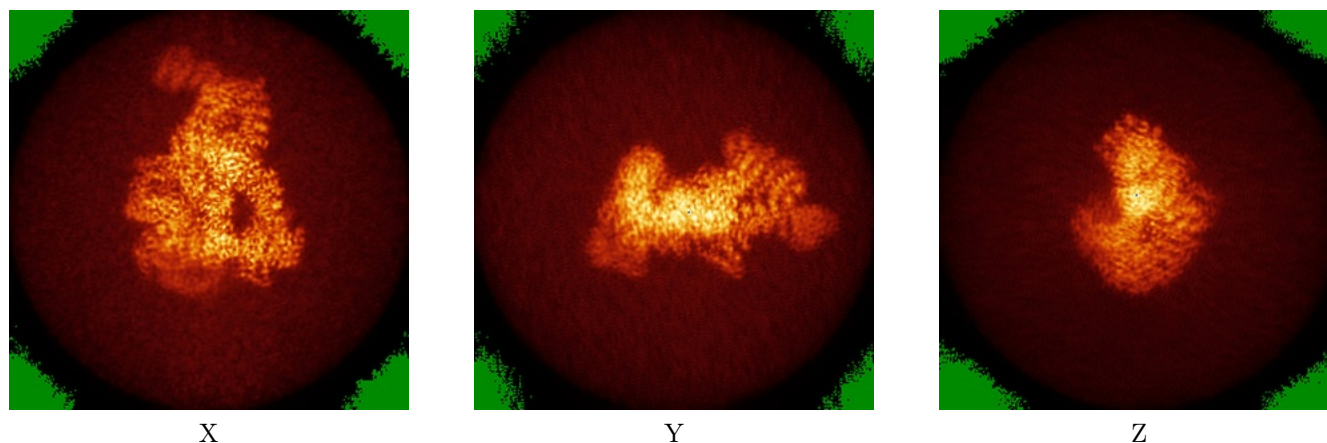


Z Index: 107

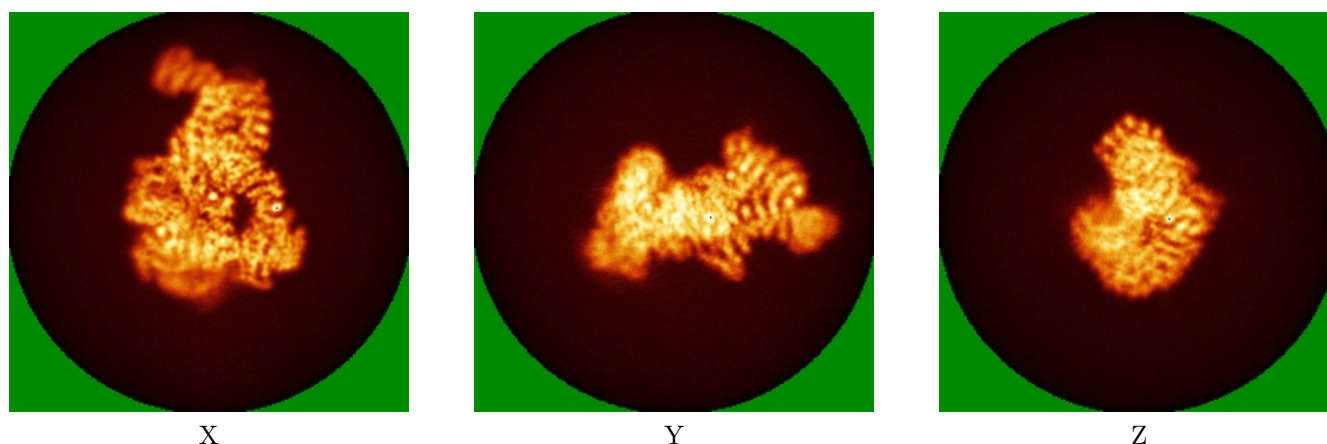
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

