



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:01 PM UTC

PDB ID : 7V05 / pdb_00007v05
EMDB ID : EMD-26936
Title : Complex of Plasmodium falciparum circumsporozoite protein with 850 Fab
Authors : Kucharska, I.; Prieto, K.; Rubinstein, J.L.; Julien, J.P.
Deposited on : 2022-05-09
Resolution : 3.40 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

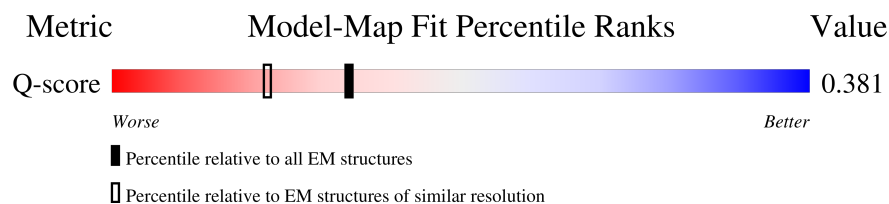
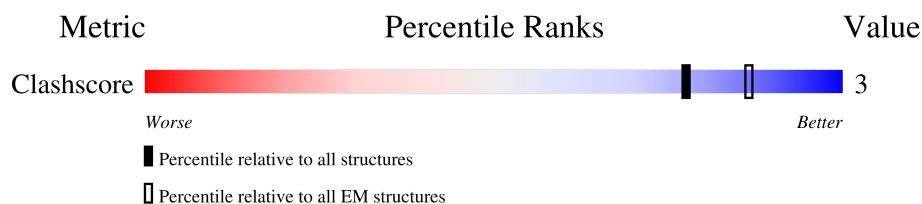
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

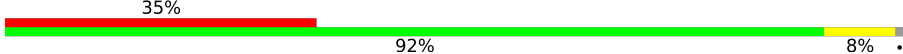
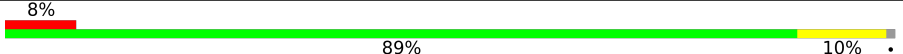
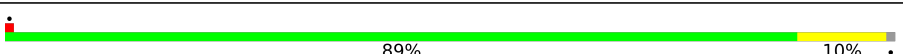
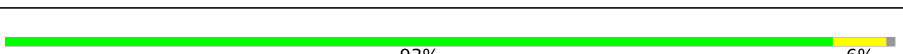
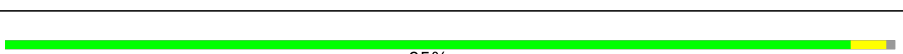
The reported resolution of this entry is 3.40 Å.

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



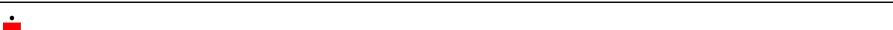
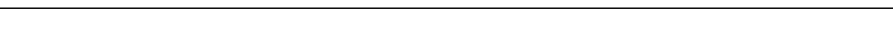
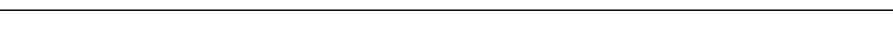
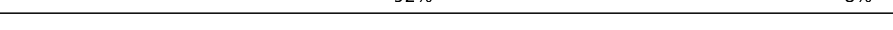
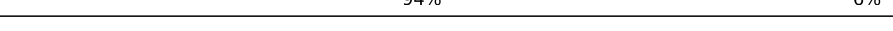
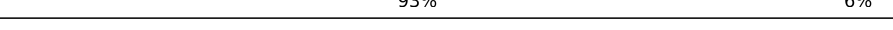
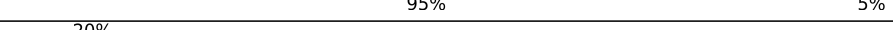
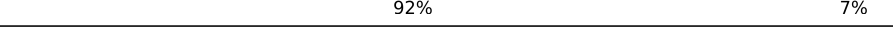
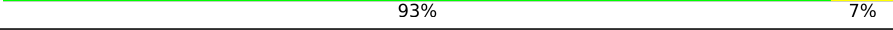
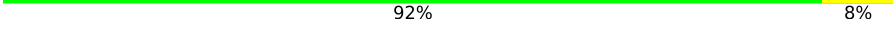
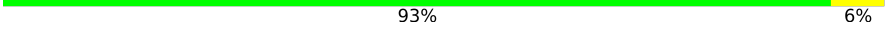
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	226	
1	B	226	
1	C	226	
1	D	226	
1	E	226	
1	F	226	

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Mol	Chain	Length	Quality of chain
1	G	226	 90% 9%
1	H	226	 92% 7%
1	I	226	 92% 7%
1	J	226	 19% 91% 8%
1	K	226	 93% 6%
1	L	226	 94% 5%
1	M	226	 92% 7%
1	N	226	 6% 92% 7%
2	a	213	 36% 92% 7%
2	b	213	 9% 91% 9%
2	c	213	 91% 8%
2	d	213	 92% 8%
2	e	213	 93% 6%
2	f	213	 92% 8%
2	g	213	 94% 6%
2	h	213	 93% 6%
2	i	213	 95% 5%
2	j	213	 20% 90% 9%
2	k	213	 92% 7%
2	l	213	 93% 7%
2	m	213	 92% 8%
2	n	213	 93% 6%
3	X	372	 24% 6% 70%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 47382 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 850 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	B	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	C	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	D	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	E	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	F	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	G	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	H	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	I	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	J	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	K	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	L	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	M	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		
1	N	224	Total	C	N	O	S	0	0
			1689	1068	283	332	6		

- Molecule 2 is a protein called 850 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	c	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	d	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	e	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	f	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	g	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	h	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	i	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	j	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	k	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	l	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	m	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		
2	n	212	Total	C	N	O	S	0	0
			1640	1029	272	334	5		

- Molecule 3 is a protein called Circumsporozoite protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	X	111	Total	C	N	O	0	0
			776	444	166	166		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	74	ALA	VAL	conflict	UNP Q7K740
X	75	ASN	ASP	conflict	UNP Q7K740
X	258	GLN	ASN	conflict	UNP Q7K740
X	261	PRO	-	expression tag	UNP Q7K740
X	262	HIS	-	expression tag	UNP Q7K740
X	263	HIS	-	expression tag	UNP Q7K740

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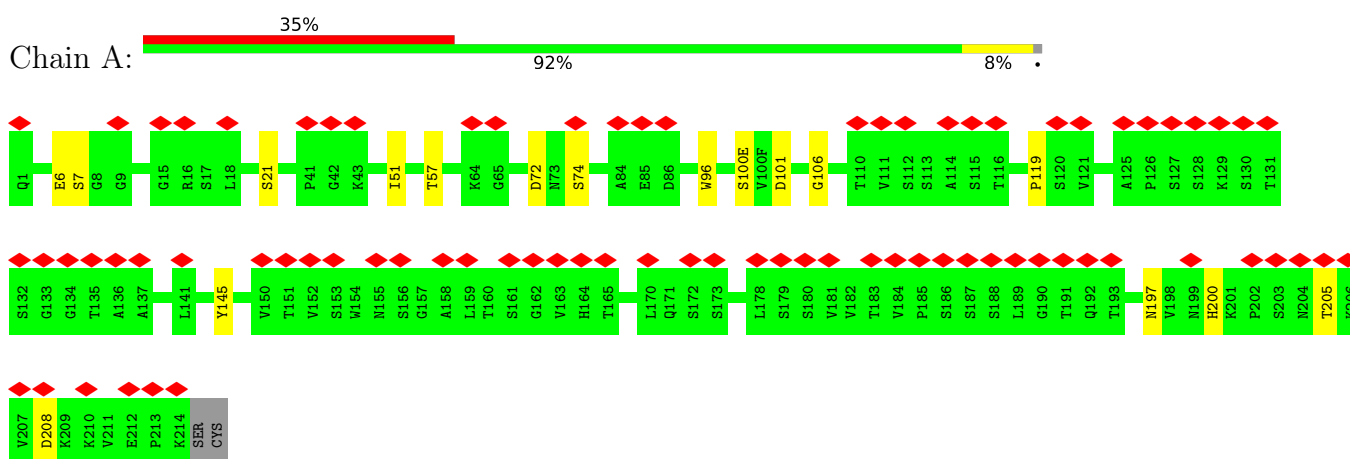
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Chain	Residue	Modelled	Actual	Comment	Reference
X	264	HIS	-	expression tag	UNP Q7K740
X	265	HIS	-	expression tag	UNP Q7K740
X	266	HIS	-	expression tag	UNP Q7K740
X	267	HIS	-	expression tag	UNP Q7K740

