



wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 07:40 pm BST

PDB ID : 9SKI / pdb_00009ski
EMDB ID : EMD-54965
Title : Polysaccharide co-polymerase FepE open 7 subunit complex
Authors : Wiseman, B.; Hogbom, M.
Deposited on : 2025-09-02
Resolution : 3.10 Å(reported)
Based on initial model : .

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:

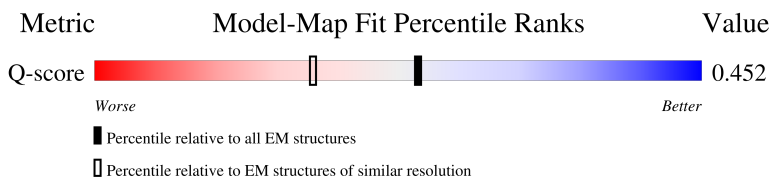
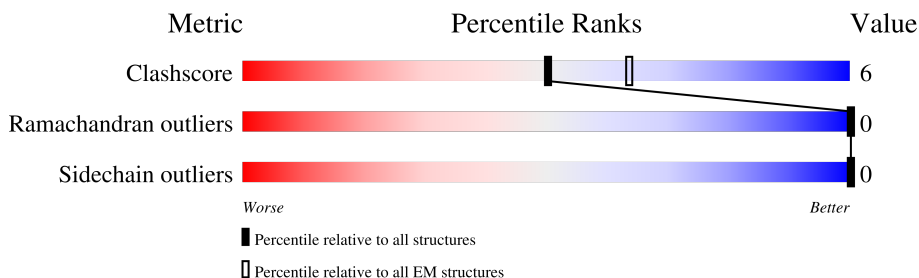
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	392	 69% 10% 21%
1	B	392	 74% 10% 16%
1	C	392	 72% 12% 16%
1	D	392	 74% 10% 16%

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Mol	Chain	Length	Quality of chain
1	E	392	 74% 10% 16%
1	F	392	 76% 8% 16%
1	G	392	 54% 17% 29%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17689 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 Ferric enterobactin transport protein FepE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	311	Total	C	N	O	S	0	0
			2451	1573	407	465	6		
1	B	330	Total	C	N	O	S	0	0
			2599	1667	431	495	6		
1	C	330	Total	C	N	O	S	0	0
			2599	1667	431	495	6		
1	D	330	Total	C	N	O	S	0	0
			2599	1667	431	495	6		
1	E	330	Total	C	N	O	S	0	0
			2599	1667	431	495	6		
1	F	330	Total	C	N	O	S	0	0
			2599	1667	431	495	6		
1	G	280	Total	C	N	O	S	0	0
			2243	1429	374	438	2		

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	378	GLU	-	expression tag	UNP P26266
A	379	PHE	-	expression tag	UNP P26266
A	380	ARG	-	expression tag	UNP P26266
A	381	VAL	-	expression tag	UNP P26266
A	382	PRO	-	expression tag	UNP P26266
A	383	GLY	-	expression tag	UNP P26266
A	384	SER	-	expression tag	UNP P26266
A	385	HIS	-	expression tag	UNP P26266
A	386	HIS	-	expression tag	UNP P26266
A	387	HIS	-	expression tag	UNP P26266
A	388	HIS	-	expression tag	UNP P26266
A	389	HIS	-	expression tag	UNP P26266
A	390	HIS	-	expression tag	UNP P26266
A	391	HIS	-	expression tag	UNP P26266
A	392	HIS	-	expression tag	UNP P26266
B	378	GLU	-	expression tag	UNP P26266

