



wwPDB EM Validation Summary Report ⓘ

Aug 28, 2025 – 10:19 AM EDT

PDB ID : 9MLK / pdb_00009mlk
EMDB ID : EMD-48374
Title : Post-fusion HERV-K Envelope Protein in complex with Kenv-4 Fab
Authors : Sun, C.; Shek, J.; Hastie, K.; Saphire, E.O.
Deposited on : 2024-12-19
Resolution : 2.84 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:

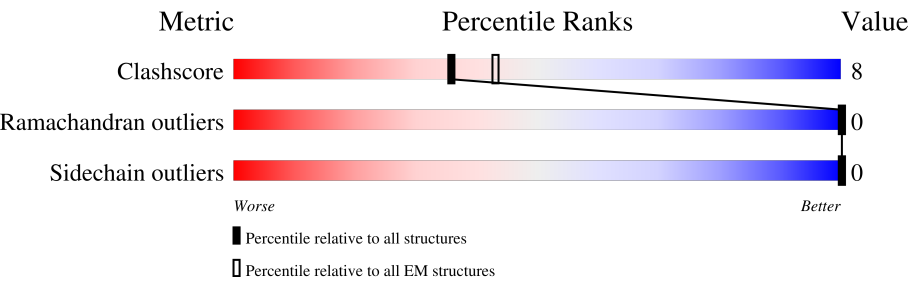
EMDB validation analysis : 0.0.1.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.84 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	H	449	<div><div>22%5%73%</div></div>
1	I	449	<div><div>22%5%73%</div></div>
1	J	449	<div><div>23%73%</div></div>
2	L	213	<div><div>41%9%50%</div></div>
2	M	213	<div><div>42%8%50%</div></div>
2	N	213	<div><div>38%12%50%</div></div>
3	A	135	<div><div>9%47%12%41%</div></div>
3	B	135	<div><div>14%53%10%38%</div></div>

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Mol	Chain	Length	Quality of chain
3	C	135	<div><div></div><div>14%</div><div>49%</div><div>13%</div><div>38%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7335 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 Kenv-4 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	120	Total	C	N	O	S	0	0
			942	602	152	185	3		
1	I	121	Total	C	N	O	S	0	0
			948	605	153	187	3		
1	J	121	Total	C	N	O	S	0	0
			948	605	153	187	3		

- Molecule 2 is a protein called Kenv-4 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	106	Total	C	N	O	S	0	0
			804	506	128	163	7		
2	M	107	Total	C	N	O	S	0	0
			815	512	132	164	7		
2	N	106	Total	C	N	O	S	0	0
			804	506	128	163	7		

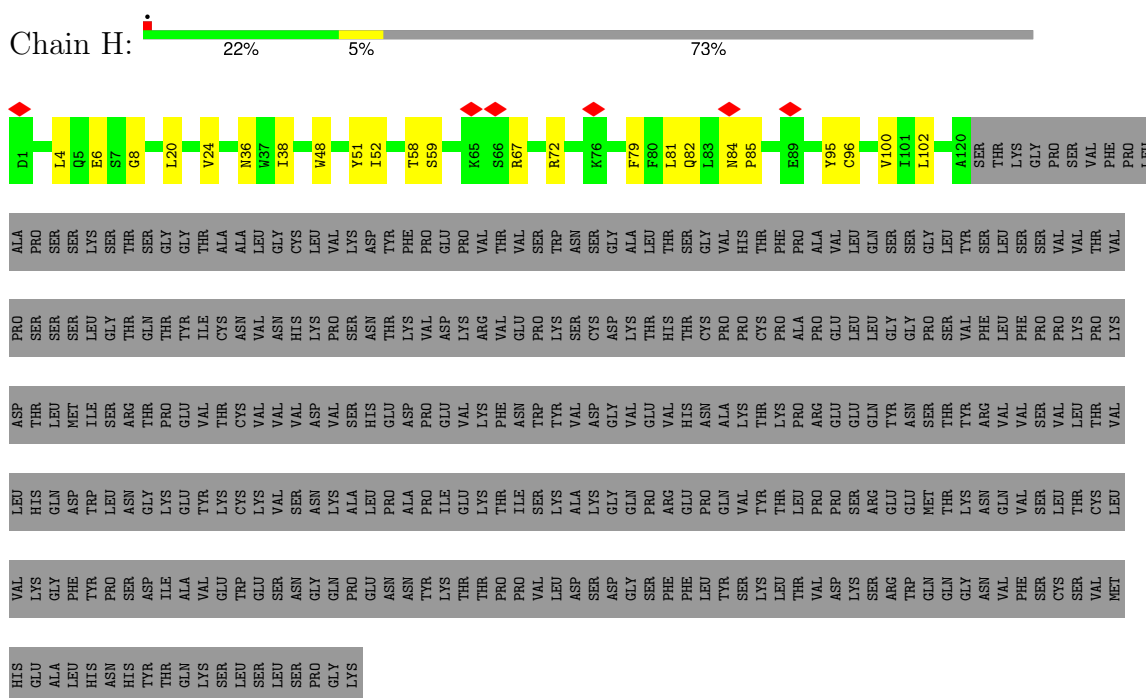
- Molecule 3 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	80	Total	C	N	O	S	0	0
			668	408	130	127	3		
3	C	84	Total	C	N	O	S	0	0
			703	430	135	135	3		
3	B	84	Total	C	N	O	S	0	0
			703	430	135	135	3		

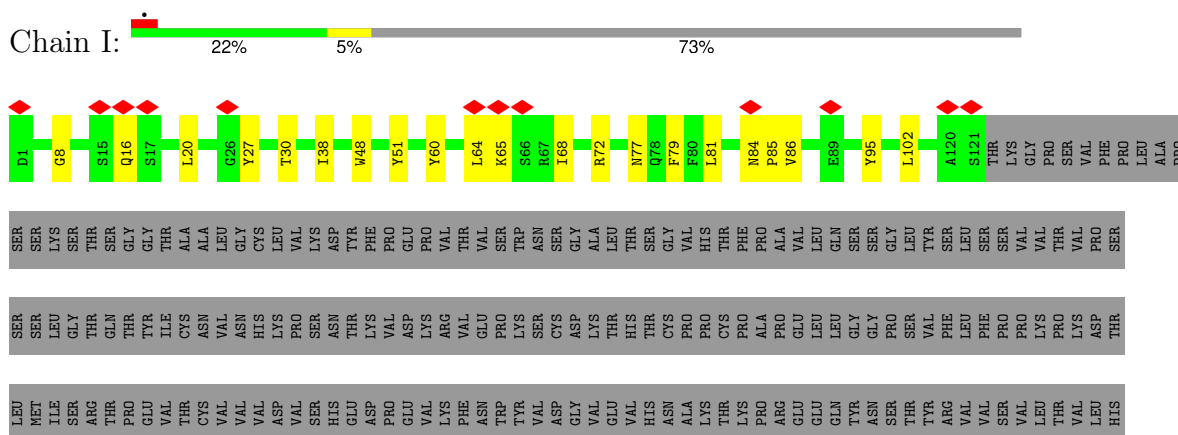
3 Residue-property plots [i](#)

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.