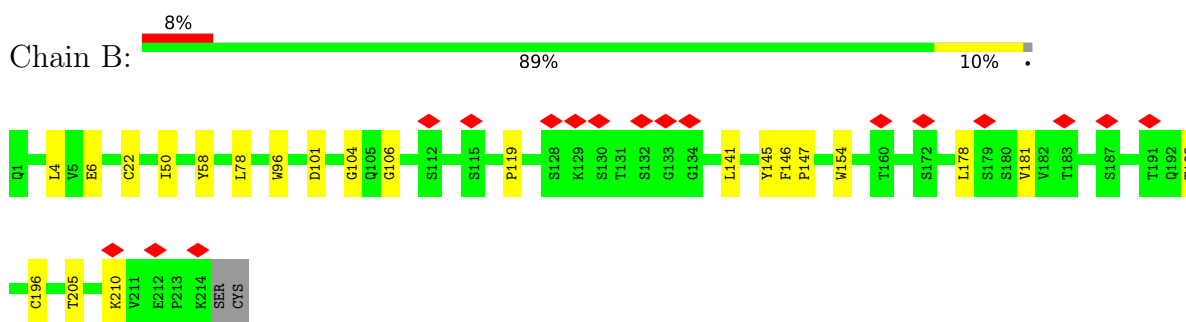
3 Residue-property plots

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.

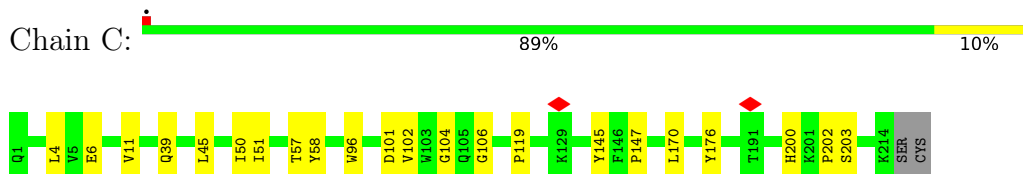
• Molecule 1: 850 Fab Heavy Chain



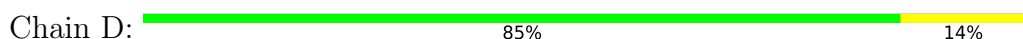
• Molecule 1: 850 Fab Heavy Chain



• Molecule 1: 850 Fab Heavy Chain



• Molecule 1: 850 Fab Heavy Chain





- Molecule 1: 850 Fab Heavy Chain

Chain E: 93% 6%



- Molecule 1: 850 Fab Heavy Chain

Chain F: 95% 5%



- Molecule 1: 850 Fab Heavy Chain

Chain G: 90% 9%



- Molecule 1: 850 Fab Heavy Chain

Chain H: 92% 7%



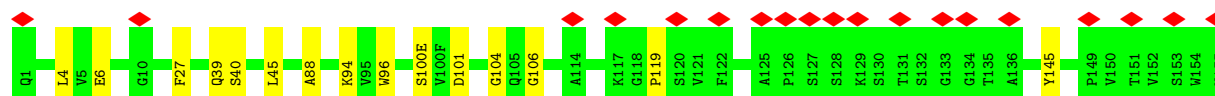
- Molecule 1: 850 Fab Heavy Chain

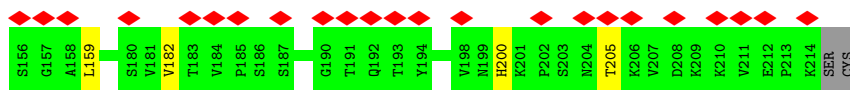
Chain I: 92% 7%



- Molecule 1: 850 Fab Heavy Chain

Chain J: 19% 91% 8%





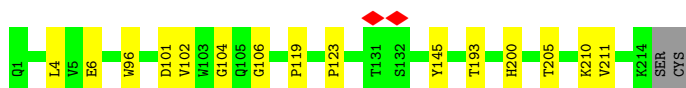
• Molecule 1: 850 Fab Heavy Chain



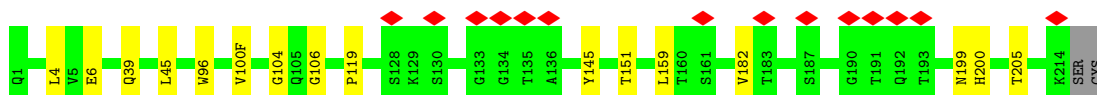
• Molecule 1: 850 Fab Heavy Chain



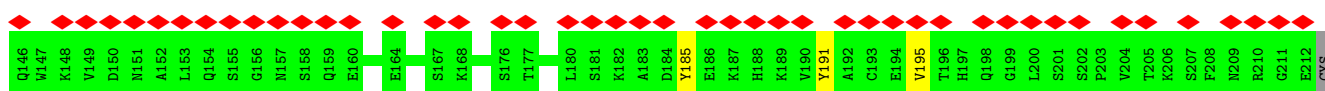
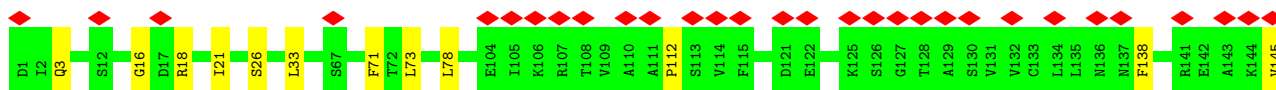
• Molecule 1: 850 Fab Heavy Chain



