



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2024 – 06:22 AM EST

PDB ID : 7MOP
EMDB ID : EMD-23925
Title : Cryo-EM structure of human HUWE1 in complex with DDIT4
Authors : Hunkeler, M.; Fischer, E.S.
Deposited on : 2021-05-03
Resolution : 3.30 Å (reported)
Based on initial model : 7JQ9

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.dev113
MolProbity : 4.02b-467
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) : 2.39

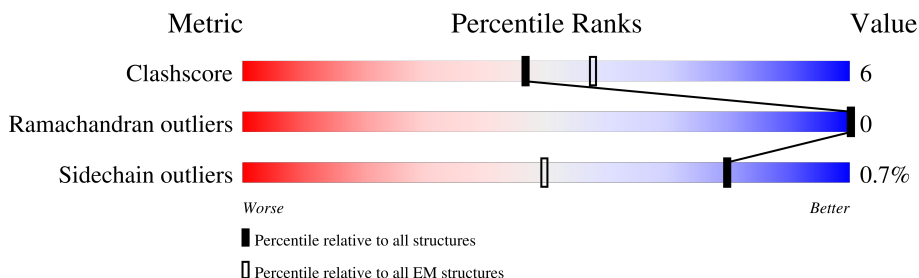
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	A	4411	
2	B	259	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 39049 atoms, of which 19681 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 E3 ubiquitin-protein ligase HUWE1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2445	Total	C	H	N	O	S	0	0
			38929	12313	19625	3314	3555	122		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-36	MET	-	expression tag	UNP Q7Z6Z7
A	-35	ASP	-	expression tag	UNP Q7Z6Z7
A	-34	TYR	-	expression tag	UNP Q7Z6Z7
A	-33	LYS	-	expression tag	UNP Q7Z6Z7
A	-32	ASP	-	expression tag	UNP Q7Z6Z7
A	-31	ASP	-	expression tag	UNP Q7Z6Z7
A	-30	ASP	-	expression tag	UNP Q7Z6Z7
A	-29	ASP	-	expression tag	UNP Q7Z6Z7
A	-28	LYS	-	expression tag	UNP Q7Z6Z7
A	-27	LEU	-	expression tag	UNP Q7Z6Z7
A	-26	ALA	-	expression tag	UNP Q7Z6Z7
A	-25	ALA	-	expression tag	UNP Q7Z6Z7
A	-24	ALA	-	expression tag	UNP Q7Z6Z7
A	-23	ASN	-	expression tag	UNP Q7Z6Z7
A	-22	SER	-	expression tag	UNP Q7Z6Z7
A	-21	SER	-	expression tag	UNP Q7Z6Z7
A	-20	ILE	-	expression tag	UNP Q7Z6Z7
A	-19	ASP	-	expression tag	UNP Q7Z6Z7
A	-18	LEU	-	expression tag	UNP Q7Z6Z7
A	-17	ILE	-	expression tag	UNP Q7Z6Z7
A	-16	SER	-	expression tag	UNP Q7Z6Z7
A	-15	THR	-	expression tag	UNP Q7Z6Z7
A	-14	SER	-	expression tag	UNP Q7Z6Z7
A	-13	LEU	-	expression tag	UNP Q7Z6Z7
A	-12	TYR	-	expression tag	UNP Q7Z6Z7
A	-11	LYS	-	expression tag	UNP Q7Z6Z7
A	-10	LYS	-	expression tag	UNP Q7Z6Z7
A	-9	ALA	-	expression tag	UNP Q7Z6Z7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	GLY	-	expression tag	UNP Q7Z6Z7
A	-7	PHE	-	expression tag	UNP Q7Z6Z7
A	-6	LYS	-	expression tag	UNP Q7Z6Z7
A	-5	GLY	-	expression tag	UNP Q7Z6Z7
A	-4	THR	-	expression tag	UNP Q7Z6Z7
A	-3	ASN	-	expression tag	UNP Q7Z6Z7
A	-2	SER	-	expression tag	UNP Q7Z6Z7
A	-1	VAL	-	expression tag	UNP Q7Z6Z7
A	0	ASP	-	expression tag	UNP Q7Z6Z7

- Molecule 2 is a protein called DNA damage-inducible transcript 4 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	7	Total	C	H	N	O	0	0
			120	42	56	11	11		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-26	MET	-	expression tag	UNP Q9NX09
B	-25	ASP	-	expression tag	UNP Q9NX09
B	-24	SER	-	expression tag	UNP Q9NX09
B	-23	ALA	-	expression tag	UNP Q9NX09
B	-22	TRP	-	expression tag	UNP Q9NX09
B	-21	SER	-	expression tag	UNP Q9NX09
B	-20	HIS	-	expression tag	UNP Q9NX09
B	-19	PRO	-	expression tag	UNP Q9NX09
B	-18	GLN	-	expression tag	UNP Q9NX09
B	-17	PHE	-	expression tag	UNP Q9NX09
B	-16	GLU	-	expression tag	UNP Q9NX09
B	-15	LYS	-	expression tag	UNP Q9NX09
B	-14	SER	-	expression tag	UNP Q9NX09
B	-13	ALA	-	expression tag	UNP Q9NX09
B	-12	VAL	-	expression tag	UNP Q9NX09
B	-11	ASP	-	expression tag	UNP Q9NX09
B	-10	GLU	-	expression tag	UNP Q9NX09
B	-9	ASN	-	expression tag	UNP Q9NX09
B	-8	LEU	-	expression tag	UNP Q9NX09
B	-7	TYR	-	expression tag	UNP Q9NX09
B	-6	PHE	-	expression tag	UNP Q9NX09
B	-5	GLN	-	expression tag	UNP Q9NX09
B	-4	GLY	-	expression tag	UNP Q9NX09

