



wwPDB EM Validation Summary Report ⓘ

May 13, 2025 – 11:01 PM EDT

PDB ID : 8T9A / pdb_00008t9a
EMDB ID : EMD-41105
Title : CryoEM structure of human DDB1-DCAF12 in complex with MAGEA3
Authors : Duda, D.; Righetto, G.; Li, Y.; Loppnau, P.; Seitova, A.; Santhakumar, V.;
Halabelian, L.; Yin, Y.
Deposited on : 2023-06-23
Resolution : 3.17 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

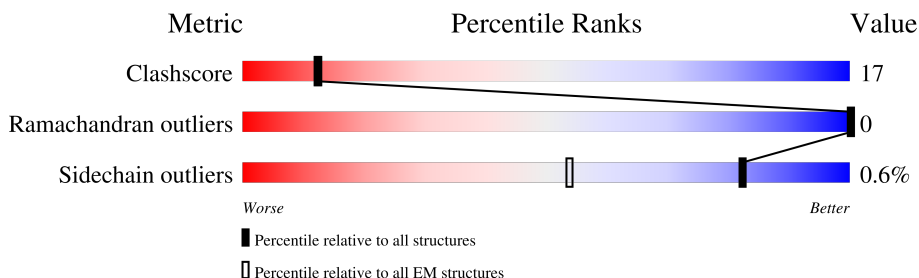
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.17 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1140	<div> <div>27%</div> <div>70%</div> <div>27%</div> <div>.</div> </div>
2	B	471	<div> <div>12%</div> <div>47%</div> <div>33%</div> <div>20%</div> </div>
3	C	212	<div> <div>98%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11785 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1114	Total	C	N	O	S	0	0
			8744	5540	1473	1683	48		

- Molecule 2 is a protein called DDB1- and CUL4-associated factor 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	379	Total	C	N	O	S	0	0
			2998	1905	529	553	11		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	initiating methionine	UNP Q5T6F0
B	-16	HIS	-	expression tag	UNP Q5T6F0
B	-15	HIS	-	expression tag	UNP Q5T6F0
B	-14	HIS	-	expression tag	UNP Q5T6F0
B	-13	HIS	-	expression tag	UNP Q5T6F0
B	-12	HIS	-	expression tag	UNP Q5T6F0
B	-11	HIS	-	expression tag	UNP Q5T6F0
B	-10	SER	-	expression tag	UNP Q5T6F0
B	-9	SER	-	expression tag	UNP Q5T6F0
B	-8	GLY	-	expression tag	UNP Q5T6F0
B	-7	ARG	-	expression tag	UNP Q5T6F0
B	-6	GLU	-	expression tag	UNP Q5T6F0
B	-5	ASN	-	expression tag	UNP Q5T6F0
B	-4	LEU	-	expression tag	UNP Q5T6F0
B	-3	TYR	-	expression tag	UNP Q5T6F0
B	-2	PHE	-	expression tag	UNP Q5T6F0
B	-1	GLN	-	expression tag	UNP Q5T6F0
B	0	GLY	-	expression tag	UNP Q5T6F0
B	131	GLN	ARG	variant	UNP Q5T6F0

- Molecule 3 is a protein called Melanoma-associated antigen 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	5	Total	C	N	O	0	0
			43	23	8	12		

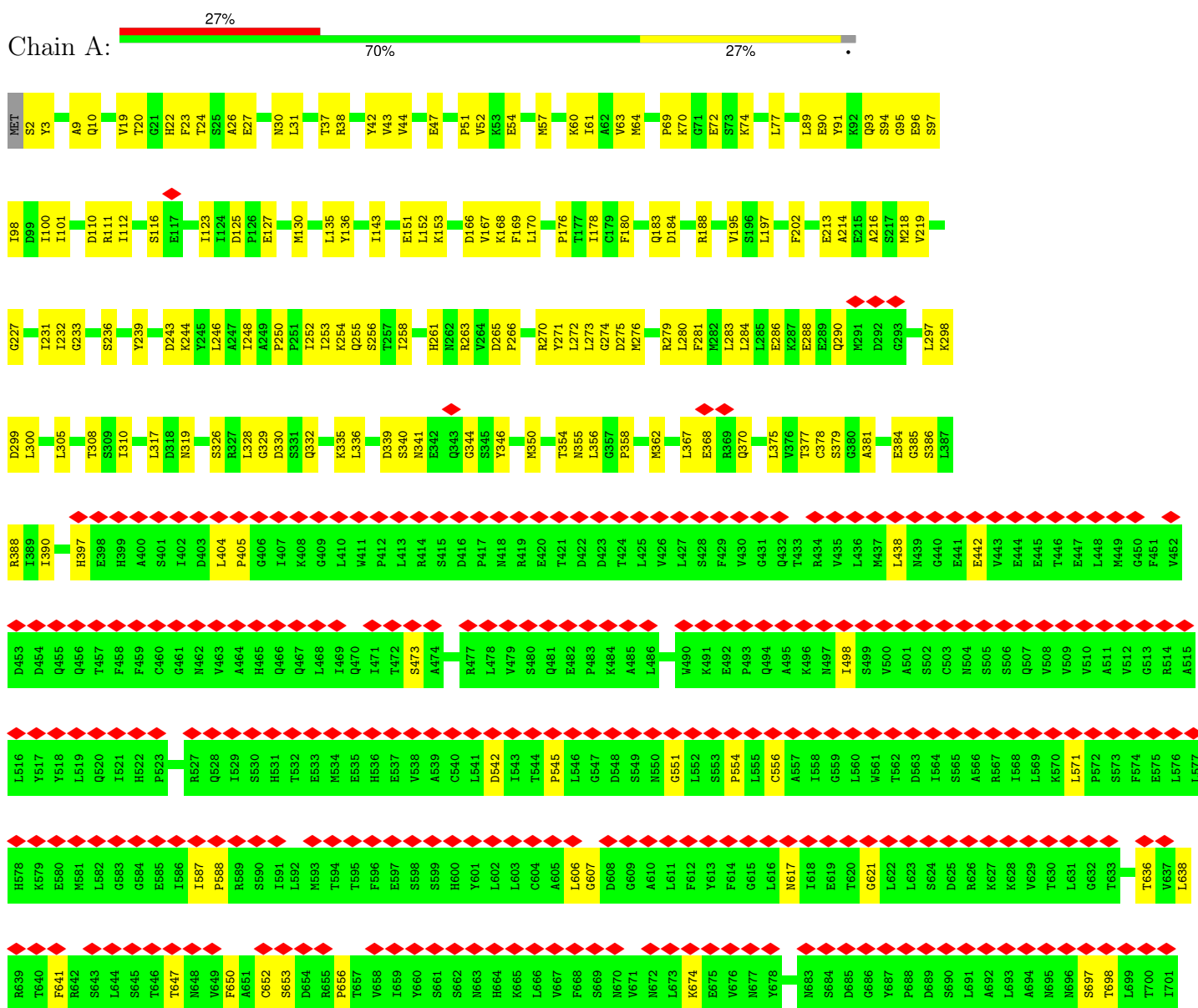
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	103	MET	-	initiating methionine	UNP P43357

