



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 06:37 PM UTC

PDB ID : 8RLM / pdb_00008rlm
EMDB ID : EMD-19341
Title : TRIF Oligomerisation
Authors : Moncrieffe, M.C.; Verstak, B.; Whitely, L.; Symmoms, M.F.; Soares, S.G.;
Egelman, E.H.; Klenerman, D.; Bryant, C.E.; Gay, N.J.
Deposited on : 2024-01-03
Resolution : 3.50 Å(reported)
Based on initial model : ?

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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

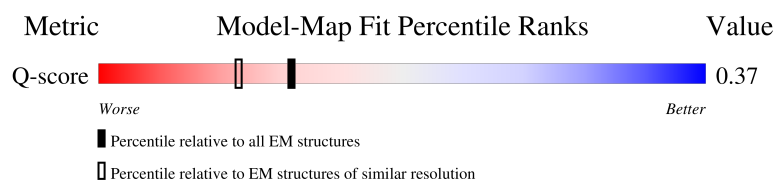
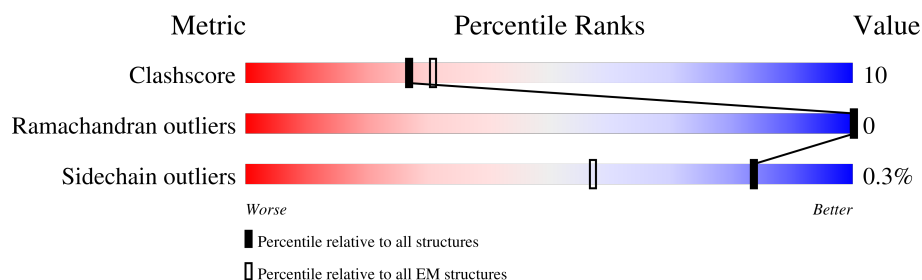
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	721	 6% 17% 17% 5% 55% 78%
1	B	721	 5% 17% 17% 5% 55% 78%
1	C	721	 5% 17% 17% 5% 55% 78%
1	D	721	 5% 17% 17% 5% 55% 78%

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Mol	Chain	Length	Quality of chain
1	E	721	
1	F	721	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14670 atoms, of which 7236 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 TIR domain-containing adapter molecule 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0
1	B	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0
1	C	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0
1	D	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0
1	E	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0
1	F	157	Total 2445	C 777	H 1206	N 229	O 226	S 7	0	0

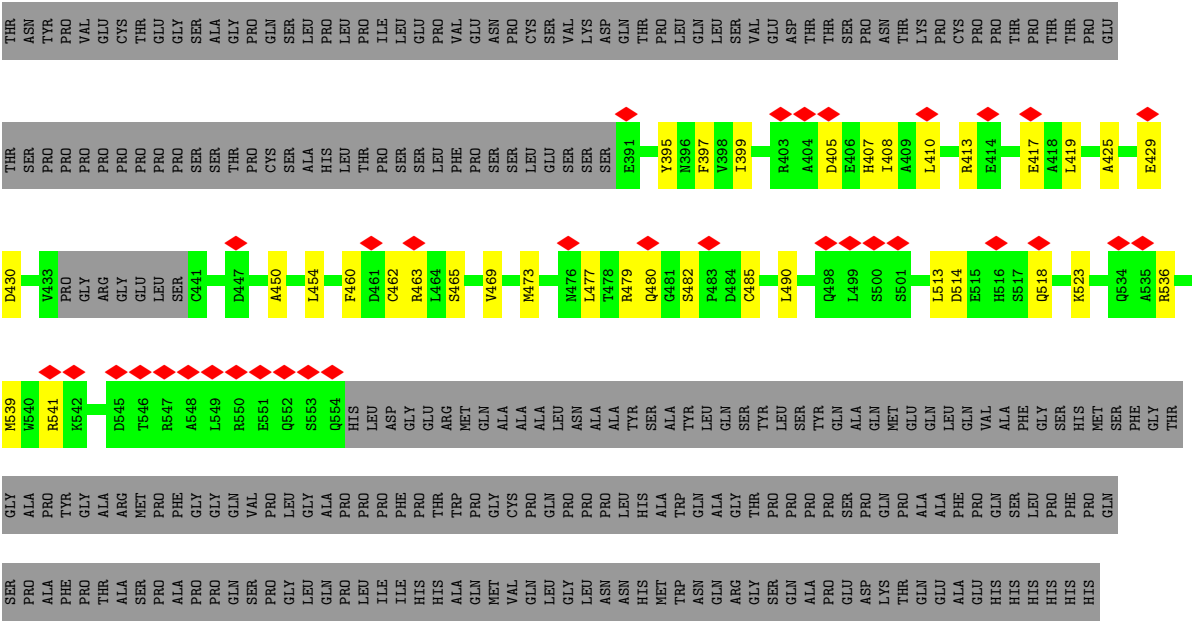
There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q8IUC6
A	-1	ASN	-	expression tag	UNP Q8IUC6
A	0	ALA	-	expression tag	UNP Q8IUC6
A	323	GLU	LYS	conflict	UNP Q8IUC6
A	713	HIS	-	expression tag	UNP Q8IUC6
A	714	HIS	-	expression tag	UNP Q8IUC6
A	715	HIS	-	expression tag	UNP Q8IUC6
A	716	HIS	-	expression tag	UNP Q8IUC6
A	717	HIS	-	expression tag	UNP Q8IUC6
A	718	HIS	-	expression tag	UNP Q8IUC6
B	-2	SER	-	expression tag	UNP Q8IUC6
B	-1	ASN	-	expression tag	UNP Q8IUC6
B	0	ALA	-	expression tag	UNP Q8IUC6
B	323	GLU	LYS	conflict	UNP Q8IUC6
B	713	HIS	-	expression tag	UNP Q8IUC6
B	714	HIS	-	expression tag	UNP Q8IUC6
B	715	HIS	-	expression tag	UNP Q8IUC6
B	716	HIS	-	expression tag	UNP Q8IUC6

