



wwPDB EM Validation Summary Report ⓘ

Dec 4, 2025 – 04:10 PM EST

PDB ID : 9Z3Q / pdb_00009z3q
EMDB ID : EMD-73789
Title : Cryo-EM structure of KSHV glycoprotein gHgL in complex with MLKH3 and MLKH10 FABs
Authors : Lang, K.; Aldridge, N.; Pancera, M.
Deposited on : 2025-11-07
Resolution : 3.51 Å (reported)
Based on initial models : 7CZF, .

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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

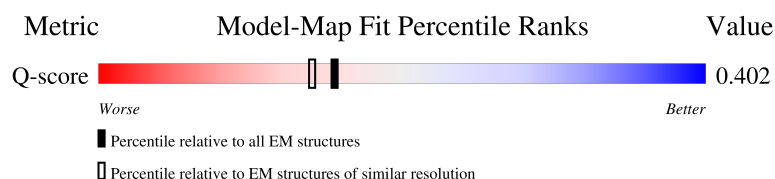
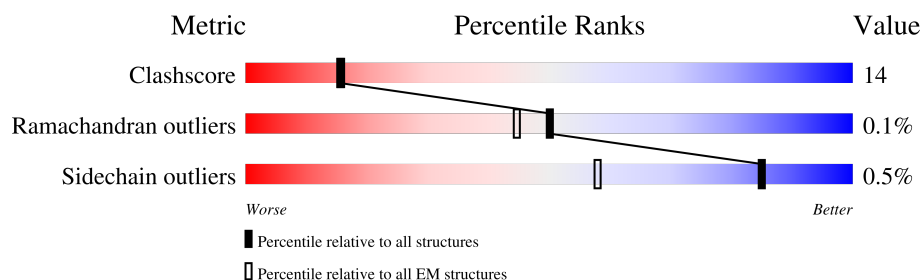
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.51 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13085 (3.01 - 4.01)

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	112	
2	B	121	
3	C	107	
4	D	122	

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Mol	Chain	Length	Quality of chain
5	E	728	<div><div></div><div>13%</div><div>62%</div><div>26%</div><div>12%</div></div>
6	F	176	<div><div></div><div>40%</div><div>23%</div><div>36%</div></div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9433 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 MLKH10 Light chain FV.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	112	Total	C	N	O	S	0	0
			875	553	146	173	3		

- Molecule 2 is a protein called MLKH10 Heavy chain FV.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	S	0	0
			925	576	161	184	4		

- Molecule 3 is a protein called MLKH3 Light chain FV.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			813	514	136	161	2		

- Molecule 4 is a protein called MLKH3 Heavy chain FV.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	121	Total	C	N	O	S	0	0
			909	569	150	186	4		

- Molecule 5 is a protein called Envelope glycoprotein H.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	642	Total	C	N	O	S	0	0
			5049	3229	849	943	28		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	MET	-	initiating methionine	UNP F5HAK9
E	-2	ASP	-	expression tag	UNP F5HAK9
E	-1	ALA	-	expression tag	UNP F5HAK9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	MET	-	expression tag	UNP F5HAK9
E	1	LYS	-	expression tag	UNP F5HAK9
E	2	ARG	-	expression tag	UNP F5HAK9
E	3	GLY	-	expression tag	UNP F5HAK9
E	4	LEU	-	expression tag	UNP F5HAK9
E	5	CYS	-	expression tag	UNP F5HAK9
E	6	CYS	-	expression tag	UNP F5HAK9
E	7	VAL	-	expression tag	UNP F5HAK9
E	8	LEU	-	expression tag	UNP F5HAK9
E	9	LEU	-	expression tag	UNP F5HAK9
E	10	LEU	-	expression tag	UNP F5HAK9
E	11	CYS	-	expression tag	UNP F5HAK9
E	12	GLY	-	expression tag	UNP F5HAK9
E	13	ALA	-	expression tag	UNP F5HAK9
E	14	VAL	-	expression tag	UNP F5HAK9
E	15	PHE	-	expression tag	UNP F5HAK9
E	16	VAL	-	expression tag	UNP F5HAK9
E	17	SER	-	expression tag	UNP F5HAK9
E	18	PRO	-	expression tag	UNP F5HAK9
E	19	SER	-	expression tag	UNP F5HAK9
E	20	ALA	-	expression tag	UNP F5HAK9
E	21	SER	-	expression tag	UNP F5HAK9
E	22	ALA	-	expression tag	UNP F5HAK9
E	699	GLY	-	expression tag	UNP F5HAK9
E	700	SER	-	expression tag	UNP F5HAK9
E	701	GLY	-	expression tag	UNP F5HAK9
E	702	SER	-	expression tag	UNP F5HAK9
E	703	GLY	-	expression tag	UNP F5HAK9
E	704	HIS	-	expression tag	UNP F5HAK9
E	705	HIS	-	expression tag	UNP F5HAK9
E	706	HIS	-	expression tag	UNP F5HAK9
E	707	HIS	-	expression tag	UNP F5HAK9
E	708	HIS	-	expression tag	UNP F5HAK9
E	709	HIS	-	expression tag	UNP F5HAK9
E	710	GLY	-	expression tag	UNP F5HAK9
E	711	LEU	-	expression tag	UNP F5HAK9
E	712	ASN	-	expression tag	UNP F5HAK9
E	713	ASP	-	expression tag	UNP F5HAK9
E	714	ILE	-	expression tag	UNP F5HAK9
E	715	PHE	-	expression tag	UNP F5HAK9
E	716	GLU	-	expression tag	UNP F5HAK9
E	717	ALA	-	expression tag	UNP F5HAK9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	718	GLN	-	expression tag	UNP F5HAK9
E	719	LYS	-	expression tag	UNP F5HAK9
E	720	ILE	-	expression tag	UNP F5HAK9
E	721	GLU	-	expression tag	UNP F5HAK9
E	722	TRP	-	expression tag	UNP F5HAK9
E	723	HIS	-	expression tag	UNP F5HAK9
E	724	GLU	-	expression tag	UNP F5HAK9