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Chain	Residue	Modelled	Actual	Comment	Reference
B	379	PHE	-	expression tag	UNP P26266
B	380	ARG	-	expression tag	UNP P26266
B	381	VAL	-	expression tag	UNP P26266
B	382	PRO	-	expression tag	UNP P26266
B	383	GLY	-	expression tag	UNP P26266
B	384	SER	-	expression tag	UNP P26266
B	385	HIS	-	expression tag	UNP P26266
B	386	HIS	-	expression tag	UNP P26266
B	387	HIS	-	expression tag	UNP P26266
B	388	HIS	-	expression tag	UNP P26266
B	389	HIS	-	expression tag	UNP P26266
B	390	HIS	-	expression tag	UNP P26266
B	391	HIS	-	expression tag	UNP P26266
B	392	HIS	-	expression tag	UNP P26266
C	378	GLU	-	expression tag	UNP P26266
C	379	PHE	-	expression tag	UNP P26266
C	380	ARG	-	expression tag	UNP P26266
C	381	VAL	-	expression tag	UNP P26266
C	382	PRO	-	expression tag	UNP P26266
C	383	GLY	-	expression tag	UNP P26266
C	384	SER	-	expression tag	UNP P26266
C	385	HIS	-	expression tag	UNP P26266
C	386	HIS	-	expression tag	UNP P26266
C	387	HIS	-	expression tag	UNP P26266
C	388	HIS	-	expression tag	UNP P26266
C	389	HIS	-	expression tag	UNP P26266
C	390	HIS	-	expression tag	UNP P26266
C	391	HIS	-	expression tag	UNP P26266
C	392	HIS	-	expression tag	UNP P26266
D	378	GLU	-	expression tag	UNP P26266
D	379	PHE	-	expression tag	UNP P26266
D	380	ARG	-	expression tag	UNP P26266
D	381	VAL	-	expression tag	UNP P26266
D	382	PRO	-	expression tag	UNP P26266
D	383	GLY	-	expression tag	UNP P26266
D	384	SER	-	expression tag	UNP P26266
D	385	HIS	-	expression tag	UNP P26266
D	386	HIS	-	expression tag	UNP P26266
D	387	HIS	-	expression tag	UNP P26266
D	388	HIS	-	expression tag	UNP P26266
D	389	HIS	-	expression tag	UNP P26266
D	390	HIS	-	expression tag	UNP P26266

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Chain	Residue	Modelled	Actual	Comment	Reference
D	391	HIS	-	expression tag	UNP P26266
D	392	HIS	-	expression tag	UNP P26266
E	378	GLU	-	expression tag	UNP P26266
E	379	PHE	-	expression tag	UNP P26266
E	380	ARG	-	expression tag	UNP P26266
E	381	VAL	-	expression tag	UNP P26266
E	382	PRO	-	expression tag	UNP P26266
E	383	GLY	-	expression tag	UNP P26266
E	384	SER	-	expression tag	UNP P26266
E	385	HIS	-	expression tag	UNP P26266
E	386	HIS	-	expression tag	UNP P26266
E	387	HIS	-	expression tag	UNP P26266
E	388	HIS	-	expression tag	UNP P26266
E	389	HIS	-	expression tag	UNP P26266
E	390	HIS	-	expression tag	UNP P26266
E	391	HIS	-	expression tag	UNP P26266
E	392	HIS	-	expression tag	UNP P26266
F	378	GLU	-	expression tag	UNP P26266
F	379	PHE	-	expression tag	UNP P26266
F	380	ARG	-	expression tag	UNP P26266
F	381	VAL	-	expression tag	UNP P26266
F	382	PRO	-	expression tag	UNP P26266
F	383	GLY	-	expression tag	UNP P26266
F	384	SER	-	expression tag	UNP P26266
F	385	HIS	-	expression tag	UNP P26266
F	386	HIS	-	expression tag	UNP P26266
F	387	HIS	-	expression tag	UNP P26266
F	388	HIS	-	expression tag	UNP P26266
F	389	HIS	-	expression tag	UNP P26266
F	390	HIS	-	expression tag	UNP P26266
F	391	HIS	-	expression tag	UNP P26266
F	392	HIS	-	expression tag	UNP P26266
G	378	GLU	-	expression tag	UNP P26266
G	379	PHE	-	expression tag	UNP P26266
G	380	ARG	-	expression tag	UNP P26266
G	381	VAL	-	expression tag	UNP P26266
G	382	PRO	-	expression tag	UNP P26266
G	383	GLY	-	expression tag	UNP P26266
G	384	SER	-	expression tag	UNP P26266
G	385	HIS	-	expression tag	UNP P26266
G	386	HIS	-	expression tag	UNP P26266
G	387	HIS	-	expression tag	UNP P26266

