wwPDB EM Validation Summary Report

Oct 26, 2026 – 03:01 PM EDT

PDB ID	:	9O5X / pdb_00009o5x
EMDB ID	:	EMD-70152
Title	:	VAR2CSA in complex with V2C.014 Fab
Authors	:	Raghavan, S.S.R.; Ward, A.B.
Deposited on	:	2025-04-10
Resolution	:	3.60 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:

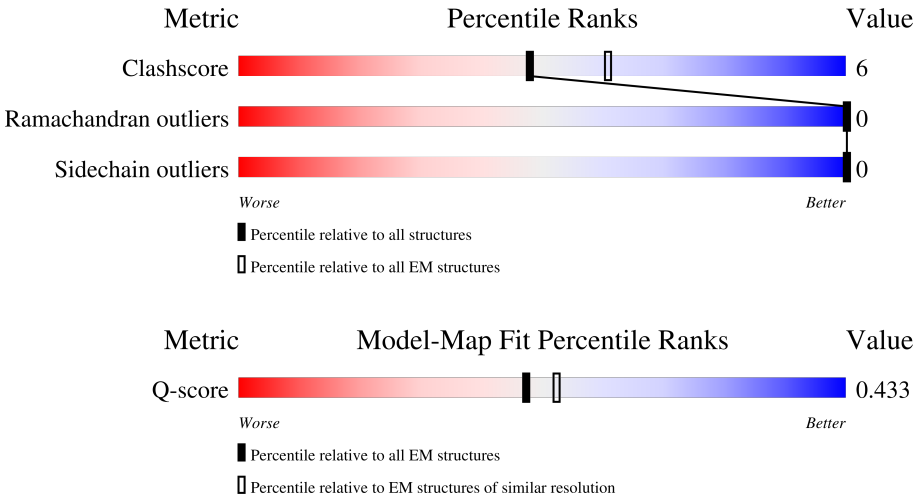
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 (3.10 - 4.10)

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 <=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	121	17% 81% 19%
2	L	107	16% 79% 21%
3	A	2683	10% 88%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4268 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 V2C.014 Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	121	Total	C	N	O	S	0	0
			938	600	155	179	4		

- Molecule 2 is a protein called V2C.014 Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	107	Total	C	N	O	S	0	0
			816	512	130	171	3		

- Molecule 3 is a protein called Erythrocyte membrane protein 1, PfEMP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	309	Total	C	N	O	S	0	0
			2514	1588	432	478	16		

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A024V5I6
A	-18	LYS	-	expression tag	UNP A0A024V5I6
A	-17	LEU	-	expression tag	UNP A0A024V5I6
A	-16	CYS	-	expression tag	UNP A0A024V5I6
A	-15	ILE	-	expression tag	UNP A0A024V5I6
A	-14	LEU	-	expression tag	UNP A0A024V5I6
A	-13	LEU	-	expression tag	UNP A0A024V5I6
A	-12	ALA	-	expression tag	UNP A0A024V5I6
A	-11	VAL	-	expression tag	UNP A0A024V5I6
A	-10	VAL	-	expression tag	UNP A0A024V5I6
A	-9	ALA	-	expression tag	UNP A0A024V5I6
A	-8	PHE	-	expression tag	UNP A0A024V5I6
A	-7	VAL	-	expression tag	UNP A0A024V5I6
A	-6	GLY	-	expression tag	UNP A0A024V5I6
A	-5	LEU	-	expression tag	UNP A0A024V5I6

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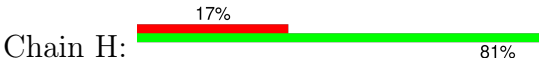
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	SER	-	expression tag	UNP A0A024V5I6
A	-3	LEU	-	expression tag	UNP A0A024V5I6
A	-2	GLY	-	expression tag	UNP A0A024V5I6
A	-1	GLY	-	expression tag	UNP A0A024V5I6
A	0	THR	-	expression tag	UNP A0A024V5I6
A	2510	GLY	GLU	conflict	UNP A0A024V5I6
A	2630	GLY	-	expression tag	UNP A0A024V5I6
A	2631	SER	-	expression tag	UNP A0A024V5I6
A	2632	GLU	-	expression tag	UNP A0A024V5I6
A	2633	ASN	-	expression tag	UNP A0A024V5I6
A	2634	LEU	-	expression tag	UNP A0A024V5I6
A	2635	TYR	-	expression tag	UNP A0A024V5I6
A	2636	PHE	-	expression tag	UNP A0A024V5I6
A	2637	GLN	-	expression tag	UNP A0A024V5I6
A	2638	SER	-	expression tag	UNP A0A024V5I6
A	2639	ALA	-	expression tag	UNP A0A024V5I6
A	2640	SER	-	expression tag	UNP A0A024V5I6
A	2641	GLY	-	expression tag	UNP A0A024V5I6
A	2642	LEU	-	expression tag	UNP A0A024V5I6
A	2643	ASN	-	expression tag	UNP A0A024V5I6
A	2644	ASP	-	expression tag	UNP A0A024V5I6
A	2645	ILE	-	expression tag	UNP A0A024V5I6
A	2646	PHE	-	expression tag	UNP A0A024V5I6
A	2647	GLU	-	expression tag	UNP A0A024V5I6
A	2648	ALA	-	expression tag	UNP A0A024V5I6
A	2649	GLN	-	expression tag	UNP A0A024V5I6
A	2650	LYS	-	expression tag	UNP A0A024V5I6
A	2651	ILE	-	expression tag	UNP A0A024V5I6
A	2652	GLU	-	expression tag	UNP A0A024V5I6
A	2653	TRP	-	expression tag	UNP A0A024V5I6
A	2654	HIS	-	expression tag	UNP A0A024V5I6
A	2655	GLU	-	expression tag	UNP A0A024V5I6
A	2656	HIS	-	expression tag	UNP A0A024V5I6
A	2657	HIS	-	expression tag	UNP A0A024V5I6
A	2658	HIS	-	expression tag	UNP A0A024V5I6
A	2659	HIS	-	expression tag	UNP A0A024V5I6
A	2660	HIS	-	expression tag	UNP A0A024V5I6
A	2661	HIS	-	expression tag	UNP A0A024V5I6
A	2662	HIS	-	expression tag	UNP A0A024V5I6
A	2663	HIS	-	expression tag	UNP A0A024V5I6

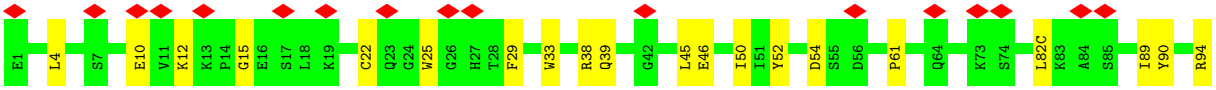
3 Residue-property plots (i)