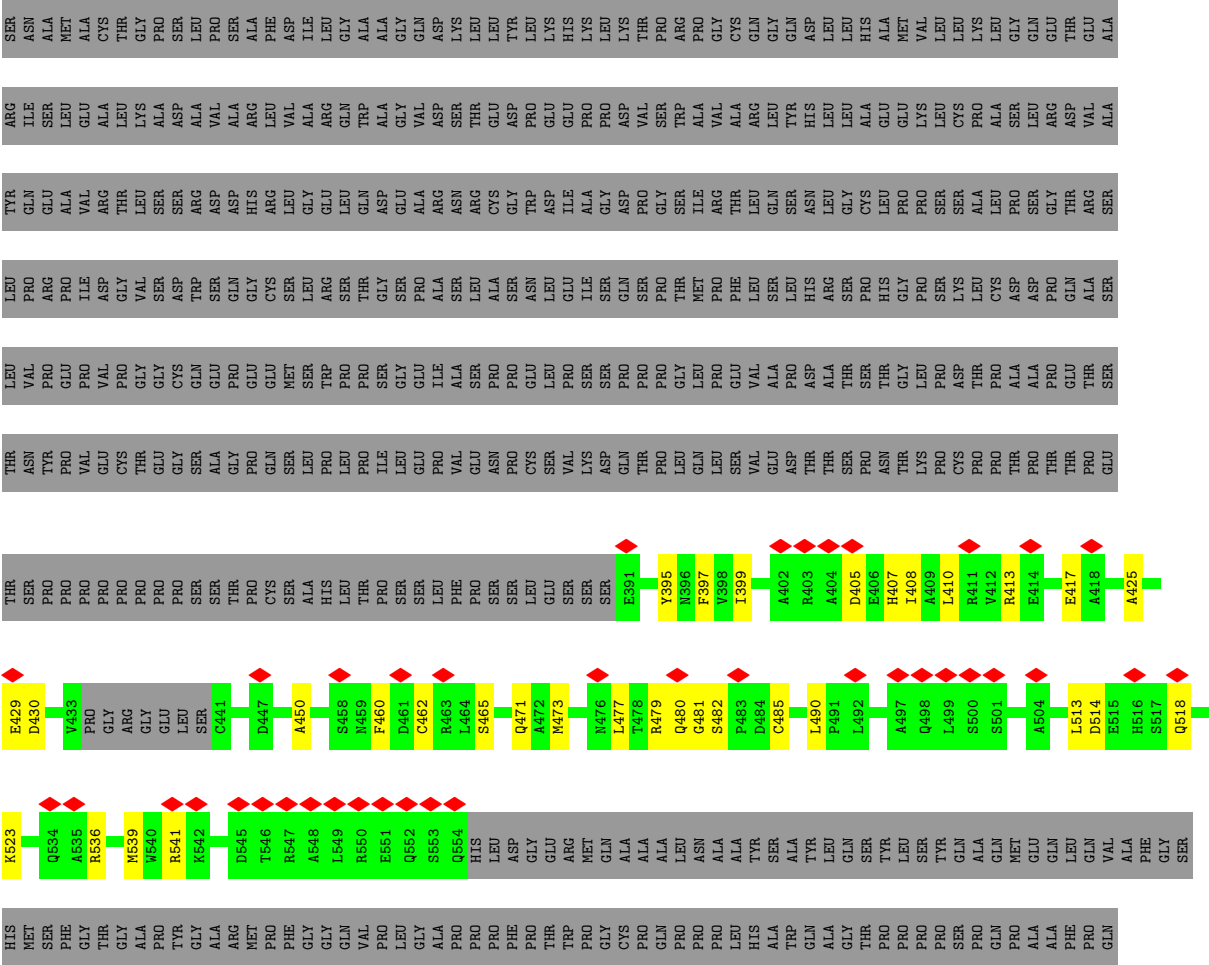
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Chain	Residue	Modelled	Actual	Comment	Reference
B	717	HIS	-	expression tag	UNP Q8IUC6
B	718	HIS	-	expression tag	UNP Q8IUC6
C	-2	SER	-	expression tag	UNP Q8IUC6
C	-1	ASN	-	expression tag	UNP Q8IUC6
C	0	ALA	-	expression tag	UNP Q8IUC6
C	323	GLU	LYS	conflict	UNP Q8IUC6
C	713	HIS	-	expression tag	UNP Q8IUC6
C	714	HIS	-	expression tag	UNP Q8IUC6
C	715	HIS	-	expression tag	UNP Q8IUC6
C	716	HIS	-	expression tag	UNP Q8IUC6
C	717	HIS	-	expression tag	UNP Q8IUC6
C	718	HIS	-	expression tag	UNP Q8IUC6
D	-2	SER	-	expression tag	UNP Q8IUC6
D	-1	ASN	-	expression tag	UNP Q8IUC6
D	0	ALA	-	expression tag	UNP Q8IUC6
D	323	GLU	LYS	conflict	UNP Q8IUC6
D	713	HIS	-	expression tag	UNP Q8IUC6
D	714	HIS	-	expression tag	UNP Q8IUC6
D	715	HIS	-	expression tag	UNP Q8IUC6
D	716	HIS	-	expression tag	UNP Q8IUC6
D	717	HIS	-	expression tag	UNP Q8IUC6
D	718	HIS	-	expression tag	UNP Q8IUC6
E	-2	SER	-	expression tag	UNP Q8IUC6
E	-1	ASN	-	expression tag	UNP Q8IUC6
E	0	ALA	-	expression tag	UNP Q8IUC6
E	323	GLU	LYS	conflict	UNP Q8IUC6
E	713	HIS	-	expression tag	UNP Q8IUC6
E	714	HIS	-	expression tag	UNP Q8IUC6
E	715	HIS	-	expression tag	UNP Q8IUC6
E	716	HIS	-	expression tag	UNP Q8IUC6
E	717	HIS	-	expression tag	UNP Q8IUC6
E	718	HIS	-	expression tag	UNP Q8IUC6
F	-2	SER	-	expression tag	UNP Q8IUC6
F	-1	ASN	-	expression tag	UNP Q8IUC6
F	0	ALA	-	expression tag	UNP Q8IUC6
F	323	GLU	LYS	conflict	UNP Q8IUC6
F	713	HIS	-	expression tag	UNP Q8IUC6
F	714	HIS	-	expression tag	UNP Q8IUC6
F	715	HIS	-	expression tag	UNP Q8IUC6
F	716	HIS	-	expression tag	UNP Q8IUC6
F	717	HIS	-	expression tag	UNP Q8IUC6
F	718	HIS	-	expression tag	UNP Q8IUC6



• Molecule 1: TIR domain-containing adapter molecule 1



- Molecule 1: TIR domain-containing adapter molecule 1



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

Tyr	Gln	Glu	Ala	Val	Arg	Thr	Leu	Ser	Ser	Arg	Asp	Asp	His	Arg	Gly	Gly	Leu	Glu	Gln	Asp	Glu	Ala	Arg	Asn	Arg	Cys	Gly	Trp	Asp	Leu	Ala	Gly	Asp	Pro	Gly	Ser	Ser	Arg	Arg	Thr	Leu	Gln	Ser	Asn	Leu	Gly	Cys	Pro	Pro	Leu	Ala	Leu	Ser	Ser	Gly	Thr	Arg	Ser
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LEU PRO ARG ARG ARG ILE ASP GLY VAL SER ASP TRP SER THR GLN GLY CYS SER LEU LEU ARG SER SER THR GLY GLY PRO PRO ALA ALA SER SER LEU LEU GLJ TLE SER SER GLN SER PRO SER THR MET MET PRO PHE SER LEU LEU SER LEU LEU HIS ARG ARG PRO PRO GLY HIS GLY PRO SER LYS LEU CYS ASP ASP PRO PRO GLN ALA FER

LEU	VAL	PRO	PRO	GLU	PRO	VAL	PRO	GLY	GLY	CYS	GLN	GLU	PRO	GLU	GLU	GLU	GLU	ILE	ALA	ALA	PRO	PRO	PRO	PRO	TRP	PRO	PRO	SER	SER	GLY	GLY	GLU	LEU	PRO	PRO	SER	SER	PRO	PRO	PRO	PRO	GLY	LEU	PRO	PRO	GLU	GLU	VAL	ALA	ALA	PRO	ASP	ALA	ALA	THR	THR	SER	SER	THR	THR	GLY	PRO	PRO	LEU	PRO	ASP	THR	THR	PRO	PRO	ALA	ALA	ALA	PRO	PRO	GLU	GLU	THR	THR	SER
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THR	ASN	TYR	PRO	VAL	GLU	CYS	THR	GLY	SER	ALA	GLY	PRO	GLN	SER	LEU	LEU	PRO	PRO	ILE	LEU	GLU	PRO	VAL	GLU	ASN	PRO	CYS	SER	VAL	LYS	ASP	GLN	THR	PRO	LEU	LEU	LEU	SER	SER	ASN	THR	PRO	CYS	PRO	PRO	THR	THR	THR	PRO	GLU
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Label	Value
THR	0.00
SER	0.00
PRO	0.00
PRO	0.00
PRO	0.00
PRO	0.00
PRO	0.00
PRO	0.00
SER	0.00
SER	0.00
THR	0.00
CYS	0.00
ALA	0.00
HTS	0.00
LEU	0.00
THR	0.00
PRO	0.00
SER	0.00
SER	0.00
LEU	0.00
PHI	0.00
PRO	0.00
SER	0.00
SER	0.00
LEU	0.00
GLU	0.00
SER	0.00
SER	0.00
SER	0.00
E391	0.00
Y396	0.00
N396	0.00
F397	0.00
V398	0.00
I399	0.00
R403	0.00
A404	0.00
D405	0.00
E406	0.00
H407	0.00
I408	0.00
A409	0.00
L410	0.00
R413	0.00
E414	0.00
E417	0.00
A425	0.00
E429	0.00
D430	0.00
F431	0.00

Figure 1: Schematic representation of the 120 amino acid residues of the protein. The sequence is shown as a horizontal bar with residues grouped into blocks. Residues are color-coded: yellow for Q432, V433, P434, G435, ARG, GLY, GLU, LEU, SER, C441, A450, L454, N459, F460, D461, C462, L463, S465, V469, N470, Q471, A472, M473, N476, L477, T478, R479, Q480, G481, S482, P483, D484, C485, L490, A497, Q498, L499, S500, S501, L513, D514, E515, H516, S517, Q518, K523, and Q534. Red diamonds above the bar indicate specific residues: D447, N459, D461, N476, G481, P483, D484, A497, E515, H516, S517, Q518, and Q534.

