



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:09 PM UTC

PDB ID : 7L2K / pdb_00007l2k
EMDB ID : EMD-23131
Title : Cryo-EM structure of full-length TRPV1 at pH6b state
Authors : Zhang, K.; Julius, D.; Cheng, Y.
Deposited on : 2020-12-17
Resolution : 3.89 Å(reported)

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.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

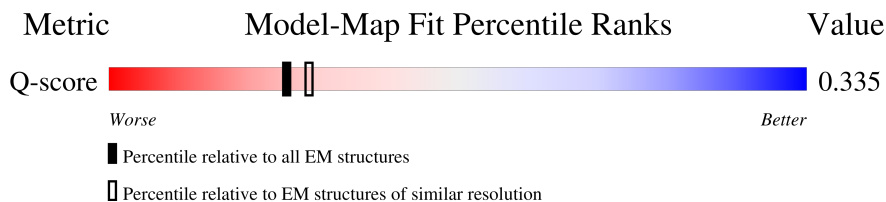
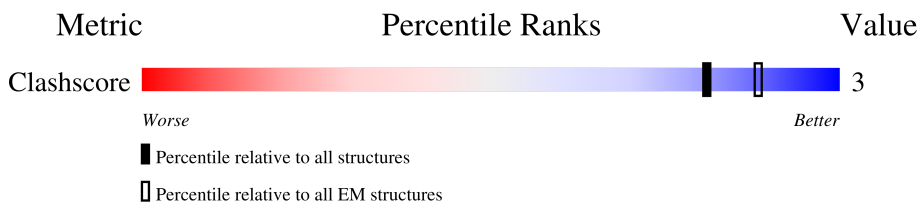
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

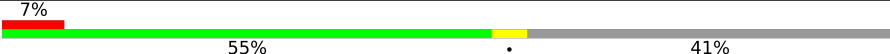
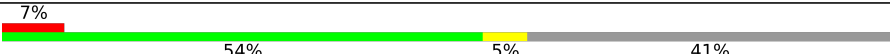
The reported resolution of this entry is 3.89 Å.

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	-
Q-score	-	25397	8712 (3.39 - 4.39)

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	842	 7% 55% . 41%
1	B	842	 7% 55% . 41%
1	C	842	 7% 54% 5% 41%
1	D	842	 7% 55% . 41%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15998 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 V member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	494	Total	C	N	O	S	0	0
			4000	2624	647	704	25		
1	C	494	Total	C	N	O	S	0	0
			4000	2624	647	704	25		
1	D	494	Total	C	N	O	S	0	0
			3998	2622	647	704	25		
1	B	494	Total	C	N	O	S	0	0
			4000	2624	647	704	25		

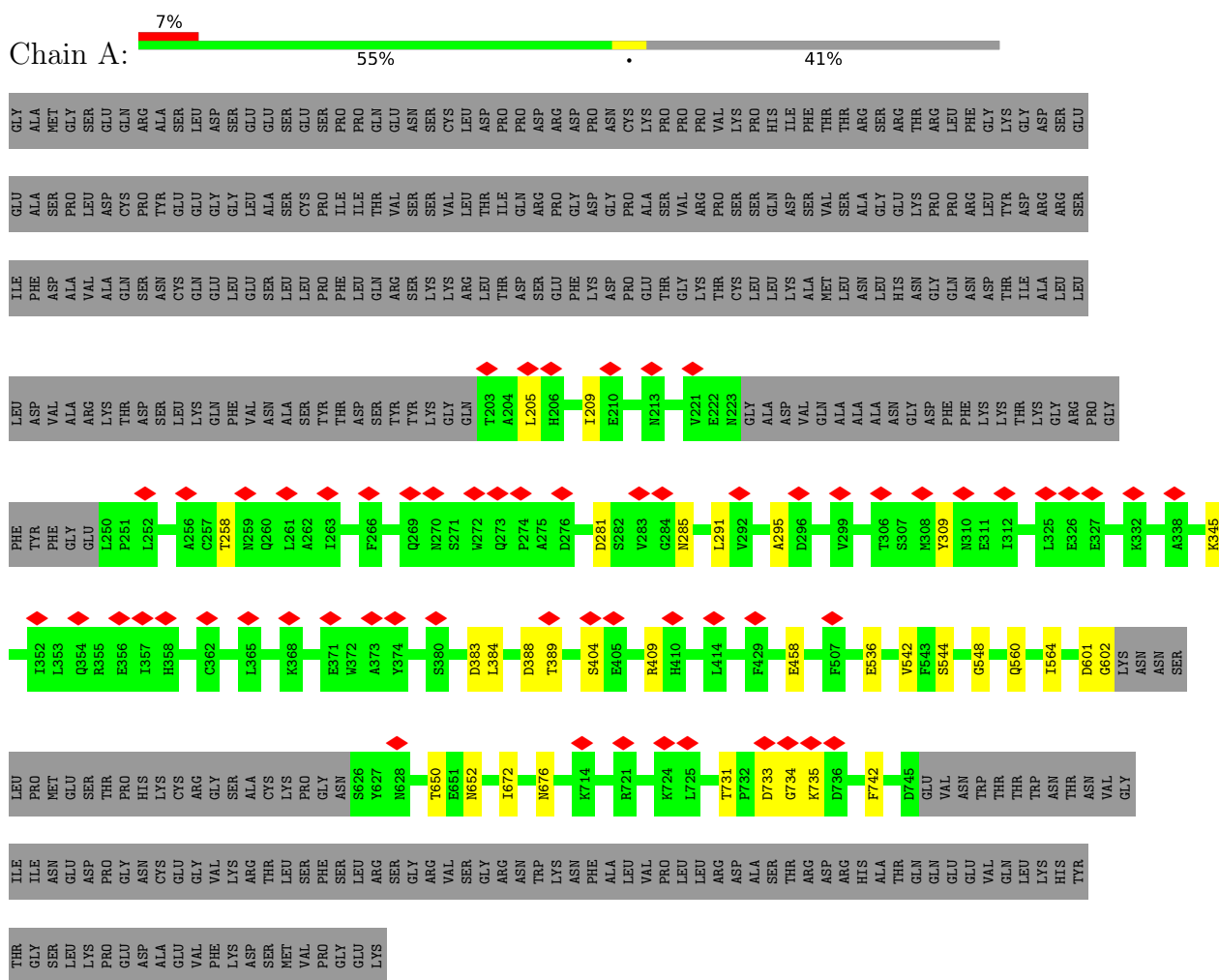
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP O35433
A	-2	ALA	-	expression tag	UNP O35433
A	-1	MET	-	expression tag	UNP O35433
A	0	GLY	-	expression tag	UNP O35433
A	1	SER	-	expression tag	UNP O35433
C	-3	GLY	-	expression tag	UNP O35433
C	-2	ALA	-	expression tag	UNP O35433
C	-1	MET	-	expression tag	UNP O35433
C	0	GLY	-	expression tag	UNP O35433
C	1	SER	-	expression tag	UNP O35433
D	-3	GLY	-	expression tag	UNP O35433
D	-2	ALA	-	expression tag	UNP O35433
D	-1	MET	-	expression tag	UNP O35433
D	0	GLY	-	expression tag	UNP O35433
D	1	SER	-	expression tag	UNP O35433
B	-3	GLY	-	expression tag	UNP O35433
B	-2	ALA	-	expression tag	UNP O35433
B	-1	MET	-	expression tag	UNP O35433
B	0	GLY	-	expression tag	UNP O35433
B	1	SER	-	expression tag	UNP O35433