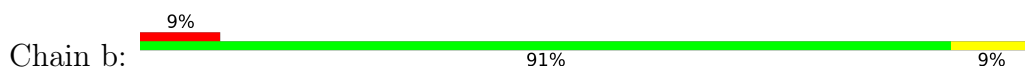
• Molecule 1: 850 Fab Heavy Chain

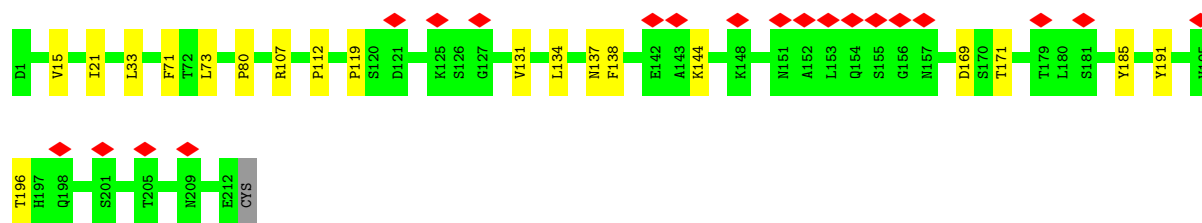


• Molecule 2: 850 Fab Light Chain

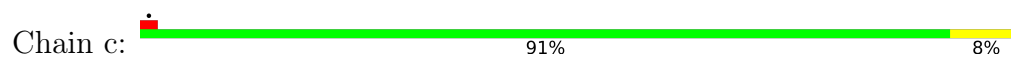


• Molecule 2: 850 Fab Light Chain





• Molecule 2: 850 Fab Light Chain



• Molecule 2: 850 Fab Light Chain



• Molecule 2: 850 Fab Light Chain



• Molecule 2: 850 Fab Light Chain



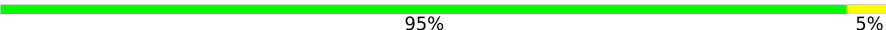
• Molecule 2: 850 Fab Light Chain



• Molecule 2: 850 Fab Light Chain

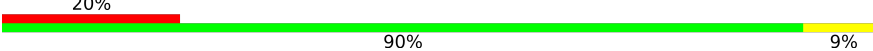


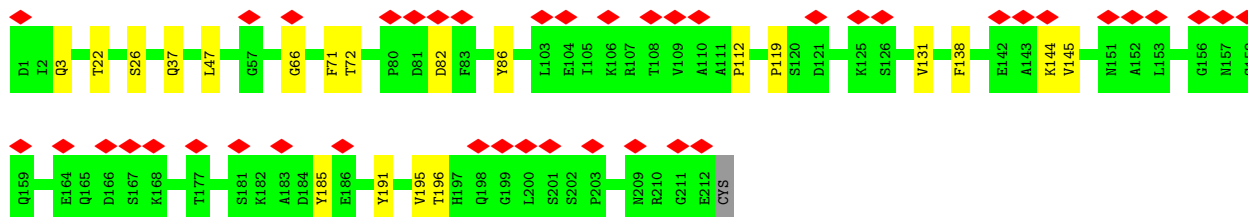
- Molecule 2: 850 Fab Light Chain

Chain i:  95% 5%

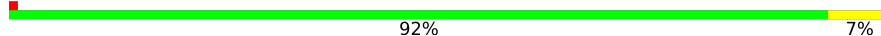


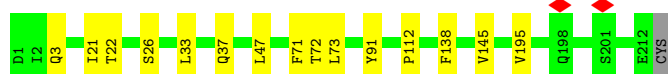
- Molecule 2: 850 Fab Light Chain

Chain j:  20% 90% 9%

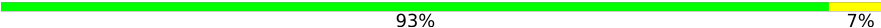


- Molecule 2: 850 Fab Light Chain

Chain k:  92% 7%

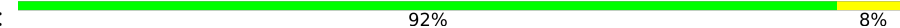


- Molecule 2: 850 Fab Light Chain

Chain l:  93% 7%



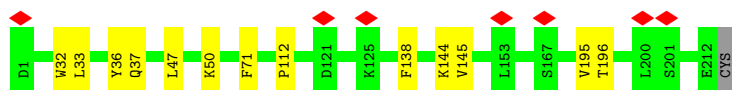
- Molecule 2: 850 Fab Light Chain

Chain m:  92% 8%



- Molecule 2: 850 Fab Light Chain

Chain n:  93% 6%



- Molecule 3: Circumsporozoite protein

HIS	SER	PRO		A46	ASN	PHE
HIS	THR	ASN		A47	GLU	GLN
HIS	GLU	ALA		N47	ASP	GLY
HIS	TRP	ASN		P48	ASN	TYR
	SER	PRO			GLU	CYS
	PRO	ASN		A62	LYS	TYR
	CYS	LYS		N63	LEU	GLY
	SER	ASN		P64	ARG	SER
	VAL	ASN		N65	LYS	SER
	THR	GLN			PRO	SER
	CYS	GLY		A70	LYS	SER
	GLY	ASN		N71	HIS	ASN
	ASN	GLY		P72	LYS	THR
	ILE	GLN			LEU	ARG
	GLN	HIS		A78	LYS	VAL
	VAL	ASN		N79	GLN	ASN
	ARG	MET		P80	PRO	GLU
	ILE	PRO		A86	ALA	LEU
	LYS	ASN		N87	ASP	ASN
	PRO	ASP		P88	GLY	TYR
	GLY	PRO			ASN	ASP
	SER	ASN		A94	PRO	ASN
	ALA	ARG		N95	ASP	ALA
	ASN	ASN		P96	PRO	GLY
	LYS	VAL			ASN	THR
	PRO	ASP		A110	ALA	LEU
	LYS	GLN		N111	ASN	TYR
	ASP	GLU		P112	PRO	ASN
	GLU	ALA		N113	ASN	GLY
	LEU	ASN		A114	VAL	LEU
	ASP	ALA		ASN	ASP	GLU
	TYR	ASN		PRO	PRO	MET
	ALA	SER		ASN	ASN	ASN
	ASN	ALA		ALA	ALA	ASN
	ASP	VAL		ASN	ASN	TYR
	ILE	LYS		PRO	PRO	TYR
	GLU	ASN		ASN	ASN	GLY
	LYS	ASN		ALA	VAL	LYS
	LYS	ASN		ASN	ASP	GLN
	ILE	ASN		PRO	PRO	GLU
	CYS	GLU		ASN	ASN	ASN
	LYS	GLU		ALA	VAL	LYS
	MET	PRO		ASN	ALA	TYR
	GLU	SER		PRO	PRO	SER
	LYS	ASP		ASN	ASN	LEU
	CYS	HIS		ALA	VAL	LYS
	SER	ILE		PRO	ASP	LYS
	VAL	LYS		ALA	F4	ASN
	ASN	TYR		ASN	N21	SER
	VAL	LEU		PRO	ALA	ARG
	VAL	ASN		ASN	A30	LEU
	GLN	LYS		ALA	N31	GLY
	SER	ILE		ASN	P32	GLU
	SER	ILE		ASN		ASN
	SER	GLN		PRO	A38	ASP
	PRO	ASN		ASN	N39	ASP
	HIS	SER		ALA	P40	GLY
	HIS	LEU		ASN	N41	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	165747	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.24	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.494	Depositor
Minimum map value	-1.458	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.071	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	350.19998, 350.19998, 350.19998	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	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	A	0.12	0/1732	0.28	0/2361
1	B	0.19	0/1732	0.31	0/2361
1	C	0.29	0/1732	0.34	0/2361
1	D	0.41	0/1732	0.37	0/2361
1	E	0.45	0/1732	0.34	0/2361
1	F	0.43	0/1732	0.35	0/2361
1	G	0.46	0/1732	0.37	0/2361
1	H	0.43	0/1732	0.35	0/2361
1	I	0.44	0/1732	0.37	0/2361
1	J	0.20	0/1732	0.30	0/2361
1	K	0.37	0/1732	0.35	0/2361
1	L	0.43	0/1732	0.35	0/2361
1	M	0.41	0/1732	0.36	0/2361
1	N	0.30	0/1732	0.33	0/2361
2	a	0.13	0/1677	0.30	0/2279
2	b	0.21	0/1677	0.31	0/2279
2	c	0.27	0/1677	0.34	0/2279
2	d	0.34	0/1677	0.35	0/2279
2	e	0.38	0/1677	0.36	0/2279
2	f	0.37	0/1677	0.35	0/2279
2	g	0.38	0/1677	0.36	0/2279
2	h	0.37	0/1677	0.36	0/2279
2	i	0.36	0/1677	0.36	0/2279
2	j	0.11	0/1677	0.29	0/2279
2	k	0.26	0/1677	0.34	0/2279
2	l	0.39	0/1677	0.36	0/2279
2	m	0.33	0/1677	0.35	0/2279
2	n	0.17	0/1677	0.32	0/2279
3	X	0.53	0/803	0.48	0/1133
All	All	0.34	0/48529	0.35	0/66093

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	A	1689	0	1637	9	0
1	B	1689	0	1637	13	0
1	C	1689	0	1637	13	0
1	D	1689	0	1637	20	0
1	E	1689	0	1637	8	0
1	F	1689	0	1637	5	0
1	G	1689	0	1637	13	0
1	H	1689	0	1637	9	0
1	I	1689	0	1637	10	0
1	J	1689	0	1637	12	0
1	K	1689	0	1637	9	0
1	L	1689	0	1637	7	0
1	M	1689	0	1637	10	0
1	N	1689	0	1637	10	0
2	a	1640	0	1585	9	0
2	b	1640	0	1585	10	0
2	c	1640	0	1585	10	0
2	d	1640	0	1585	9	0
2	e	1640	0	1585	7	0
2	f	1640	0	1585	8	0
2	g	1640	0	1585	6	0
2	h	1640	0	1585	8	0
2	i	1640	0	1585	5	0
2	j	1640	0	1585	10	0
2	k	1640	0	1585	8	0
2	l	1640	0	1585	8	0
2	m	1640	0	1585	9	0
2	n	1640	0	1585	7	0
3	X	776	0	666	12	0
All	All	47382	0	45774	267	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 267 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:I:119:PRO:HB3	1:I:145:TYR:HB3	1.77	0.67
1:J:119:PRO:HB3	1:J:145:TYR:HB3	1.76	0.67
2:g:145:VAL:HG22	2:g:195:VAL:HG22	1.78	0.65
1:A:119:PRO:HB3	1:A:145:TYR:HB3	1.79	0.64
1:M:119:PRO:HD2	1:M:205:THR:HG21	1.80	0.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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.

