



Full wwPDB EM Validation Report ⓘ

Mar 25, 2025 – 12:20 pm GMT

PDB ID : 8QTB
EMDB ID : EMD-18648
Title : MUC5AC D'D3CysD1 domains. SNP rs36189285: Arg996Gln.
Authors : Trillo-Muyo, S.; Hansson, G.C.
Deposited on : 2023-10-12
Resolution : 2.94 Å(reported)
Based on initial model : .

This is a Full wwPDB EM Validation 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.dev117
MolProbity : 4.02b-467
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) : 2.41.5

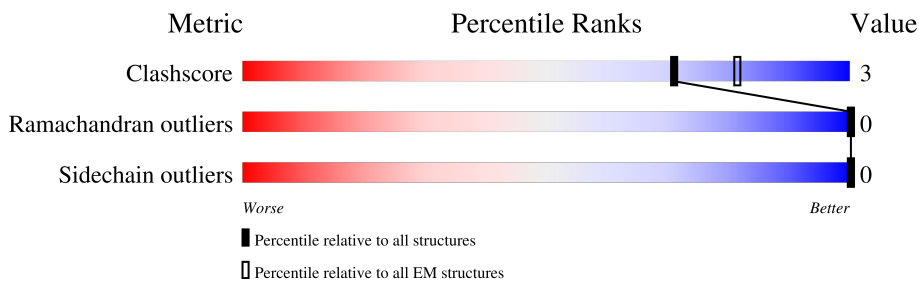
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY



The reported resolution of this entry is 2.94 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	722	
1	B	722	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5050 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 Mucin-5AC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	331	Total	C	N	O	S	0	0
			2524	1580	425	486	33		
1	B	331	Total	C	N	O	S	0	0
			2524	1580	425	486	33		

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	778	ASP	-	expression tag	UNP P98088
A	779	ALA	-	expression tag	UNP P98088
A	780	ALA	-	expression tag	UNP P98088
A	781	GLN	-	expression tag	UNP P98088
A	782	PRO	-	expression tag	UNP P98088
A	783	ALA	-	expression tag	UNP P98088
A	784	ARG	-	expression tag	UNP P98088
A	785	ARG	-	expression tag	UNP P98088
A	786	ALA	-	expression tag	UNP P98088
A	787	VAL	-	expression tag	UNP P98088
A	788	ARG	-	expression tag	UNP P98088
A	789	SER	-	expression tag	UNP P98088
A	790	SER	-	expression tag	UNP P98088
A	791	ARG	-	expression tag	UNP P98088
A	792	HIS	-	expression tag	UNP P98088
A	793	HIS	-	expression tag	UNP P98088
A	794	HIS	-	expression tag	UNP P98088
A	795	HIS	-	expression tag	UNP P98088
A	796	HIS	-	expression tag	UNP P98088
A	797	HIS	-	expression tag	UNP P98088
A	798	GLY	-	expression tag	UNP P98088
A	799	SER	ALA	conflict	UNP P98088
A	996	GLN	ARG	engineered mutation	UNP P98088
A	1482	THR	SER	conflict	UNP P98088
A	1483	SER	THR	conflict	UNP P98088
A	1484	GLU	SER	conflict	UNP P98088

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1485	GLN	SER	conflict	UNP P98088
A	1486	LYS	SER	conflict	UNP P98088
A	1487	LEU	-	expression tag	UNP P98088
A	1488	ILE	-	expression tag	UNP P98088
A	1489	SER	-	expression tag	UNP P98088
A	1490	GLU	-	expression tag	UNP P98088
A	1491	GLU	-	expression tag	UNP P98088
A	1492	ASP	-	expression tag	UNP P98088
A	1493	LEU	-	expression tag	UNP P98088
A	1494	SER	-	expression tag	UNP P98088
A	1495	ARG	-	expression tag	UNP P98088
A	1496	LYS	-	expression tag	UNP P98088
A	1497	LEU	-	expression tag	UNP P98088
A	1498	THR	-	expression tag	UNP P98088
A	1499	ARG	-	expression tag	UNP P98088
B	778	ASP	-	expression tag	UNP P98088
B	779	ALA	-	expression tag	UNP P98088
B	780	ALA	-	expression tag	UNP P98088
B	781	GLN	-	expression tag	UNP P98088
B	782	PRO	-	expression tag	UNP P98088
B	783	ALA	-	expression tag	UNP P98088
B	784	ARG	-	expression tag	UNP P98088
B	785	ARG	-	expression tag	UNP P98088
B	786	ALA	-	expression tag	UNP P98088
B	787	VAL	-	expression tag	UNP P98088
B	788	ARG	-	expression tag	UNP P98088
B	789	SER	-	expression tag	UNP P98088
B	790	SER	-	expression tag	UNP P98088
B	791	ARG	-	expression tag	UNP P98088
B	792	HIS	-	expression tag	UNP P98088
B	793	HIS	-	expression tag	UNP P98088
B	794	HIS	-	expression tag	UNP P98088
B	795	HIS	-	expression tag	UNP P98088
B	796	HIS	-	expression tag	UNP P98088
B	797	HIS	-	expression tag	UNP P98088
B	798	GLY	-	expression tag	UNP P98088
B	799	SER	ALA	conflict	UNP P98088
B	996	GLN	ARG	engineered mutation	UNP P98088
B	1482	THR	SER	conflict	UNP P98088
B	1483	SER	THR	conflict	UNP P98088
B	1484	GLU	SER	conflict	UNP P98088
B	1485	GLN	SER	conflict	UNP P98088

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1486	LYS	SER	conflict	UNP P98088
B	1487	LEU	-	expression tag	UNP P98088
B	1488	ILE	-	expression tag	UNP P98088
B	1489	SER	-	expression tag	UNP P98088
B	1490	GLU	-	expression tag	UNP P98088
B	1491	GLU	-	expression tag	UNP P98088
B	1492	ASP	-	expression tag	UNP P98088
B	1493	LEU	-	expression tag	UNP P98088
B	1494	SER	-	expression tag	UNP P98088
B	1495	ARG	-	expression tag	UNP P98088
B	1496	LYS	-	expression tag	UNP P98088
B	1497	LEU	-	expression tag	UNP P98088
B	1498	THR	-	expression tag	UNP P98088
B	1499	ARG	-	expression tag	UNP P98088