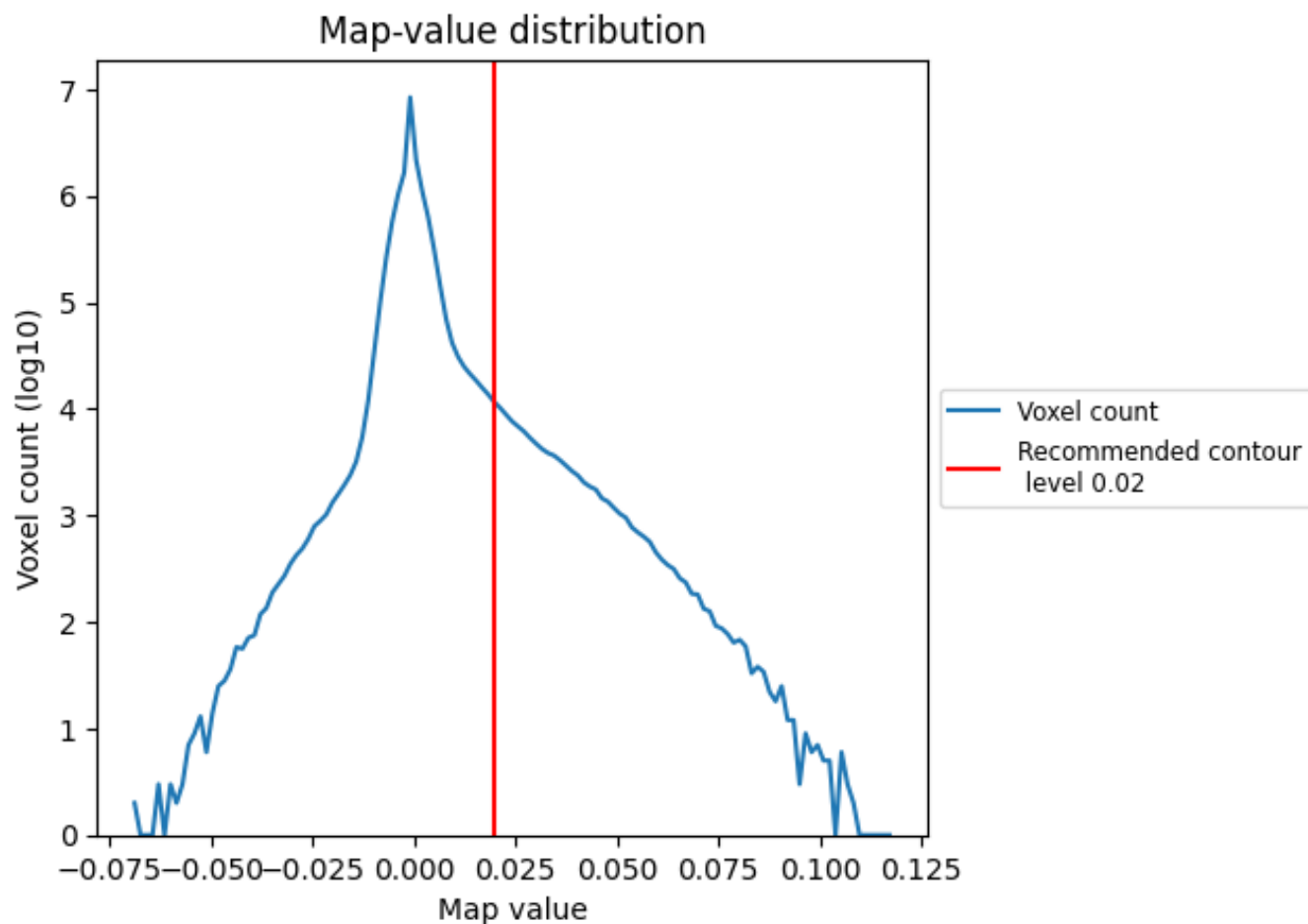
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

