



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:43 PM UTC

PDB ID : 8ODT / pdb_00008odt
EMDB ID : EMD-16816
Title : Structure of TolQR complex from E.coli
Authors : Webby, M.N.; Kleanthous, C.; Press, C.E.
Deposited on : 2023-03-09
Resolution : 4.20 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

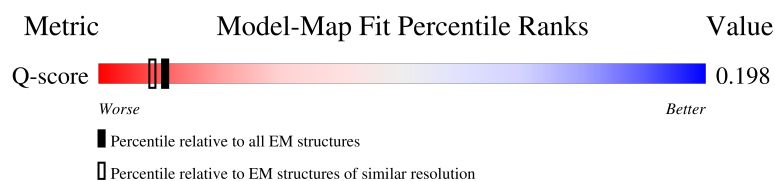
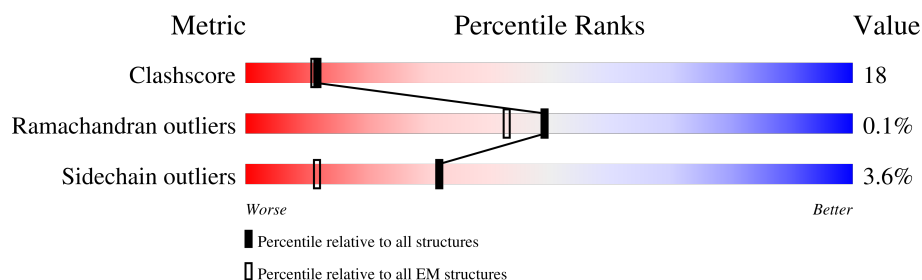
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	230	79% 73% 26% .
1	B	230	73% 67% 33% .
1	C	230	34% 61% 37% .
1	D	230	17% 64% 35% .

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Mol	Chain	Length	Quality of chain
1	E	230	27% 71% 27%
2	F	189	8% 89%
2	G	189	7% 91% 6%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 18800 atoms, of which 9496 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 Tol-Pal system protein TolQ.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	230	Total	C	H	N	O	S	0	0
			3634	1159	1831	310	325	9		
1	B	230	Total	C	H	N	O	S	0	0
			3634	1159	1831	310	325	9		
1	C	230	Total	C	H	N	O	S	0	0
			3634	1159	1831	310	325	9		
1	D	230	Total	C	H	N	O	S	0	0
			3634	1159	1831	310	325	9		
1	E	230	Total	C	H	N	O	S	0	0
			3634	1159	1831	310	325	9		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0ABU9
B	1	MET	-	initiating methionine	UNP P0ABU9
C	1	MET	-	initiating methionine	UNP P0ABU9
D	1	MET	-	initiating methionine	UNP P0ABU9
E	1	MET	-	initiating methionine	UNP P0ABU9

- Molecule 2 is a protein called Tol-Pal system protein TolR.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	F	21	Total	C	H	N	O	S	0	0
			349	112	189	22	25	1		
2	G	17	Total	C	H	N	O	S	0	0
			281	91	152	17	20	1		

There are 94 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	143	LEU	-	expression tag	UNP P0ABV6
F	144	GLU	-	expression tag	UNP P0ABV6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	145	GLU	-	expression tag	UNP P0ABV6
F	146	ASN	-	expression tag	UNP P0ABV6
F	147	LEU	-	expression tag	UNP P0ABV6
F	148	TYR	-	expression tag	UNP P0ABV6
F	149	PHE	-	expression tag	UNP P0ABV6
F	150	GLN	-	expression tag	UNP P0ABV6
F	151	GLY	-	expression tag	UNP P0ABV6
F	152	GLN	-	expression tag	UNP P0ABV6
F	153	PHE	-	expression tag	UNP P0ABV6
F	154	GLY	-	expression tag	UNP P0ABV6
F	155	SER	-	expression tag	UNP P0ABV6
F	156	TRP	-	expression tag	UNP P0ABV6
F	157	SER	-	expression tag	UNP P0ABV6
F	158	HIS	-	expression tag	UNP P0ABV6
F	159	PRO	-	expression tag	UNP P0ABV6
F	160	GLN	-	expression tag	UNP P0ABV6
F	161	PHE	-	expression tag	UNP P0ABV6
F	162	GLU	-	expression tag	UNP P0ABV6
F	163	LYS	-	expression tag	UNP P0ABV6
F	164	GLY	-	expression tag	UNP P0ABV6
F	165	GLY	-	expression tag	UNP P0ABV6
F	166	GLY	-	expression tag	UNP P0ABV6
F	167	SER	-	expression tag	UNP P0ABV6
F	168	GLY	-	expression tag	UNP P0ABV6
F	169	GLY	-	expression tag	UNP P0ABV6
F	170	GLY	-	expression tag	UNP P0ABV6
F	171	SER	-	expression tag	UNP P0ABV6
F	172	GLY	-	expression tag	UNP P0ABV6
F	173	GLY	-	expression tag	UNP P0ABV6
F	174	GLY	-	expression tag	UNP P0ABV6
F	175	SER	-	expression tag	UNP P0ABV6
F	176	TRP	-	expression tag	UNP P0ABV6
F	177	SER	-	expression tag	UNP P0ABV6
F	178	HIS	-	expression tag	UNP P0ABV6
F	179	PRO	-	expression tag	UNP P0ABV6
F	180	GLN	-	expression tag	UNP P0ABV6
F	181	PHE	-	expression tag	UNP P0ABV6
F	182	GLU	-	expression tag	UNP P0ABV6
F	183	LYS	-	expression tag	UNP P0ABV6
F	184	HIS	-	expression tag	UNP P0ABV6
F	185	HIS	-	expression tag	UNP P0ABV6
F	186	HIS	-	expression tag	UNP P0ABV6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	187	HIS	-	expression tag	UNP P0ABV6
F	188	HIS	-	expression tag	UNP P0ABV6
F	189	HIS	-	expression tag	UNP P0ABV6
G	143	LEU	-	expression tag	UNP P0ABV6
G	144	GLU	-	expression tag	UNP P0ABV6
G	145	GLU	-	expression tag	UNP P0ABV6
G	146	ASN	-	expression tag	UNP P0ABV6
G	147	LEU	-	expression tag	UNP P0ABV6
G	148	TYR	-	expression tag	UNP P0ABV6
G	149	PHE	-	expression tag	UNP P0ABV6
G	150	GLN	-	expression tag	UNP P0ABV6
G	151	GLY	-	expression tag	UNP P0ABV6
G	152	GLN	-	expression tag	UNP P0ABV6
G	153	PHE	-	expression tag	UNP P0ABV6
G	154	GLY	-	expression tag	UNP P0ABV6
G	155	SER	-	expression tag	UNP P0ABV6
G	156	TRP	-	expression tag	UNP P0ABV6
G	157	SER	-	expression tag	UNP P0ABV6
G	158	HIS	-	expression tag	UNP P0ABV6
G	159	PRO	-	expression tag	UNP P0ABV6
G	160	GLN	-	expression tag	UNP P0ABV6
G	161	PHE	-	expression tag	UNP P0ABV6
G	162	GLU	-	expression tag	UNP P0ABV6
G	163	LYS	-	expression tag	UNP P0ABV6
G	164	GLY	-	expression tag	UNP P0ABV6
G	165	GLY	-	expression tag	UNP P0ABV6
G	166	GLY	-	expression tag	UNP P0ABV6
G	167	SER	-	expression tag	UNP P0ABV6
G	168	GLY	-	expression tag	UNP P0ABV6
G	169	GLY	-	expression tag	UNP P0ABV6
G	170	GLY	-	expression tag	UNP P0ABV6
G	171	SER	-	expression tag	UNP P0ABV6
G	172	GLY	-	expression tag	UNP P0ABV6
G	173	GLY	-	expression tag	UNP P0ABV6
G	174	GLY	-	expression tag	UNP P0ABV6
G	175	SER	-	expression tag	UNP P0ABV6
G	176	TRP	-	expression tag	UNP P0ABV6
G	177	SER	-	expression tag	UNP P0ABV6
G	178	HIS	-	expression tag	UNP P0ABV6
G	179	PRO	-	expression tag	UNP P0ABV6
G	180	GLN	-	expression tag	UNP P0ABV6
G	181	PHE	-	expression tag	UNP P0ABV6