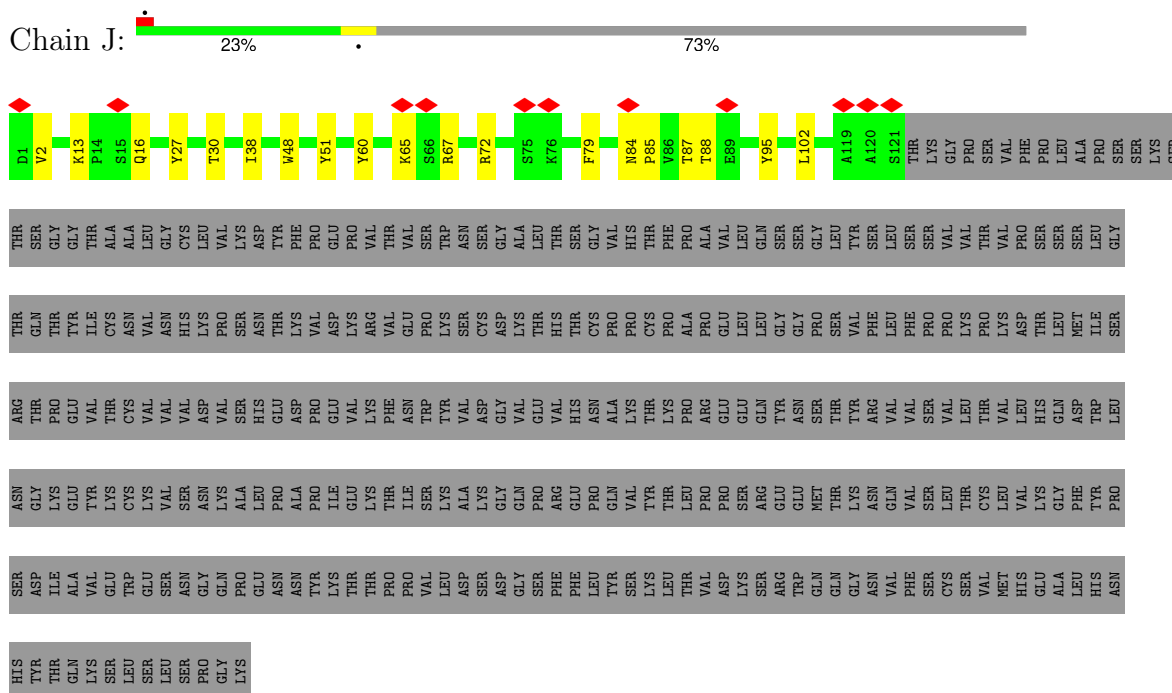
• Molecule 1: Kenv-4 Fab Heavy Chain



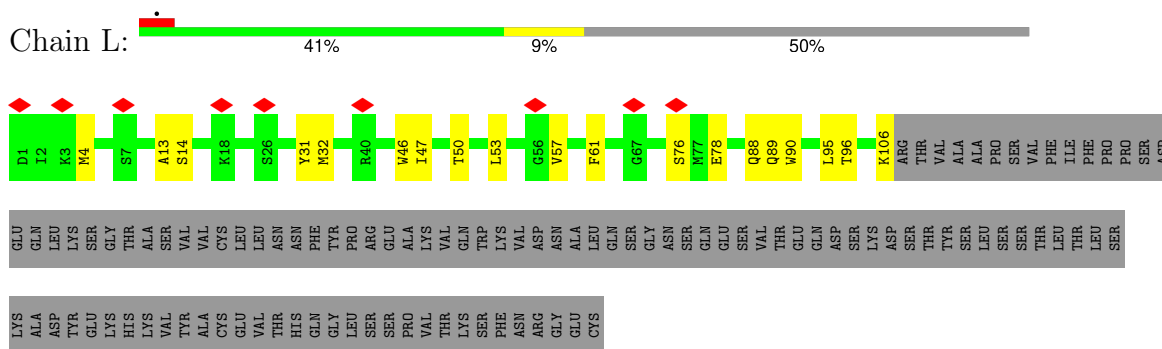
• Molecule 1: Kenv-4 Fab Heavy Chain



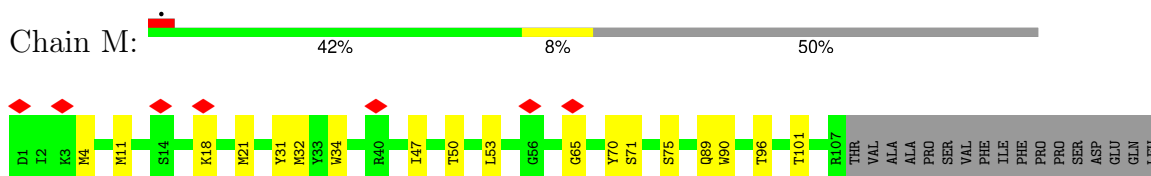
- Molecule 1: Kenv-4 Fab Heavy Chain



- Molecule 2: Kenv-4 Fab Light Chain

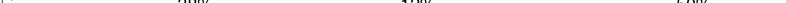


- Molecule 2: Kenv-4 Fab Light Chain



[illegible]

- Molecule 2: Kenv-4 Fab Light Chain

Chain N: 

SER	THR	TYR	SER	LEU	SER	THR	THR	THR	SER	LYS	ALA	ASP	GLY	HIS	LYS	VAL	TYR	ALA	CYS	GLU	VAL	THR	PHE	ASN	ARG	GLY	CYS																				
D1	I2	K3	Q6	S7	P8	M11	S14	V19	T20	M21	S26	Y31	Y33	W34	Y35	R40	P45	W46	I47	Y48	L49	T50	L53	A54	G65	T68	S69	Y70	I74	M77	A82	C87	W90	T101	E104	I105	K106	ARG	THR	VAL							
ALA	ALA	PRO	SER	VAL	PHE	TLE	PHE	PRO	PRO	ASP	GLU	GLN	LEU	LYS	GLY	THR	ALA	SER	VAL	VAL	CYS	LEU	ASN	ASN	PHE	TYR	PRO	ARG	GLU	ALA	LYS	VAL	GLN	SER	GLY	ASN	SER	GLN	GLU	VAL	THR	GLU	GLN	ASP	SER	LYS	ASP

- Molecule 3: Transmembrane protein

Chain A:

Residue	Position	Score	Conservation	Annotations
VAL	5502	0.95	High	
ASN	5503	0.95	High	
PHE	5520	0.95	High	
VAL	5524	0.95	High	
LEU	5525	0.95	High	
PRO	5528	0.95	High	
GLY	5537	0.95	High	
THR	5540	0.95	High	
GLU	5541	0.95	High	
ALA	5545	0.95	High	
ILE	5546	0.95	High	
VAL	5547	0.95	High	
ALA	5548	0.95	High	
ASP	5549	0.95	High	
GLY	5550	0.95	High	
LEU	5551	0.95	High	
LEU	5552	0.95	High	
ALA	5553	0.95	High	
ASN	5554	0.95	High	
ASN	5555	0.95	High	
PRO	5556	0.95	High	
VAL	5557	0.95	High	
THR	5558	0.95	High	
THR	5559	0.95	High	
ASP	5560	0.95	High	
PHE	5561	0.95	High	
CYS	5562	0.95	High	
ILE	5563	0.95	High	
THR	5564	0.95	High	
PRO	5565	0.95	High	
GLN	5566	0.95	High	
ILE	5567	0.95	High	
TYR	5568	0.95	High	
ASN	5569	0.95	High	
GLU	5570	0.95	High	
SER	5571	0.95	High	
ASP	5572	0.95	High	
THR	5573	0.95	High	
GLN	5574	0.95	High	
ASP	5575	0.95	High	
LEU	5576	0.95	High	
ASP	5577	0.95	High	
THR	5578	0.95	High	
LEU	5579	0.95	High	
ASP	5580	0.95	High	
THR	5581	0.95	High	
LEU	5582	0.95	High	
ASP	5583	0.95	High	
THR	5584	0.95	High	
LEU	5585	0.95	High	
ASP	5586	0.95	High	
THR	5587	0.95	High	
LEU	5588	0.95	High	
ASP	5589	0.95	High	
THR	5590	0.95	High	
LEU	5591	0.95	High	
ASP	5592	0.95	High	
THR	5593	0.95	High	
LEU	5594	0.95	High	
ASP	5595	0.95	High	
THR	5596	0.95	High	
LEU	5597	0.95	High	
ASP	5598	0.95	High	
THR	5599	0.95	High	
LEU	5600	0.95	High	
ASP	5601	0.95	High	
THR	5602	0.95	High	
LEU	5603	0.95	High	
ASP	5604	0.95	High	
THR	5605	0.95	High	
LEU	5606	0.95	High	
ASP	5607	0.95	High	
THR	5608	0.95	High	
LEU	5609	0.95	High	
ASP	5610	0.95	High	
THR	5611	0.95	High	
LEU	5612	0.95	High	
ASP	5613	0.95	High	
THR	5614	0.95	High	
LEU	5615	0.95	High	
ASP	5616	0.95	High	
THR	5617	0.95	High	
LEU	5618	0.95	High	
ASP	5619	0.95	High	
THR	5620	0.95	High	
LEU	5621	0.95	High	
ASP	5622	0.95	High	
THR				

