



wwPDB EM Validation Summary Report ⓘ

May 27, 2026 – 12:57 PM JST

PDB ID : 22BK / pdb_000022bk
EMDB ID : EMD-68153
Title : KCNQ2/3 heterotetramer with 2:2 stoichiometry
Authors : Lu, F.; Fan, X.; Huang, J.
Deposited on : 2026-01-05
Resolution : 2.70 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

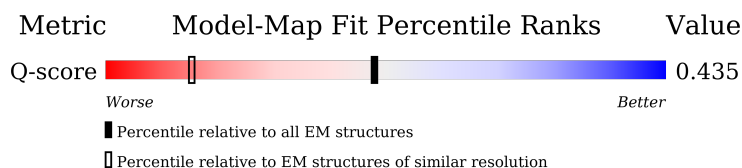
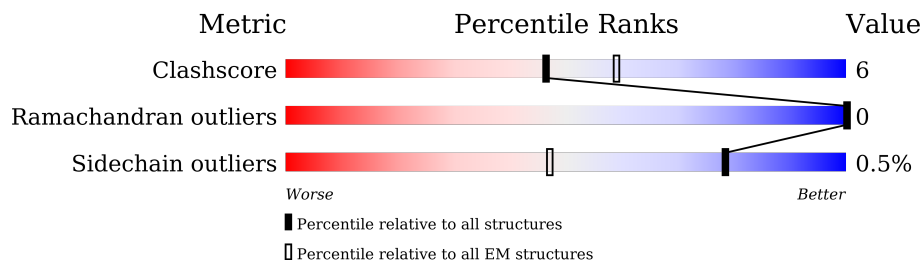
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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

Mol	Chain	Length	Quality of chain
1	A	872	
1	C	872	
2	B	872	
2	D	872	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8089 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 Potassium voltage-gated channel subfamily KQT member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	248	Total	C	N	O	S	0	0
			2016	1339	339	329	9		
1	C	249	Total	C	N	O	S	0	0
			2027	1345	343	330	9		

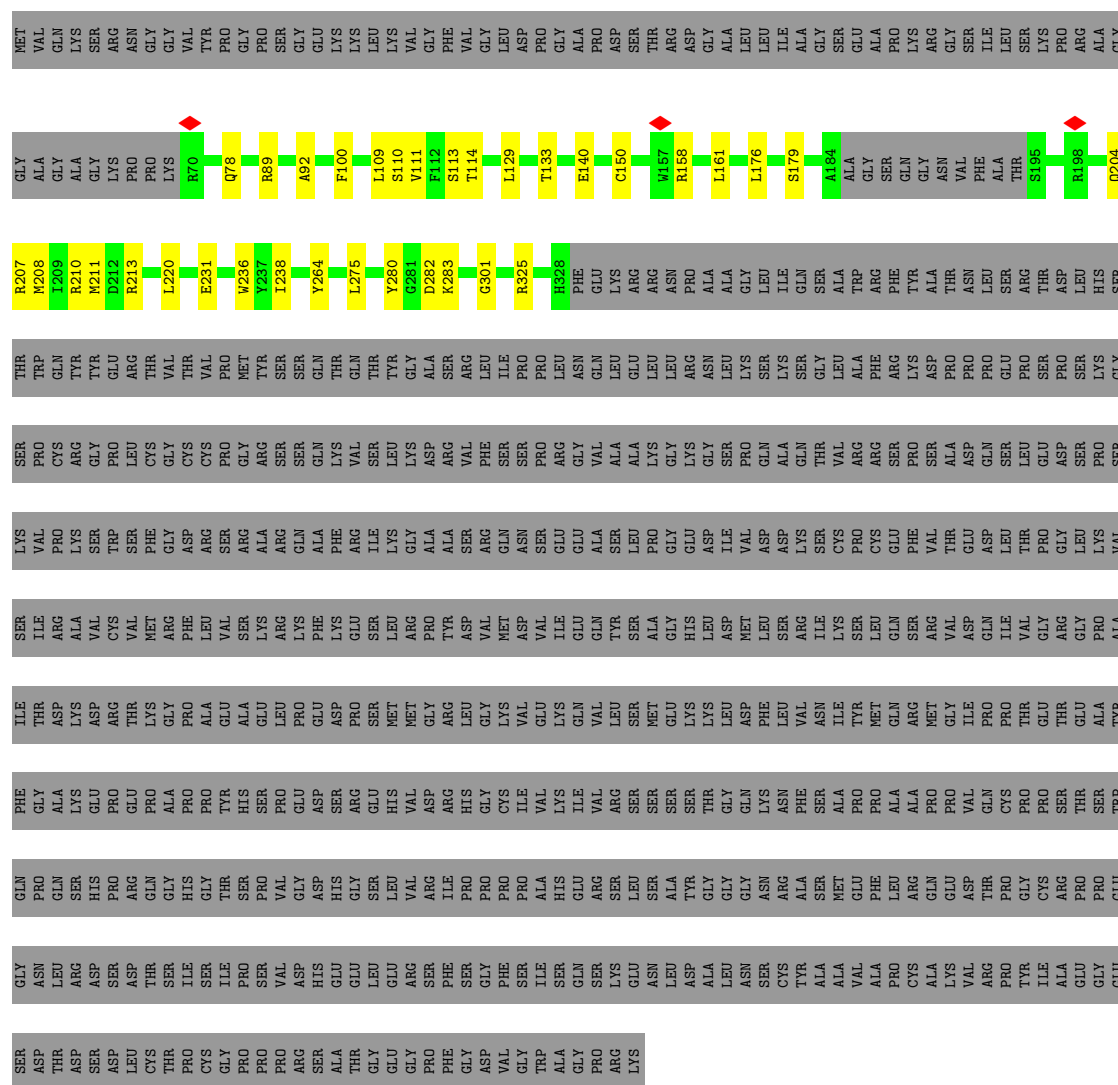
- Molecule 2 is a protein called Potassium voltage-gated channel subfamily KQT member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	251	Total	C	N	O	S	0	0
			2021	1341	337	333	10		
2	B	251	Total	C	N	O	S	0	0
			2021	1341	337	333	10		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

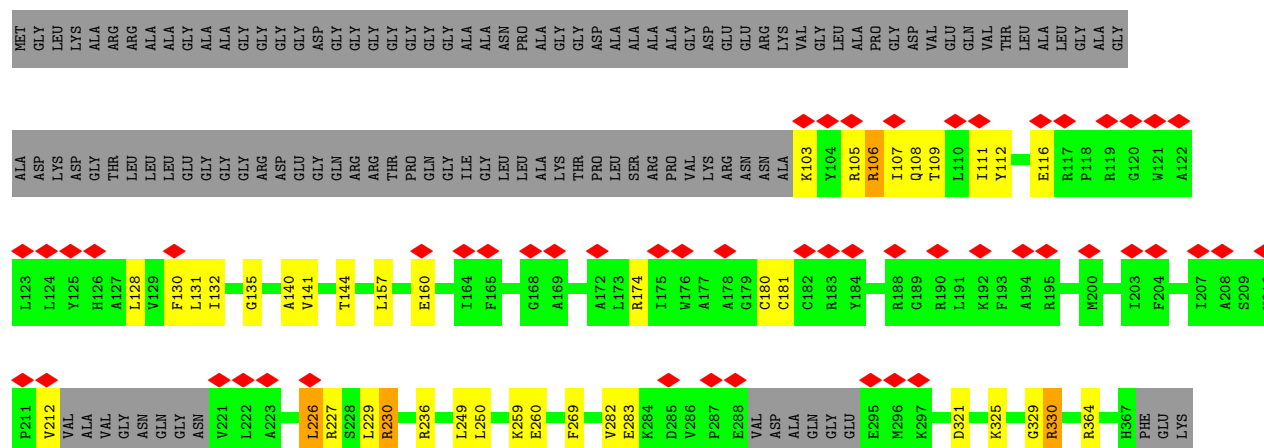
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	K	0
			1	1	
3	C	2	Total	K	0
			2	2	
3	B	1	Total	K	0
			1	1	

