



wwPDB EM Validation Summary Report ⓘ

Oct 17, 2026 – 10:10 am BST

PDB ID : 9TE5 / pdb_00009te5
EMDB ID : EMD-55820
Title : Cryo-EM structure of C5*-CVFBb (state 2.0)
Authors : Joergensen, M.H.; Andersen, G.R.; Almeida, A.V.d.
Deposited on : 2025-11-25
Resolution : 3.09 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:

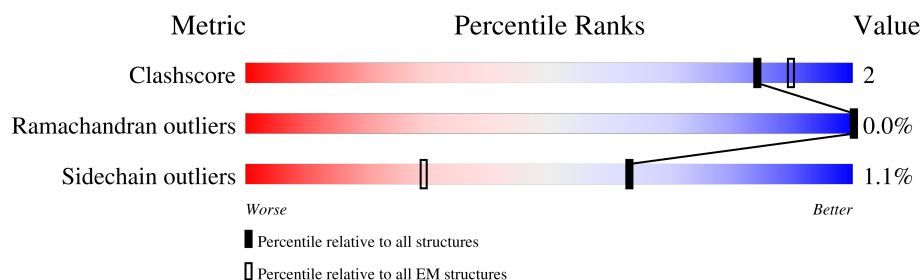
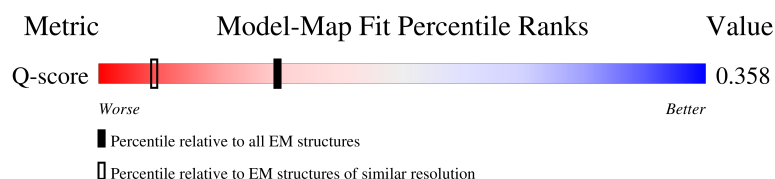
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 3.09 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	14003 (2.59 - 3.59)

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	659	 90% 10%
2	C	999	 16% 83%
3	B	627	 93% 7%
4	D	252	 87% 6% 7%

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Mol	Chain	Length	Quality of chain
5	E	379	<div><div></div><div>12%</div><div>89%</div><div>7%</div><div></div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16261 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 Complement C5 beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	657	Total	C	N	O	S	0	0
			5195	3330	838	1014	13		

- Molecule 2 is a protein called Complement C5 alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	172	Total	C	N	O	S	0	0
			1364	877	230	250	7		

- Molecule 3 is a protein called Cobra venom factor alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	624	Total	C	N	O	S	0	0
			4881	3117	822	926	16		

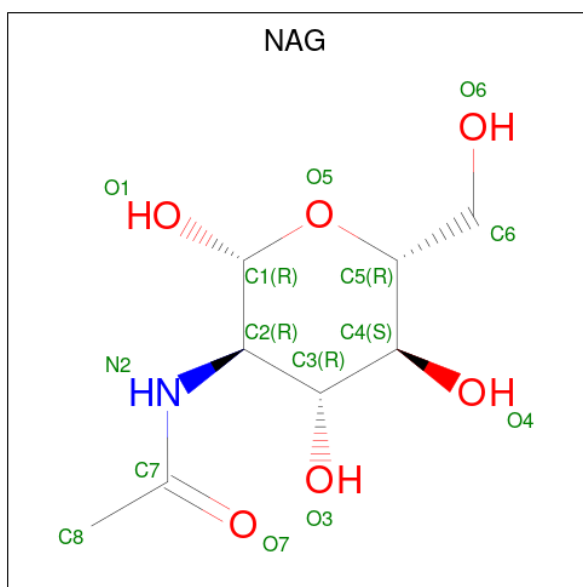
- Molecule 4 is a protein called Cobra venom factor gamma chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	234	Total	C	N	O	S	0	0
			1865	1199	312	349	5		

- Molecule 5 is a protein called Cobra venom factor beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	364	Total	C	N	O	S	0	0
			2942	1856	494	573	19		

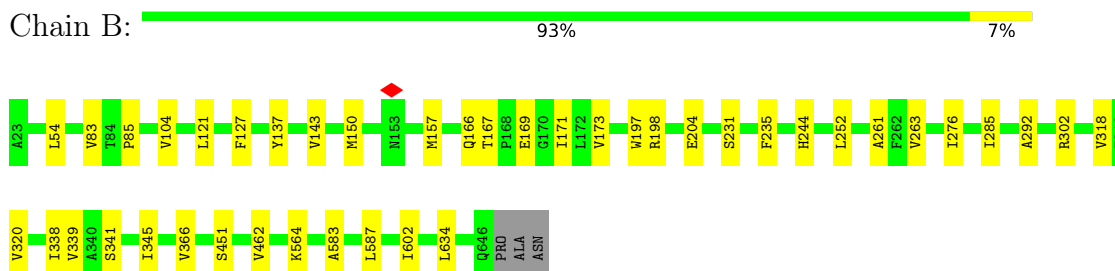
- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



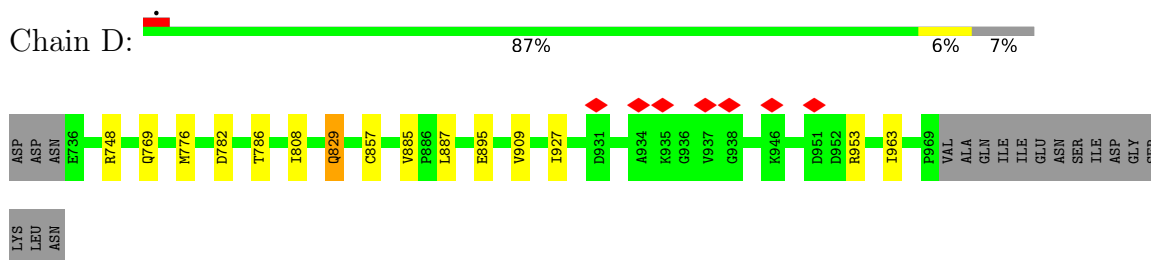
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	C	1	14	8	1	5	0

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

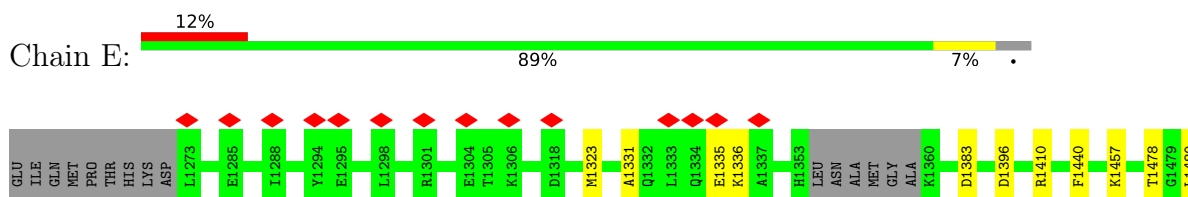
- Molecule 3: Cobra venom factor alpha chain

