



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 10:30 AM EST

PDB ID : 6V9W
EMDB ID : EMD-21128
Title : Structure of TRPA1 (ligand-free) with bound calcium, LMNG
Authors : Zhao, J.; Lin King, J.V.; Paulsen, C.E.; Cheng, Y.; Julius, D.
Deposited on : 2019-12-16
Resolution : 3.10 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

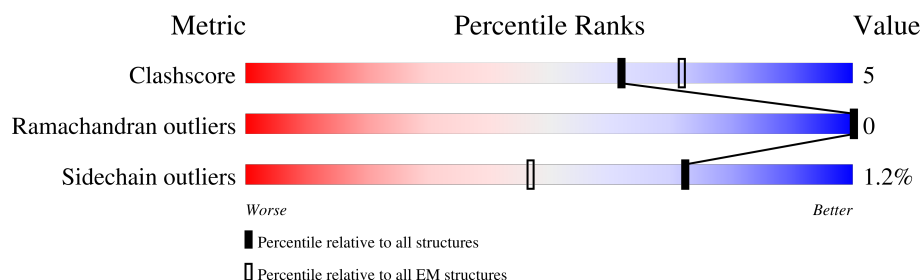
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1119	
1	B	1119	
1	C	1119	
1	D	1119	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18812 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 Transient receptor potential cation channel subfamily A member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	597	Total	C	N	O	S	0	0
			4702	3088	781	799	34		
1	B	597	Total	C	N	O	S	0	0
			4702	3088	781	799	34		
1	D	597	Total	C	N	O	S	0	0
			4702	3088	781	799	34		
1	C	597	Total	C	N	O	S	0	0
			4702	3088	781	799	34		

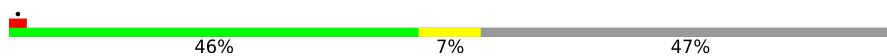
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	966	ASP	GLU	engineered mutation	UNP O75762
B	966	ASP	GLU	engineered mutation	UNP O75762
D	966	ASP	GLU	engineered mutation	UNP O75762
C	966	ASP	GLU	engineered mutation	UNP O75762

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

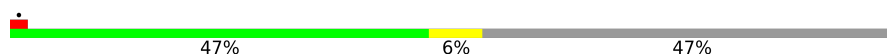
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Ca	0
			1	1	
2	B	1	Total	Ca	0
			1	1	
2	D	1	Total	Ca	0
			1	1	
2	C	1	Total	Ca	0
			1	1	

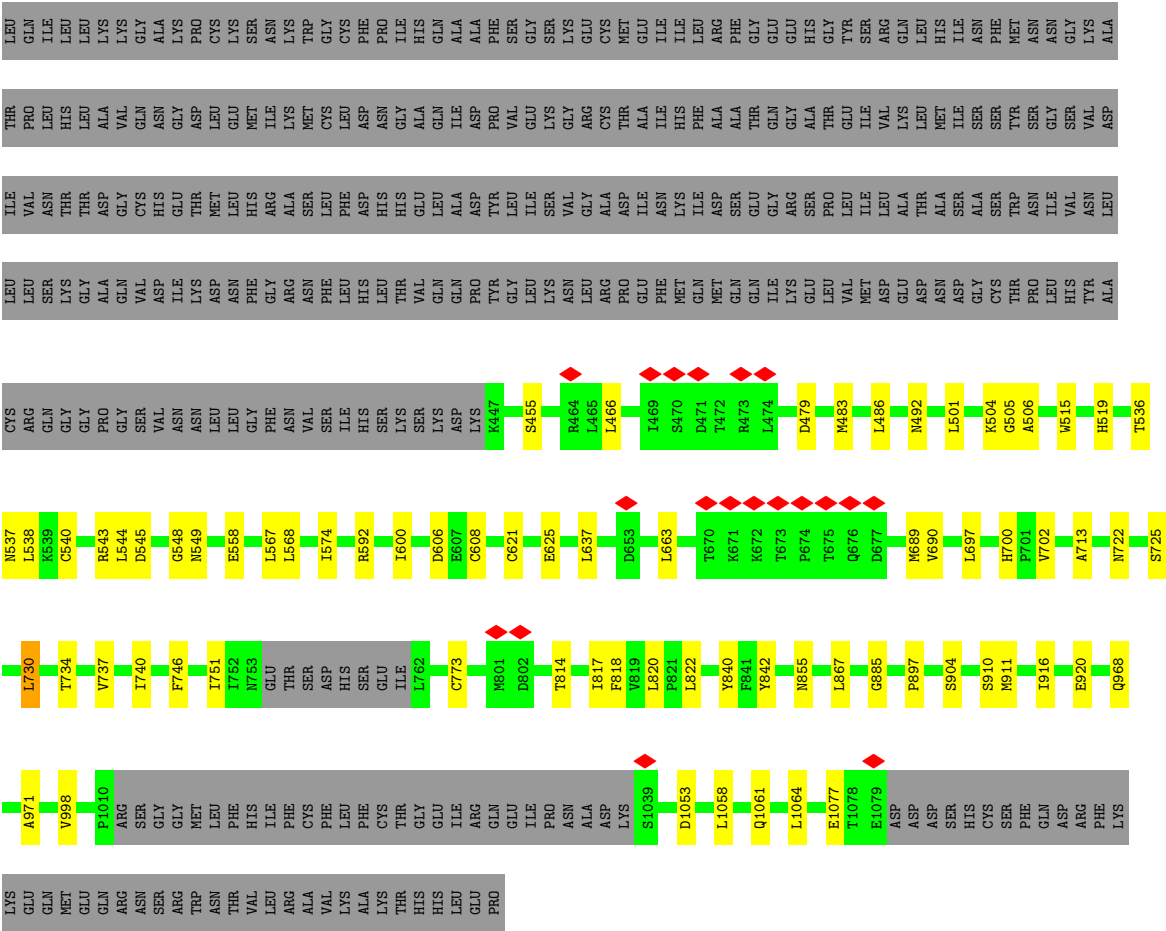
Chain B:



ASP	L880	L697	T516	CYS	LEU	ILE	THR	LEU	ASP	THR	LEU	GLN	GLY	ASP	THR	MET
ASP	L880	H700	H519	ARG	LEU	VAL	PRO	LEU	ASP	PRO	LEU	GLN	ALA	MET	LYS	LYS
SER	A883	V701	H519	GLN	SER	ASN	ASN	ASN	ASN	THR	HIS	ILE	ASN	ASP	ASP	ASP
HIS	V702	V702	T536	GLY	GLY	THR	THR	GLY	THR	THR	LEU	LEU	ASN	PHE	THR	THR
CYS	S910	W711	N537	PRO	ALA	ASP	ALA	GLN	ASP	ALA	ALA	LYS	LEU	PHE	ARG	ARG
SER	E920	L712	K539	GLY	VAL	CYS	VAL	VAL	GLY	GLN	VAL	LYS	ARG	LEU	LYS	LYS
PHE	L712	A713	K539	SER	VAL	ASN	VAL	ASP	HIS	ASN	HIS	GLY	ALA	TYR	MET	MET
GLN	A713	A713	C540	ASN	ASN	ASN	ASN	ILE	GLU	GLY	GLY	LYS	PHE	TYR	ARG	ARG
ASP	E924	F716	T541	ASN	LYS	THR	ASP	LYS	THR	ASP	ASP	PRO	MET	ALA	PRO	GLY
ARG	E924	F716	D542	LEU	ASP	MET	LEU	ASP	LEU	LEU	LEU	CYS	MET	ALA	ALA	GLY
PHE	E928	N722	E543	LEU	ASN	LEU	LEU	ASN	LEU	GLU	GLU	LYS	ALA	GLU	GLU	GLY
LYS	E928	N722	E543	LEU	ASN	LEU	LEU	ASN	LEU	GLU	GLU	LYS	ALA	GLU	GLU	GLY
LYS	Q969	S725	L544	GLY	PHE	GLY	GLY	PHE	HIS	MET	MET	LYS	PRO	GLY	LYS	LYS
GLU	Q969	S725	D545	PHE	GLY	GLY	GLY	GLY	HIS	ILE	ASN	ASN	LEU	GLN	VAL	VAL
GLU	A971	L730	E546	ASN	VAL	ASN	ASN	PHE	LEU	CYS	CYS	GLY	ALA	LEU	GLN	GLN
MET	A971	L730	D547	VAL	VAL	ASN	ASN	ASN	LEU	ASN	ASN	TRP	ILE	GLY	PRO	PRO
GLU	V998	T734	G548	SER	SER	PHE	SER	LEU	LEU	CYS	CYS	GLY	ALA	LEU	LEU	GLN
GLN	V998	T734	N549	ILE	ILE	LEU	ILE	LEU	LEU	LEU	LEU	CYS	VAL	MET	GLY	GLY
ARG	P1010	V737	E558	HIS	HIS	LEU	HIS	HIS	ASP	ASP	ASP	PHE	GLN	GLY	VAL	VAL
ASN	P1010	V737	E558	SER	SER	LEU	SER	LEU	ASN	ASN	ASN	GLN	GLN	ASN	ARG	ASN
SER	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ARG	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
TRP	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ASN	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LEU	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ARG	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LYS	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LYS	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LEU	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ARG	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LYS	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
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LEU	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ARG	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
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ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
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LEU	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
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VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LYS	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
VAL	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
LEU	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ARG	P1010	V737	E558	LYS	LYS	THR	LYS	THR	THR	THR	THR	HIS	ASN	THR	THR	GLY
ALA	P1010	V737	E558	LYS	LYS	THR	LY									

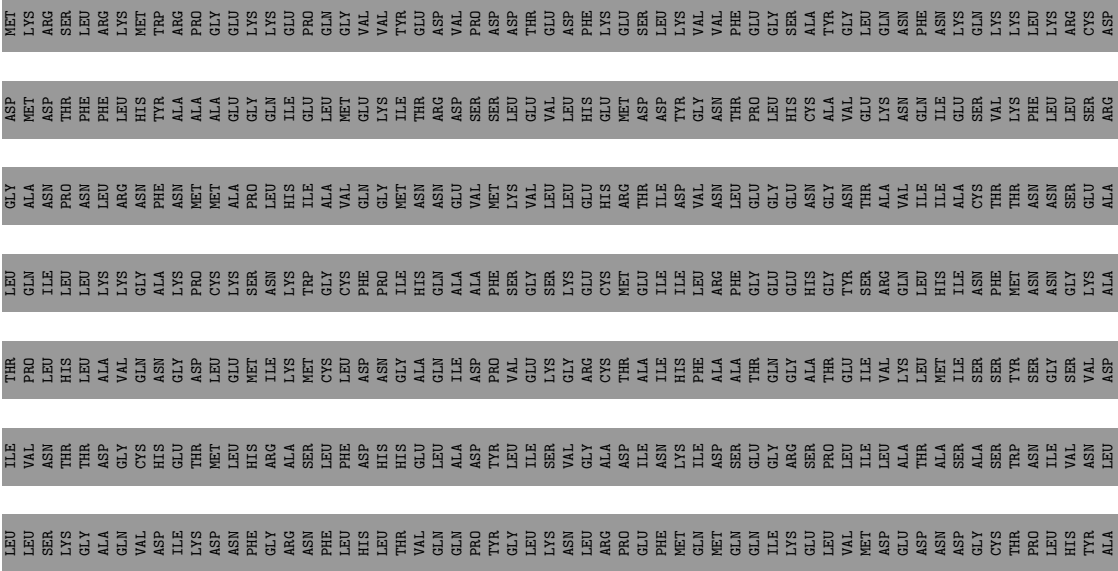
Chain D:

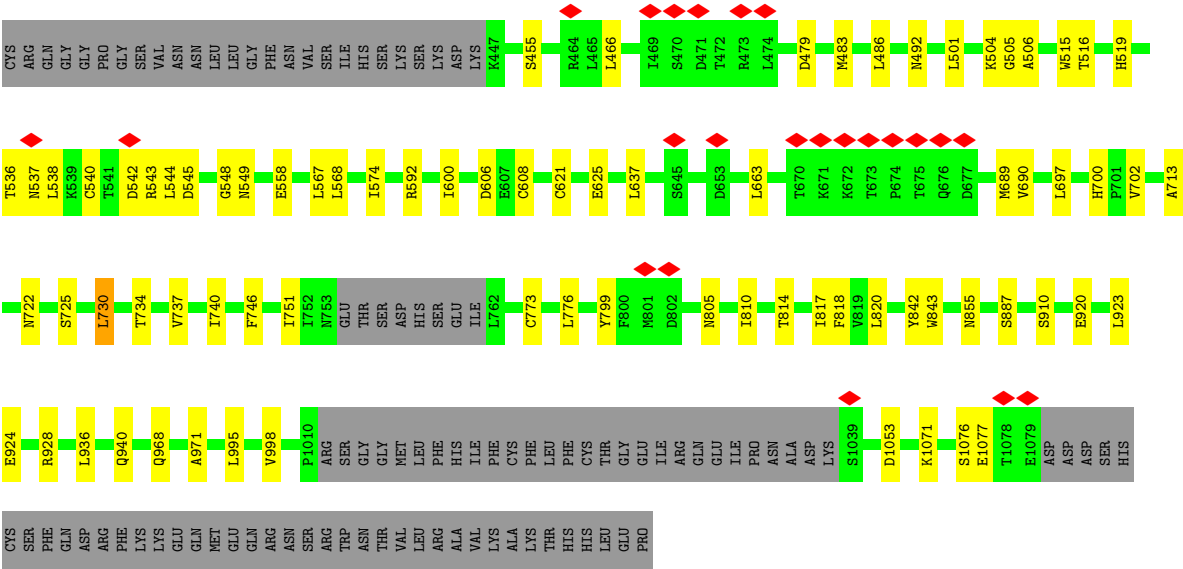
[illegible]



● Molecule 1: Transient receptor potential cation channel subfamily A member 1

Chain C: 46% 7% 47%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	130595	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	33.166	Depositor
Minimum map value	-14.046	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.8	Depositor
Map size (Å)	311.1936, 311.1936, 311.1936	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2156, 1.2156, 1.2156	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	0.41	0/4810	0.55	1/6527 (0.0%)
1	B	0.41	0/4810	0.55	1/6527 (0.0%)
1	C	0.41	0/4810	0.55	1/6527 (0.0%)
1	D	0.41	0/4810	0.55	1/6527 (0.0%)
All	All	0.41	0/19240	0.55	4/26108 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	538	LEU	CA-CB-CG	6.76	130.85	115.30
1	A	538	LEU	CA-CB-CG	6.75	130.81	115.30
1	B	538	LEU	CA-CB-CG	6.75	130.82	115.30
1	C	538	LEU	CA-CB-CG	6.74	130.80	115.30

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	4702	0	4733	47	0
1	B	4702	0	4733	45	0
1	C	4702	0	4733	46	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4702	0	4733	42	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	18812	0	18932	171	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 5.