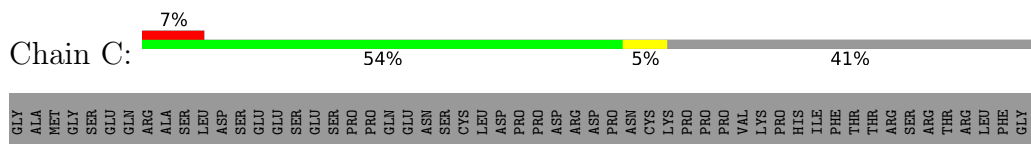
3 Residue-property plots

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: Transient receptor potential cation channel subfamily V member 1



- Molecule 1: Transient receptor potential cation channel subfamily V member 1



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

- Molecule 1: Transient receptor potential cation channel subfamily V member 1



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

PHE	GLY	GLU	L250	P251	L252	T258	N259	Q260	L261	A262	I263	V264	K265	F266	Q269	N270	S271	W272	Q273	P274	A275	D276	D281	S282	V283	G284	N285	L291	V292	D296	V299	T306	Y309	N310	E311	I312	L325	E326	E327	K332	L339	I352	L353	Q354	R355	E356	I357
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H358	C362	L365	F369	T370	E371	W372	A373	Y374	G375	S380	D383	L384	D388	T389	S404	E405	R409	M412	L413	L414	E458	F507	S544	G548	Q560	I564	V583	T593	V596	D601	G602	LYS	ASN	ASN	SER	LEU	PRO	MET	GLU	SER
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THR	PRO	HIS	LYS	CYS	ARG	GLY	SER	ALA	CYS	LYS	PRO	GLY	ASN	S626	Y627	N628	T641	T650	E651	N652	I672	L675	N676	M682	Q691	K714	R721	S722	G723	K724	L725	T731	P732	D733	G734	K735	D736	D745	GLU	VAL	ASN	TRP	THR	THR	ASN	THR	VAL
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GLY	ILE	ASN	GLU	ASP	PRO	GLY	ASP	ASN	ALA	CYS	GLY	VAL	LYS	ARG	THR	LEU	PHE	SER	LEU	ARG	GLY	ARG	VAL	SER	GLY	ARG	ASN	TRP	LYS	ASN	PHE	ALA	LEU	VAL	PRO	LEU	LEU	ARG	ASP	ALA	SER	THR	ARG	ASP	ARG	HIS	ALA	THR	GLN	GLN	GLU	GLU	TRP	VAL	GLN	LEU	LYS	HIS
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TYR	THR	GLY	SER	LEU	LYS	PRO	GLU	ASP	ALA	GLU	VAL	PHE	LYS	ASP	SER	MET	VAL	PRO	GLY	LYS
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11276	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	76.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.009	Depositor
Map size ($\text{\AA}$)	257.6, 257.6, 257.6	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.15, 1.15, 1.15	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.37	0/4091	0.48	0/5539
1	B	0.39	1/4091 (0.0%)	0.49	0/5539
1	C	0.39	1/4091 (0.0%)	0.49	1/5539 (0.0%)
1	D	0.37	0/4089	0.50	0/5536
All	All	0.38	2/16362 (0.0%)	0.49	1/22153 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	652	ASN	C-N	-7.93	1.22	1.33
1	C	652	ASN	C-N	-5.34	1.26	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	652	ASN	O-C-N	5.32	129.66	122.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4000	0	4061	21	0
1	B	4000	0	4061	21	0
1	C	4000	0	4061	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3998	0	4054	19	0
All	All	15998	0	16237	84	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 (84) 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:C:651:GLU:OE1	1:C:656:LYS:NZ	2.07	0.85
1:D:672:ILE:O	1:D:676:ASN:ND2	2.11	0.83
1:C:672:ILE:O	1:C:676:ASN:ND2	2.13	0.81
1:A:672:ILE:O	1:A:676:ASN:ND2	2.13	0.81
1:B:672:ILE:O	1:B:676:ASN:ND2	2.16	0.79
1:C:731:THR:OG1	1:C:733:ASP:O	2.03	0.75
1:D:731:THR:OG1	1:D:733:ASP:O	2.03	0.75
1:A:731:THR:OG1	1:A:733:ASP:O	2.01	0.74
1:D:513:GLU:N	1:D:513:GLU:OE1	2.22	0.73
1:C:513:GLU:N	1:C:513:GLU:OE1	2.22	0.73
1:A:733:ASP:OD2	1:A:735:LYS:NZ	2.23	0.71