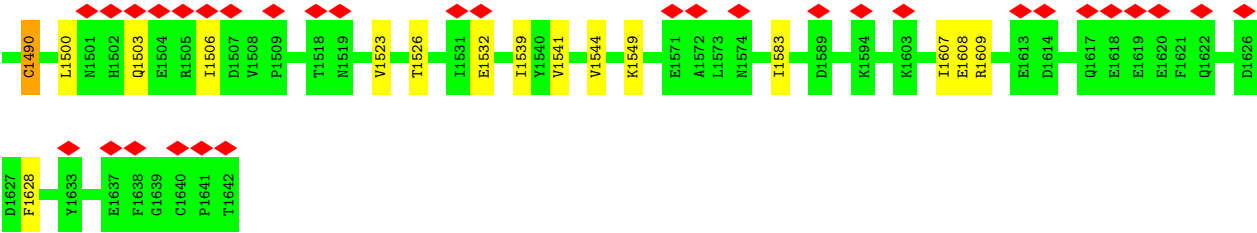


- Molecule 4: Cobra venom factor gamma chain



- Molecule 5: Cobra venom factor beta chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	206847	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 ($e^-/\text{\AA}^2$)	59.9	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.179	Depositor
Minimum map value	-0.494	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	330.24, 330.24, 330.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.29, 1.29, 1.29	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.26	0/5316	0.61	3/7230 (0.0%)
2	C	0.26	0/1395	0.67	0/1891
3	B	0.24	0/4991	0.57	1/6790 (0.0%)
4	D	0.23	0/1903	0.54	1/2582 (0.0%)
5	E	0.25	0/2994	0.62	1/4049 (0.0%)
All	All	0.25	0/16599	0.60	6/22542 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1
5	E	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1410	ARG	CA-CB-CG	5.97	126.04	114.10
4	D	769	GLN	CB-CG-CD	5.31	121.63	112.60
3	B	157	MET	CA-CB-CG	5.25	124.59	114.10
1	A	311	SER	CA-C-N	5.14	131.36	121.54
1	A	311	SER	C-N-CA	5.14	131.36	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	885	ARG	Sidechain
5	E	1541	VAL	Peptide

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	5195	0	5114	31	0
2	C	1364	0	1379	7	0
3	B	4881	0	4884	21	0
4	D	1865	0	1906	10	0
5	E	2942	0	2894	14	0
6	C	14	0	13	0	0
All	All	16261	0	16190	75	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 2.

The worst 5 of 75 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)
3:B:127:PHE:HB2	3:B:150:MET:HB3	1.78	0.65
2:C:835:ARG:HA	2:C:902:PRO:HG2	1.83	0.59
4:D:963:ILE:HG23	5:E:1323:MET:HE1	1.84	0.59
1:A:132:LYS:HB2	1:A:609:VAL:HG11	1.85	0.58
5:E:1523:VAL:HG23	5:E:1549:LYS:HE2	1.86	0.56

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	655/659 (99%)	624 (95%)	30 (5%)	1 (0%)	43	73
2	C	170/999 (17%)	166 (98%)	4 (2%)	0	100	100
3	B	622/627 (99%)	604 (97%)	18 (3%)	0	100	100
4	D	232/252 (92%)	229 (99%)	3 (1%)	0	100	100
5	E	360/379 (95%)	349 (97%)	11 (3%)	0	100	100
All	All	2039/2916 (70%)	1972 (97%)	66 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	312	TYR

5.3.2 Protein sidechains ⓘ

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	582/584 (100%)	570 (98%)	12 (2%)	47	71
2	C	156/886 (18%)	155 (99%)	1 (1%)	78	83
3	B	546/548 (100%)	541 (99%)	5 (1%)	70	80
4	D	211/227 (93%)	210 (100%)	1 (0%)	81	85
5	E	333/345 (96%)	331 (99%)	2 (1%)	78	83
All	All	1828/2590 (71%)	1807 (99%)	21 (1%)	63	78

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	204	GLU
3	B	634	LEU
5	E	1490	CYS
4	D	829	GLN

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Mol	Chain	Res	Type
3	B	462	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	806	ASN
5	E	1415	ASN
3	B	59	HIS
5	E	1511	GLN
4	D	889	GLN

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	C	1701	2	14,14,15	0.77	0	17,19,21	3.06	7 (41%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	1701	2	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1701	NAG	C2-N2-C7	8.30	134.72	122.90
6	C	1701	NAG	C1-C2-N2	5.58	120.02	110.49
6	C	1701	NAG	O5-C1-C2	-4.54	104.11	111.29
6	C	1701	NAG	C1-O5-C5	3.17	116.49	112.19
6	C	1701	NAG	C4-C3-C2	3.05	115.48	111.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	1701	NAG	O5-C5-C6-O6
6	C	1701	NAG	C4-C5-C6-O6
6	C	1701	NAG	C3-C2-N2-C7
6	C	1701	NAG	C1-C2-N2-C7

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.

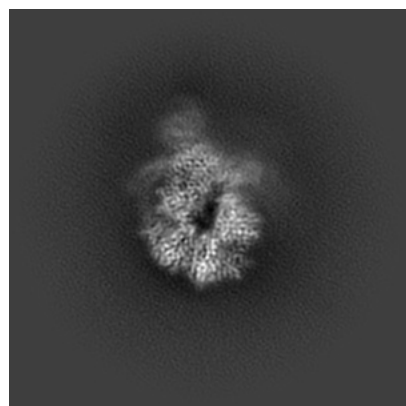
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55820. These allow visual inspection of the internal detail of the map and identification of artifacts.

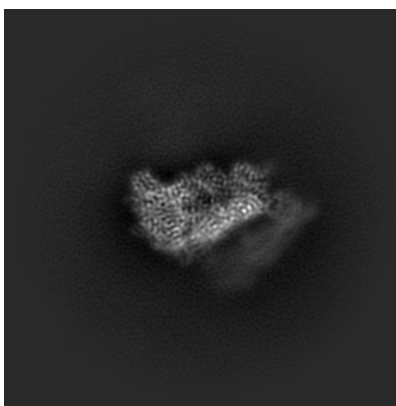
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