- Molecule 6 is a protein called Envelope glycoprotein L.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	112	Total	C	N	O	S	0	0
			862	548	154	155	5		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-8	MET	-	initiating methionine	UNP F5HDB7
F	-7	ASP	-	expression tag	UNP F5HDB7
F	-6	ALA	-	expression tag	UNP F5HDB7
F	-5	MET	-	expression tag	UNP F5HDB7
F	-4	LYS	-	expression tag	UNP F5HDB7
F	-3	ARG	-	expression tag	UNP F5HDB7
F	-2	GLY	-	expression tag	UNP F5HDB7
F	-1	LEU	-	expression tag	UNP F5HDB7
F	0	CYS	-	expression tag	UNP F5HDB7
F	1	CYS	-	expression tag	UNP F5HDB7
F	2	VAL	-	expression tag	UNP F5HDB7
F	3	LEU	-	expression tag	UNP F5HDB7
F	4	LEU	-	expression tag	UNP F5HDB7
F	5	LEU	-	expression tag	UNP F5HDB7
F	6	CYS	-	expression tag	UNP F5HDB7
F	7	GLY	-	expression tag	UNP F5HDB7
F	8	ALA	-	expression tag	UNP F5HDB7
F	9	VAL	-	expression tag	UNP F5HDB7
F	10	PHE	-	expression tag	UNP F5HDB7
F	11	VAL	-	expression tag	UNP F5HDB7
F	12	SER	-	expression tag	UNP F5HDB7
F	13	PRO	-	expression tag	UNP F5HDB7
F	14	SER	-	expression tag	UNP F5HDB7
F	15	ALA	-	expression tag	UNP F5HDB7
F	16	SER	-	expression tag	UNP F5HDB7

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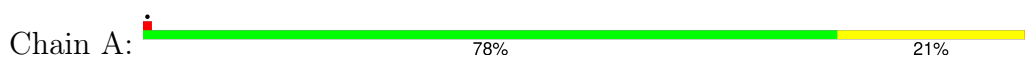
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Chain	Residue	Modelled	Actual	Comment	Reference
F	17	ASP	-	expression tag	UNP F5HDB7
F	18	GLY	-	expression tag	UNP F5HDB7
F	19	ILE	-	expression tag	UNP F5HDB7
F	20	GLN	-	expression tag	UNP F5HDB7

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: MLKH10 Light chain FV



- Molecule 2: MLKH10 Heavy chain FV



- Molecule 3: MLKH3 Light chain FV



- Molecule 4: MLKH3 Heavy chain FV



- Molecule 5: Envelope glycoprotein H



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75257	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.918	Depositor
Minimum map value	-3.352	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.181	Depositor
Recommended contour level	0.658	Depositor
Map size (Å)	240.108, 240.108, 238.986	wwPDB
Map dimensions	214, 214, 213	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.122, 1.122, 1.122	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	0.13	0/897	0.36	0/1219
2	B	0.14	0/946	0.40	0/1281
3	C	0.18	0/833	0.45	0/1133
4	D	0.14	0/926	0.39	0/1257
5	E	0.16	0/5159	0.44	0/7014
6	F	0.17	0/881	0.45	0/1202
All	All	0.16	0/9642	0.42	0/13106

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	A	875	0	844	22	0
2	B	925	0	862	33	0
3	C	813	0	790	21	0
4	D	909	0	882	20	0
5	E	5049	0	5029	149	0
6	F	862	0	852	35	0
All	All	9433	0	9259	269	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 14.

The worst 5 of 269 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)
5:E:472:THR:HB	5:E:506:LEU:H	1.41	0.84
2:B:51:ILE:HD13	2:B:71:ARG:HB3	1.61	0.83
3:C:94:PHE:HB3	3:C:95:PRO:HD2	1.64	0.78
2:B:33:GLY:HA2	2:B:71:ARG:HH12	1.52	0.75
5:E:294:ILE:HD11	5:E:312:VAL:HG21	1.69	0.74

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	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
2	B	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
3	C	105/107 (98%)	94 (90%)	10 (10%)	1 (1%)	13	45
4	D	119/122 (98%)	114 (96%)	5 (4%)	0	100	100
5	E	638/728 (88%)	597 (94%)	41 (6%)	0	100	100
6	F	110/176 (62%)	104 (94%)	6 (6%)	0	100	100
All	All	1201/1366 (88%)	1119 (93%)	81 (7%)	1 (0%)	50	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	95	PRO

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	98/98 (100%)	97 (99%)	1 (1%)	73	84
2	B	97/97 (100%)	97 (100%)	0	100	100
3	C	90/90 (100%)	89 (99%)	1 (1%)	70	83
4	D	99/100 (99%)	98 (99%)	1 (1%)	73	84
5	E	561/627 (90%)	559 (100%)	2 (0%)	89	94
6	F	94/143 (66%)	94 (100%)	0	100	100
All	All	1039/1155 (90%)	1034 (100%)	5 (0%)	85	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	TYR
3	C	94	PHE
4	D	102	ILE
5	E	61	ASN
5	E	91	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	131	ASN
5	E	175	ASN
6	F	44	HIS
5	E	679	HIS
2	B	73	ASN

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 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.

