wwPDB EM Validation Summary Report

Aug 24, 2026 – 11:34 AM EDT

PDB ID	:	9Q3E / pdb_00009q3e
EMDB ID	:	EMD-72190
Title	:	Cryo-EM structure of RotavirusA NSP1-ELOB-ELOC-CUL3
Authors	:	Baek, K.; Glassman, C.R.; Fischer, E.S.
Deposited on	:	2025-08-18
Resolution	:	3.30 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:

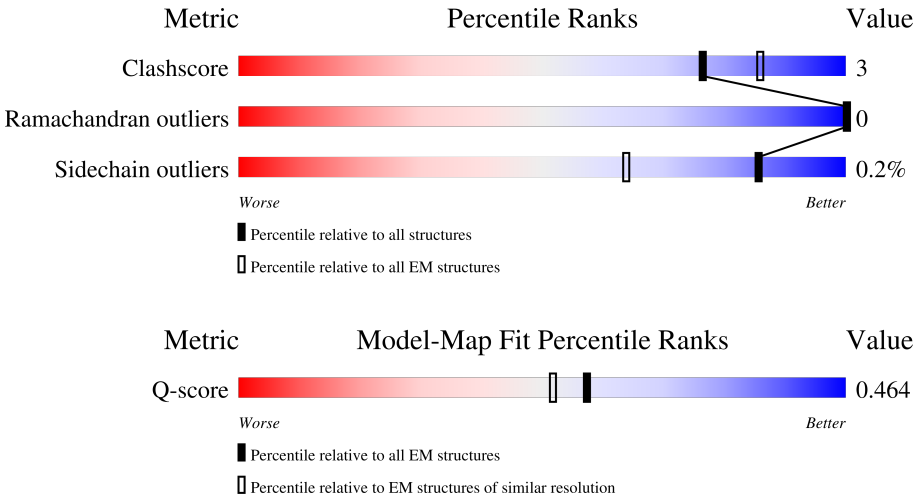
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 3.30 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	15087 (2.80 - 3.80)

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 <=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	N	486	86% 6% 8%
2	B	118	75% 5% 20%
3	C	112	87% 10%
4	L	771	17% 82%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6028 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 Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	448	Total	C	N	O	S	0	0
			3454	2224	580	618	32		

- Molecule 2 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	94	Total	C	N	O	S	0	0
			669	429	116	121	3		

- Molecule 3 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	101	Total	C	N	O	S	0	0
			752	485	124	136	7		

- Molecule 4 is a protein called Cullin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	142	Total	C	N	O	S	0	0
			1150	728	205	210	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	GLY	-	expression tag	UNP Q13618
L	-1	GLY	-	expression tag	UNP Q13618
L	0	ARG	-	expression tag	UNP Q13618

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	N	3	Total	Zn	0
			3	3	

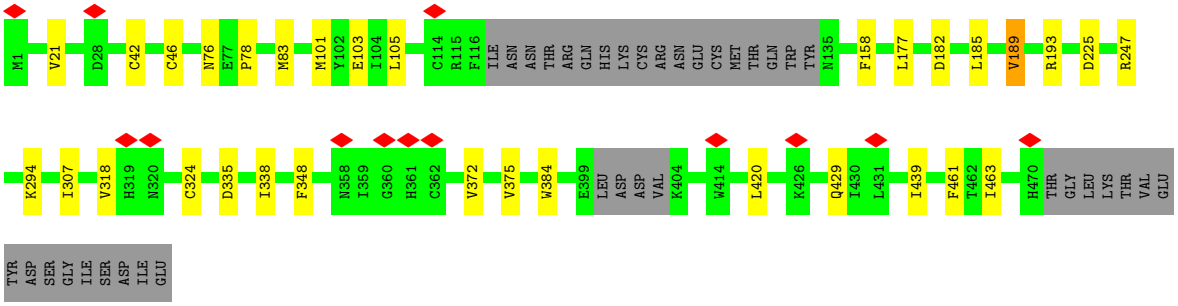
3 Residue-property plots (i)

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

- Molecule 1: Non-structural protein 1

Chain N:

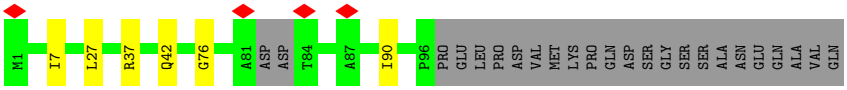




- Molecule 2: Elongin-B

Chain B:

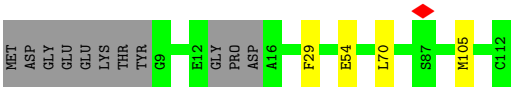




- Molecule 3: Elongin-C

Chain C:

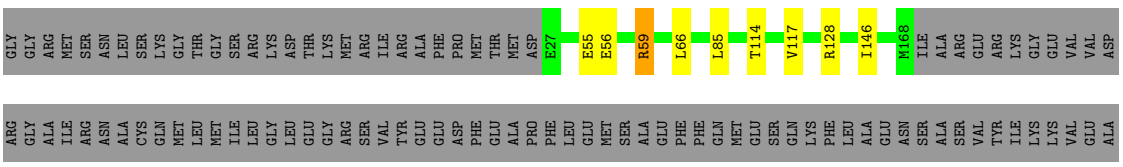


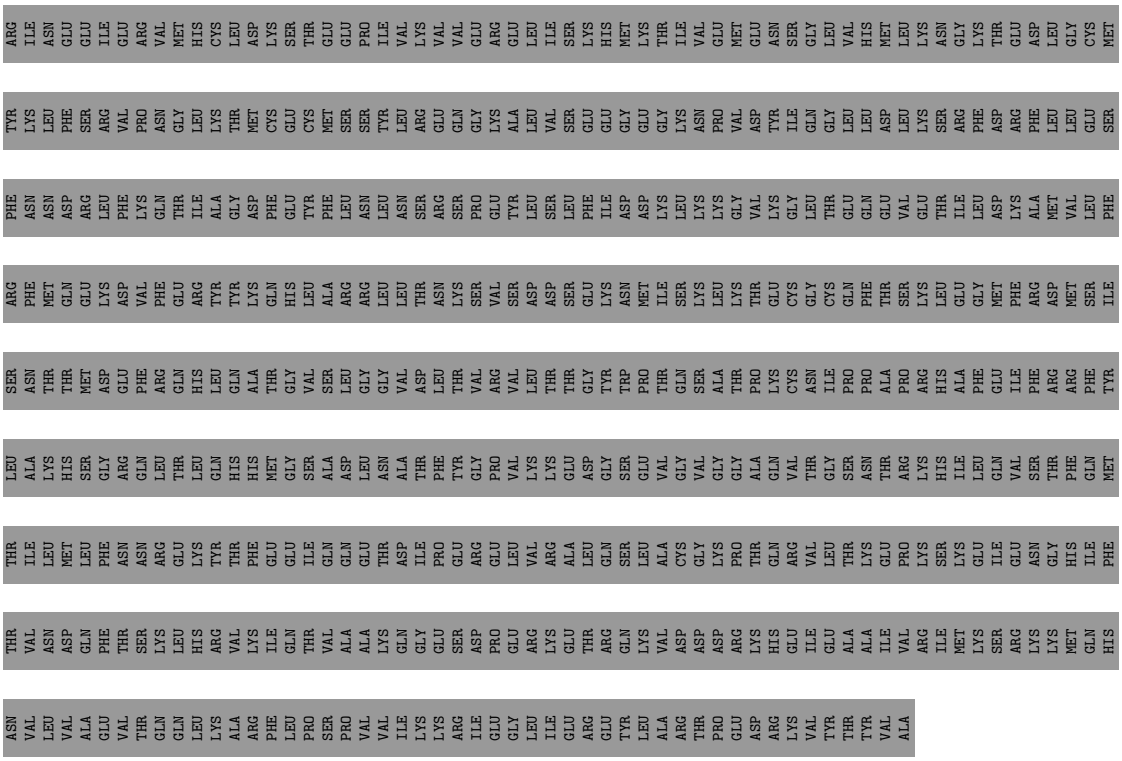


- Molecule 4: Cullin-3

Chain L:






ARG ILE ASN GLU GLU ILE GLU ARG VAL MET HIS CYS LEU ASP LYS SER THR GLU GLU PRO ILE VAL LYS VAL VAL GLU ARG GLU LEU ILE SER LYS HIS MET LYS THR ILE VAL GLU MET GLU ASN SER GLY LEU VAL HIS MET LEU LYS ASN GLY LYS THR GLU ASP LEU GLY CYS MET
TYR LYS LEU PHE SER ARG VAL PRO ASN GLY LEU LYS THR MET CYS GLU CYS MET SER SER TYR LEU ARG GLU GLN GLY LYS ALA LEU VAL SER GLU GLU GLY GLU GLY LYS ASN PRO VAL ASP TYR ILE GLN GLY LEU LEU ASP LEU LYS SER ARG PHE ASP ARG PHE LEU LEU GLU SER
PHE ASN ASN ASP ARG LEU PHE LYS GLN THR ILE ALA GLY ASP PHE GLU TYR PHE LEU ASN SER ARG SER PRO GLU TYR LEU SER LEU PHE ILE ASP ASP LYS LEU LYS LYS GLY VAL LYS GLY LEU THR GLU GLN GLU VAL GLU LYS ASP LYS ALA MET VAL LEU PHE
ARG PHE MET GLN GLU LYS ASP VAL PHE GLU ARG TYR TYR LYS GLN HIS LEU ALA ARG ARG LEU LEU THR ASN LYS SER VAL SER ASP ASP SER GLU LYS ASN MET ILE SER LYS LEU LYS THR GLU CYS GLY CYS GLN PHE THR SER LYS LEU GLU GLY MET PHE ARG ASP MET SER ILE
SER ASN THR THR MET ASP GLU PHE ARG GLN HIS LEU GLN ALA THR GLY VAL SER LEU GLY GLY VAL ASP LEU THR VAL ARG VAL LEU THR THR GLY TYR TRP PRO THR GLN SER ALA THR PRO LYS CYS ASN ILE PRO PRO ALA PRO ARG HIS ALA PHE GLU ILE PHE ARG ARG PHE TYR
LEU ALA LYS HIS SER GLY ARG GLN LEU THR LEU GLN HIS HIS MET GLY SER ALA ASP LEU ASN ALA THR PHE TYR GLY PRO VAL LYS LYS GLU ASP GLY SER GLU VAL GLY VAL GLY GLY ALA GLN VAL THR GLY SER ASN THR ARG LYS HIS ILE LEU GLN VAL SER THR PHE GLN MET
THR ILE LEU MET LEU PHE ASN ASN ARG GLU LYS TYR THR PHE GLU GLU ILE GLN GLN GLU THR ASP ILE PRO GLU ARG GLU LEU VAL ARG ALA LEU GLN SER LEU ALA CYS GLY LYS PRO THR GLN ARG VAL LEU THR LYS GLU PRO LYS SER LYS GLU ILE GLU ASN ASP GLY HIS ILE PHE
THR VAL ASN ASP GLN PHE THR SER LYS LEU HIS ARG VAL LYS ILE GLN THR VAL ALA ALA LYS GLN GLY GLU SER ASP PRO GLU ARG LYS GLU THR ARG GLN LYS VAL ASP ASP ARG LYS HIS GLU ILE GLU ALA ALA ILE VAL ARG ILE MET LYS SER ARG LYS LYS MET GLN HIS
ASN VAL LEU VAL ALA GLU VAL THR GLN GLN LEU LYS ALA ARG PHE LEU PRO SER PRO VAL VAL ILE LYS LYS ARG ILE GLU GLY LEU ILE GLU ARG GLU TYR LEU ALA ARG THR PRO GLU ASP ARG LYS VAL TYR THR TYR VAL ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	173093	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 ($e^-/Å^2$)	50.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.051	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	283.008, 283.008, 283.008	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.737, 0.737, 0.737	Depositor

5 Model quality

5.1 Standard geometry

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

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	N	0.23	0/3533	0.47	1/4814 (0.0%)
2	B	0.25	0/681	0.41	0/928
3	C	0.20	0/768	0.40	0/1040
4	L	0.23	0/1167	0.48	0/1580
All	All	0.23	0/6149	0.46	1/8362 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	N	189	VAL	N-CA-C	-5.44	104.15	111.44

There are no chirality outliers.

There are no planarity outliers.

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	N	3454	0	3219	24	0
2	B	669	0	638	4	0
3	C	752	0	721	3	0
4	L	1150	0	1127	6	0
5	N	3	0	0	0	0
All	All	6028	0	5705	35	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 3.