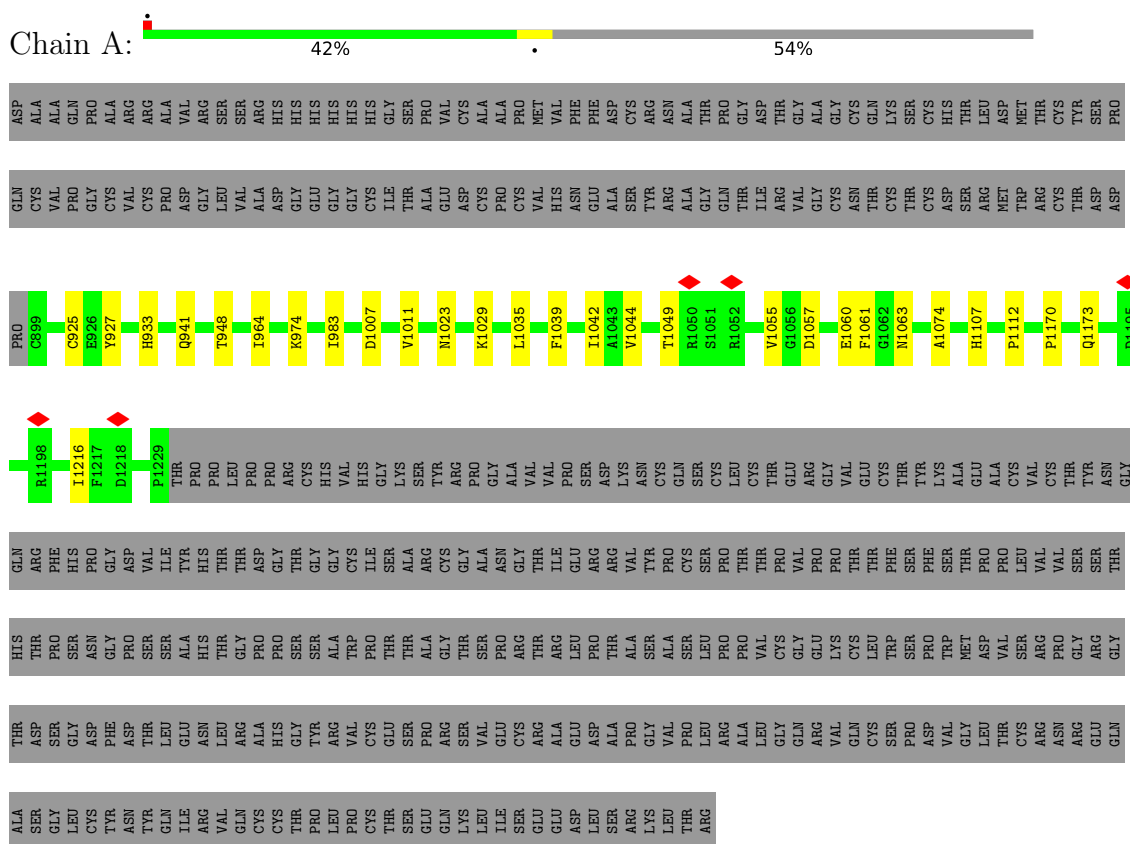
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Ca 1 1	0
2	B	1	Total Ca 1 1	0

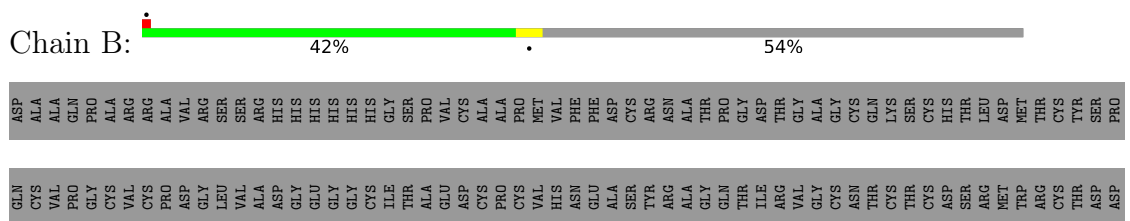
3 Residue-property plots

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: Mucin-5AC



• Molecule 1: Mucin-5AC



PRO	C899	C925	E926	Y927	H933	Q941	T948	K962	A963	I964	K974	I983	D1007	V1011	N1023	K1029	F1039	T1049	R1050	S1051	R1052	V1055	G1056	D1057	E1060	F1061	G1062	N1063	A1074	H1107	P1112	P1170	Q1173	D1195	R1198	D1218									
THR	PRO	PRO	LEU	PRO	PRO	ARG	CYS	HIS	VAL	HIS	GLY	LYS	TYR	ARG	PRO	GLY	ALA	VAL	VAL	PRO	ASP	LYS	ASN	CYS	GLN	PRO	CYS	THR	TYR	LYS	ALA	GLU	ALA	CYS	VAL	CYS	THR	ASN	GLY	GLN	ARG	PHE	HIS	PRO	GLY
ASP	VAL	THR	ILE	TYR	HIS	ASN	THR	THR	GLY	ASP	THR	THR	GLY	GLY	ALA	TRP	ALA	ARG	GLY	THR	GLY	ALA	THR	PRO	ASP	THR	THR	PHE	THR	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	SER	SER	ALA	ALA	HIS	THR	THR	GLY	PRO	PRO	SER	THR	TYR	SER	ALA	TRP	ALA	ARG	GLY	THR	GLY	ALA	THR	PRO	ASP	THR	THR	PHE	THR	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASP	THR	LEU	GLU	ASN	ARG	LEU	VAL	ARG	ALA	HIS	THR	THR	GLY	PRO	PRO	ASP	THR	ALA	ARG	GLY	THR	GLY	ALA	THR	PRO	ASP	THR	THR	PHE	THR	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	TYR	GLN	ILE	ARG	VAL	GLN	CYS	CYS	CYS	THR	PRO	LEU	THR	PRO	LEU	LEU	ARG	ALA	ALA	VAL	GLY	GLN	ARG	VAL	VAL	GLN	CYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	426711	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 ($e^-/\text{\AA}^2$)	1.29	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.392	Depositor
Minimum map value	-0.171	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	220.16, 220.16, 220.16	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.24	0/2590	0.45	0/3526
1	B	0.24	0/2590	0.45	0/3526
All	All	0.24	0/5180	0.45	0/7052

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

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	2524	0	2355	17	0
1	B	2524	0	2355	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	5050	0	4710	32	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.

All (32) 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:948:THR:HG22	1:A:964:ILE:HG12	1.86	0.58
1:A:933:HIS:NE2	1:A:941:GLN:O	2.37	0.57
1:B:948:THR:HG22	1:B:964:ILE:HG12	1.86	0.57
1:A:1055:VAL:HG12	1:A:1057:ASP:H	1.71	0.56
1:A:1049:THR:HG22	1:A:1061:PHE:HA	1.88	0.56
1:B:1049:THR:HG22	1:B:1061:PHE:HA	1.88	0.56
1:A:1063:ASN:HD21	1:A:1074:ALA:HB3	1.70	0.55
1:B:933:HIS:NE2	1:B:941:GLN:O	2.37	0.55
1:B:1063:ASN:HD21	1:B:1074:ALA:HB3	1.70	0.55
1:B:1055:VAL:HG12	1:B:1057:ASP:H	1.70	0.55
1:A:974:LYS:HB2	1:A:983:ILE:HD11	1.92	0.52
1:B:974:LYS:HB2	1:B:983:ILE:HD11	1.92	0.51
1:A:1107:HIS:CD2	1:A:1112:PRO:HG3	2.49	0.47
1:B:1107:HIS:CD2	1:B:1112:PRO:HG3	2.49	0.47
1:A:1007:ASP:OD1	1:A:1007:ASP:N	2.45	0.46
1:B:1170:PRO:HG2	1:B:1173:GLN:HB2	1.98	0.46
1:A:1170:PRO:HG2	1:A:1173:GLN:HB2	1.98	0.45
1:A:1011:VAL:HG23	1:A:1023:ASN:HB2	2.00	0.44
1:B:1011:VAL:HG23	1:B:1023:ASN:HB2	2.00	0.44
1:B:925:CYS:HB3	1:B:927:TYR:CZ	2.53	0.43
1:B:1007:ASP:OD1	1:B:1007:ASP:N	2.45	0.43
1:A:1029:LYS:HE3	1:A:1029:LYS:HB2	1.81	0.43
1:A:925:CYS:HB3	1:A:927:TYR:CZ	2.53	0.43
1:B:1029:LYS:HE3	1:B:1029:LYS:HB2	1.82	0.42
1:B:1029:LYS:HG3	1:B:1039:PHE:O	2.20	0.42
1:A:1029:LYS:HG3	1:A:1039:PHE:O	2.20	0.41
1:A:1035:LEU:HD23	1:A:1035:LEU:HA	1.92	0.41
1:A:1057:ASP:HB3	1:A:1060:GLU:HB2	2.02	0.41
1:A:1042:ILE:HG22	1:A:1044:VAL:HG22	2.03	0.41
1:B:1057:ASP:HB3	1:B:1060:GLU:HB2	2.02	0.40
1:A:1216:ILE:H	1:A:1216:ILE:HG12	1.73	0.40
1:B:962:LYS:HE2	1:B:962:LYS:HB3	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	329/722 (46%)	318 (97%)	11 (3%)	0	100	100
1	B	329/722 (46%)	318 (97%)	11 (3%)	0	100	100
All	All	658/1444 (46%)	636 (97%)	22 (3%)	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	280/611 (46%)	280 (100%)	0	100	100
1	B	280/611 (46%)	280 (100%)	0	100	100
All	All	560/1222 (46%)	560 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