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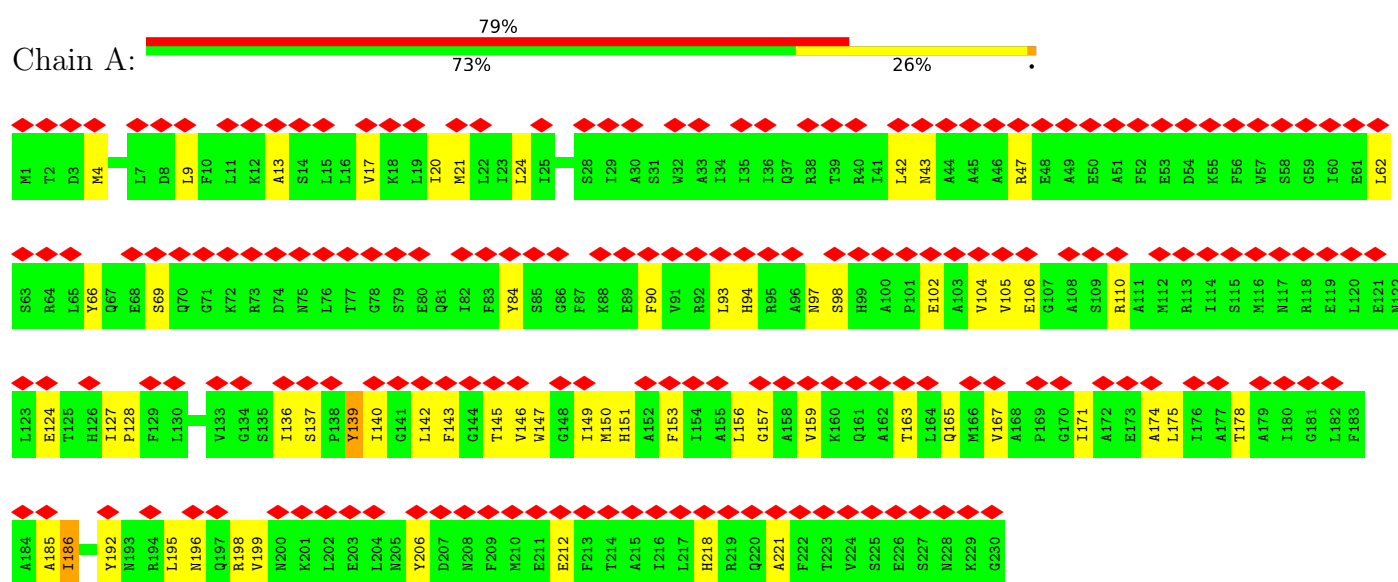
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Chain	Residue	Modelled	Actual	Comment	Reference
G	182	GLU	-	expression tag	UNP P0ABV6
G	183	LYS	-	expression tag	UNP P0ABV6
G	184	HIS	-	expression tag	UNP P0ABV6
G	185	HIS	-	expression tag	UNP P0ABV6
G	186	HIS	-	expression tag	UNP P0ABV6
G	187	HIS	-	expression tag	UNP P0ABV6
G	188	HIS	-	expression tag	UNP P0ABV6
G	189	HIS	-	expression tag	UNP P0ABV6

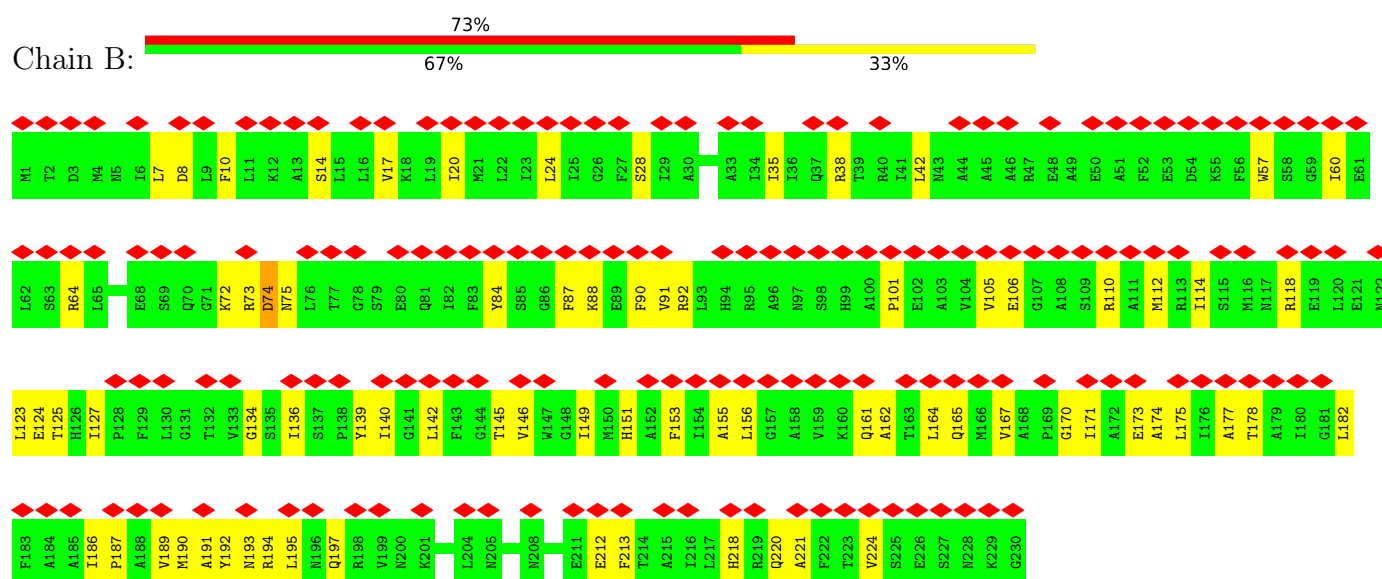
3 Residue-property plots

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.

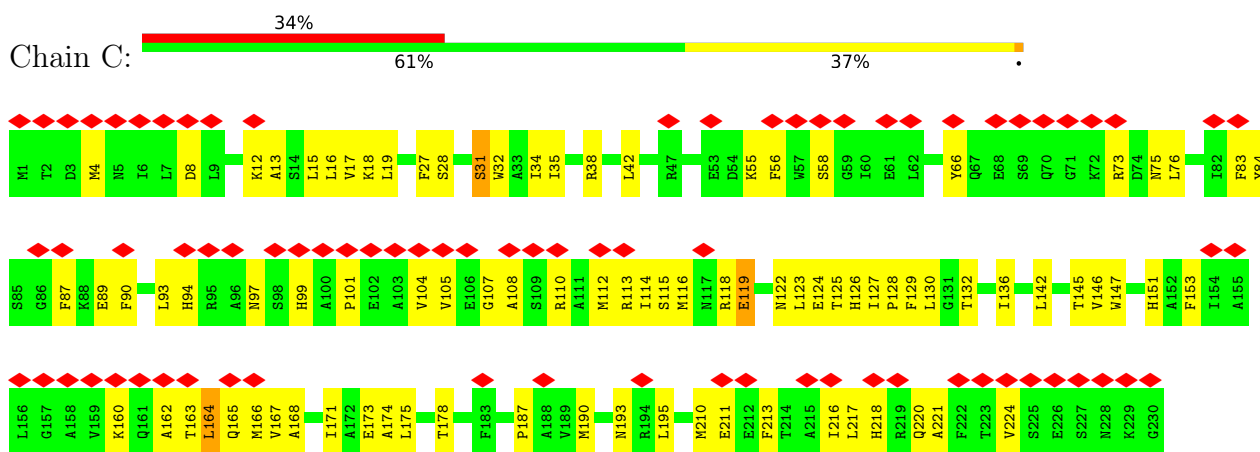
• Molecule 1: Tol-Pal system protein TolQ