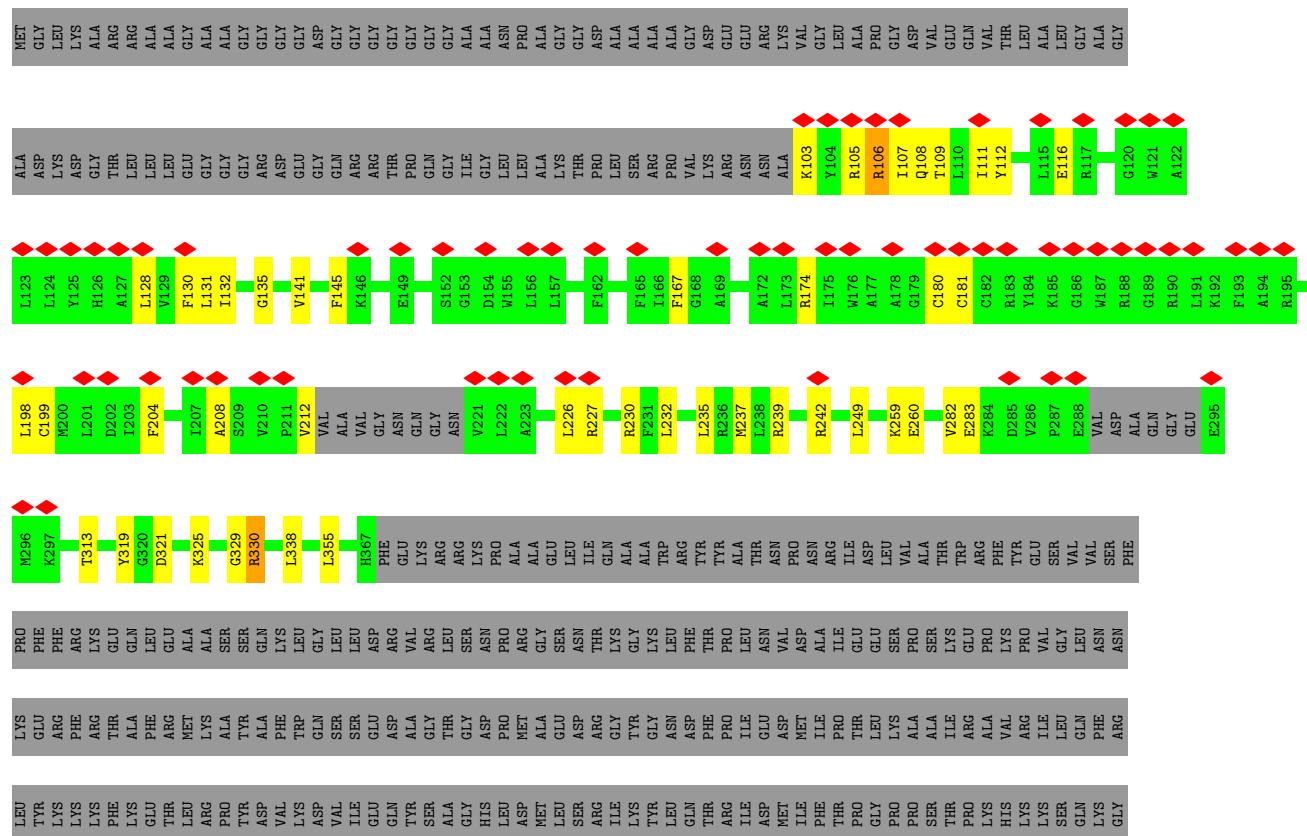
Chain C:  25% 71%



• Molecule 2: Potassium voltage-gated channel subfamily KQT member 3

Chain D:  6% 24% 71%





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	124975	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.357	Depositor
Minimum map value	-0.871	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	262.08, 262.08, 262.08	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93599993, 0.93599993, 0.93599993	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.10	0/2071	0.25	0/2805
1	C	0.11	0/2082	0.23	0/2819
2	B	0.22	0/2070	0.35	0/2801
2	D	0.21	0/2070	0.33	0/2801
All	All	0.17	0/8293	0.30	0/11226

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
1	A	0	1
1	C	0	1
2	B	0	4
2	D	0	4
All	All	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	ARG	Sidechain
1	C	213	ARG	Sidechain
2	D	105	ARG	Sidechain
2	D	106	ARG	Sidechain
2	D	227	ARG	Sidechain

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	2016	0	2053	26	0
1	C	2027	0	2066	25	0
2	B	2021	0	2101	45	0
2	D	2021	0	2101	26	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
All	All	8089	0	8321	100	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 6.

The worst 5 of 100 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:208:ALA:HB1	2:B:232:LEU:HD12	1.61	0.82
1:A:264:TYR:CD2	2:B:141:VAL:HG22	2.19	0.77
2:B:212:VAL:CG1	2:B:226:LEU:HD12	2.15	0.77
2:B:212:VAL:HG13	2:B:226:LEU:HD12	1.68	0.75
1:A:264:TYR:HD2	2:B:141:VAL:HG22	1.53	0.72

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	244/872 (28%)	244 (100%)	0	0	100	100
1	C	245/872 (28%)	244 (100%)	1 (0%)	0	100	100
2	B	245/872 (28%)	240 (98%)	5 (2%)	0	100	100
2	D	245/872 (28%)	240 (98%)	5 (2%)	0	100	100
All	All	979/3488 (28%)	968 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	207/728 (28%)	207 (100%)	0	100	100
1	C	208/728 (29%)	208 (100%)	0	100	100
2	B	209/725 (29%)	208 (100%)	1 (0%)	81	92
2	D	209/725 (29%)	206 (99%)	3 (1%)	59	82
All	All	833/2906 (29%)	829 (100%)	4 (0%)	78	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	226	LEU
2	D	230	ARG
2	D	330	ARG
2	B	330	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	HIS
1	C	78	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](#)

Of 4 ligands modelled in this entry, 4 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.