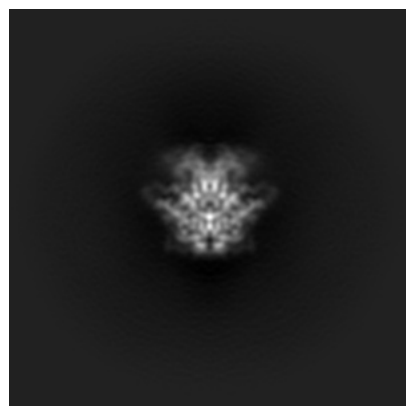
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18648. These allow visual inspection of the internal detail of the map and identification of artifacts.

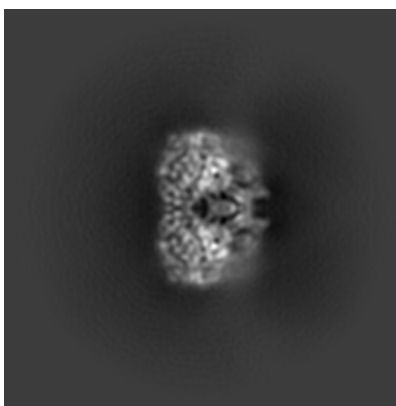
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

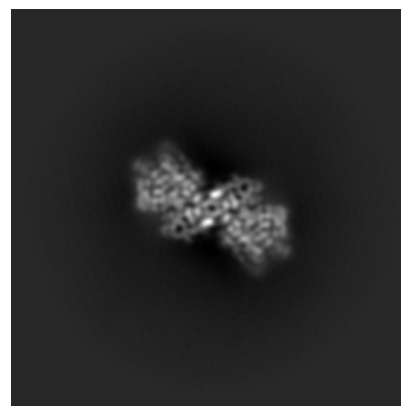
6.1.1 Primary map



X

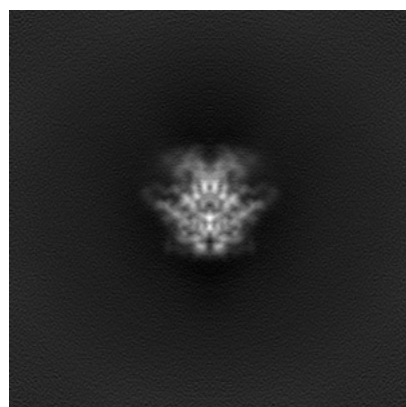


Y

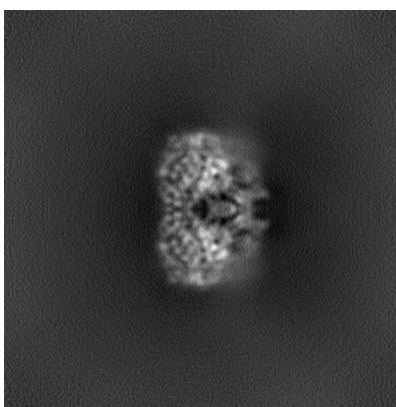


Z

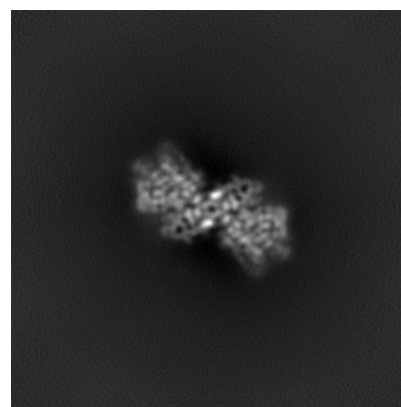
6.1.2 Raw map



X



Y

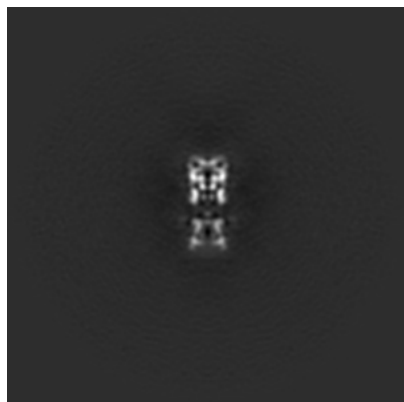


Z

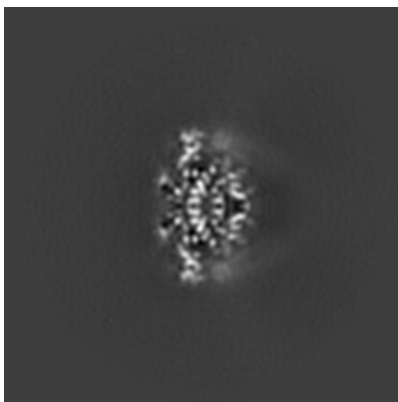
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