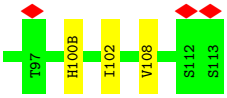
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: V2C.014 Heavy chain

Chain H:



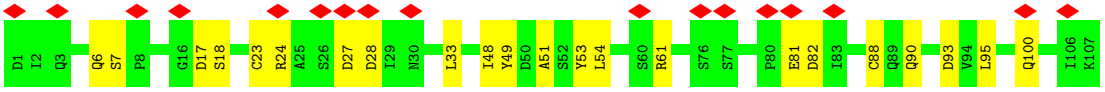




• Molecule 2: V2C.014 Light chain

Chain L:

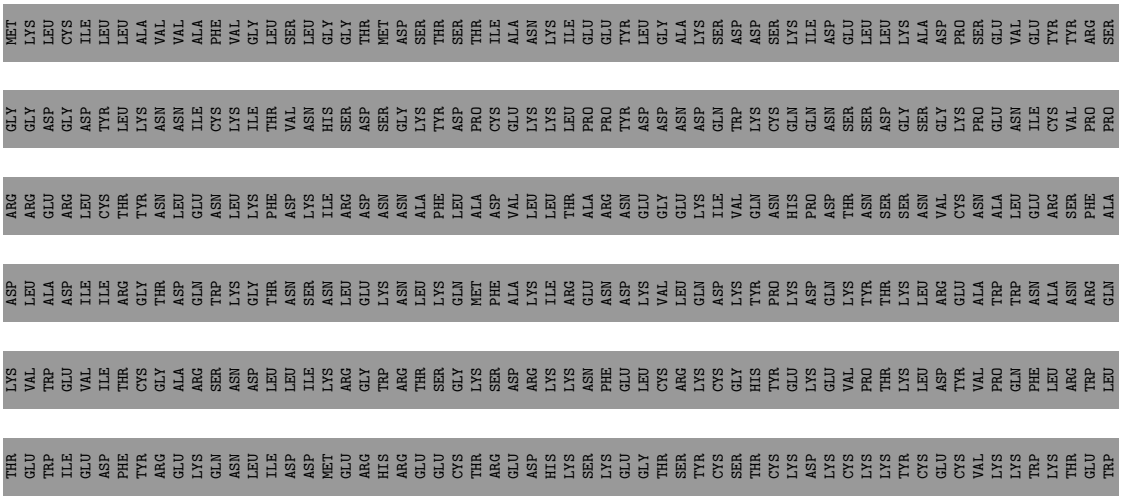


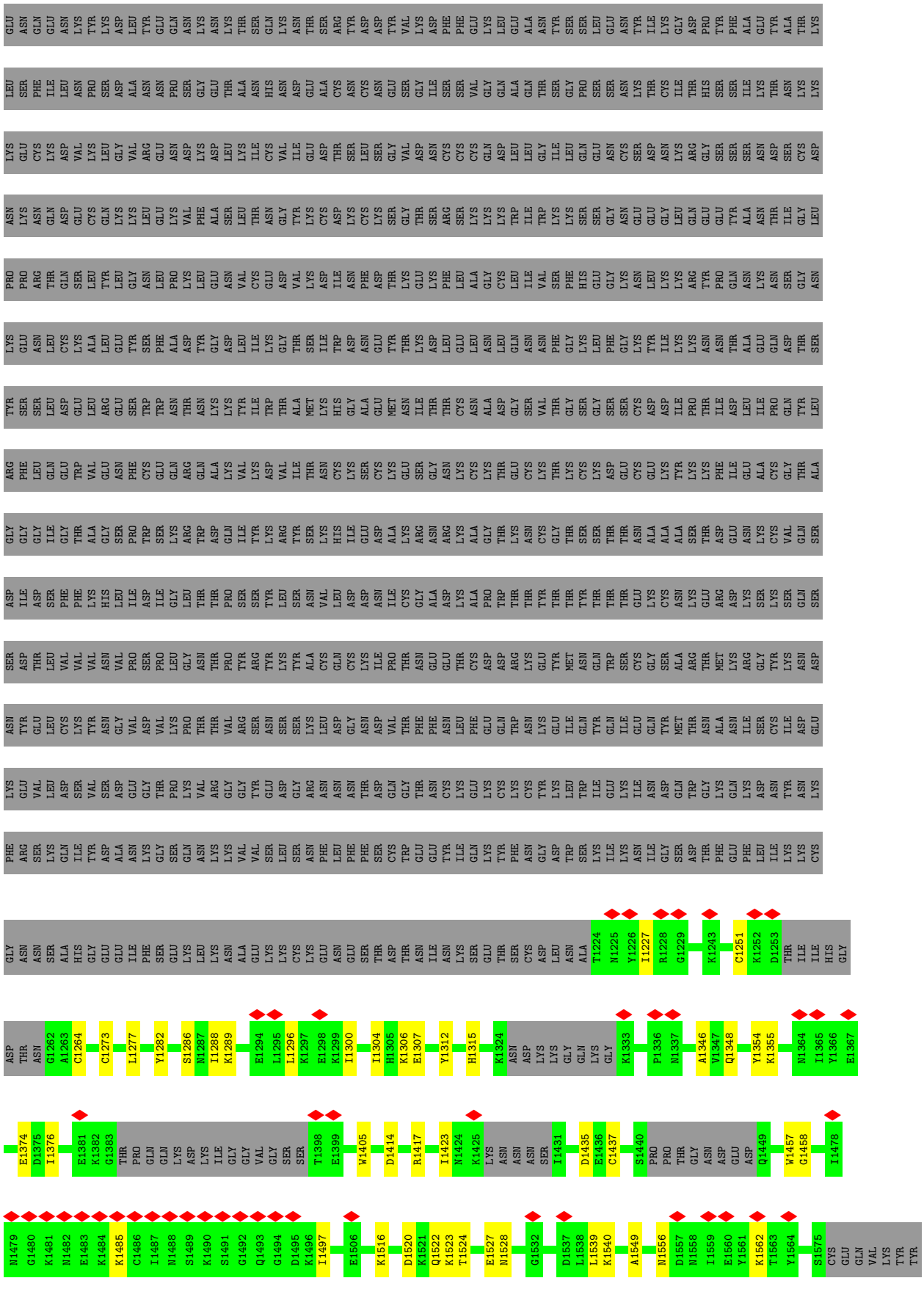


• Molecule 3: Erythrocyte membrane protein 1, PfEMP1

Chain A:







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

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

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

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

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

ILE MET ALA PRO THR VAL ILE ASP TYR LEU ASN ASN ILE GLY ALA TYR ASN THR VAL THR THR SER GLY GLU GLU GLU GLU LYS GLY PRO LEU ASP LEU