1:C:733:ASP:OD2	1:C:735:LYS:NZ	2.26	0.68
1:D:733:ASP:OD2	1:D:735:LYS:NZ	2.26	0.67
1:A:536:GLU:N	1:A:536:GLU:OE1	2.29	0.65
1:C:536:GLU:N	1:C:536:GLU:OE1	2.29	0.65
1:B:733:ASP:OD2	1:B:735:LYS:NZ	2.29	0.65
1:D:536:GLU:N	1:D:536:GLU:OE1	2.33	0.62
1:C:291:LEU:HD22	1:C:309:TYR:CE1	2.36	0.60
1:B:731:THR:OG1	1:B:733:ASP:O	2.14	0.59
1:C:745:ASP:N	1:C:745:ASP:OD1	2.35	0.57
1:A:383:ASP:OD1	1:A:384:LEU:N	2.38	0.56
1:A:650:THR:OG1	1:A:652:ASN:OD1	2.23	0.56
1:A:281:ASP:OD1	1:A:285:ASN:N	2.39	0.56
1:C:388:ASP:OD1	1:C:389:THR:N	2.39	0.56
1:B:458:GLU:OE1	1:B:458:GLU:N	2.39	0.56
1:B:383:ASP:OD1	1:B:384:LEU:N	2.40	0.54
1:B:281:ASP:OD1	1:B:285:ASN:N	2.41	0.54
1:C:383:ASP:OD1	1:C:384:LEU:N	2.40	0.54
1:C:458:GLU:N	1:C:458:GLU:OE1	2.41	0.53
1:A:388:ASP:OD1	1:A:389:THR:N	2.41	0.53
1:D:458:GLU:N	1:D:458:GLU:OE1	2.41	0.53
1:A:458:GLU:OE1	1:A:458:GLU:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:ASP:OD1	1:C:285:ASN:N	2.43	0.52
1:B:650:THR:OG1	1:B:652:ASN:OD1	2.28	0.52
1:A:560:GLN:O	1:A:564:ILE:HD12	2.11	0.51
1:A:676:ASN:HB2	1:B:682:MET:HE1	1.92	0.51
1:D:641:THR:HG23	1:D:675:LEU:HD11	1.93	0.51
1:B:691:GLN:N	1:B:691:GLN:OE1	2.42	0.51
1:B:388:ASP:OD1	1:B:389:THR:N	2.42	0.51
1:C:601:ASP:OD1	1:C:602:GLY:N	2.43	0.50
1:B:296:ASP:N	1:B:296:ASP:OD1	2.44	0.50
1:D:560:GLN:O	1:D:564:ILE:HD12	2.11	0.50
1:C:691:GLN:OE1	1:C:691:GLN:N	2.44	0.50
1:D:601:ASP:OD1	1:D:602:GLY:N	2.42	0.50
1:A:205:LEU:O	1:A:209:ILE:HG22	2.13	0.49
1:D:281:ASP:OD1	1:D:285:ASN:N	2.46	0.49
1:B:291:LEU:HD22	1:B:309:TYR:CE1	2.48	0.49
1:B:601:ASP:OD1	1:B:602:GLY:N	2.44	0.49
1:B:560:GLN:O	1:B:564:ILE:HD12	2.13	0.48
1:C:650:THR:OG1	1:C:652:ASN:OD1	2.31	0.48
1:D:296:ASP:N	1:D:296:ASP:OD1	2.44	0.47
1:A:209:ILE:HD11	1:A:258:THR:HG21	1.96	0.47
1:C:296:ASP:OD1	1:C:296:ASP:N	2.47	0.47
1:D:733:ASP:OD1	1:D:734:GLY:N	2.46	0.47
1:D:291:LEU:HD22	1:D:309:TYR:CE1	2.50	0.47
1:A:291:LEU:HD22	1:A:309:TYR:CE1	2.51	0.46
1:B:404:SER:O	1:B:409:ARG:NH1	2.49	0.46
1:D:544:SER:O	1:D:548:GLY:N	2.40	0.46
1:B:209:ILE:HD11	1:B:258:THR:HG21	1.98	0.46
1:B:593:THR:HA	1:B:596:VAL:HG12	1.96	0.46
1:D:593:THR:HA	1:D:596:VAL:HG12	1.99	0.45
1:C:593:THR:HA	1:C:596:VAL:HG12	1.97	0.45
1:A:384:LEU:HD11	1:A:742:PHE:HB3	1.97	0.45
1:C:298:THR:O	1:C:302:THR:N	2.50	0.45
1:C:560:GLN:O	1:C:564:ILE:HD12	2.18	0.44
1:C:733:ASP:OD1	1:C:734:GLY:N	2.50	0.44
1:B:641:THR:HG23	1:B:675:LEU:HD11	1.98	0.44
1:D:295:ALA:O	1:D:345:LYS:NZ	2.51	0.44
1:A:295:ALA:O	1:A:345:LYS:NZ	2.51	0.43
1:A:542:VAL:HG12	1:D:597:THR:HG23	2.00	0.43
1:C:298:THR:O	1:C:302:THR:OG1	2.31	0.43
1:B:544:SER:O	1:B:548:GLY:N	2.41	0.43
1:A:733:ASP:OD1	1:A:734:GLY:N	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:565:TYR:HE1	1:B:583:VAL:HG21	1.85	0.42
1:A:404:SER:O	1:A:409:ARG:NH1	2.53	0.42
1:C:357:ILE:HD13	1:C:362:CYS:O	2.19	0.42
1:A:601:ASP:OD1	1:A:602:GLY:N	2.49	0.42
1:C:384:LEU:HA	1:C:387:ILE:HD12	2.01	0.42
1:A:544:SER:O	1:A:548:GLY:N	2.42	0.41
1:D:371:GLU:OE1	1:D:743:ARG:NH1	2.46	0.41
1:C:640:PHE:CD2	1:C:667:VAL:HG22	2.56	0.41
1:B:733:ASP:OD1	1:B:734:GLY:N	2.51	0.41
1:C:544:SER:O	1:C:548:GLY:N	2.41	0.41
1:D:721:ARG:NH2	1:D:740:TRP:O	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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