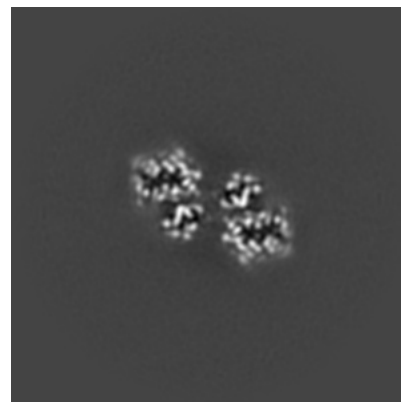
6.2.1 Primary map



X Index: 128

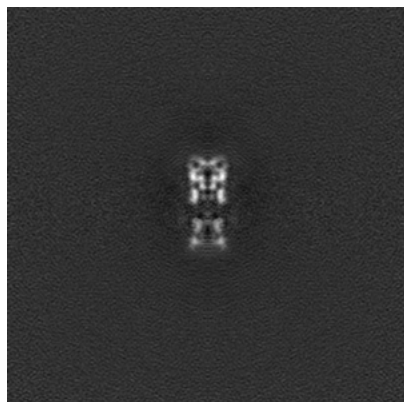


Y Index: 128

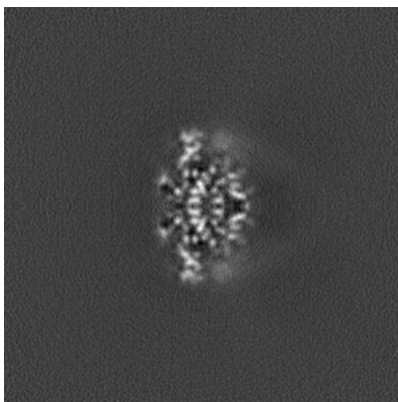


Z Index: 128

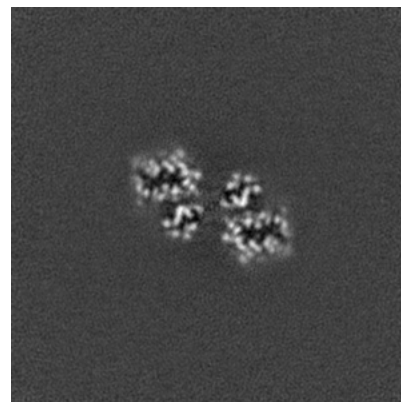
6.2.2 Raw map



X Index: 128



Y Index: 128

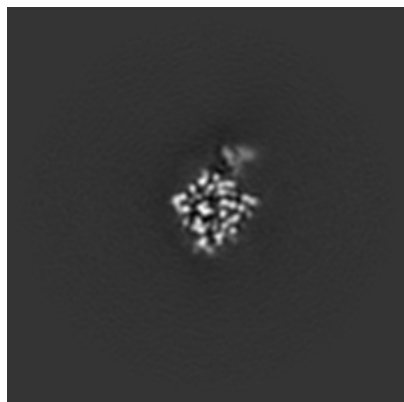


Z Index: 128

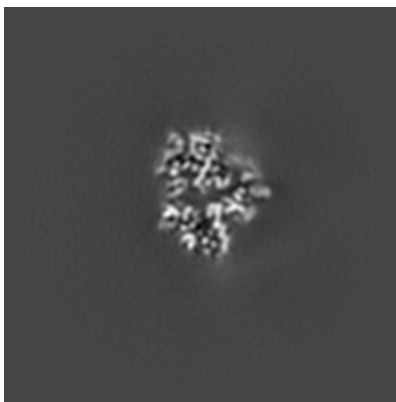
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

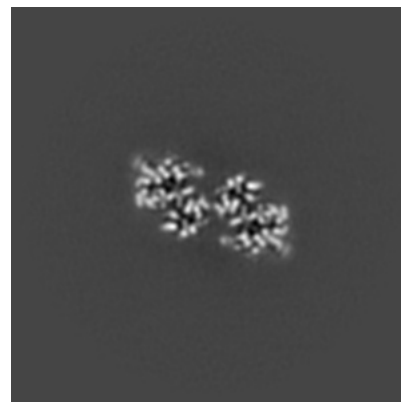
6.3.1 Primary map



X Index: 113

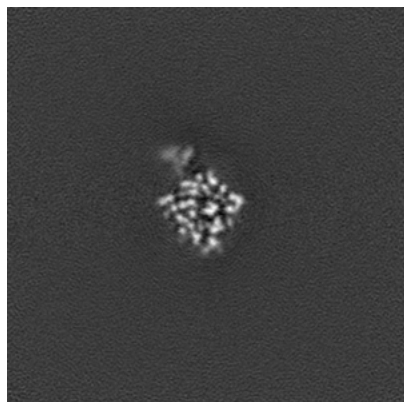


Y Index: 119

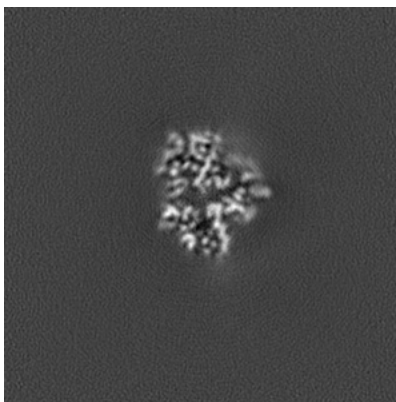


Z Index: 124

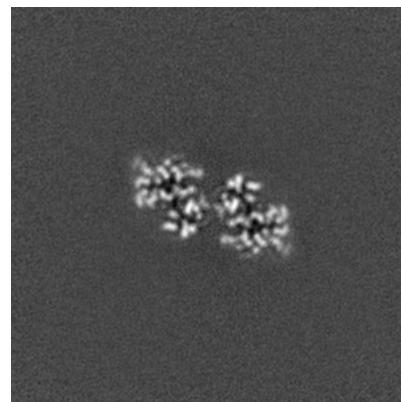
6.3.2 Raw map



X Index: 143



Y Index: 119

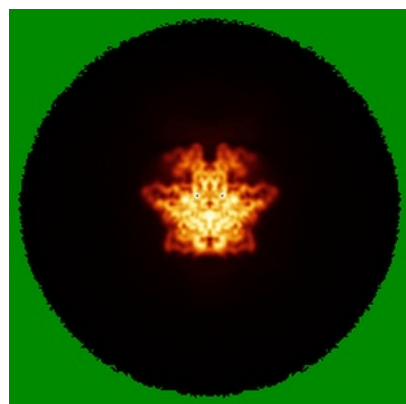


Z Index: 125

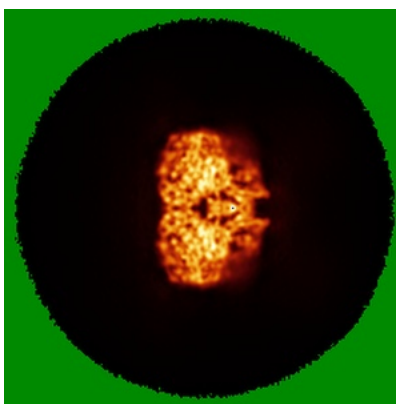
The images above show the largest variance slices of the map in three orthogonal directions.