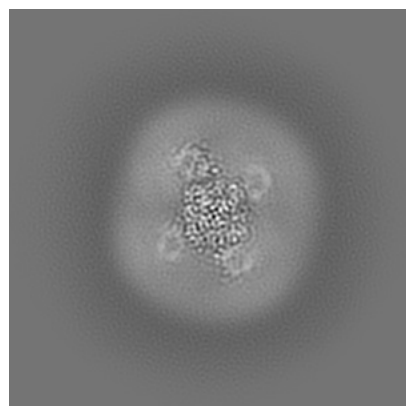
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68153. These allow visual inspection of the internal detail of the map and identification of artifacts.

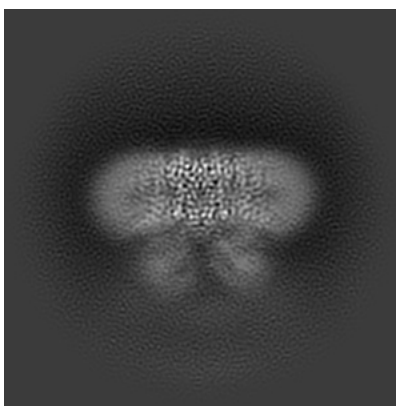
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

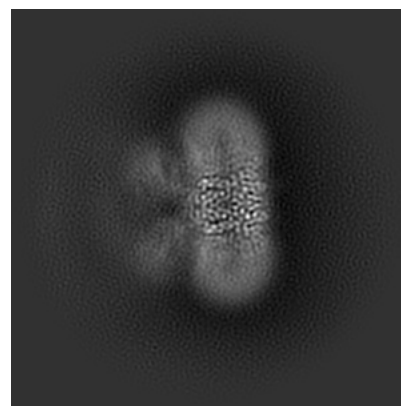
6.1.1 Primary map



X

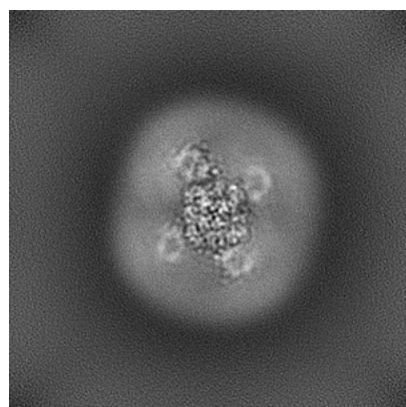


Y

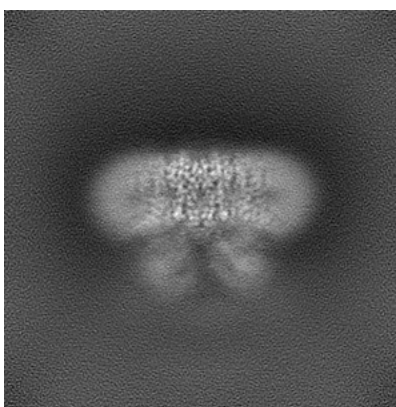


Z

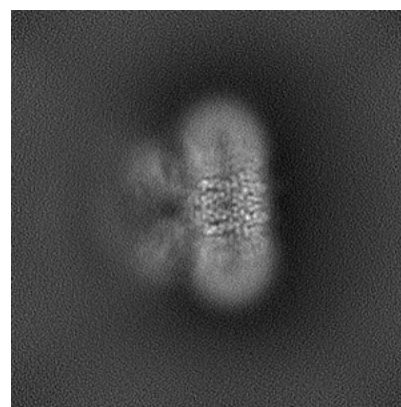
6.1.2 Raw map



X



Y

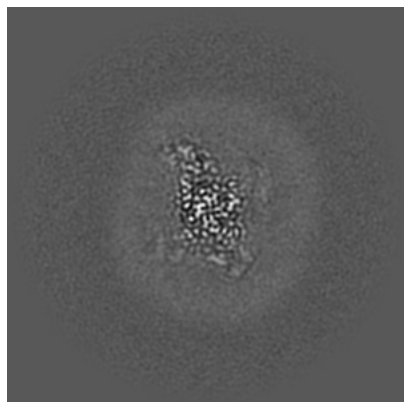


Z

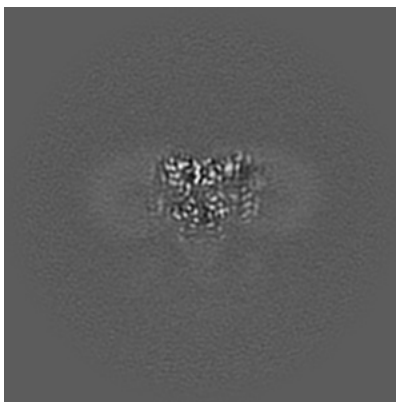
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

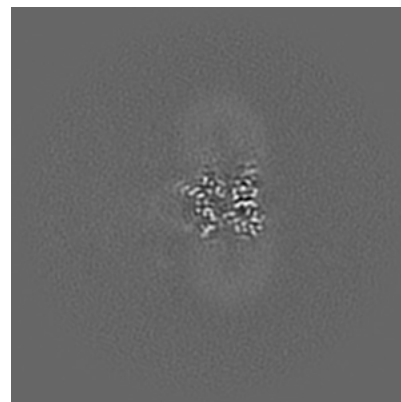
6.2.1 Primary map



X Index: 140

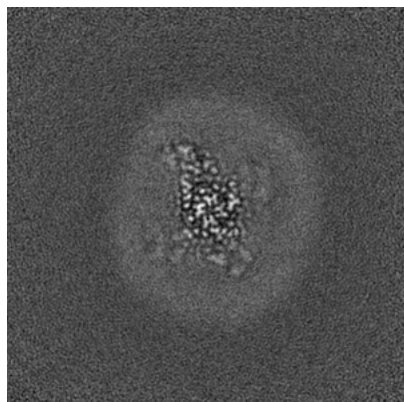


Y Index: 140

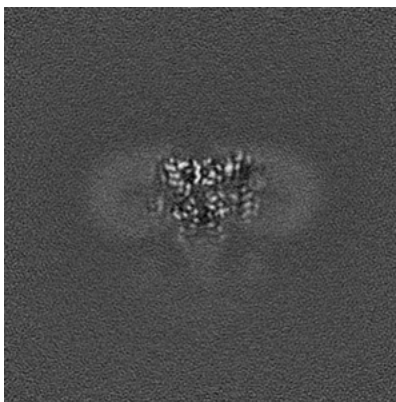


Z Index: 140

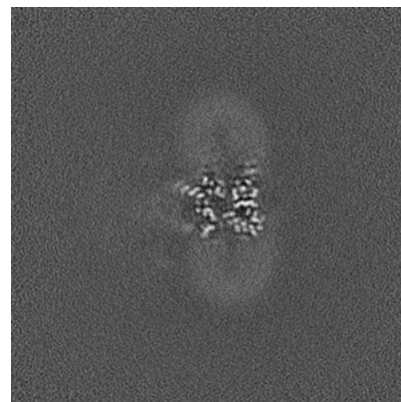
6.2.2 Raw map



X Index: 140



Y Index: 140

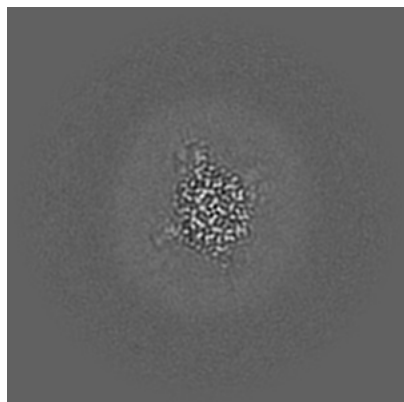


Z Index: 140

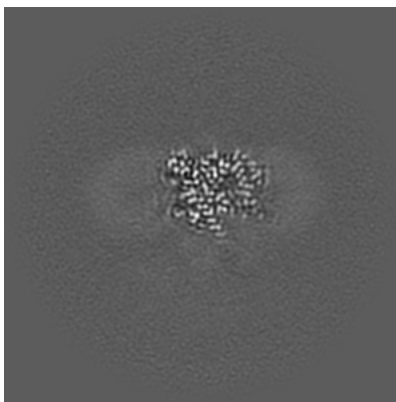
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