There are no ligands in this entry.

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.

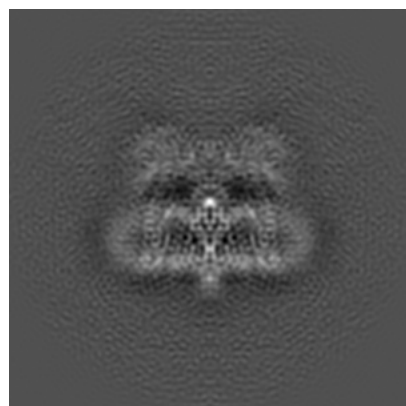
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23131. These allow visual inspection of the internal detail of the map and identification of artifacts.

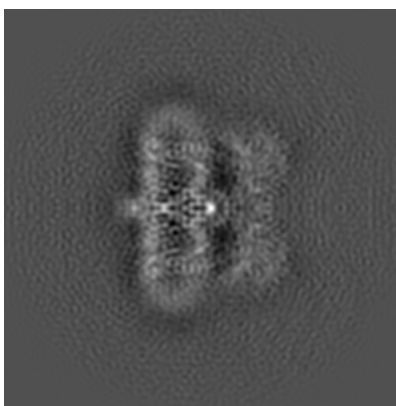
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

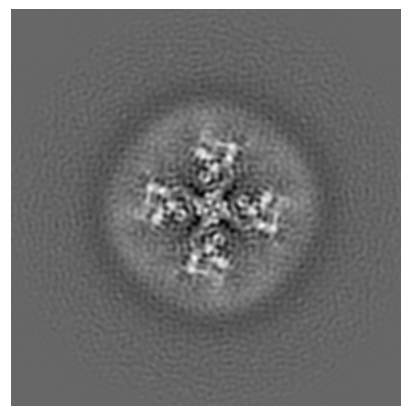
6.1.1 Primary map



X

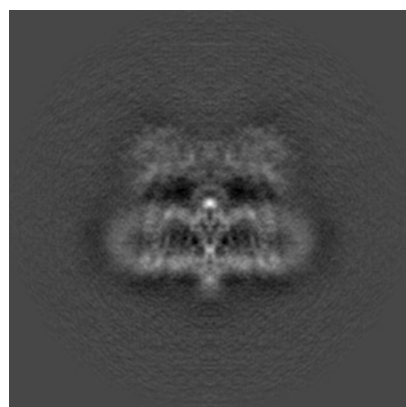


Y

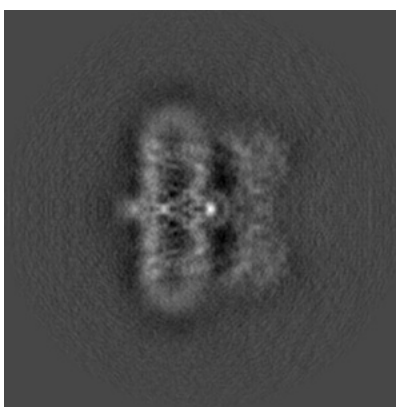


Z

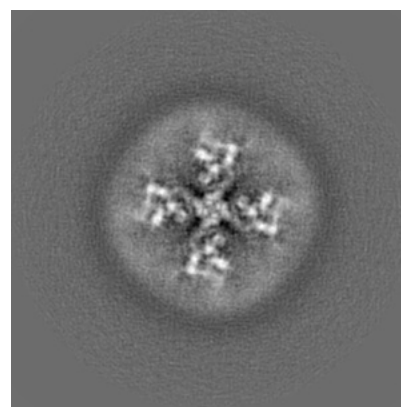
6.1.2 Raw map



X



Y

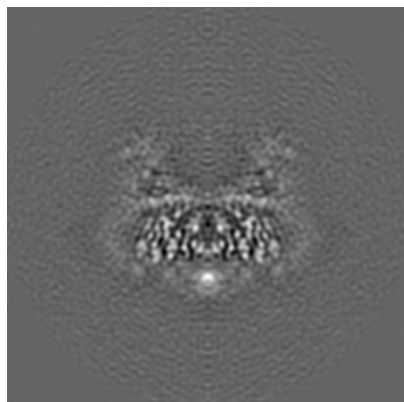


Z

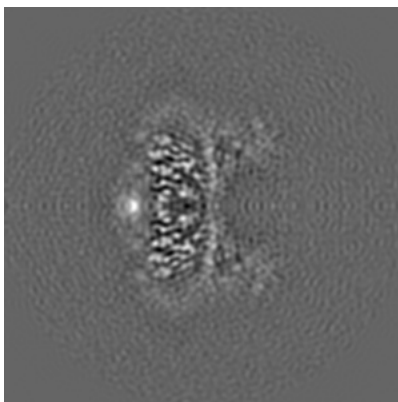
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

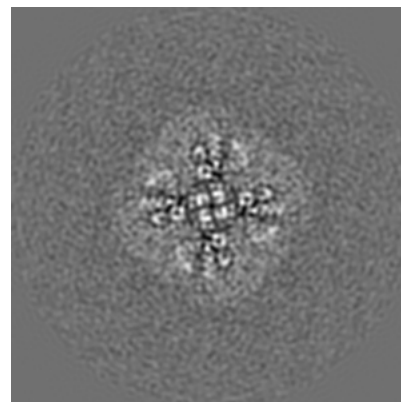
6.2.1 Primary map



X Index: 112

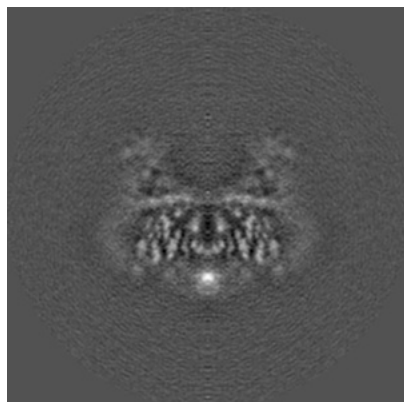


Y Index: 112

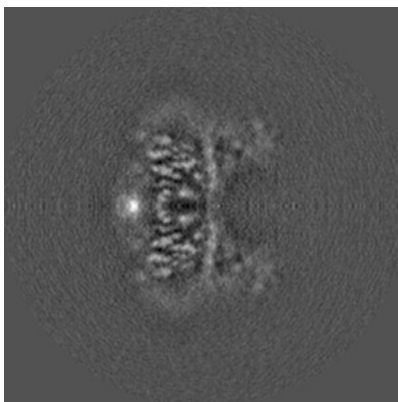


Z Index: 112

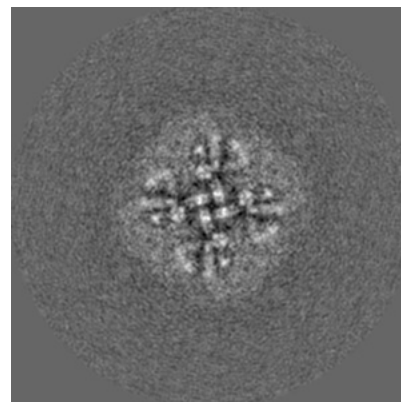
6.2.2 Raw map



X Index: 112



Y Index: 112

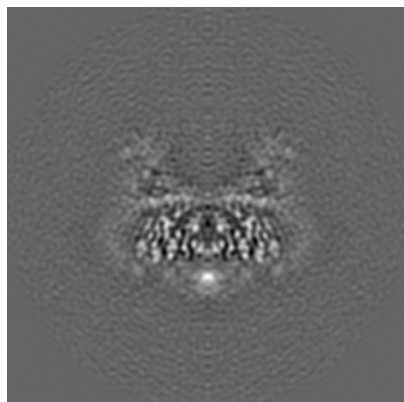


Z Index: 112

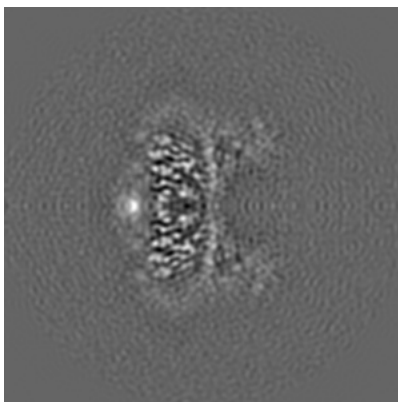
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