The worst 5 of 35 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)
4:L:85:LEU:HD11	4:L:146:ILE:HG22	1.73	0.70
4:L:56:GLU:OE1	4:L:59:ARG:NH2	2.25	0.68
1:N:42:CYS:O	1:N:46:CYS:N	2.29	0.65
1:N:429:GLN:N	1:N:429:GLN:OE1	2.30	0.64
3:C:54:GLU:N	3:C:54:GLU:OE1	2.31	0.63

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	N	442/486 (91%)	432 (98%)	10 (2%)	0	100	100
2	B	90/118 (76%)	86 (96%)	4 (4%)	0	100	100
3	C	97/112 (87%)	96 (99%)	1 (1%)	0	100	100
4	L	140/771 (18%)	138 (99%)	2 (1%)	0	100	100
All	All	769/1487 (52%)	752 (98%)	17 (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	
1	N	361/466 (78%)	361 (100%)	0	100	100
2	B	64/103 (62%)	64 (100%)	0	100	100
3	C	76/96 (79%)	76 (100%)	0	100	100
4	L	123/694 (18%)	122 (99%)	1 (1%)	73	79
All	All	624/1359 (46%)	623 (100%)	1 (0%)	85	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	59	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	N	277	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 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

This section contains visualisations of the EMDB entry EMD-72190. These allow visual inspection of the internal detail of the map and identification of artifacts.

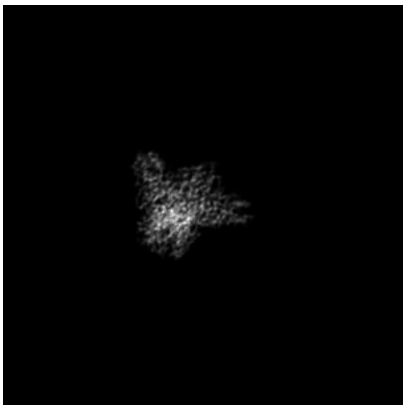
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

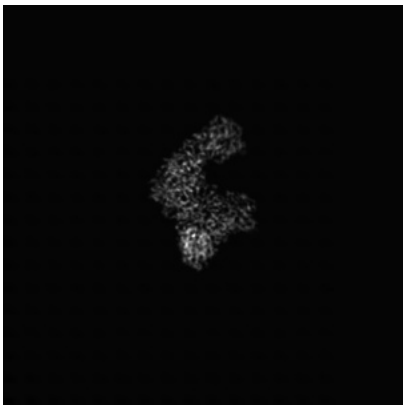
6.1.1 Primary map



X

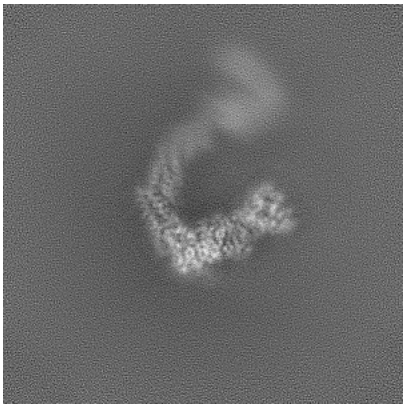


Y

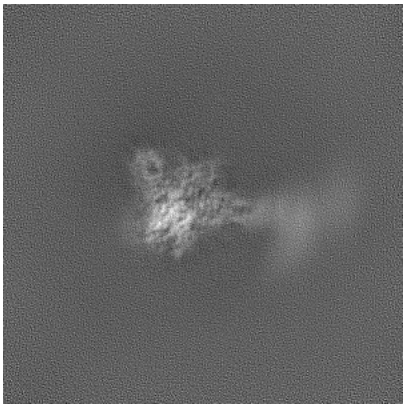


Z

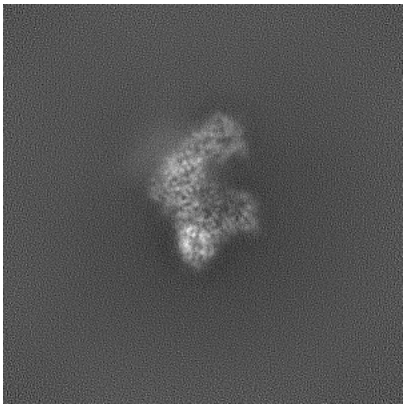
6.1.2 Raw map



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

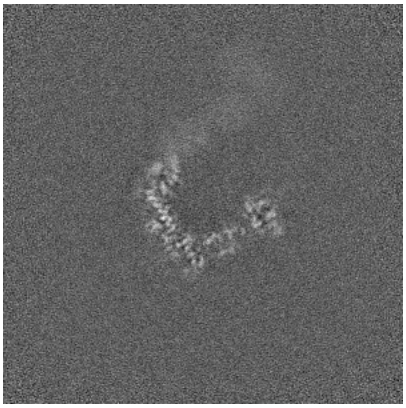


Y Index: 192

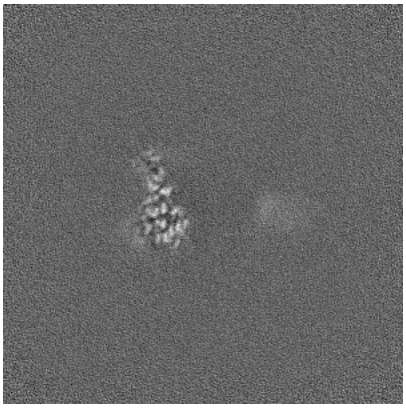


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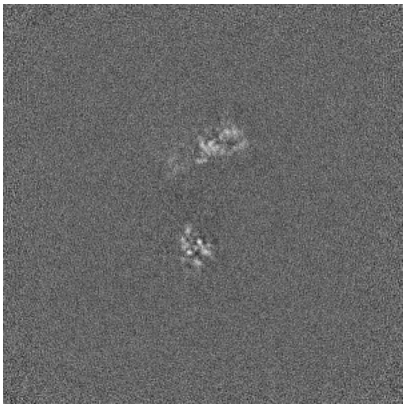
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

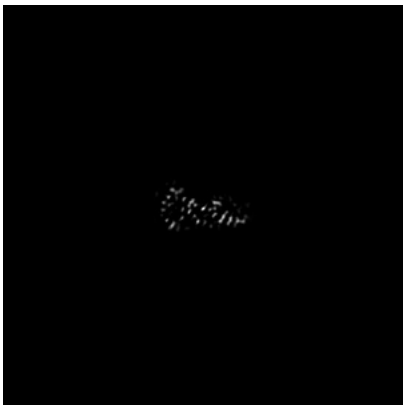
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 178