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

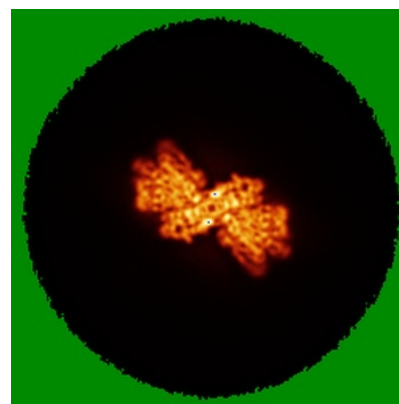
6.4.1 Primary map



X

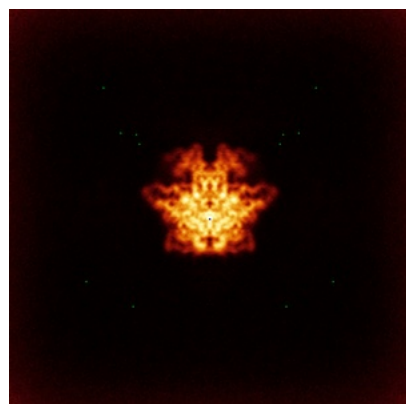


Y

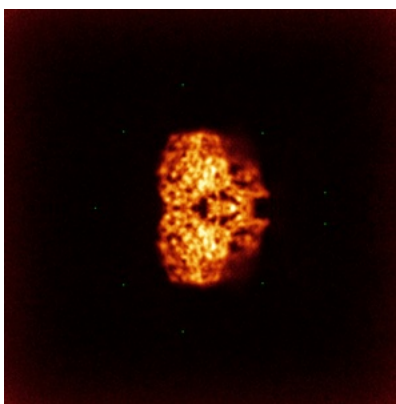


Z

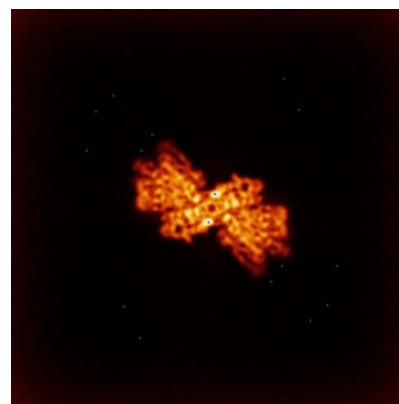
6.4.2 Raw map



X



Y

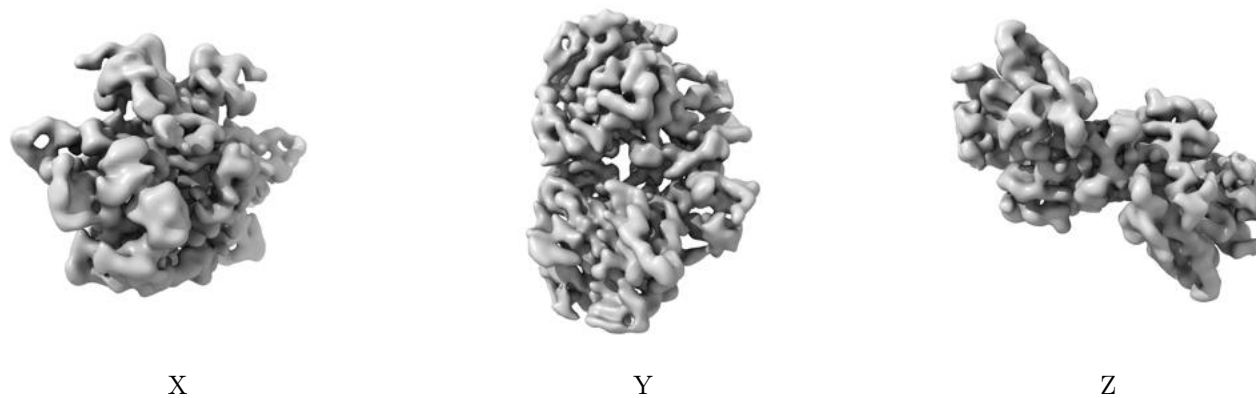


Z

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.

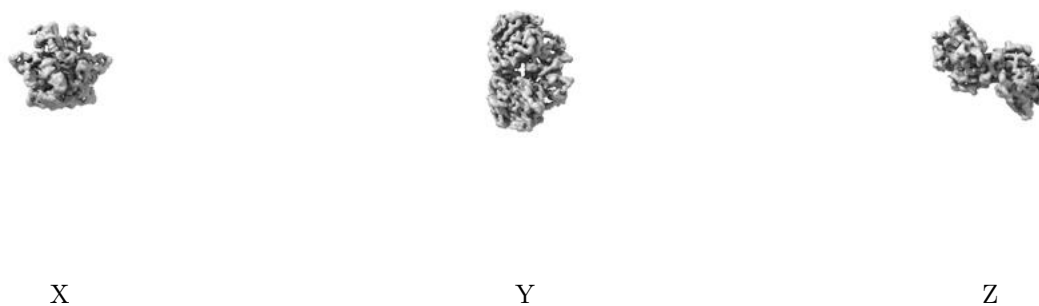
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. 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.

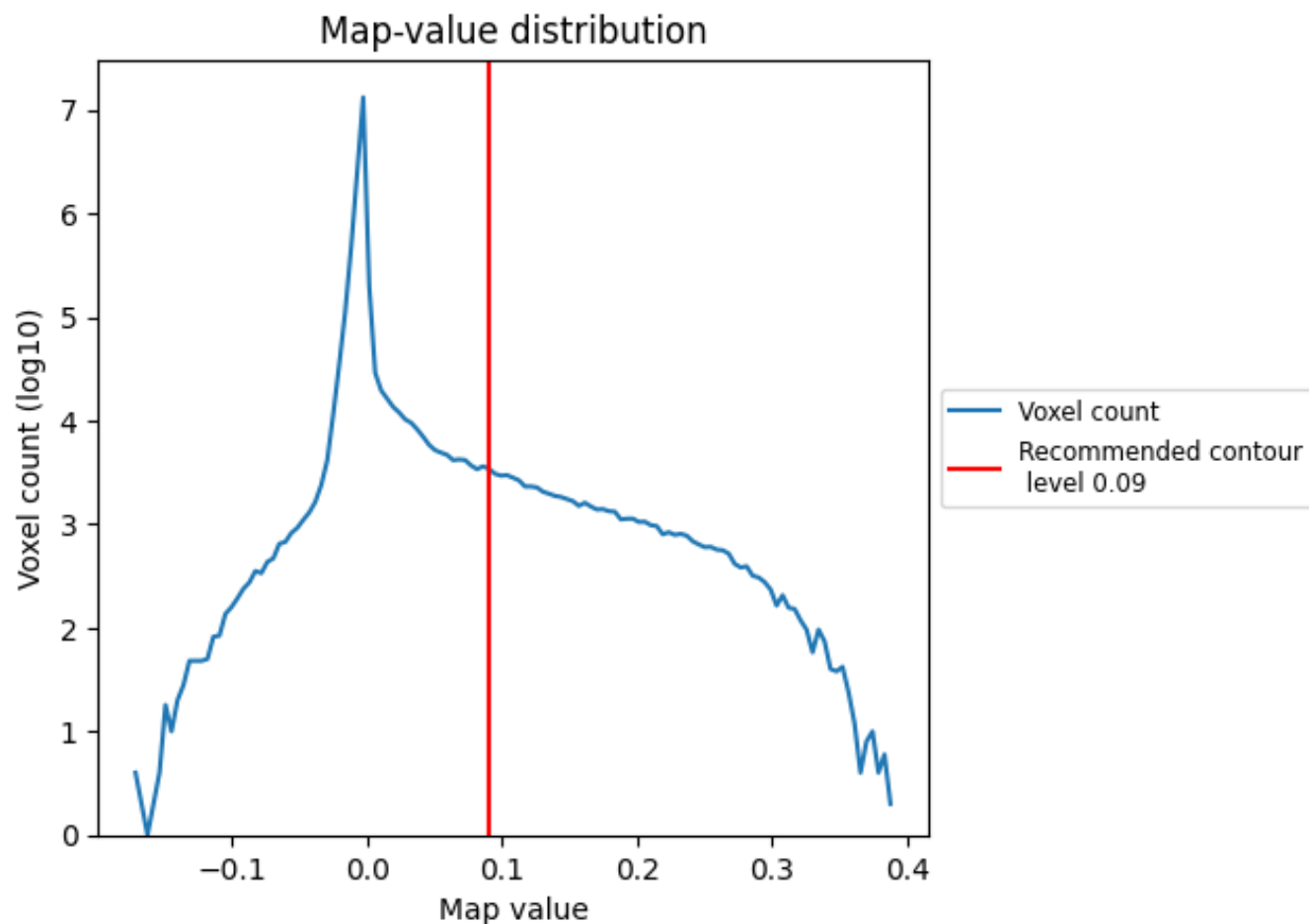
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