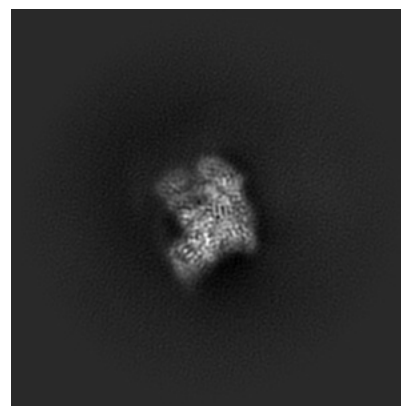
6.1.1 Primary map



X

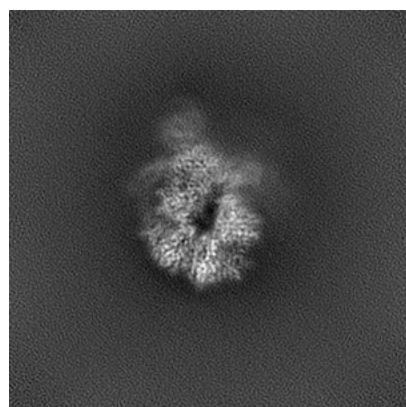


Y

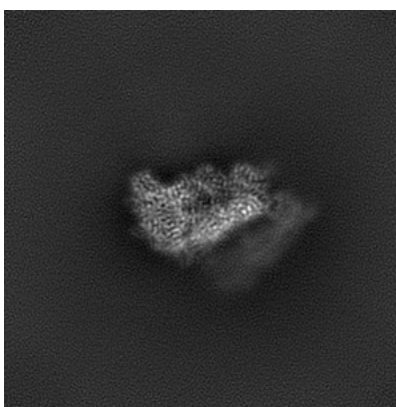


Z

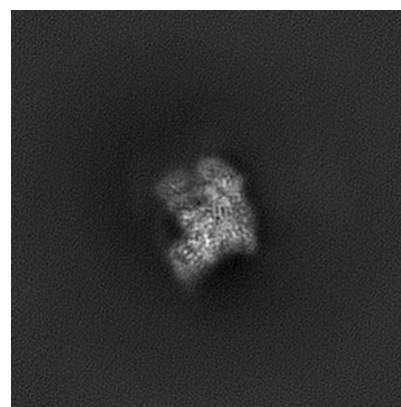
6.1.2 Raw map



X



Y

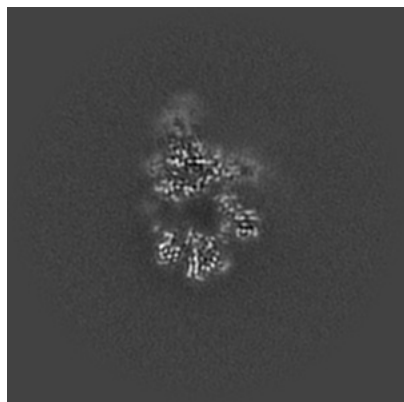


Z

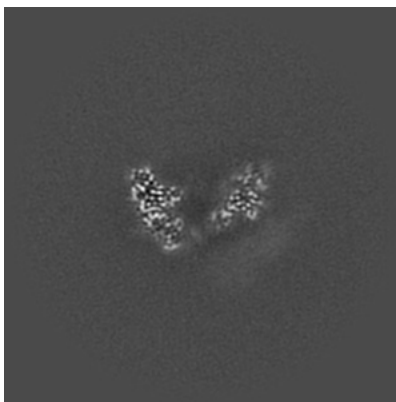
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

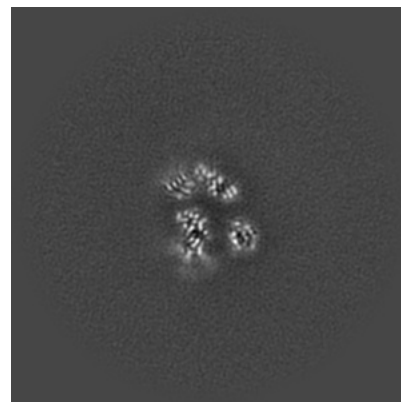
6.2.1 Primary map



X Index: 128

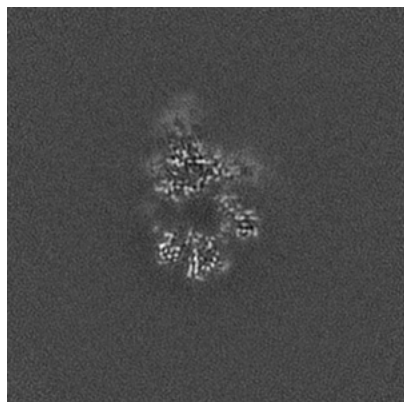


Y Index: 128

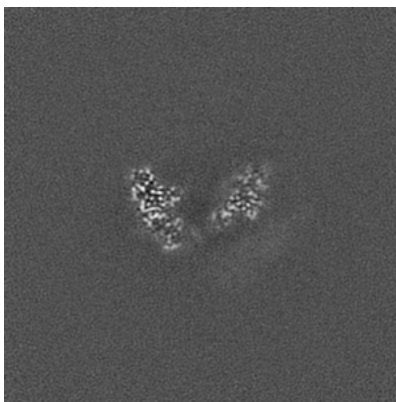


Z Index: 128

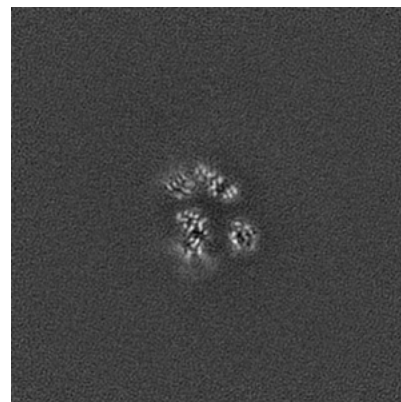
6.2.2 Raw map



X Index: 128



Y Index: 128

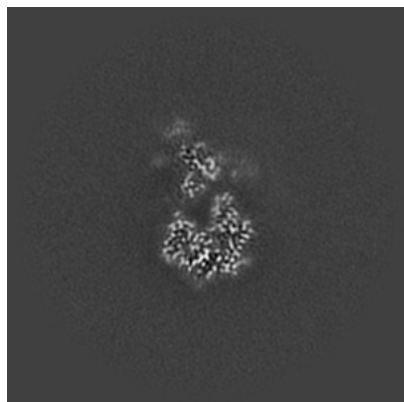


Z Index: 128

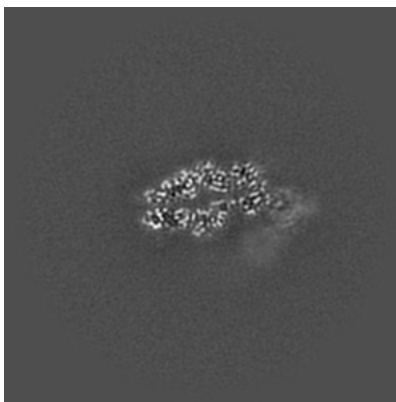
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