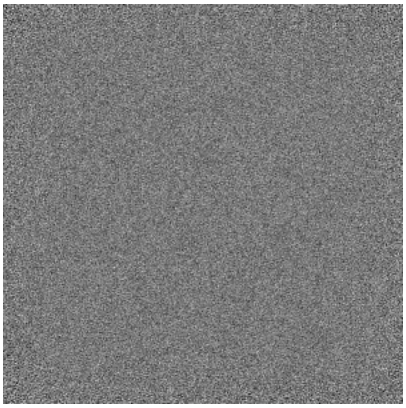


Y Index: 155

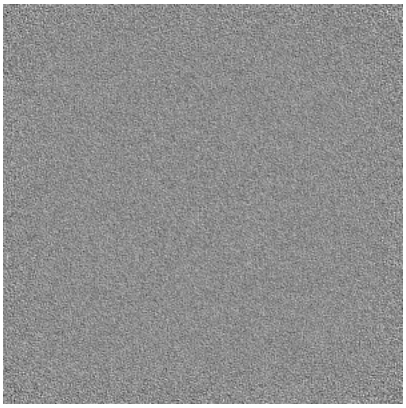


Z Index: 162

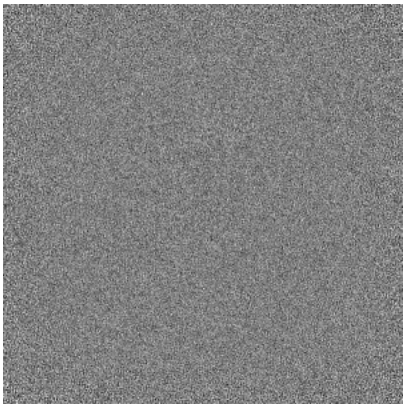
6.3.2 Raw map



X Index: 0



Y Index: 0

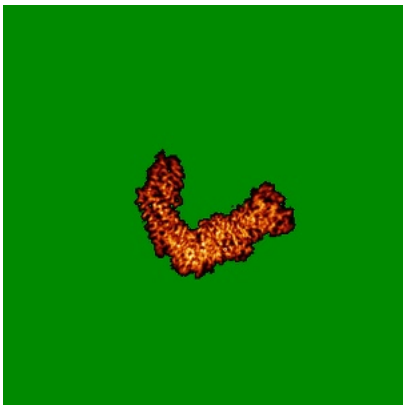


Z Index: 0

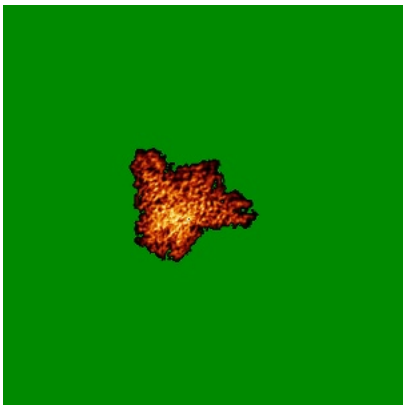
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

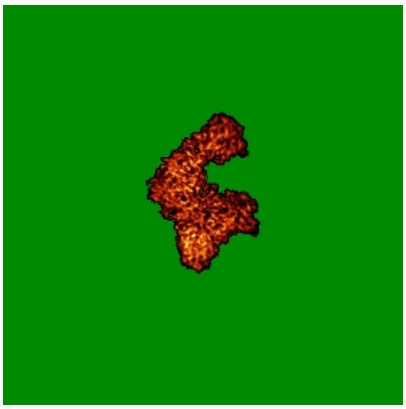
6.4.1 Primary map



X

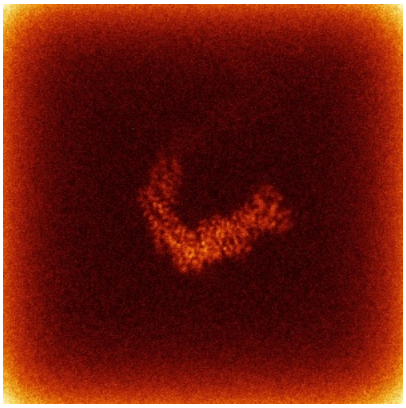


Y

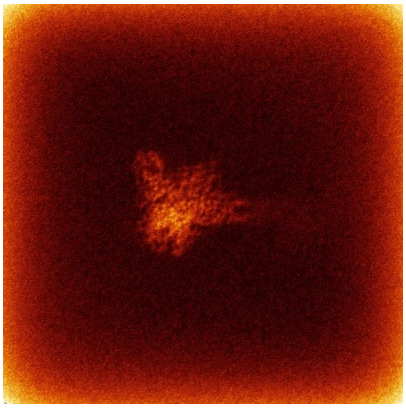


Z

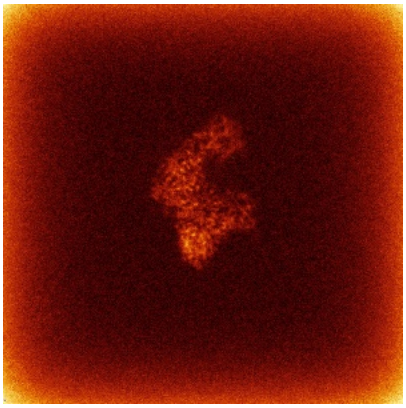
6.4.2 Raw map



X



Y

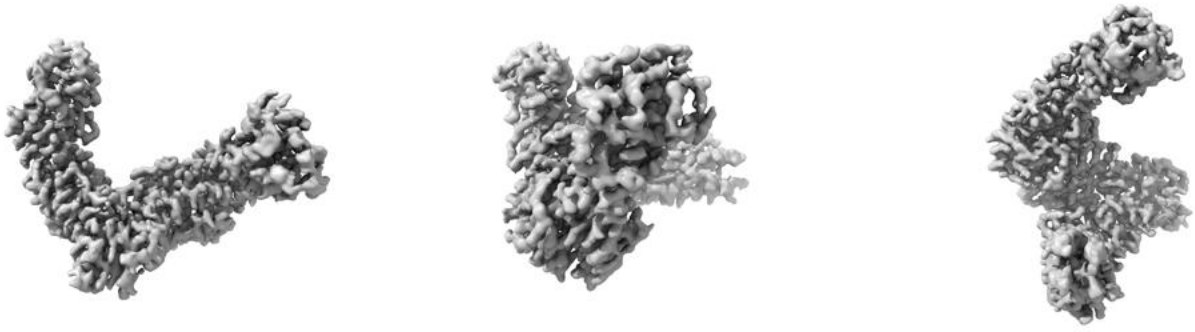


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



X Y Z

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.