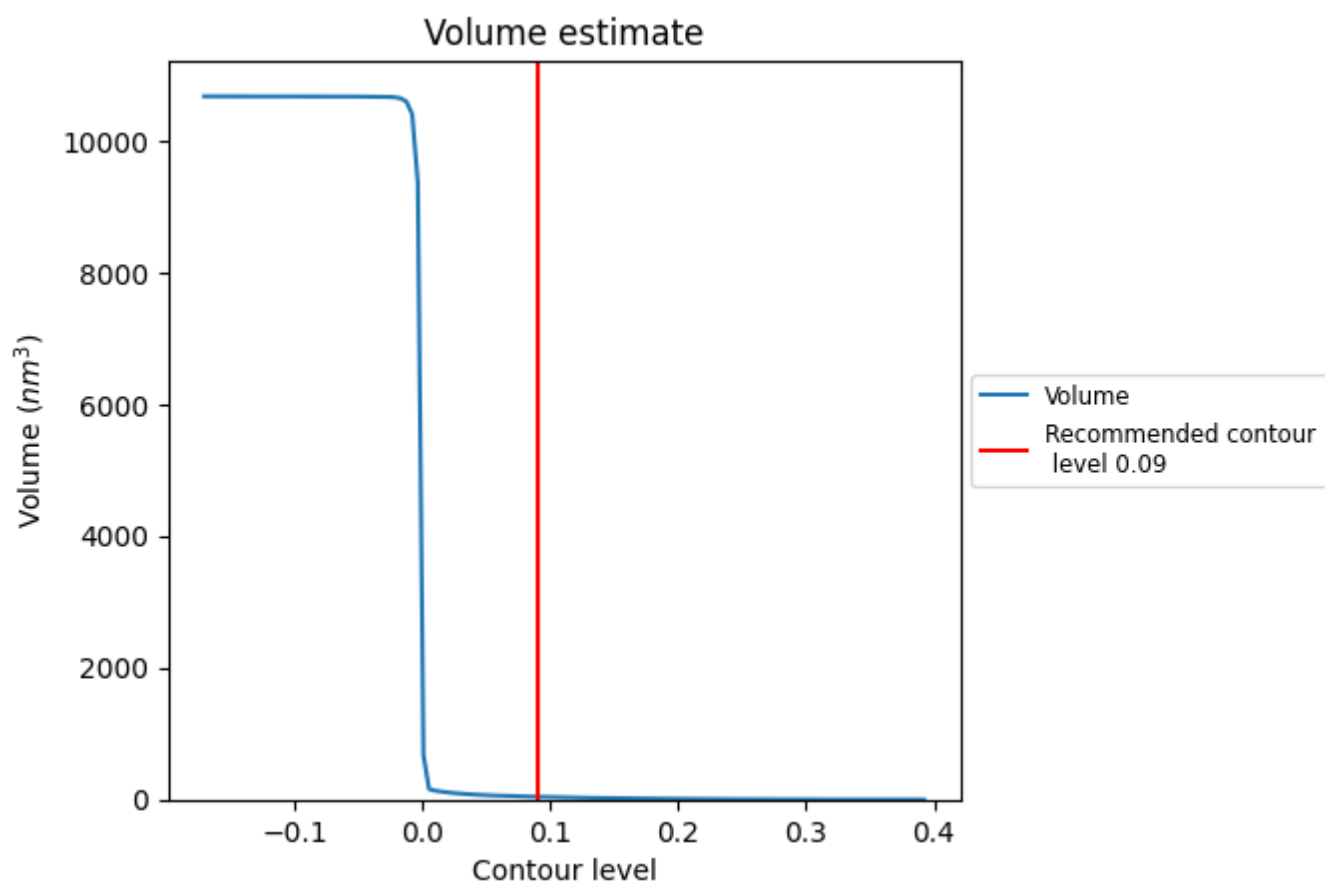
This section contains the results of statistical analysis of the map.

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.

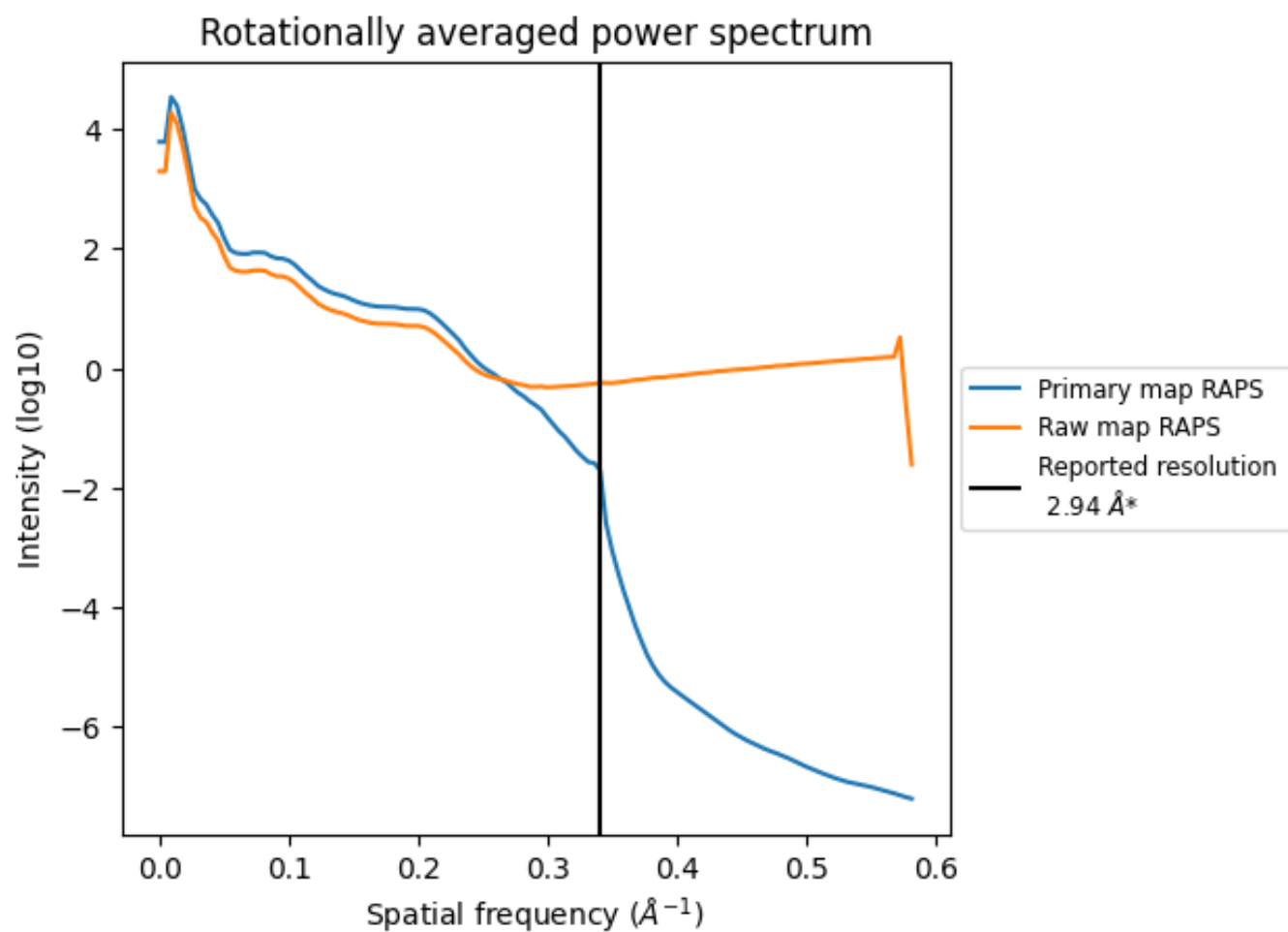
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 42 nm³; this corresponds to an approximate mass of 38 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 ⓘ