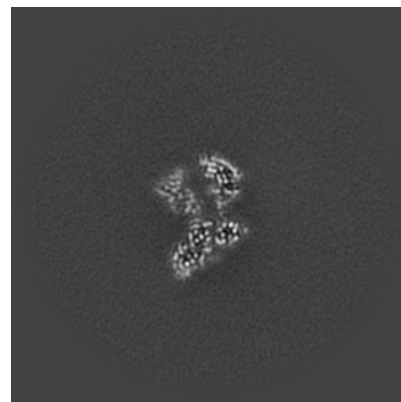
6.3.1 Primary map



X Index: 137

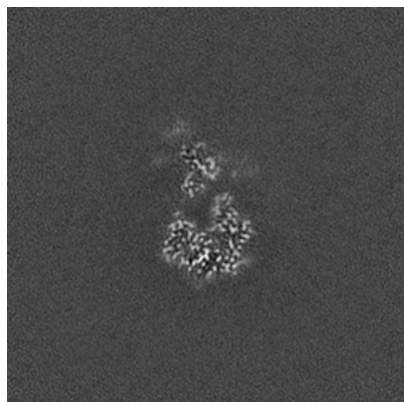


Y Index: 111

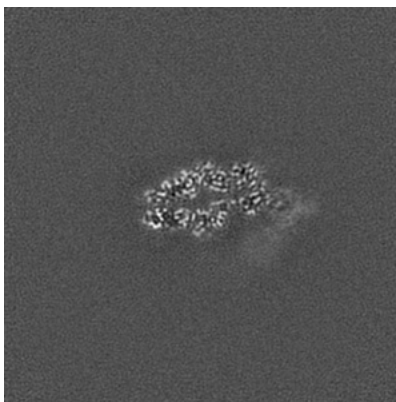


Z Index: 112

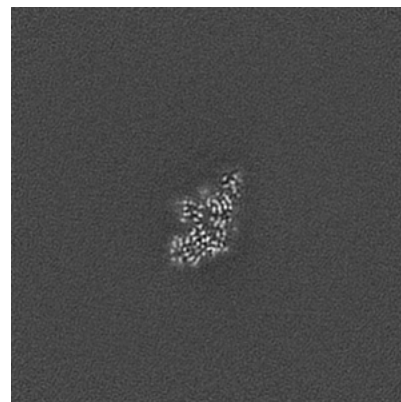
6.3.2 Raw map



X Index: 137



Y Index: 111

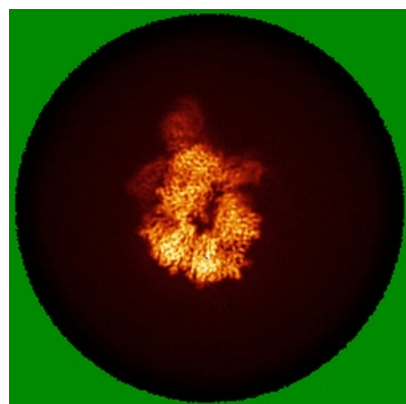


Z Index: 99

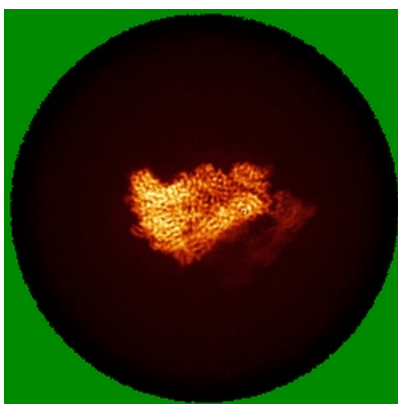
The images above show the largest variance slices of the map in three orthogonal directions.

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

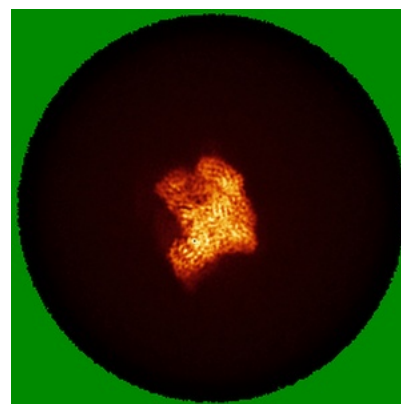
6.4.1 Primary map



X

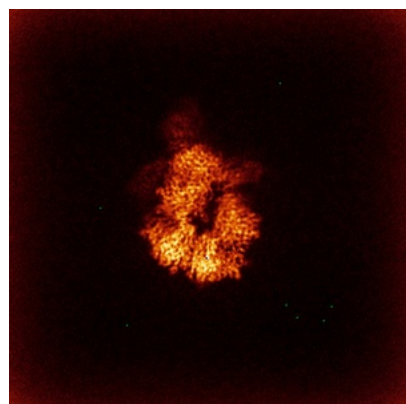


Y

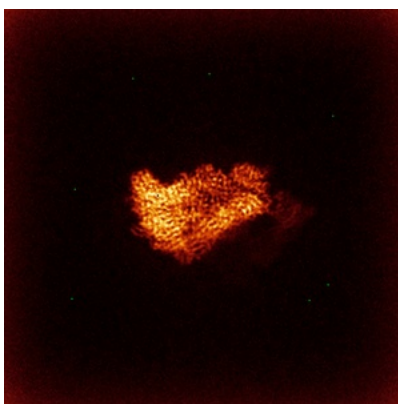


Z

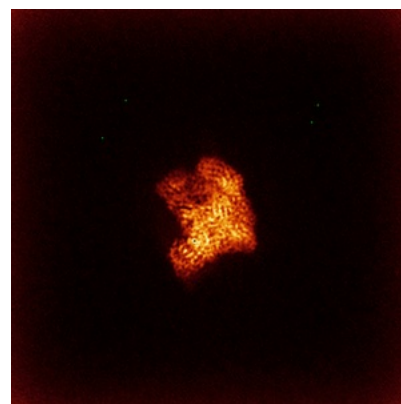
6.4.2 Raw map



X



Y

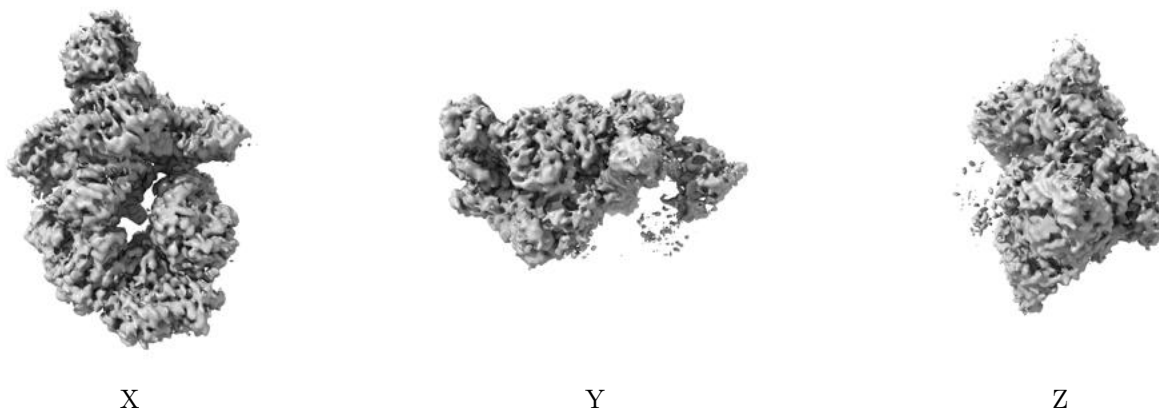


Z

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.