- Molecule 3: Transmembrane protein

Chain C: 

Accession	Protein	Length	Start	End	Score	Annotations
K602	HIS	4603	1	4603	100	Hisidine
A603	LEU	4603	1	4603	100	Leucine
N502	ASN	502	1	502	100	Asparagine
D503	LEU	503	1	503	100	Leucine
K506	VAL	506	1	506	100	Valine
R510	PRO	510	1	510	100	Proline
	GLY	510	1	510	100	Glycine
	THR	510	1	510	100	Threonine
	GLU	510	1	510	100	Glutamic acid
	ALA	510	1	510	100	Alanine
L522	ILE	522	1	522	100	Isoleucine
Q525	ALA	525	1	525	100	Alanine
I526	GLY	526	1	526	100	Glycine
N527	VAL	527	1	527	100	Valine
D528	ALA	528	1	528	100	Alanine
L529	ASP	529	1	529	100	Aspartic acid
R530	GLY	530	1	530	100	Glycine
	LEU	530	1	530	100	Leucine
H545	ALA	545	1	545	100	Alanine
R546	ASN	546	1	546	100	Asparagine
F547	LEU	547	1	547	100	Leucine
Q548	ASN	548	1	548	100	Asparagine
	PRO	548	1	548	100	Proline
	VAL	548	1	548	100	Valine
	THR	548	1	548	100	Threonine
	TRP	548	1	548	100	Tryptophan
	VAL	548	1	548	100	Valine
	LYS	548	1	548	100	Lysine
	THR	548	1	548	100	Threonine
VAL						
ASN						
PHE						
N502						
D503						
K506						
R510						
L522						
Q525						
I526						
N527						
D528						
L529						
R530						
H545						
R546						
F547						
Q548						
LEU						
GLN						
CYS						
ASP						
TRP						
ASN						
THR						
SER						
ASP						
PHE						
CYS						
ILE						
THR						
PRO						
GLN						
ILE						
TYR						
ASN						
E567						
S568						
E569						
H570						
H571						
N574						
V575						
R582						
E583						
D584						
N585						

- Molecule 3: Transmembrane protein

Chain B: 

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	143318	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.609	Depositor
Minimum map value	-0.321	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.155	Depositor
Map size (\AA)	337.91998, 337.91998, 337.91998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.87999994, 0.87999994, 0.87999994	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	H	0.13	0/968	0.31	0/1324
1	I	0.12	0/974	0.29	0/1332
1	J	0.11	0/974	0.30	0/1332
2	L	0.13	0/825	0.32	0/1120
2	M	0.12	0/836	0.31	0/1134
2	N	0.16	0/825	0.36	0/1120
3	A	0.10	0/677	0.28	0/907
3	B	0.10	0/713	0.26	0/955
3	C	0.10	0/713	0.28	0/955
All	All	0.12	0/7505	0.30	0/10179

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	H	942	0	901	18	0
1	I	948	0	906	12	0
1	J	948	0	906	11	0
2	L	804	0	778	13	0
2	M	815	0	791	12	0
2	N	804	0	778	16	0
3	A	668	0	649	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	703	0	677	12	0
3	C	703	0	677	18	0
All	All	7335	0	7063	109	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 8.

The worst 5 of 109 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:C:545:HIS:NE2	3:C:569:GLU:OE1	2.22	0.71
1:J:67:ARG:HB2	1:J:85:PRO:HD2	1.79	0.64
1:J:102:LEU:HD22	3:A:578:HIS:HB3	1.79	0.64
1:H:82:GLN:NE2	1:H:84:ASN:OD1	2.32	0.63
2:L:4:MET:HE1	2:L:32:MET:HE1	1.82	0.60

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	H	118/449 (26%)	116 (98%)	2 (2%)	0	100	100
1	I	119/449 (26%)	114 (96%)	5 (4%)	0	100	100
1	J	119/449 (26%)	115 (97%)	4 (3%)	0	100	100
2	L	104/213 (49%)	101 (97%)	3 (3%)	0	100	100
2	M	105/213 (49%)	103 (98%)	2 (2%)	0	100	100
2	N	104/213 (49%)	102 (98%)	2 (2%)	0	100	100
3	A	76/135 (56%)	71 (93%)	5 (7%)	0	100	100
3	B	80/135 (59%)	78 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	80/135 (59%)	76 (95%)	4 (5%)	0	100	100
All	All	905/2391 (38%)	876 (97%)	29 (3%)	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	H	104/403 (26%)	104 (100%)	0	100	100
1	I	105/403 (26%)	105 (100%)	0	100	100
1	J	105/403 (26%)	105 (100%)	0	100	100
2	L	91/187 (49%)	91 (100%)	0	100	100
2	M	92/187 (49%)	92 (100%)	0	100	100
2	N	91/187 (49%)	91 (100%)	0	100	100
3	A	74/123 (60%)	74 (100%)	0	100	100
3	B	78/123 (63%)	78 (100%)	0	100	100
3	C	78/123 (63%)	78 (100%)	0	100	100
All	All	818/2139 (38%)	818 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	515	GLN
3	C	520	GLN
3	B	585	ASN
1	I	111	GLN
2	M	89	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](#)

There are no ligands in this entry.

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.

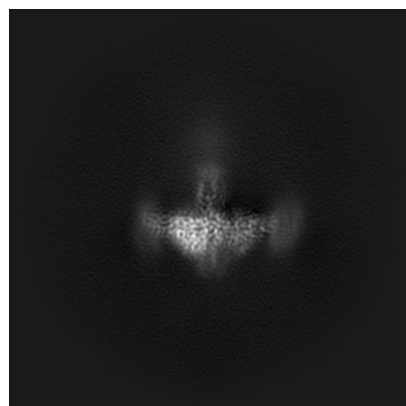
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48374. These allow visual inspection of the internal detail of the map and identification of artifacts.

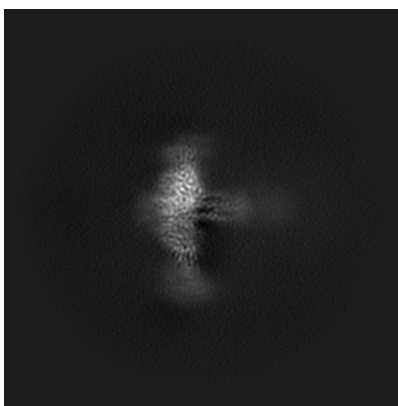
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