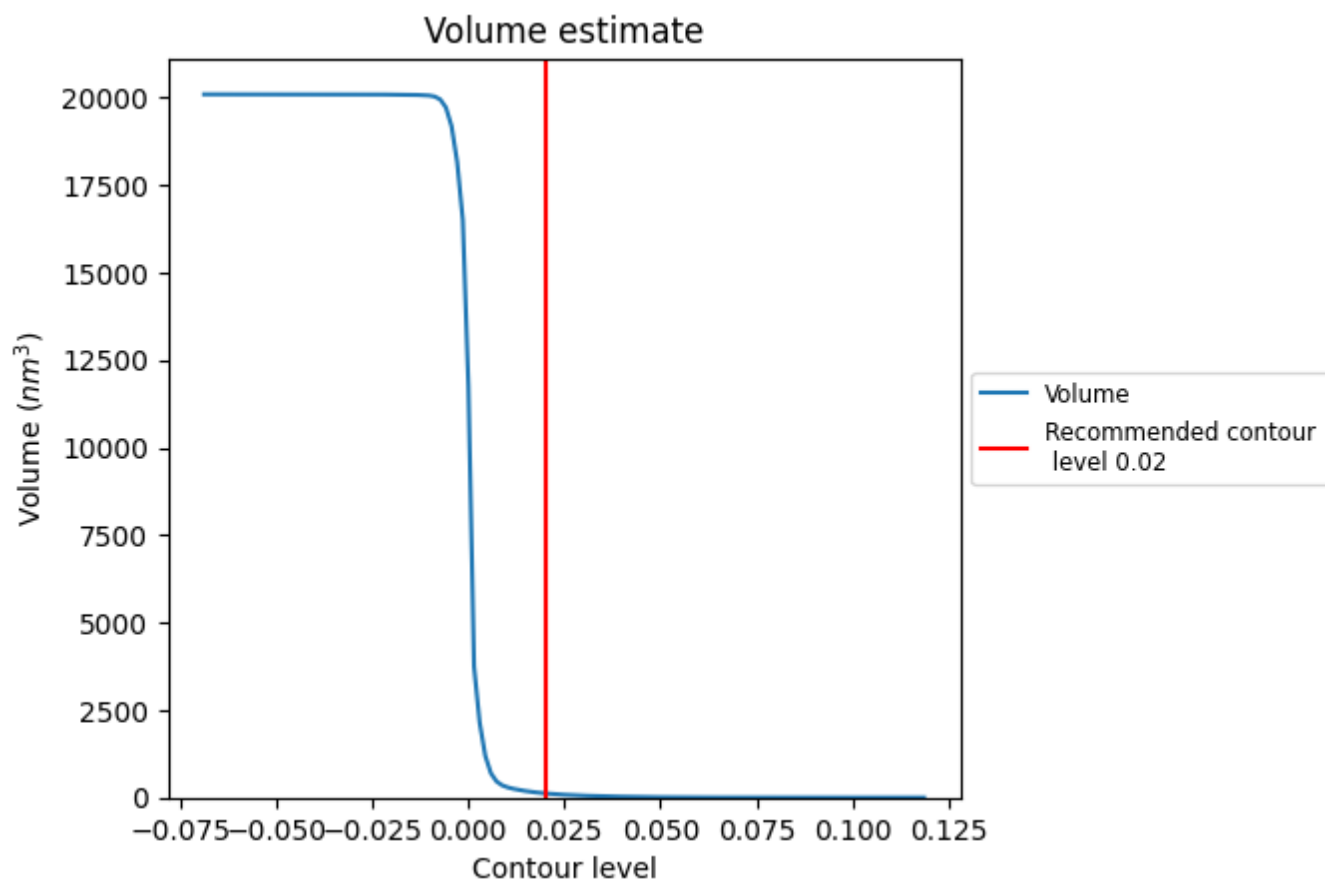
This section contains the results of statistical analysis of the map.