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

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

GLU PHE LYS GLU GLU ILE LEU LYS GLY ALA GLN SER GLU GLY LYS PHE LEU GLY ASN TYR TYR LYS GLU HIS LYS ASP LYS GLU LYS ALA LEU GLU ALA MET LYS ASN SER PHE TYR ASP TYR GLU ASP ILE ILE LYS GLY THR ASP MET LEU THR ASN ILE GLU PHE LYS ASP LYS

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

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

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

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

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

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

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

SER LYS CYS THR HIS ALA CYS VAL ASN TYR LYS ASP ASN GLU PHE LYS ASN LYS ASN SER ASN ASP LYS ASP ALA PRO ASP TYR LEU ASN LYS GLU LYS CYS ASN GLU GLY SER VAL ASP ASN LYS

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

HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97069	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 ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.357	Depositor
Minimum map value	-0.214	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	371.2, 371.2, 371.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.725, 0.725, 0.725	Depositor

5 Model quality

5.1 Standard geometry

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	0.17	0/964	0.43	0/1311
2	L	0.18	0/833	0.44	0/1134
3	A	0.15	0/2562	0.36	0/3427
All	All	0.16	0/4359	0.39	0/5872

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

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	938	0	902	13	0
2	L	816	0	784	14	0
3	A	2514	0	2458	25	0
All	All	4268	0	4144	50	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 50 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:H:39:GLN:HB2	1:H:45:LEU:HD23	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:38:ARG:NH1	1:H:90:TYR:OH	2.30	0.64
2:L:6:GLN:H	2:L:100:GLN:HE22	1.47	0.61
2:L:61:ARG:NH2	2:L:81:GLU:OE2	2.36	0.58
1:H:94:ARG:HH21	1:H:102:ILE:HD13	1.68	0.58

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	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
2	L	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
3	A	297/2683 (11%)	289 (97%)	8 (3%)	0	100	100
All	All	521/2911 (18%)	498 (96%)	23 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	100/100 (100%)	100 (100%)	0	100	100
2	L	93/93 (100%)	93 (100%)	0	100	100
3	A	273/2429 (11%)	273 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	466/2622 (18%)	466 (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. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	58	ASN
3	A	1271	ASN

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

This section contains visualisations of the EMDB entry EMD-70152. These allow visual inspection of the internal detail of the map and identification of artifacts.

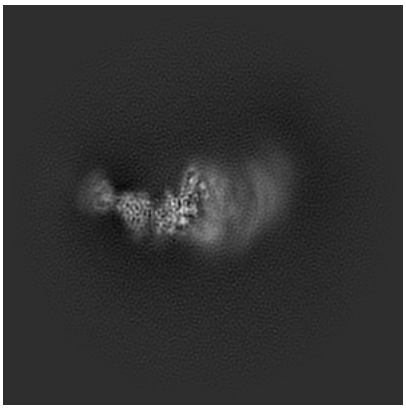
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

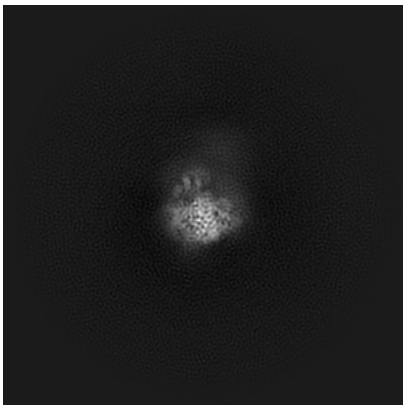
6.1.1 Primary map



X

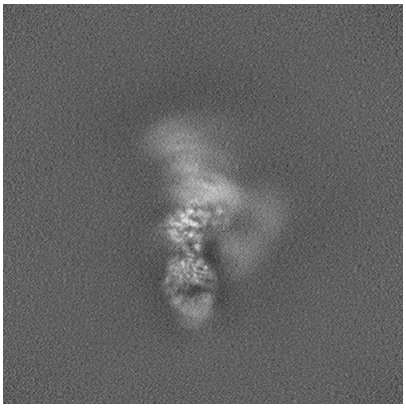


Y

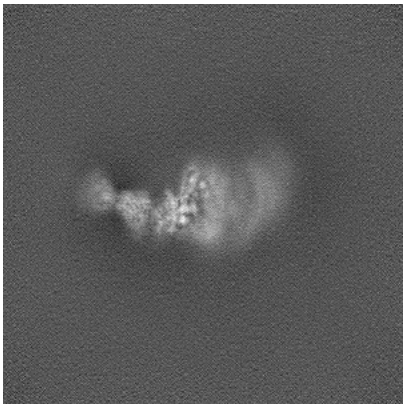


Z

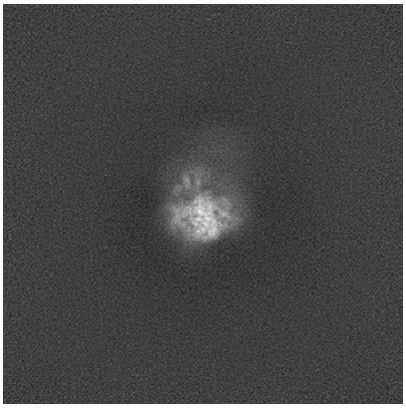
6.1.2 Raw map



X



Y

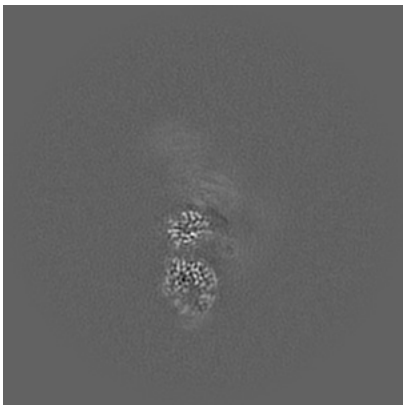


Z

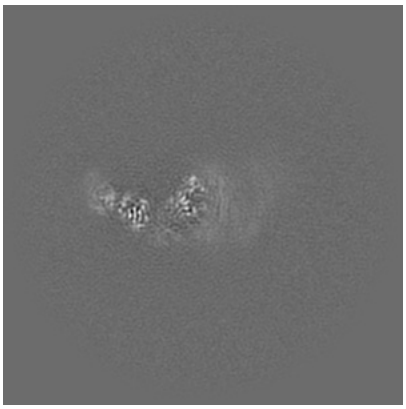
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