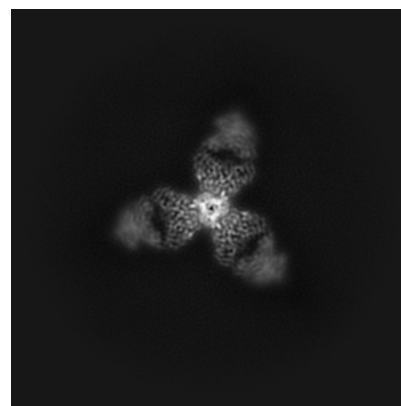
6.1.1 Primary map



X

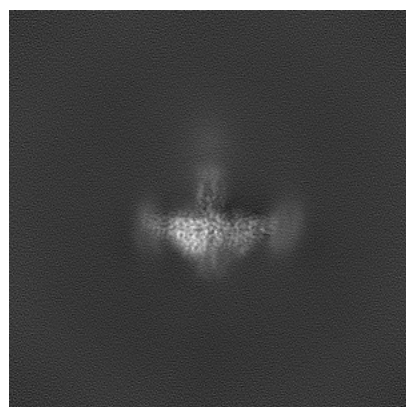


Y

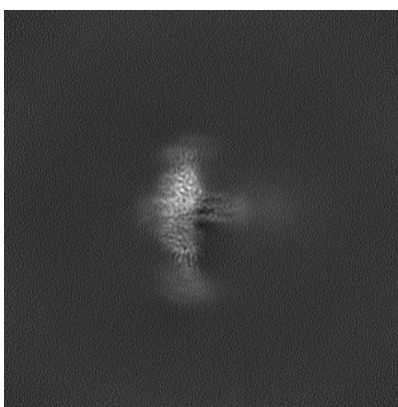


Z

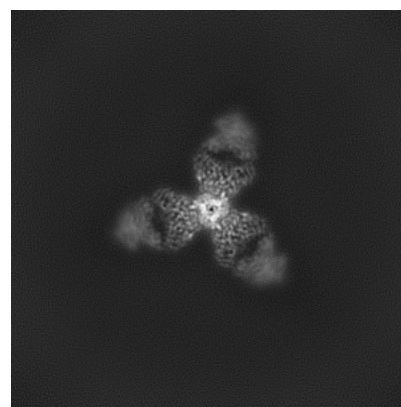
6.1.2 Raw map



X



Y

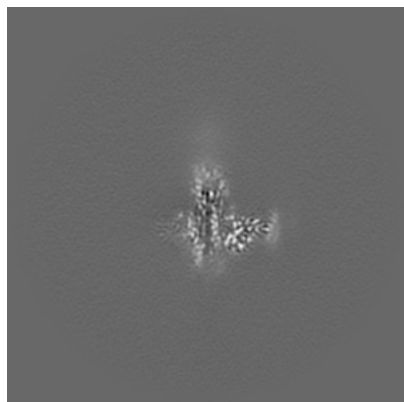


Z

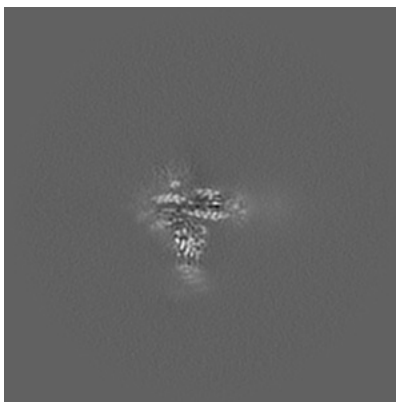
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

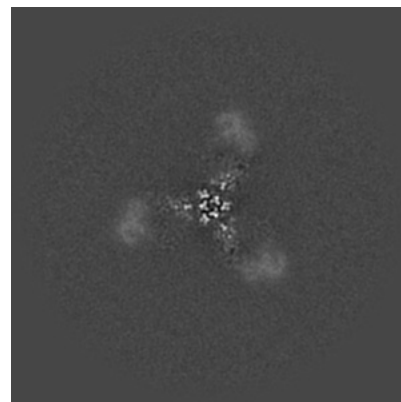
6.2.1 Primary map



X Index: 192

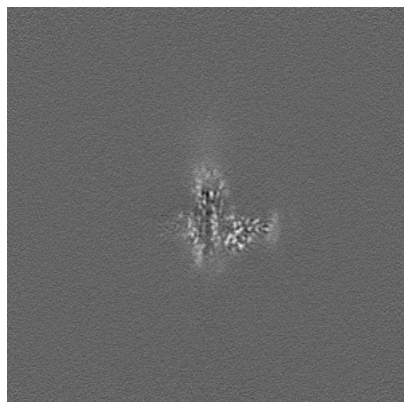


Y Index: 192

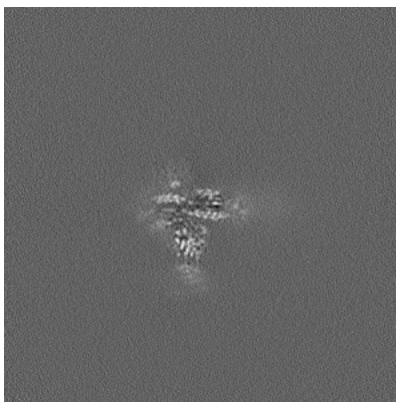


Z Index: 192

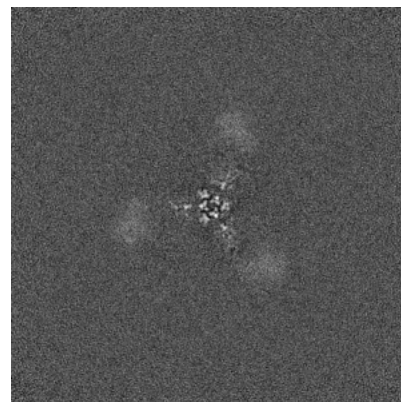
6.2.2 Raw map



X Index: 192



Y Index: 192

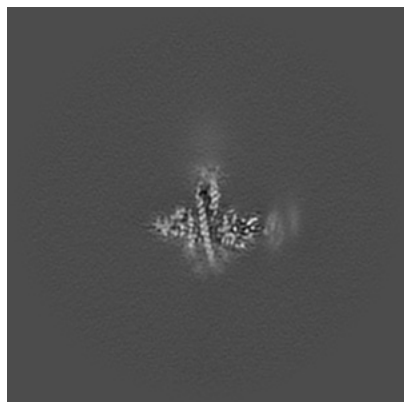


Z Index: 192

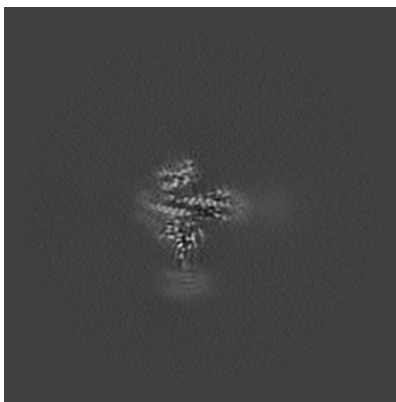
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

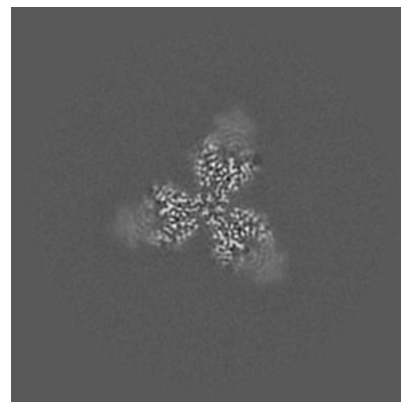
6.3.1 Primary map



X Index: 198

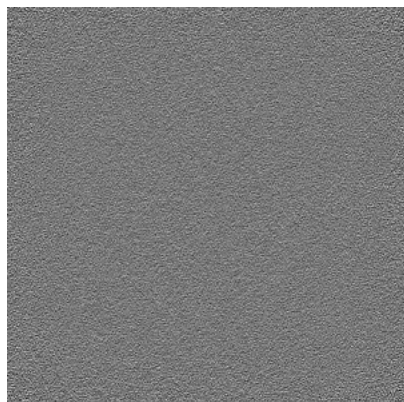


Y Index: 186

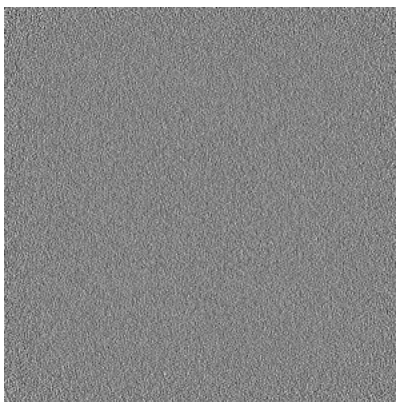


Z Index: 170

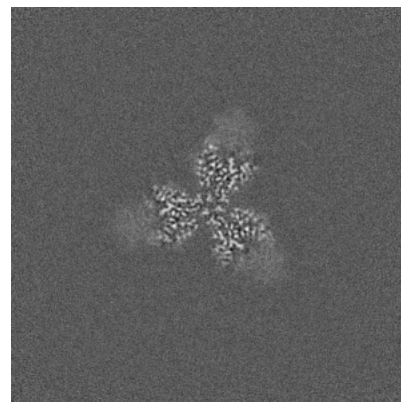
6.3.2 Raw map



X Index: 0



Y Index: 0

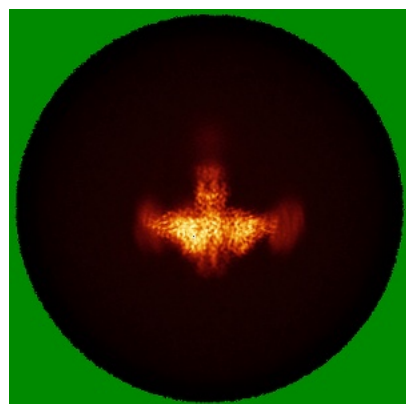


Z Index: 170

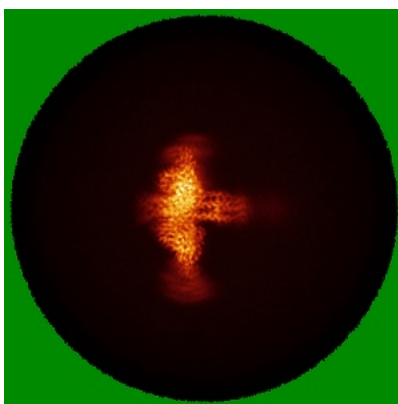
The images above show the largest variance slices of the map in three orthogonal directions.