3 Residue-property plots

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: DNA damage-binding protein 1





Tyr	Val	Leu	Glu	Met
	Lys	Leu	Glu	Phe
	Val	Ser	Leu	Gln
	Leu	Val	Met	Ala
	His	Leu	Glu	Ala
	His	Met	Val	Ser
	Val	Val	Arg	Ser
	Lys	Glu	Pro	Arg
	Ile	Glu	Ile	Lys
	Ser	Arg	Gly	Val
	Gly	Glu	His	Ala
	Gly	Glu	Leu	Ala
	Pro	Asp	Tyr	Leu
	Pro	Ser	Val	Leu
R310	Pro	Pro	Leu	
	Pro	Pro	Gly	
	Leu	Lys	Lys	
	His	Leu	Ser	
	Glu	Leu	Tyr	
	Trp	Thr	Ala	
	Val	Gln	Arg	
	Leu	His	Glu	
		Phe	Val	
		Val	Thr	
		Gln	Lys	
		Glu	Ala	
		Asn	Gln	
		Trp	Ile	
G312	Leu	Met	Leu	
		Pro	Gly	
		Lys	Ser	
		Ala	Val	
		Val	Val	
		Gln	Gly	
		Pro	Leu	
		Gly	Ile	
		Ser	Trp	
		Asp	Val	
		Pro	Leu	
		Ala	Ala	
		Trp	Gly	
		Gly	Val	
E313	Pro	Arg	Phe	
	Arg	Ala	Thr	
	Ala	Val	Ile	
	Val	Leu	Ala	
	Val	Glu	Val	
	Val	Glu	Val	
	Val	Glu	Gln	
	Val	Lys	Leu	
	Thr	Thr	Ile	
	Ser	Ser	Phe	
			Val	
			Ala	
			Thr	
			Met	
E314			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
			Val	
		Val		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	476215	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.362	Depositor
Minimum map value	-0.131	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.105	Depositor
Map size (Å)	242.688, 242.688, 242.688	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.948, 0.948, 0.948	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	A	0.51	0/8902	0.59	0/12056
2	B	0.38	0/3070	0.52	0/4163
3	C	0.33	0/42	0.56	0/52
All	All	0.48	0/12014	0.57	0/16271

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	8744	0	8715	226	0
2	B	2998	0	2950	122	0
3	C	43	0	33	1	0
All	All	11785	0	11698	345	0

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

The worst 5 of 345 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:GLU:HB2	1:A:298:LYS:HB2	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:588:PRO:HA	1:A:606:LEU:HA	1.58	0.86
1:A:851:PHE:HB3	1:A:860:THR:HA	1.59	0.84
1:A:617:ASN:O	1:A:621:GLY:N	2.13	0.82
1:A:743:GLN:HG2	1:A:749:THR:HG22	1.61	0.81

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	A	1104/1140 (97%)	961 (87%)	143 (13%)	0	100	100
2	B	369/471 (78%)	312 (85%)	57 (15%)	0	100	100
3	C	3/212 (1%)	0	3 (100%)	0	100	100
All	All	1476/1823 (81%)	1273 (86%)	203 (14%)	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	A	979/999 (98%)	973 (99%)	6 (1%)	84	92
2	B	329/403 (82%)	328 (100%)	1 (0%)	91	95
3	C	4/183 (2%)	3 (75%)	1 (25%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1312/1585 (83%)	1304 (99%)	8 (1%)	82 92

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	314	GLU
2	B	323	ASP
1	A	848	ILE
1	A	831	VAL
1	A	883	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	224	HIS
2	B	144	HIS
1	A	1055	GLN
2	B	102	GLN
1	A	1009	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

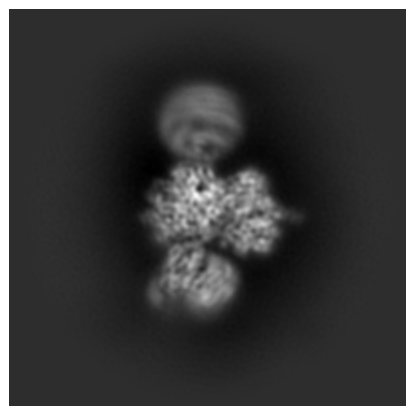
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41105. These allow visual inspection of the internal detail of the map and identification of artifacts.

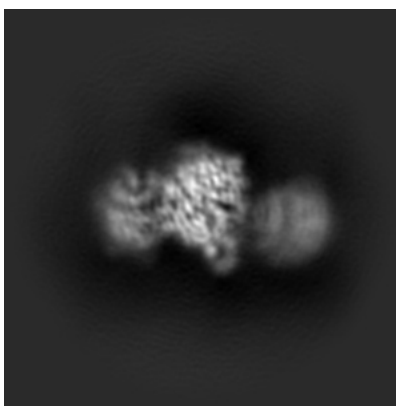
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