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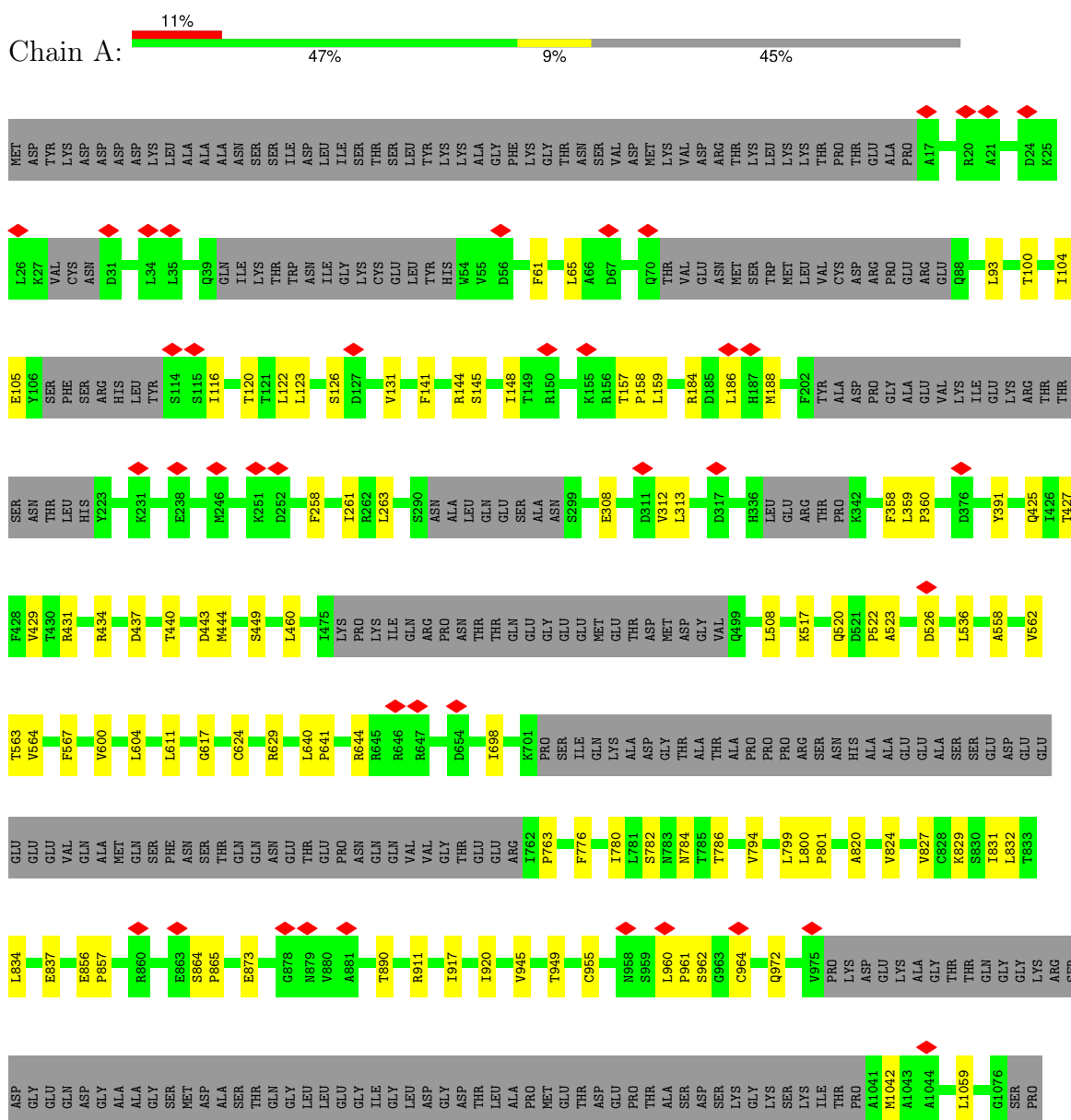
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q9NX09
B	-2	GLY	-	expression tag	UNP Q9NX09
B	-1	ARG	-	expression tag	UNP Q9NX09
B	0	THR	-	expression tag	UNP Q9NX09

3 Residue-property plots

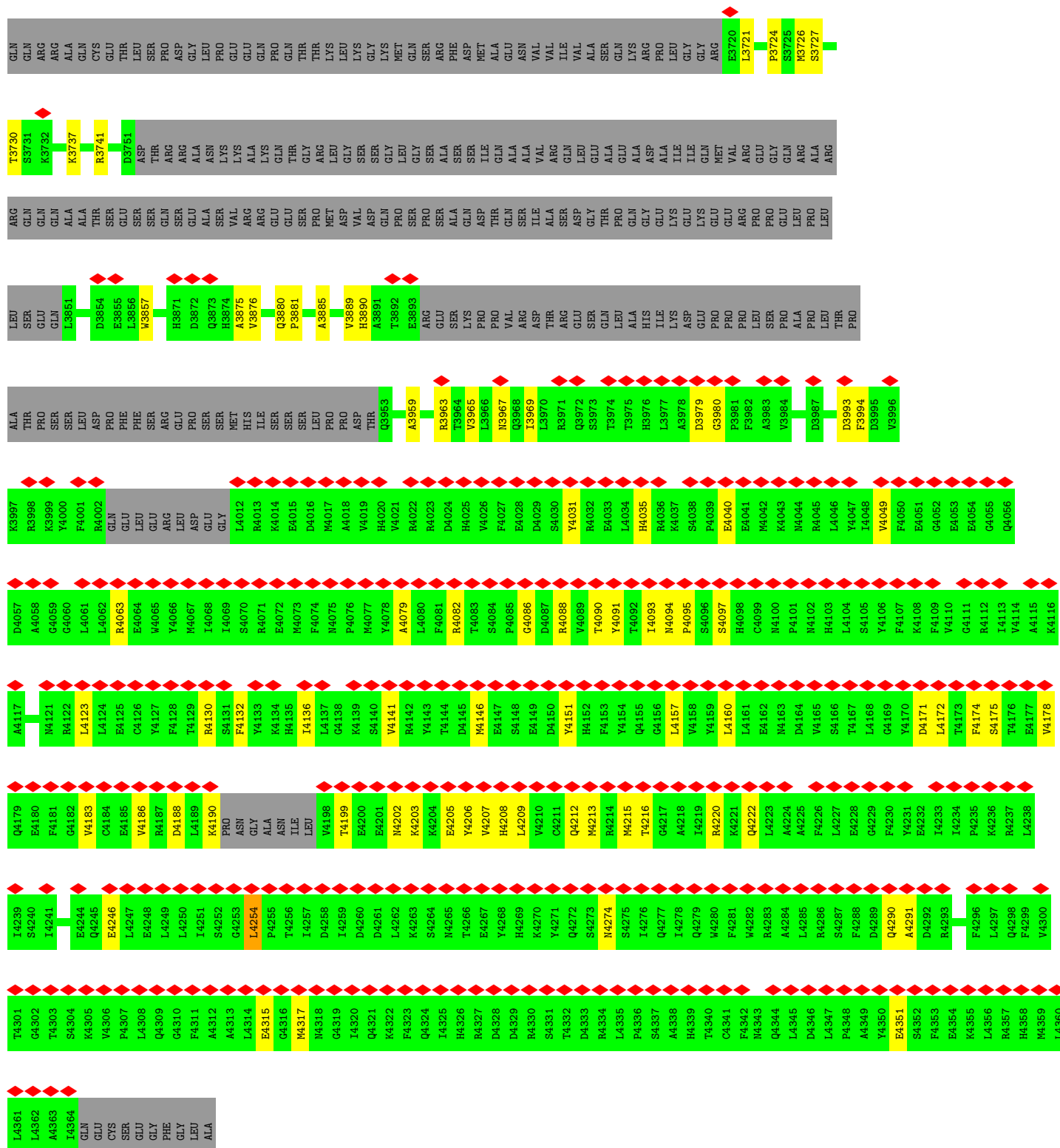
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: E3 ubiquitin-protein ligase HUWE1









- Molecule 2: DNA damage-inducible transcript 4 protein

97%

MET	THR	GLN	HIS
ASP	ARG	LEU	SER
ALA	GLU	LEU	VAL
TRP	GLY	GLN	GLY
SER	PHE	GLU	TYR
HIS	ASP	SER	SER
PRO	ARG	LEU	ALA
GLN	ASP	ALA	LEU
PHE	THR	PRO	ASP
GLU	SER	ARG	PRO
LYS	LEU	SER	LEU
SER	GLY	LEU	VAL
ALA	SER	SER	PRO
VAL	SER	ARG	THR
ASP	ASP	ARG	PHE
GLU	CYS	PRO	GLN
ASN	GLY	ALA	LEU
LEU	SER	ARG	THR
TYR	LEU	LEU	LEU
PHE	ASP	LEU	VAL
GLN	SER	MET	LEU
GLY	SER	PRO	ARG
GLY	ASN	SER	LEU
ARG	SER	GLN	ASP
THR	GLY	LEU	SER
MET	PHE	VAL	ARG
PRO	GLY	SER	LEU
S3	PRO	GLN	TRP
S9	GLU	VAL	PRO
S9	GLY	GLY	LYS
SER	ASP	LYS	ILE
SER	THR	GLU	GLN
SER	ALA	LEU	GLY
SER	TYR	LEU	GLY
SER	LEU	LEU	LEU
SER	THR	ARG	PHE
SER	LEU	LEU	SER
SER	ASP	ALA	SER
SER	GLY	TYR	ALA
SER	VAL	SER	ASN
SER	LEU	SER	SER
SER	PRO	PRO	PRO
LEU	ASP	PHE	PHE
PRO	PHE	GLY	LEU
ARG	GLU	LEU	PRO
THR	LEU	ARG	GLY
PRO	SER	ALA	PHE
PRO	THR	SER	SER
ASP	PRO	GLN	GLN
ARG	ASP	LEU	SER
PRO	GLU	ASP	LEU
PRO	ASP	VAL	THR
PRO	GLU	CYS	LEU
ARG	HIS	VAL	SER
SER	LEU	GLY	THR
ALA	CYS	GLN	GLY
TRP	ALA	GLY	PHE
GLY	ASN	LYS	ARG
SER	LEU	VAL	VAL
ALA	MET	CYS	ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	312798	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; standard correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53.34	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.050	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	300.3, 300.3, 300.3	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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	0.31	0/19649	0.50	0/26599
2	B	0.31	0/66	0.48	0/88
All	All	0.31	0/19715	0.50	0/26687