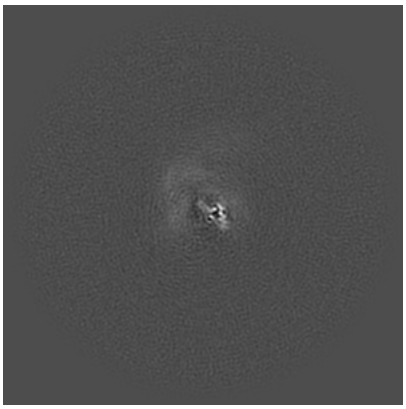
6.2.1 Primary map



X Index: 256

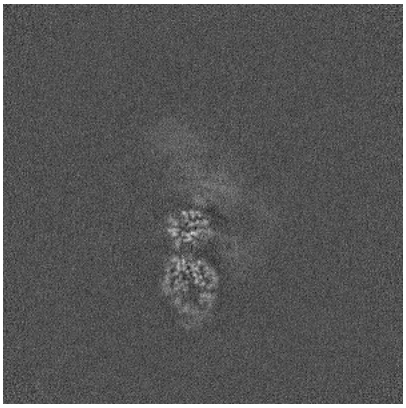


Y Index: 256

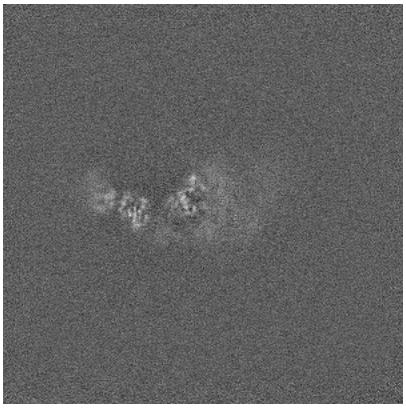


Z Index: 256

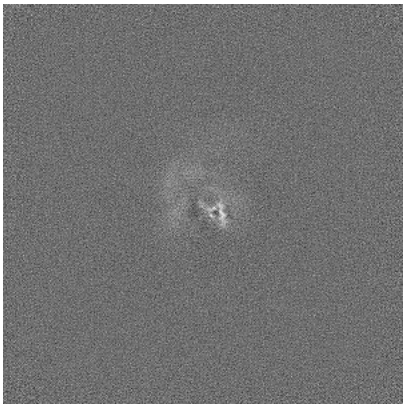
6.2.2 Raw map



X Index: 256



Y Index: 256

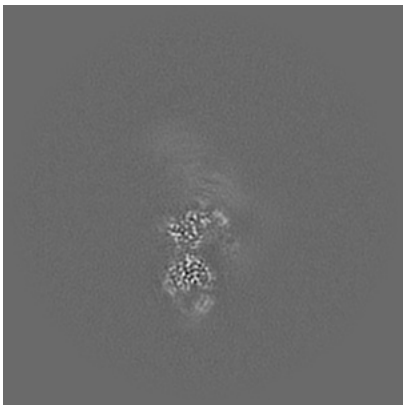


Z Index: 256

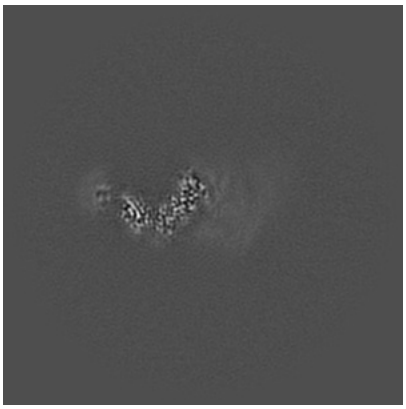
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