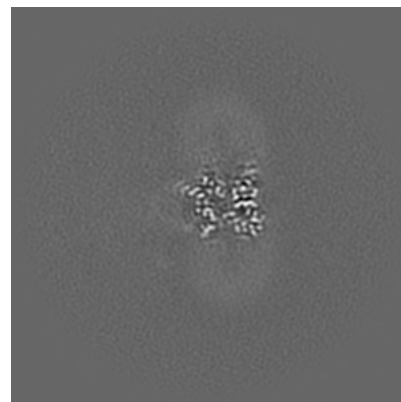
6.3.1 Primary map



X Index: 166

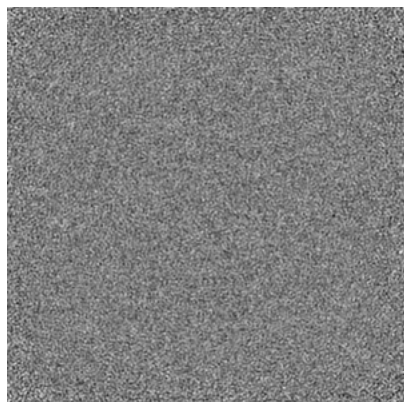


Y Index: 135

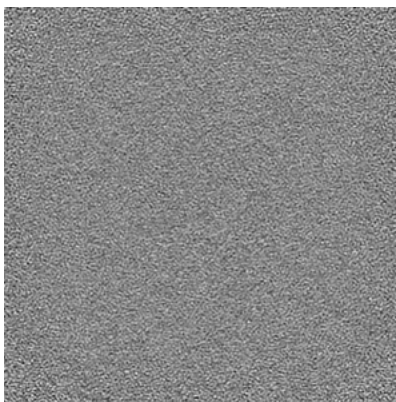


Z Index: 140

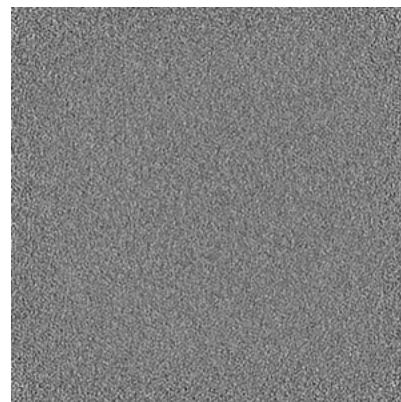
6.3.2 Raw map



X Index: 0



Y Index: 0

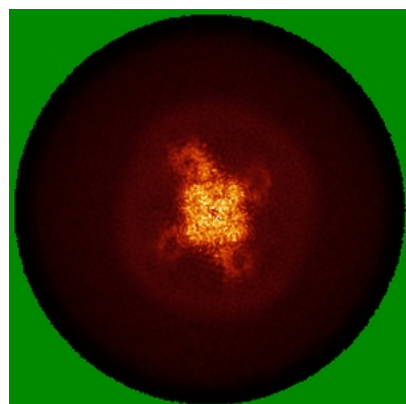


Z Index: 279

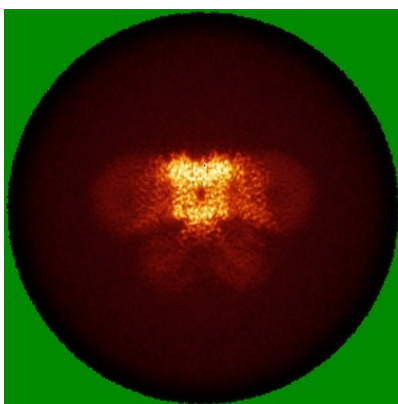
The images above show the largest variance slices of the map in three orthogonal directions.