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	19304	19625	19682	231	0
2	B	64	56	56	0	0
All	All	19368	19681	19738	231	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 231 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:A:3967:ASN:OD1	1:A:3993:ASP:N	2.14	0.78
1:A:116:ILE:O	1:A:120:THR:HG23	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:LEU:HD21	1:A:3294:LEU:HD21	1.71	0.71
1:A:1829:GLU:OE2	1:A:2082:TYR:OH	2.12	0.68
1:A:3288:VAL:HG12	1:A:3300:ILE:HD12	1.76	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2383/4411 (54%)	2317 (97%)	66 (3%)	0	100	100
2	B	5/259 (2%)	5 (100%)	0	0	100	100
All	All	2388/4670 (51%)	2322 (97%)	66 (3%)	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	A	2166/3839 (56%)	2151 (99%)	15 (1%)	81	88
2	B	7/229 (3%)	7 (100%)	0	100	100
All	All	2173/4068 (53%)	2158 (99%)	15 (1%)	80	88

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2235	SER
1	A	4209	LEU
1	A	2663	MET
1	A	4254	LEU
1	A	4175	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4208	HIS
1	A	4202	ASN
1	A	3206	HIS
1	A	924	GLN
1	A	3976	HIS

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.

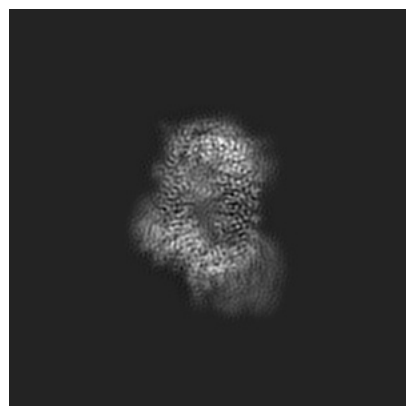
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23925. These allow visual inspection of the internal detail of the map and identification of artifacts.

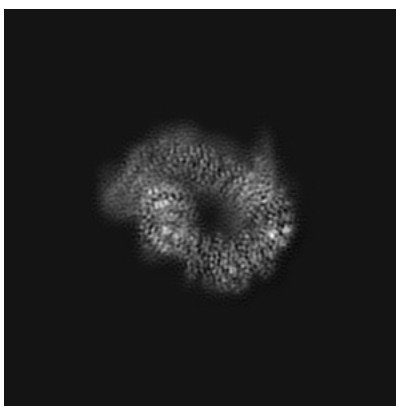
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

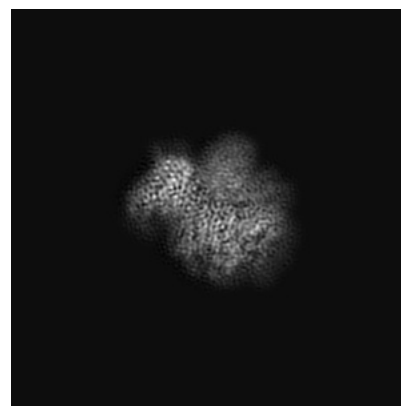
6.1.1 Primary map



X

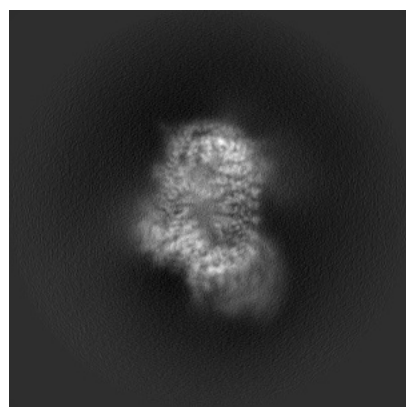


Y

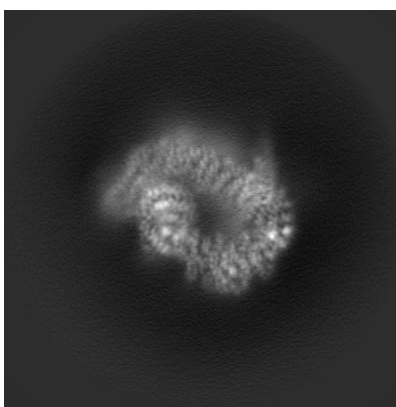


Z

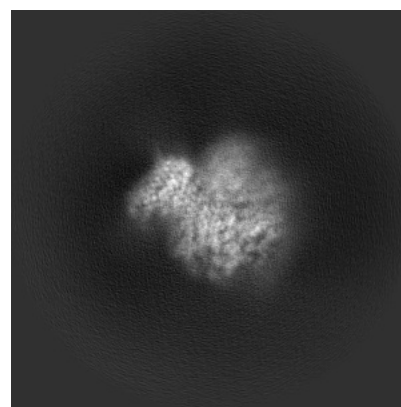
6.1.2 Raw map



X



Y

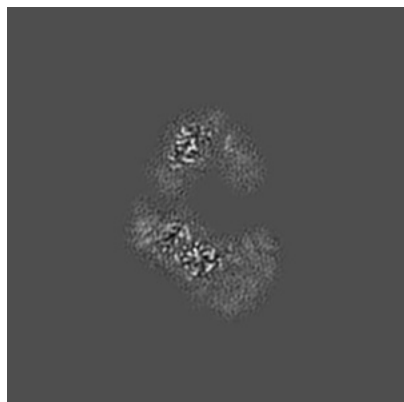


Z

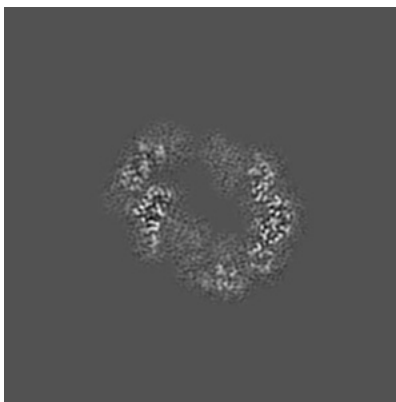
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