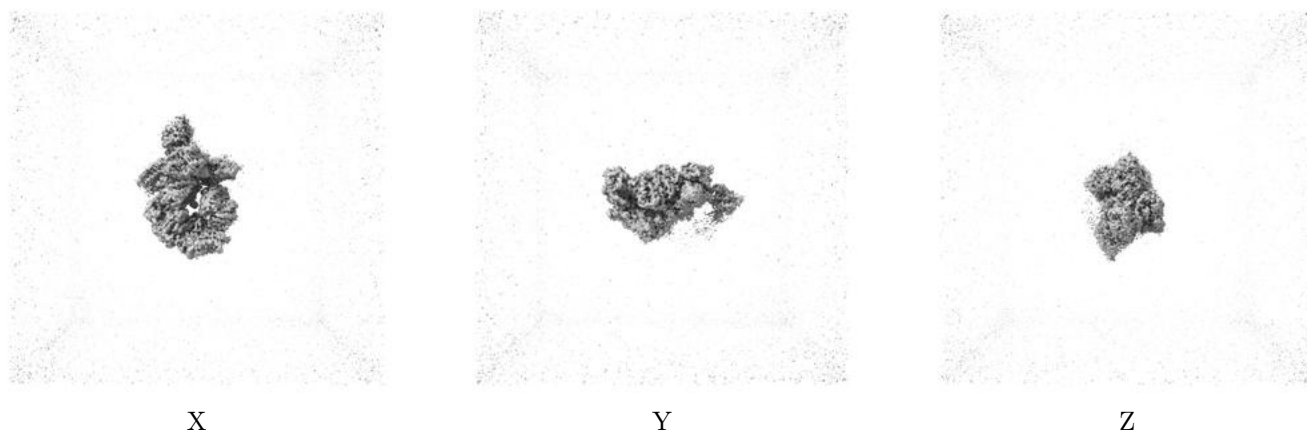
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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.

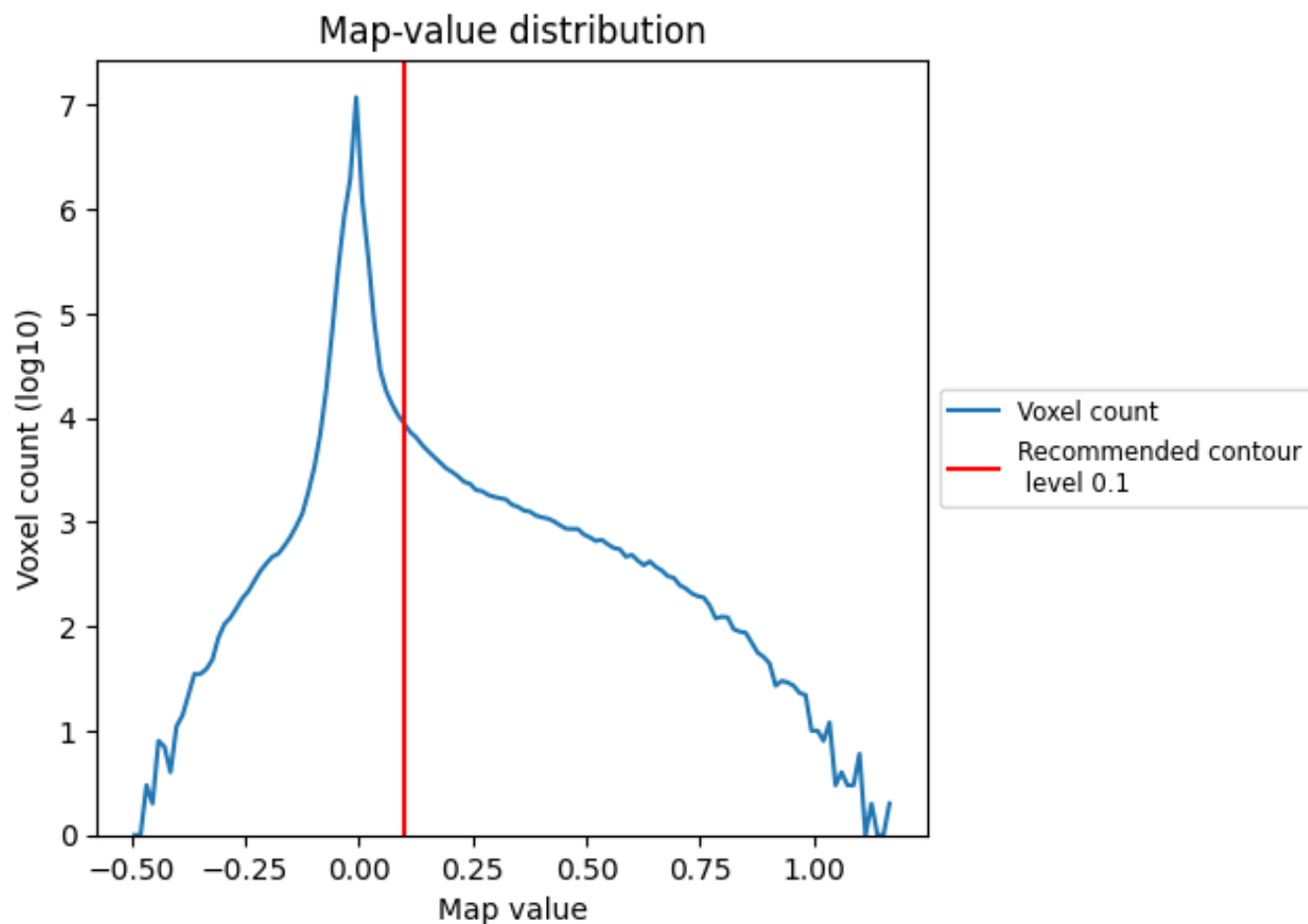
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