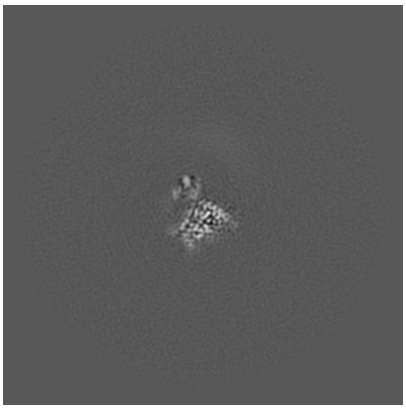
6.3.1 Primary map



X Index: 251

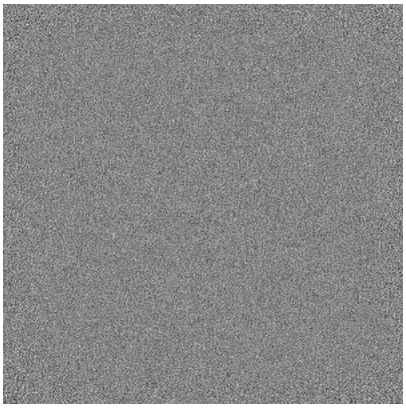


Y Index: 245

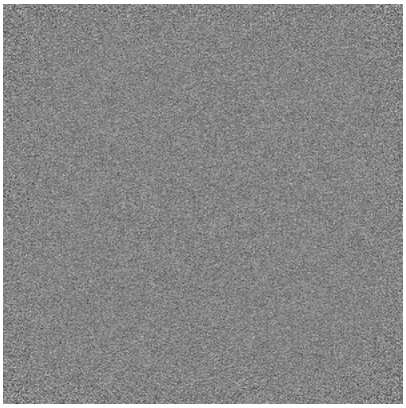


Z Index: 229

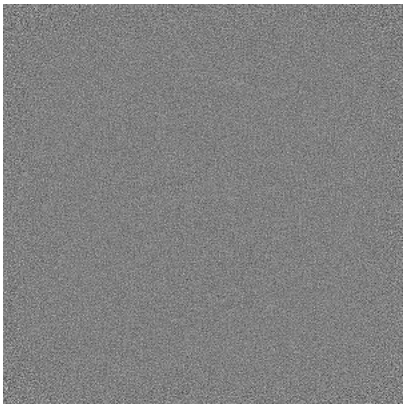
6.3.2 Raw map



X Index: 0



Y Index: 0

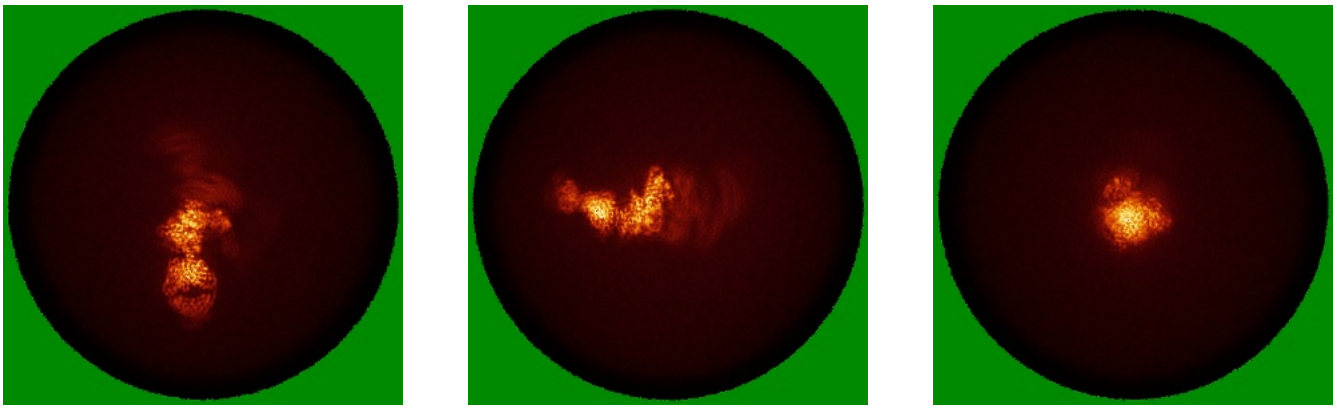


Z Index: 0

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

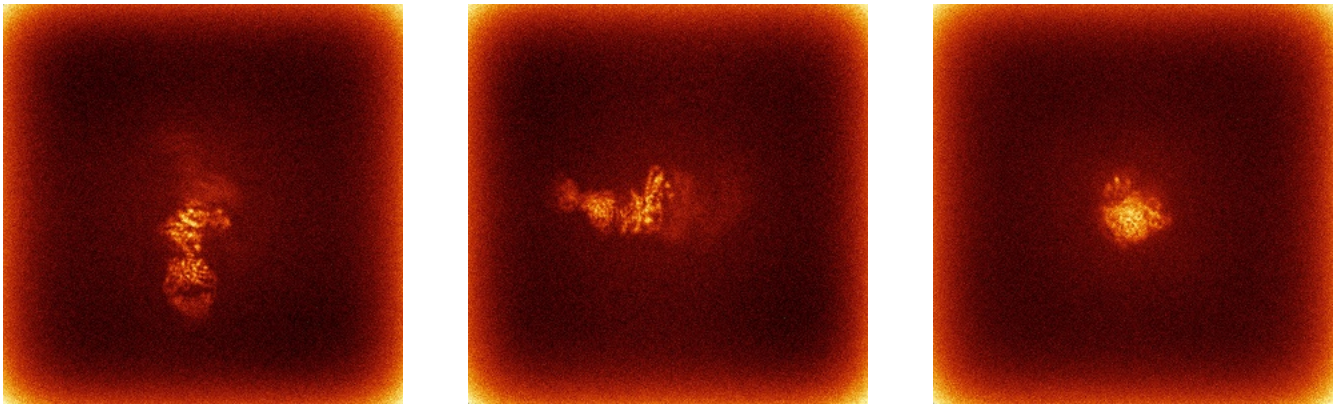
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



X Y Z

6.4.2 Raw map

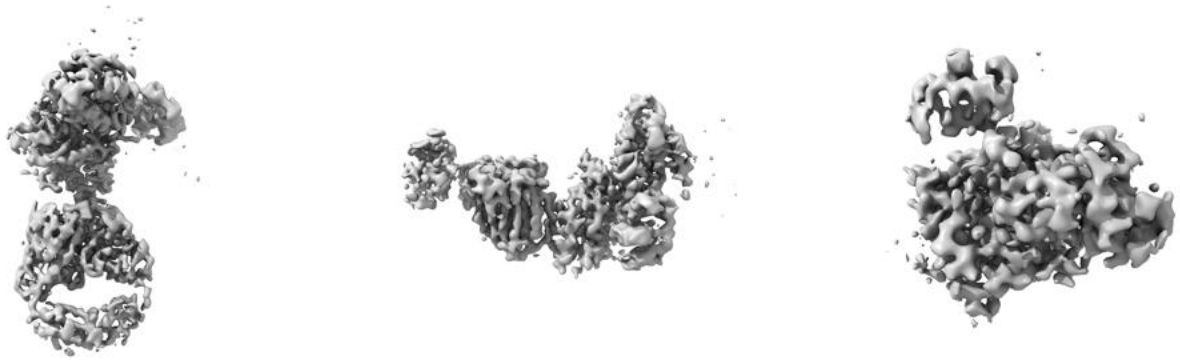


X Y Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. 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



X Y Z

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.

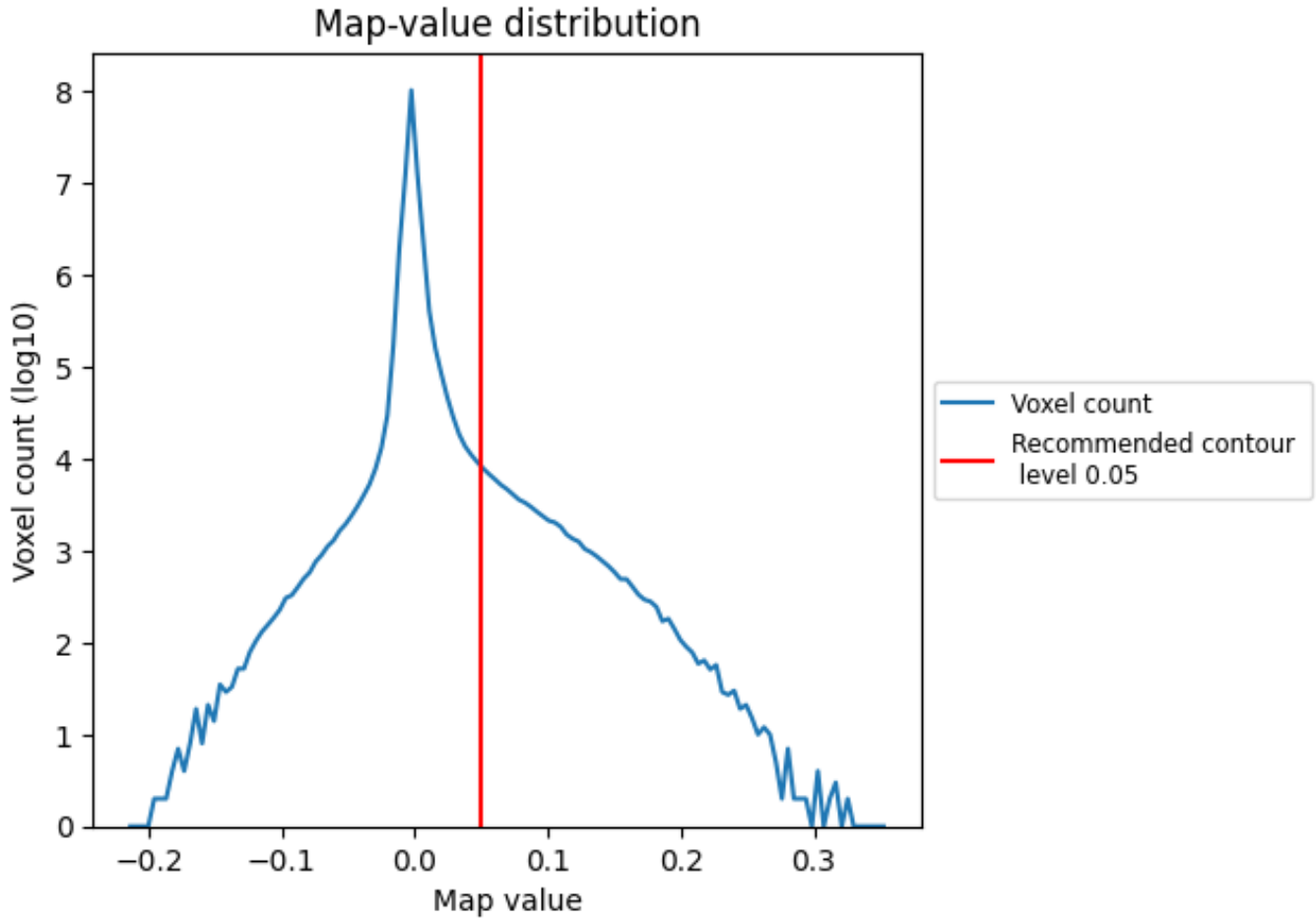
6.6 Mask visualisation (i)