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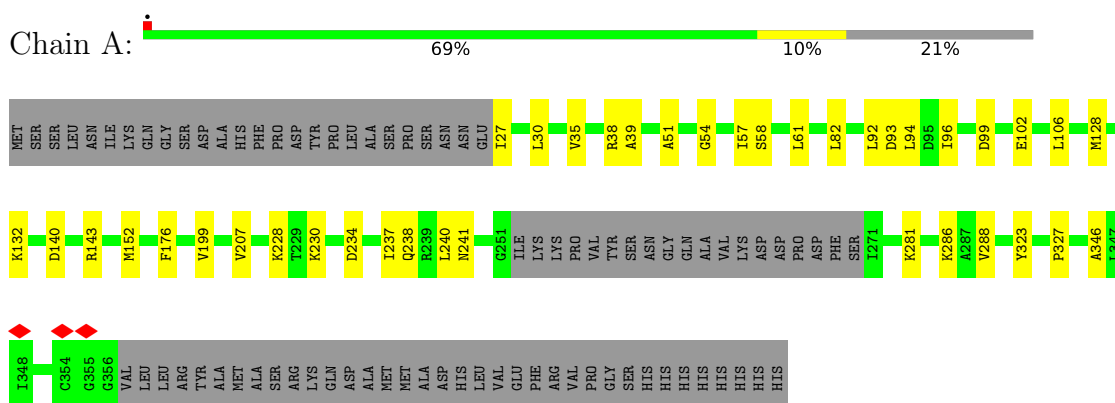
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Chain	Residue	Modelled	Actual	Comment	Reference
G	388	HIS	-	expression tag	UNP P26266
G	389	HIS	-	expression tag	UNP P26266
G	390	HIS	-	expression tag	UNP P26266
G	391	HIS	-	expression tag	UNP P26266
G	392	HIS	-	expression tag	UNP P26266

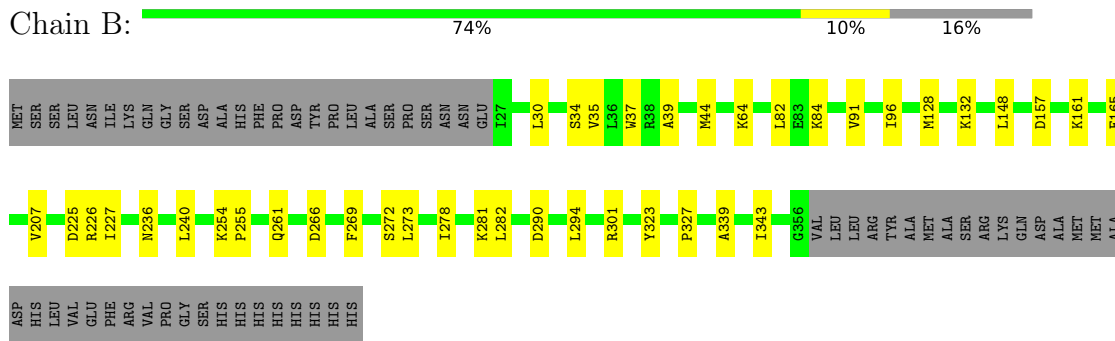
3 Residue-property plots

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.

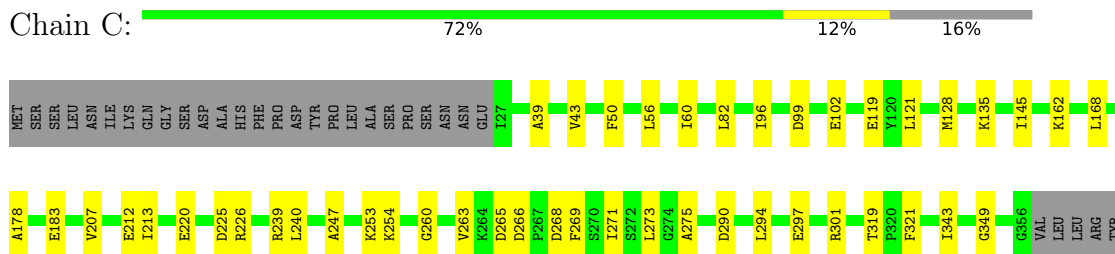
- Molecule 1: Ferric enterobactin transport protein FepE