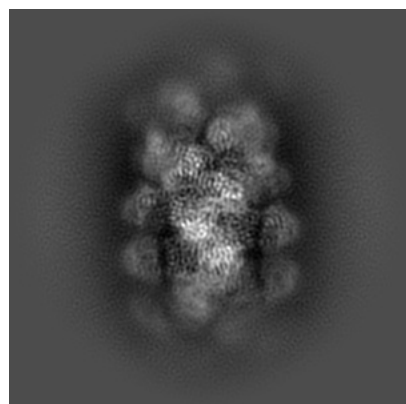
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26936. These allow visual inspection of the internal detail of the map and identification of artifacts.

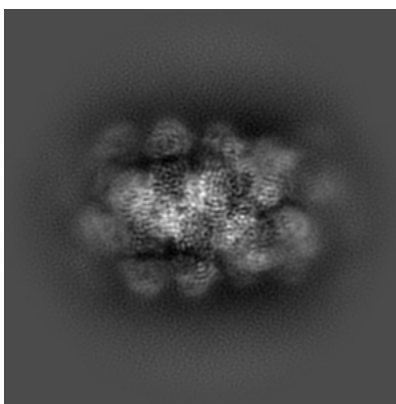
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

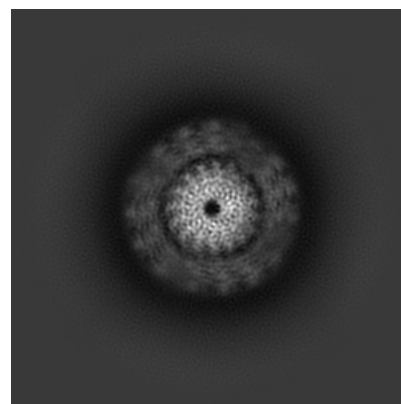
6.1.1 Primary map



X

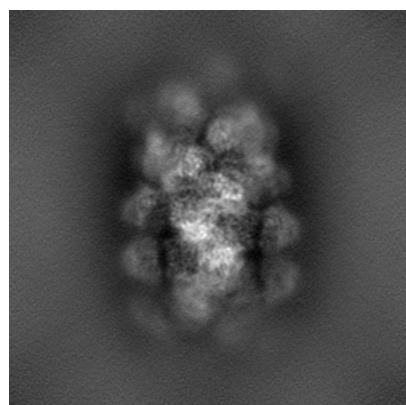


Y

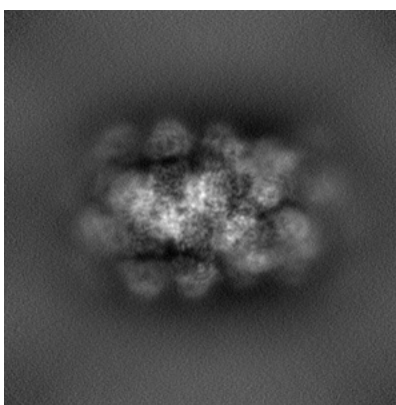


Z

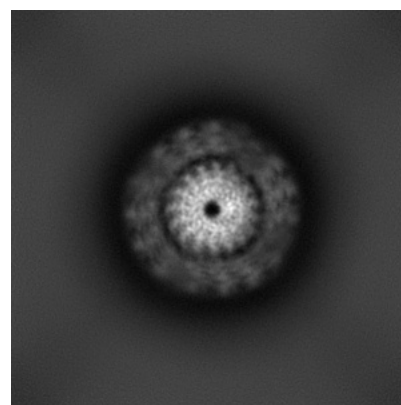
6.1.2 Raw map



X



Y

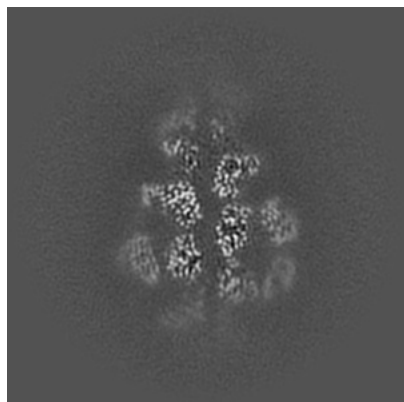


Z

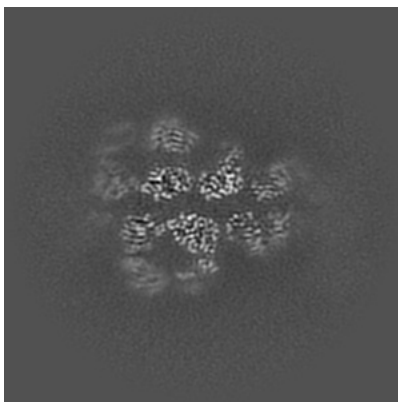
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