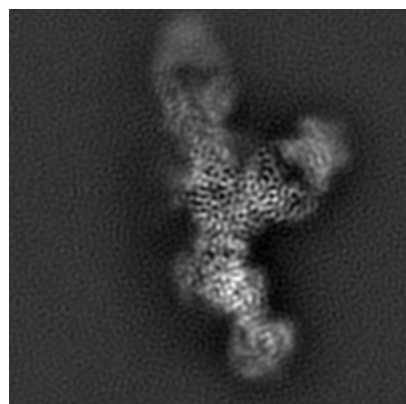
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73789. These allow visual inspection of the internal detail of the map and identification of artifacts.

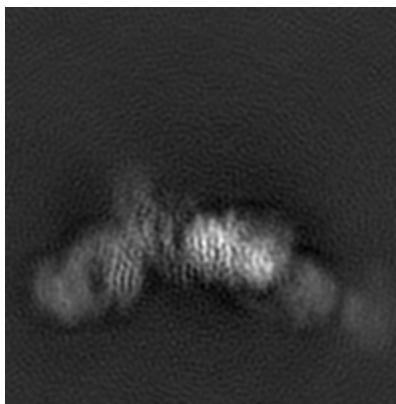
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

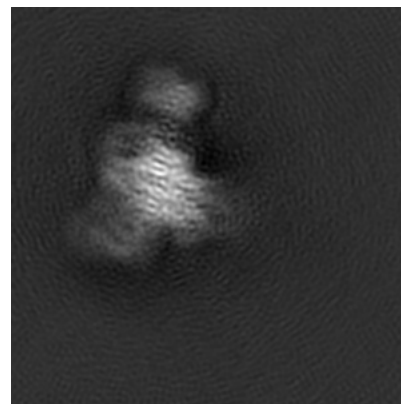
6.1.1 Primary map



X

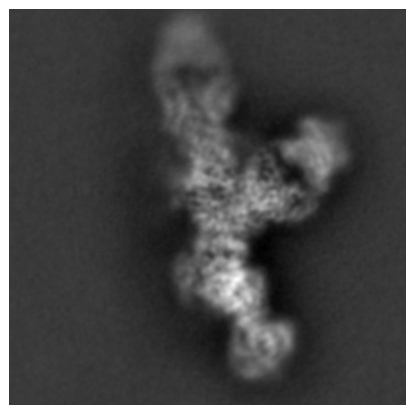


Y

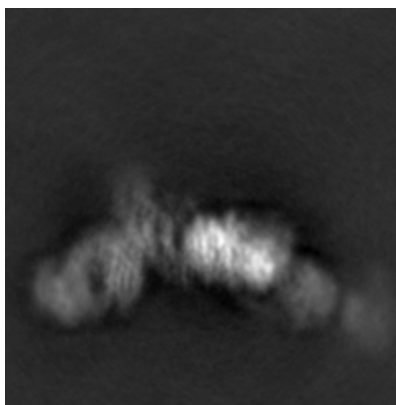


Z

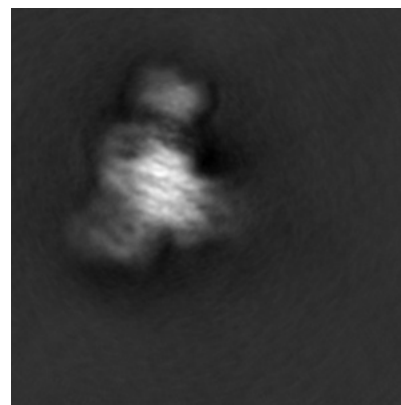
6.1.2 Raw map



X



Y

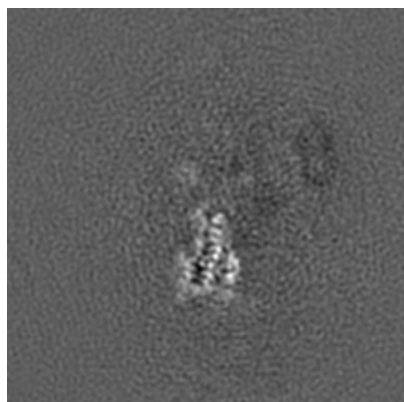


Z

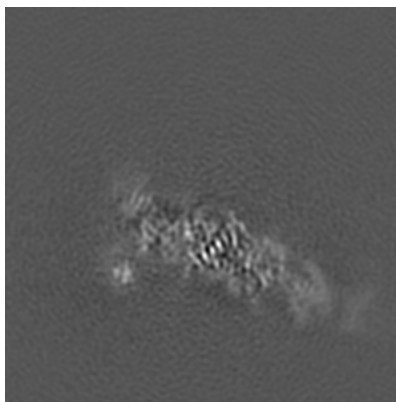
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