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.

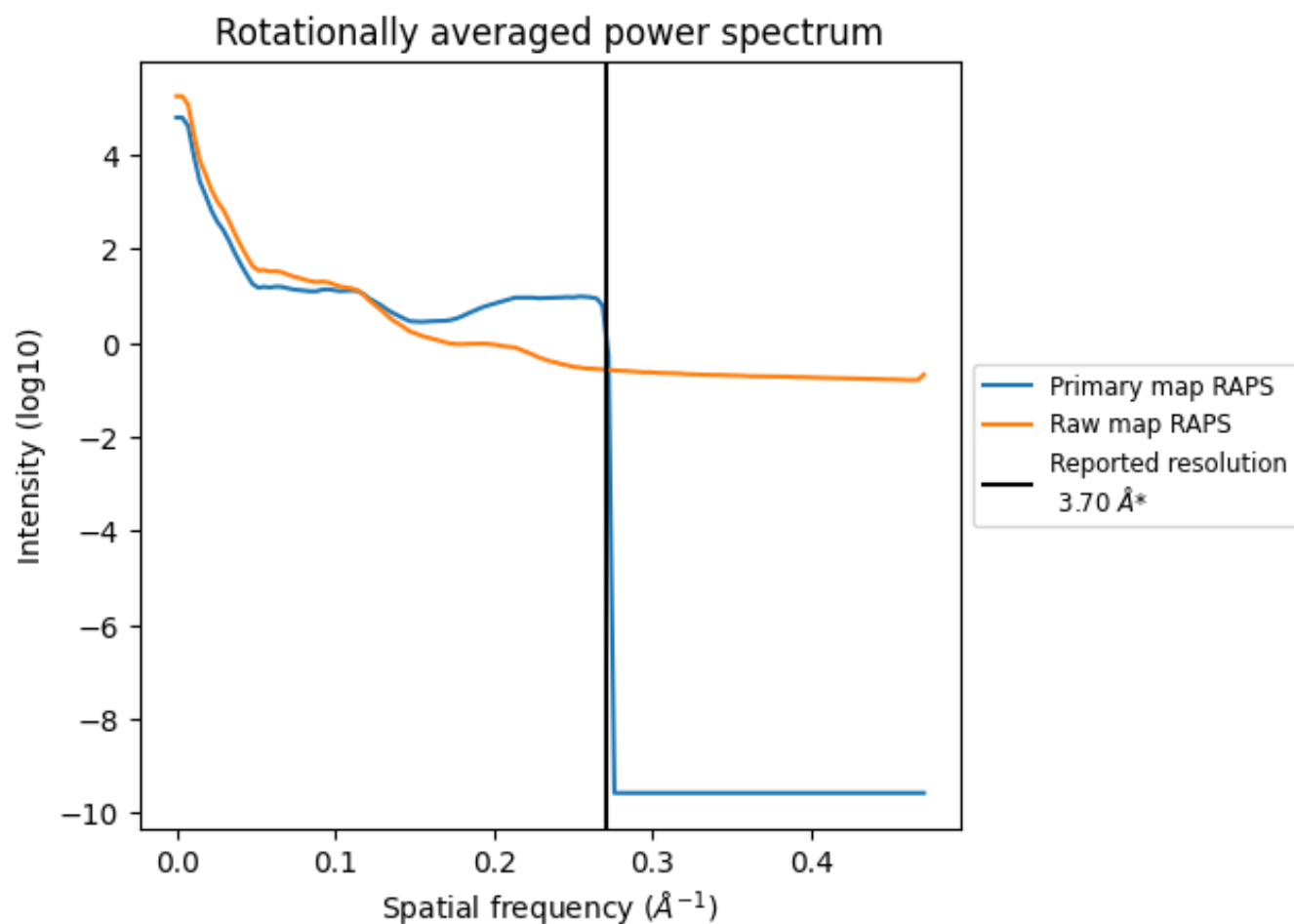
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 120 nm³; 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 ⓘ