The worst 5 of 171 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:D:600:ILE:HD11	1:D:637:LEU:HD13	1.75	0.69
1:C:740:ILE:HD12	1:C:751:ILE:HD11	1.75	0.69
1:B:740:ILE:HD12	1:B:751:ILE:HD11	1.75	0.69
1:C:600:ILE:HD11	1:C:637:LEU:HD13	1.75	0.68
1:D:740:ILE:HD12	1:D:751:ILE:HD11	1.75	0.67

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	591/1119 (53%)	563 (95%)	28 (5%)	0	100	100
1	B	591/1119 (53%)	563 (95%)	28 (5%)	0	100	100
1	C	591/1119 (53%)	563 (95%)	28 (5%)	0	100	100
1	D	591/1119 (53%)	563 (95%)	28 (5%)	0	100	100
All	All	2364/4476 (53%)	2252 (95%)	112 (5%)	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	496/995 (50%)	490 (99%)	6 (1%)	71	88
1	B	496/995 (50%)	490 (99%)	6 (1%)	71	88
1	C	496/995 (50%)	490 (99%)	6 (1%)	71	88
1	D	496/995 (50%)	490 (99%)	6 (1%)	71	88
All	All	1984/3980 (50%)	1960 (99%)	24 (1%)	72	88

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	730	LEU
1	D	920	GLU
1	D	910	SER
1	C	663	LEU
1	B	663	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	907	GLN
1	C	700	HIS
1	D	512	HIS
1	C	907	GLN
1	C	494	HIS

5.3.3 RNA ⓘ

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 monosaccharides 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.

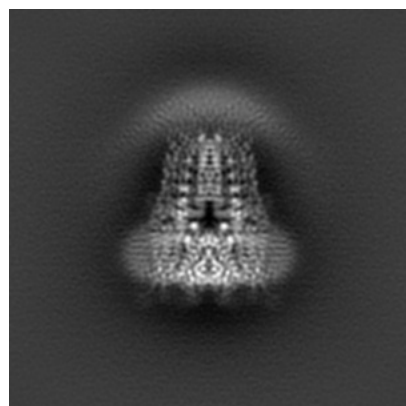
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21128. These allow visual inspection of the internal detail of the map and identification of artifacts.

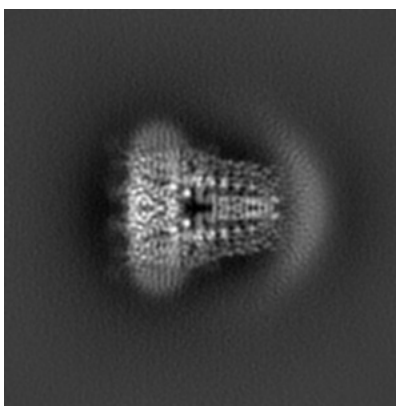
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

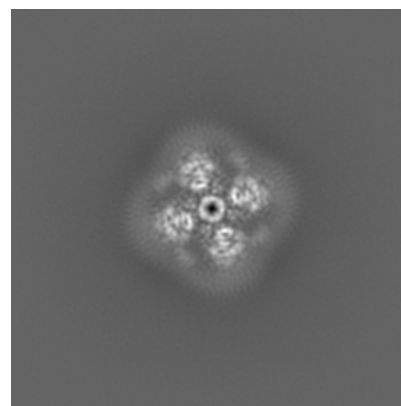
6.1.1 Primary map



X

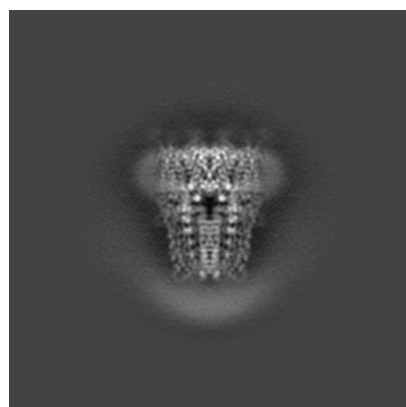


Y

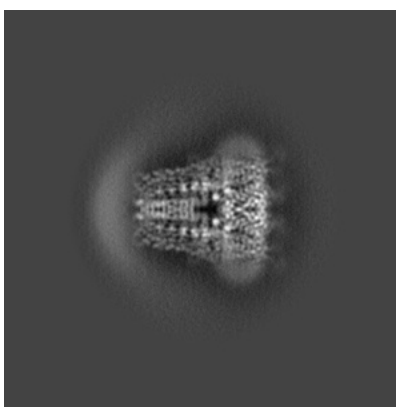


Z

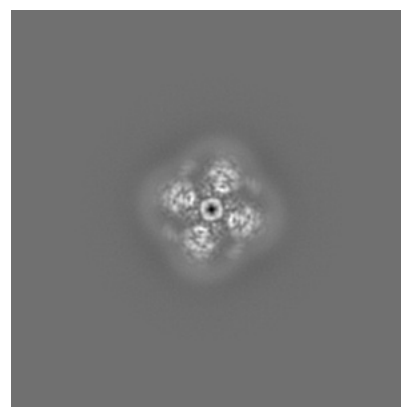
6.1.2 Raw map



X



Y

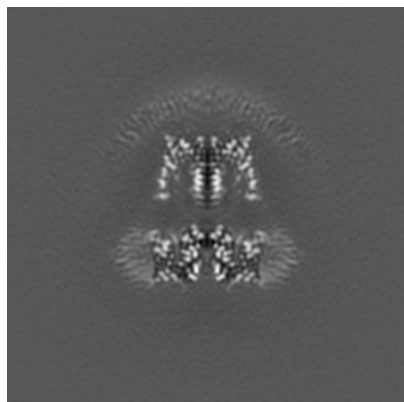


Z

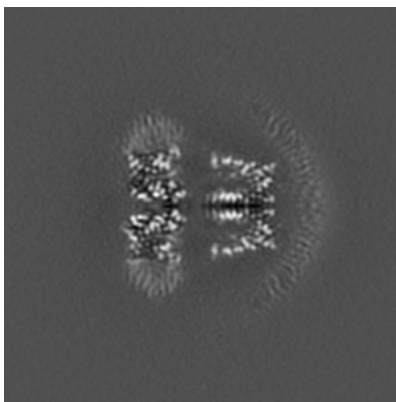
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