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

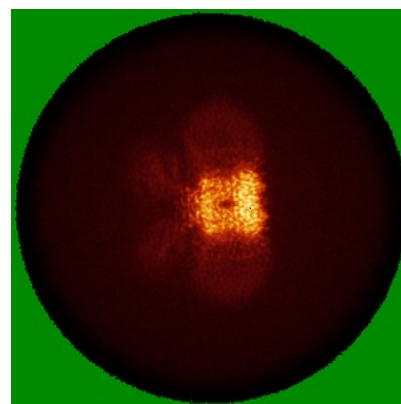
6.4.1 Primary map



X

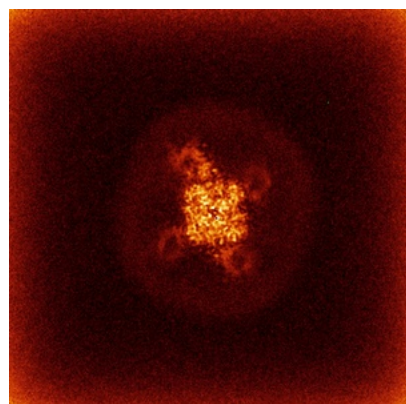


Y

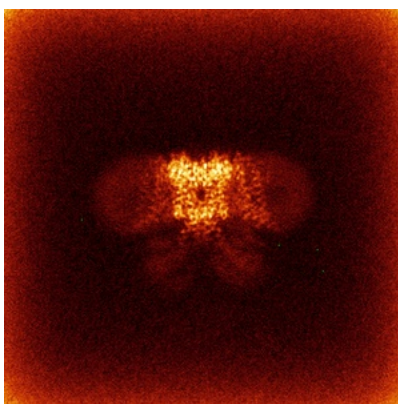


Z

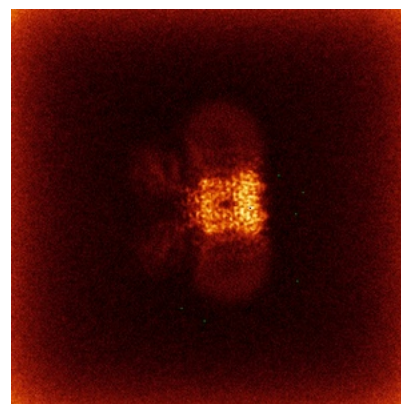
6.4.2 Raw map



X



Y

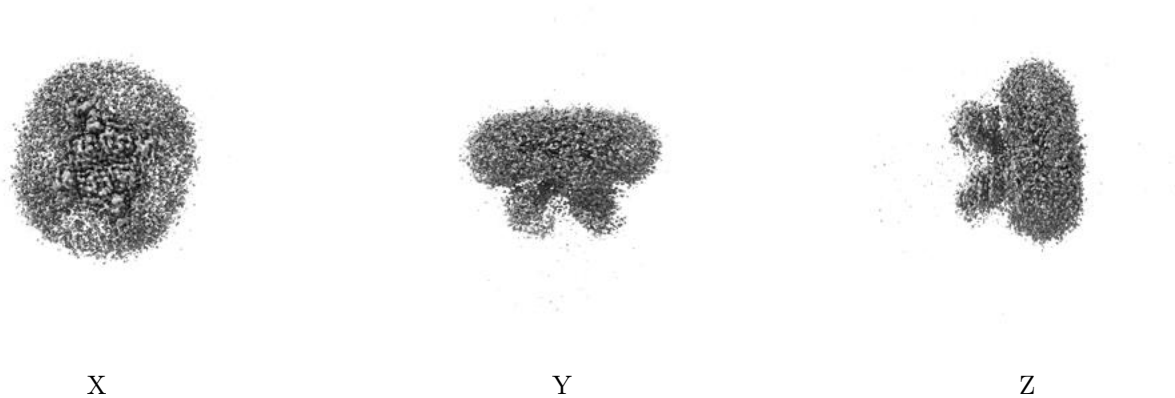


Z

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.

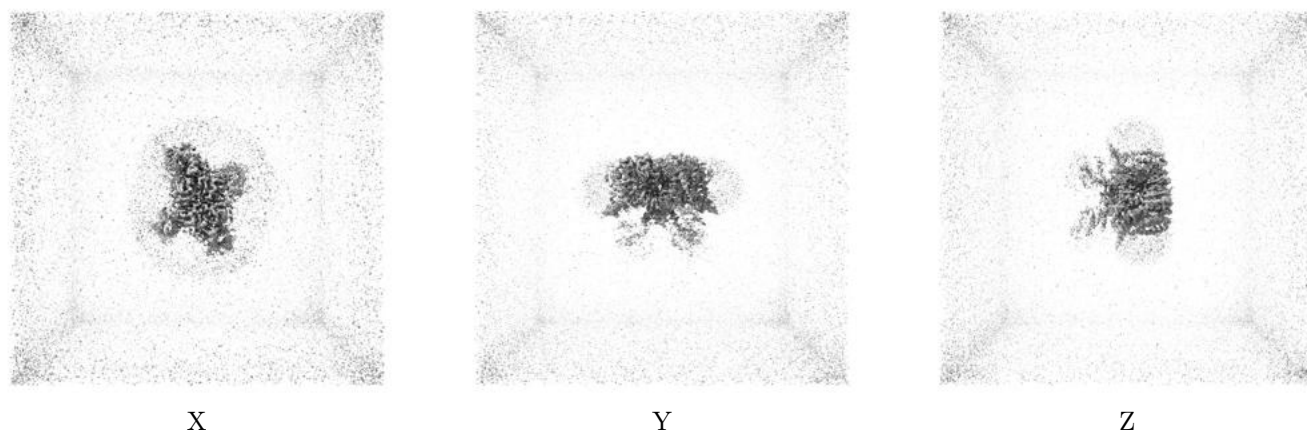
6.5 Orthogonal surface views [i](#)

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.

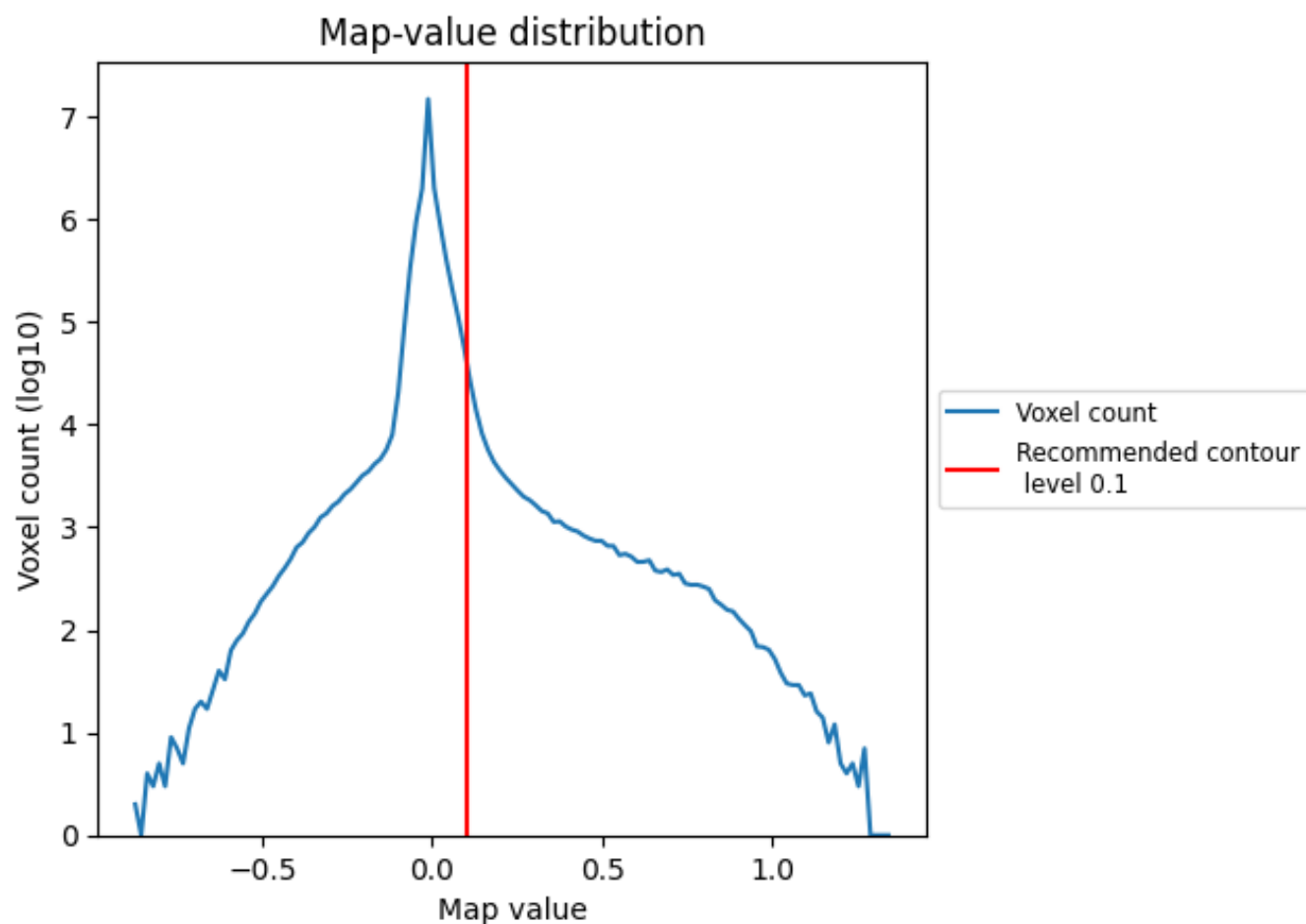
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