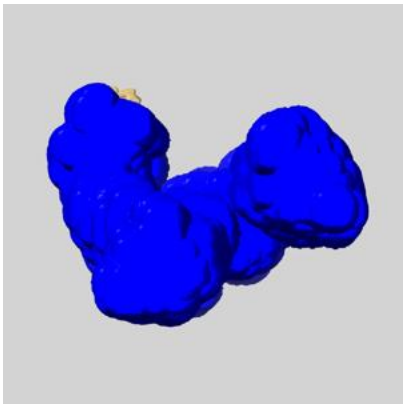
6.6 Mask visualisation

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

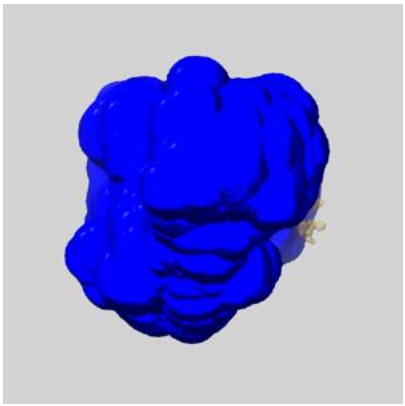
A mask typically either:

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

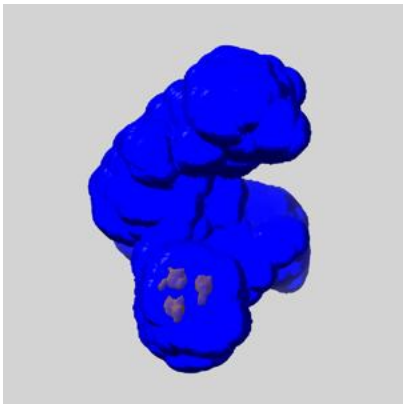