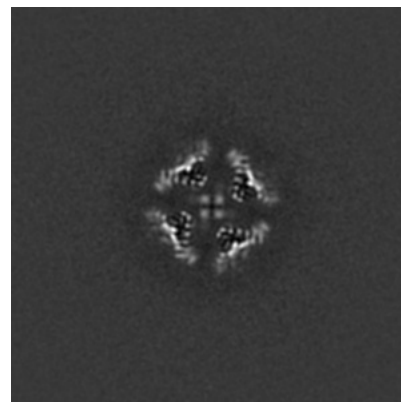
6.2.1 Primary map



X Index: 128

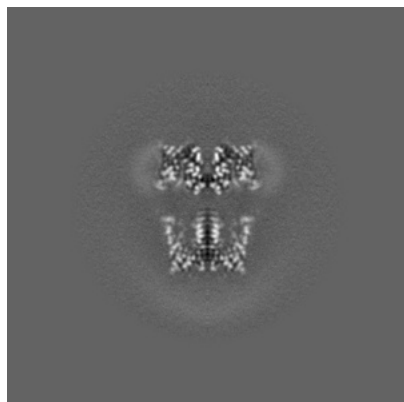


Y Index: 128

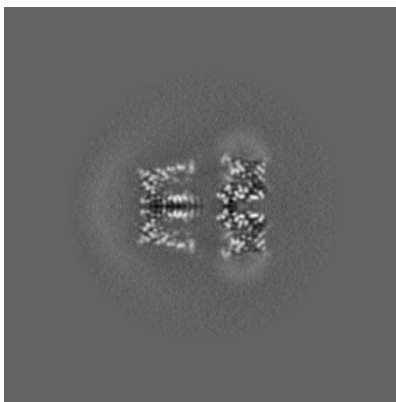


Z Index: 128

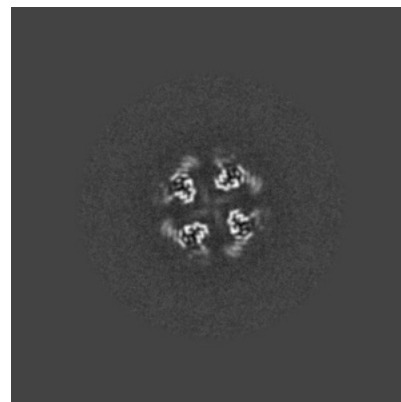
6.2.2 Raw map



X Index: 170



Y Index: 170

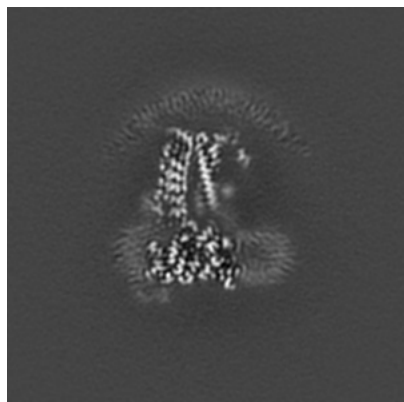


Z Index: 170

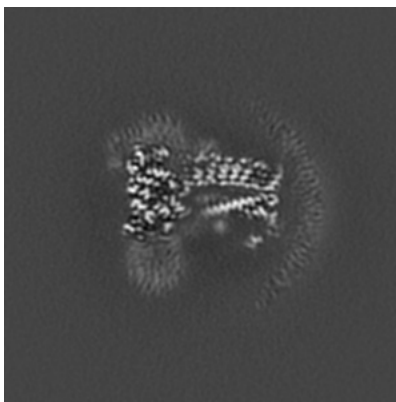
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