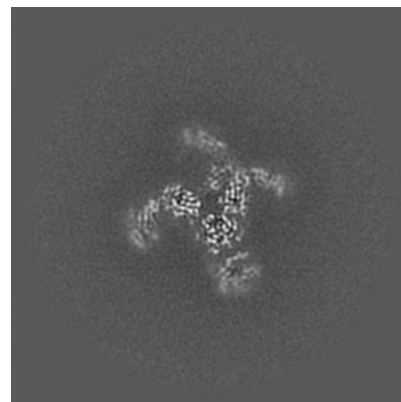
6.2.1 Primary map



X Index: 170

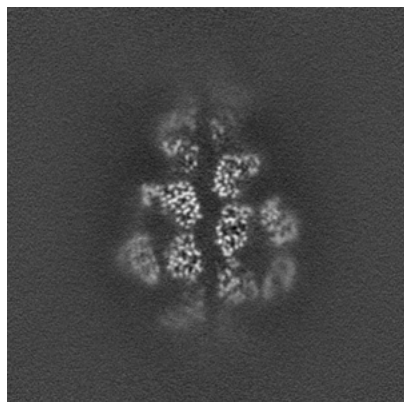


Y Index: 170

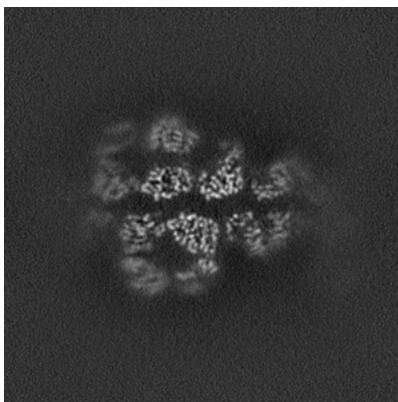


Z Index: 170

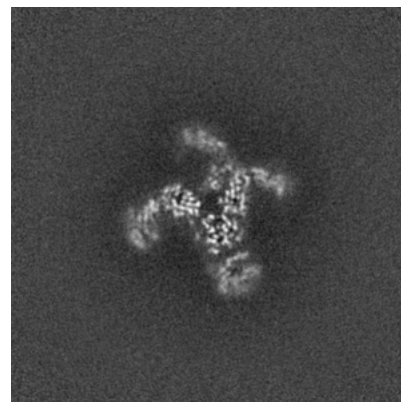
6.2.2 Raw map



X Index: 170



Y Index: 170

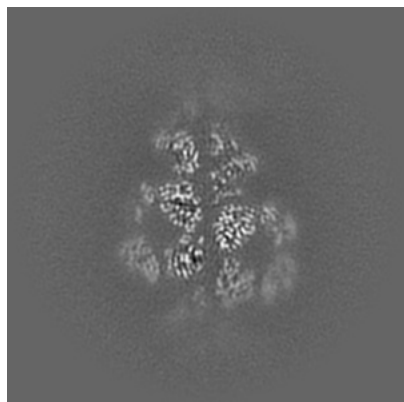


Z Index: 170

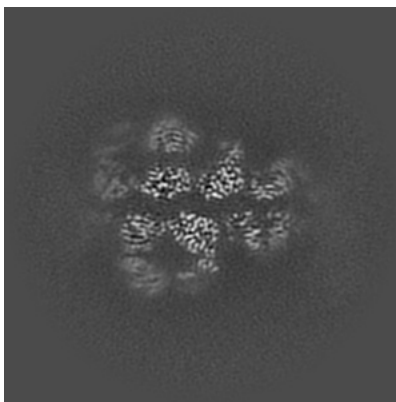
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

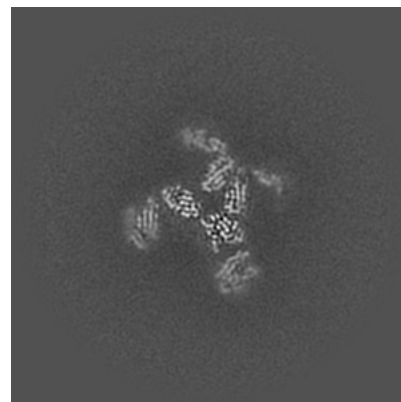
6.3.1 Primary map



X Index: 174

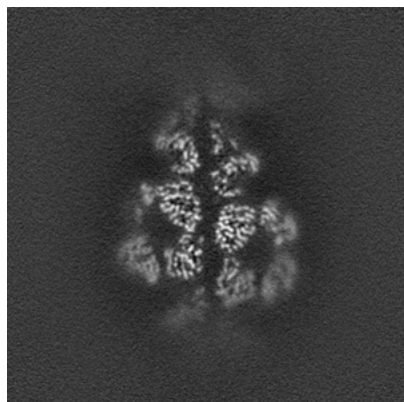


Y Index: 171

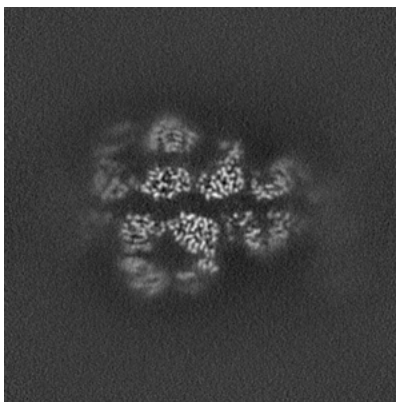


Z Index: 168

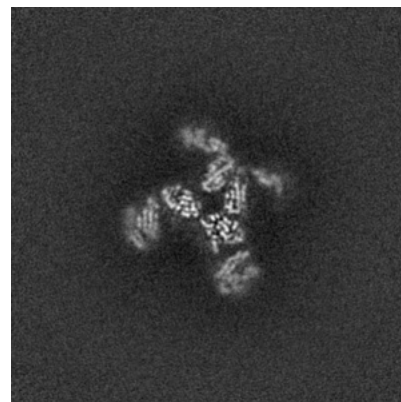
6.3.2 Raw map



X Index: 173



Y Index: 171

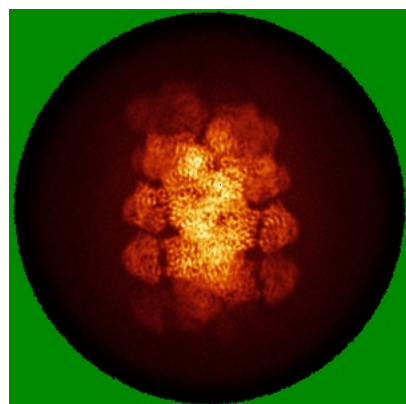


Z Index: 168

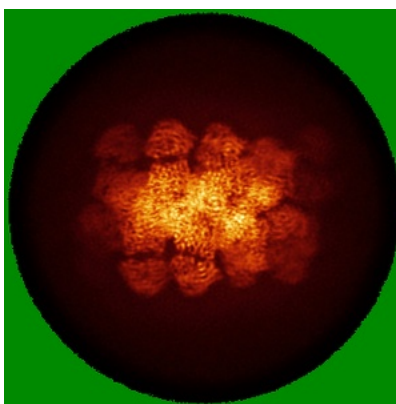
The images above show the largest variance slices of the map in three orthogonal directions.

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

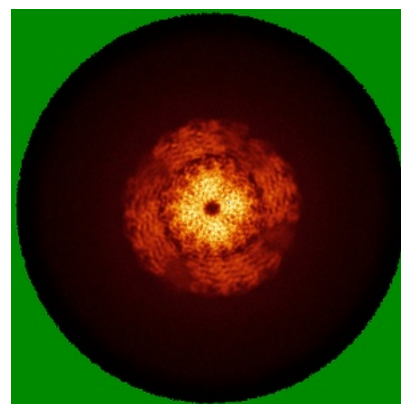
6.4.1 Primary map



X

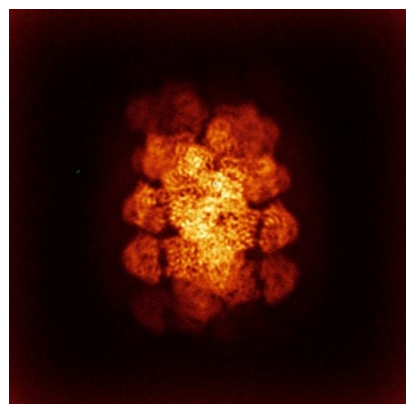


Y

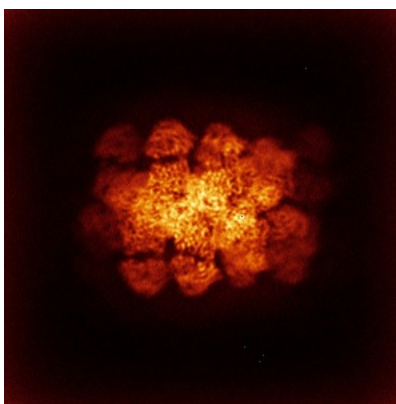


Z

6.4.2 Raw map



X



Y



Z

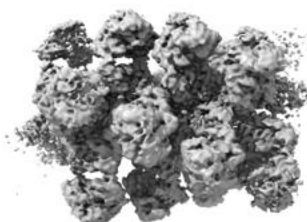
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

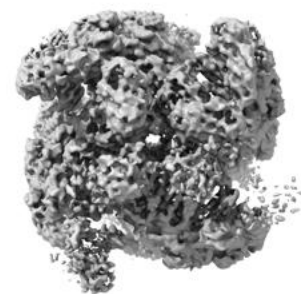
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