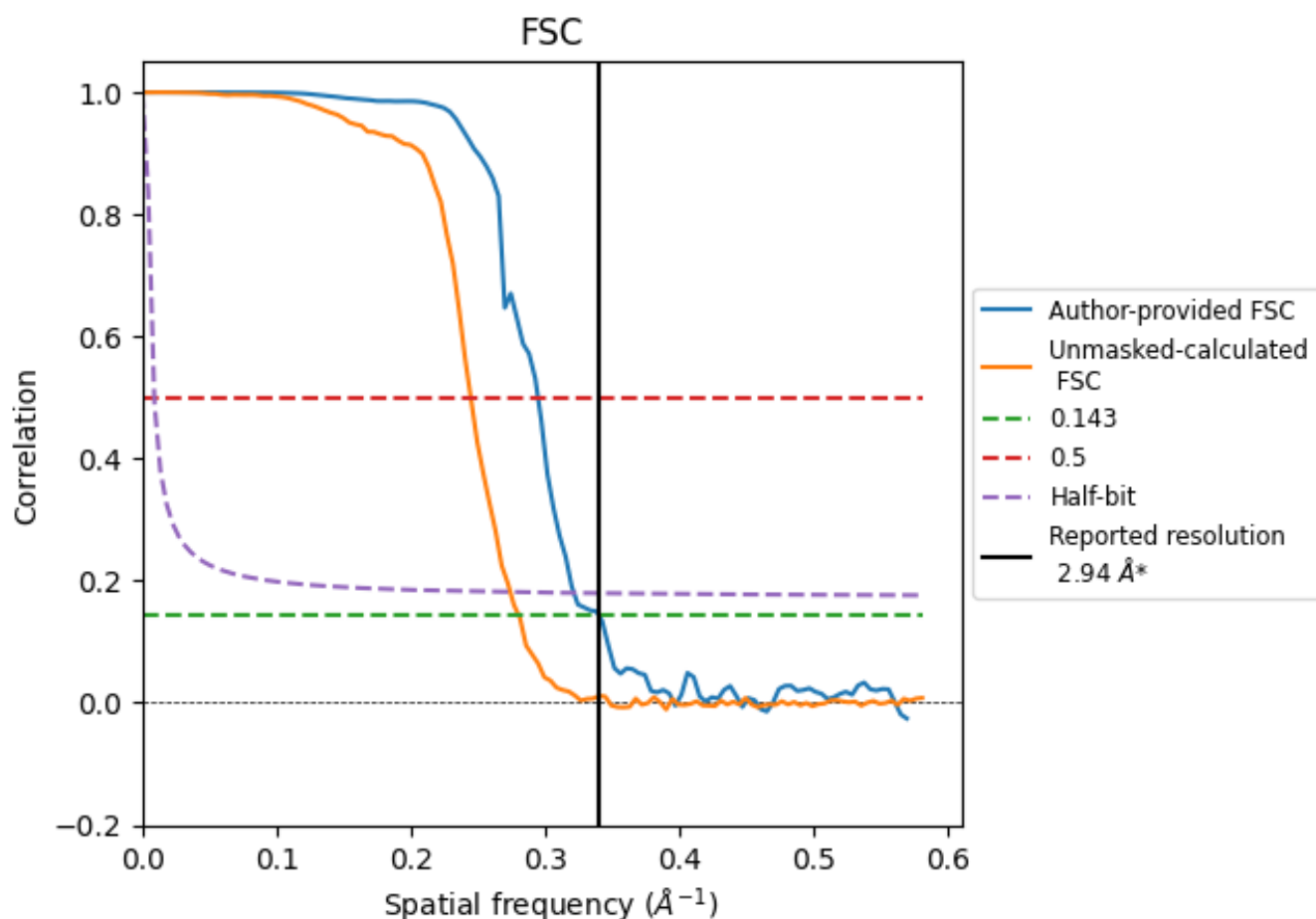


*Reported resolution corresponds to spatial frequency of 0.340 Å⁻¹

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 0.340 \AA^{-1}

8.2 Resolution estimates [i](#)

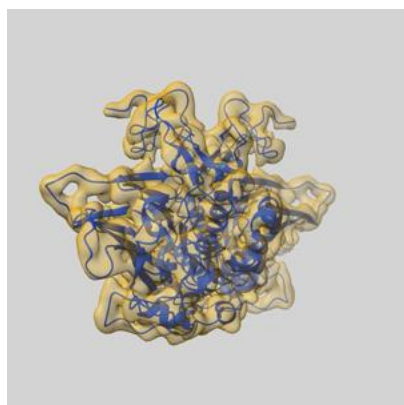
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.94	-	-
Author-provided FSC curve	2.94	3.39	3.11
Unmasked-calculated*	3.56	4.08	3.64

*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 3.56 differs from the reported value 2.94 by more than 10 %

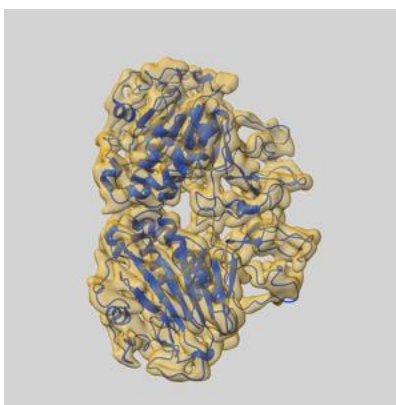
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18648 and PDB model 8QTB. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