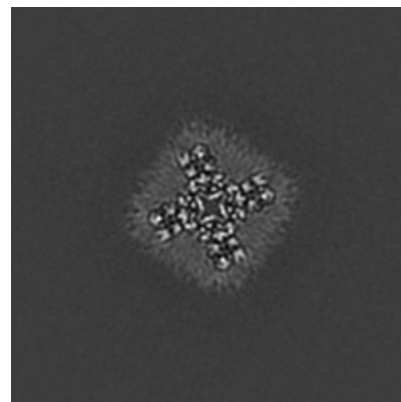
6.3.1 Primary map



X Index: 134

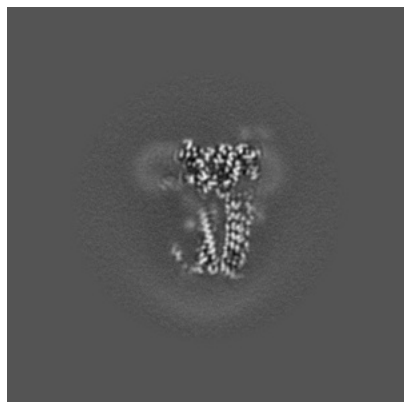


Y Index: 134

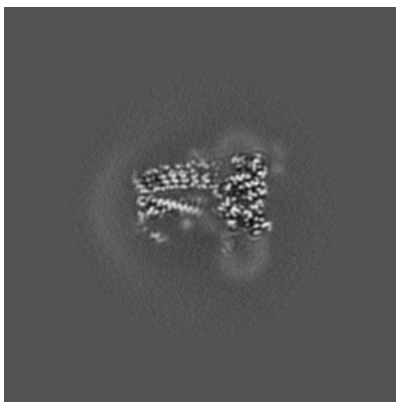


Z Index: 86

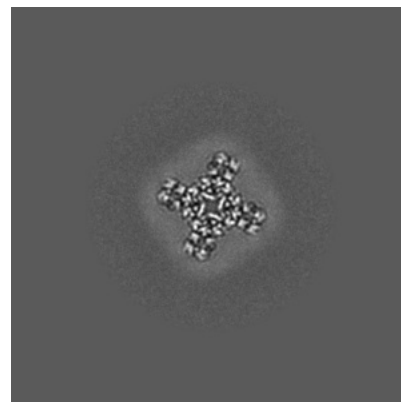
6.3.2 Raw map



X Index: 177



Y Index: 163

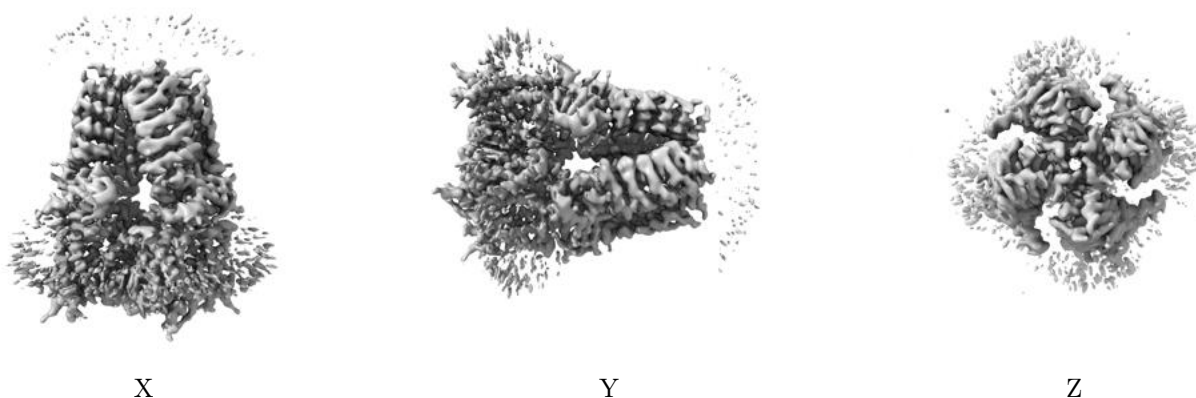


Z Index: 214

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

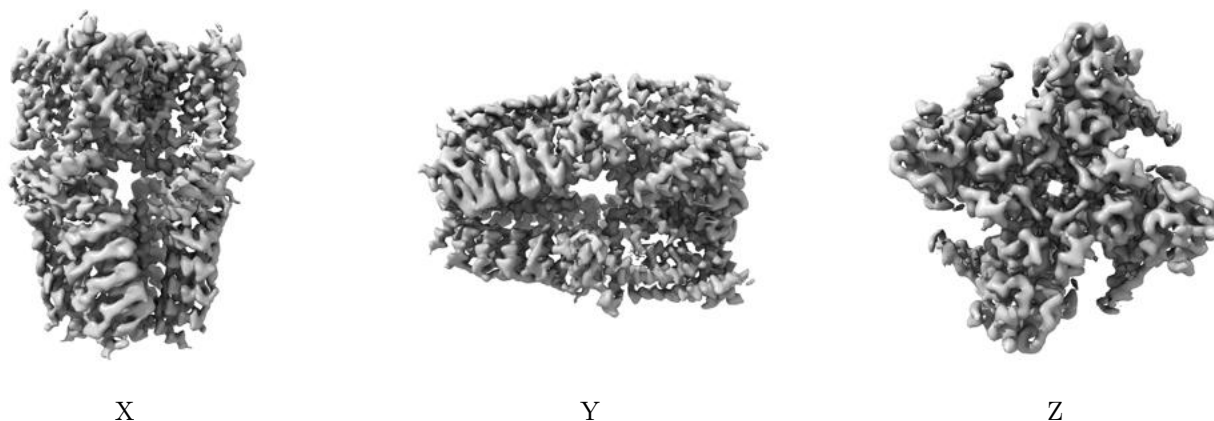
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

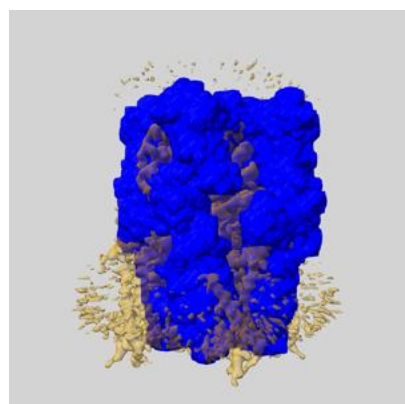
6.5 Mask visualisation [i](#)

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

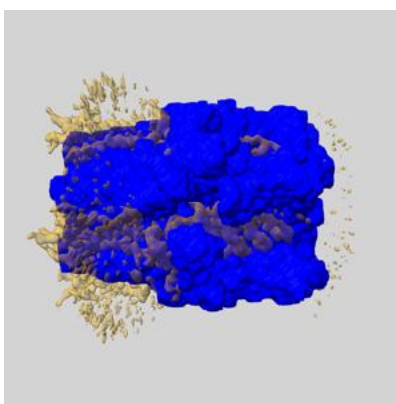
A mask typically either:

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

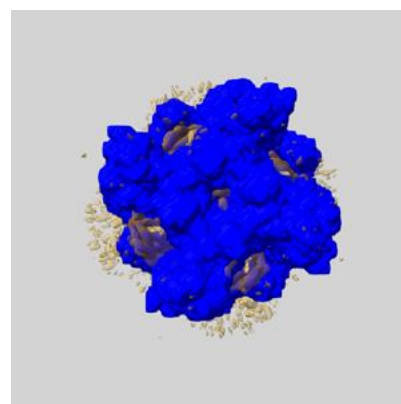
6.5.1 emd_21128_msk_1.map [i](#)