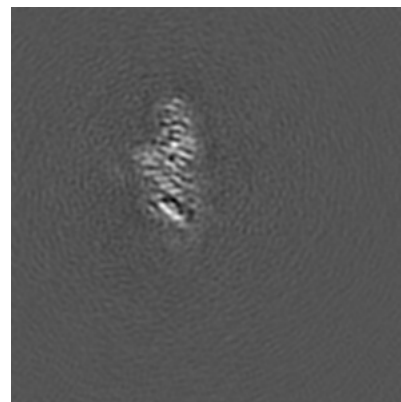
6.2.1 Primary map



X Index: 107

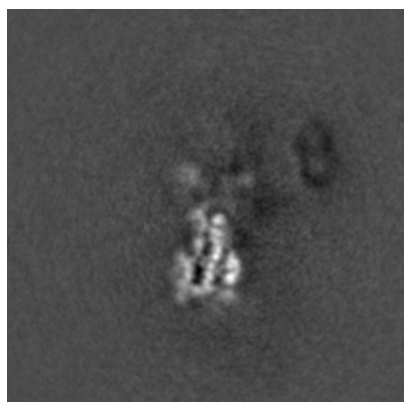


Y Index: 107

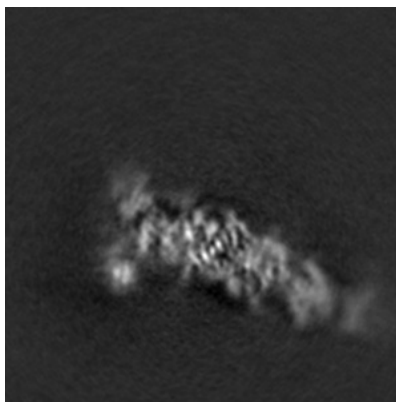


Z Index: 106

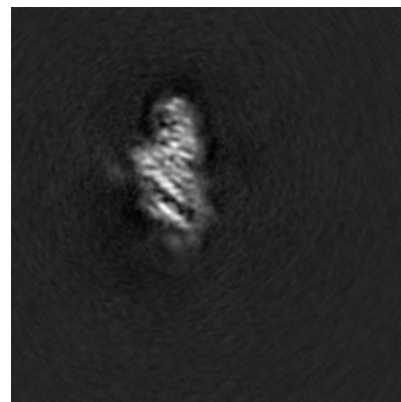
6.2.2 Raw map



X Index: 107



Y Index: 107

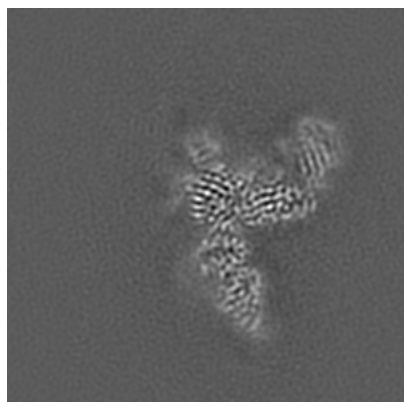


Z Index: 106

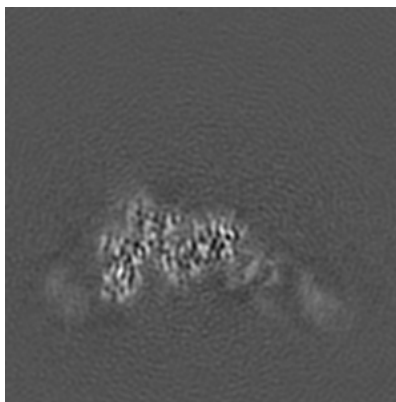
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