Amino acid sequence:

D545
T546
R547
A548
L549
R550
E551
Q552
S553
Q554

HIS
LEU
ASP
GLY
GLU
ARG
MET
GLN
ALA
ALA
ALA
ASN
LEU
ALA
ALA
TYR
SER
SER
TYR
TYR
LEU
GLN
SER
TYR
LEU
SER
SER
TYR
GLN
ALA
GLN
MET
MET
GLU
GLN
GLN
VAL
PHE
GLY
SER
HIS

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

- Molecule 1: TIR domain-containing adapter molecule 1



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



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=178.3°, rise=16.1 Å, axial sym=C1	Depositor
Number of segments used	500264	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	1.15	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.989	Depositor
Minimum map value	-0.548	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	230.256, 230.256, 230.256	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.066, 1.066, 1.066	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	0.11	0/1261	0.29	0/1702
1	B	0.12	0/1261	0.29	0/1702
1	C	0.11	0/1261	0.29	0/1702
1	D	0.11	0/1261	0.29	0/1702
1	E	0.11	0/1261	0.29	0/1702
1	F	0.11	0/1261	0.29	0/1702
All	All	0.11	0/7566	0.29	0/10212

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	1239	1206	1212	24	0
1	B	1239	1206	1212	27	0
1	C	1239	1206	1212	28	0
1	D	1239	1206	1212	26	0
1	E	1239	1206	1212	28	0
1	F	1239	1206	1212	24	0
All	All	7434	7236	7272	145	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 10.

The worst 5 of 145 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:E:523:LYS:NZ	1:F:432:GLN:O	1.96	0.99
1:C:463:ARG:NH2	1:D:479:ARG:O	2.05	0.90
1:C:479:ARG:O	1:E:463:ARG:NH2	2.09	0.85
1:F:462:CYS:O	1:F:465:SER:OG	2.04	0.77
1:E:462:CYS:O	1:E:465:SER:OG	2.03	0.76

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	153/721 (21%)	147 (96%)	6 (4%)	0	100	100
1	B	153/721 (21%)	147 (96%)	6 (4%)	0	100	100
1	C	153/721 (21%)	147 (96%)	6 (4%)	0	100	100
1	D	153/721 (21%)	148 (97%)	5 (3%)	0	100	100
1	E	153/721 (21%)	147 (96%)	6 (4%)	0	100	100
1	F	153/721 (21%)	147 (96%)	6 (4%)	0	100	100
All	All	918/4326 (21%)	883 (96%)	35 (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	A	131/610 (22%)	130 (99%)	1 (1%)	73	77
1	B	131/610 (22%)	131 (100%)	0	100	100
1	C	131/610 (22%)	130 (99%)	1 (1%)	73	77
1	D	131/610 (22%)	131 (100%)	0	100	100
1	E	131/610 (22%)	131 (100%)	0	100	100
1	F	131/610 (22%)	131 (100%)	0	100	100
All	All	786/3660 (22%)	784 (100%)	2 (0%)	84	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	419	LEU
1	C	419	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	448	HIS
1	F	476	ASN
1	F	498	GLN
1	F	448	HIS
1	C	498	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

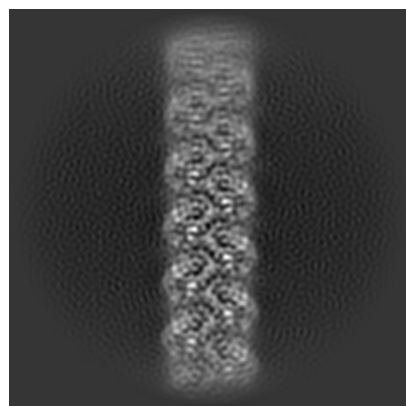
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19341. These allow visual inspection of the internal detail of the map and identification of artifacts.

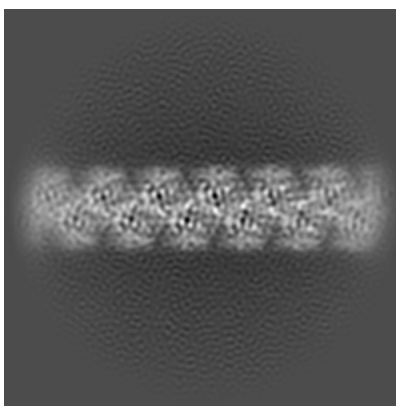
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

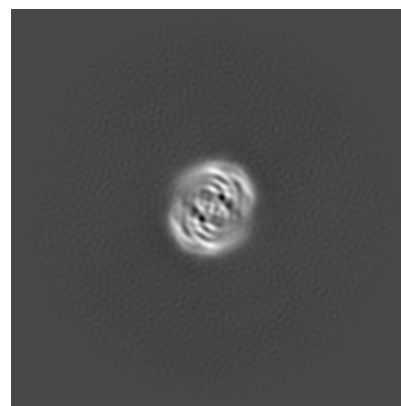
6.1.1 Primary map



X

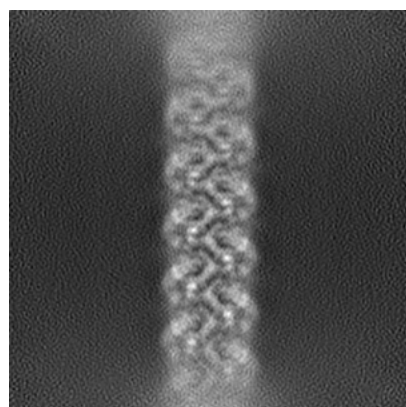


Y

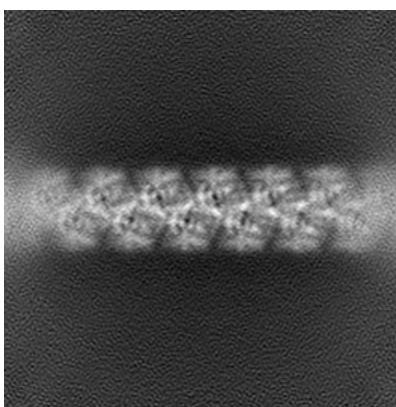


Z

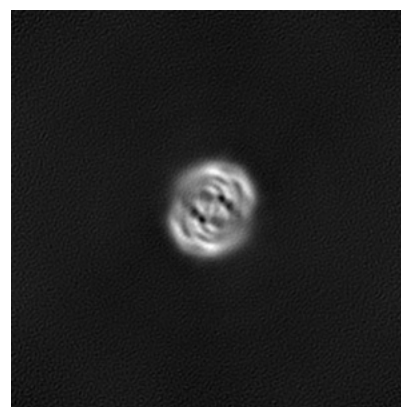
6.1.2 Raw map



X



Y

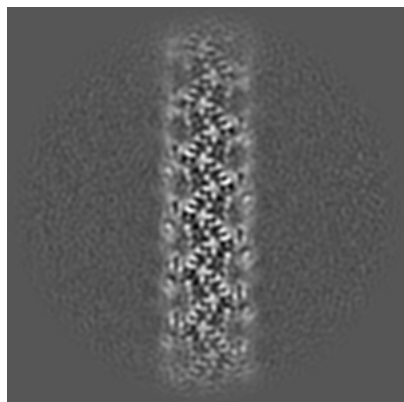


Z

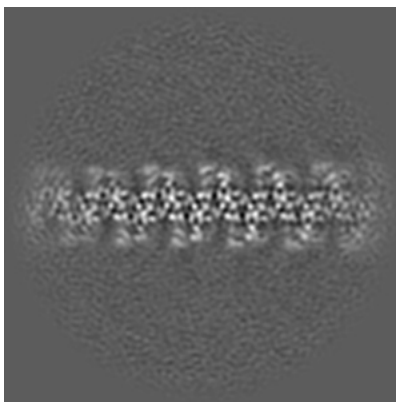
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