X



Y

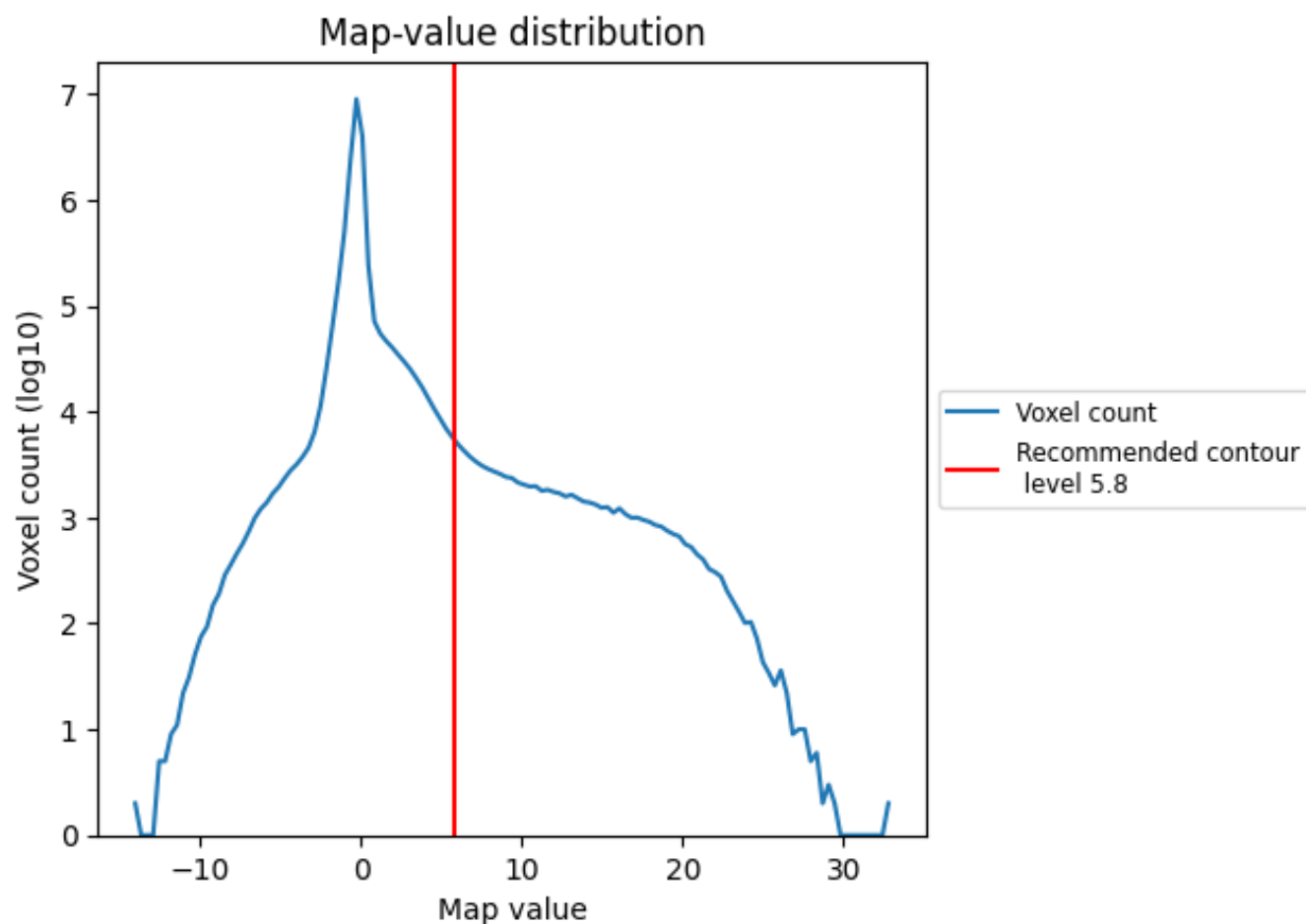


Z

7 Map analysis [i](#)

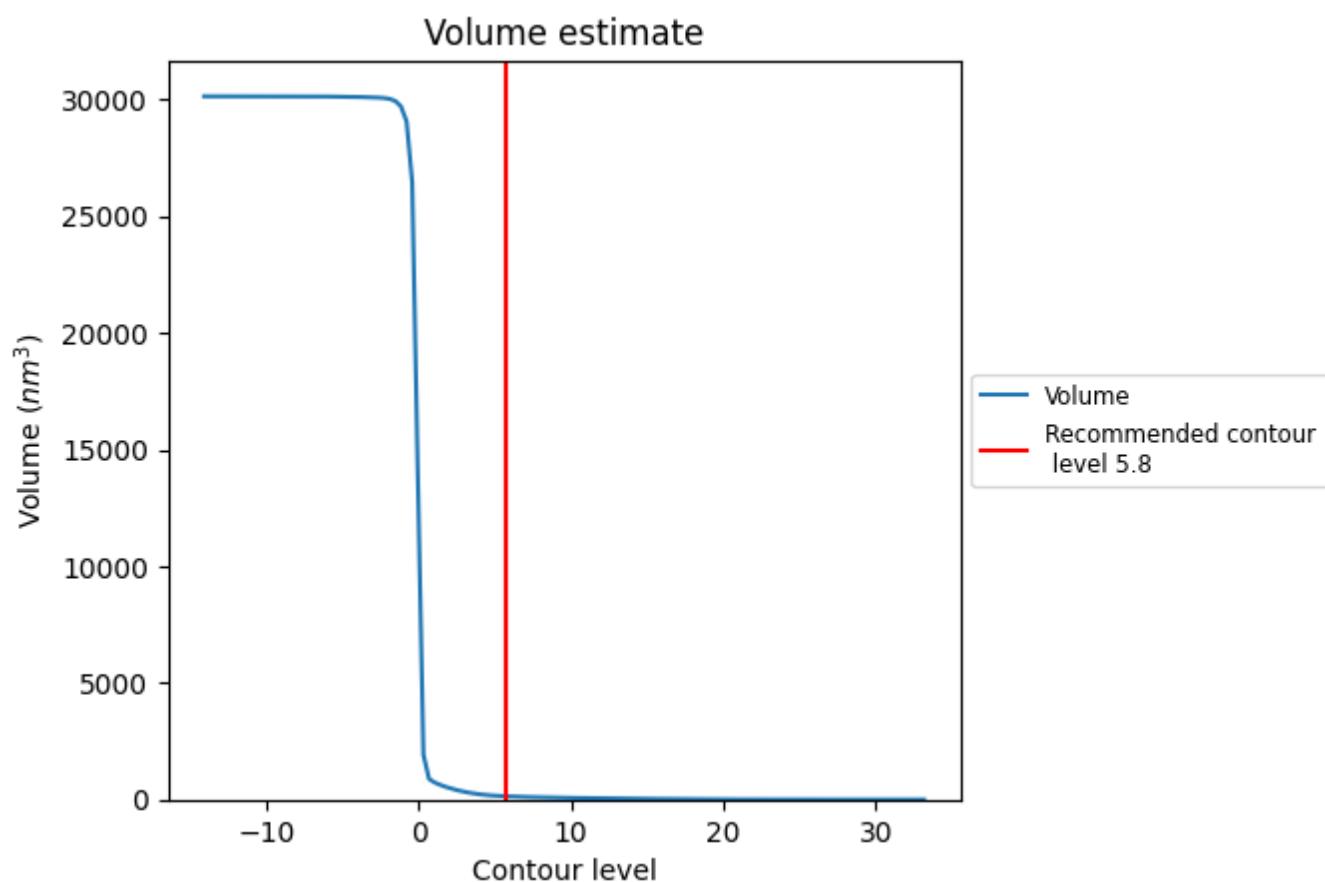
This section contains the results of statistical analysis of the map.

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.

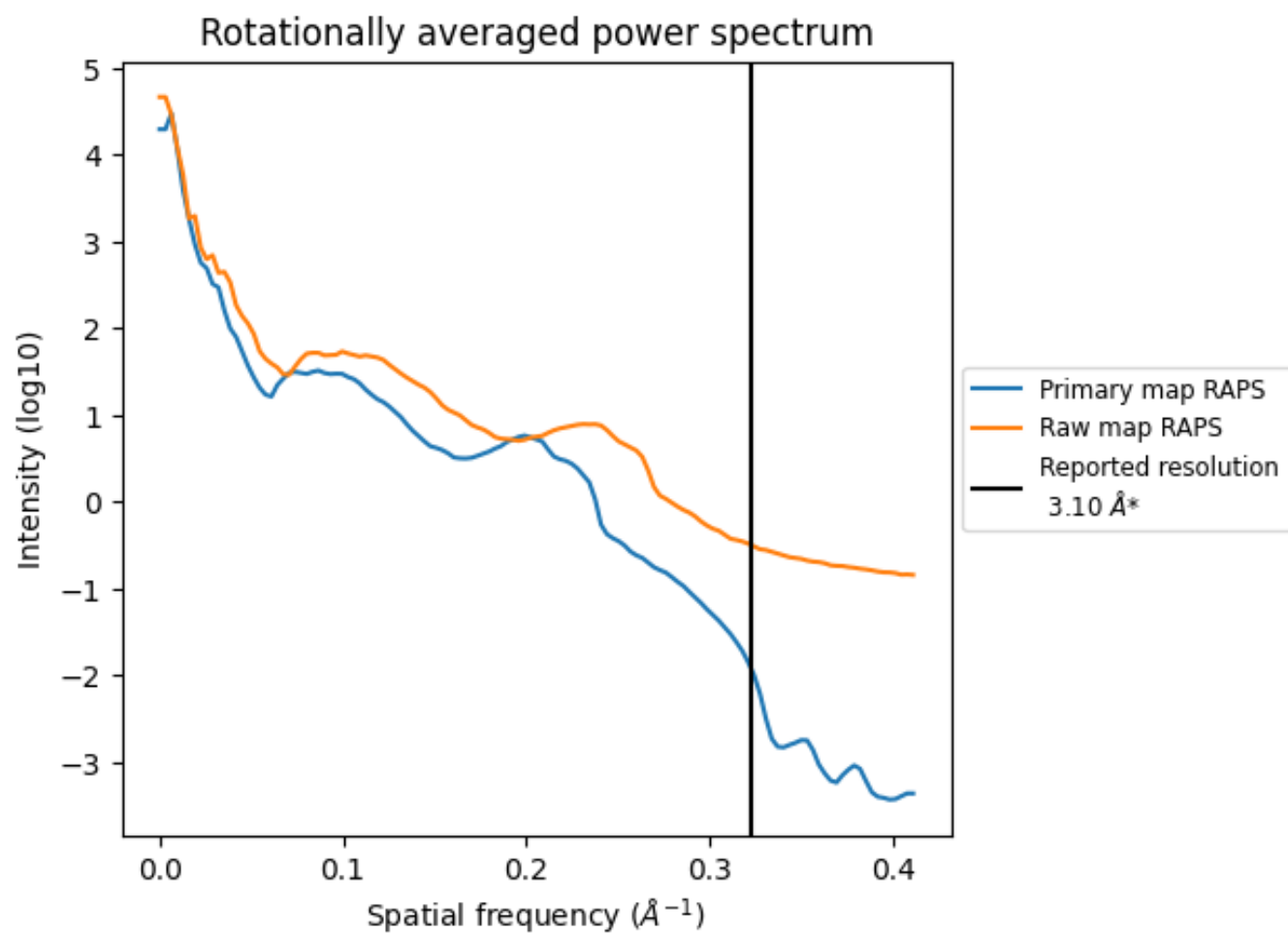
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm^3 ; this corresponds to an approximate mass of 125 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 ⓘ