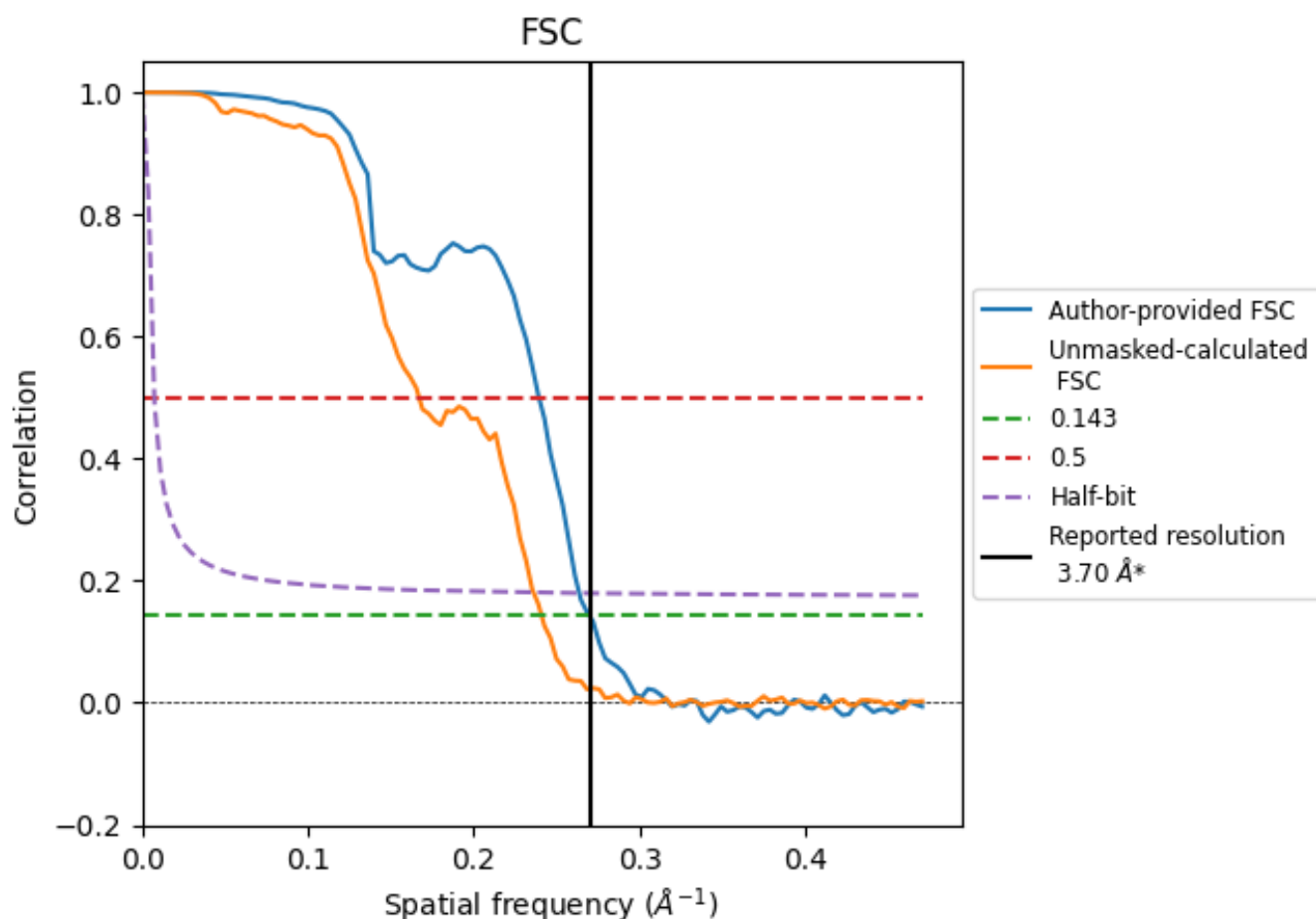


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	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 %