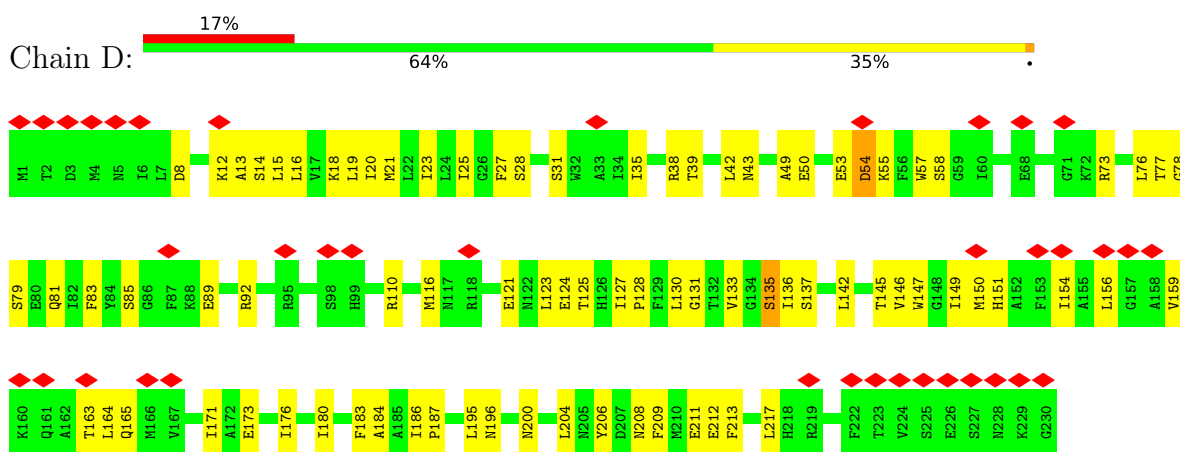
• Molecule 1: Tol-Pal system protein TolQ



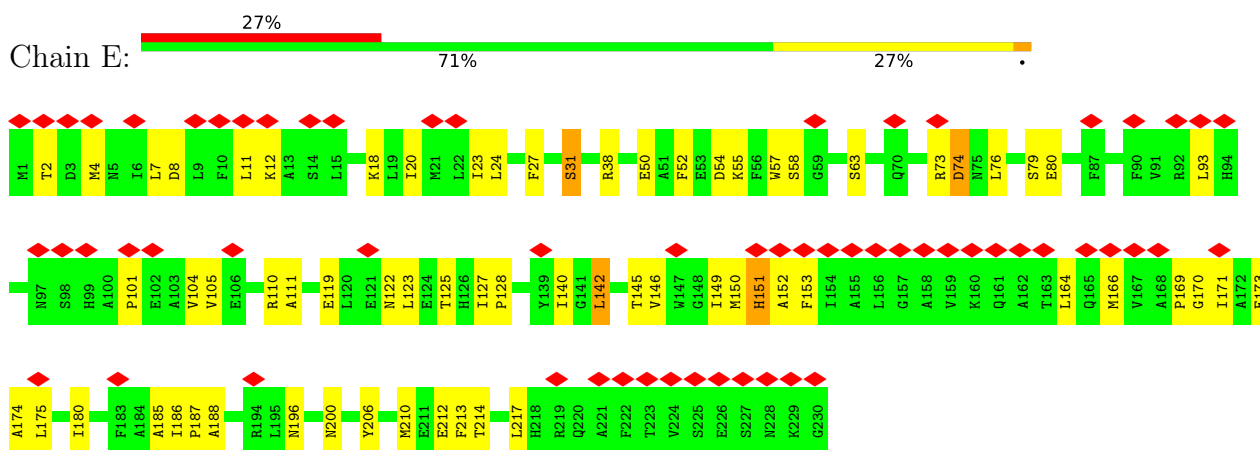
• Molecule 1: Tol-Pal system protein TolQ



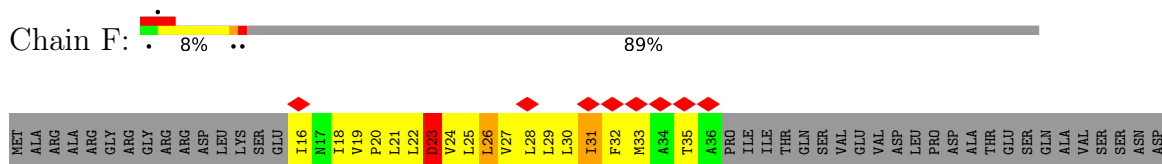
• Molecule 1: Tol-Pal system protein TolQ



• Molecule 1: Tol-Pal system protein TolQ



• Molecule 2: Tol-Pal system protein TolR



PHE
GLU
LYS
HIS
HIS
HIS
HIS
HIS
HIS

Chain G: 7% 6% 91%

PHE
GLU
LYS
HIS
HIS
HIS
HIS
HIS
HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	566486	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.39	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.609	Depositor
Minimum map value	-0.372	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.126	Depositor
Map size ($\text{\AA}$)	249.6, 249.6, 249.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.832, 0.832, 0.832	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	0.20	0/1837	0.39	0/2480
1	B	0.23	0/1837	0.39	0/2480
1	C	0.32	0/1837	0.44	0/2480
1	D	0.36	0/1837	0.46	0/2480
1	E	0.31	0/1837	0.45	0/2480
2	F	0.36	0/161	0.66	0/221
2	G	0.36	0/130	0.62	0/177
All	All	0.29	0/9476	0.43	0/12798

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	1803	1831	1831	58	0
1	B	1803	1831	1831	72	0
1	C	1803	1831	1831	78	0
1	D	1803	1831	1831	59	0
1	E	1803	1831	1831	52	0
2	F	160	189	188	37	0
2	G	129	152	152	40	0
All	All	9304	9496	9495	329	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 18.

The worst 5 of 329 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:B:142:LEU:HD13	2:G:21:LEU:HD11	1.34	1.05
1:D:196:ASN:O	1:D:200:ASN:ND2	2.02	0.92
1:E:55:LYS:O	1:E:58:SER:OG	1.88	0.90
1:B:161:GLN:NE2	1:B:162:ALA:O	2.08	0.86
1:C:55:LYS:O	1:C:58:SER:OG	1.92	0.86

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	228/230 (99%)	222 (97%)	6 (3%)	0	100	100
1	B	228/230 (99%)	223 (98%)	5 (2%)	0	100	100
1	C	228/230 (99%)	223 (98%)	5 (2%)	0	100	100
1	D	228/230 (99%)	222 (97%)	6 (3%)	0	100	100
1	E	228/230 (99%)	221 (97%)	7 (3%)	0	100	100
2	F	19/189 (10%)	16 (84%)	2 (10%)	1 (5%)	1	16
2	G	15/189 (8%)	13 (87%)	2 (13%)	0	100	100
All	All	1174/1528 (77%)	1140 (97%)	33 (3%)	1 (0%)	49	82

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	23	ASP

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	187/187 (100%)	184 (98%)	3 (2%)	55	69
1	B	187/187 (100%)	182 (97%)	5 (3%)	39	60
1	C	187/187 (100%)	180 (96%)	7 (4%)	30	51
1	D	187/187 (100%)	181 (97%)	6 (3%)	34	56
1	E	187/187 (100%)	181 (97%)	6 (3%)	34	56
2	F	19/159 (12%)	16 (84%)	3 (16%)	2	14
2	G	15/159 (9%)	10 (67%)	5 (33%)	0	2
All	All	969/1253 (77%)	934 (96%)	35 (4%)	32	52

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	26	LEU
2	F	31	ILE
2	G	28	LEU
1	C	167	VAL
1	C	164	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	208	ASN
1	D	218	HIS
1	E	200	ASN
1	E	75	ASN
1	B	197	GLN

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.

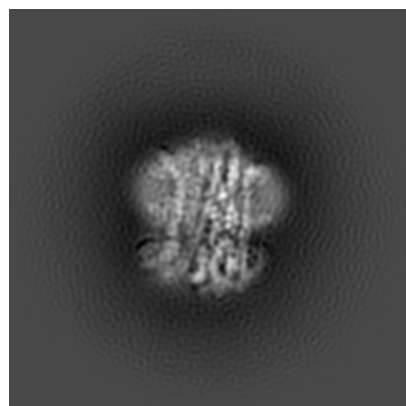
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16816. These allow visual inspection of the internal detail of the map and identification of artifacts.