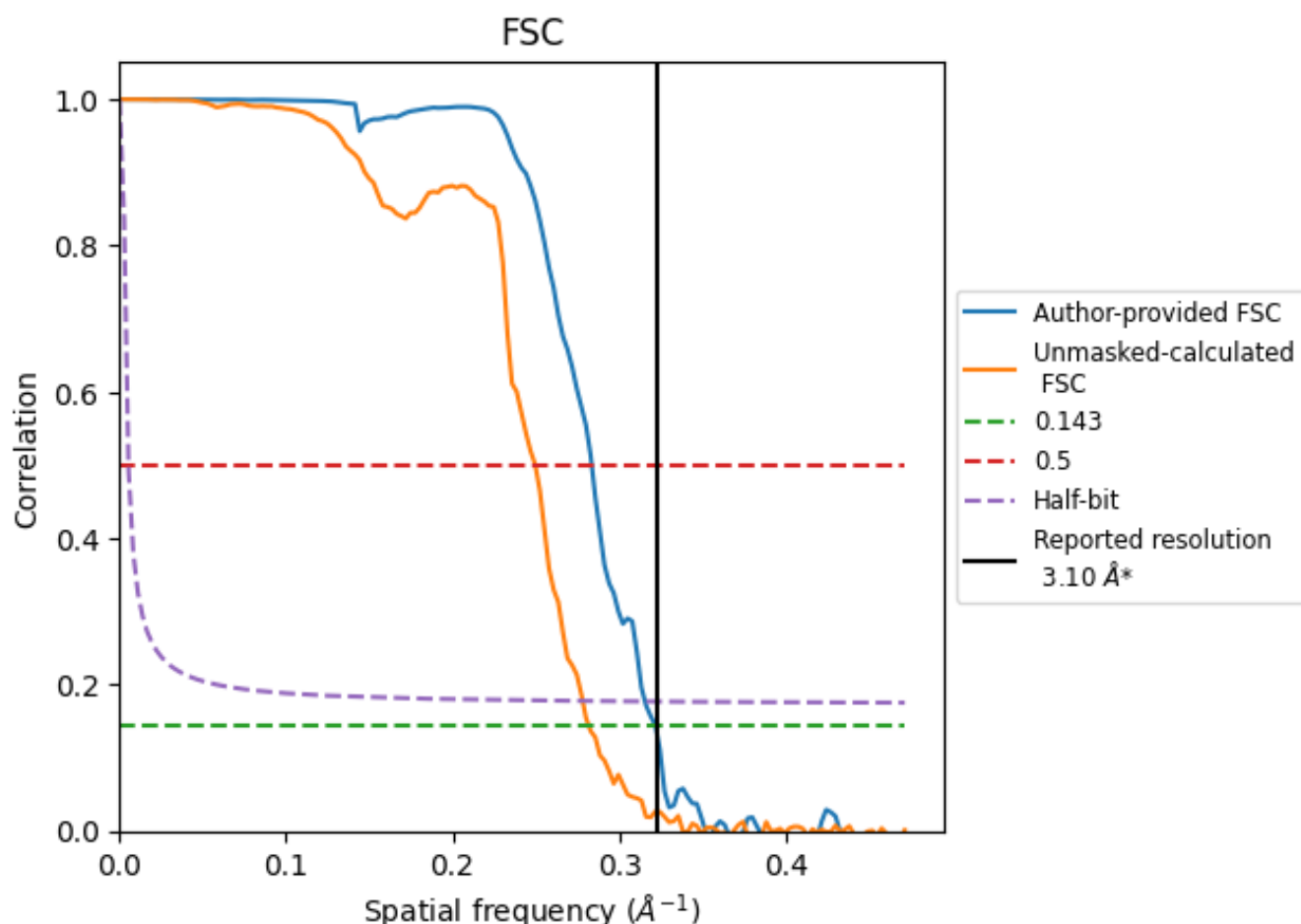


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

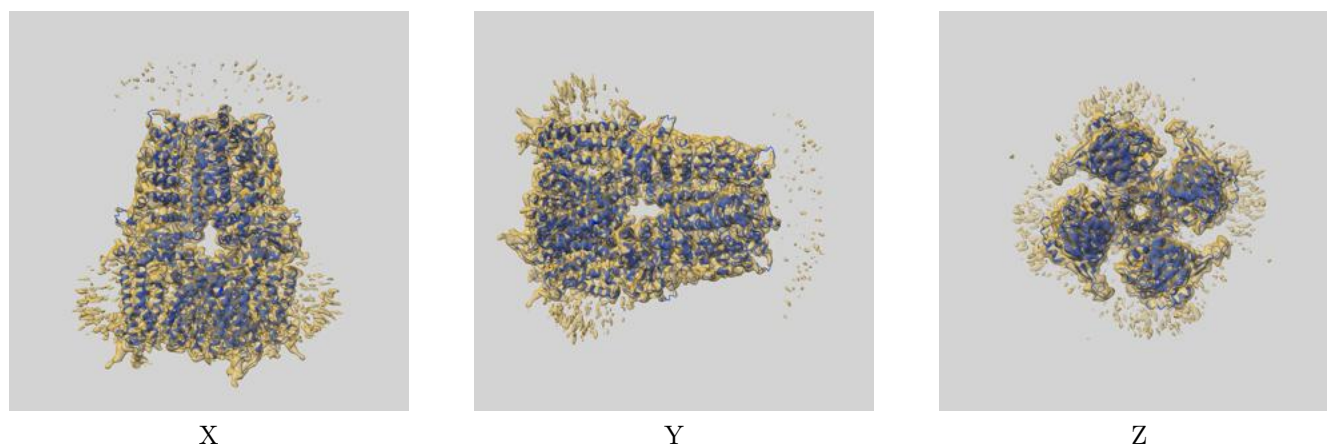
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.52	3.17
Unmasked-calculated*	3.55	4.00	3.59

*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 3.55 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