X



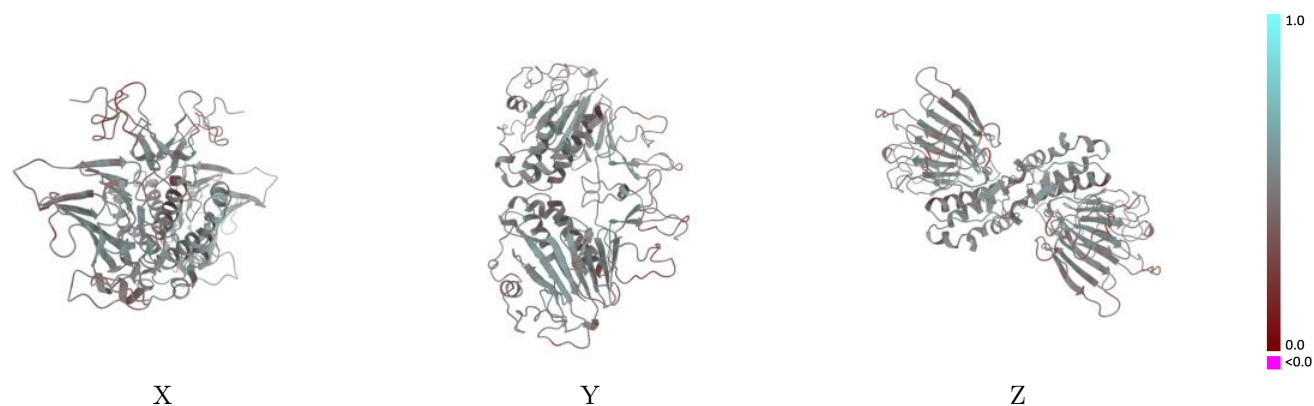
Y



Z

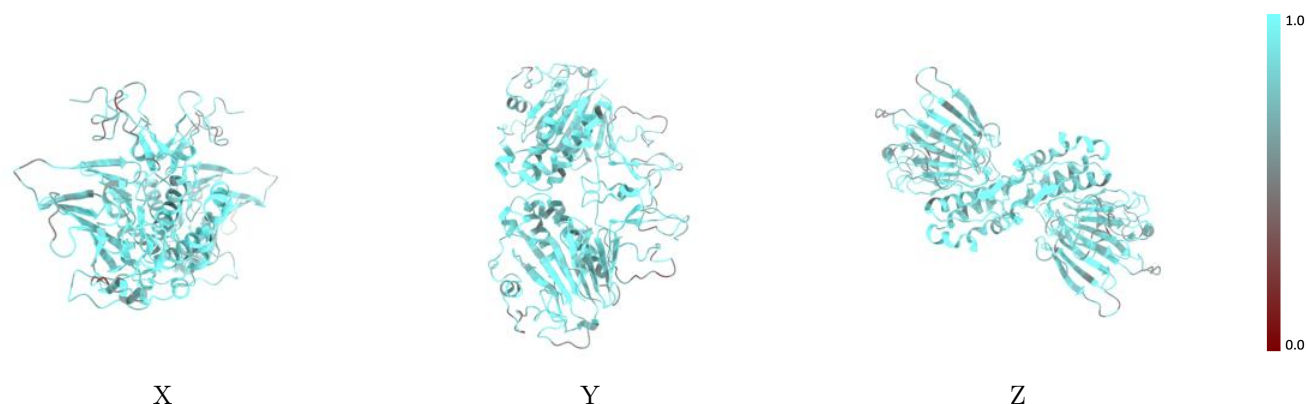
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



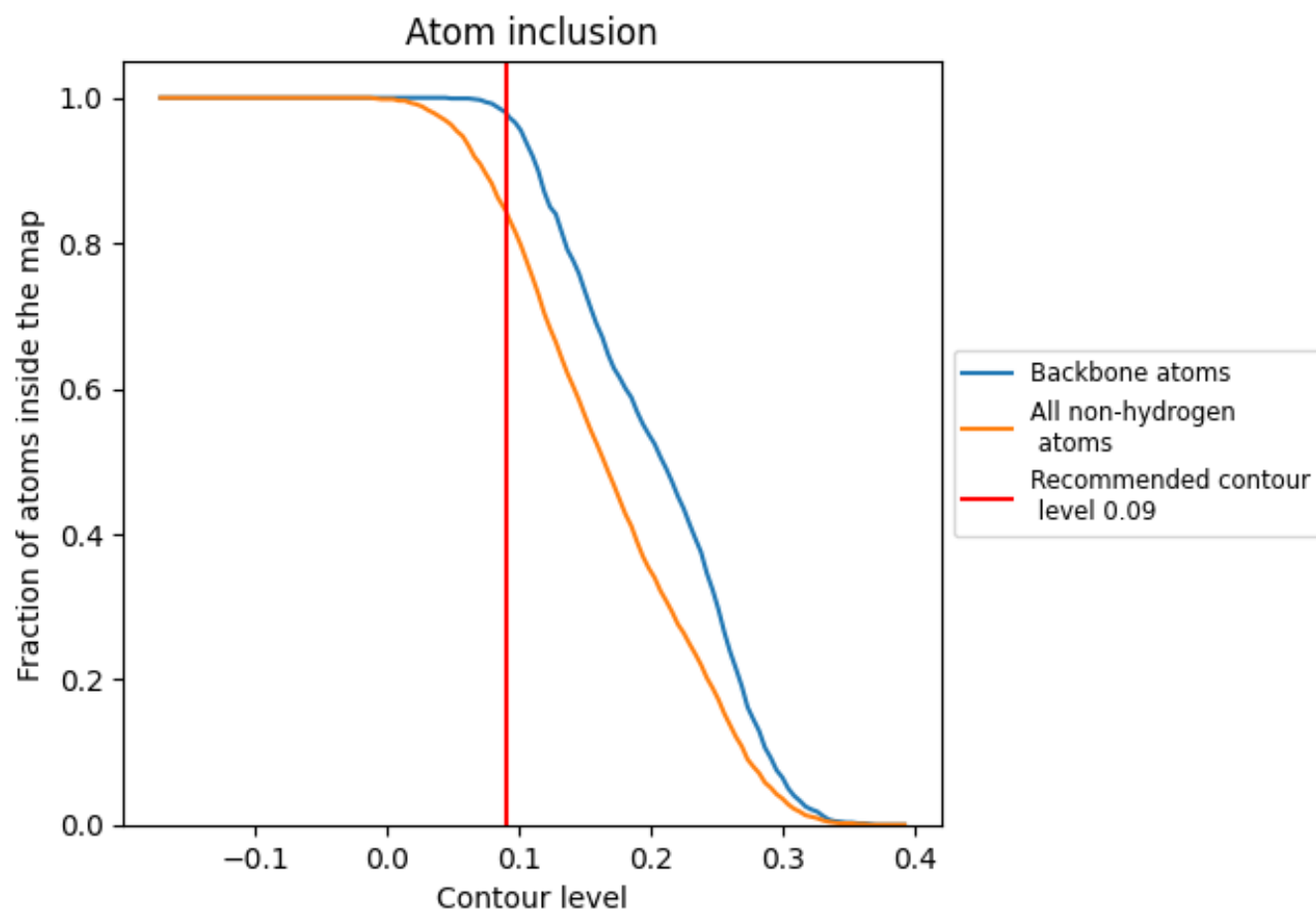
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 84% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8450	<div></div> 0.4710
A	<div></div> 0.8450	<div></div> 0.4710
B	<div></div> 0.8450	<div></div> 0.4710