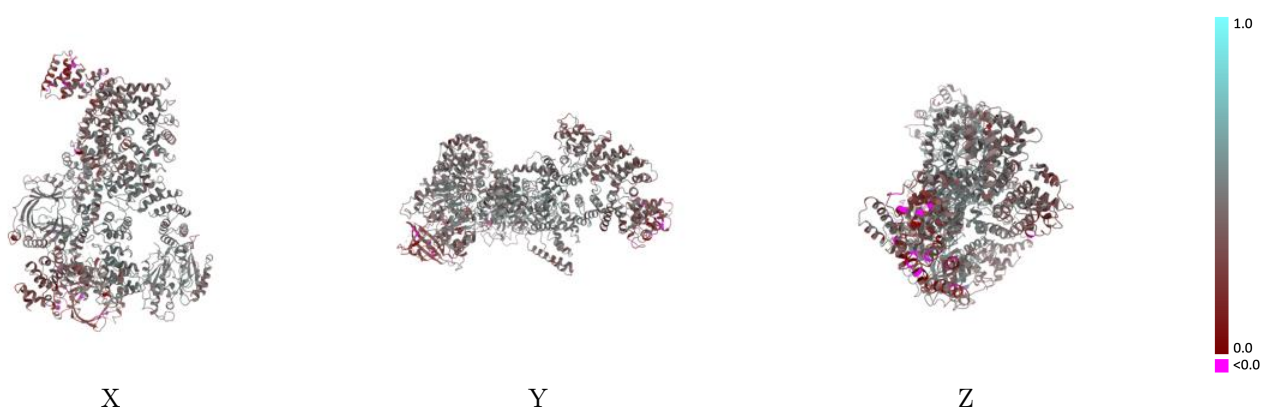
9 Map-model fit [i](#)

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 8.

9.1 Map-model overlay [i](#)

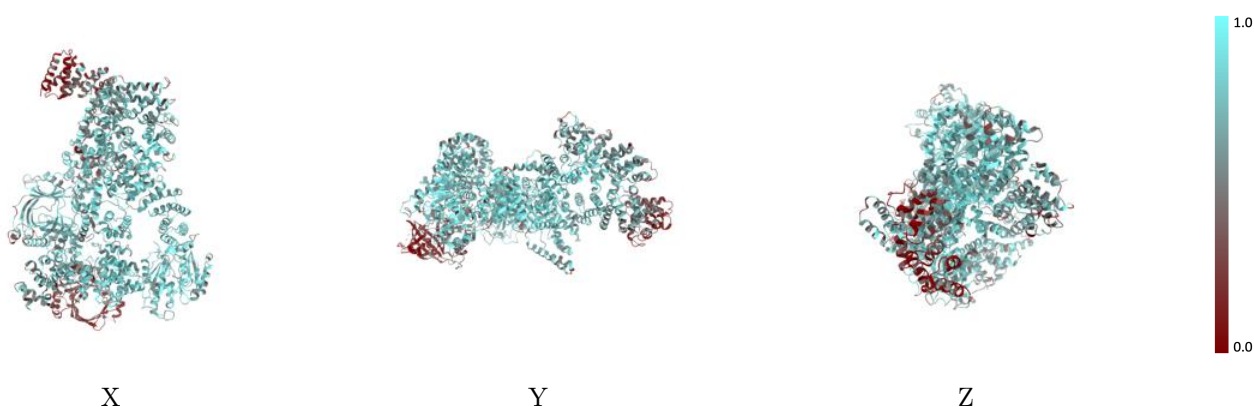
This section was not generated.