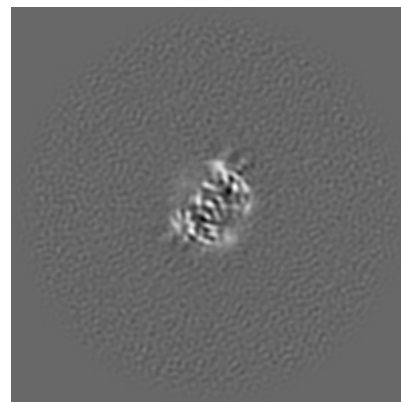
6.2.1 Primary map



X Index: 108

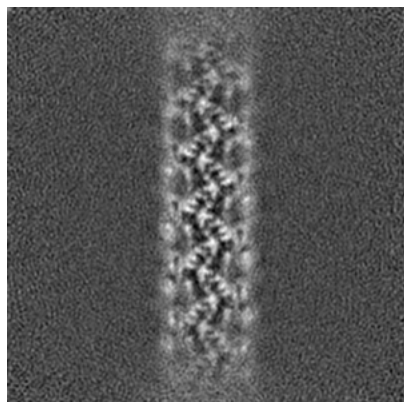


Y Index: 108

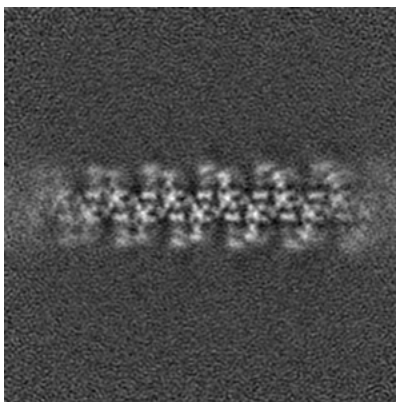


Z Index: 108

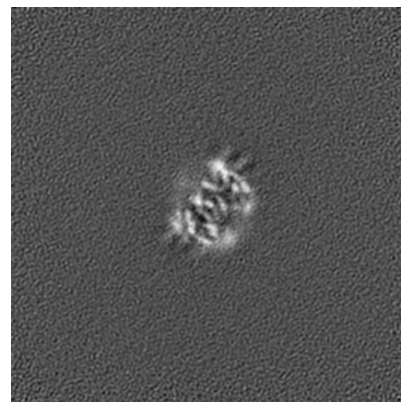
6.2.2 Raw map



X Index: 108



Y Index: 108

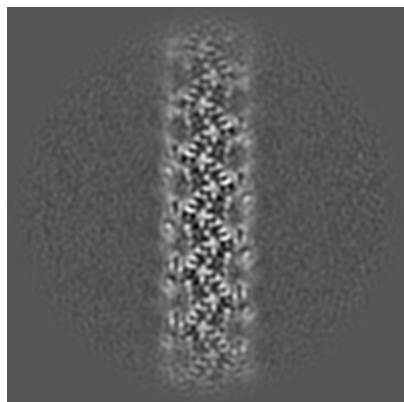


Z Index: 108

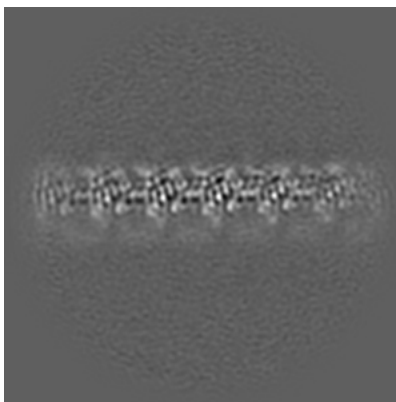
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

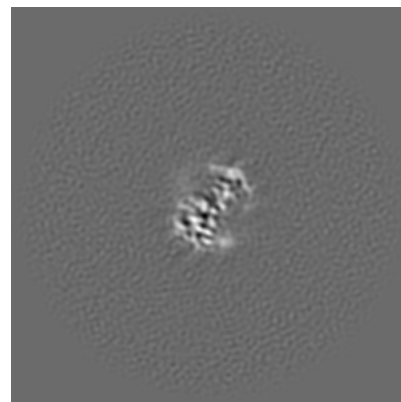
6.3.1 Primary map



X Index: 108

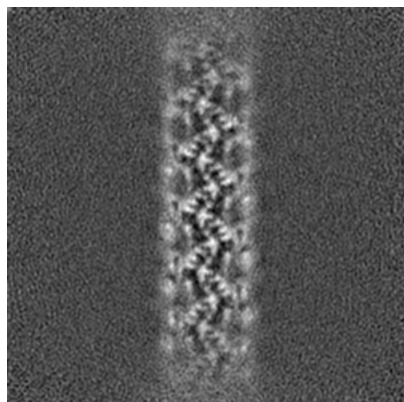


Y Index: 119

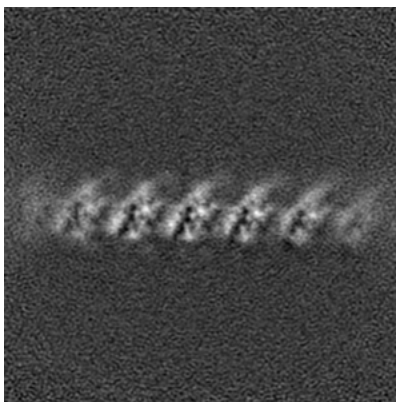


Z Index: 105

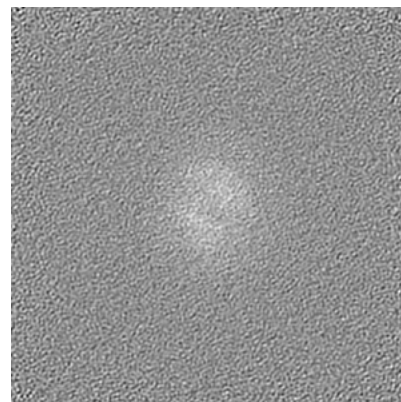
6.3.2 Raw map



X Index: 108



Y Index: 89

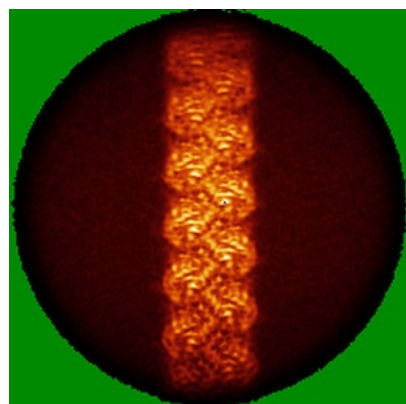


Z Index: 0

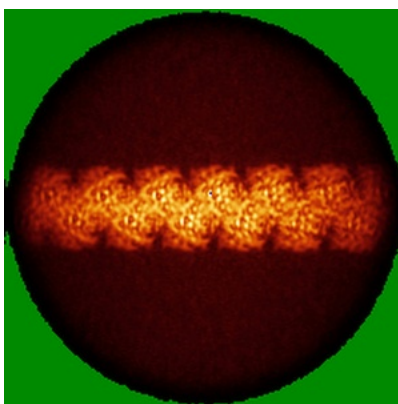
The images above show the largest variance slices of the map in three orthogonal directions.