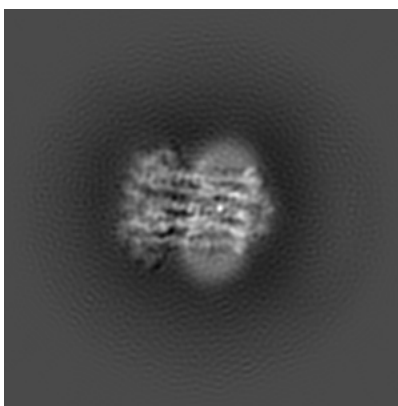
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

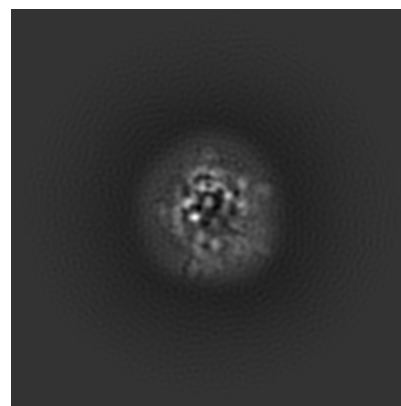
6.1.1 Primary map



X

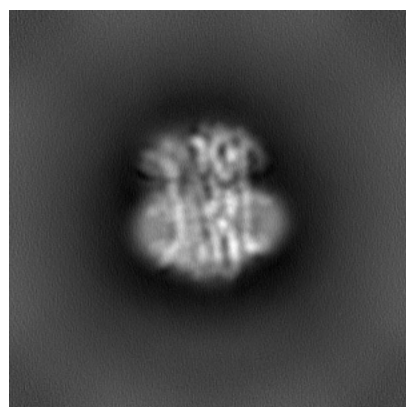


Y

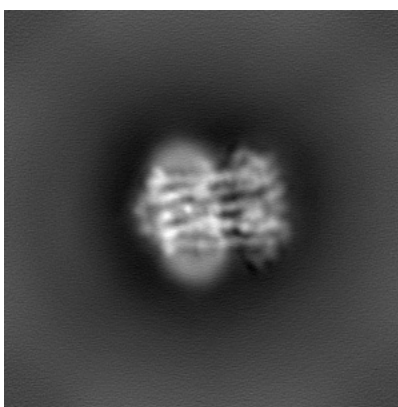


Z

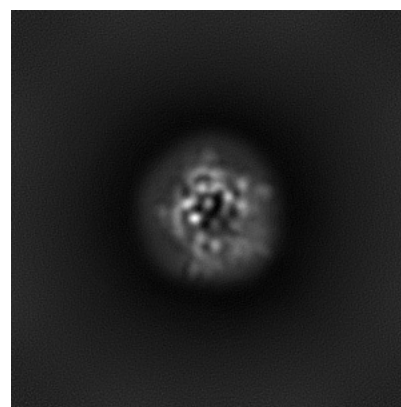
6.1.2 Raw map



X



Y

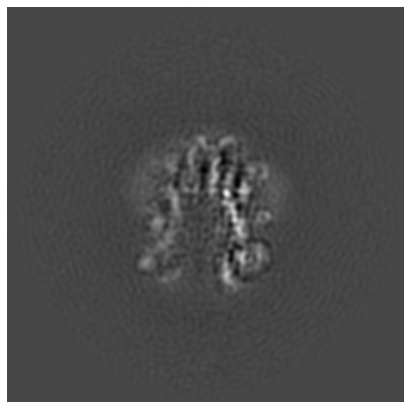


Z

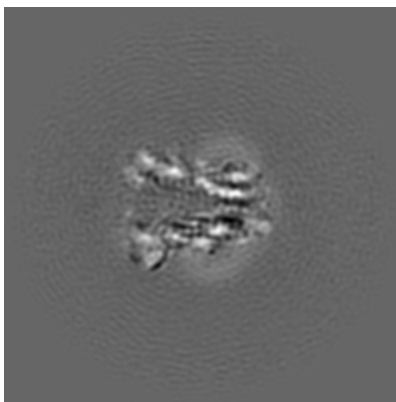
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

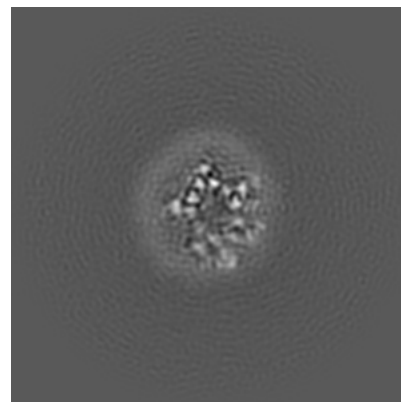
6.2.1 Primary map



X Index: 150

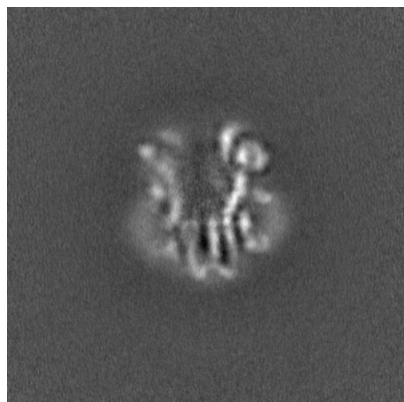


Y Index: 150

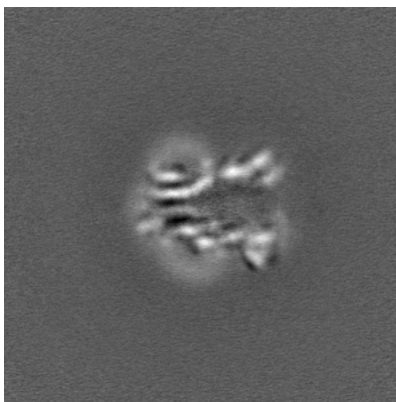


Z Index: 150

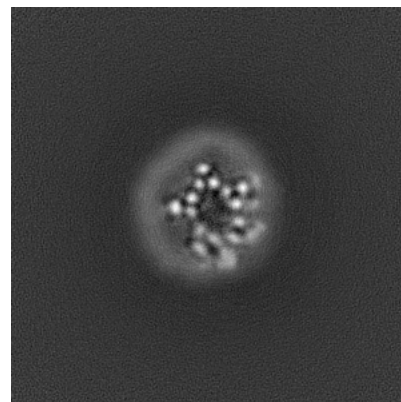
6.2.2 Raw map



X Index: 150



Y Index: 150

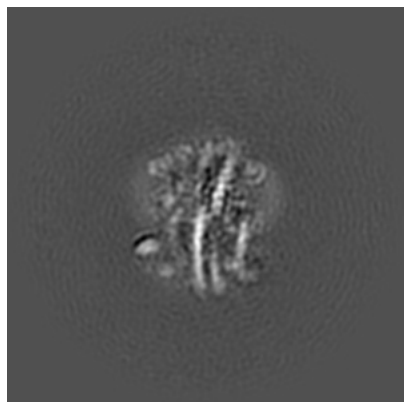


Z Index: 150

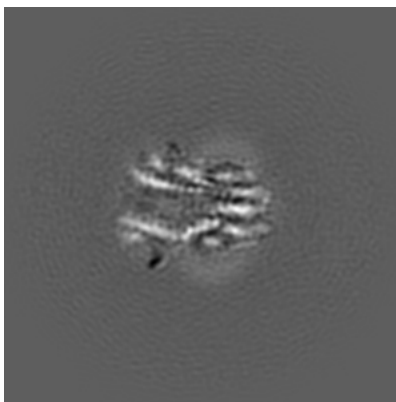
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