6.6.1 emd_72190_msk_1.map



X



Y

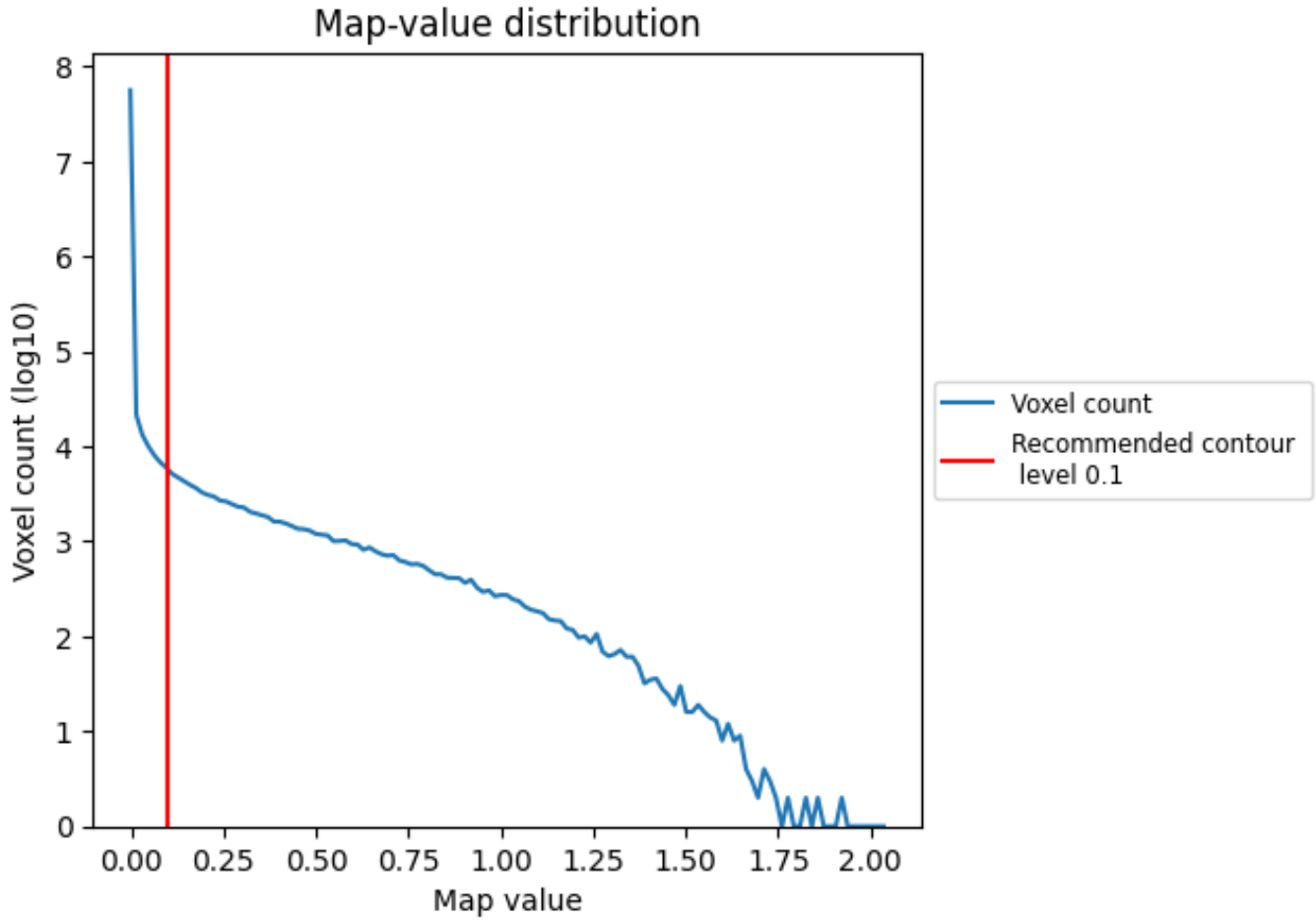


Z

7 Map analysis

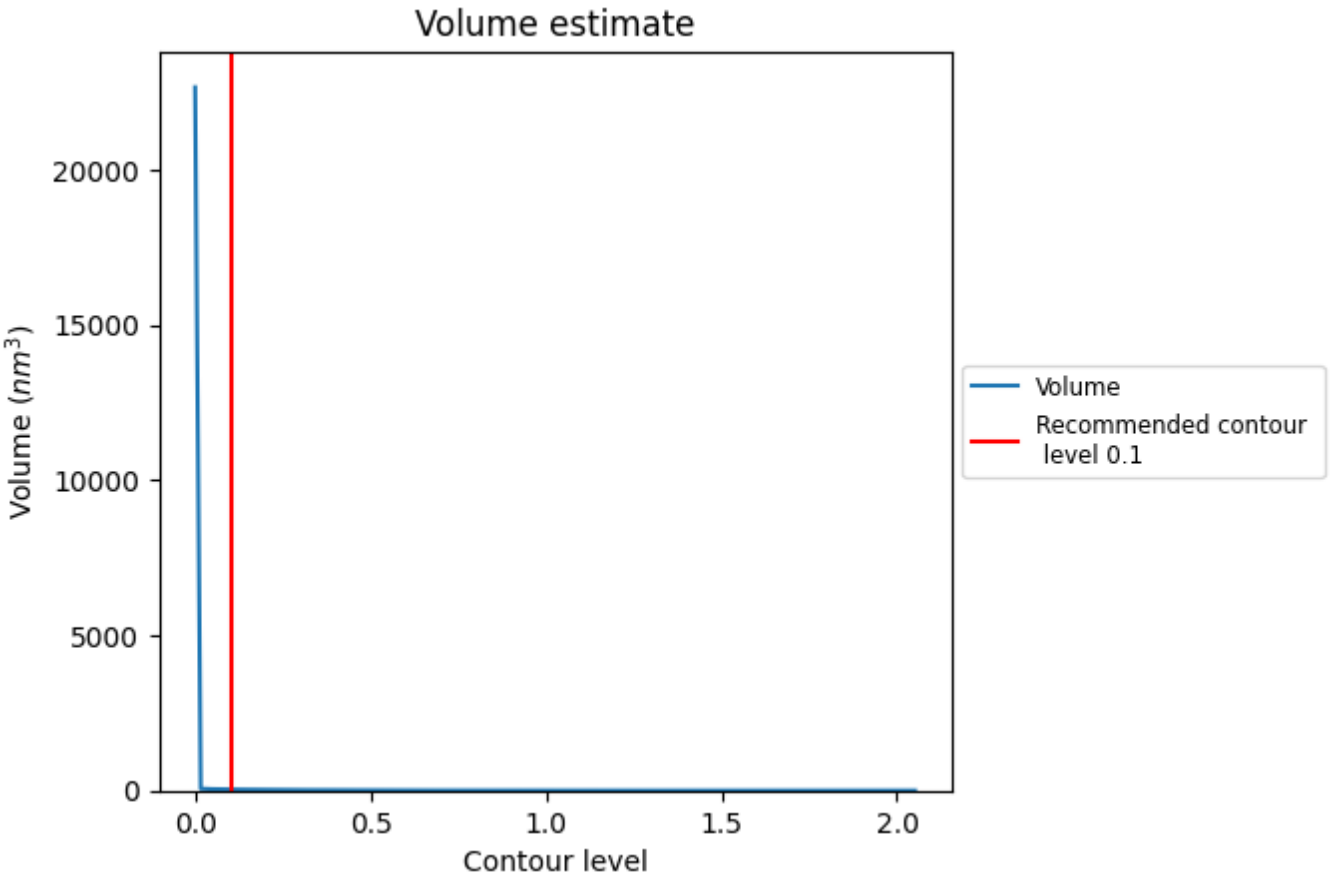
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

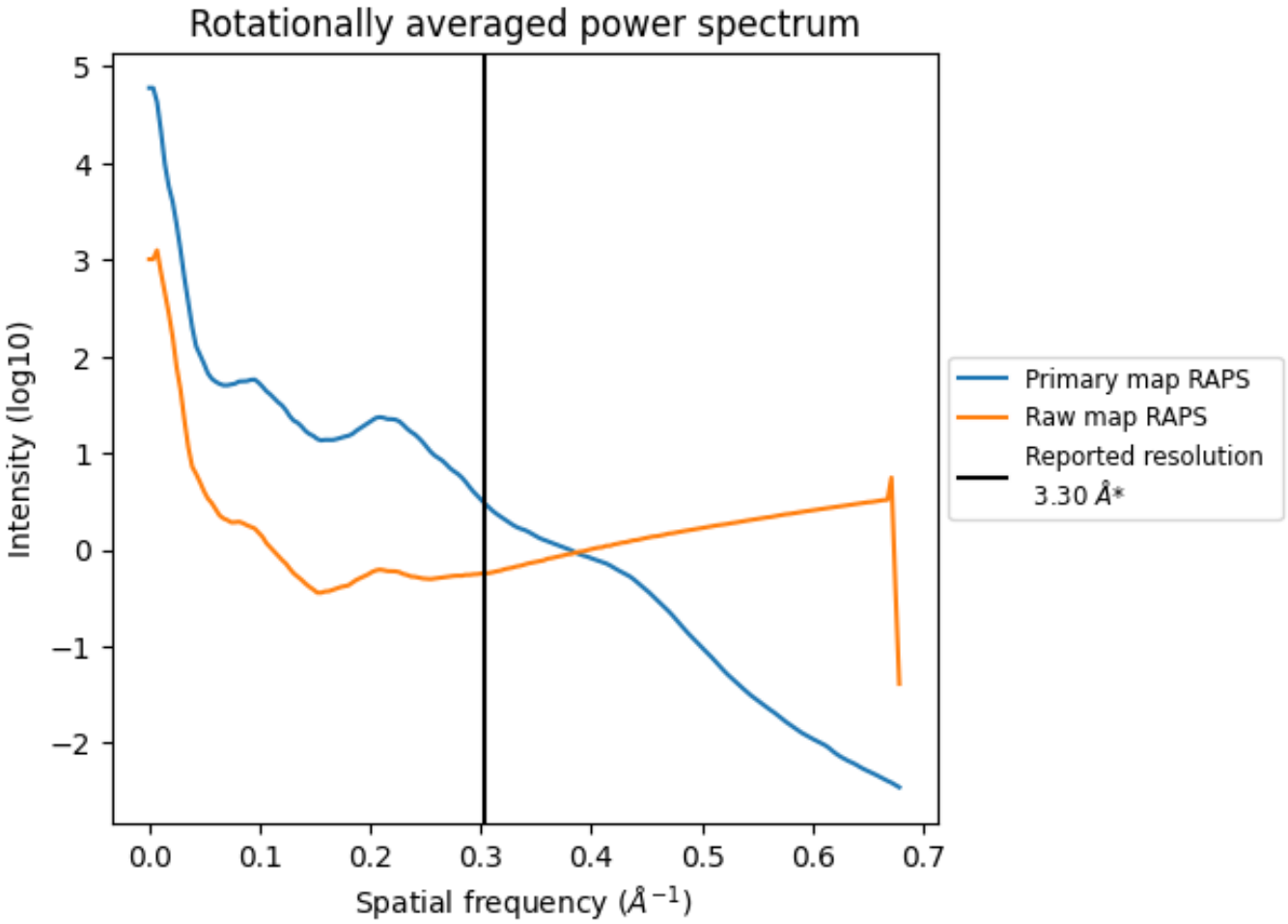
7.2 Volume estimate (i)