- Molecule 1: Ferric enterobactin transport protein FepE



- Molecule 1: Ferric enterobactin transport protein FepE



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

• Molecule 1: Ferric enterobactin transport protein FepE

Chain D: 74% 10% 16%

MET
SER
SER
LEU
ASN
ILE
LYS
GLN
GLY
ASP
ASP
ALA
HIS
HIS
PHE
PRO
ASP
TYR
PRO
LEU
ALA
SER
PRO
SER
SER
ASN
ASN
GLU
I27
L30
S34
R38
A39
K40
K41
I57
I60
L94
D95
I96
D99
E102
M105
I108
M128
D140
R143
K163

ALA
ASP
HIS
LEU
VAL
GLU
PHE
ARG
VAL
GLY
SER
GLY
SER
HIS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Ferric enterobactin transport protein FepE

Chain E: 74% 10% 16%

MET
SER
SER
LEU
ASN
ILE
LYS
GLN
GLY
ASP
ASP
ALA
HIS
HIS
PHE
PRO
ASP
TYR
PRO
LEU
ALA
SER
PRO
SER
ASN
ASN
GLU
I27
D28
L29
V46
A51
E75
L82
T87
L94
D95
I96
D99
E102
M105
L116
K135
M152
K161
K162
D164

MET
ALA
ASP
HIS
LEU
VAL
GLU
PHE
ARG
VAL
PRO
SER
SER
HIS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Ferric enterobactin transport protein FepE

Chain F: 76% 8% 16%

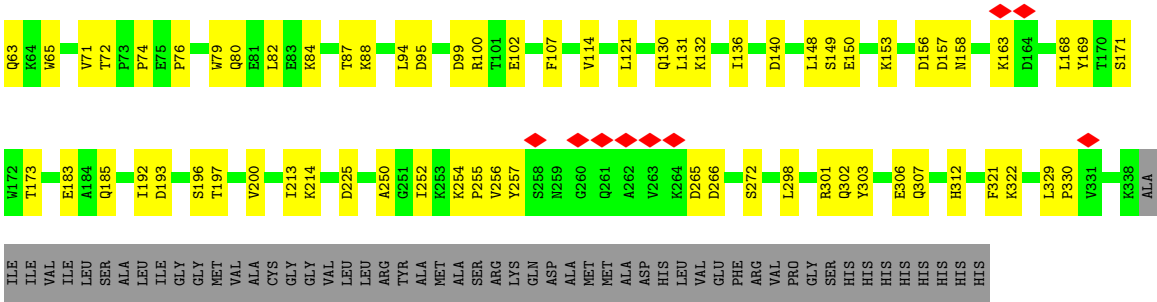
MET
SER
SER
LEU
ASN
ILE
LYS
GLN
GLY
ASP
ASP
ALA
HIS
HIS
PHE
PRO
TYR
PRO
LEU
ALA
SER
PRO
PRO
ASN
ASN
GLU
I27
D28
L29
L32
M44
K64
I96
K109
Y126
D156
A159
K163
L168
T177
E183
K201
V207
Q216

VAL
PRO
GLY
SER
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS

• Molecule 1: Ferric enterobactin transport protein FepE

Chain G: 54% 17% 29%

MET
SER
SER
LEU
ASN
ILE
LYS
GLN
GLY
ASP
ASP
ALA
HIS
HIS
PHE
PRO
ASP
TYR
PRO
LEU
ALA
SER
SER
PRO
SER
ASN
ASN
GLU
ILE
ASP
LEU
LEU
ASN
LEU
ILE
SER
VAL
LEU
TRP
ARG
VAL
LYS
LYS
THR
VAL
MET
ALA
VAL
VAL
PHE
PHE
CYS
GLY
ALA
LEU
LEU
ILE
SER
F59



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	210303	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.462	Depositor
Minimum map value	-0.228	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	372.6, 372.6, 372.6	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	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	0.10	0/2489	0.24	0/3366
1	B	0.10	0/2642	0.25	0/3575
1	C	0.16	0/2642	0.31	0/3575
1	D	0.11	0/2642	0.24	0/3575
1	E	0.11	0/2642	0.26	0/3575
1	F	0.10	0/2642	0.24	0/3575
1	G	0.11	0/2282	0.29	0/3086
All	All	0.11	0/17981	0.26	0/24327