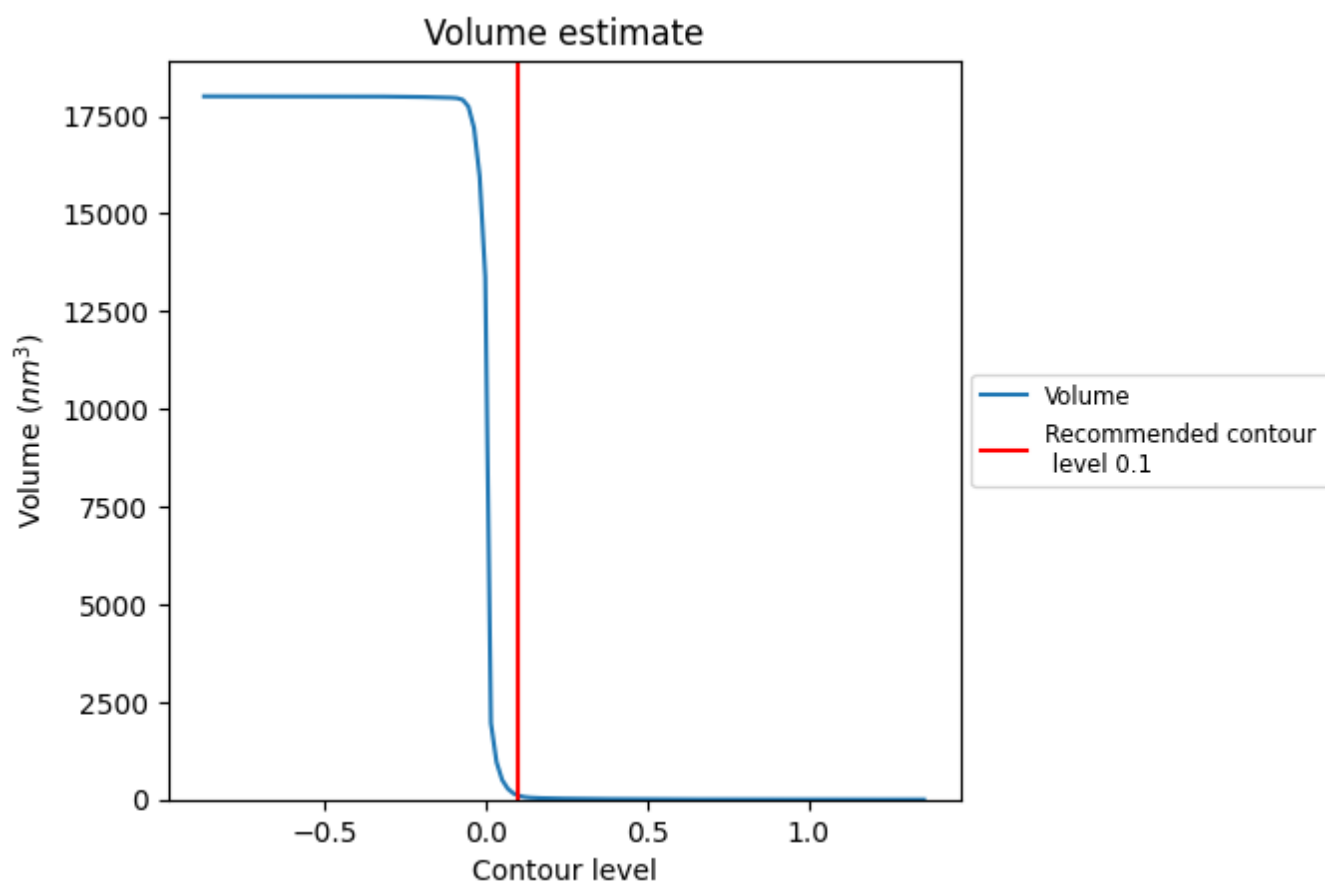
This section contains the results of statistical analysis of the map.

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.

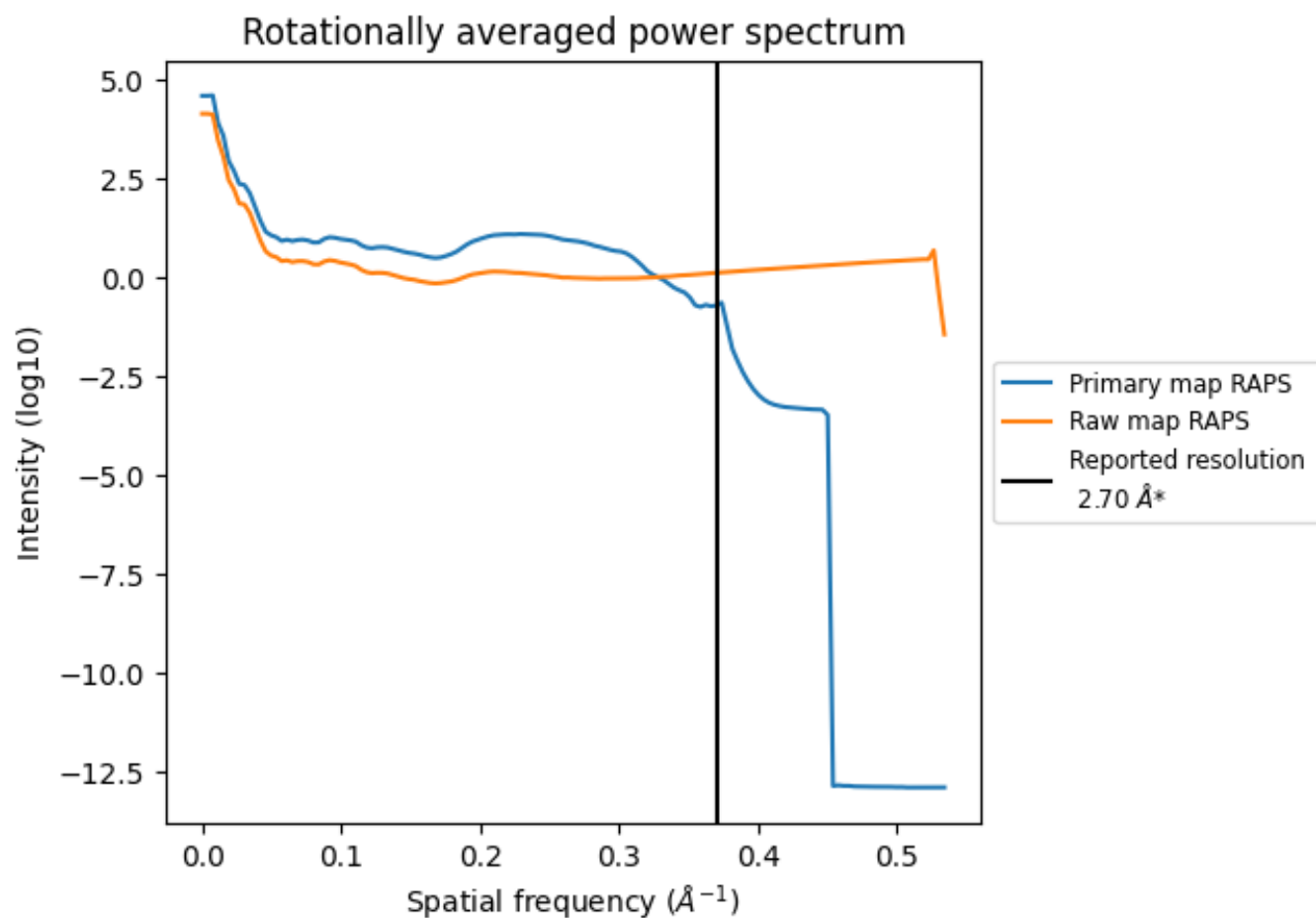
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108 nm³; this corresponds to an approximate mass of 98 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 ⓘ