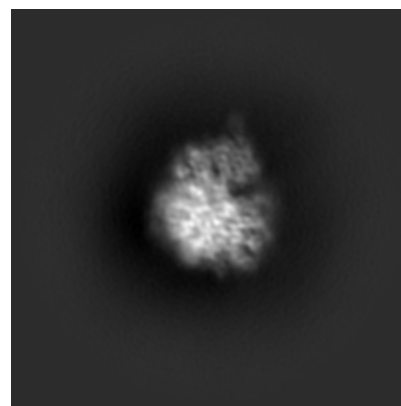
6.1.1 Primary map



X

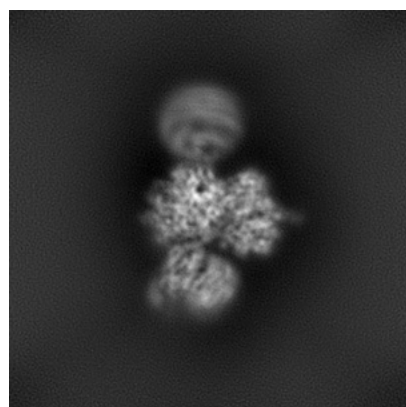


Y

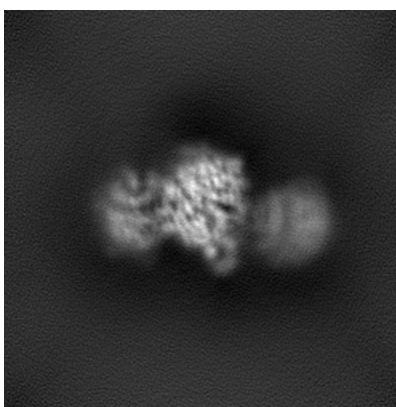


Z

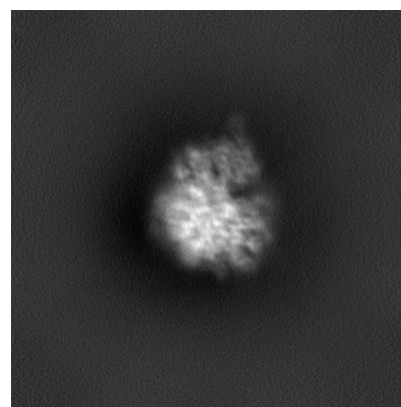
6.1.2 Raw map



X



Y

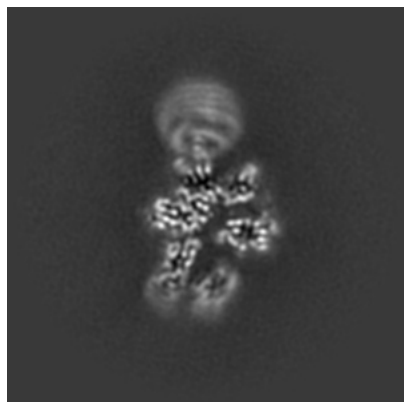


Z

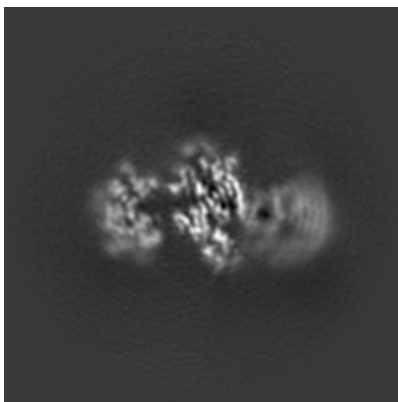
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

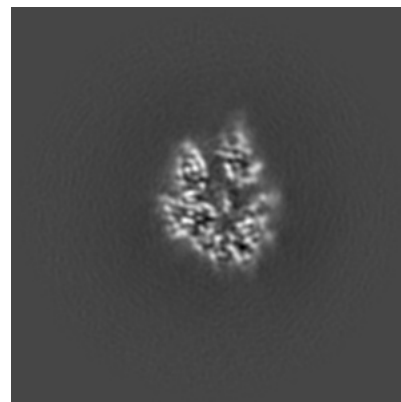
6.2.1 Primary map



X Index: 128



Y Index: 128

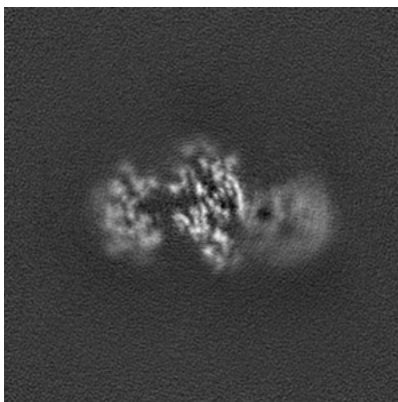


Z Index: 128

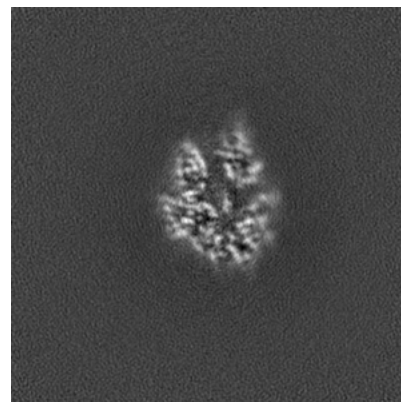
6.2.2 Raw map



X Index: 128



Y Index: 128

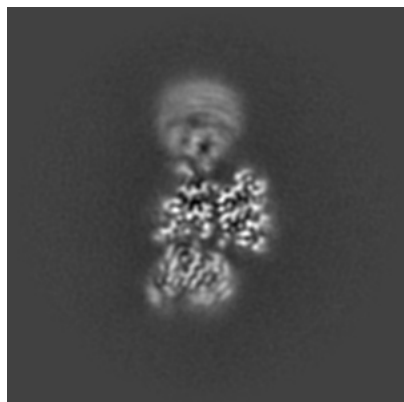


Z Index: 128

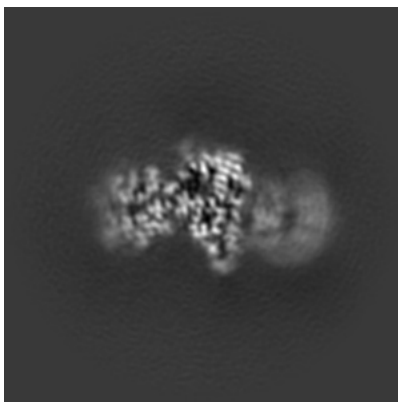
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