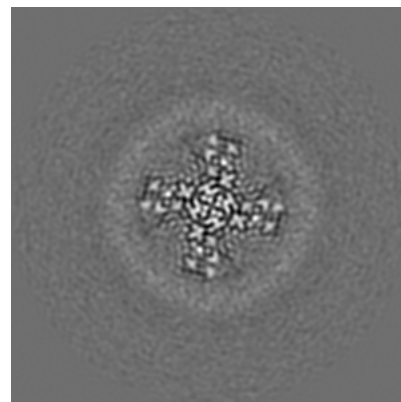
6.3.1 Primary map



X Index: 112

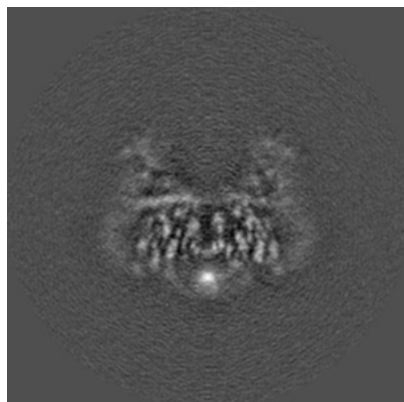


Y Index: 112

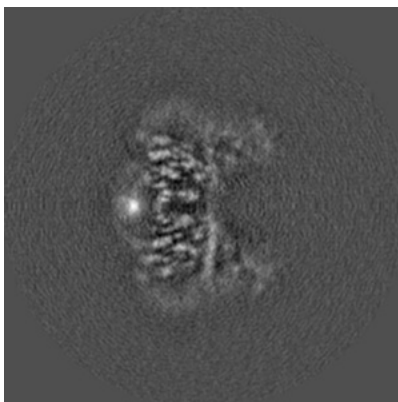


Z Index: 90

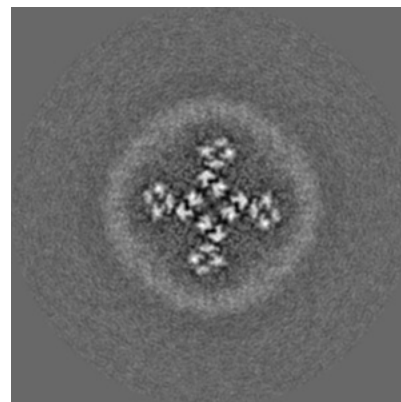
6.3.2 Raw map



X Index: 111



Y Index: 113

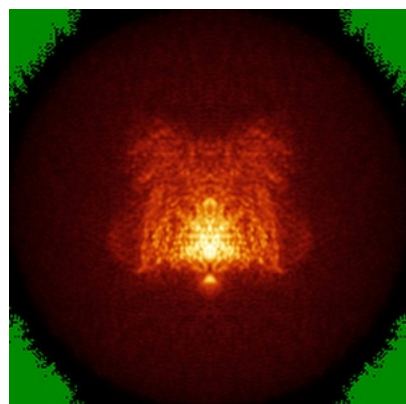


Z Index: 96

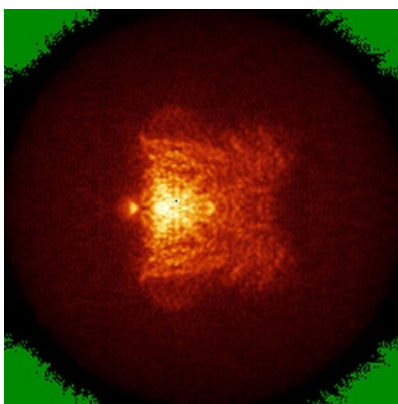
The images above show the largest variance slices of the map in three orthogonal directions.

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

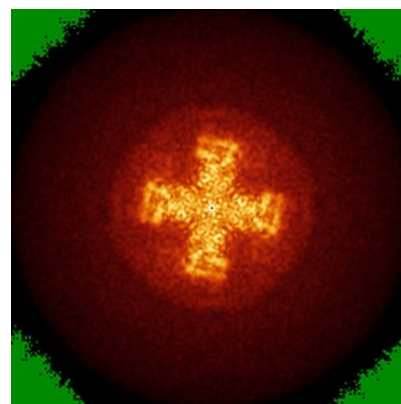
6.4.1 Primary map



X

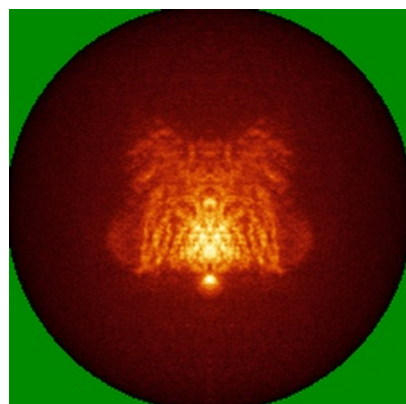


Y

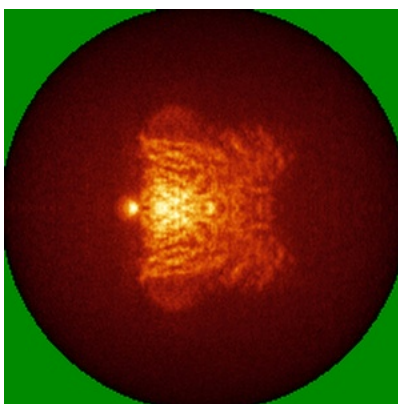


Z

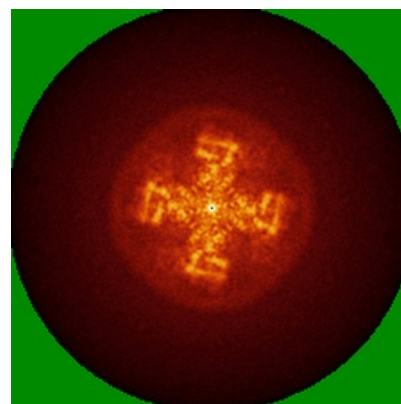
6.4.2 Raw map



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 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

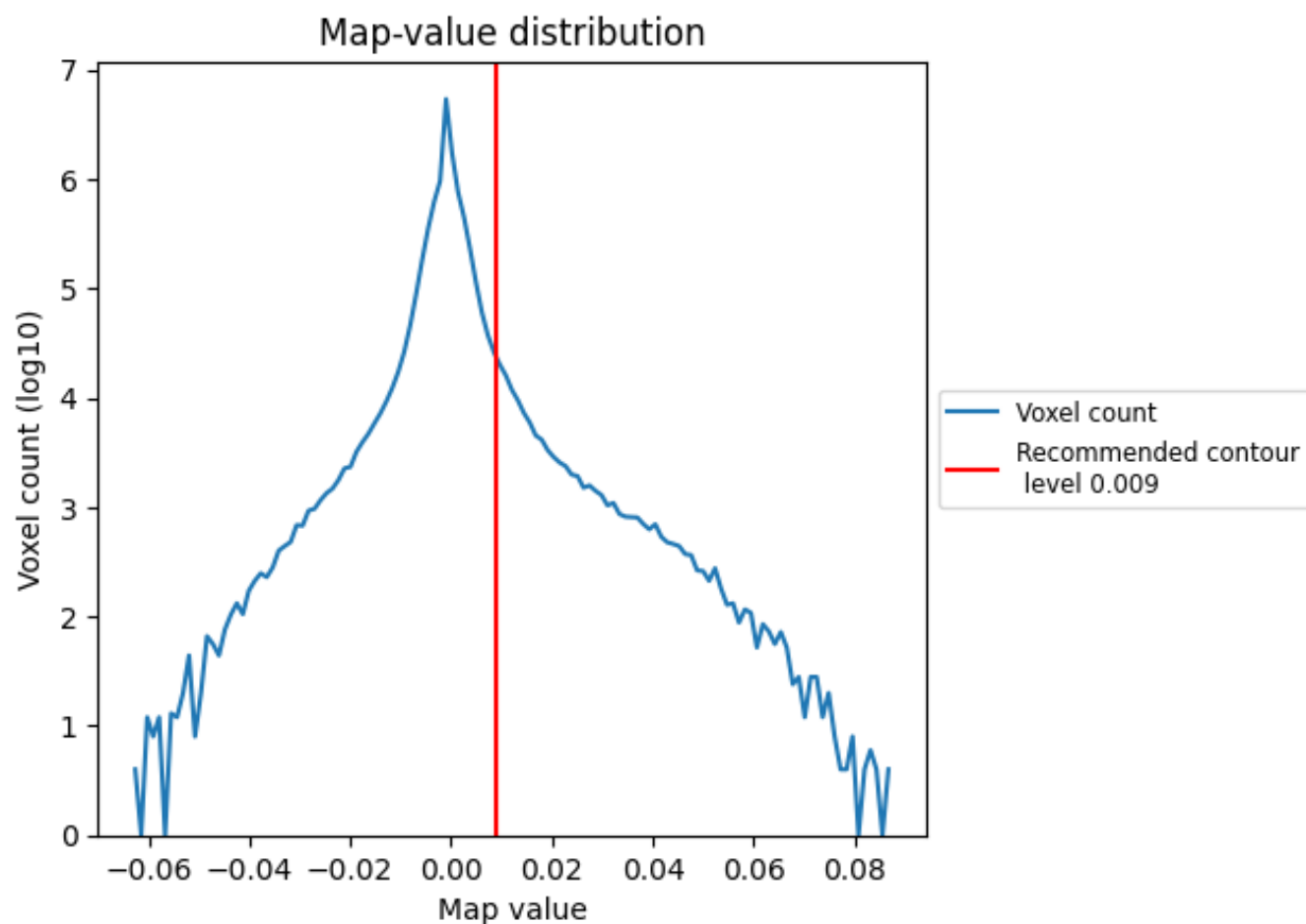
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