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

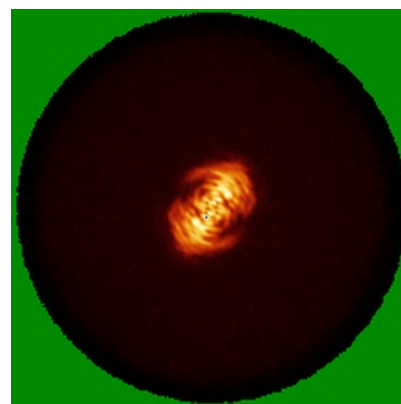
6.4.1 Primary map



X

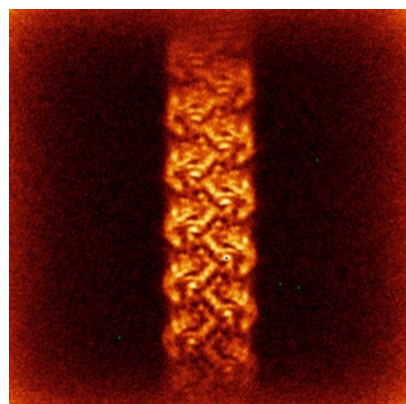


Y

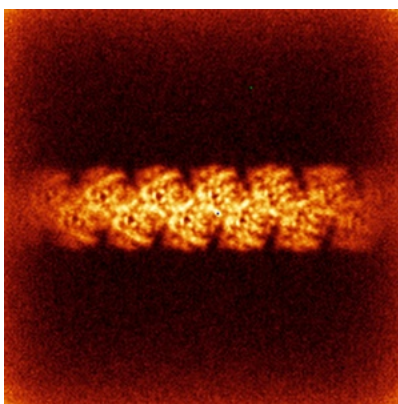


Z

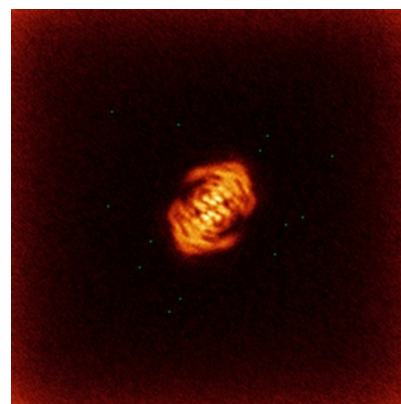
6.4.2 Raw map



X



Y

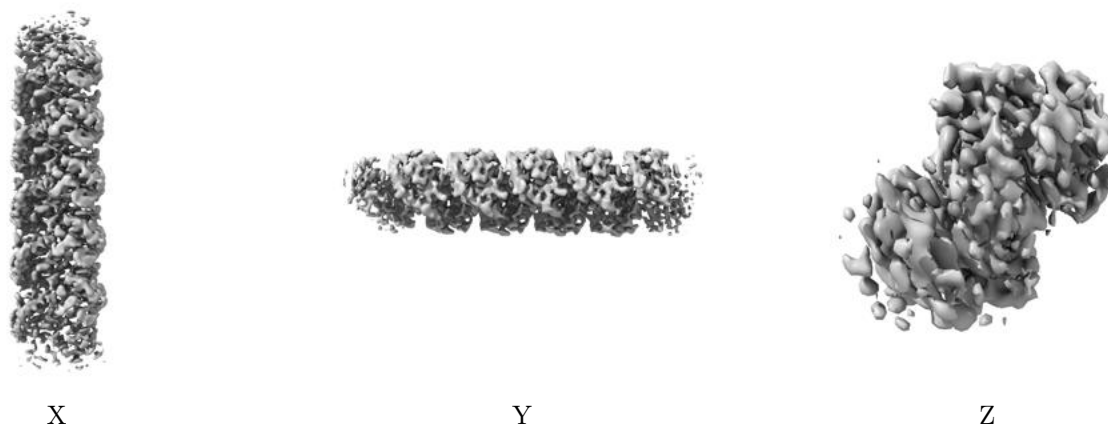


Z

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.

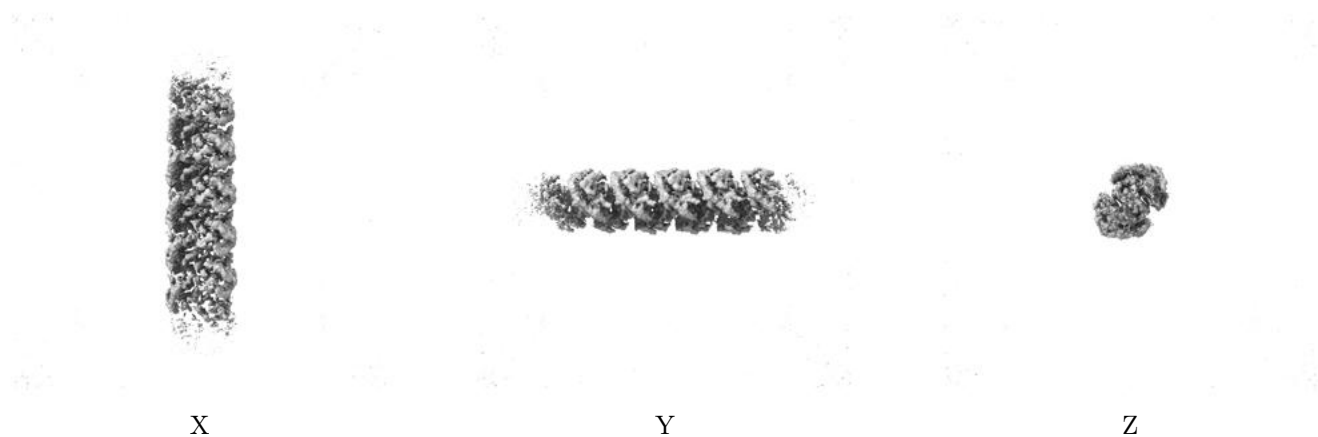
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. 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.