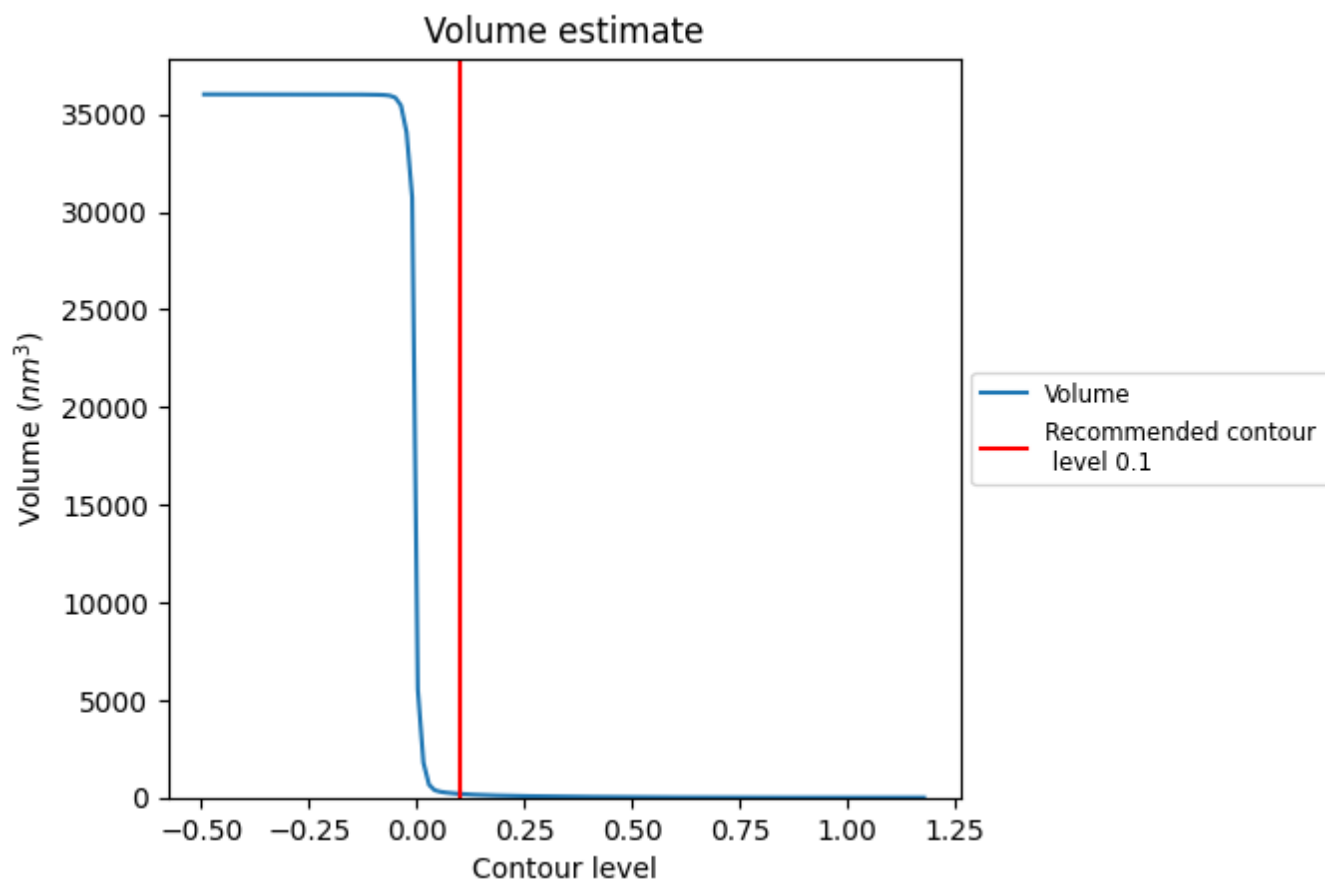
This section contains the results of statistical analysis of the map.

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.

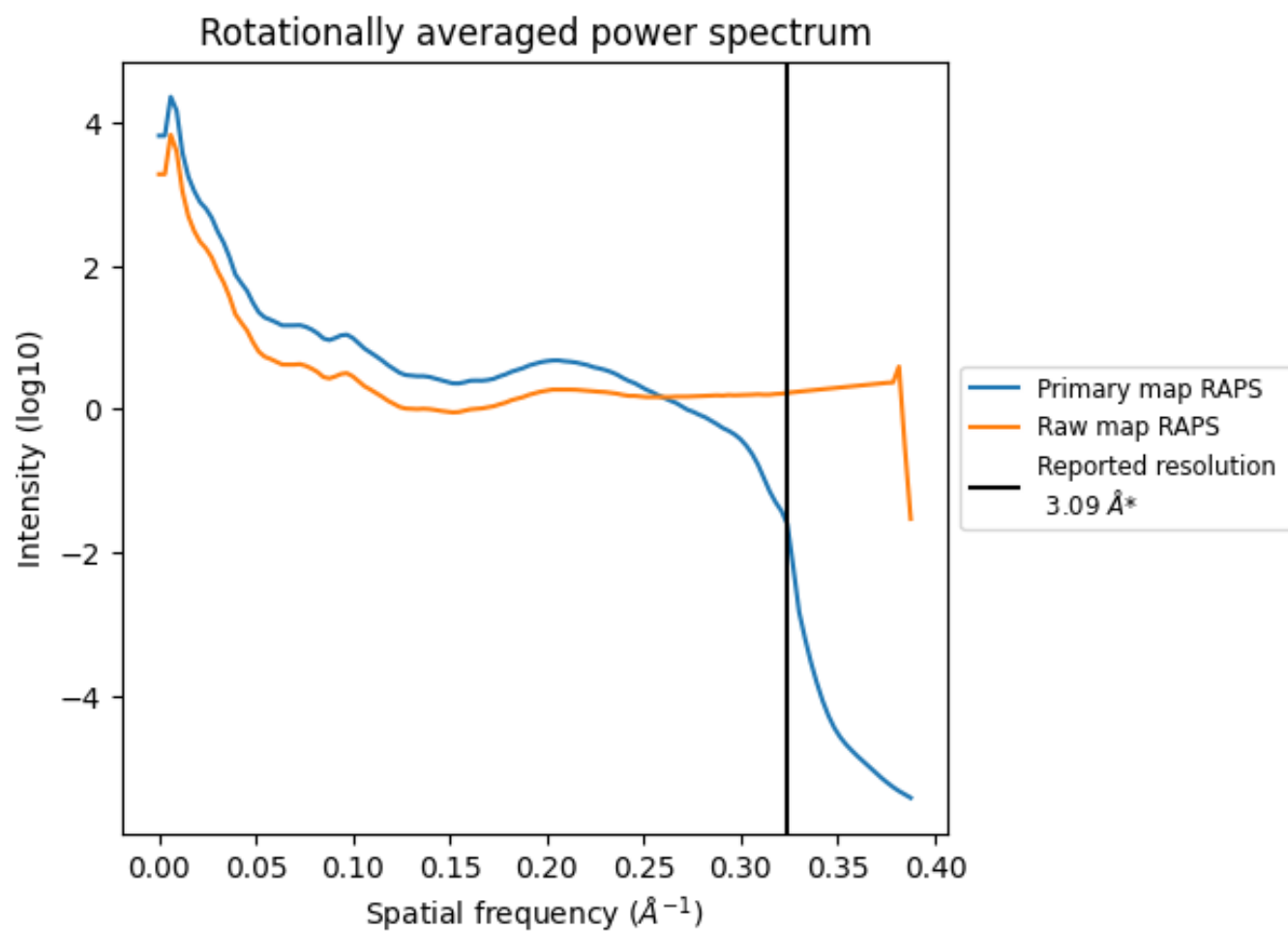
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 190 nm³; this corresponds to an approximate mass of 172 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 ⓘ