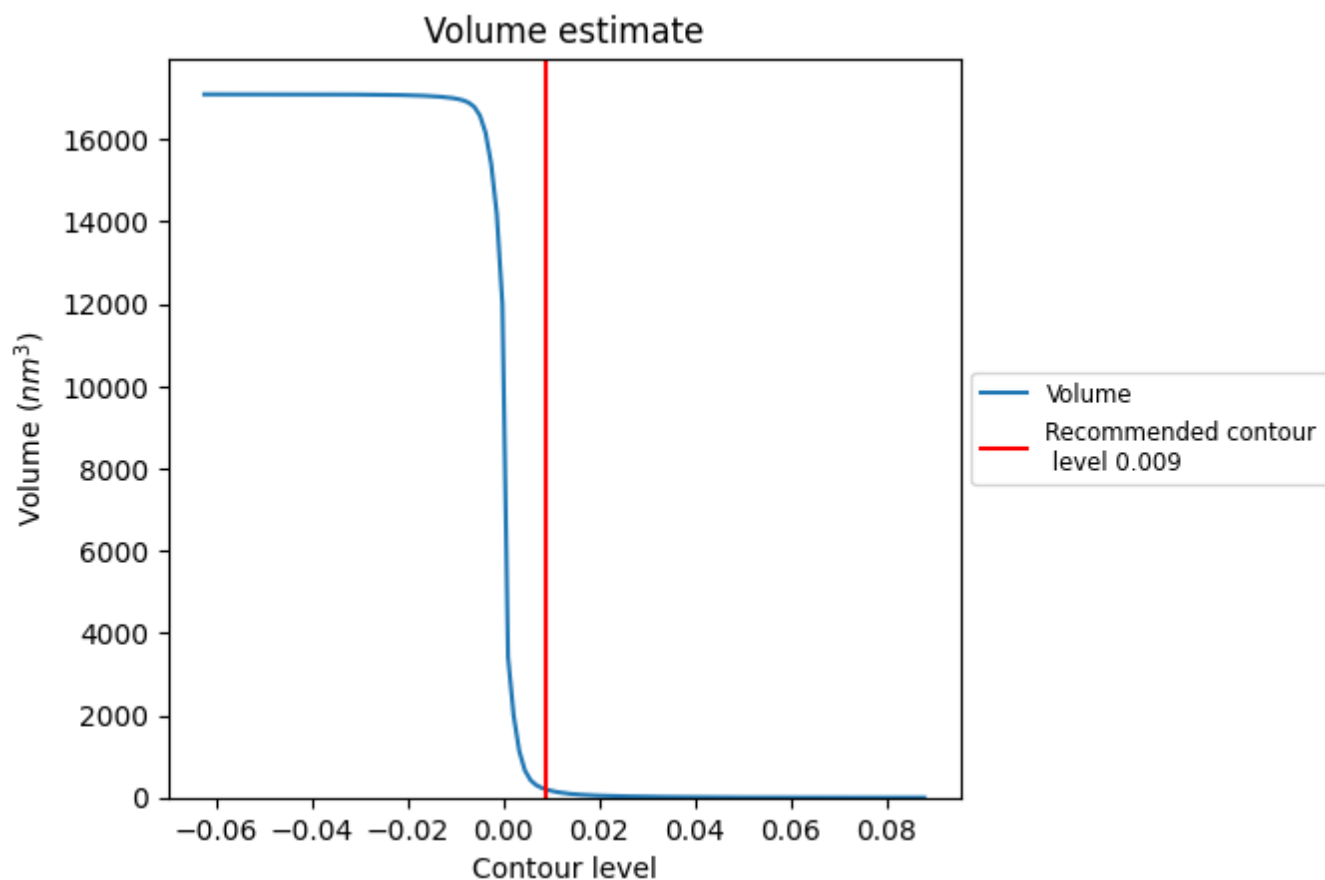
This section contains the results of statistical analysis of the map.

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.