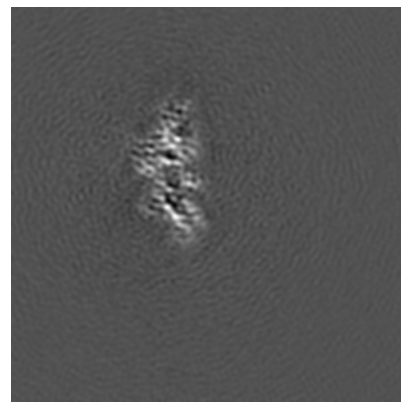
6.3.1 Primary map



X Index: 87

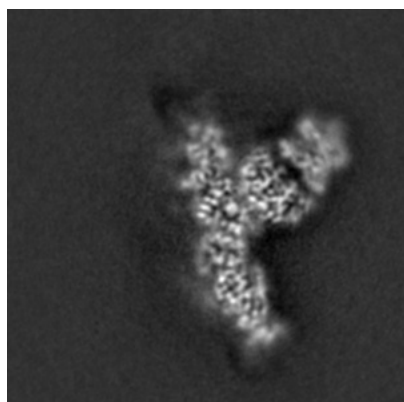


Y Index: 118

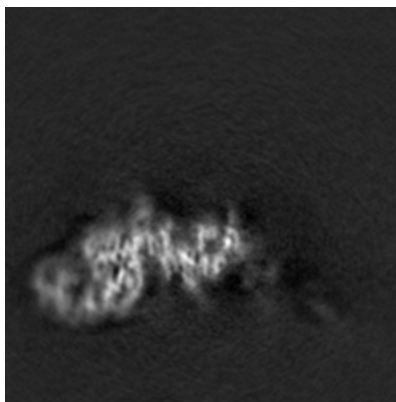


Z Index: 111

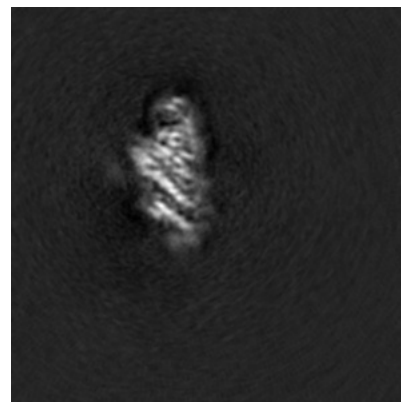
6.3.2 Raw map



X Index: 82



Y Index: 124

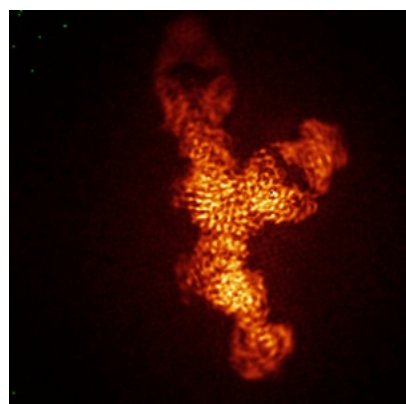


Z Index: 107

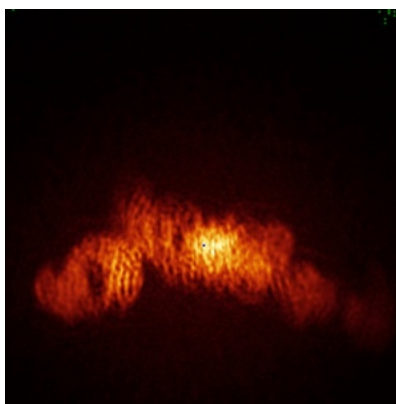
The images above show the largest variance slices of the map in three orthogonal directions.

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

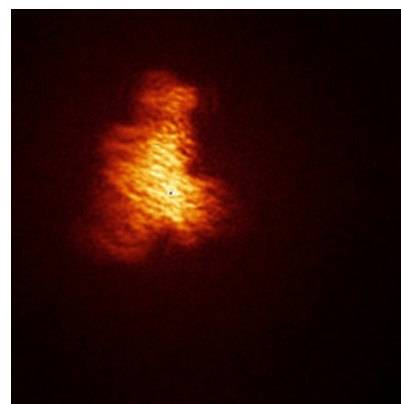
6.4.1 Primary map



X

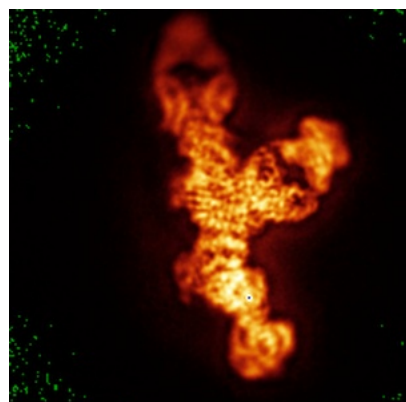


Y

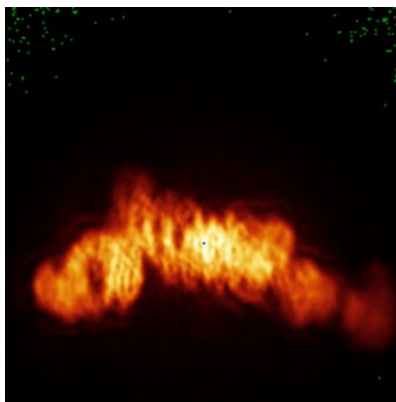


Z

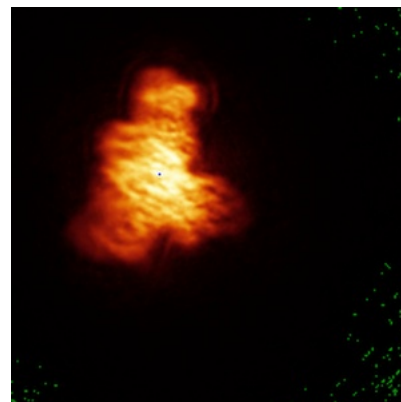
6.4.2 Raw map



X



Y

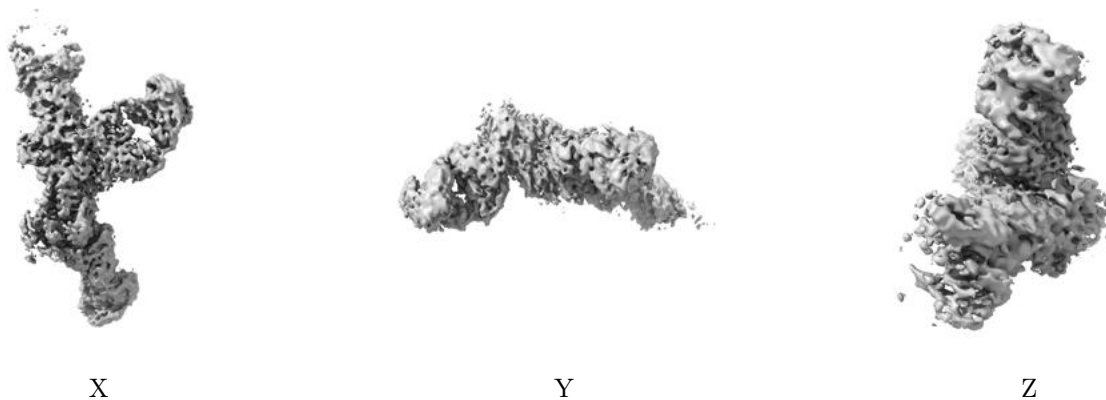


Z

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.