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	2451	0	2538	29	0
1	B	2599	0	2683	29	0
1	C	2599	0	2683	36	0
1	D	2599	0	2683	27	0
1	E	2599	0	2683	27	0
1	F	2599	0	2683	23	0
1	G	2243	0	2282	48	0
All	All	17689	0	18235	201	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 201 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:96:ILE:HD13	1:B:207:VAL:HG13	1.71	0.72
1:F:156:ASP:HB3	1:F:159:ALA:HB2	1.74	0.69
1:A:152:MET:HE1	1:A:176:PHE:HB2	1.77	0.67
1:D:259:ASN:HA	1:E:260:GLY:HA3	1.76	0.66
1:E:263:VAL:HG13	1:E:265:ASP:H	1.59	0.66

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	307/392 (78%)	298 (97%)	9 (3%)	0	100	100
1	B	328/392 (84%)	315 (96%)	13 (4%)	0	100	100
1	C	328/392 (84%)	316 (96%)	12 (4%)	0	100	100
1	D	328/392 (84%)	316 (96%)	12 (4%)	0	100	100
1	E	328/392 (84%)	315 (96%)	13 (4%)	0	100	100
1	F	328/392 (84%)	315 (96%)	13 (4%)	0	100	100
1	G	278/392 (71%)	262 (94%)	16 (6%)	0	100	100
All	All	2225/2744 (81%)	2137 (96%)	88 (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	272/343 (79%)	272 (100%)	0	100	100
1	B	289/343 (84%)	289 (100%)	0	100	100
1	C	289/343 (84%)	289 (100%)	0	100	100
1	D	289/343 (84%)	289 (100%)	0	100	100
1	E	289/343 (84%)	289 (100%)	0	100	100
1	F	289/343 (84%)	289 (100%)	0	100	100
1	G	252/343 (74%)	252 (100%)	0	100	100
All	All	1969/2401 (82%)	1969 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
1	F	324	GLN
1	G	232	GLN
1	G	312	HIS
1	G	112	GLN
1	D	259	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

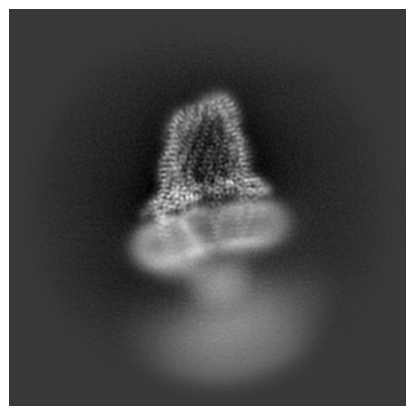
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54965. These allow visual inspection of the internal detail of the map and identification of artifacts.

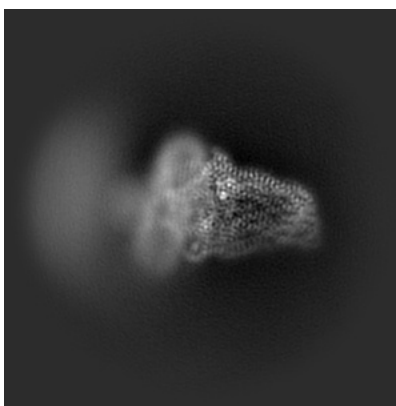
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