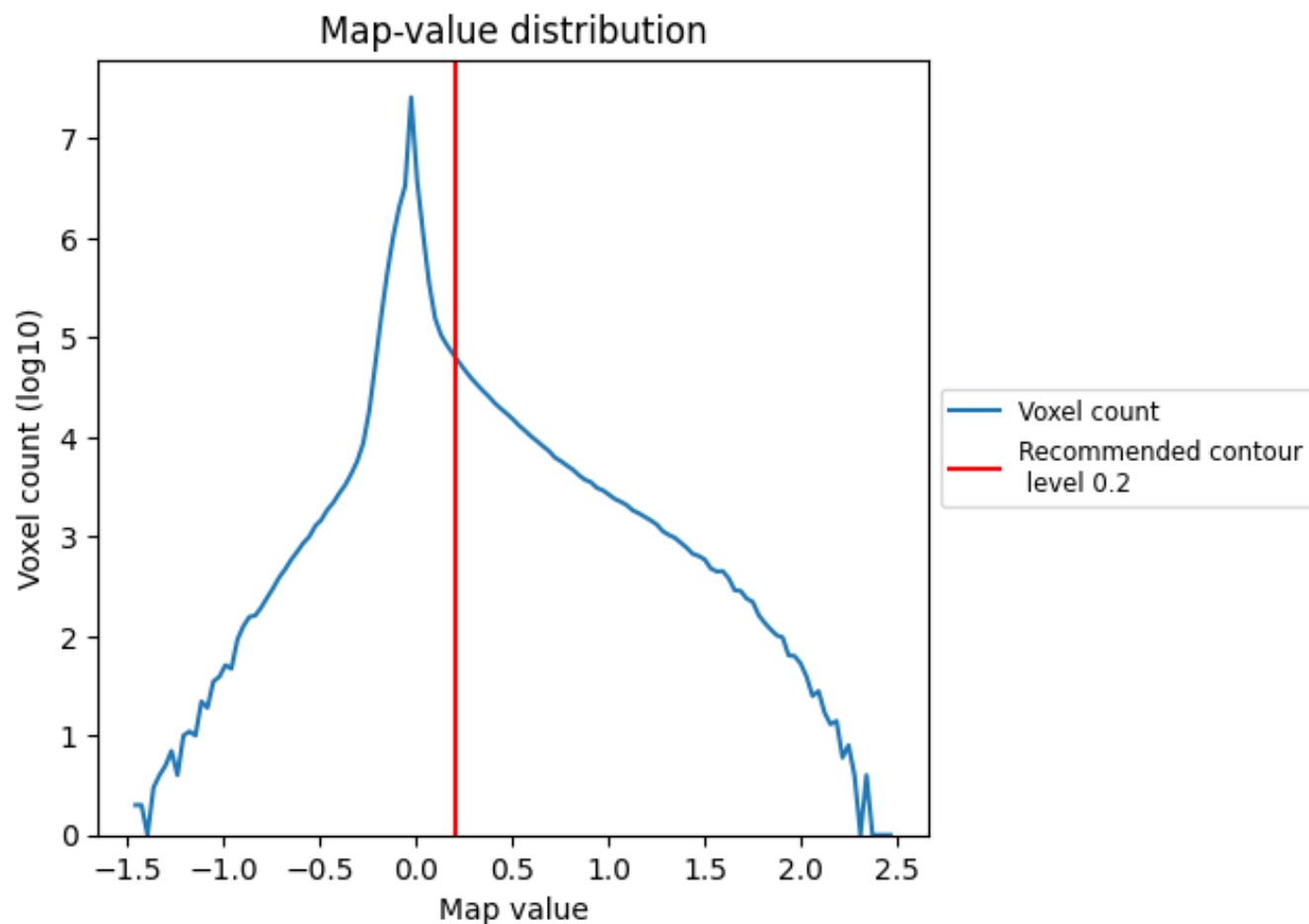
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

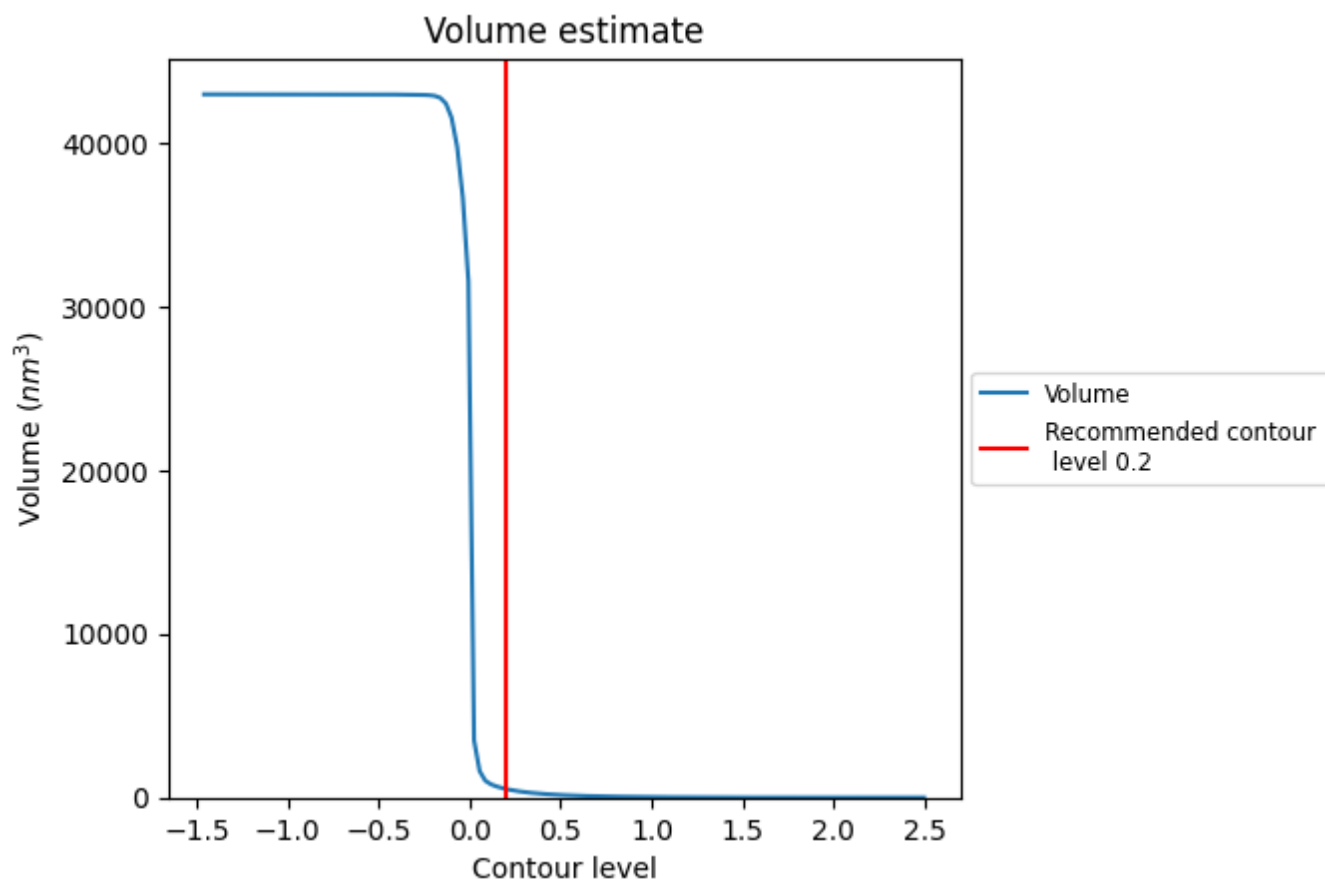
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