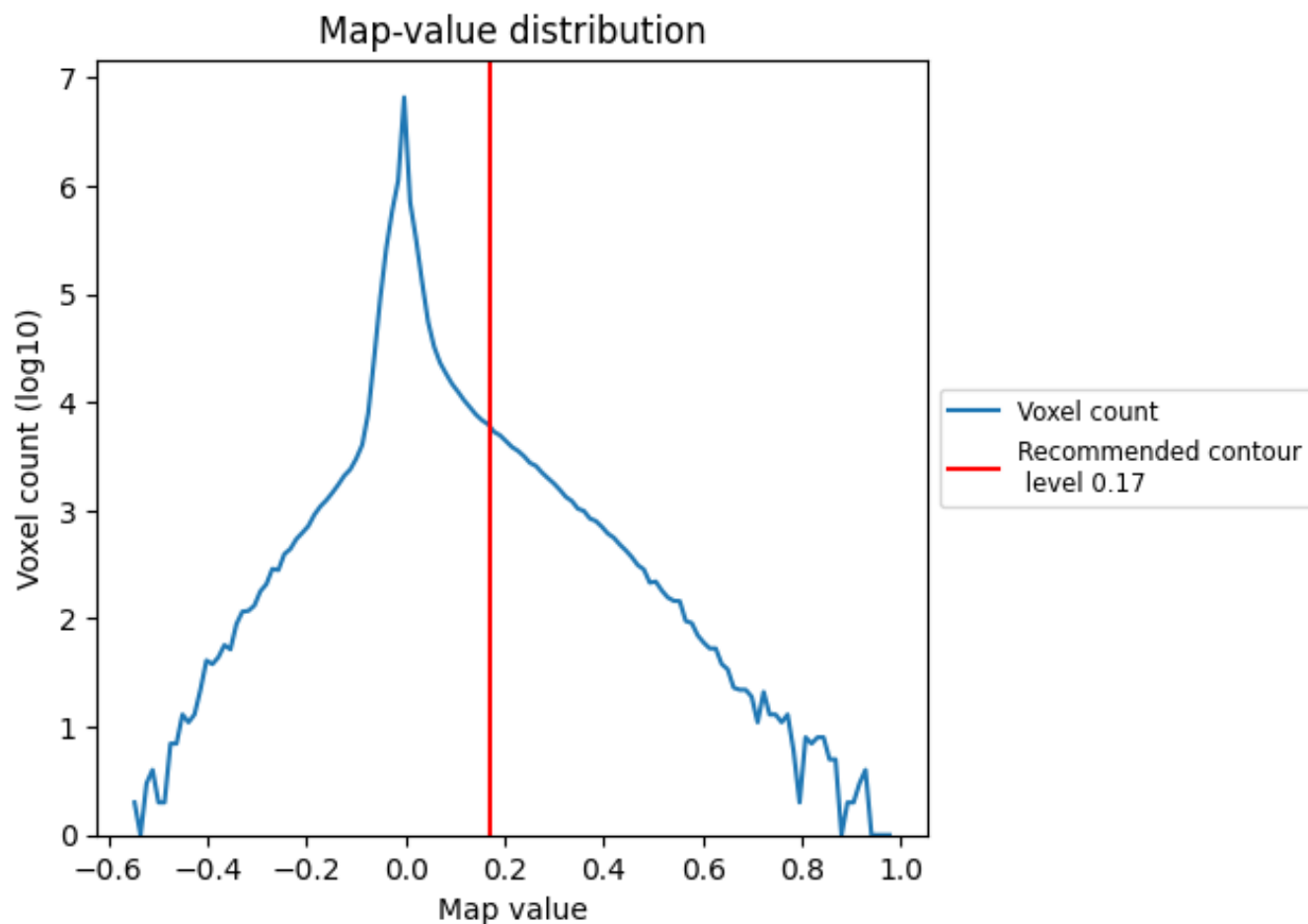
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

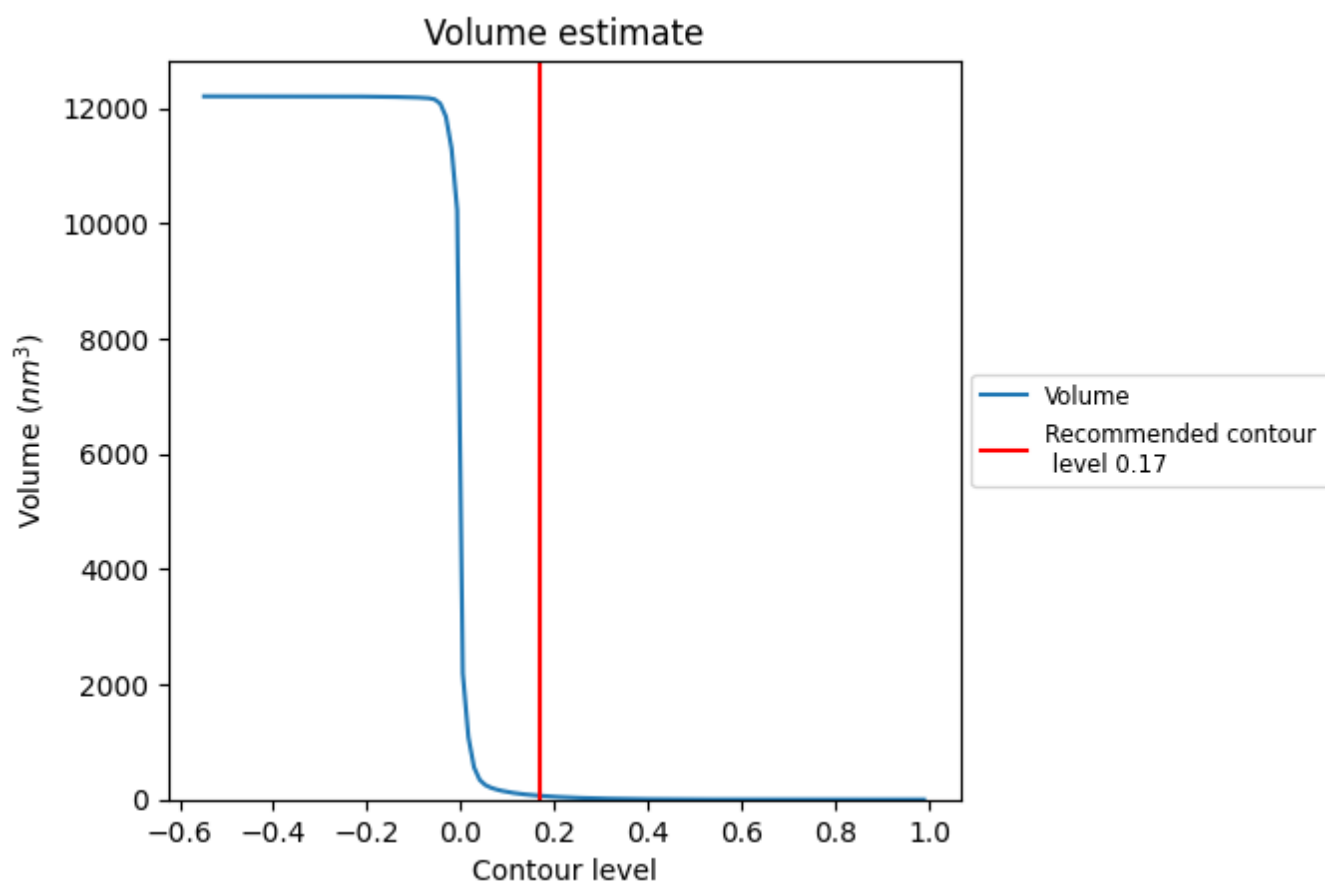
This section contains the results of statistical analysis of the map.

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.