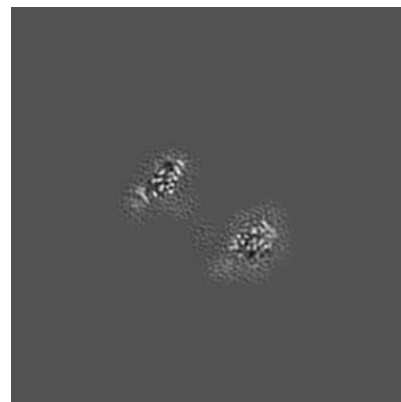
6.2.1 Primary map



X Index: 182

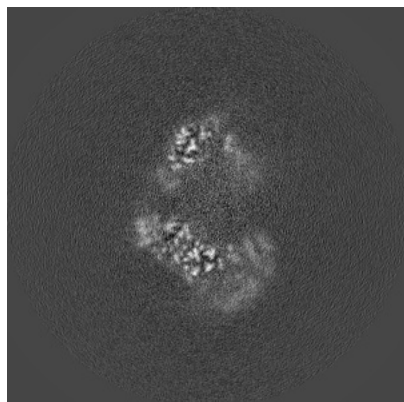


Y Index: 182

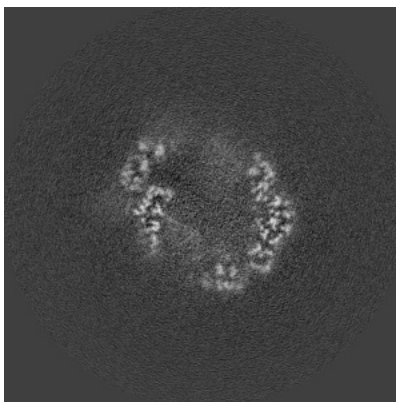


Z Index: 182

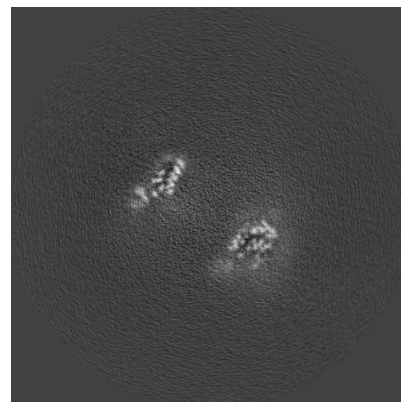
6.2.2 Raw map



X Index: 182



Y Index: 182

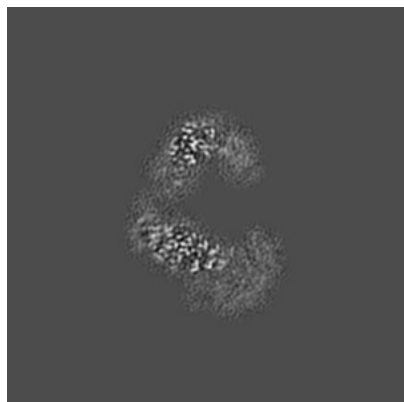


Z Index: 182

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

6.3 Largest variance slices [i](#)

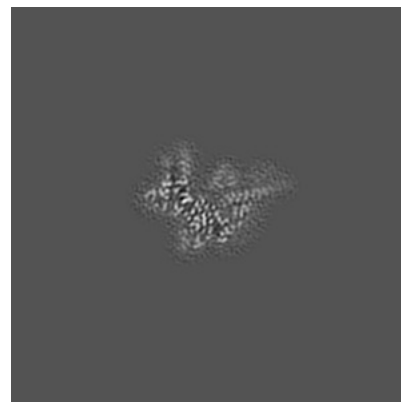
6.3.1 Primary map



X Index: 188

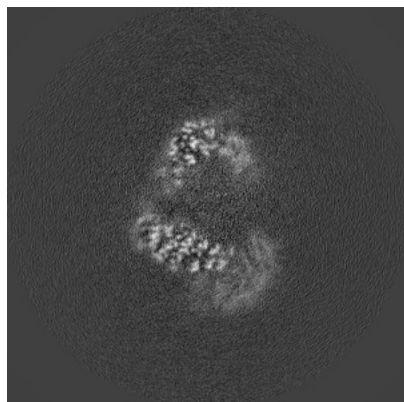


Y Index: 192

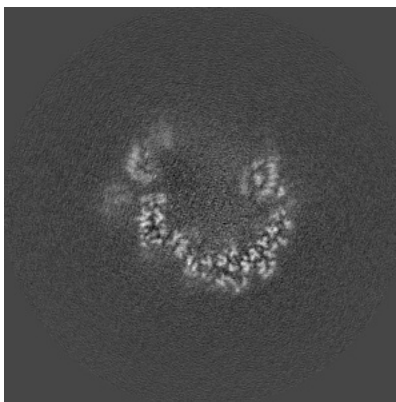


Z Index: 242

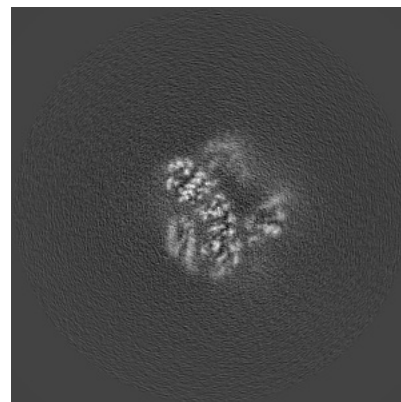
6.3.2 Raw map



X Index: 188



Y Index: 192

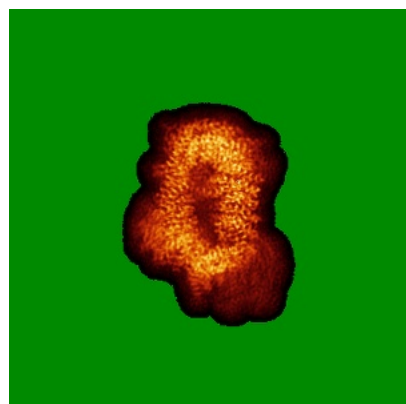


Z Index: 145

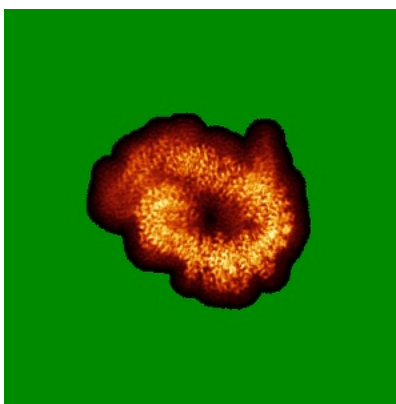
The images above show the largest variance slices of the map in three orthogonal directions.