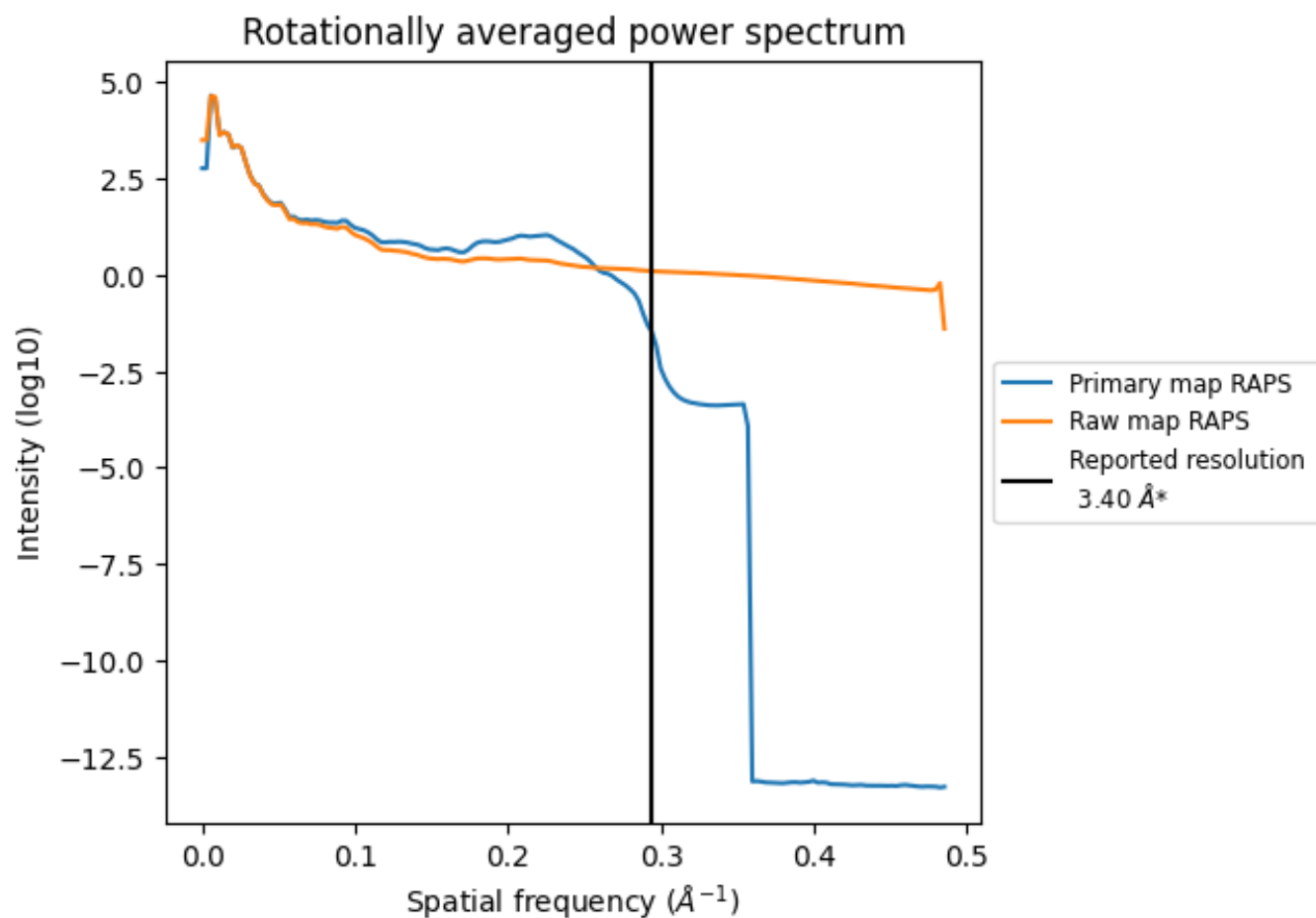
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 525 nm^3 ; this corresponds to an approximate mass of 474 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 ⓘ

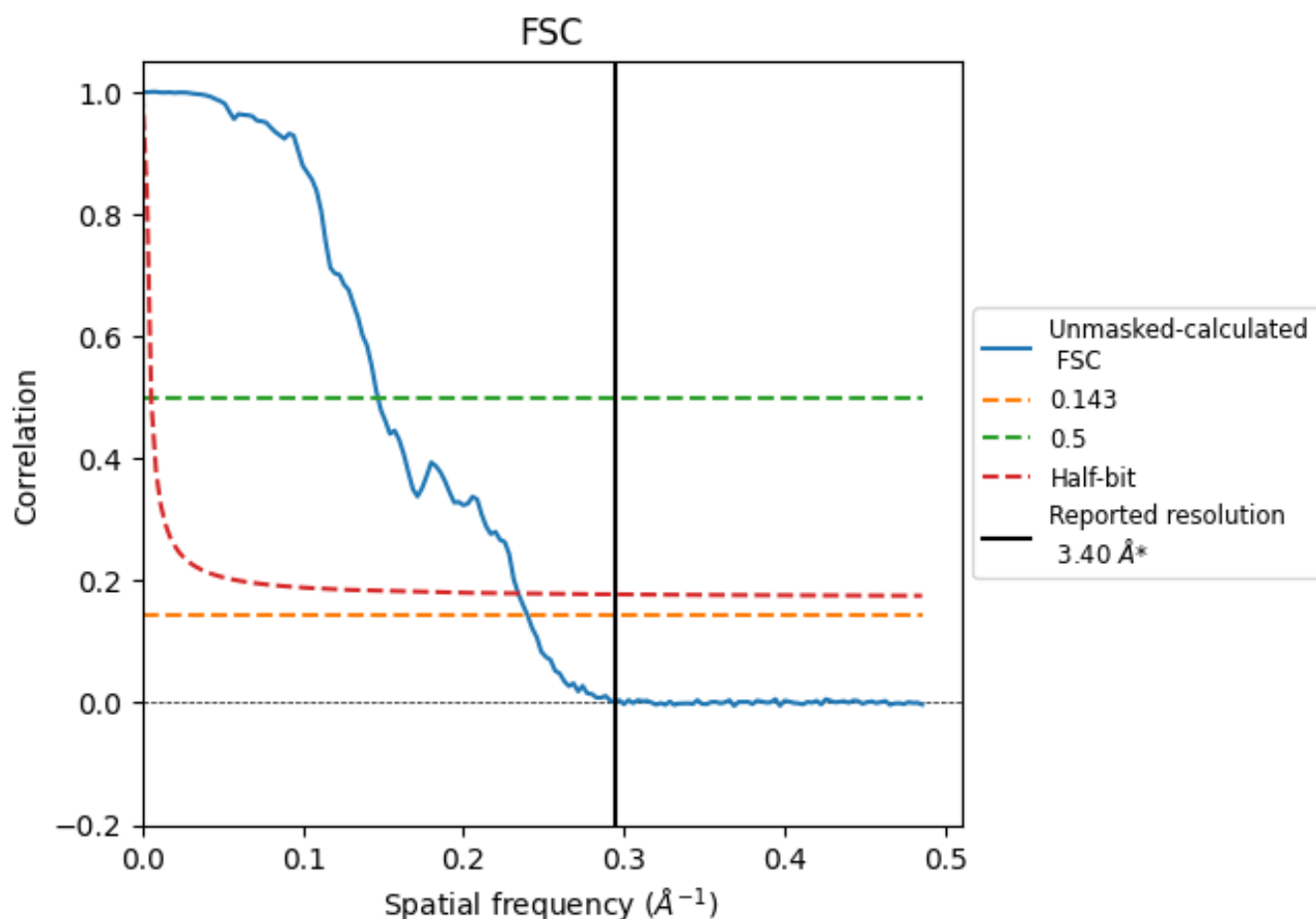


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

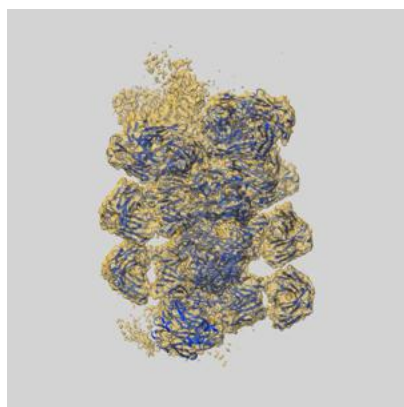
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.17	6.82	4.27

*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 4.17 differs from the reported value 3.4 by more than 10 %

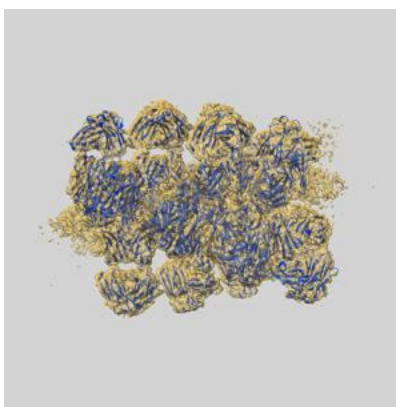
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26936 and PDB model 7V05. Per-residue inclusion information can be found in section [3](#) on page [7](#).