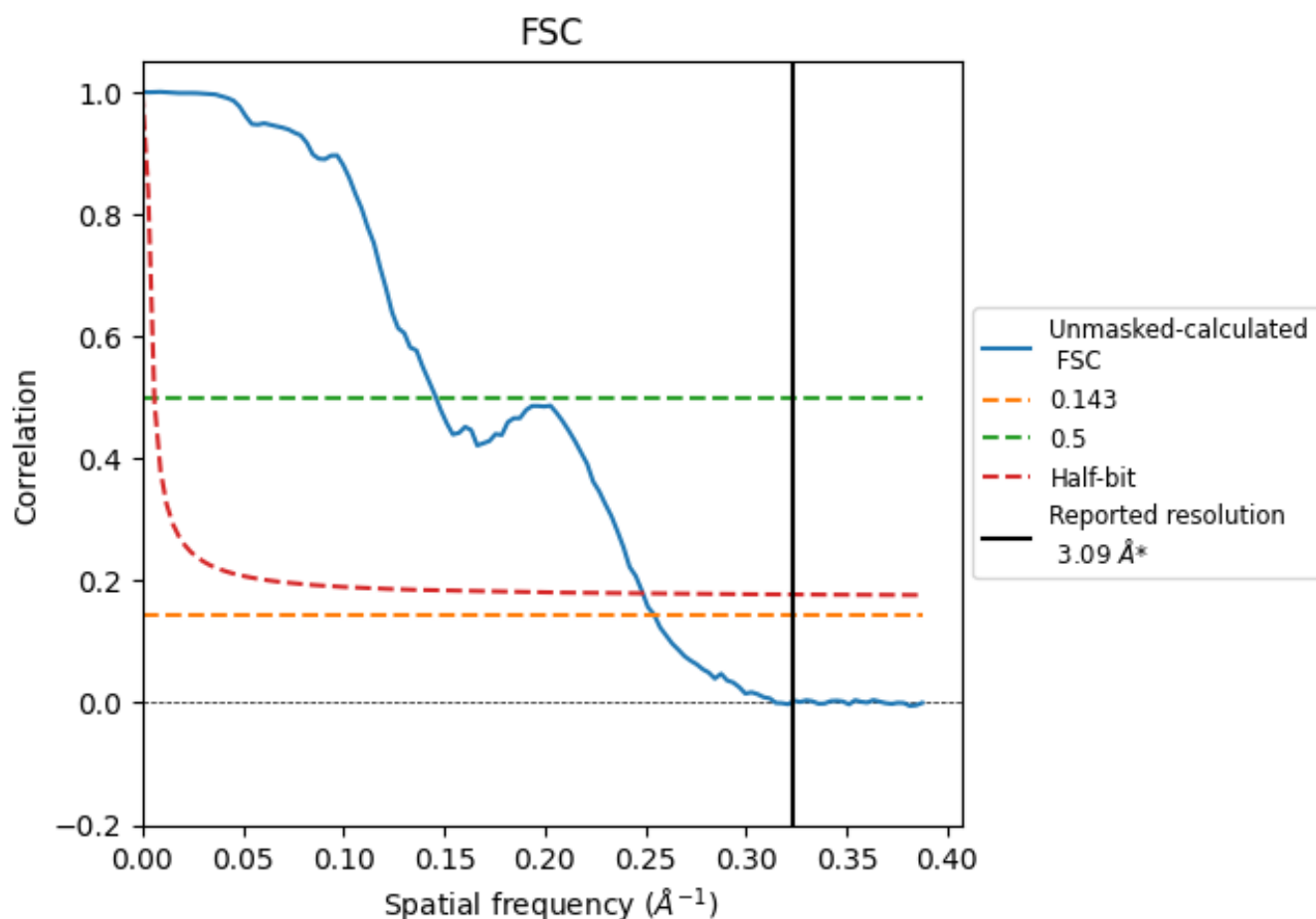


*Reported resolution corresponds to spatial frequency of $0.324 \text{ \AA}^{-1}$

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 $0.324 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

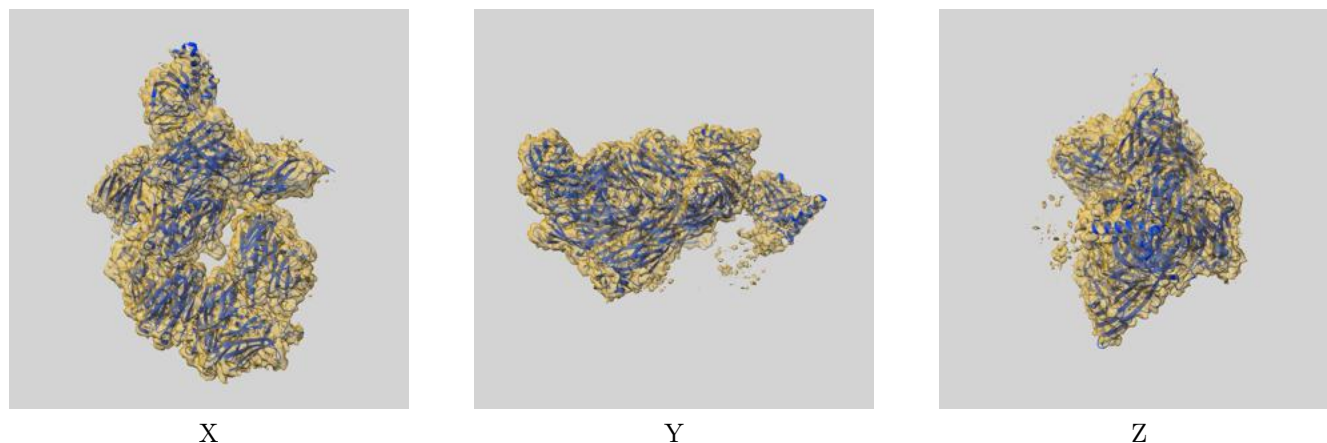
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.93	6.85	4.02

*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 3.93 differs from the reported value 3.09 by more than 10 %

9 Map-model fit [i](#)

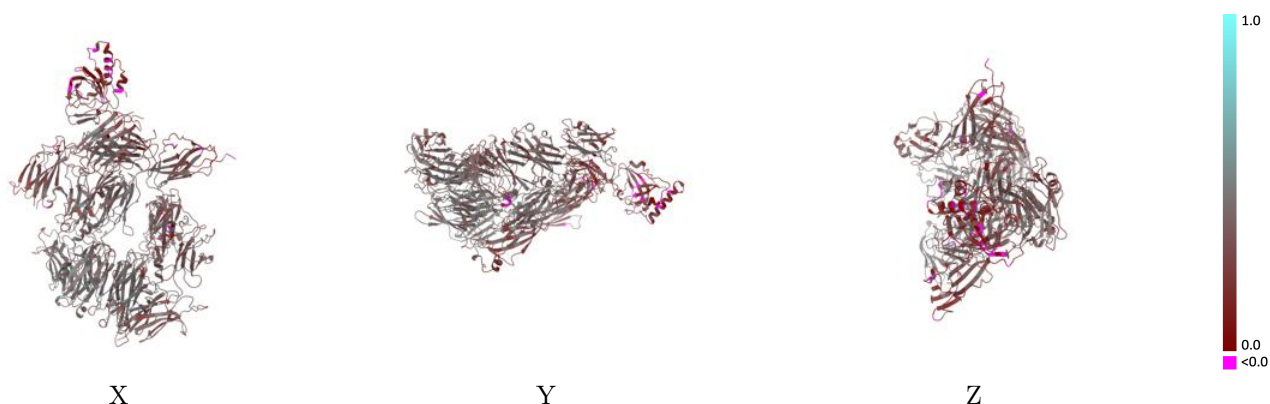
This section contains information regarding the fit between EMDB map EMD-55820 and PDB model 9TE5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