The volume at the recommended contour level is 36 nm^3; this corresponds to an approximate mass of 33 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 (i)

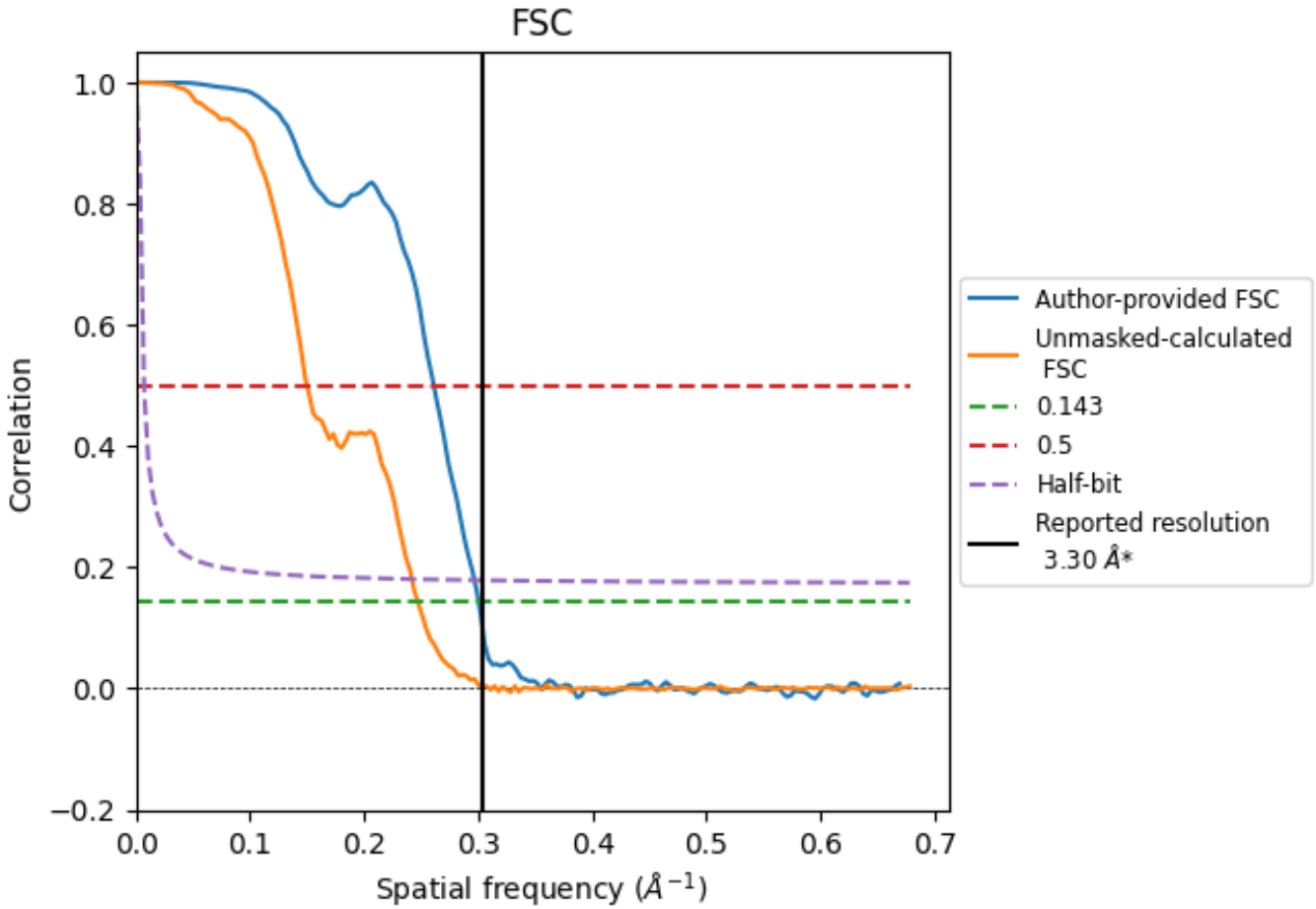


*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

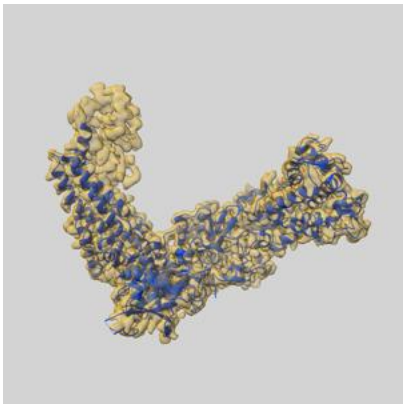
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.33	3.83	3.37
Unmasked-calculated*	4.05	6.68	4.13

*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 4.05 differs from the reported value 3.3 by more than 10 %

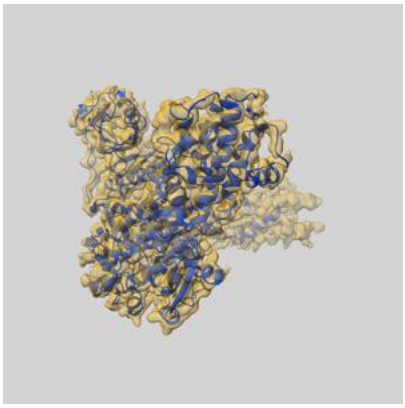
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-72190 and PDB model 9Q3E. Per-residue inclusion information can be found in section 3 on page 5.