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

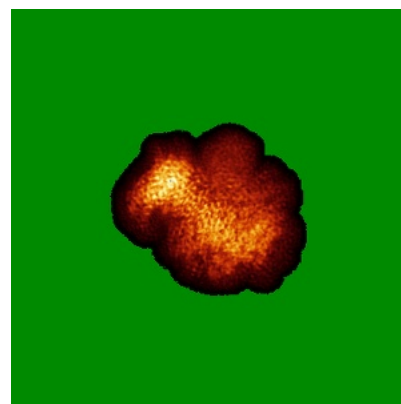
6.4.1 Primary map



X

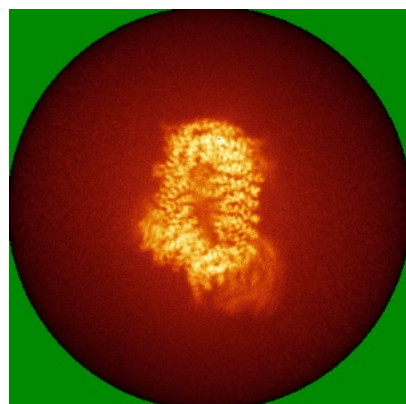


Y

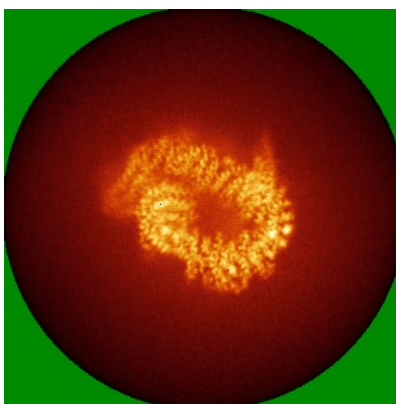


Z

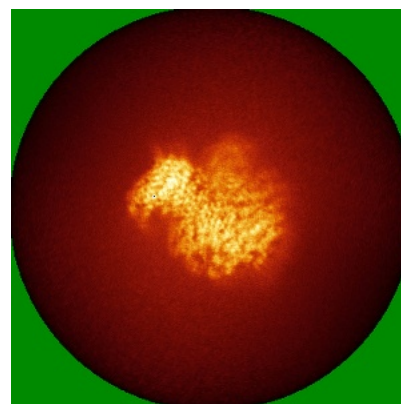
6.4.2 Raw map



X



Y

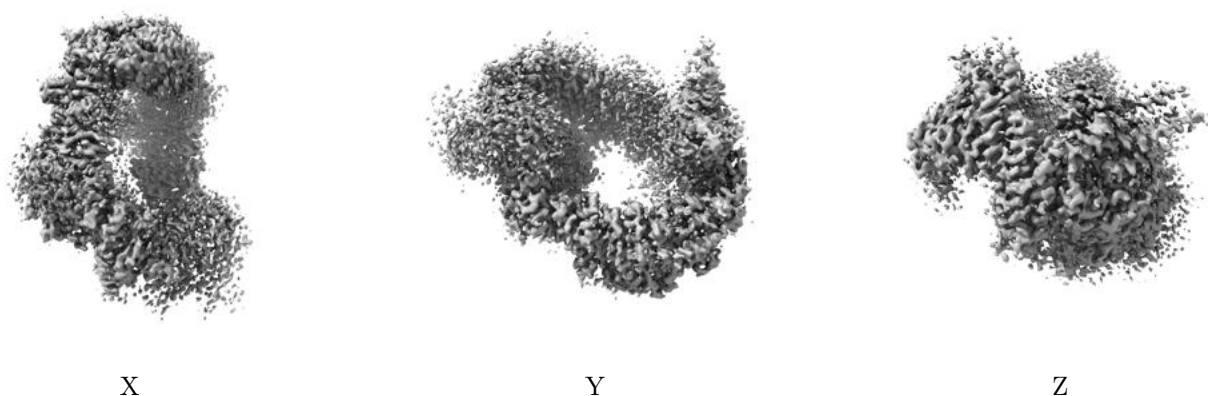


Z

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.

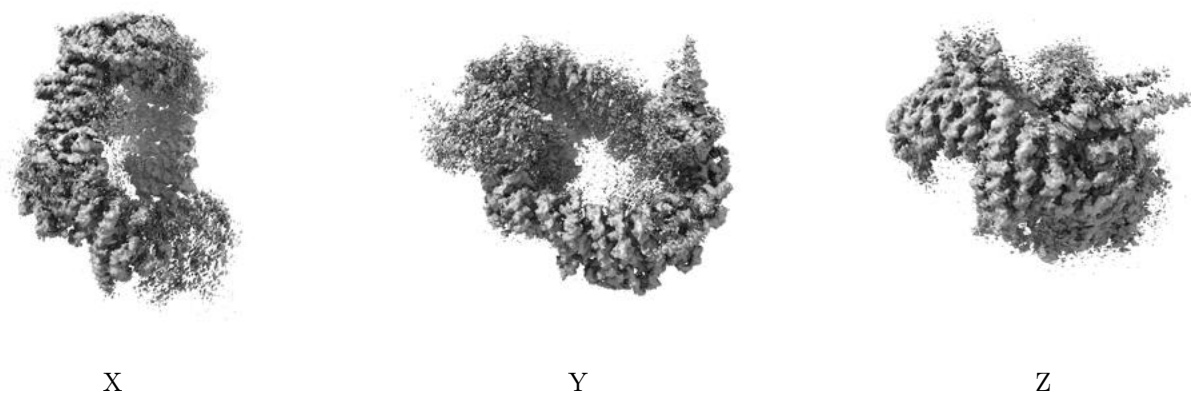
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.013. 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.

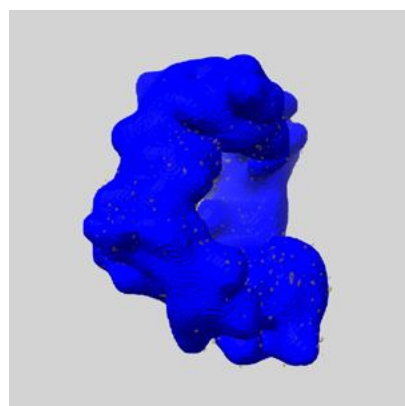
6.6 Mask visualisation [i](#)

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

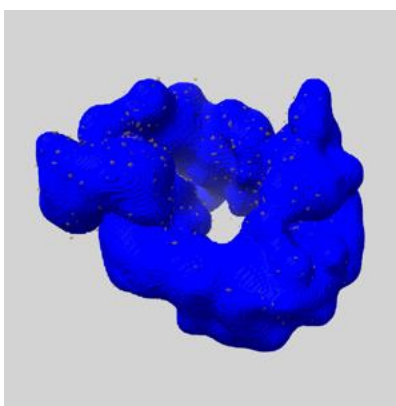
A mask typically either:

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

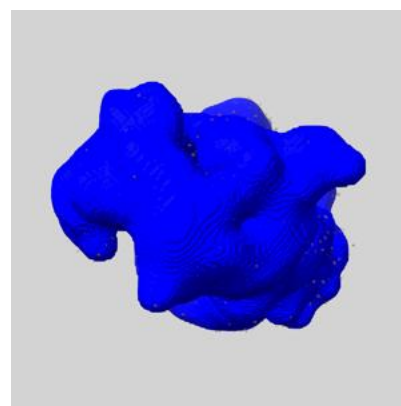
6.6.1 emd_23925_msk_1.map [i](#)