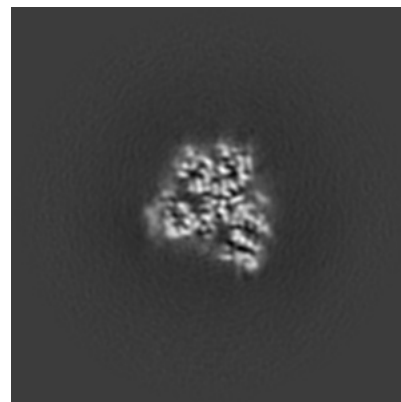
6.3.1 Primary map



X Index: 120

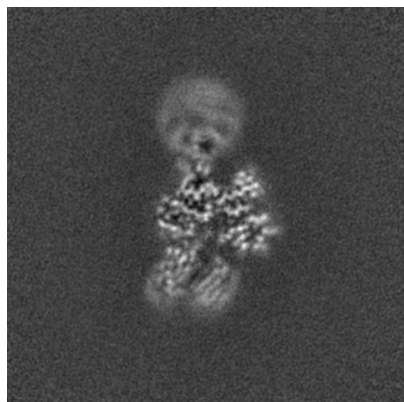


Y Index: 118

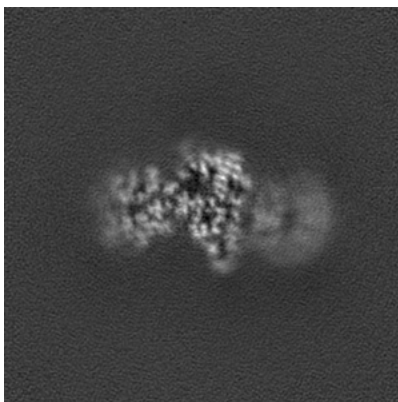


Z Index: 135

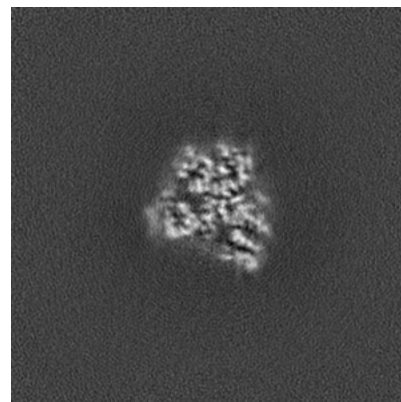
6.3.2 Raw map



X Index: 124



Y Index: 118



Z Index: 135

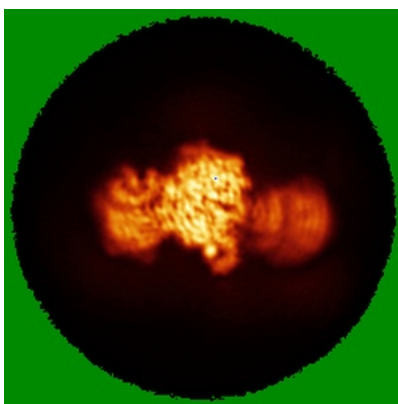
The images above show the largest variance slices of the map in three orthogonal directions.

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

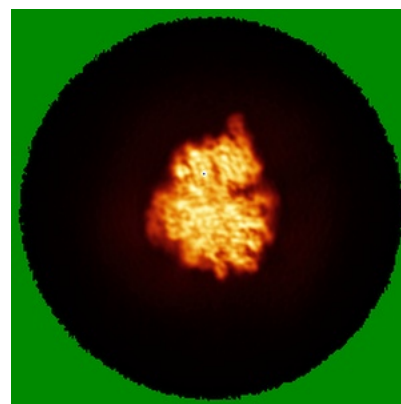
6.4.1 Primary map



X



Y

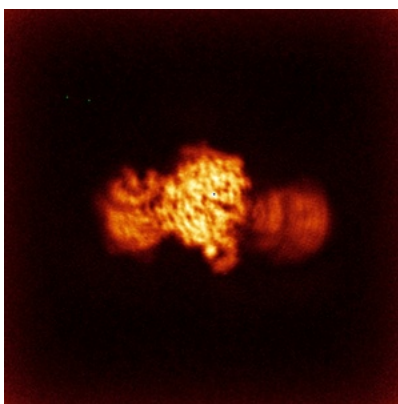


Z

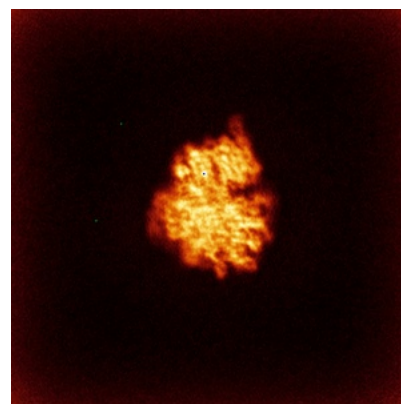
6.4.2 Raw map



X



Y

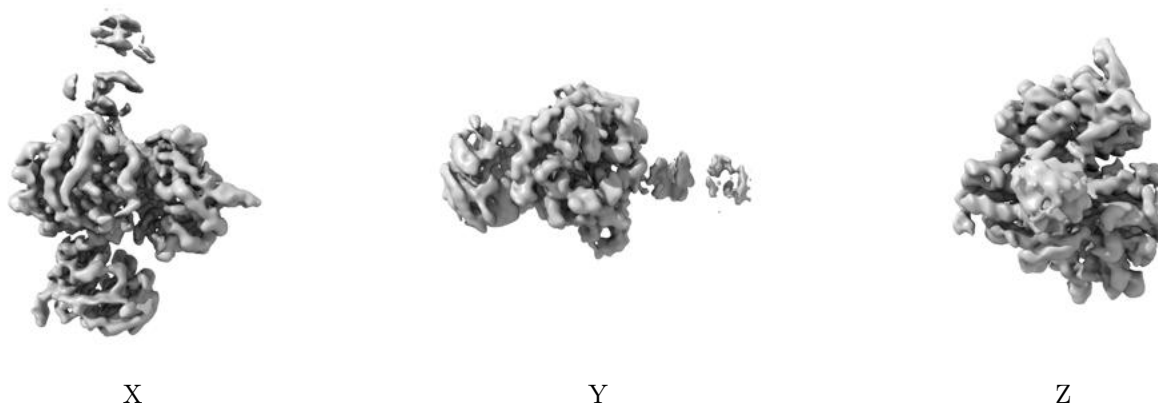


Z

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.