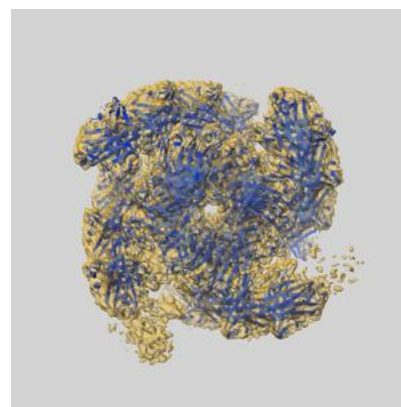
9.1 Map-model overlay [i](#)



X



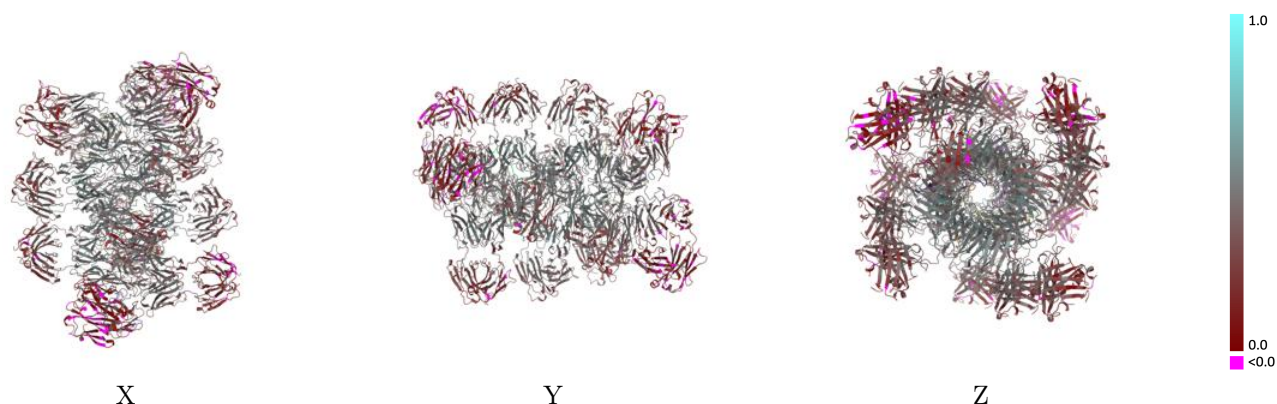
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

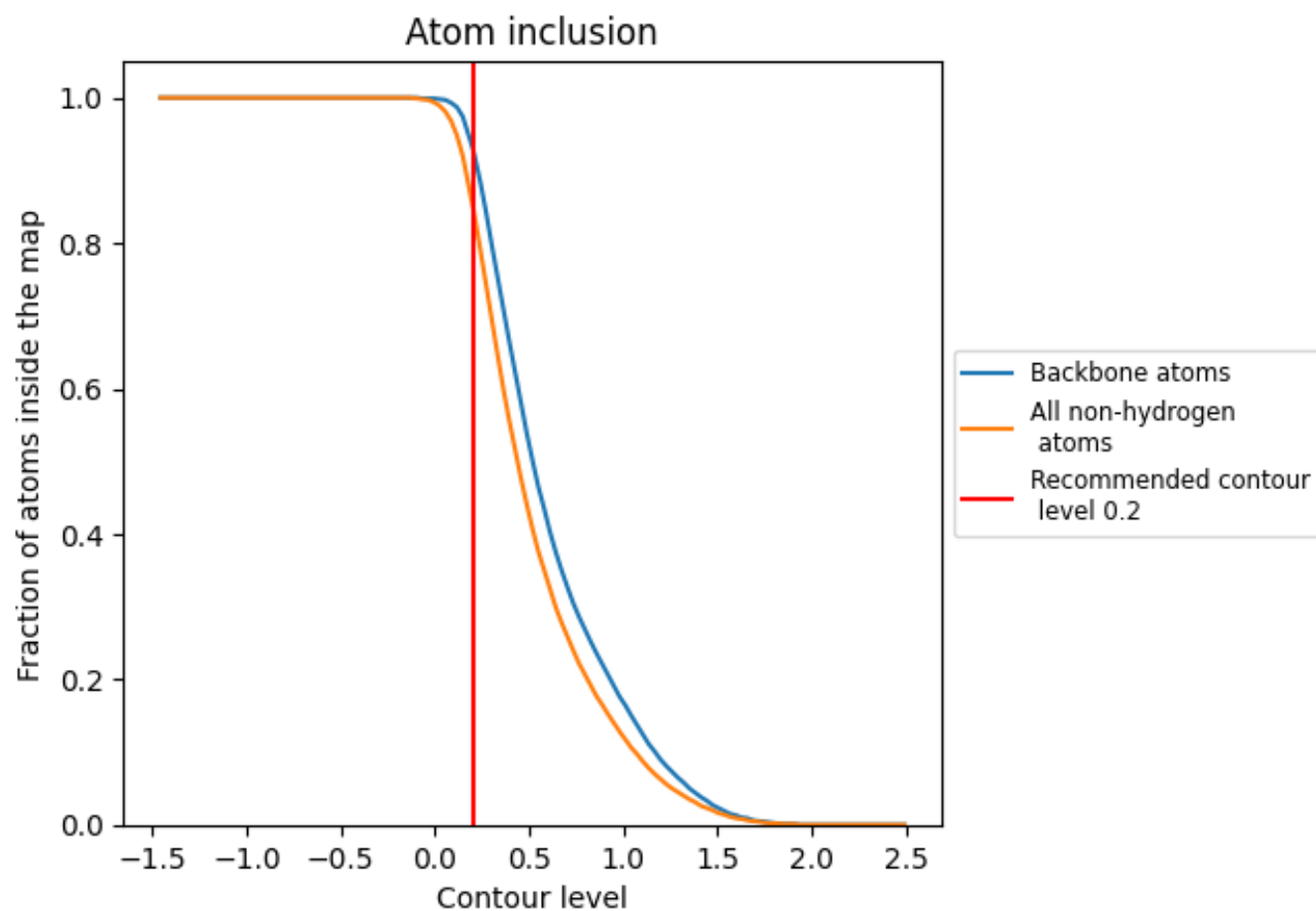


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 85% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.3810
A	 0.5320	 0.2360
B	 0.7740	 0.3090
C	 0.8740	 0.3750
D	 0.9090	 0.3960
E	 0.9500	 0.4550
F	 0.9520	 0.4560
G	 0.9400	 0.4500
H	 0.9370	 0.4440
I	 0.9280	 0.4220
J	 0.6750	 0.3050
K	 0.8810	 0.4050
L	 0.9420	 0.4520
M	 0.9160	 0.4220
N	 0.8180	 0.3640
X	 0.9690	 0.4860
a	 0.5230	 0.2510
b	 0.7550	 0.3050
c	 0.8390	 0.3490
d	 0.8880	 0.3830
e	 0.9260	 0.4340
f	 0.9270	 0.4330
g	 0.9240	 0.4230
h	 0.9170	 0.4170
i	 0.9130	 0.4140
j	 0.6360	 0.2310
k	 0.8800	 0.3610
l	 0.9340	 0.4330
m	 0.9040	 0.3890
n	 0.8070	 0.3060