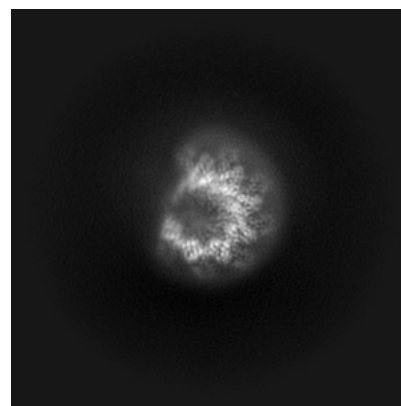
6.1.1 Primary map



X

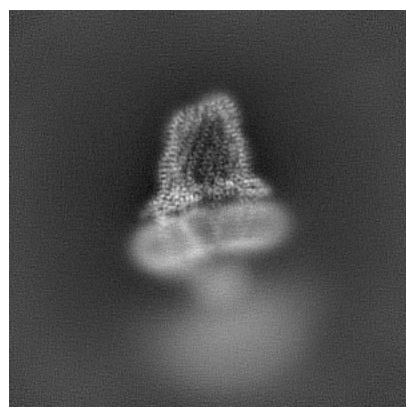


Y

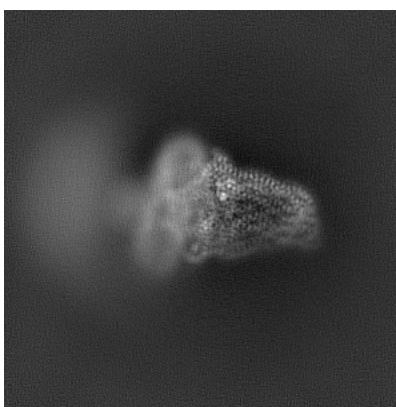


Z

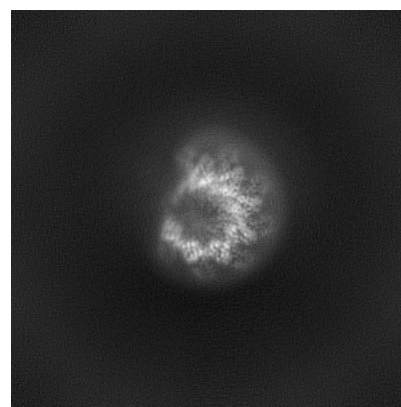
6.1.2 Raw map



X



Y

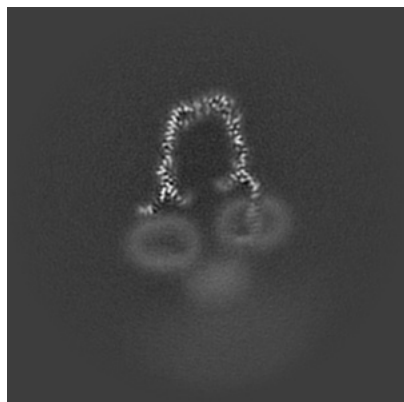


Z

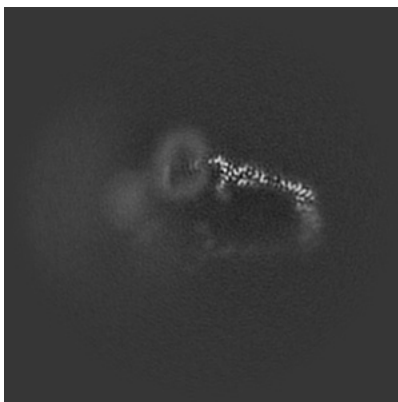
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