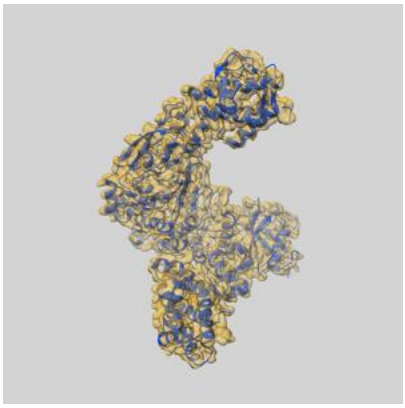
9.1 Map-model overlay



X



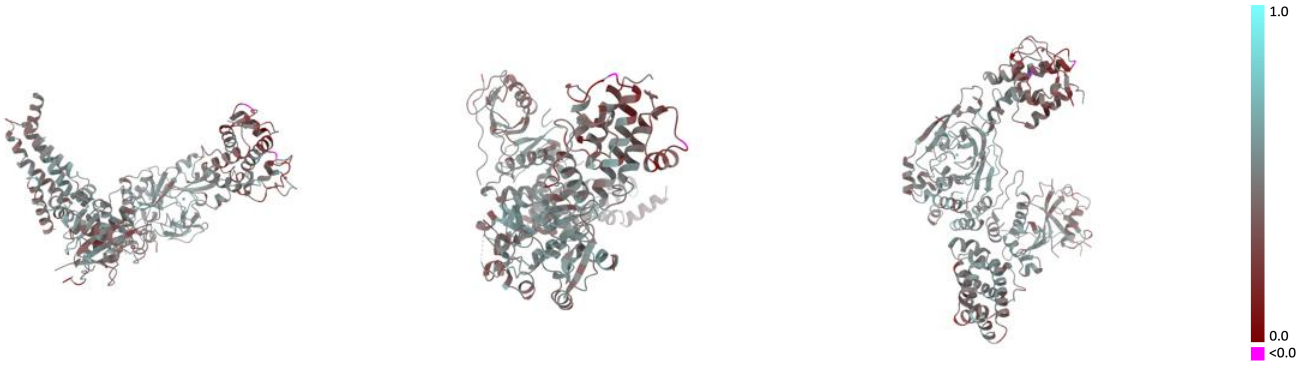
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

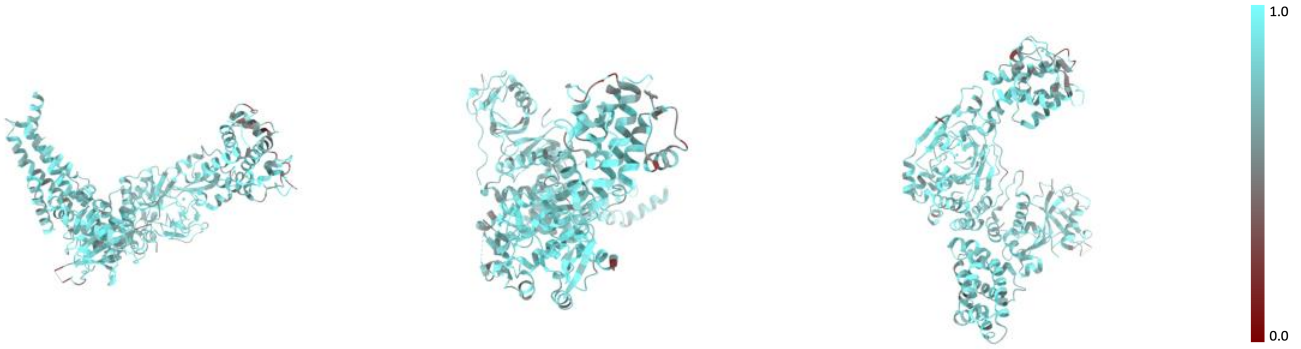
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

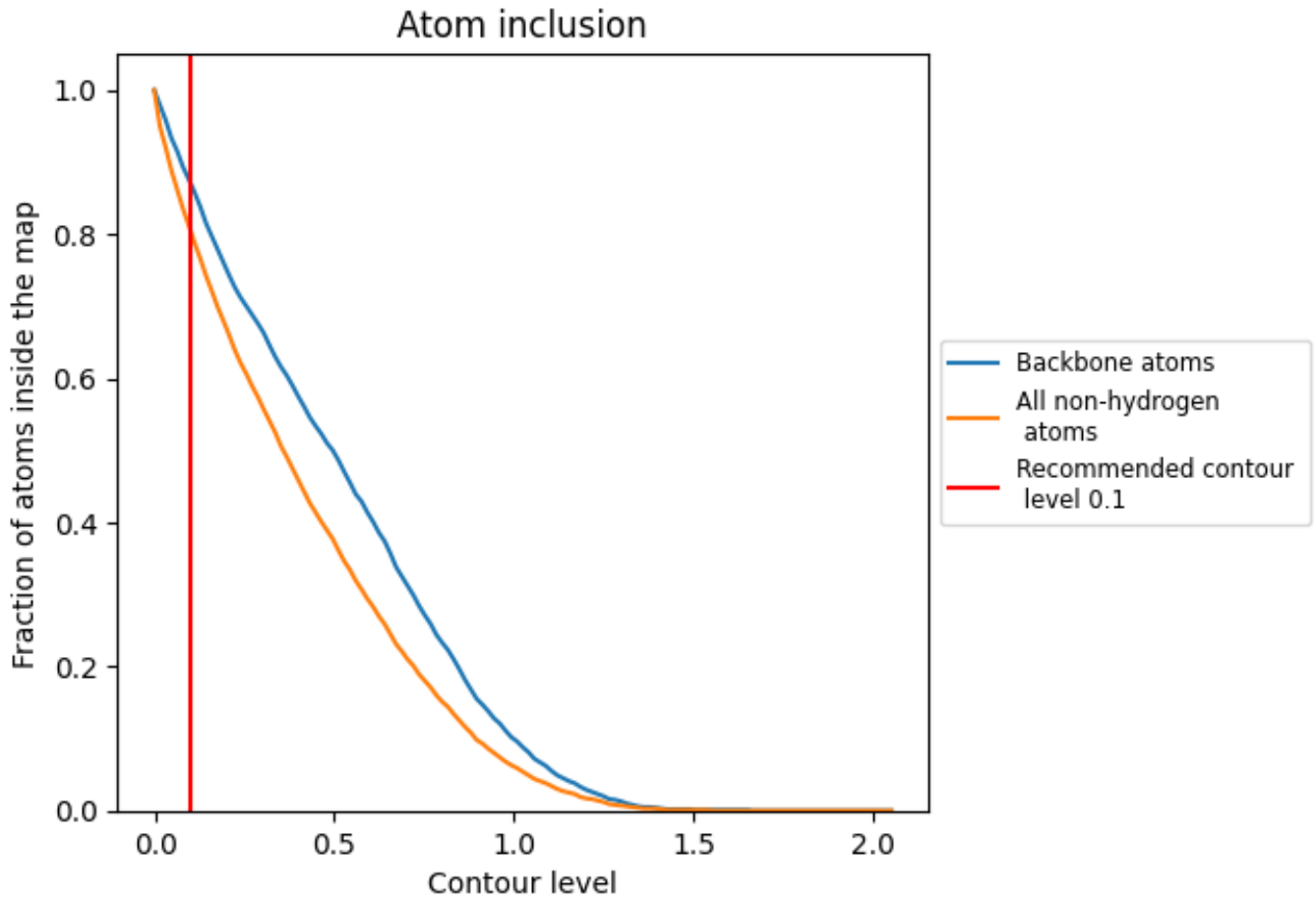
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.8040	0.4640
B	0.7640	0.4090
C	0.8170	0.4940
L	0.8080	0.4700
N	0.8070	0.4650