X



Y

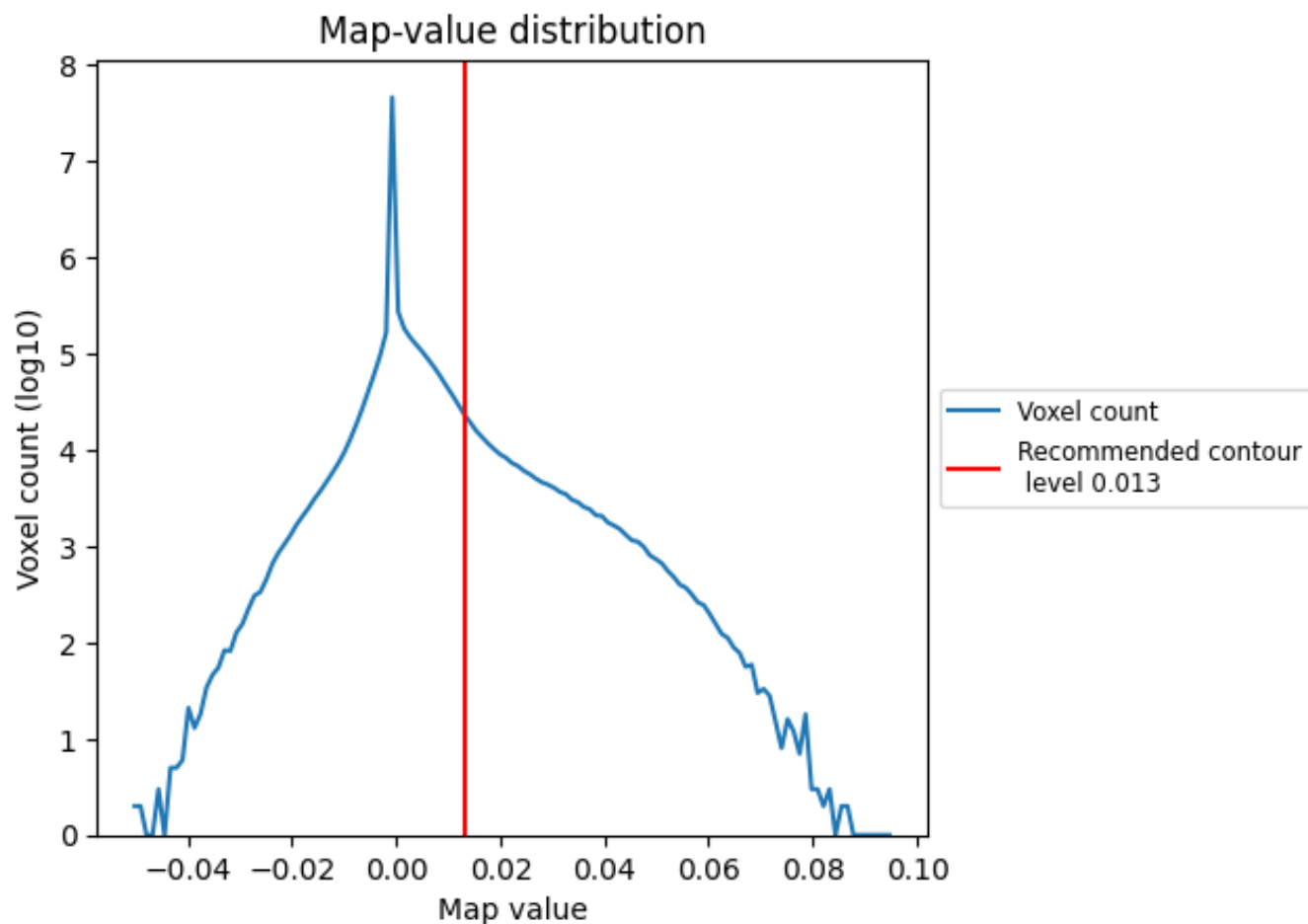


Z

7 Map analysis [i](#)

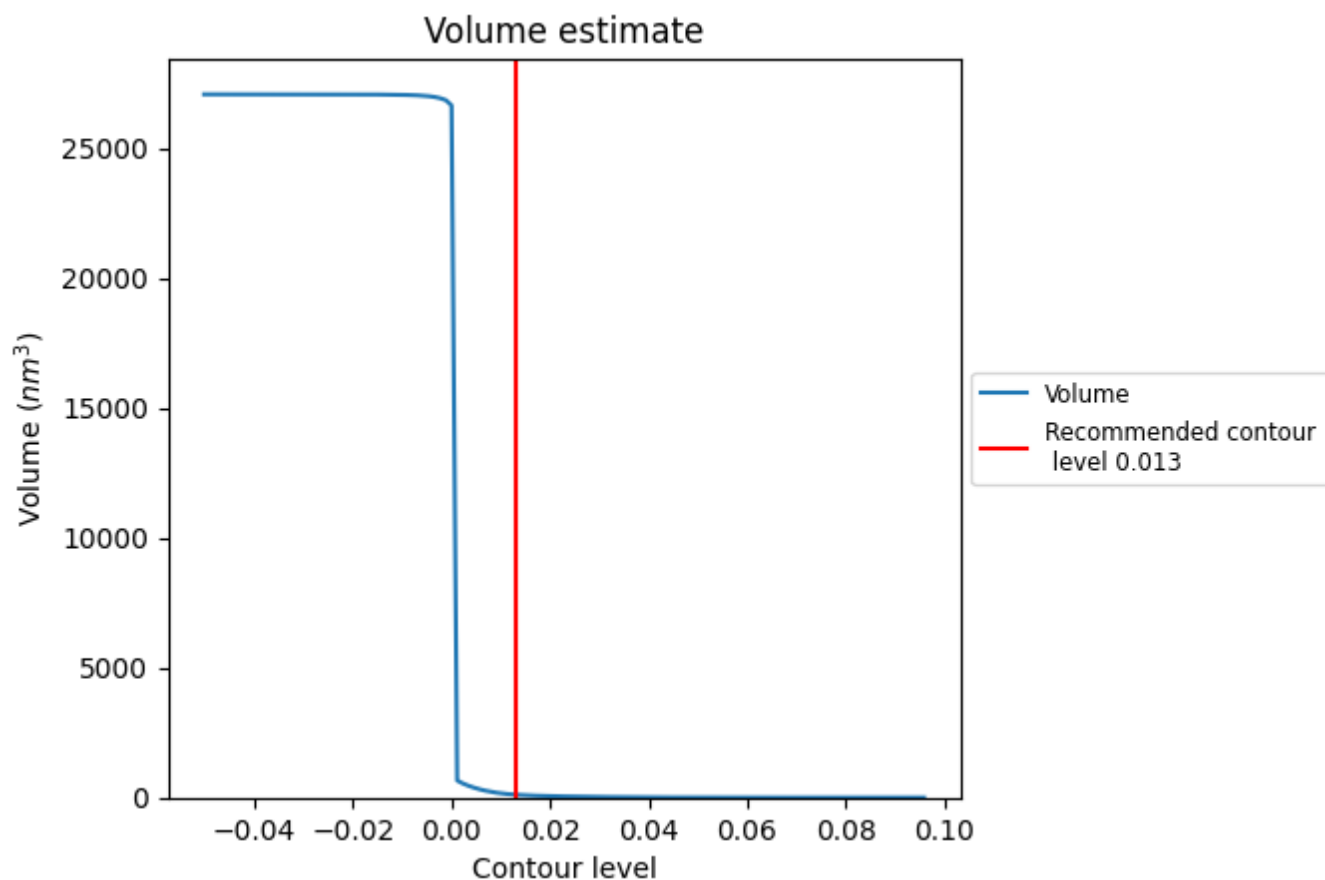
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

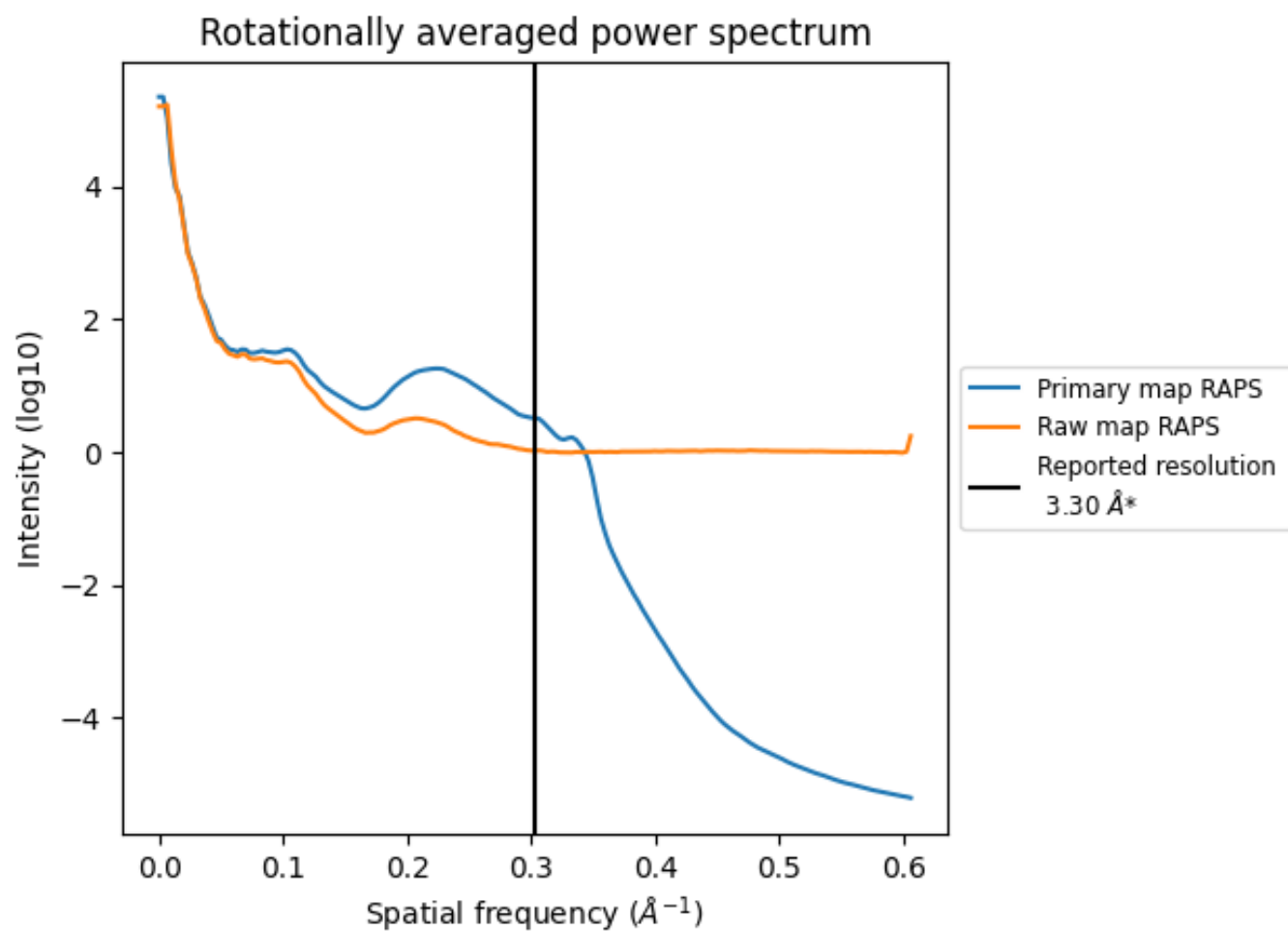
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 110 nm³; this corresponds to an approximate mass of 99 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](#)