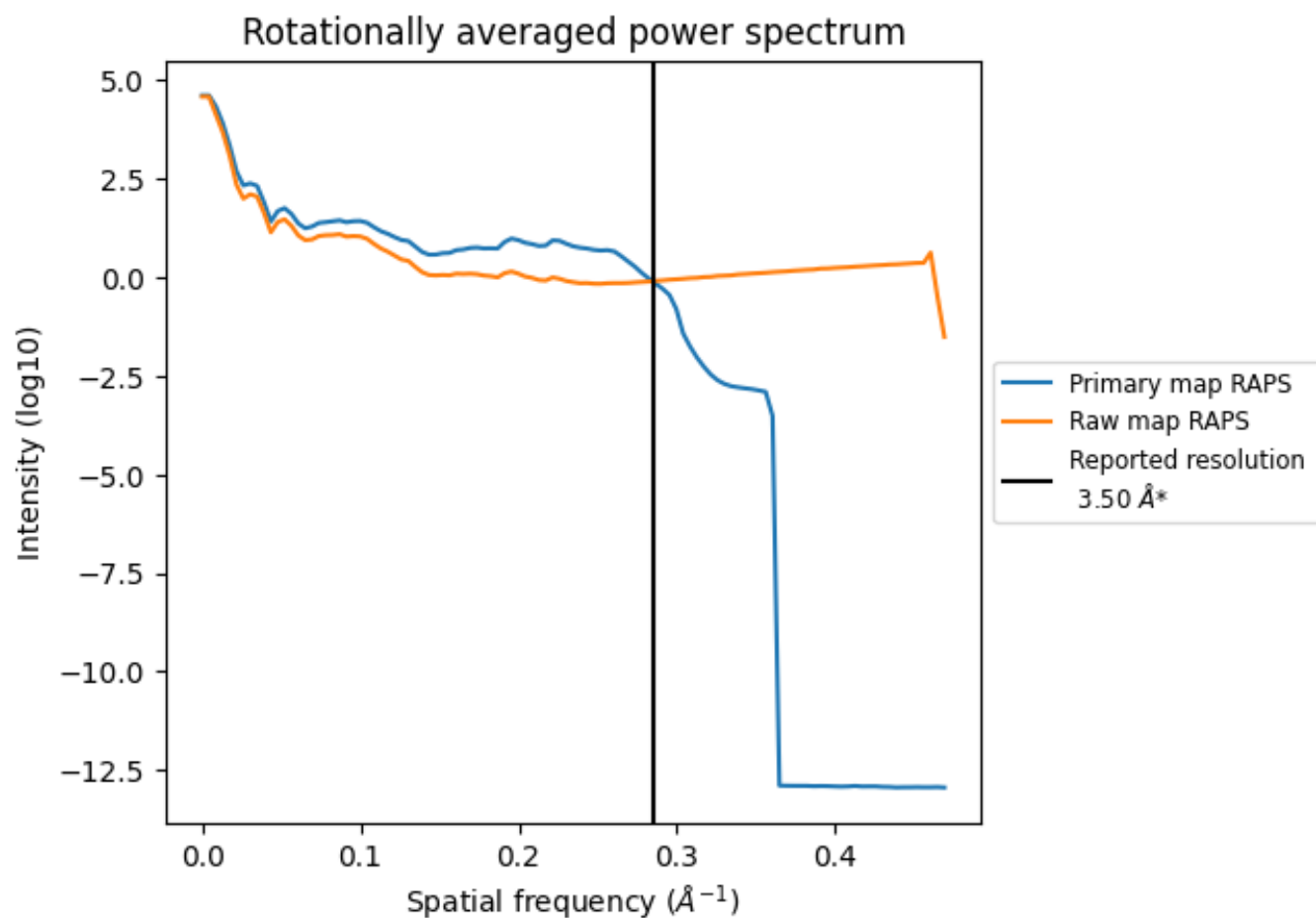
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm³; this corresponds to an approximate mass of 59 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 ⓘ

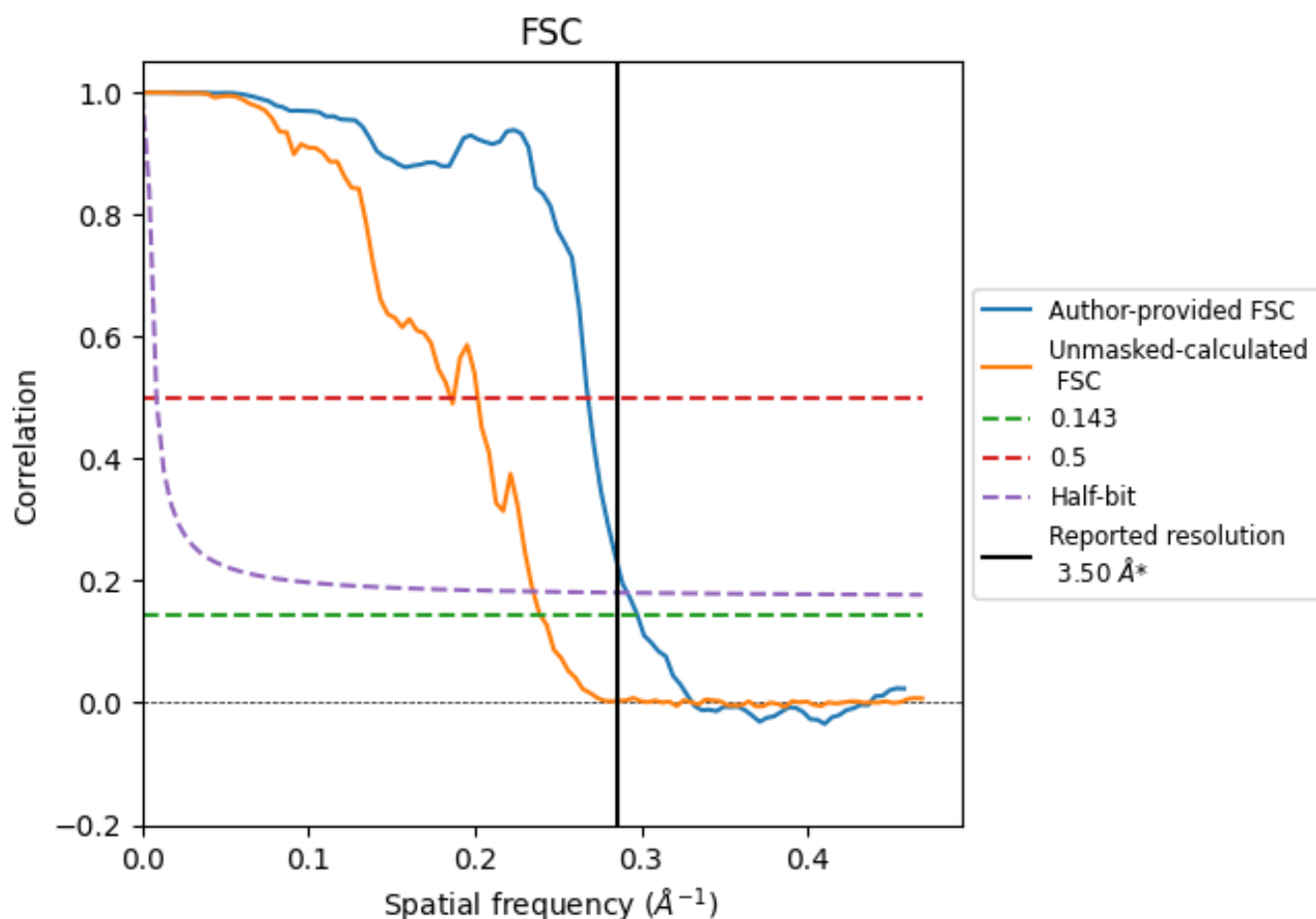


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

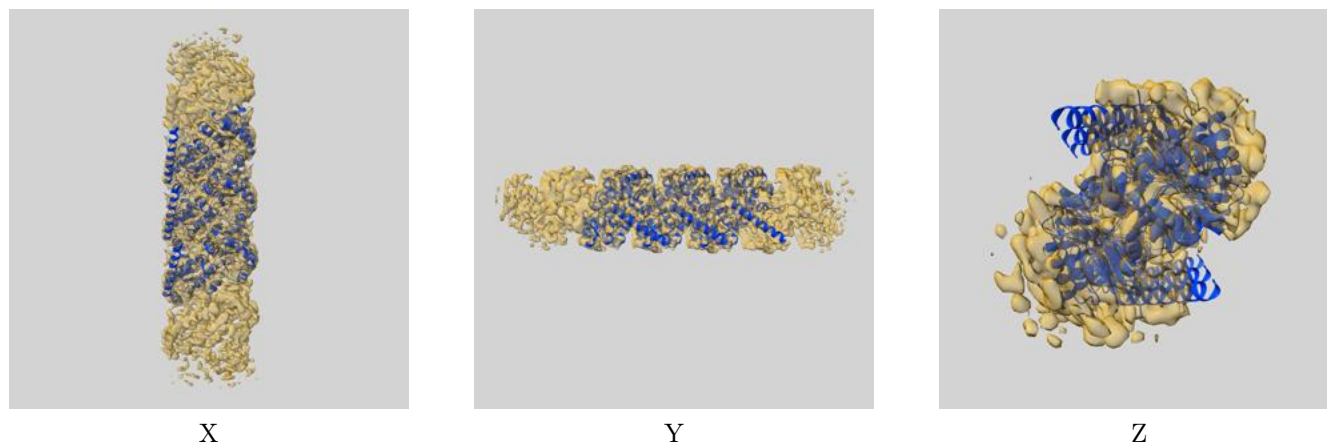
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.36	3.73	3.43
Unmasked-calculated*	4.18	5.39	4.25