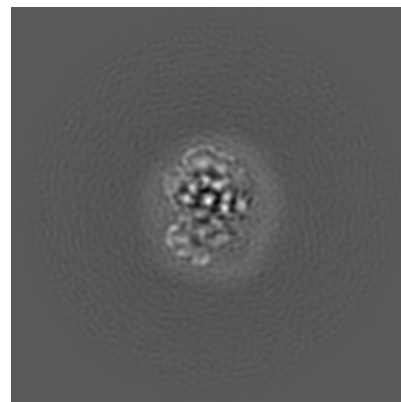
6.3.1 Primary map



X Index: 137

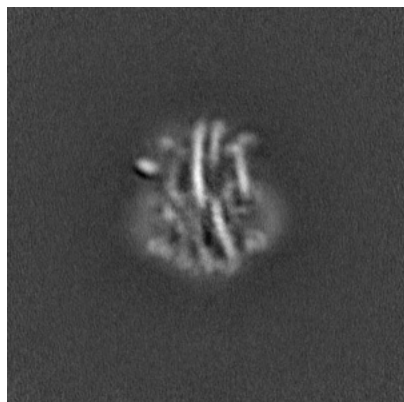


Y Index: 155

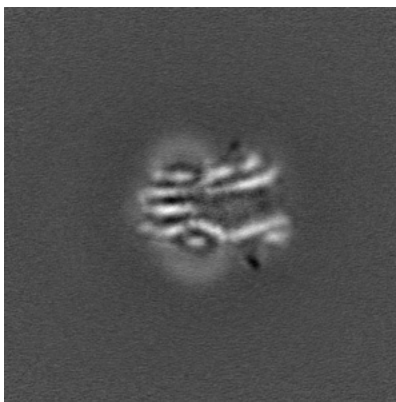


Z Index: 175

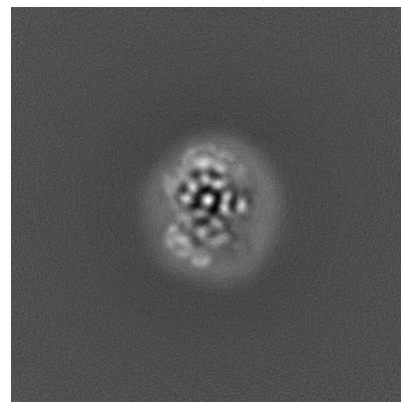
6.3.2 Raw map



X Index: 137



Y Index: 155

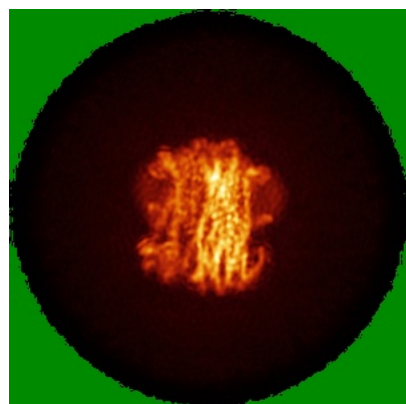


Z Index: 123

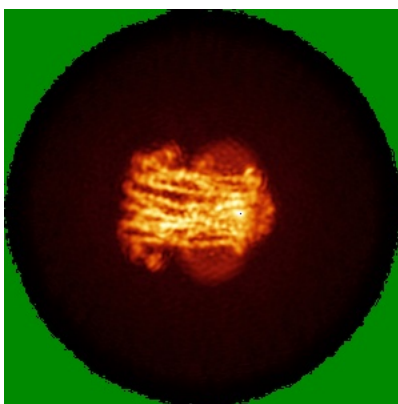
The images above show the largest variance slices of the map in three orthogonal directions.

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

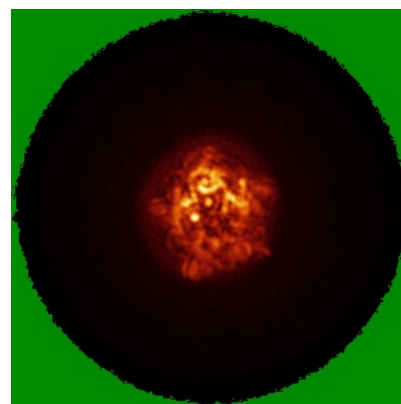
6.4.1 Primary map



X

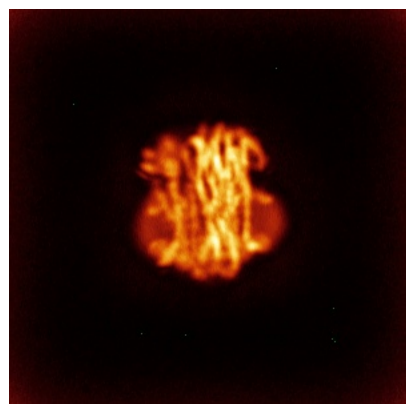


Y

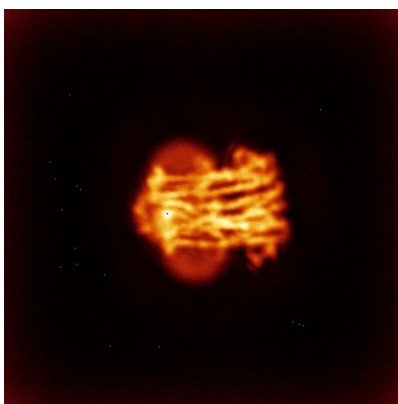


Z

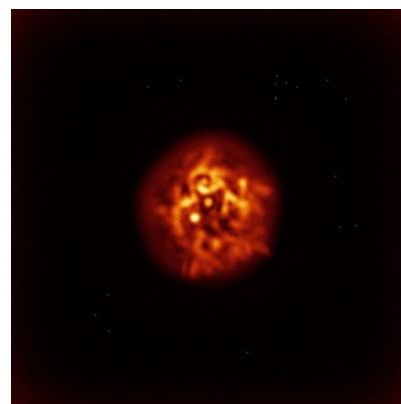
6.4.2 Raw map



X



Y

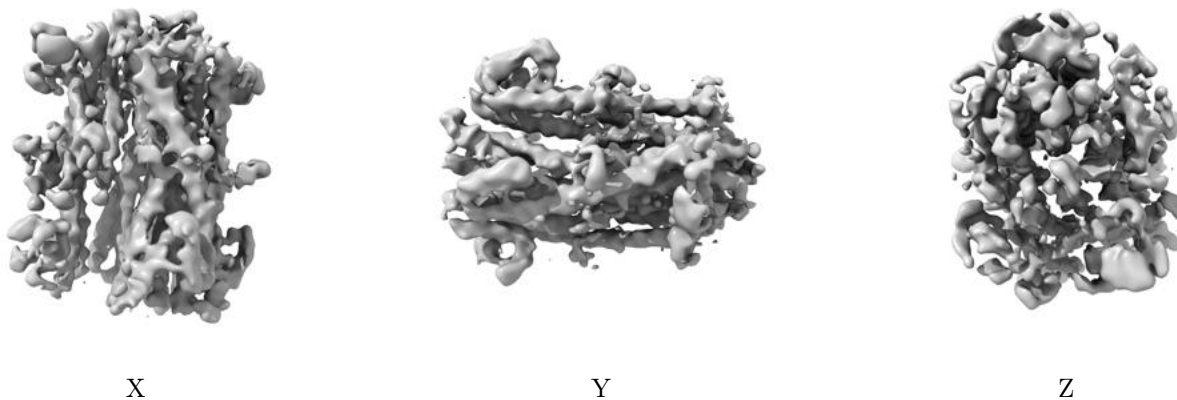


Z

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.

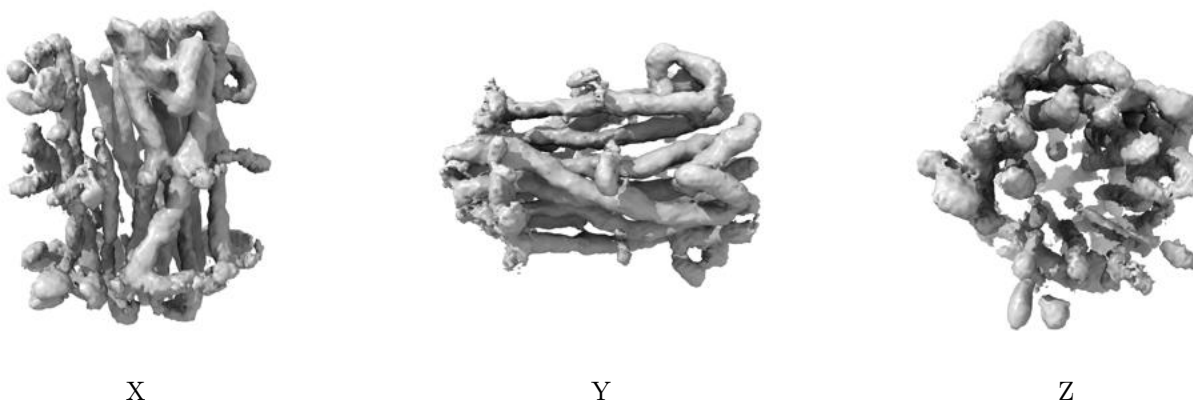
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.126. 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.