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

7 Map analysis

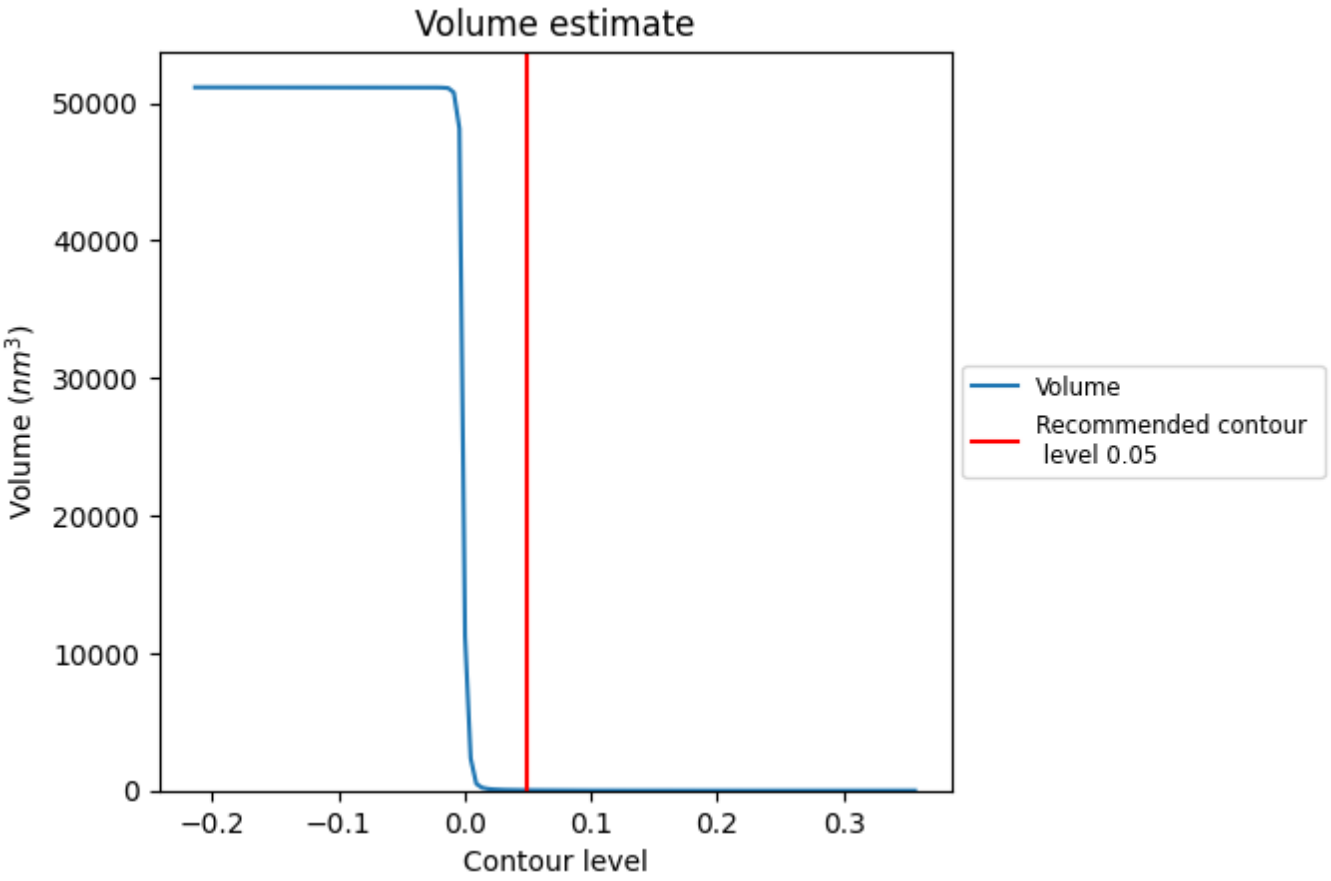
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