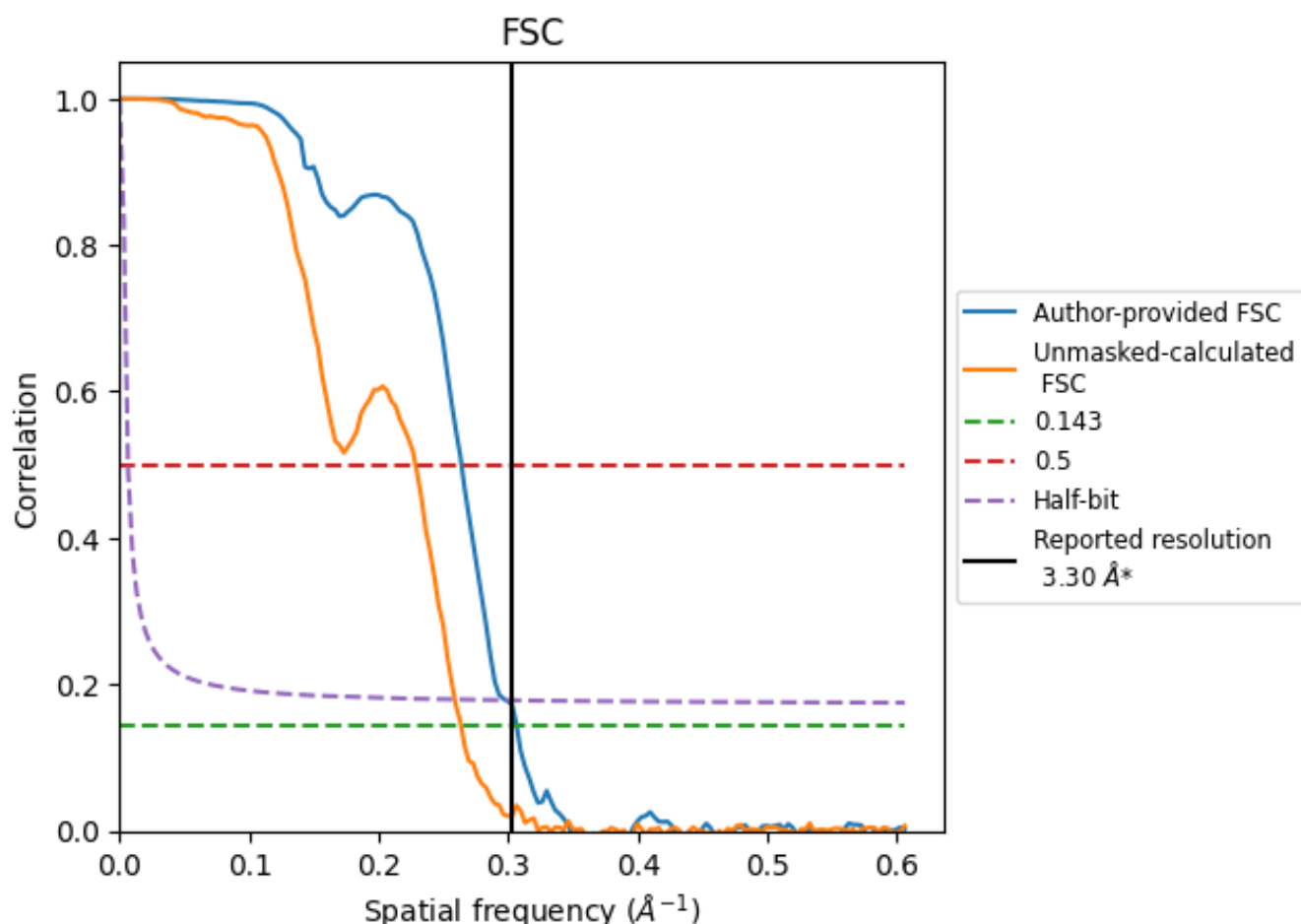


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 \AA^{-1}

8.2 Resolution estimates [i](#)

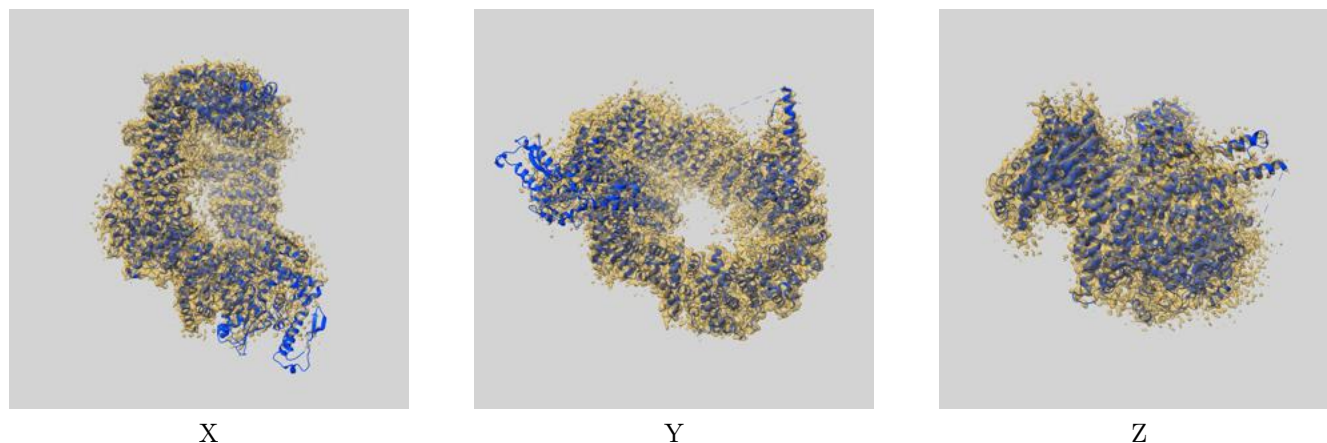
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.79	3.35
Unmasked-calculated*	3.79	4.38	3.86