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

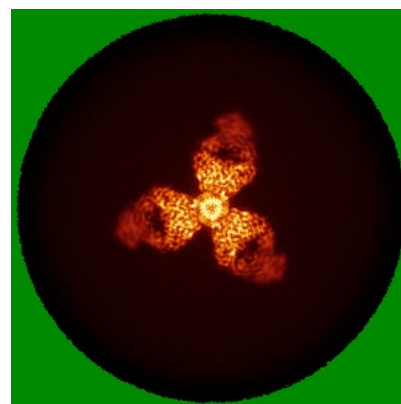
6.4.1 Primary map



X

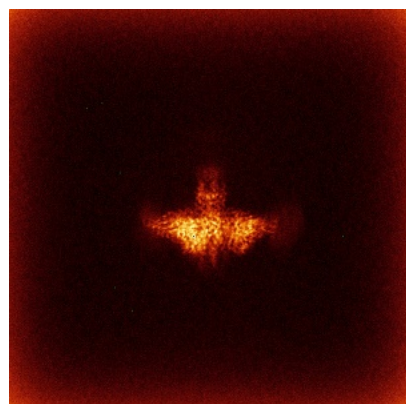


Y

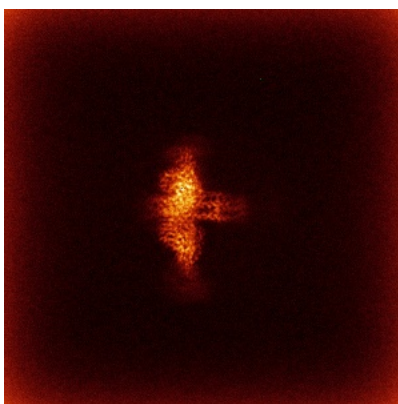


Z

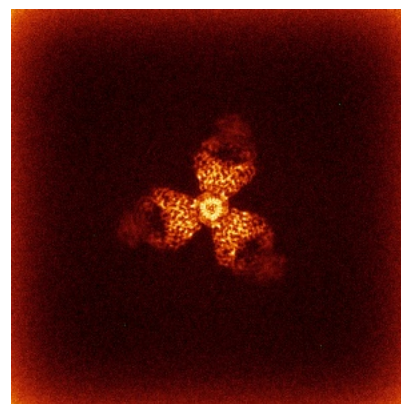
6.4.2 Raw map



X



Y

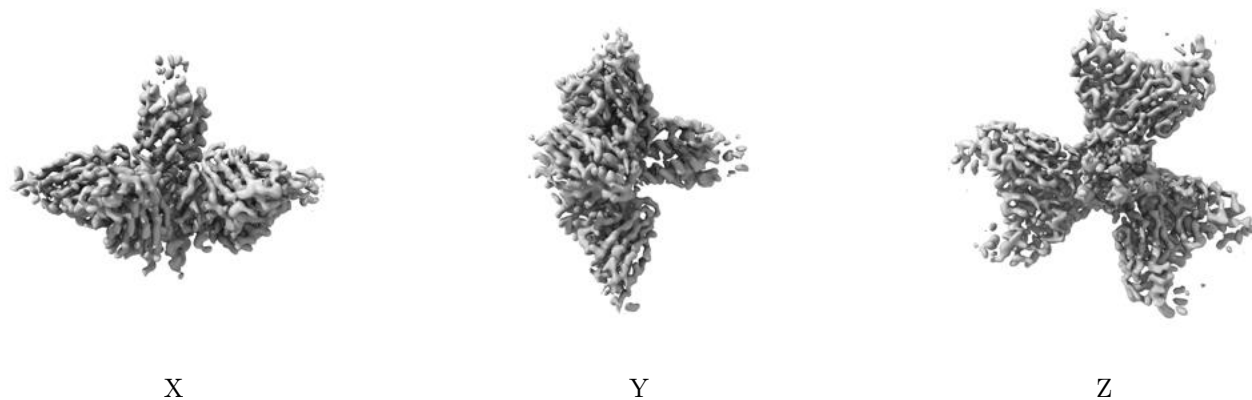


Z

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.

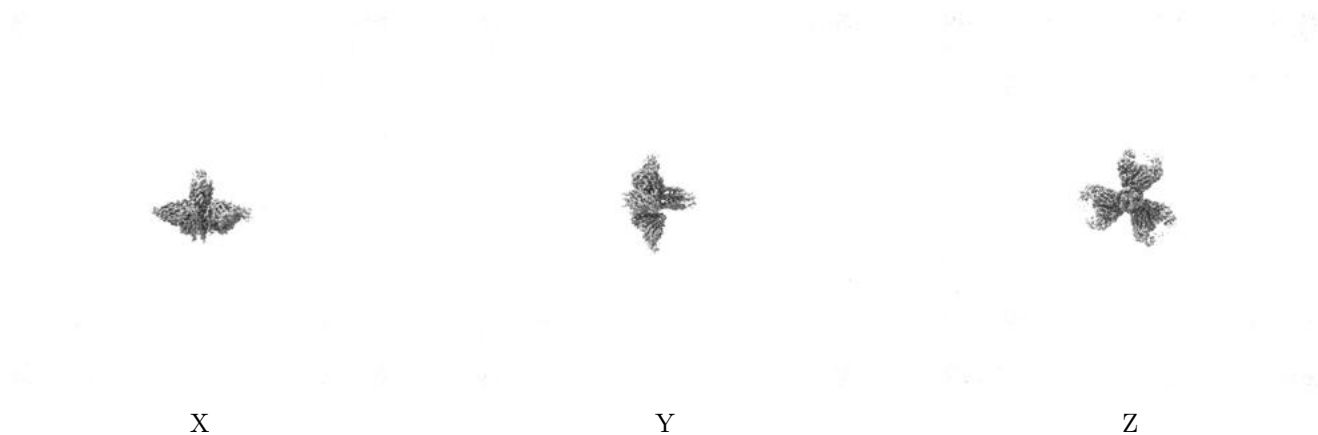
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.155. 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.