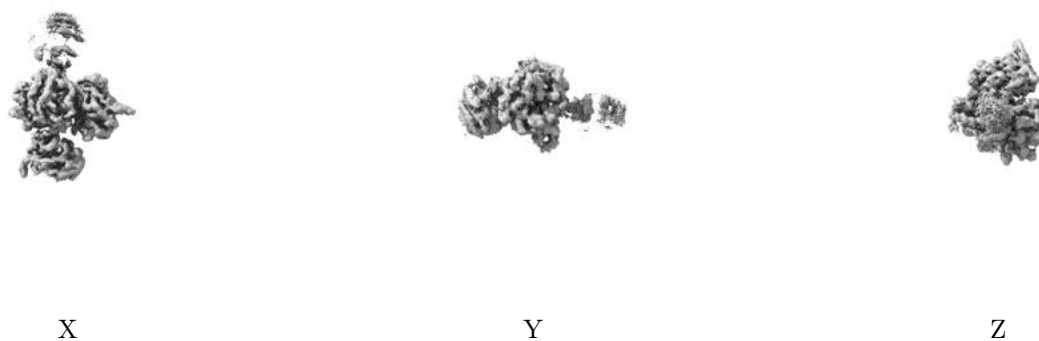
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.105. 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.

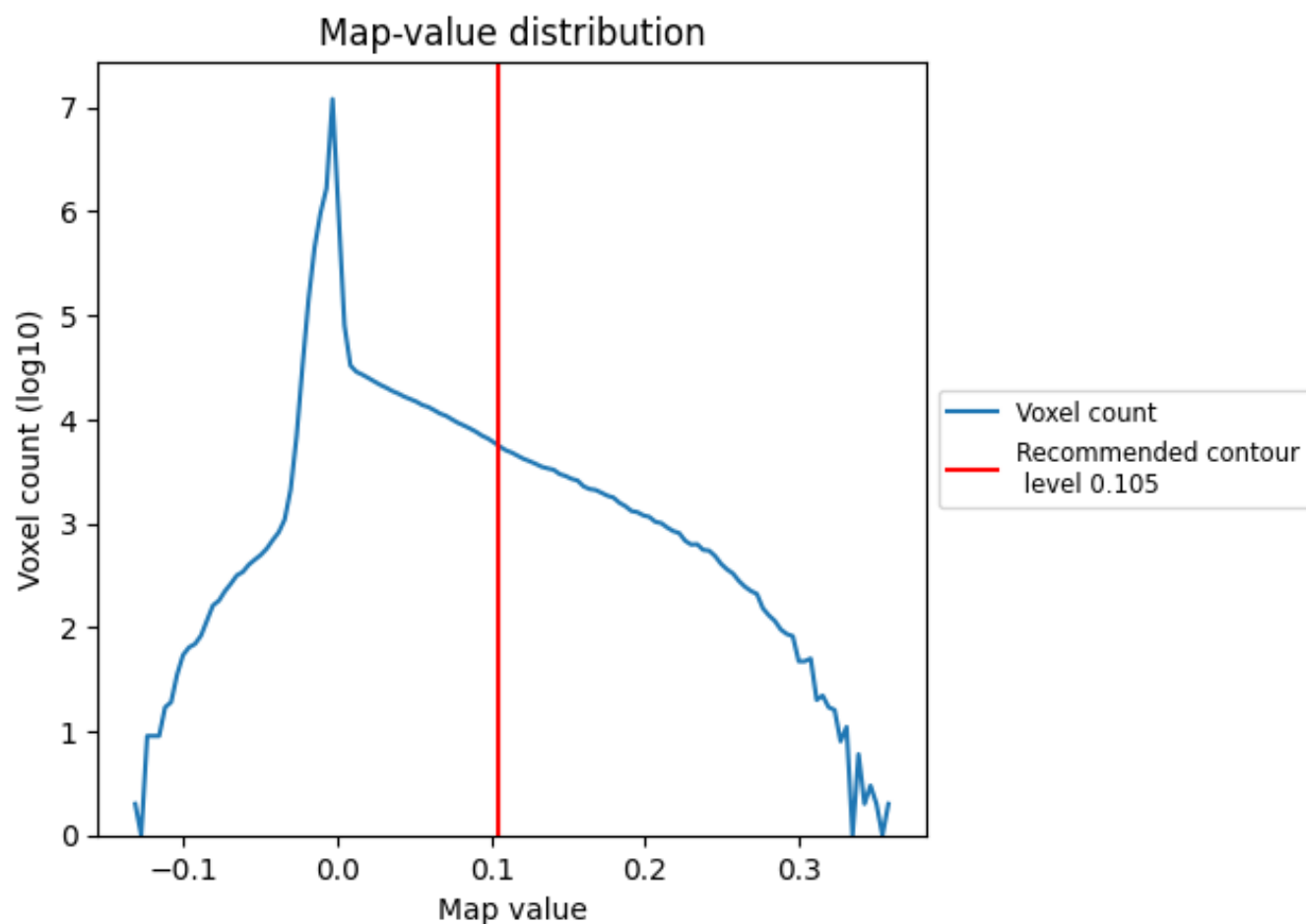
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