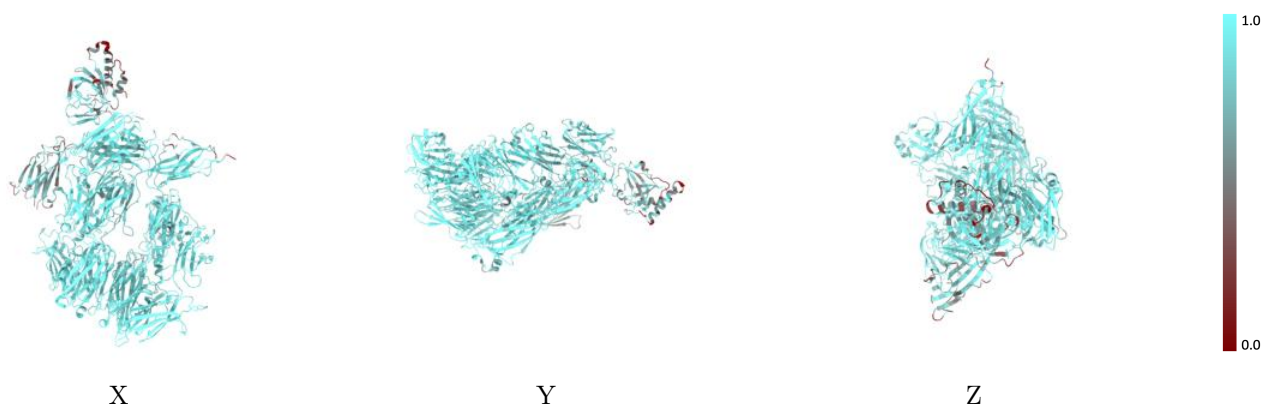
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



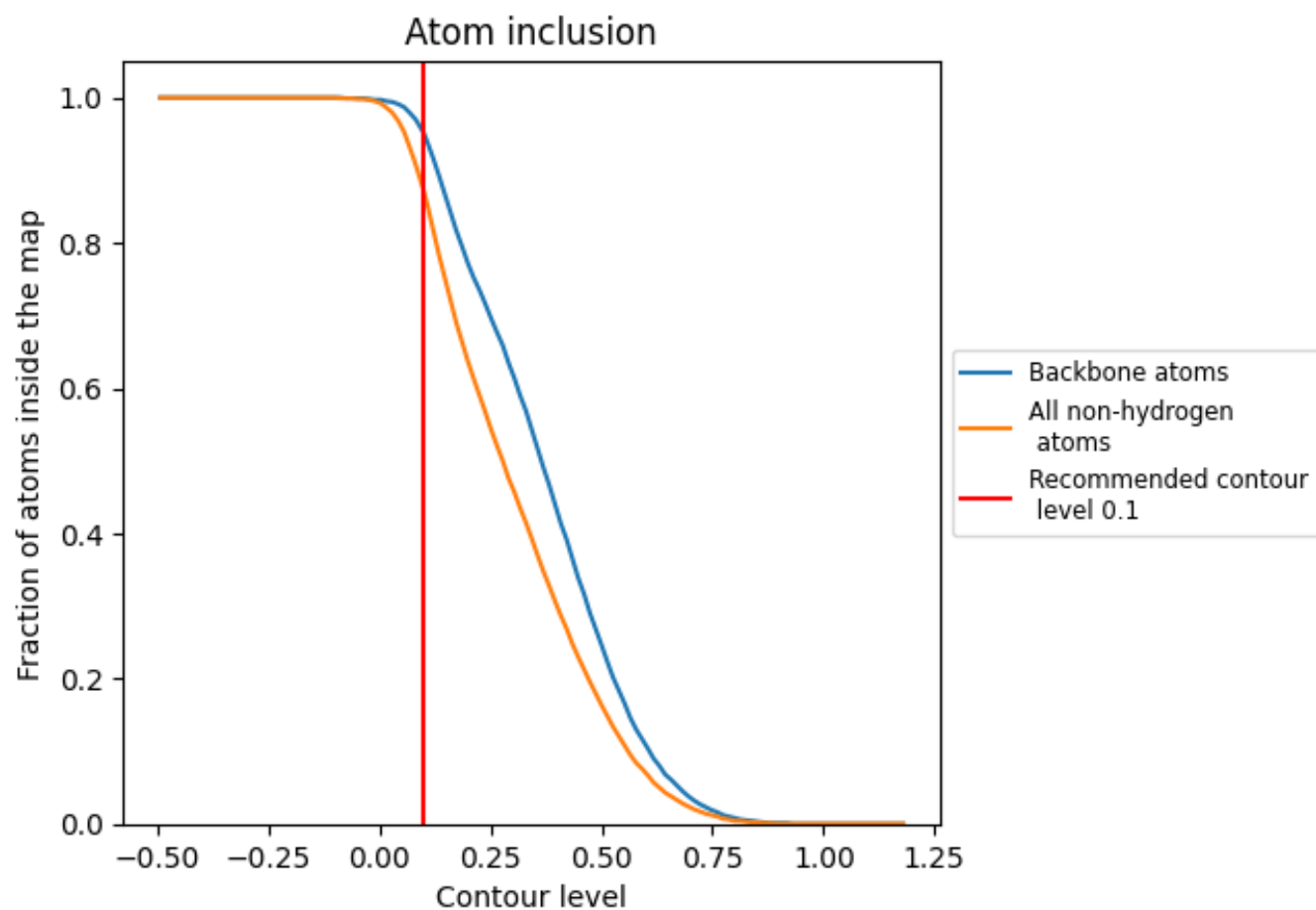
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8710</div>	<div><div></div>0.3580</div>
A	<div><div></div>0.9170</div>	<div><div></div>0.3770</div>
B	<div><div></div>0.9260</div>	<div><div></div>0.4110</div>
C	<div><div></div>0.8750</div>	<div><div></div>0.3150</div>
D	<div><div></div>0.8440</div>	<div><div></div>0.3630</div>
E	<div><div></div>0.7140</div>	<div><div></div>0.2520</div>