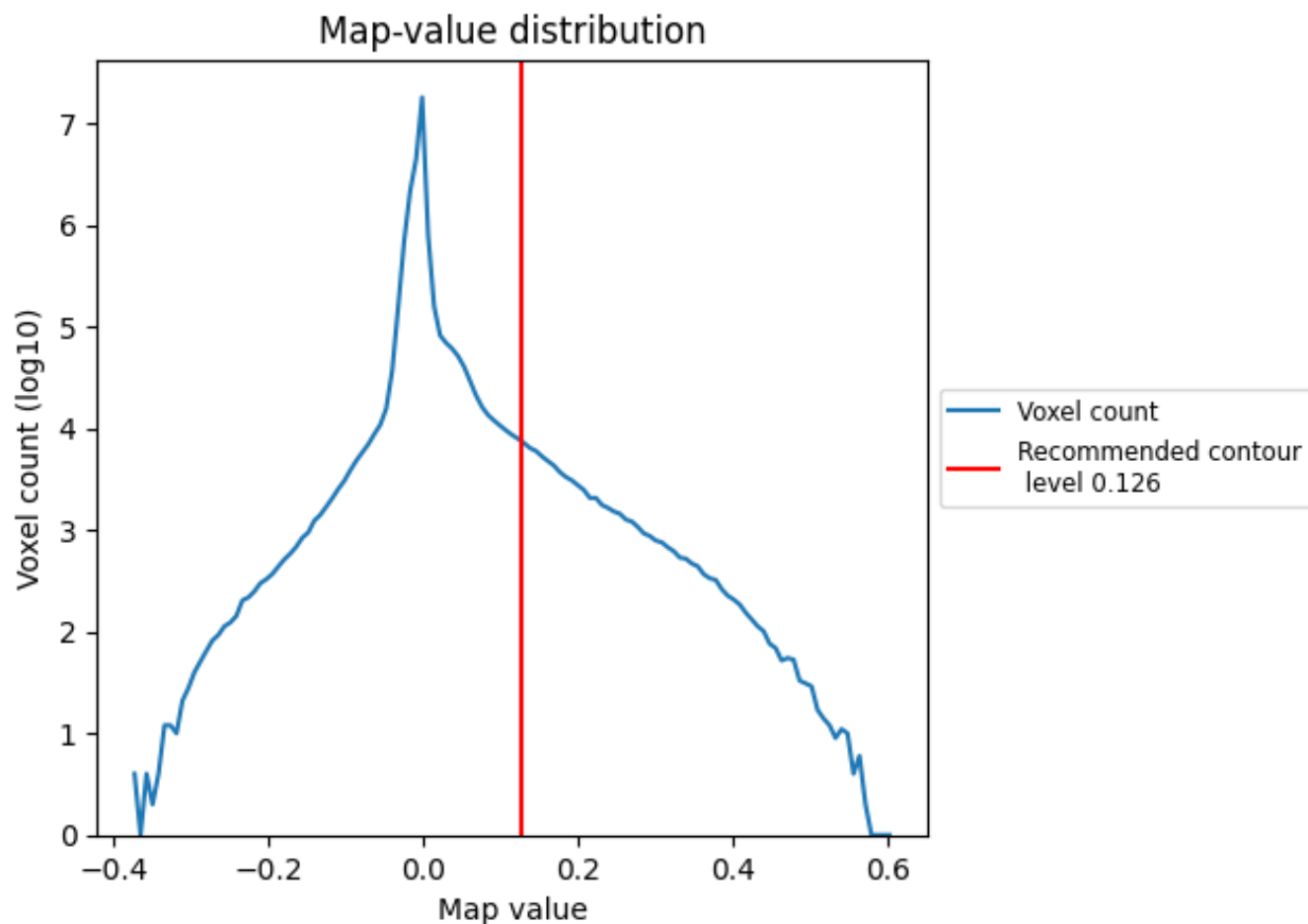
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

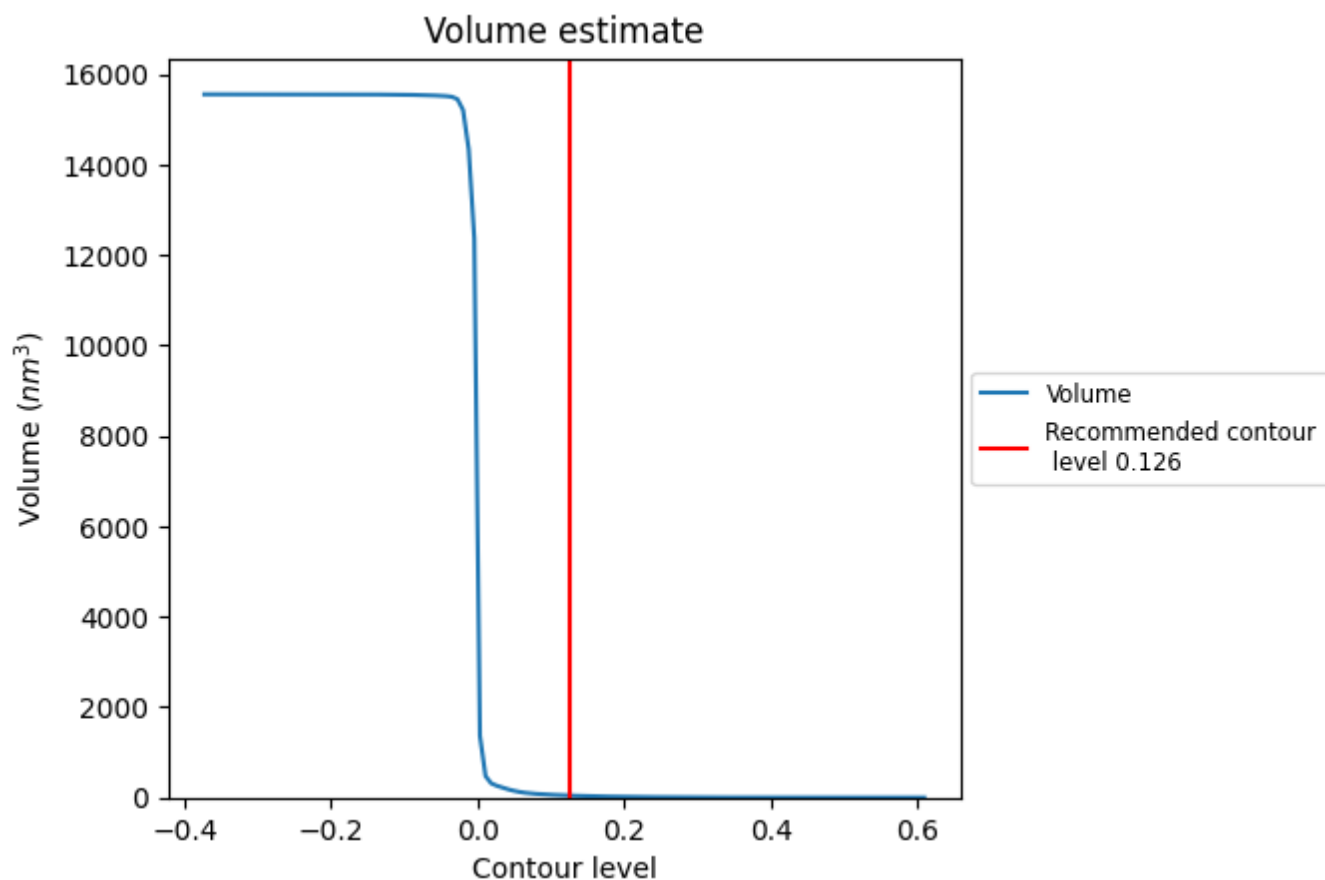
This section contains the results of statistical analysis of the map.

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.