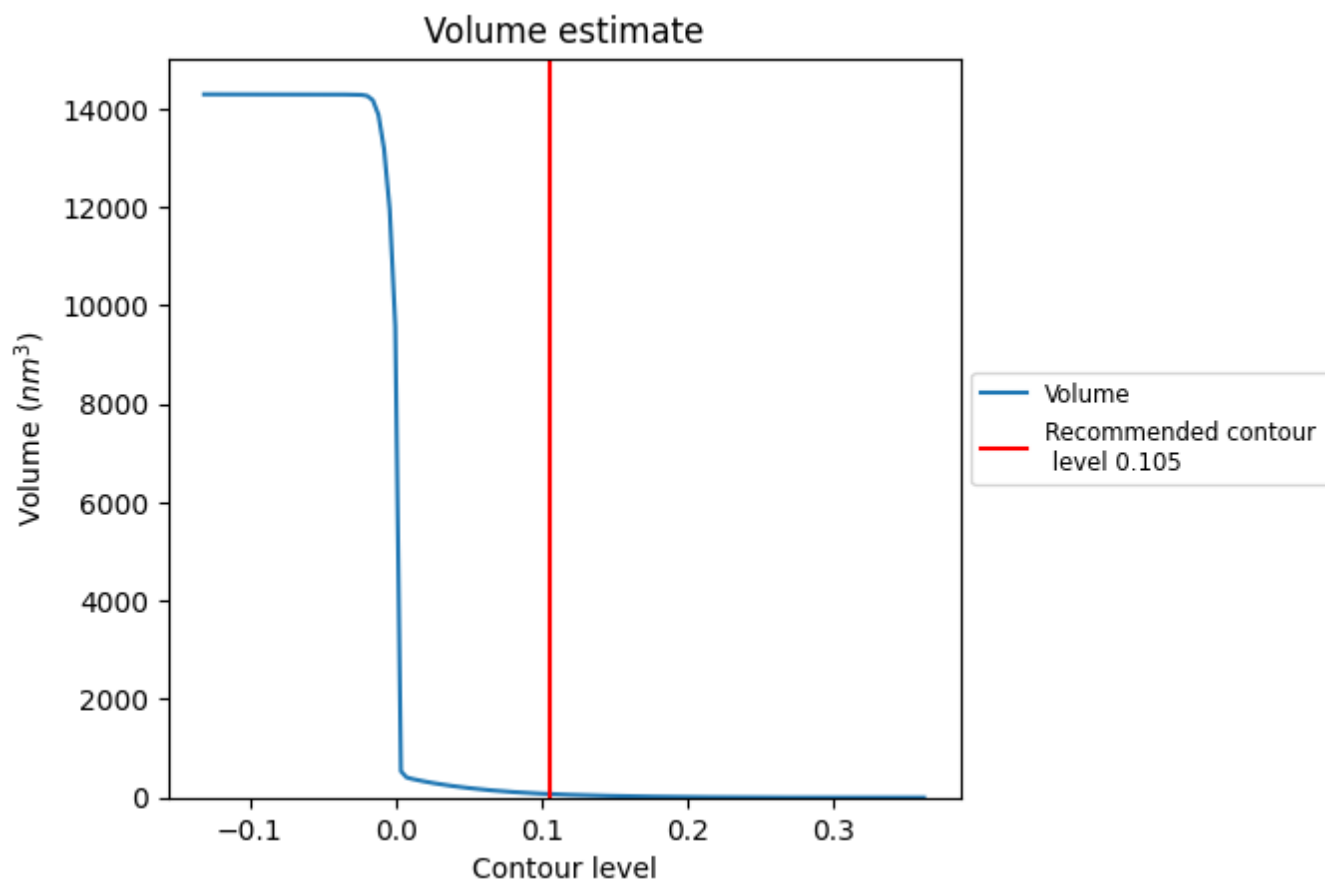
This section contains the results of statistical analysis of the map.

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.

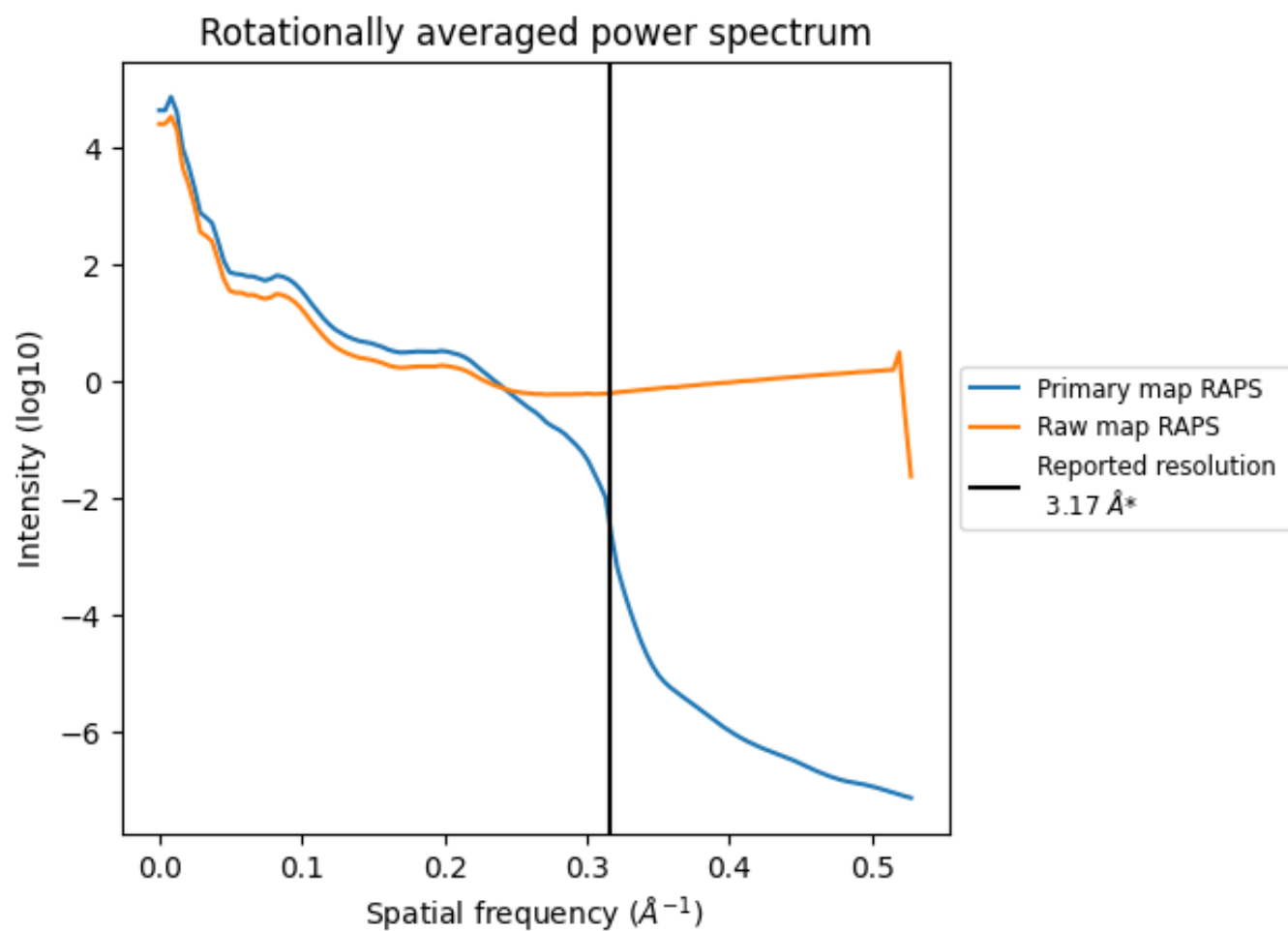
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72 nm³; this corresponds to an approximate mass of 65 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 ⓘ