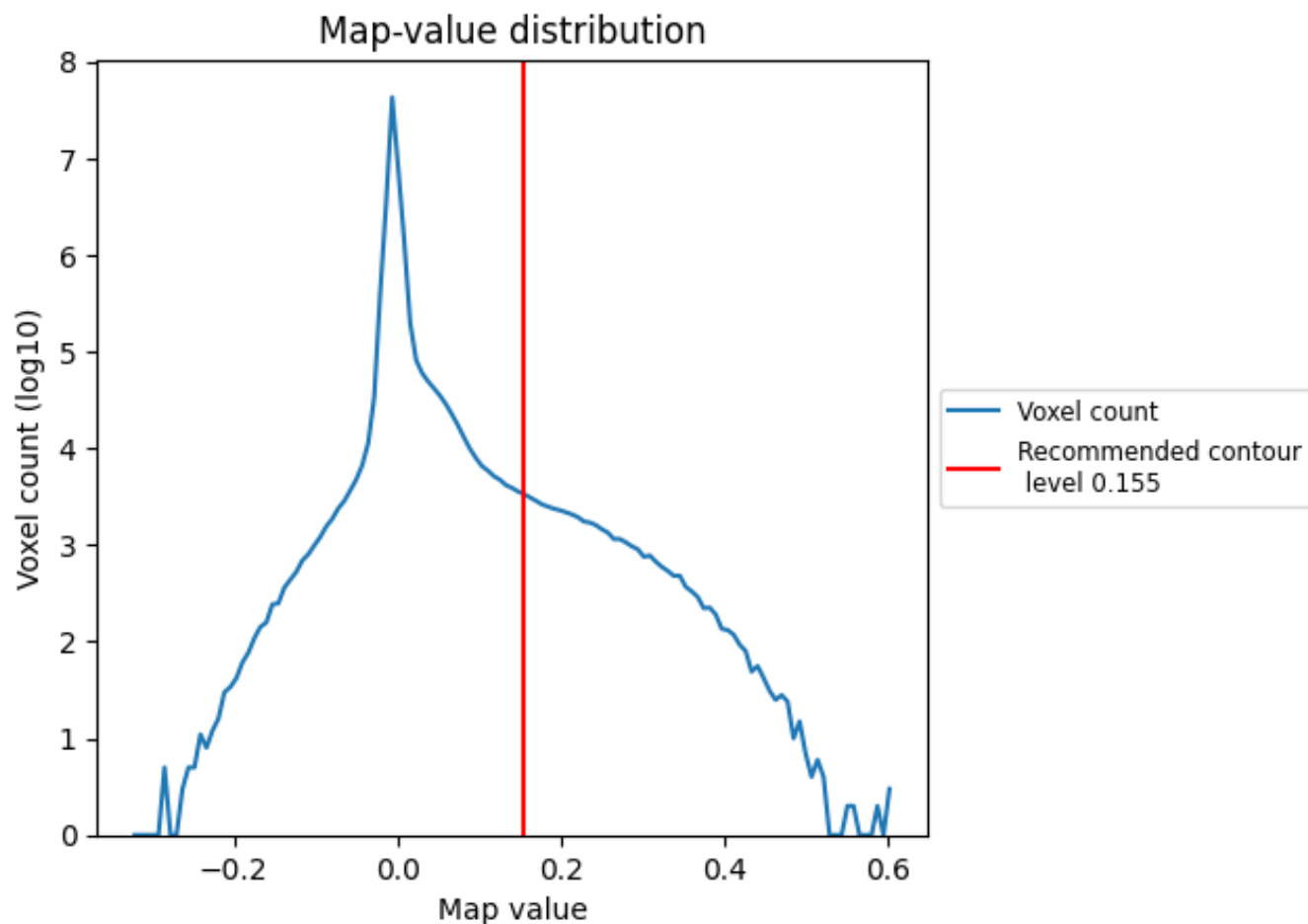
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

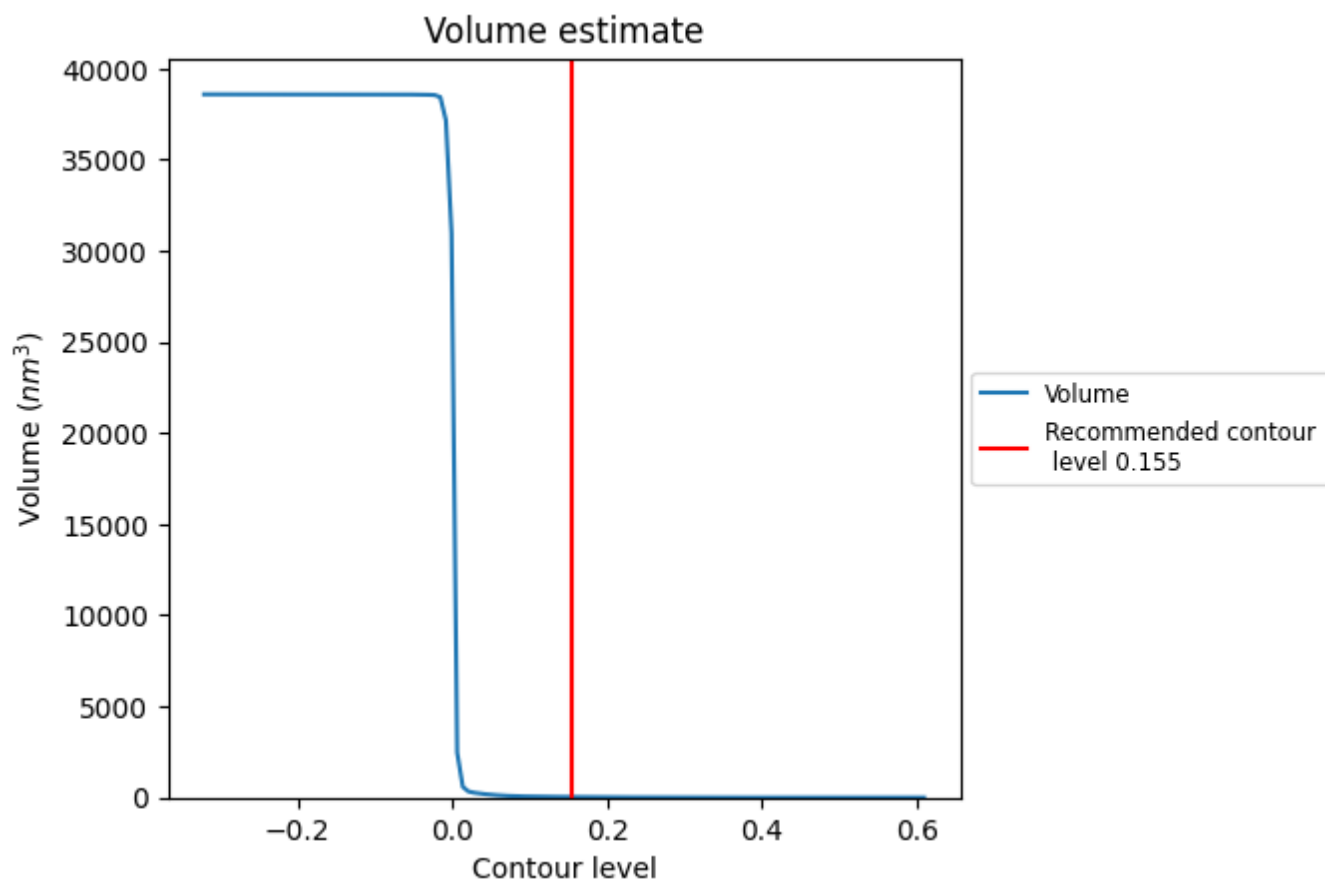
This section contains the results of statistical analysis of the map.

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.