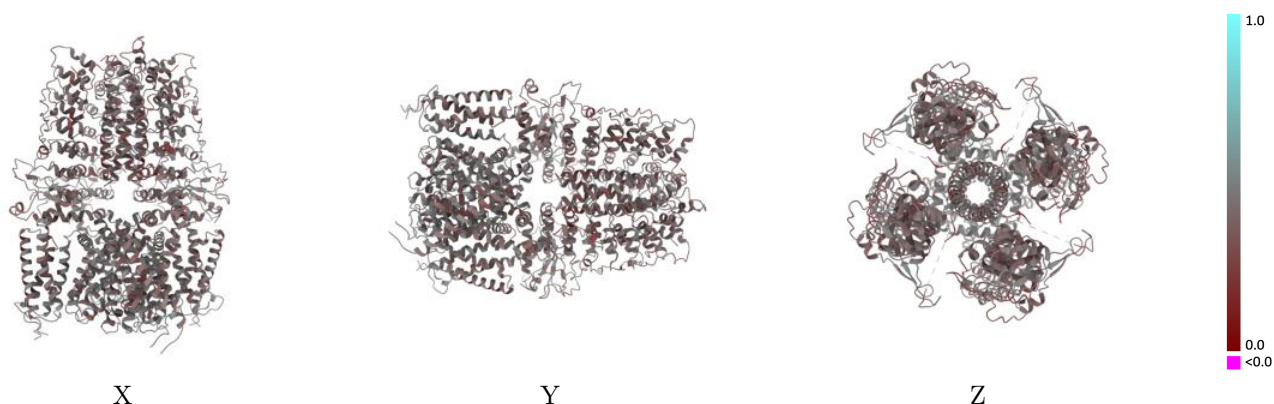
This section contains information regarding the fit between EMDB map EMD-21128 and PDB model 6V9W. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



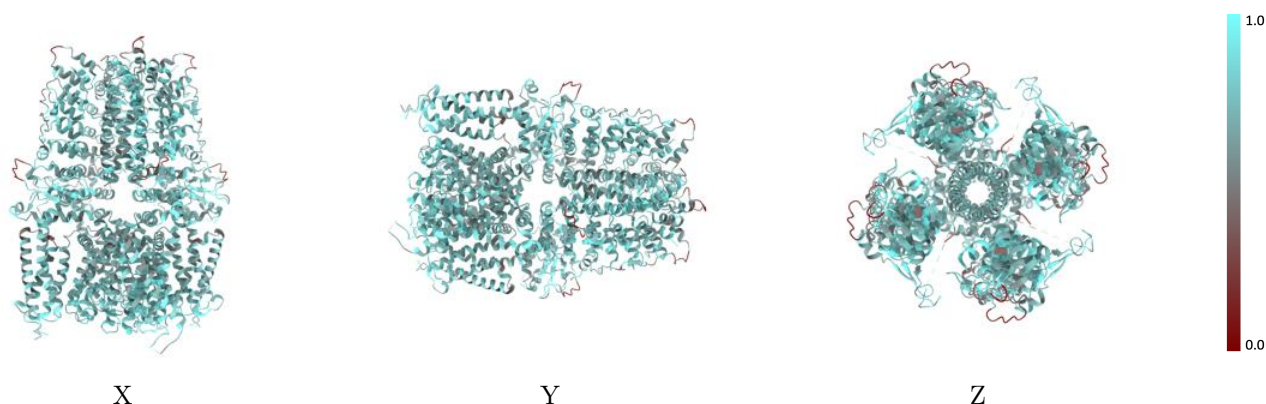
The images above show the 3D surface view of the map at the recommended contour level 5.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



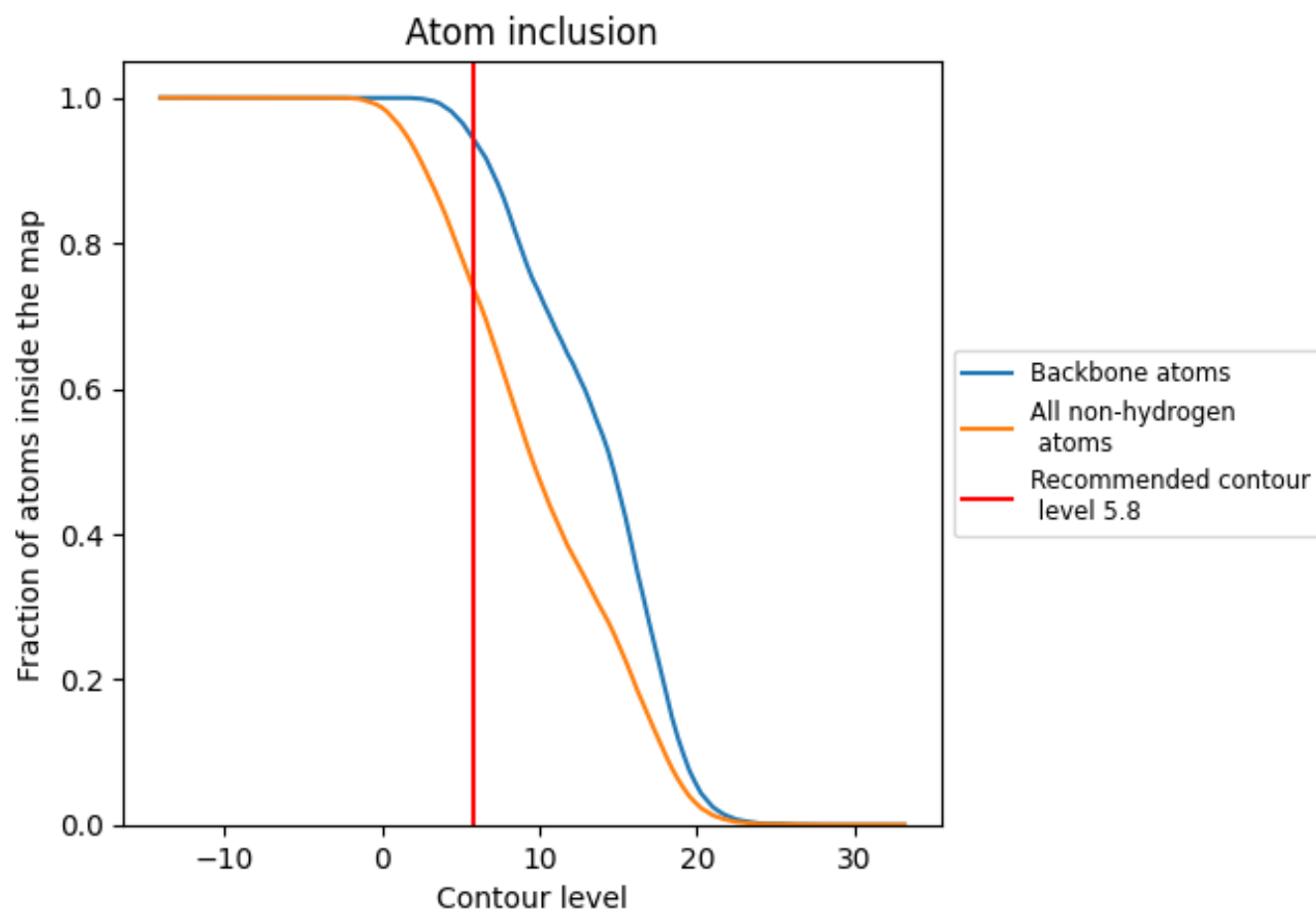
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 74% 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 (5.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7380	<div></div> 0.4190
A	<div></div> 0.7372	<div></div> 0.4210
B	<div></div> 0.7377	<div></div> 0.4190
C	<div></div> 0.7409	<div></div> 0.4200
D	<div></div> 0.7364	<div></div> 0.4180