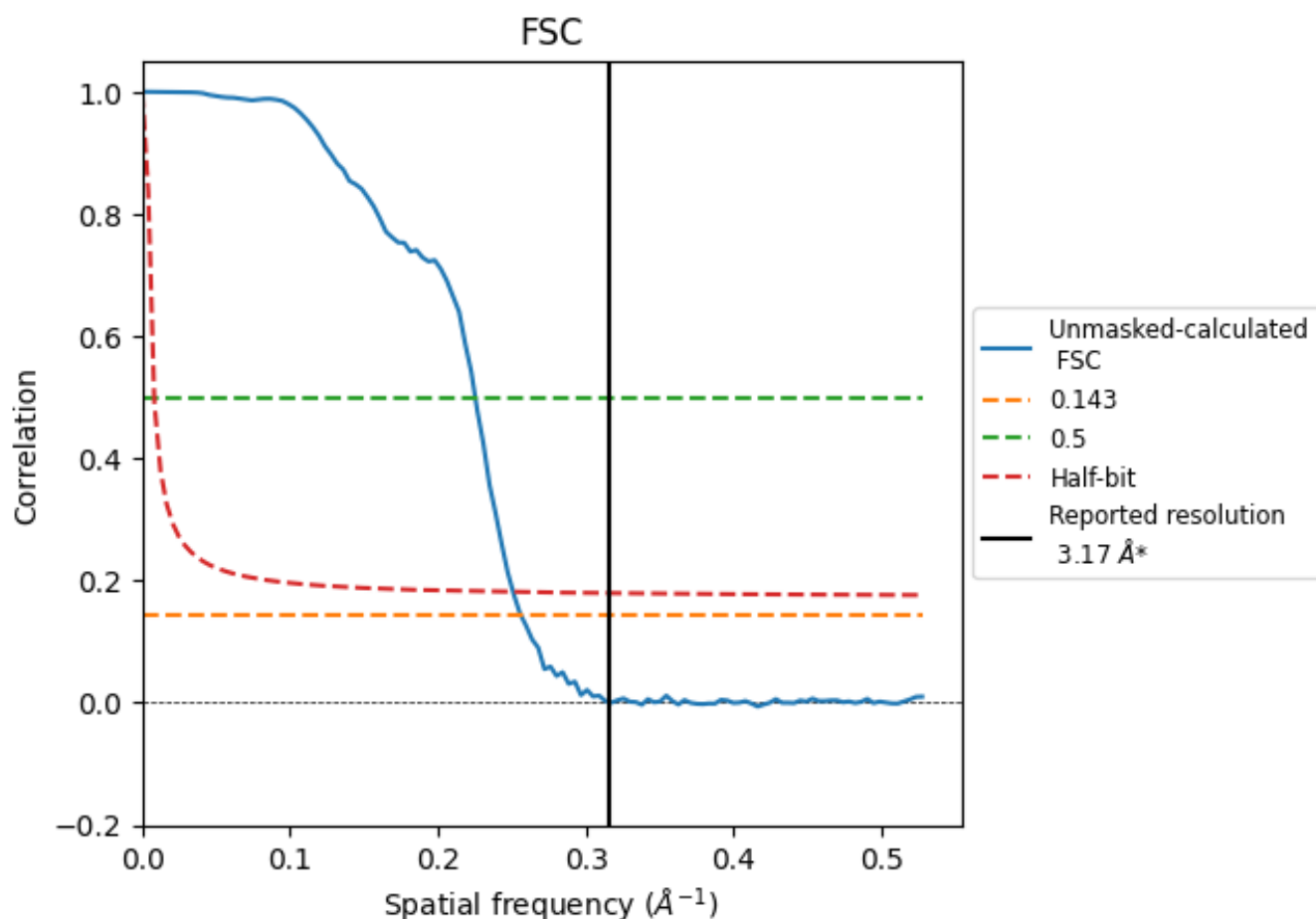


*Reported resolution corresponds to spatial frequency of 0.315 \AA^{-1}

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 0.315 Å⁻¹

8.2 Resolution estimates [i](#)

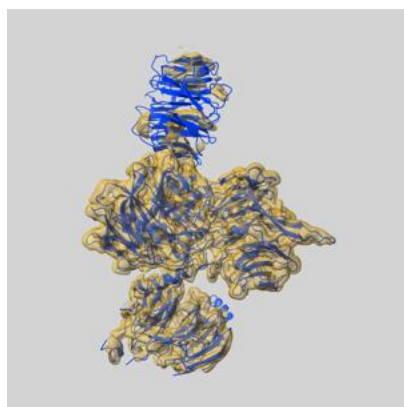
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.17	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.91	4.44	3.99

*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 3.91 differs from the reported value 3.17 by more than 10 %

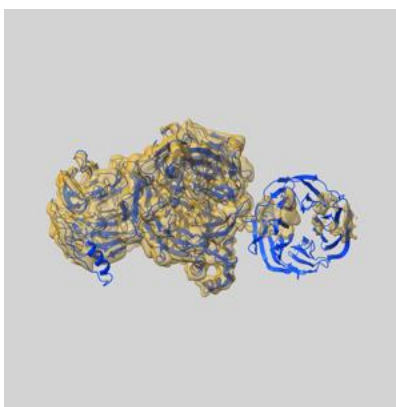
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41105 and PDB model 8T9A. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

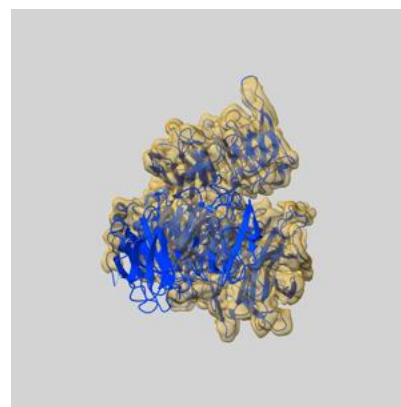
9.1 Map-model overlay [i](#)