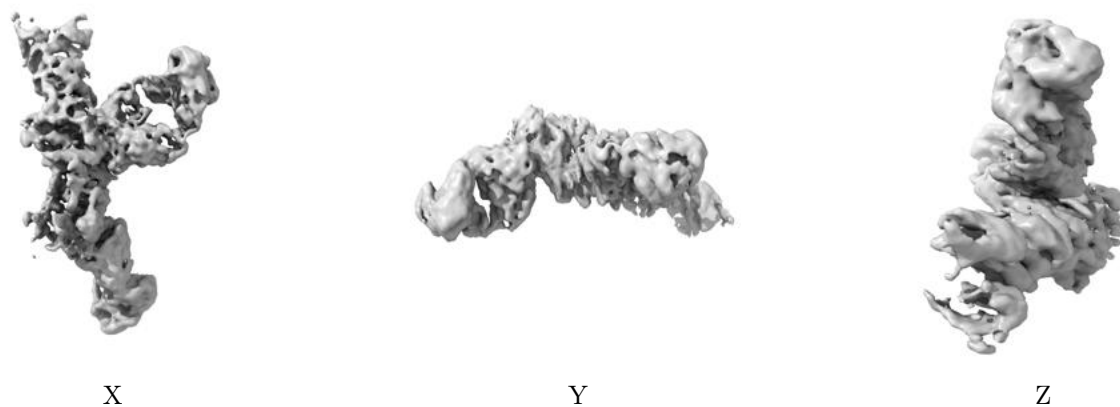
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.658. 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.

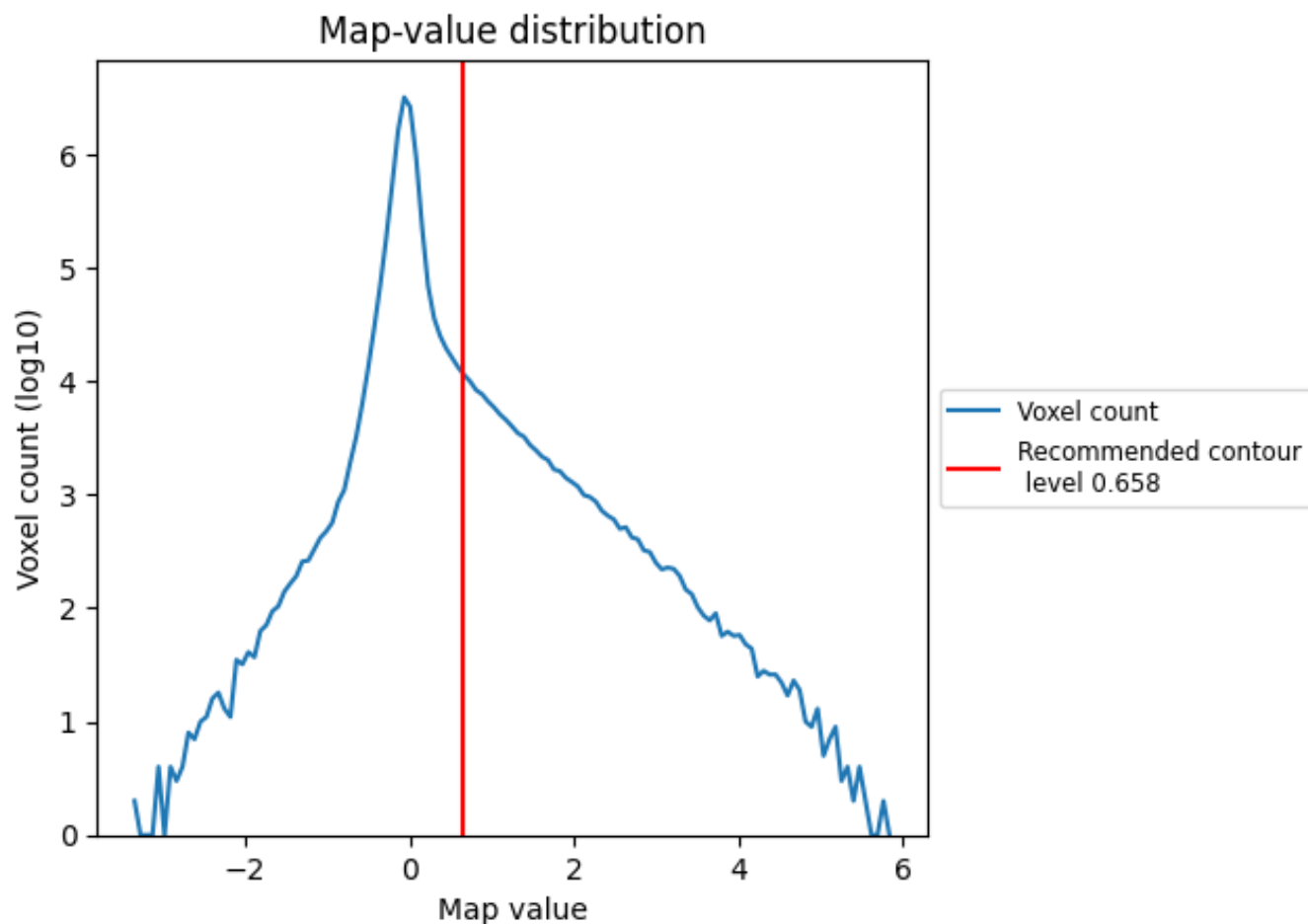
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