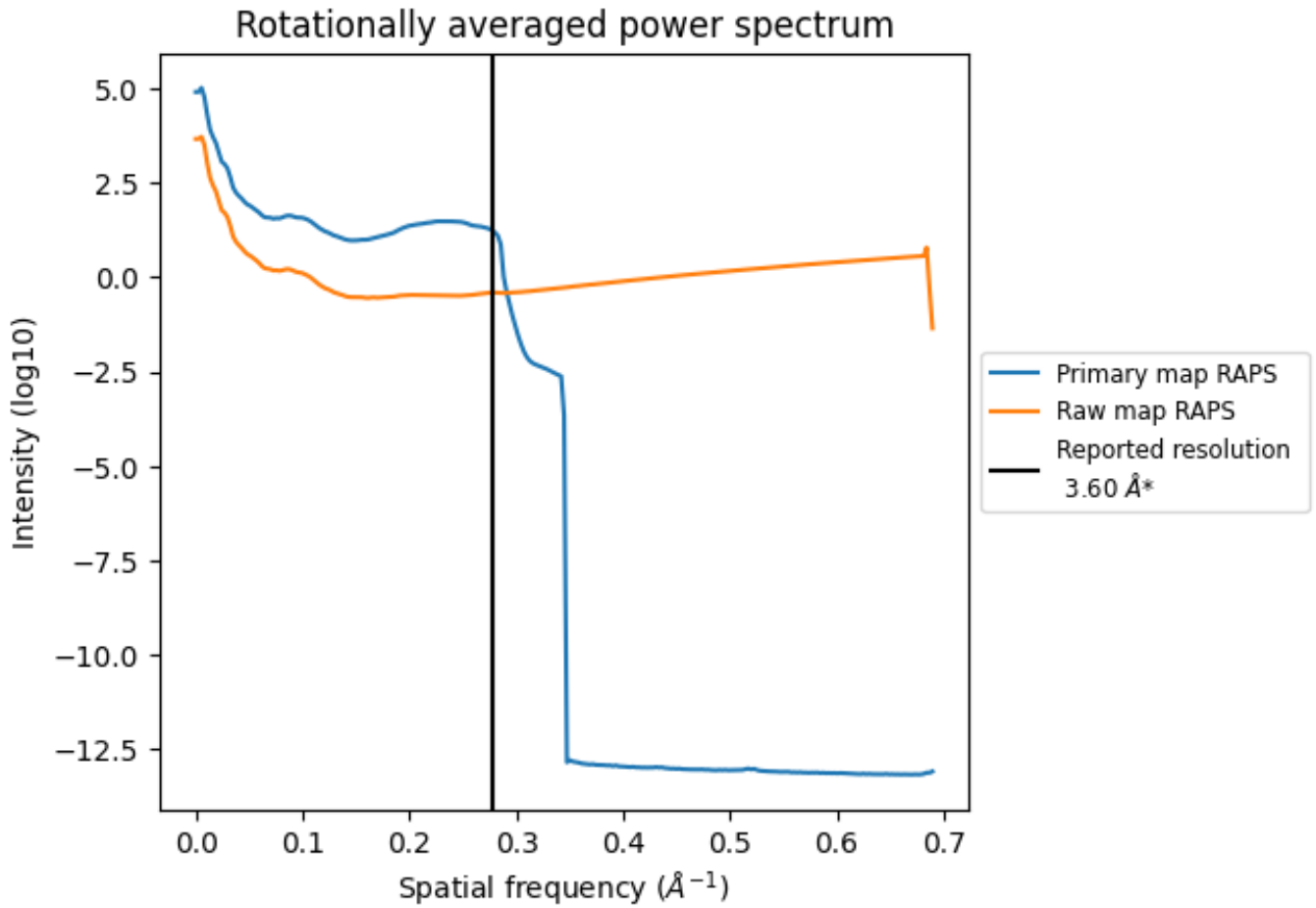
7.2 Volume estimate (i)



The volume at the recommended contour level is 27 nm^3; this corresponds to an approximate mass of 25 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)

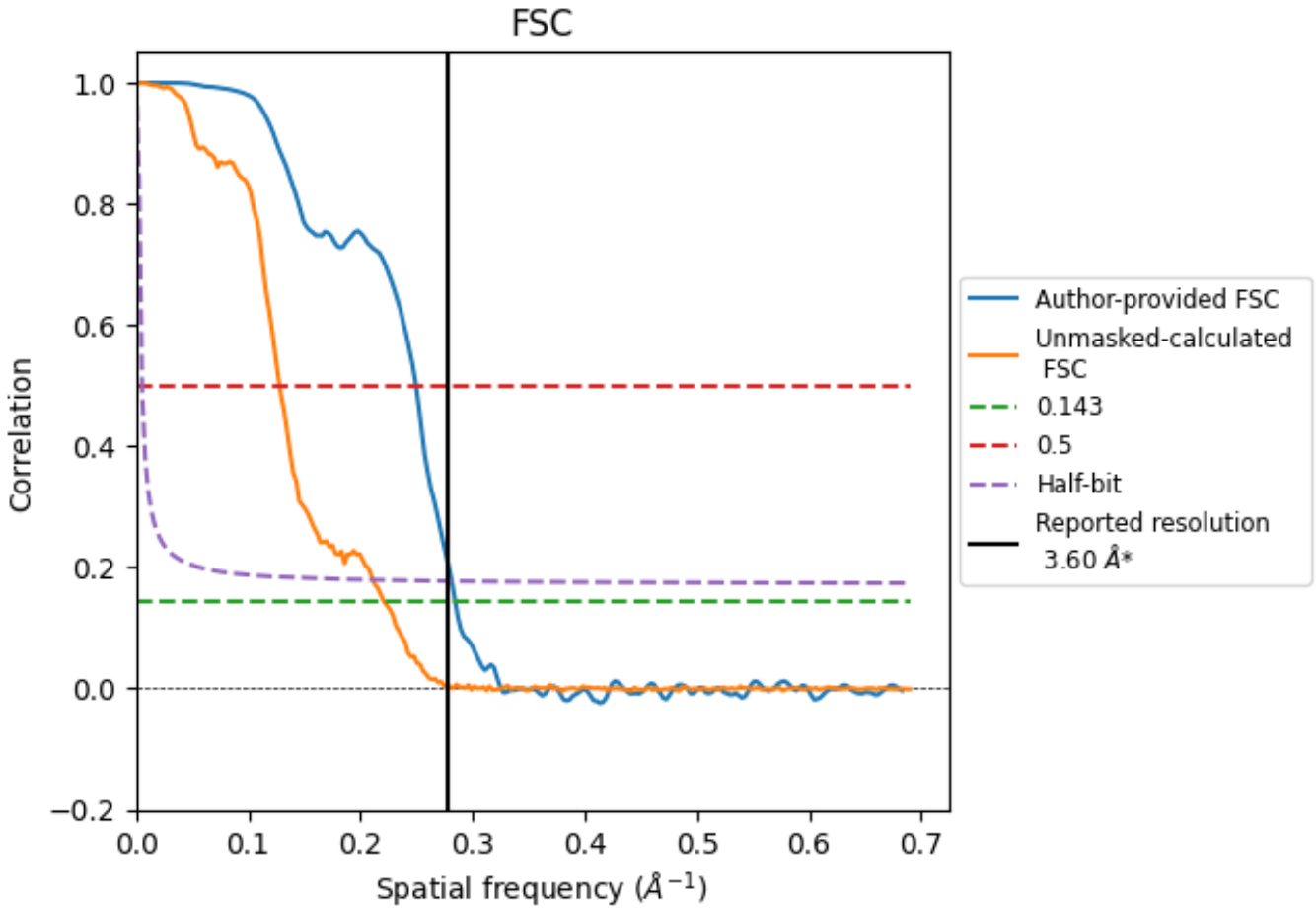


*Reported resolution corresponds to spatial frequency of 0.278 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8.2 Resolution estimates (i)

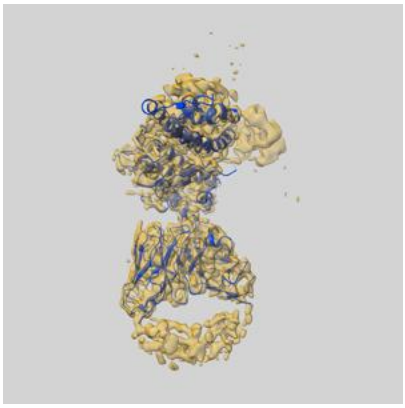
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.51	4.01	3.55
Unmasked-calculated*	4.52	7.81	4.73

*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 4.52 differs from the reported value 3.6 by more than 10 %

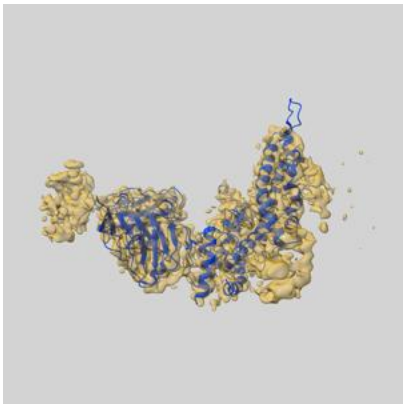
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70152 and PDB model 9O5X. Per-residue inclusion information can be found in section 3 on page 5.