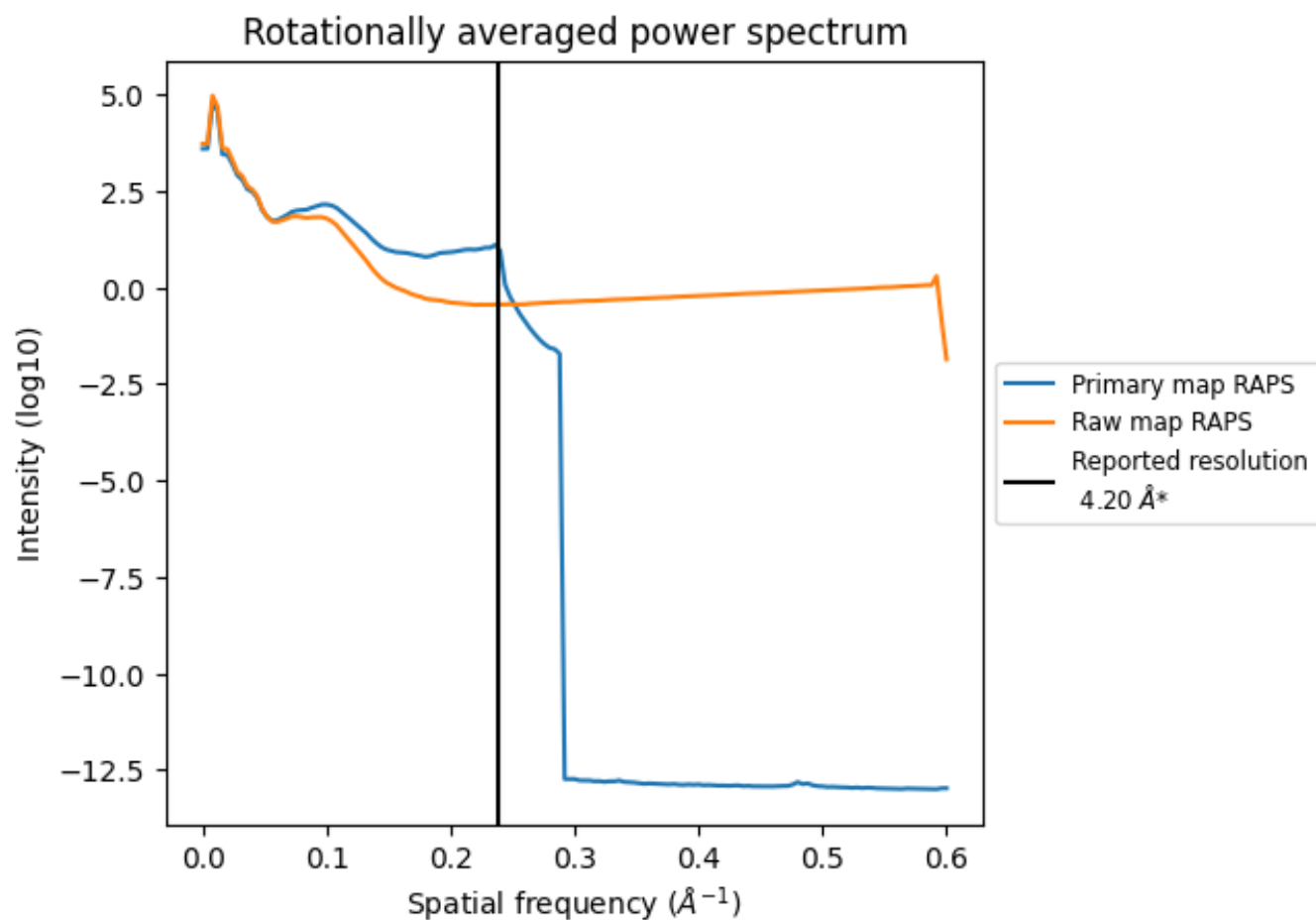
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 44 nm³; this corresponds to an approximate mass of 40 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 ⓘ

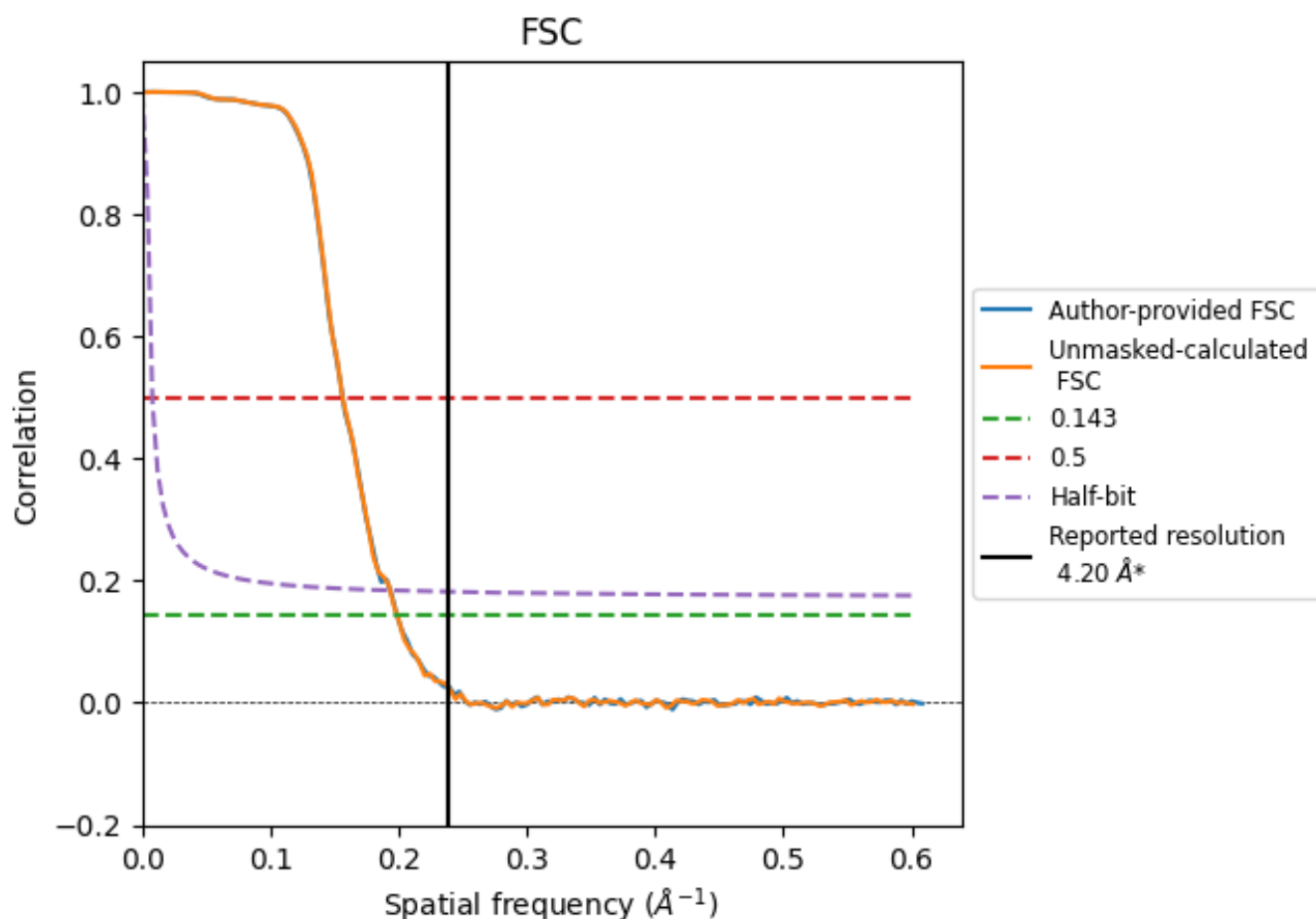


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

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 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	5.03	6.40	5.17
Unmasked-calculated*	5.03	6.40	5.17

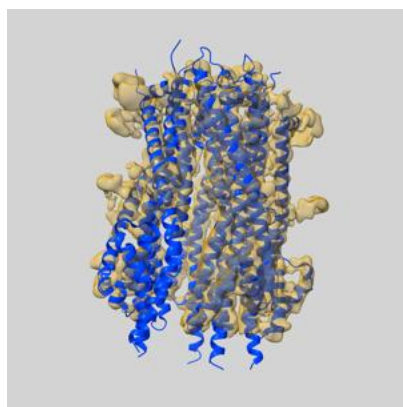
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.03 differs from the reported value 4.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.03 differs from the reported value 4.2 by more than 10 %

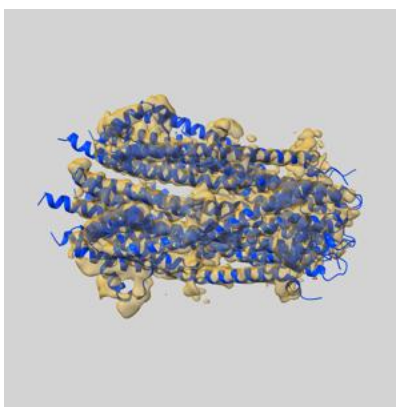
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16816 and PDB model 8ODT. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