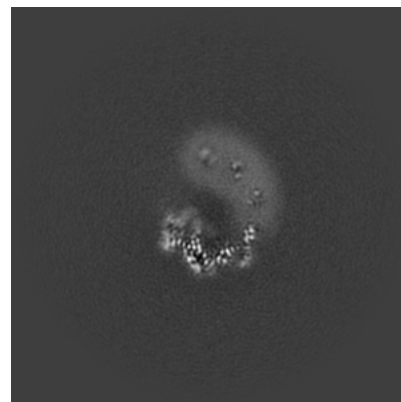
6.2.1 Primary map



X Index: 225

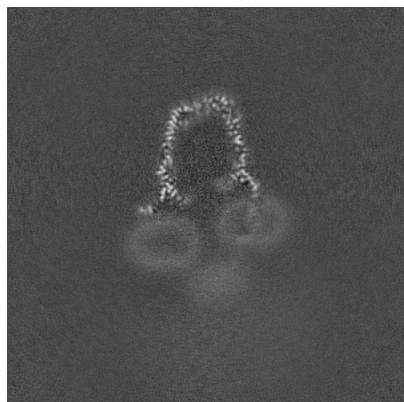


Y Index: 225

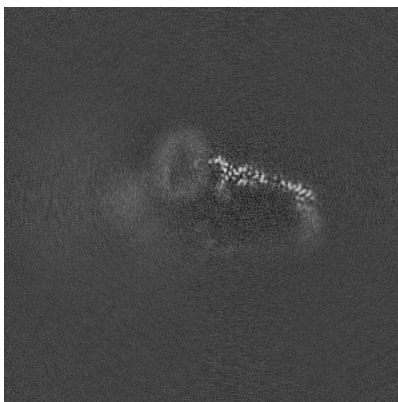


Z Index: 225

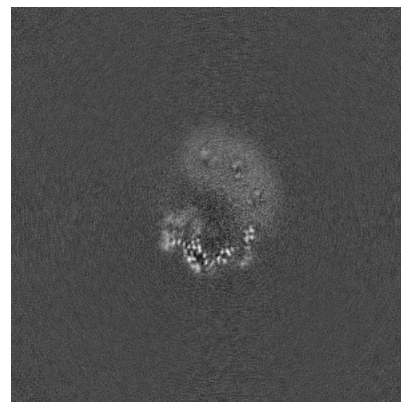
6.2.2 Raw map



X Index: 225



Y Index: 225



Z Index: 225

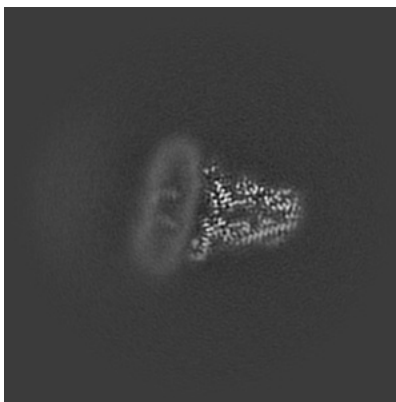
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

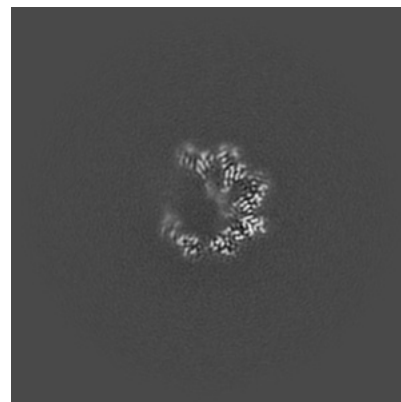
6.3.1 Primary map



X Index: 243



Y Index: 185

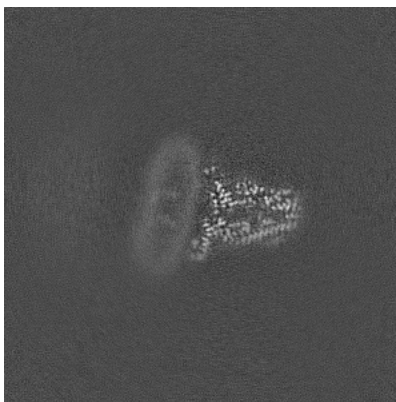


Z Index: 248

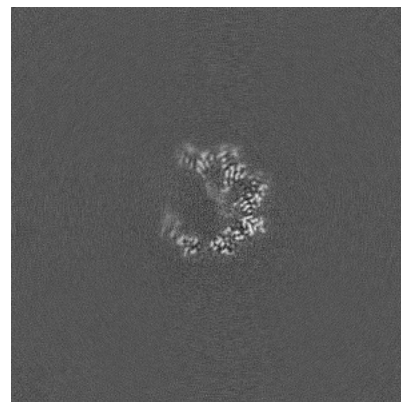
6.3.2 Raw map



X Index: 243



Y Index: 185

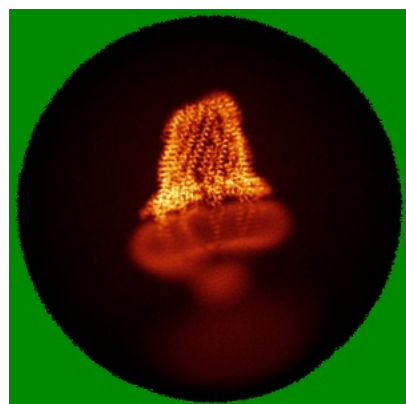


Z Index: 248

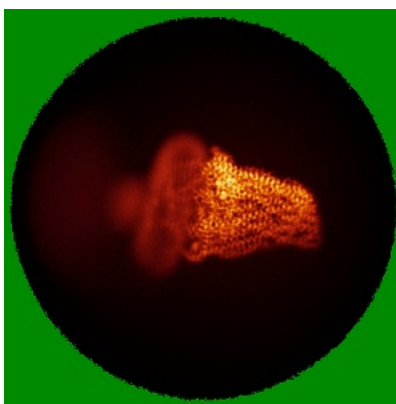
The images above show the largest variance slices of the map in three orthogonal directions.