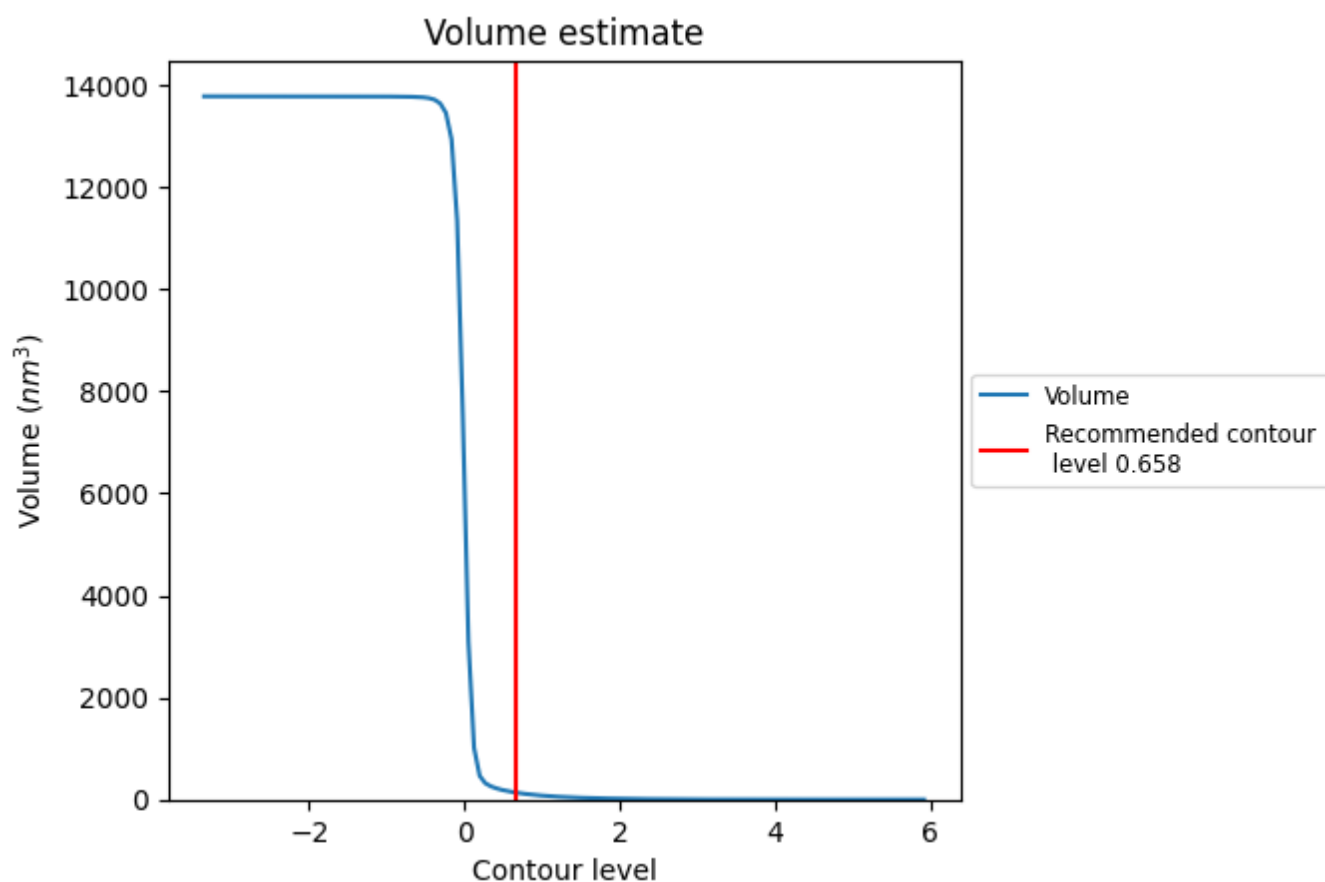
This section contains the results of statistical analysis of the map.

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 138 nm³; 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

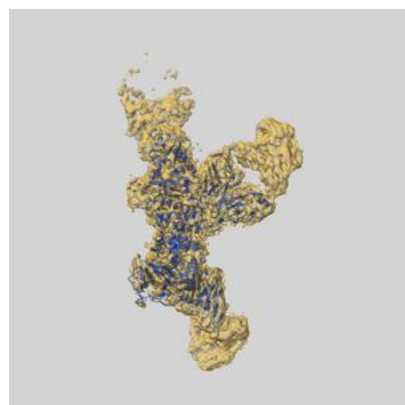
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

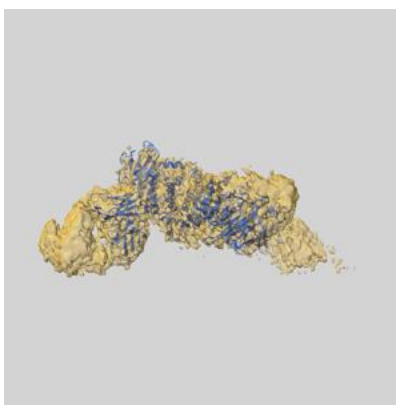
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73789 and PDB model 9Z3Q. Per-residue inclusion information can be found in section [3](#) on page [8](#).