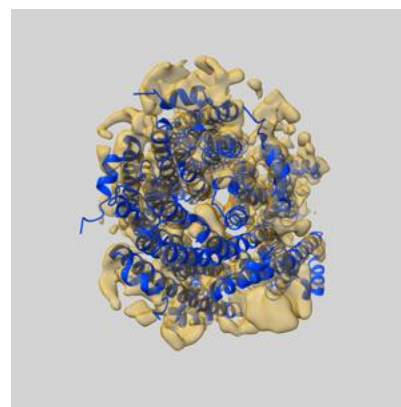
9.1 Map-model overlay [i](#)



X



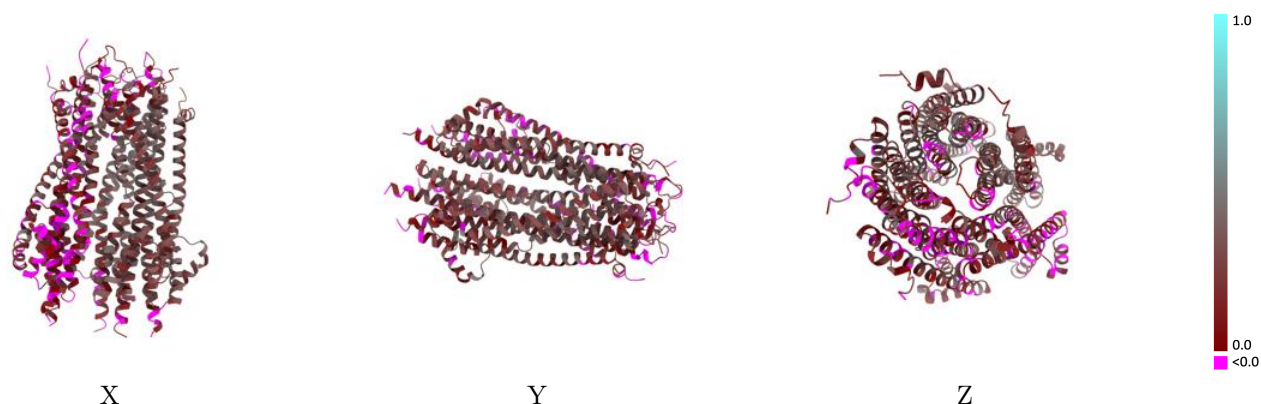
Y



Z

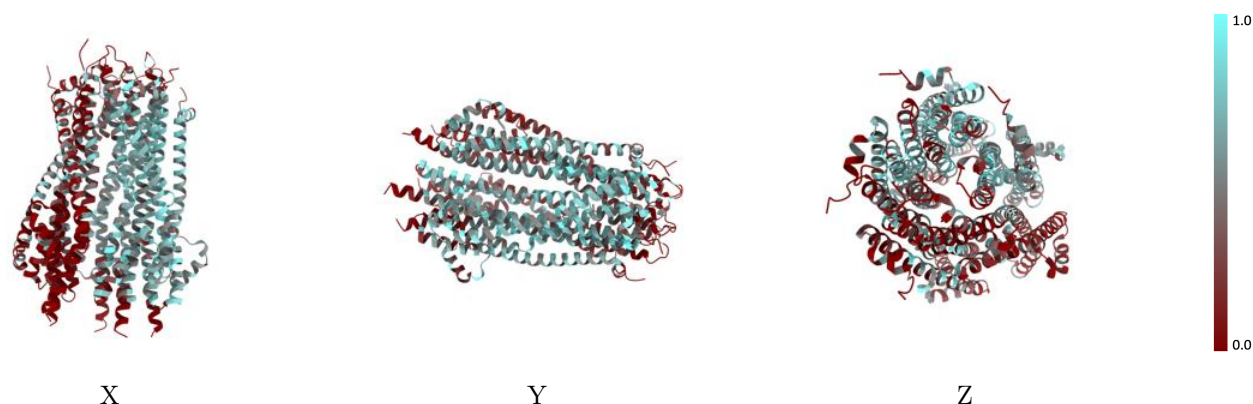
The images above show the 3D surface view of the map at the recommended contour level 0.126 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



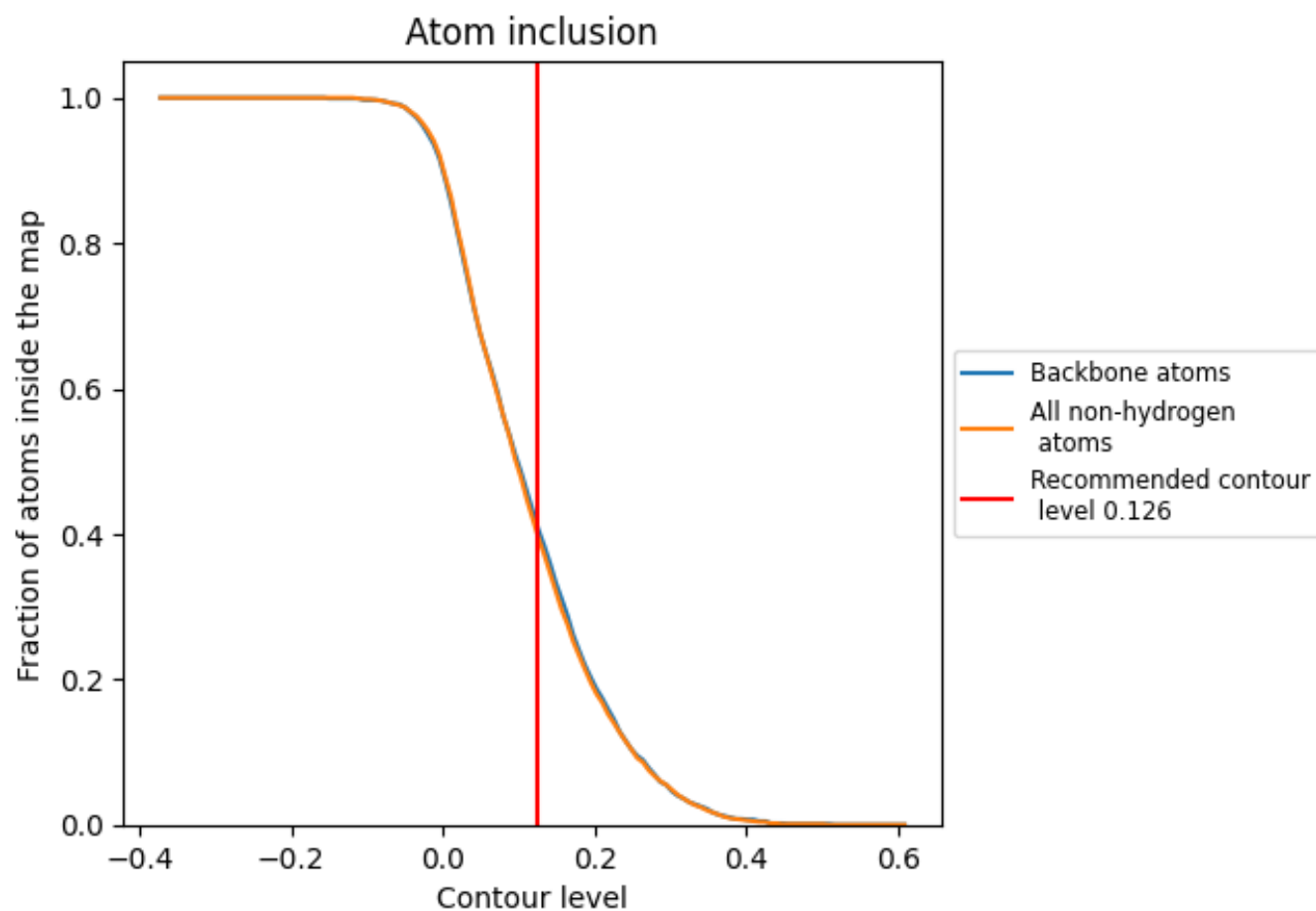
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.126).

9.4 Atom inclusion [i](#)



At the recommended contour level, 41% of all backbone atoms, 40% 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 (0.126) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3950	0.1980
A	0.1900	0.1050
B	0.2410	0.1270
C	0.4780	0.2230
D	0.5850	0.2830
E	0.5260	0.2570
F	0.4750	0.1730
G	0.2950	0.1600

1.0

0.0

<0.0