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



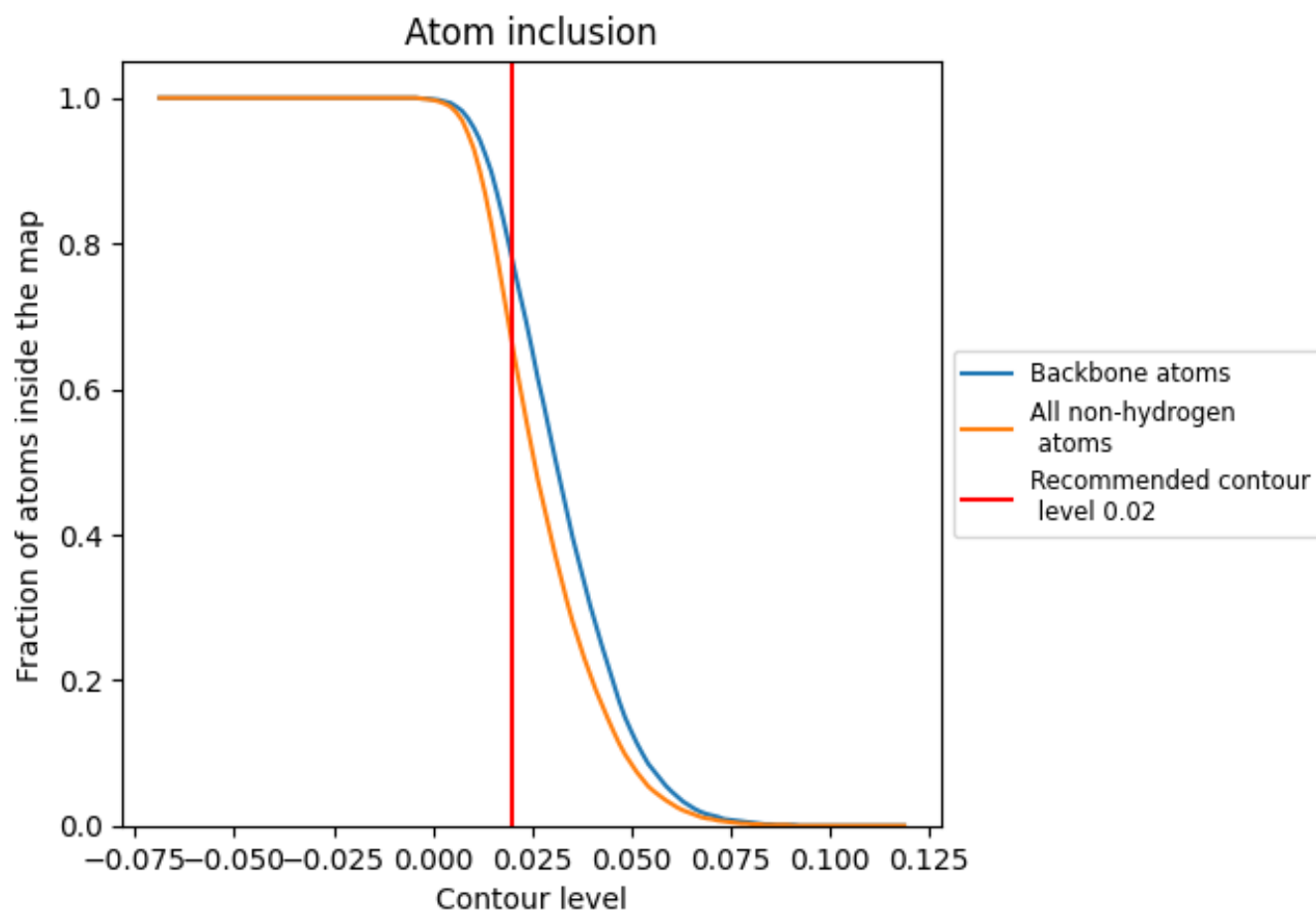
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

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	0.6610	0.4160
1	0.7270	0.4560
2	0.4140	0.3150
3	0.5540	0.3770
4	0.7310	0.4470
5	0.7540	0.4550
6	0.7550	0.4370

1.0

0.0

<0.0