X



Y



Z

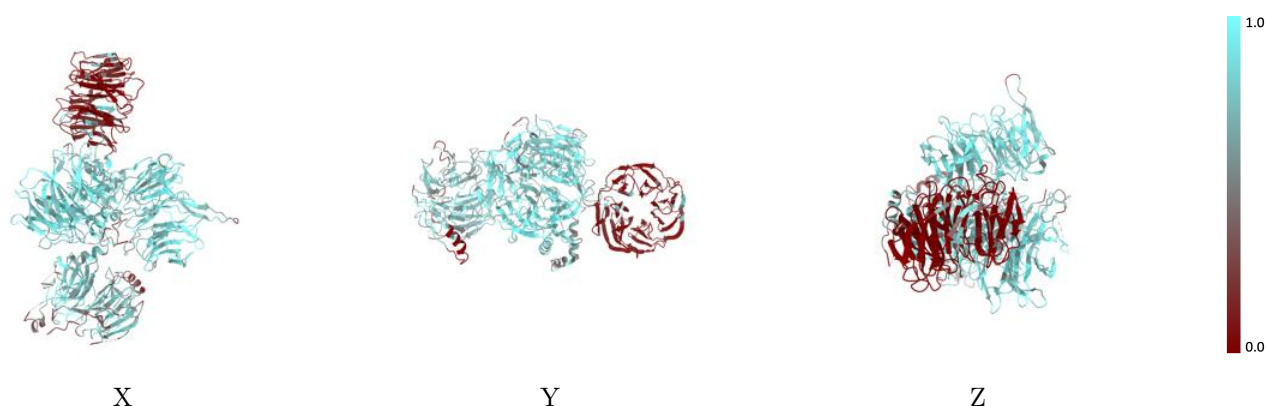
The images above show the 3D surface view of the map at the recommended contour level 0.105 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



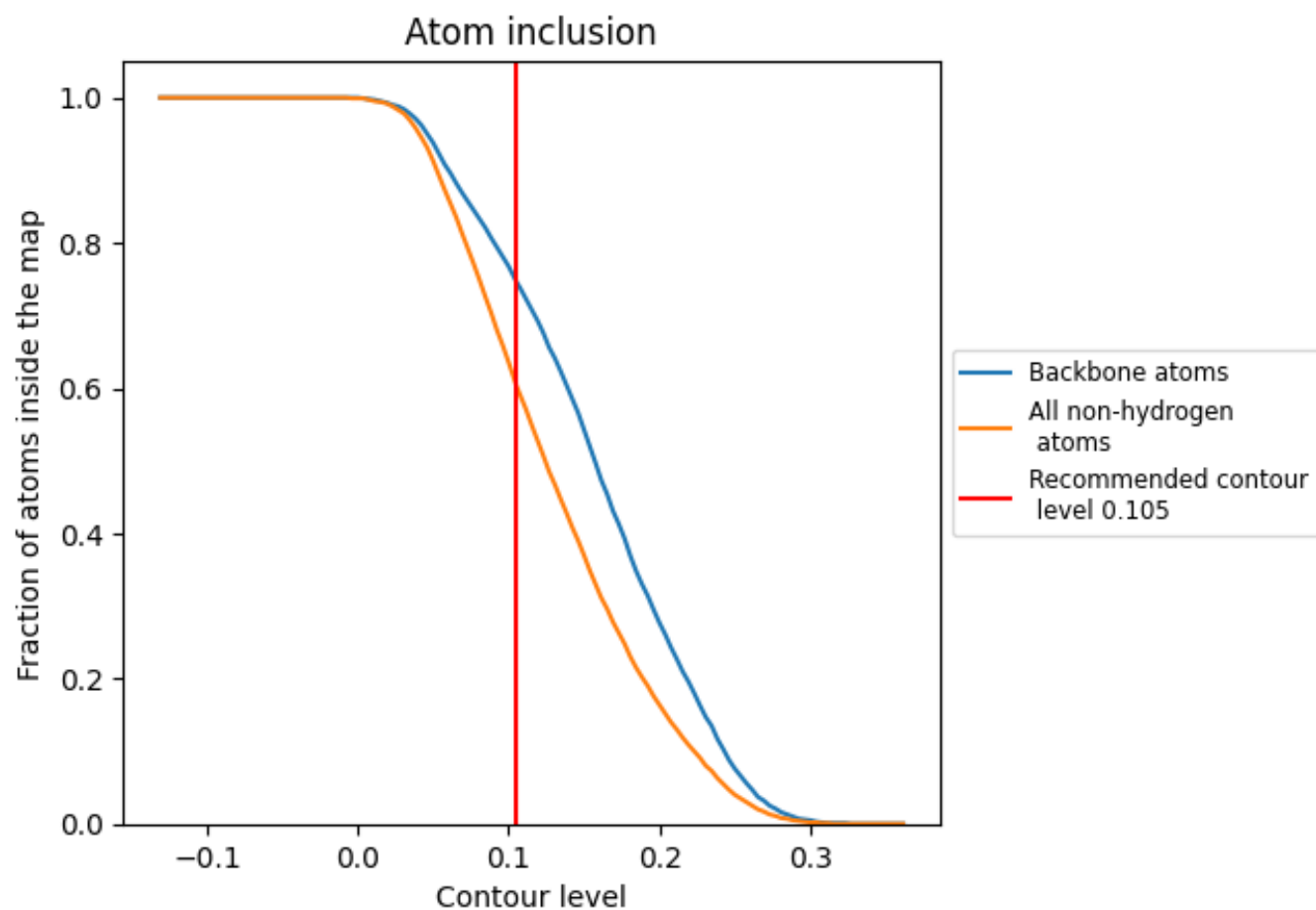
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.105).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 60% 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 (0.105) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6040	<div></div> 0.3860
A	<div></div> 0.5940	<div></div> 0.3760
B	<div></div> 0.6400	<div></div> 0.4140
C	<div></div> 0.1460	<div></div> 0.2650