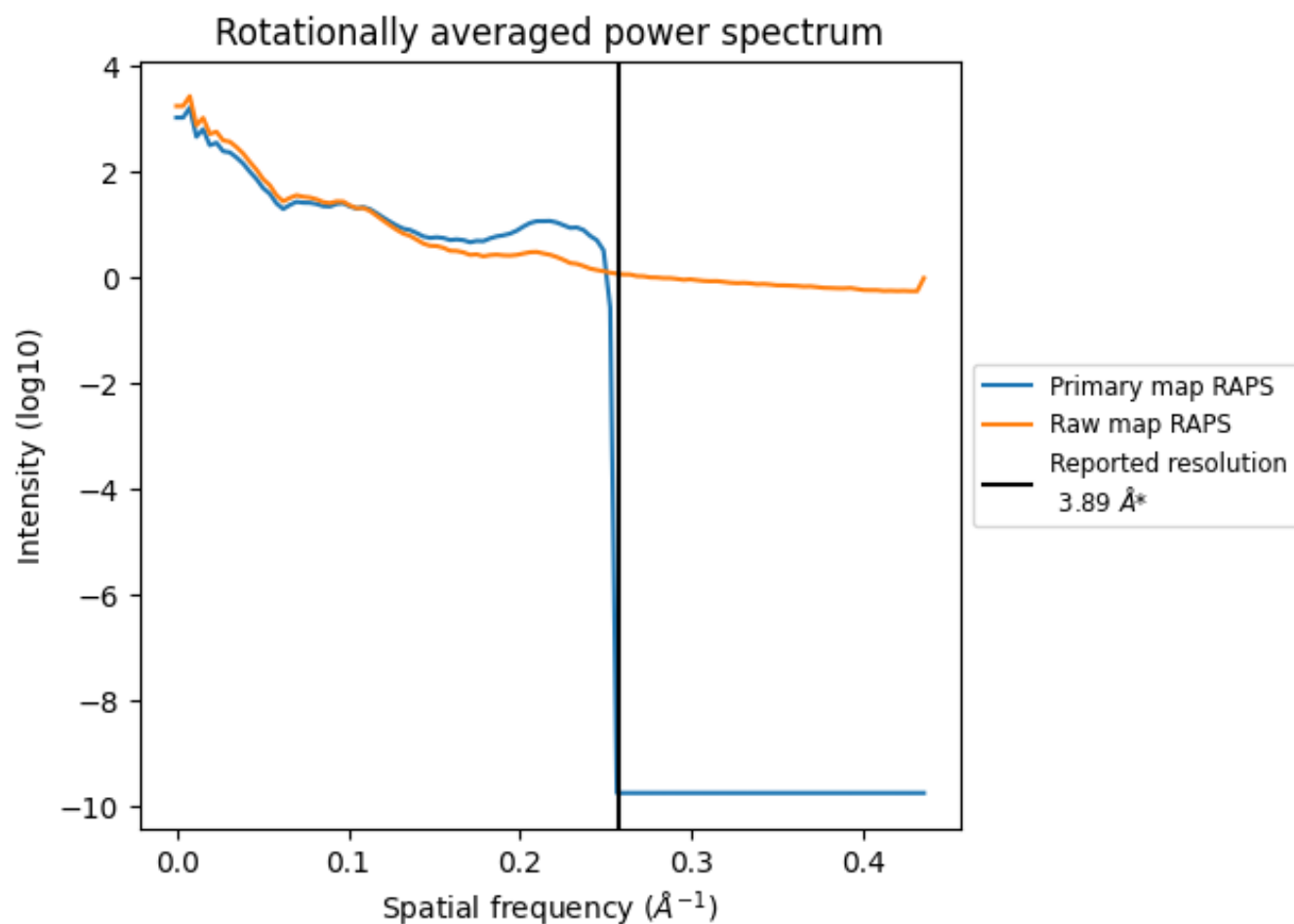
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm³; this corresponds to an approximate mass of 175 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 ⓘ

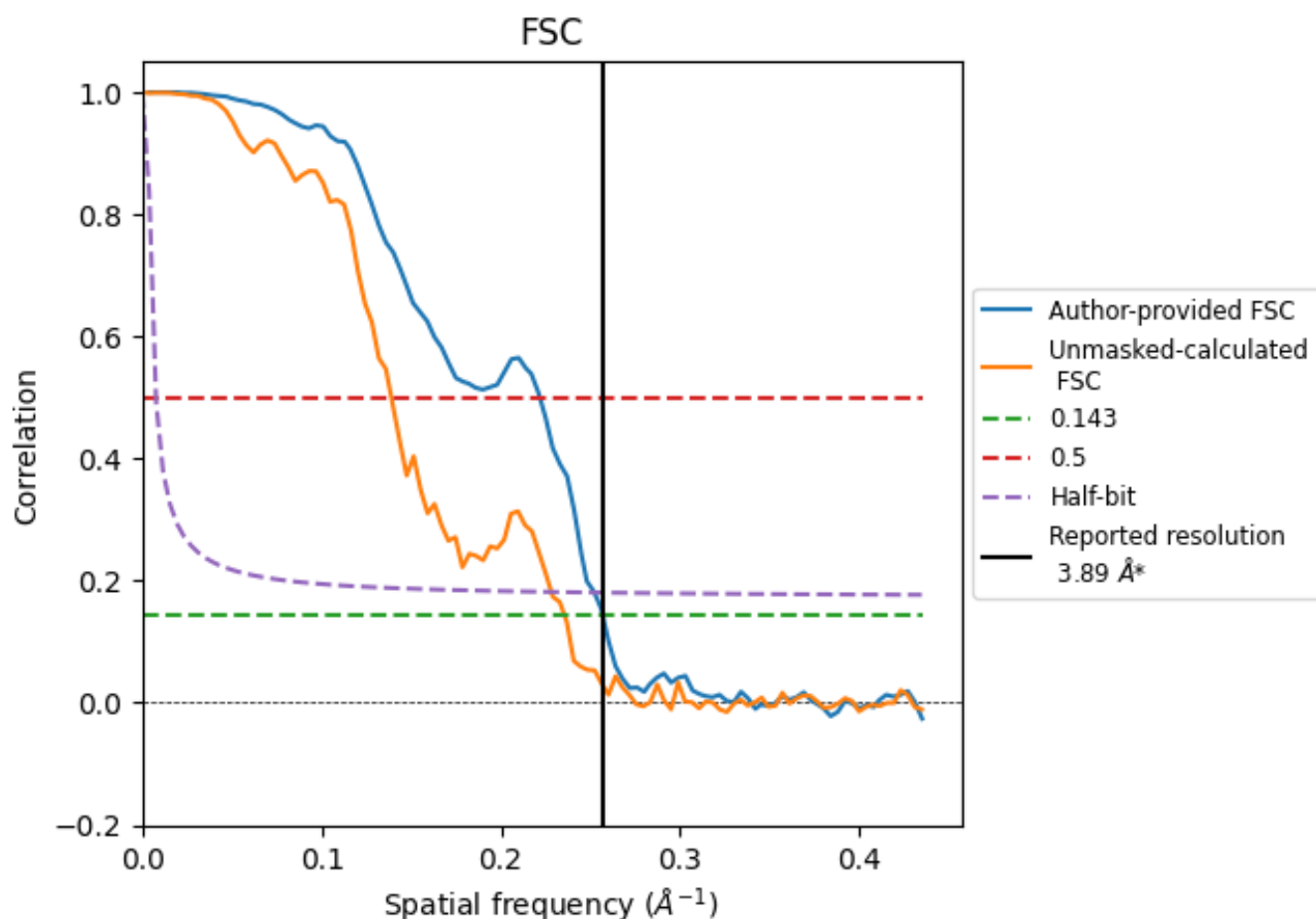


*Reported resolution corresponds to spatial frequency of 0.257 Å⁻¹

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 0.257 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