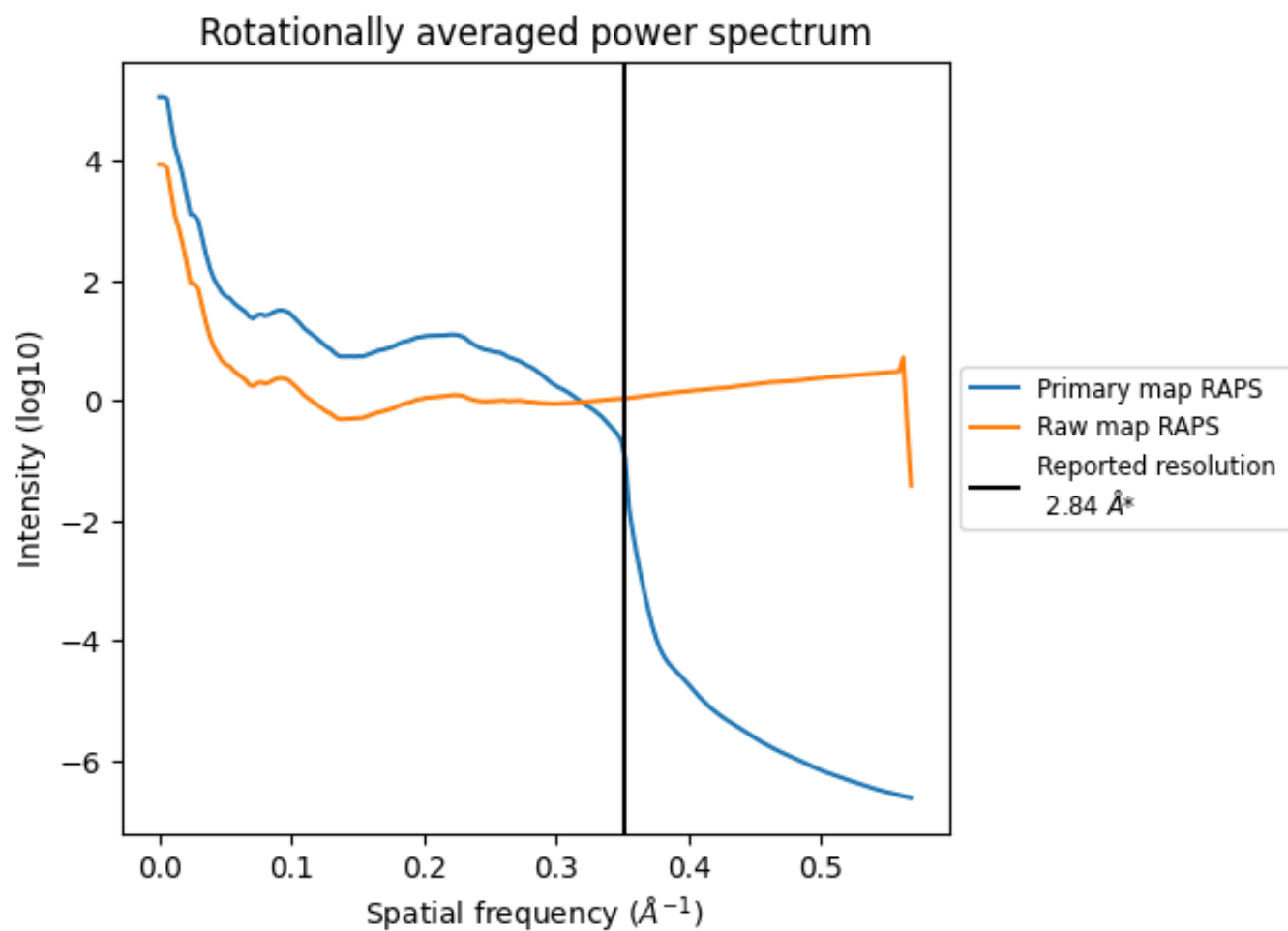
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 31 nm³; this corresponds to an approximate mass of 28 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 ⓘ

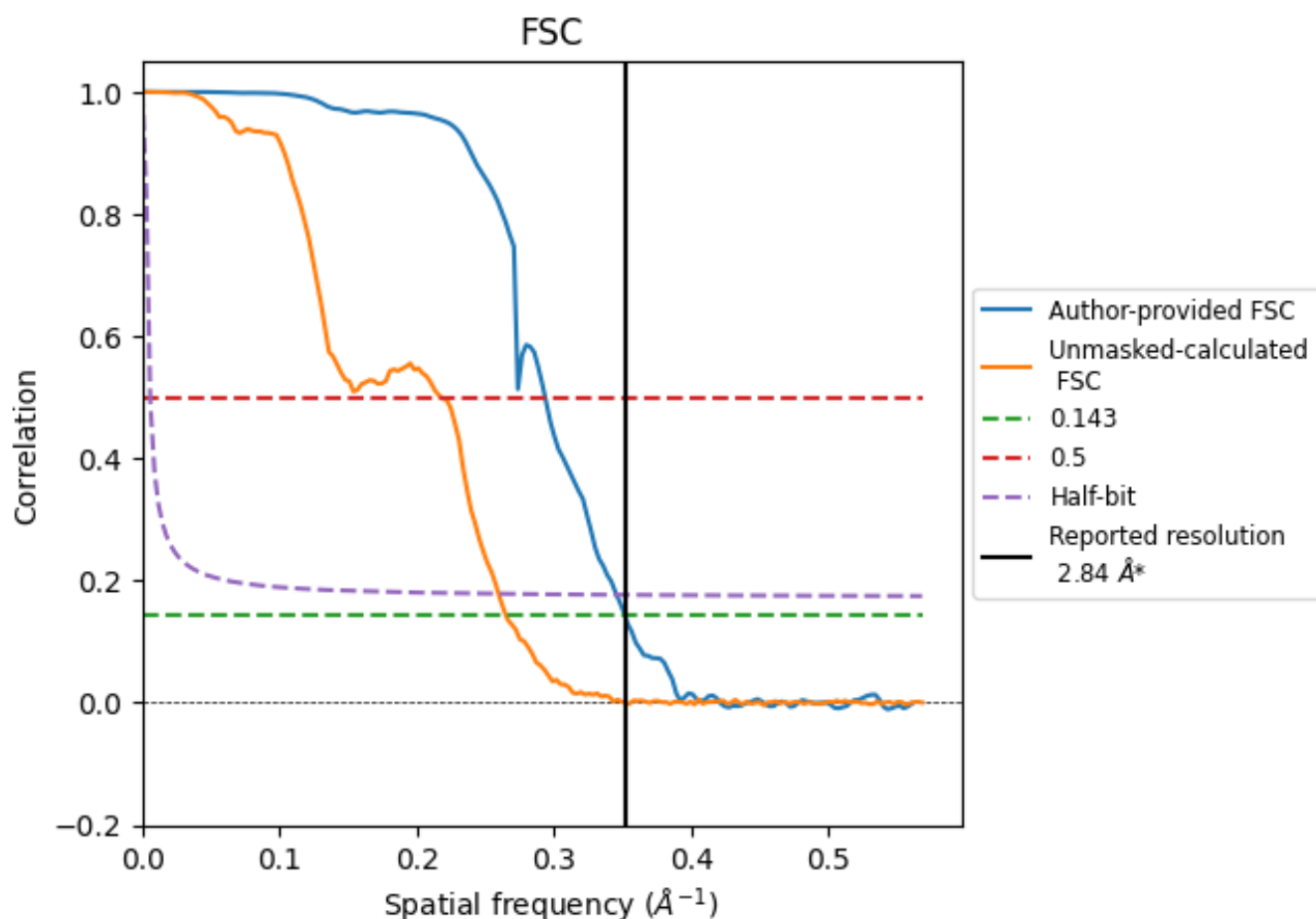


*Reported resolution corresponds to spatial frequency of 0.352\AA^{-1}

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 0.352 \AA^{-1}

8.2 Resolution estimates [i](#)

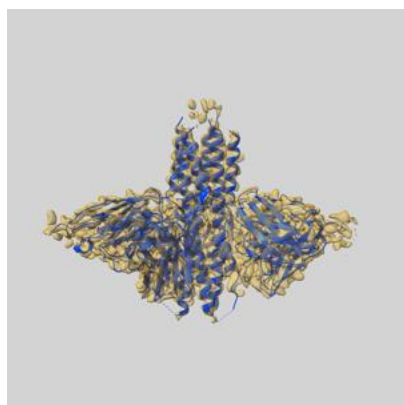
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.41	2.89
Unmasked-calculated*	3.77	4.59	3.85

*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 3.77 differs from the reported value 2.84 by more than 10 %

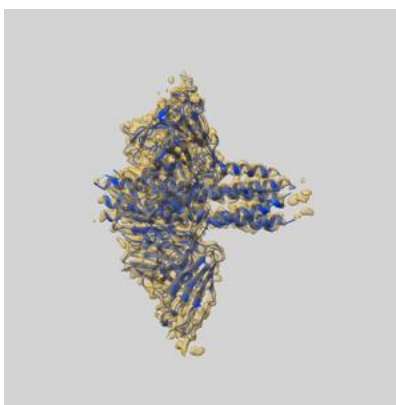
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48374 and PDB model 9MLK. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

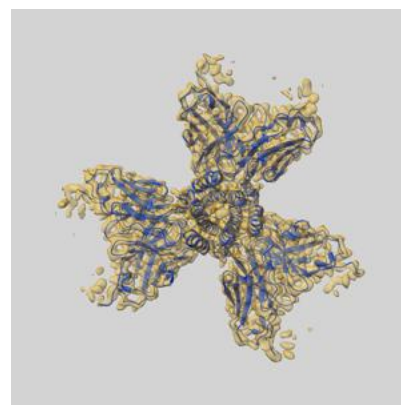
9.1 Map-model overlay [i](#)