*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 4.18 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

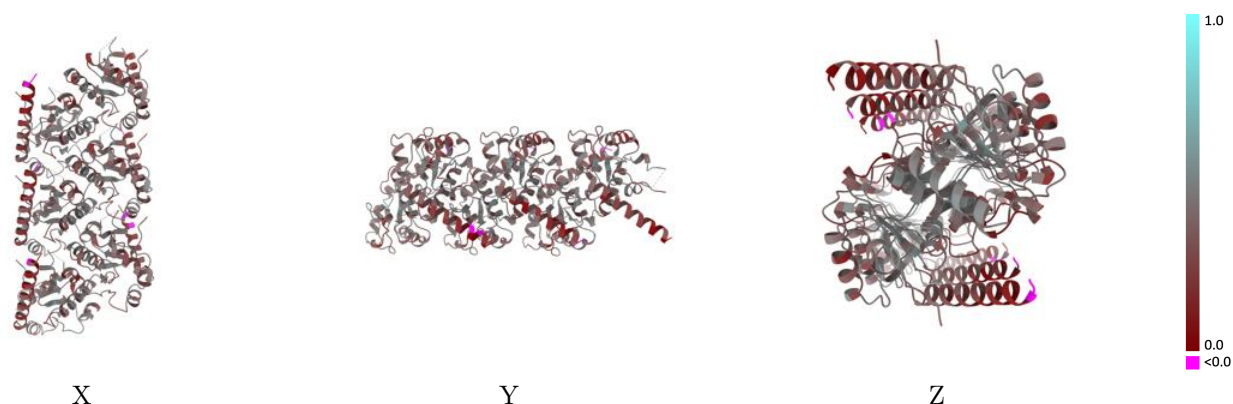
This section contains information regarding the fit between EMDB map EMD-19341 and PDB model 8RLM. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



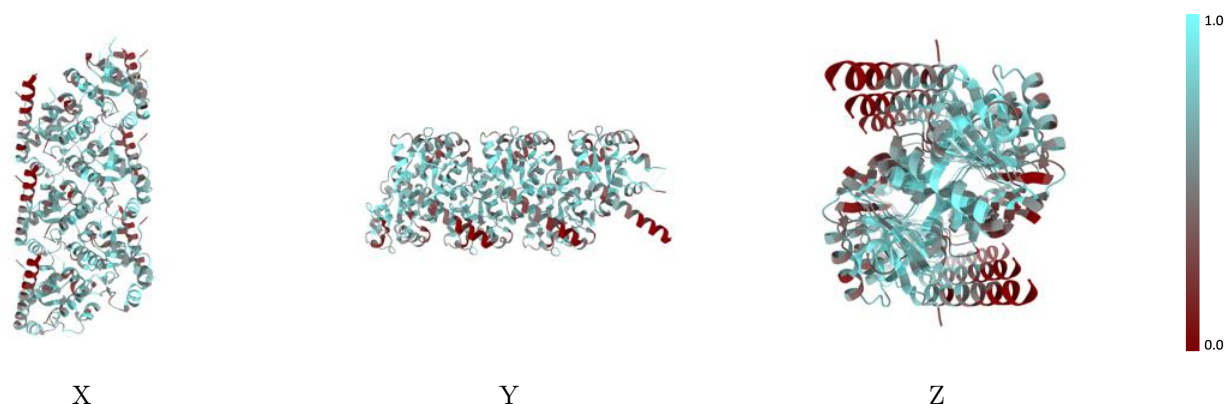
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



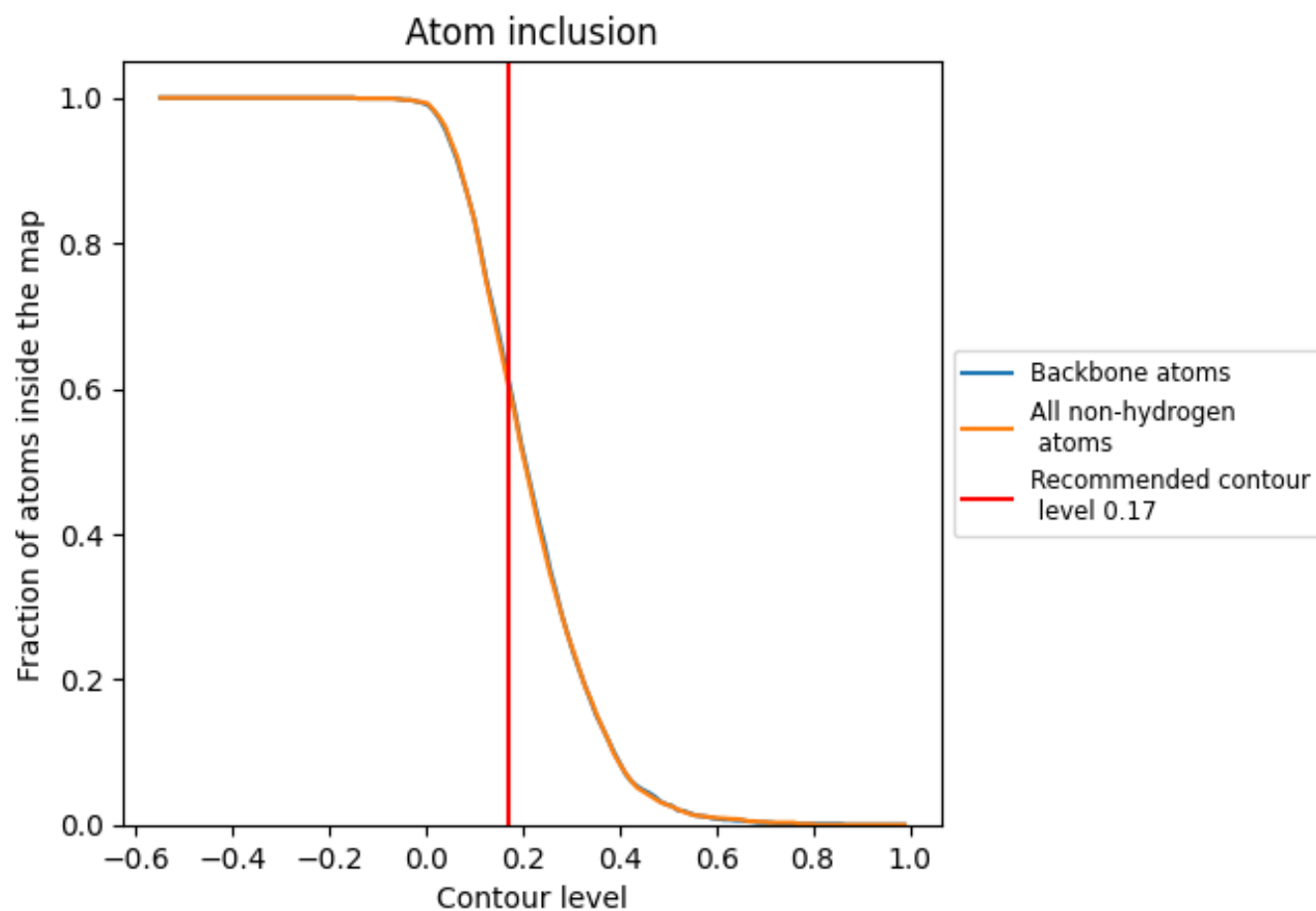
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 61% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6070	0.3700
A	0.5990	0.3690
B	0.6370	0.3790
C	0.6180	0.3660
D	0.6040	0.3700
E	0.6370	0.3750
F	0.6260	0.3590

1.0

0.0

<0.0