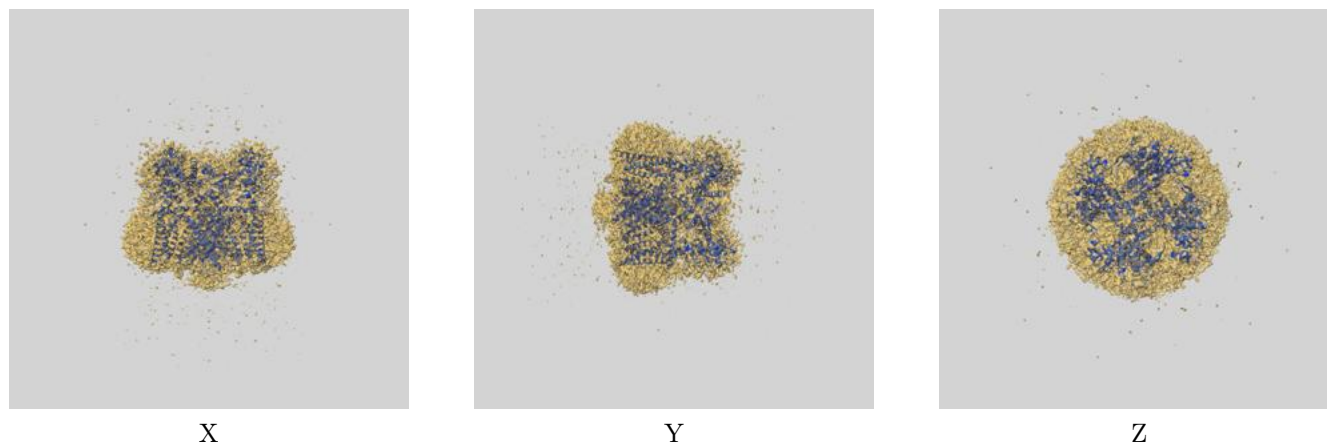
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.89	-	-
Author-provided FSC curve	3.89	4.51	3.97
Unmasked-calculated*	4.24	7.20	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

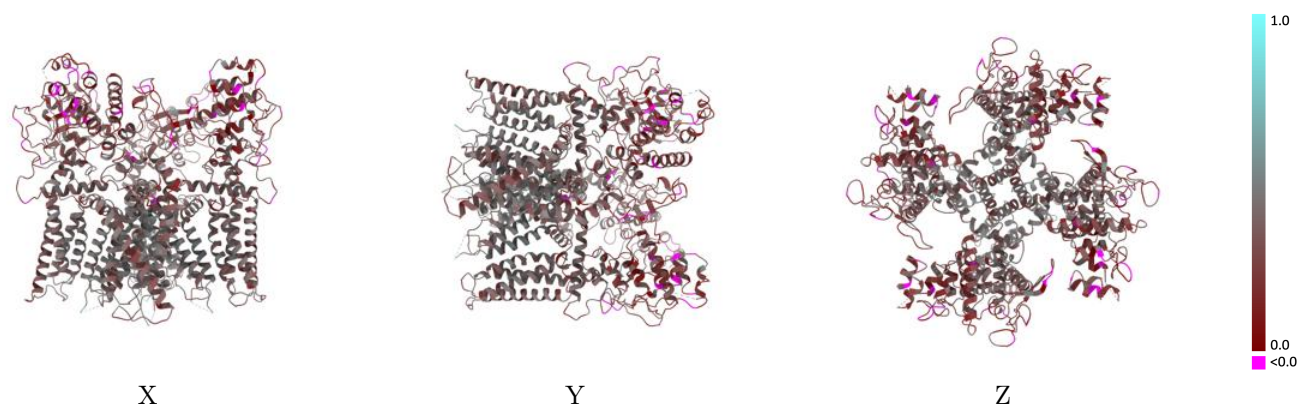
This section contains information regarding the fit between EMDB map EMD-23131 and PDB model 7L2K. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.009 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](#)

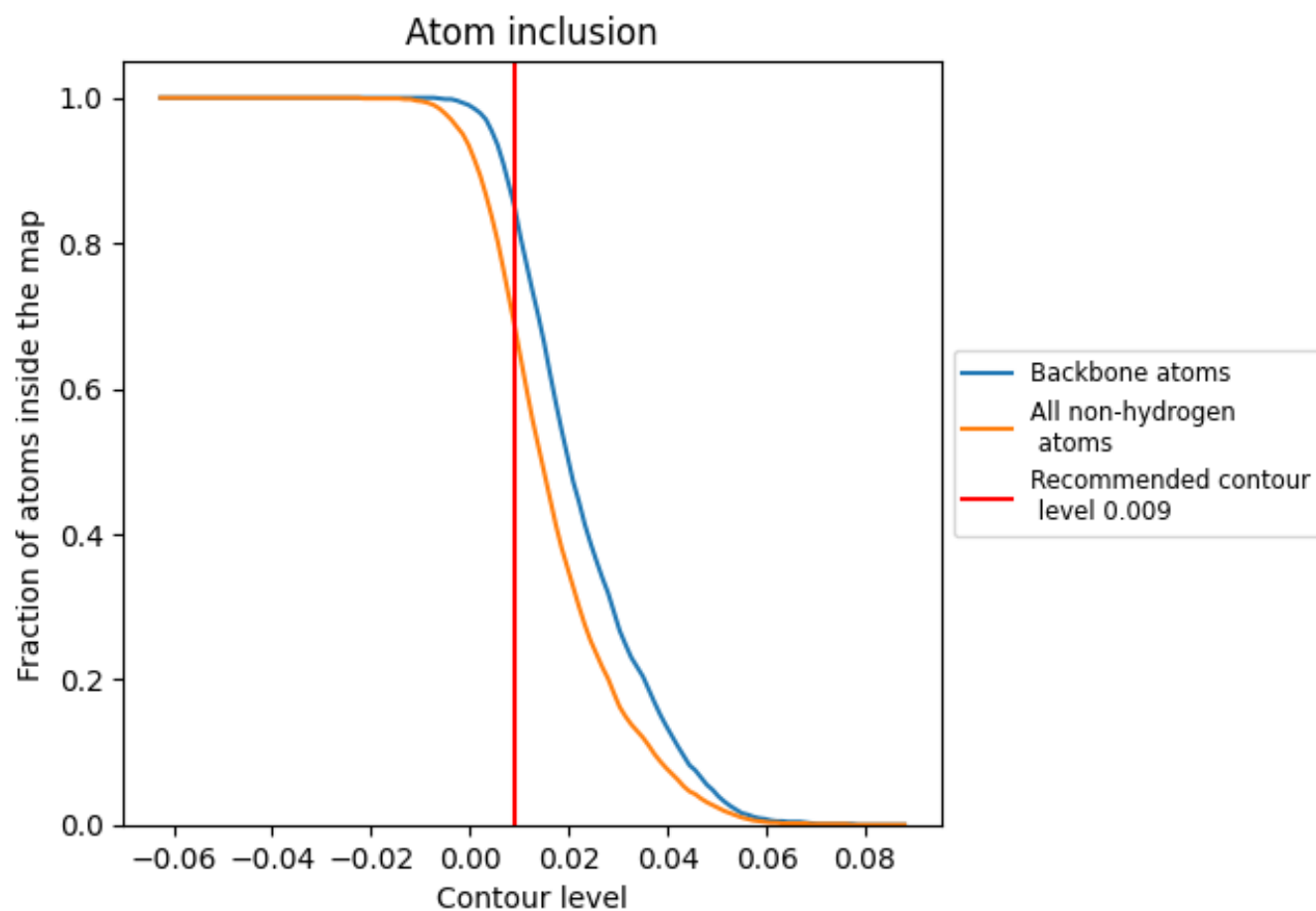


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 69% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6880	0.3350
A	0.6860	0.3340
B	0.6880	0.3360
C	0.6890	0.3330
D	0.6900	0.3350