X



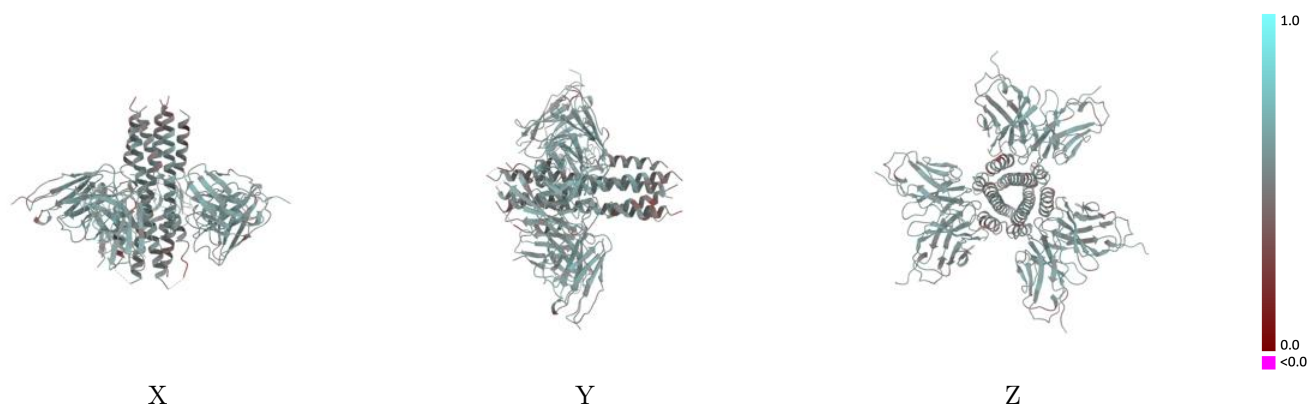
Y



Z

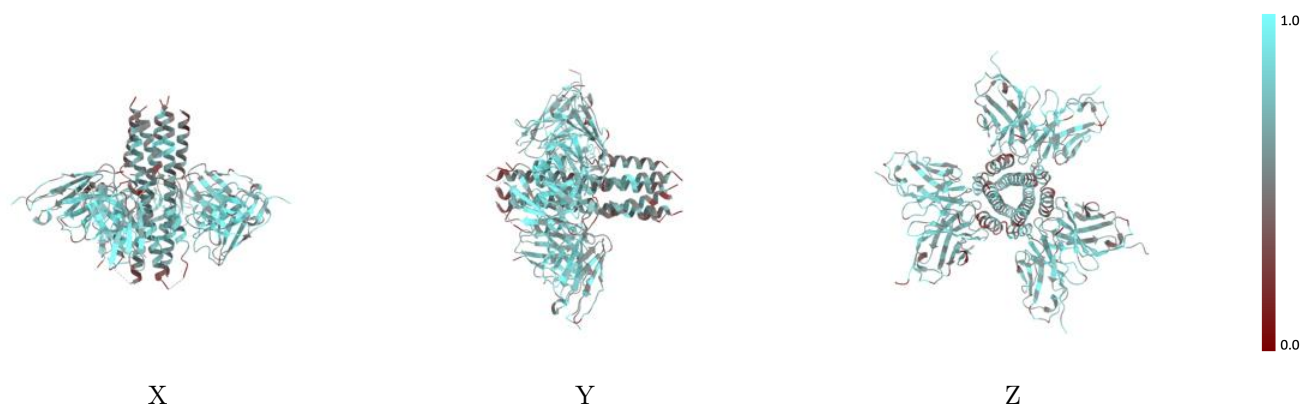
The images above show the 3D surface view of the map at the recommended contour level 0.155 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



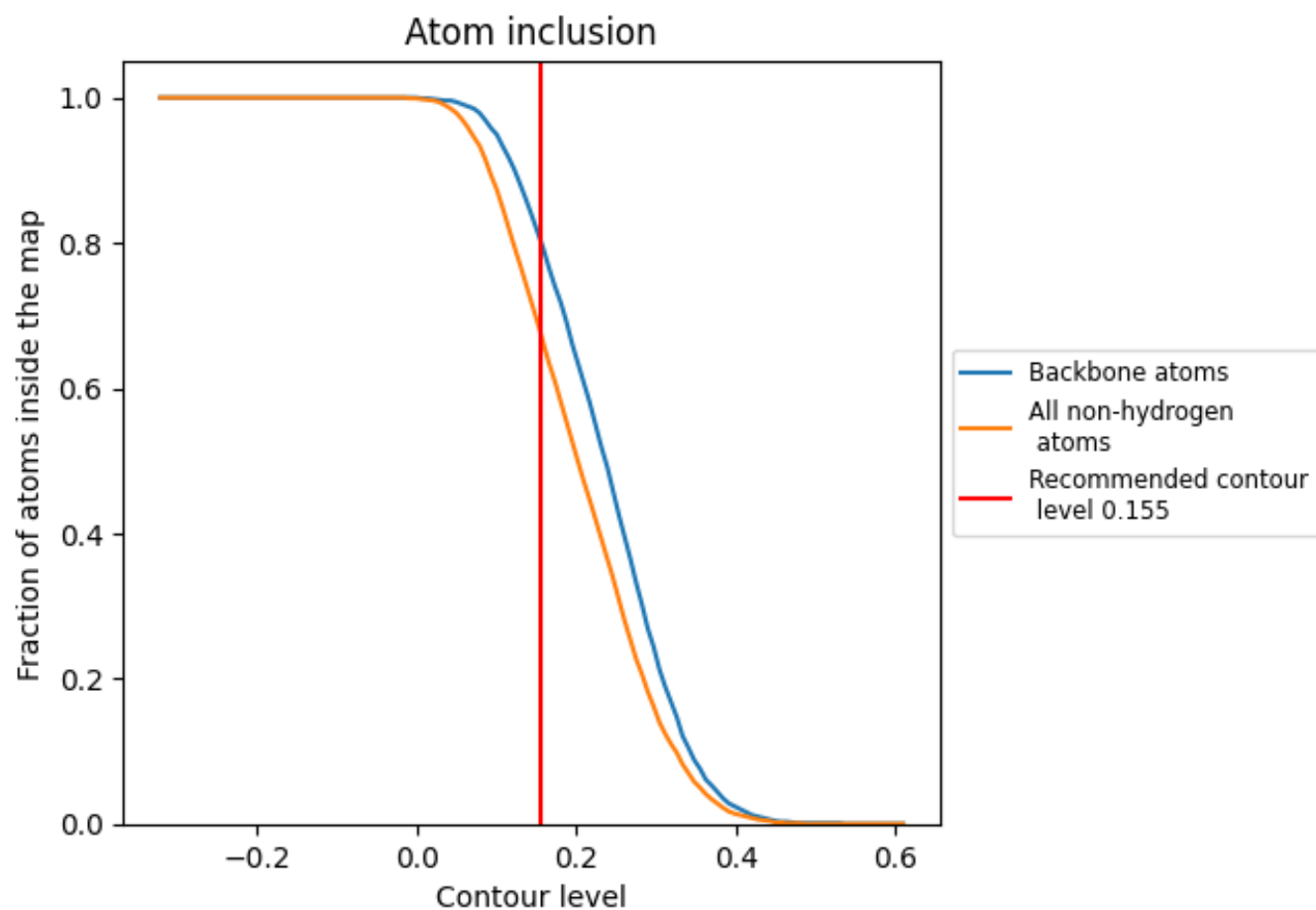
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.155).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 68% 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 (0.155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.6770	<div><div></div></div> 0.5350
A	<div><div></div></div> 0.6250	<div><div></div></div> 0.5020
B	<div><div></div></div> 0.5900	<div><div></div></div> 0.5000
C	<div><div></div></div> 0.5860	<div><div></div></div> 0.5010
H	<div><div></div></div> 0.7290	<div><div></div></div> 0.5520
I	<div><div></div></div> 0.7150	<div><div></div></div> 0.5480
J	<div><div></div></div> 0.7120	<div><div></div></div> 0.5510
L	<div><div></div></div> 0.6950	<div><div></div></div> 0.5500
M	<div><div></div></div> 0.6920	<div><div></div></div> 0.5430
N	<div><div></div></div> 0.6920	<div><div></div></div> 0.5480

1.0

0.0

<0.0