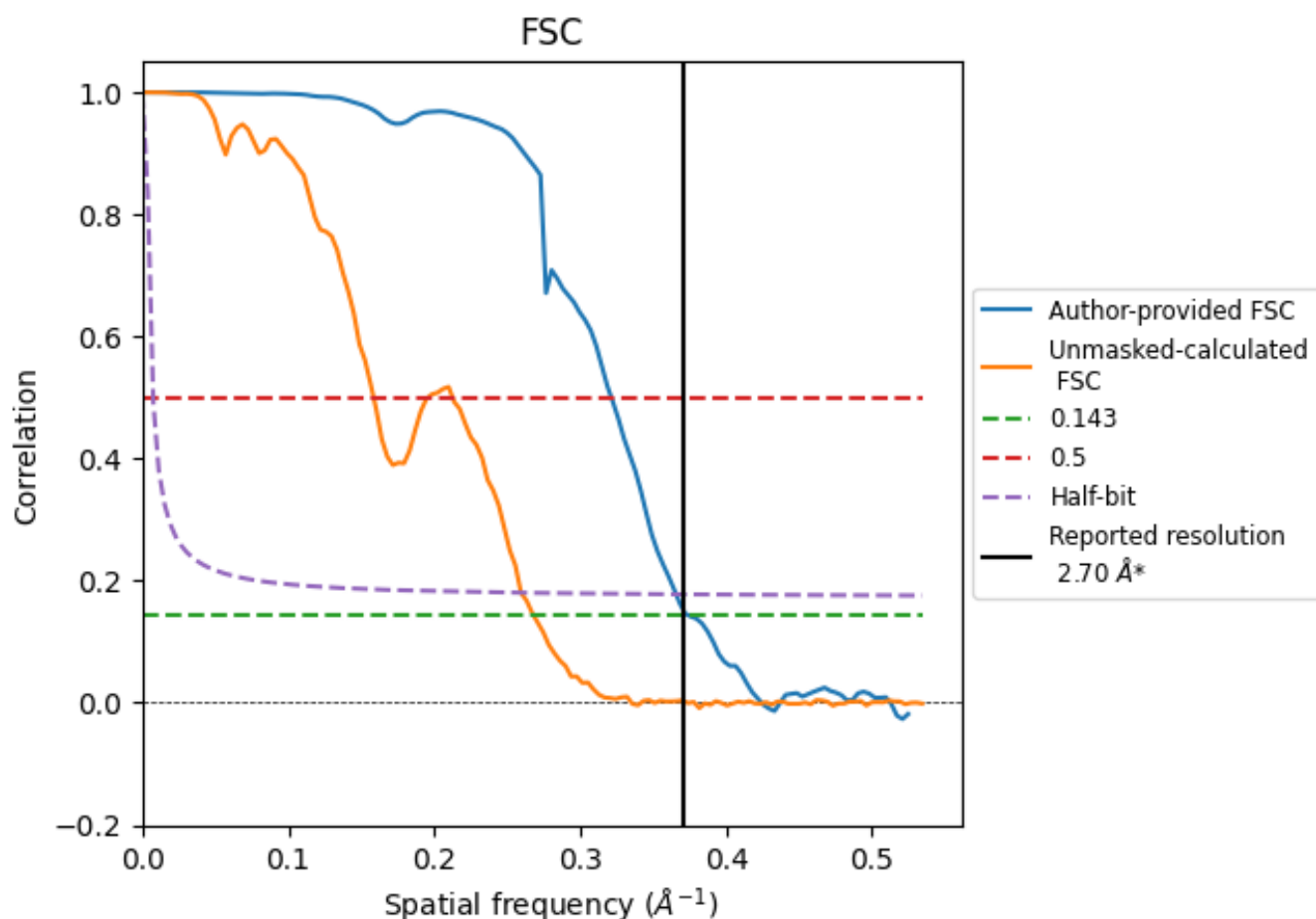


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

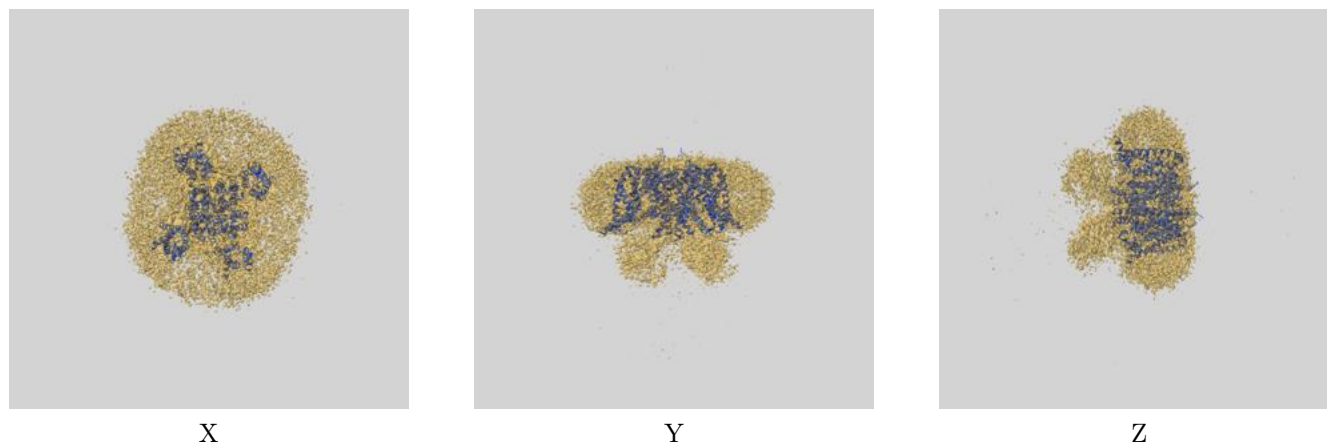
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.67	3.11	2.73
Unmasked-calculated*	3.73	6.31	3.86

*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 3.73 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