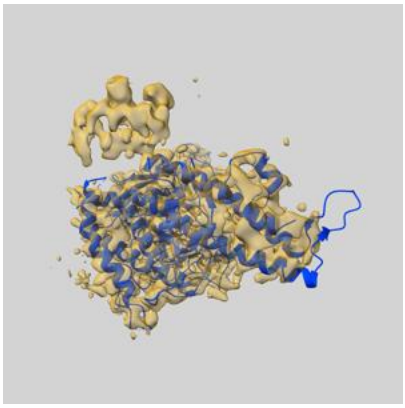
9.1 Map-model overlay



X



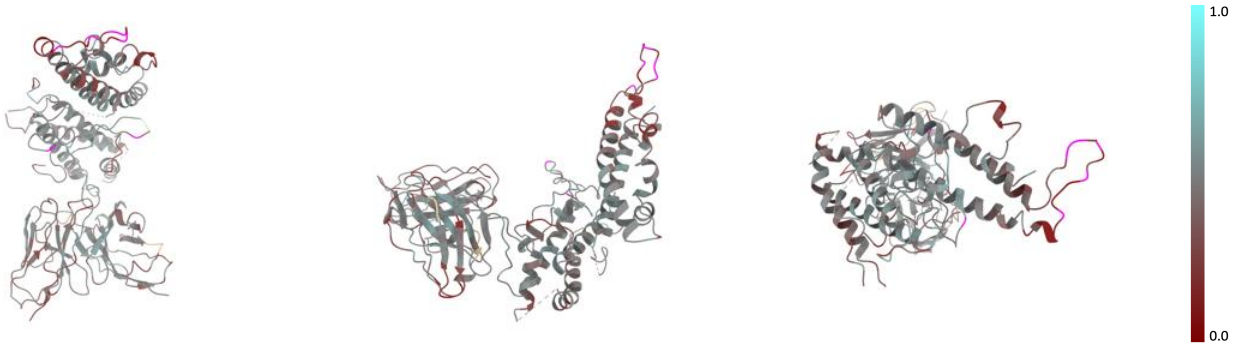
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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)



X Y Z

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.

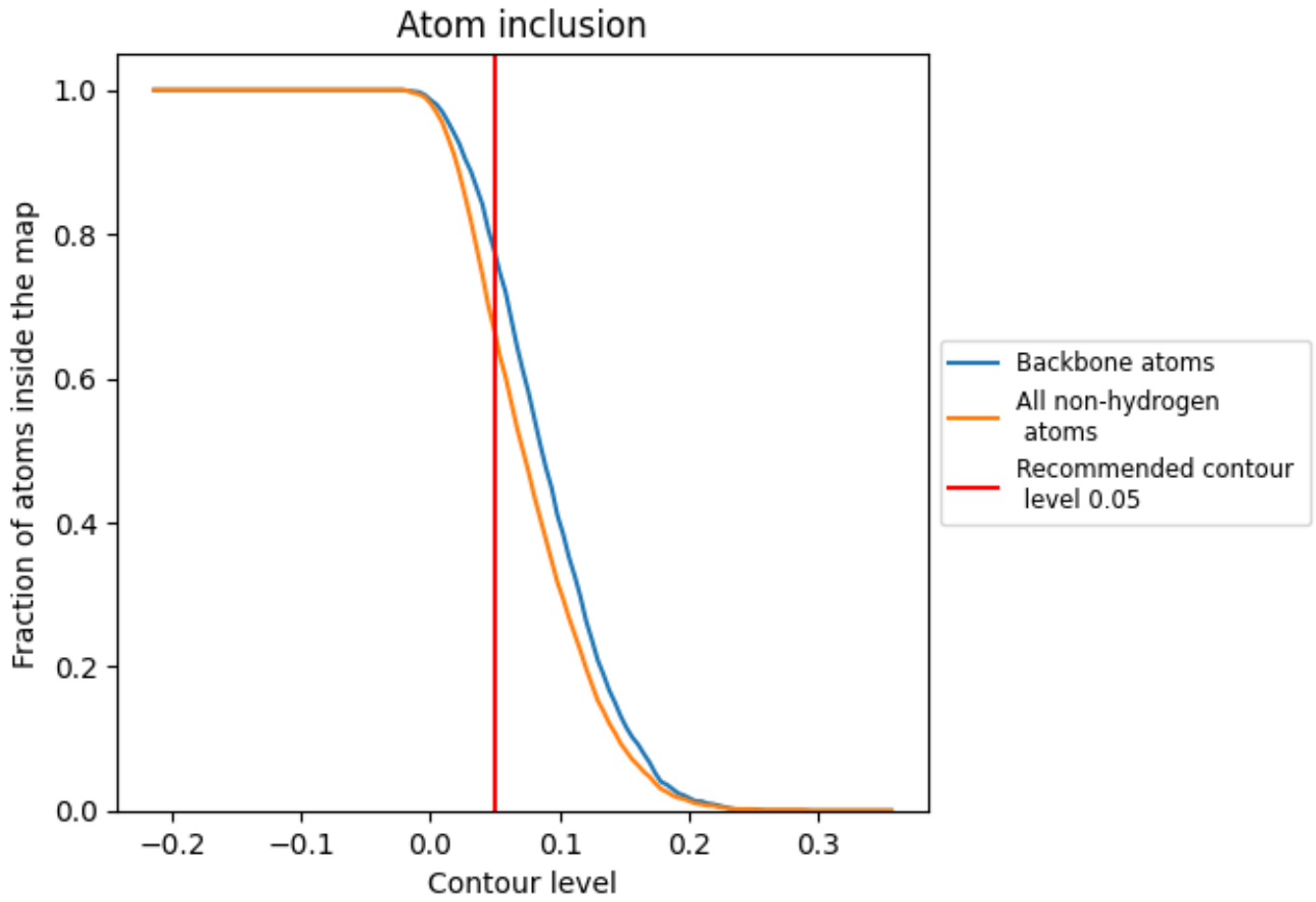
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 66% 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 (0.05) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.6630	0.4330
A	0.6740	0.4330
H	0.6660	0.4400
L	0.6280	0.4230