*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 3.79 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

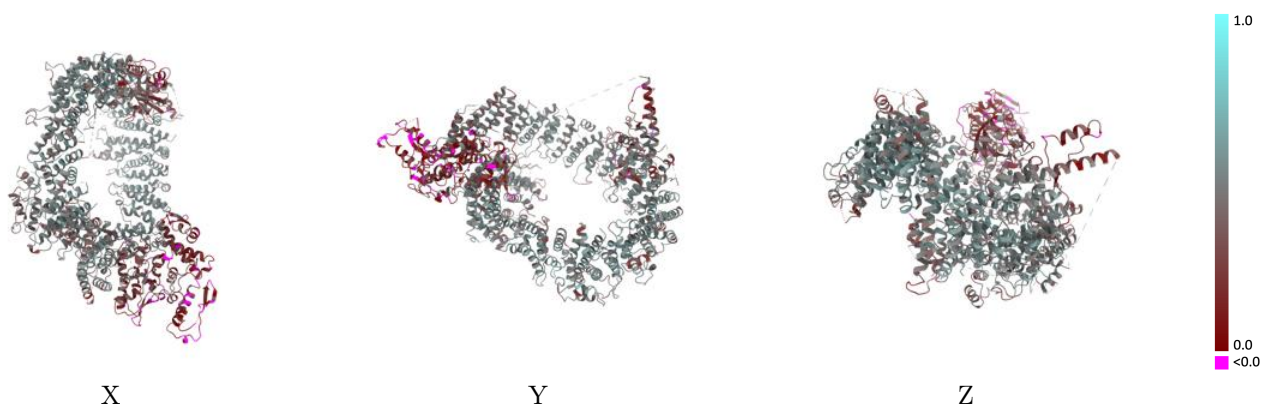
This section contains information regarding the fit between EMDB map EMD-23925 and PDB model 7MOP. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



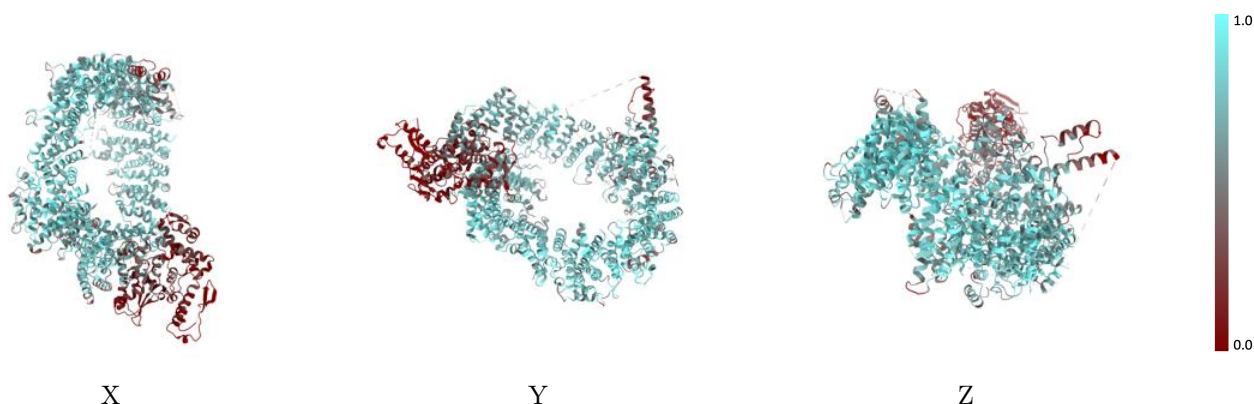
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



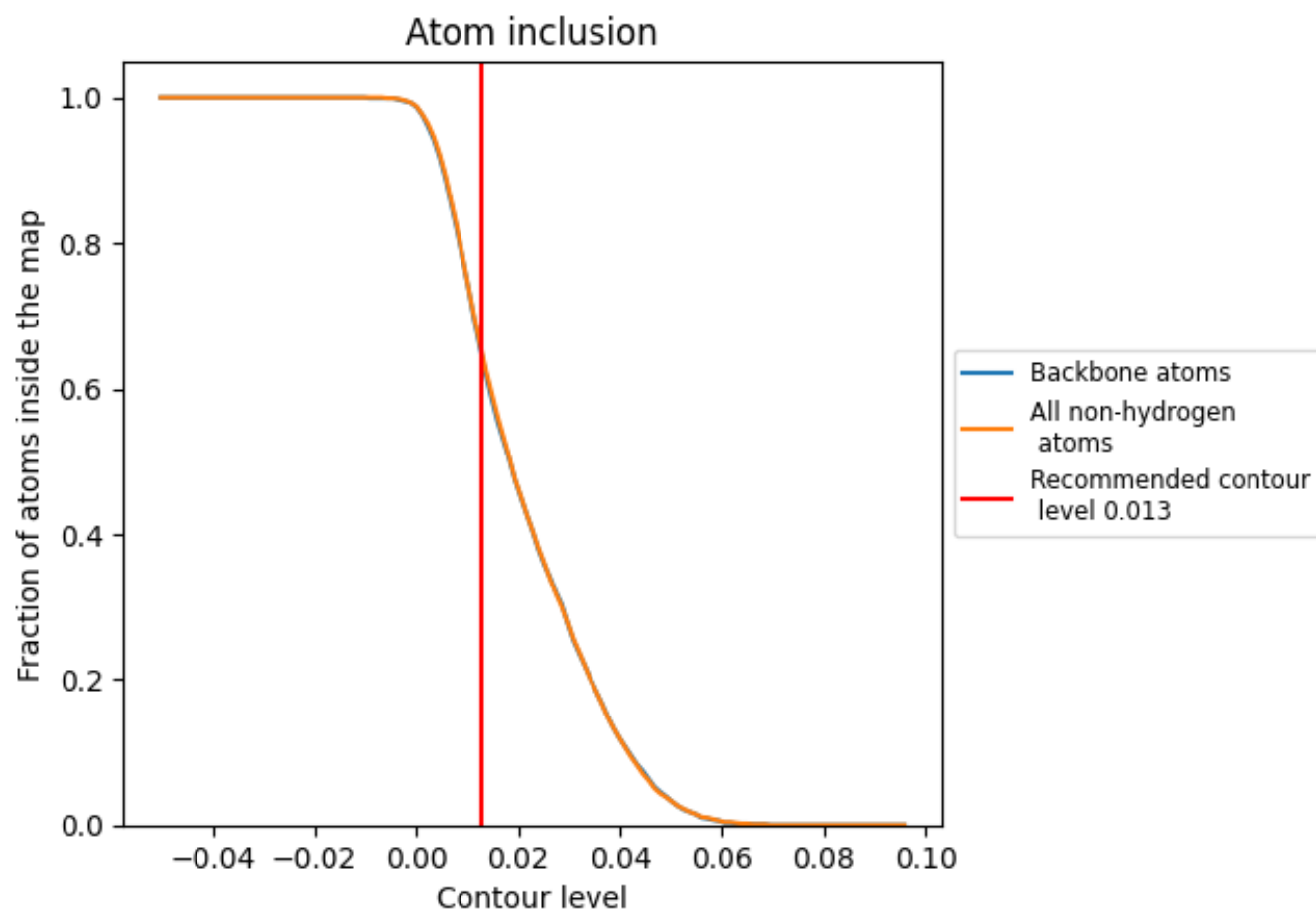
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 65% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6470	<div></div> 0.4250
A	<div></div> 0.6570	<div></div> 0.4240
B	<div></div> 0.8850	<div></div> 0.5480