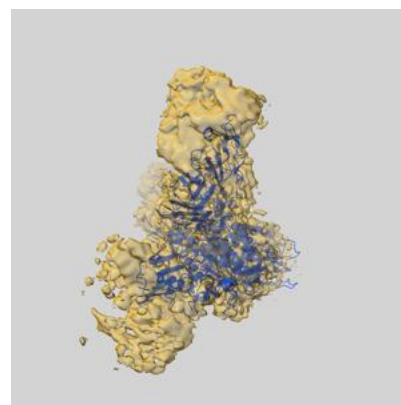
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.658 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](#)



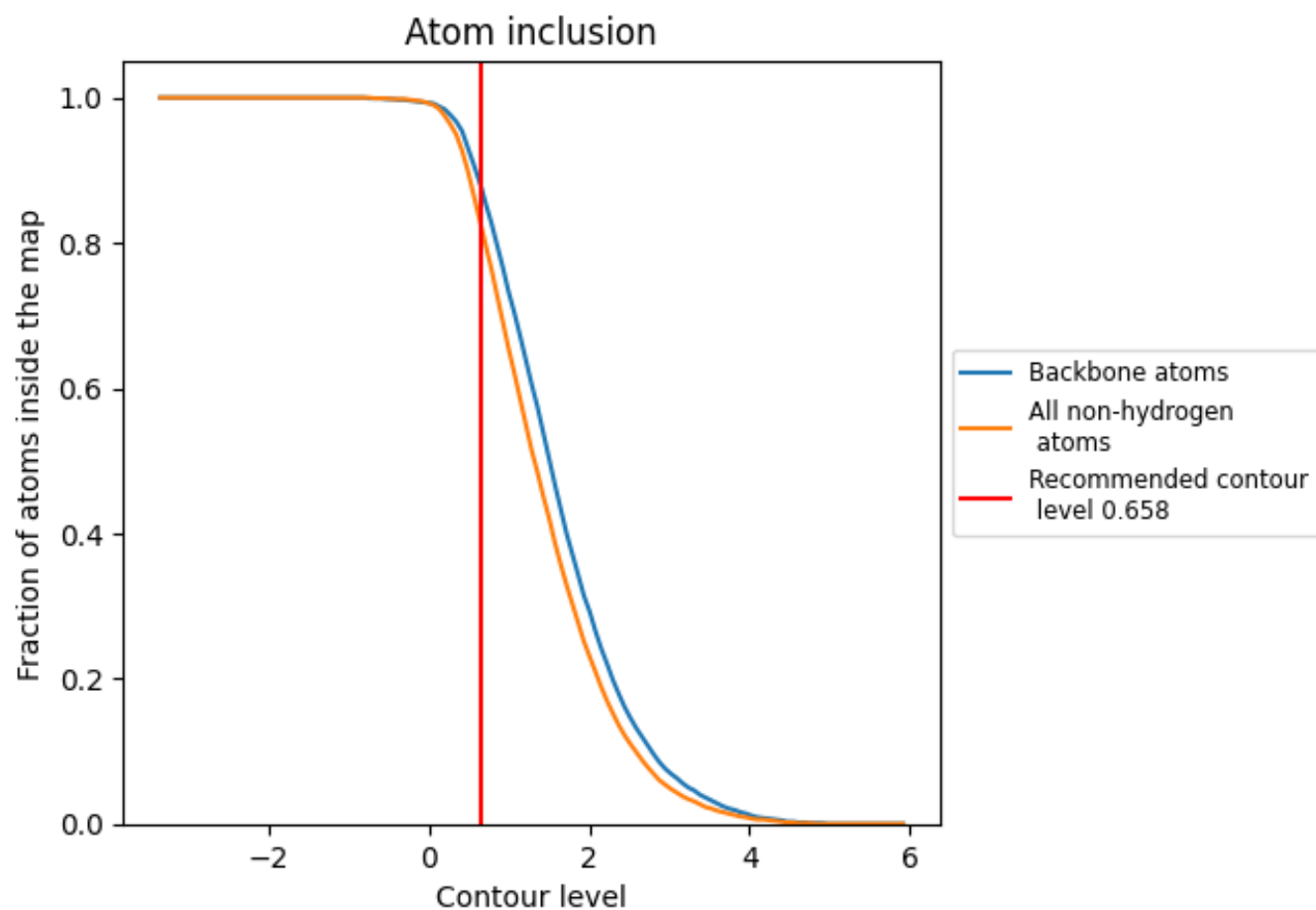
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.658).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.658) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8200	<div></div> 0.4020
A	<div></div> 0.9100	<div></div> 0.4510
B	<div></div> 0.8800	<div></div> 0.4250
C	<div></div> 0.9200	<div></div> 0.4210
D	<div></div> 0.9500	<div></div> 0.4280
E	<div></div> 0.7570	<div></div> 0.3870
F	<div></div> 0.8000	<div></div> 0.3730