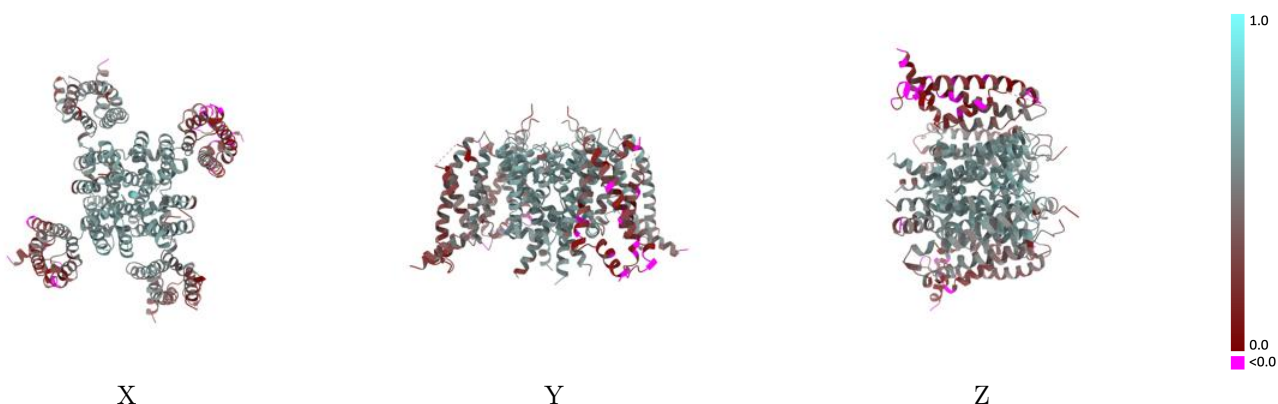
This section contains information regarding the fit between EMDB map EMD-68153 and PDB model 22BK. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



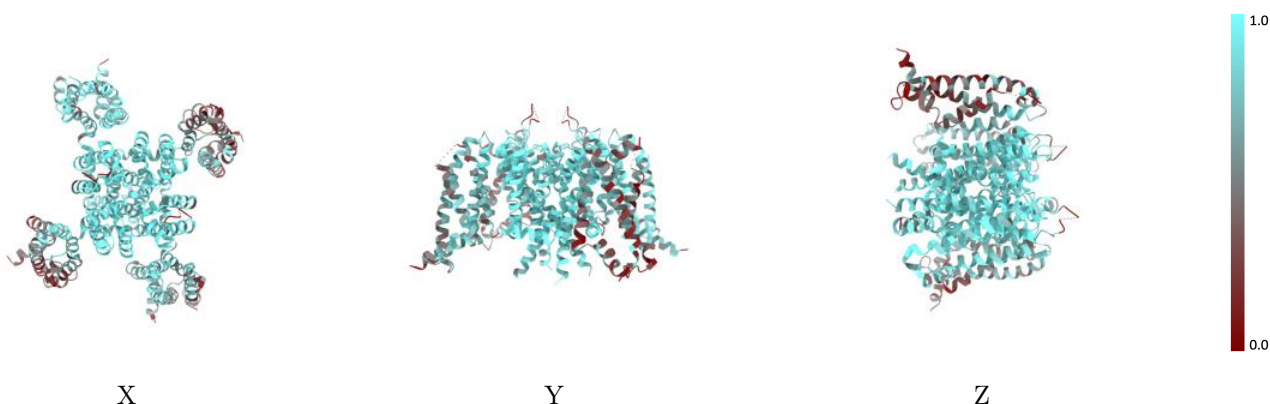
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



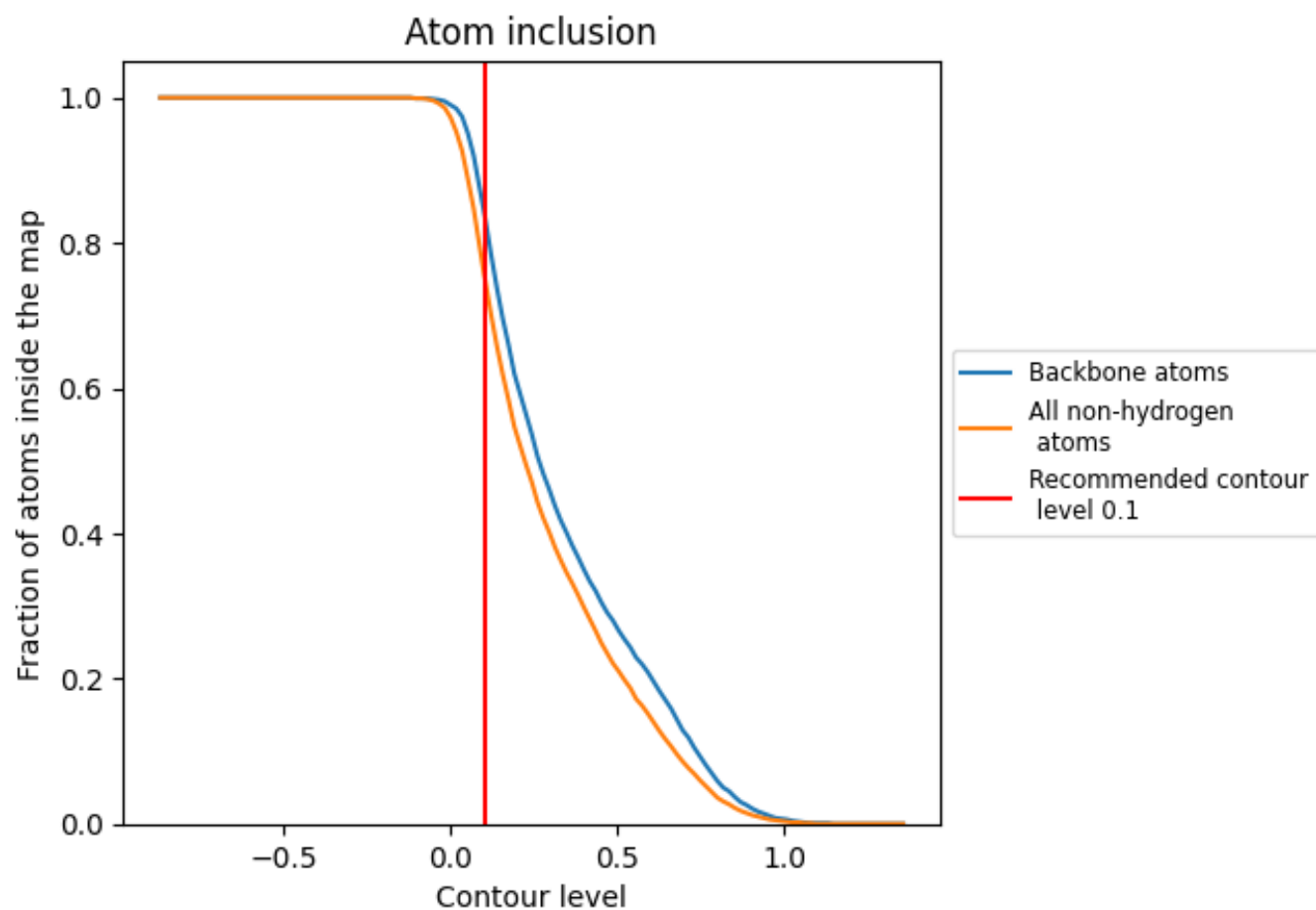
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% of all backbone atoms, 76% 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> 0.7560	<div></div> 0.4350
A	<div></div> 0.8060	<div></div> 0.4680
B	<div></div> 0.6520	<div></div> 0.3560
C	<div></div> 0.8770	<div></div> 0.5130
D	<div></div> 0.6900	<div></div> 0.4010