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

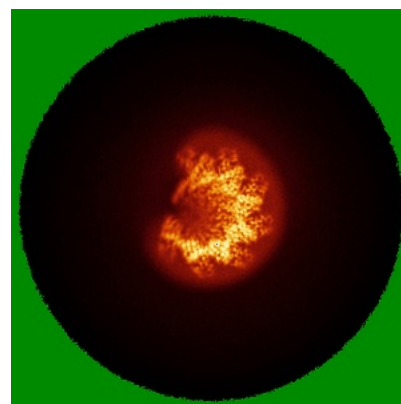
6.4.1 Primary map



X

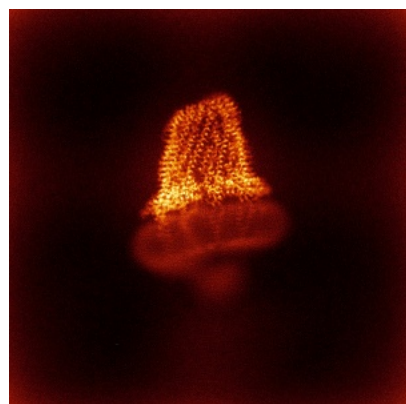


Y

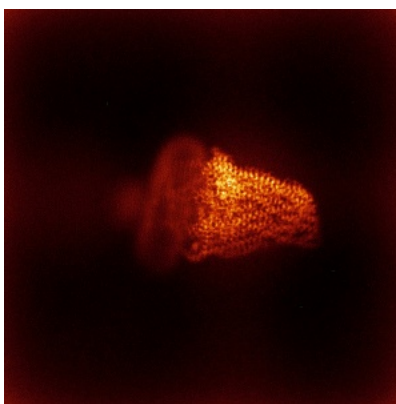


Z

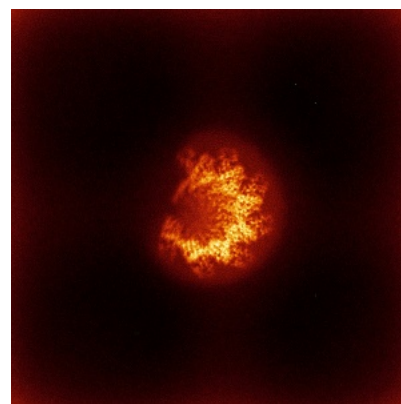
6.4.2 Raw map



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](#)

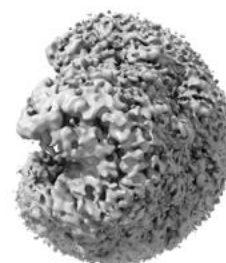
6.5.1 Primary map



X



Y



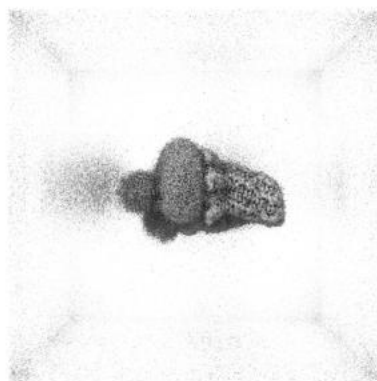
Z

The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

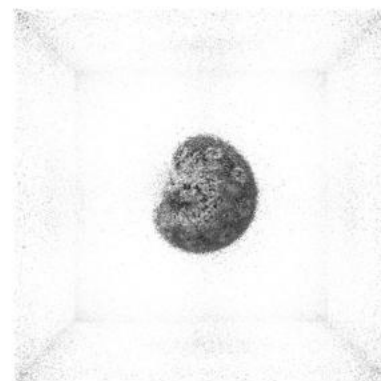
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

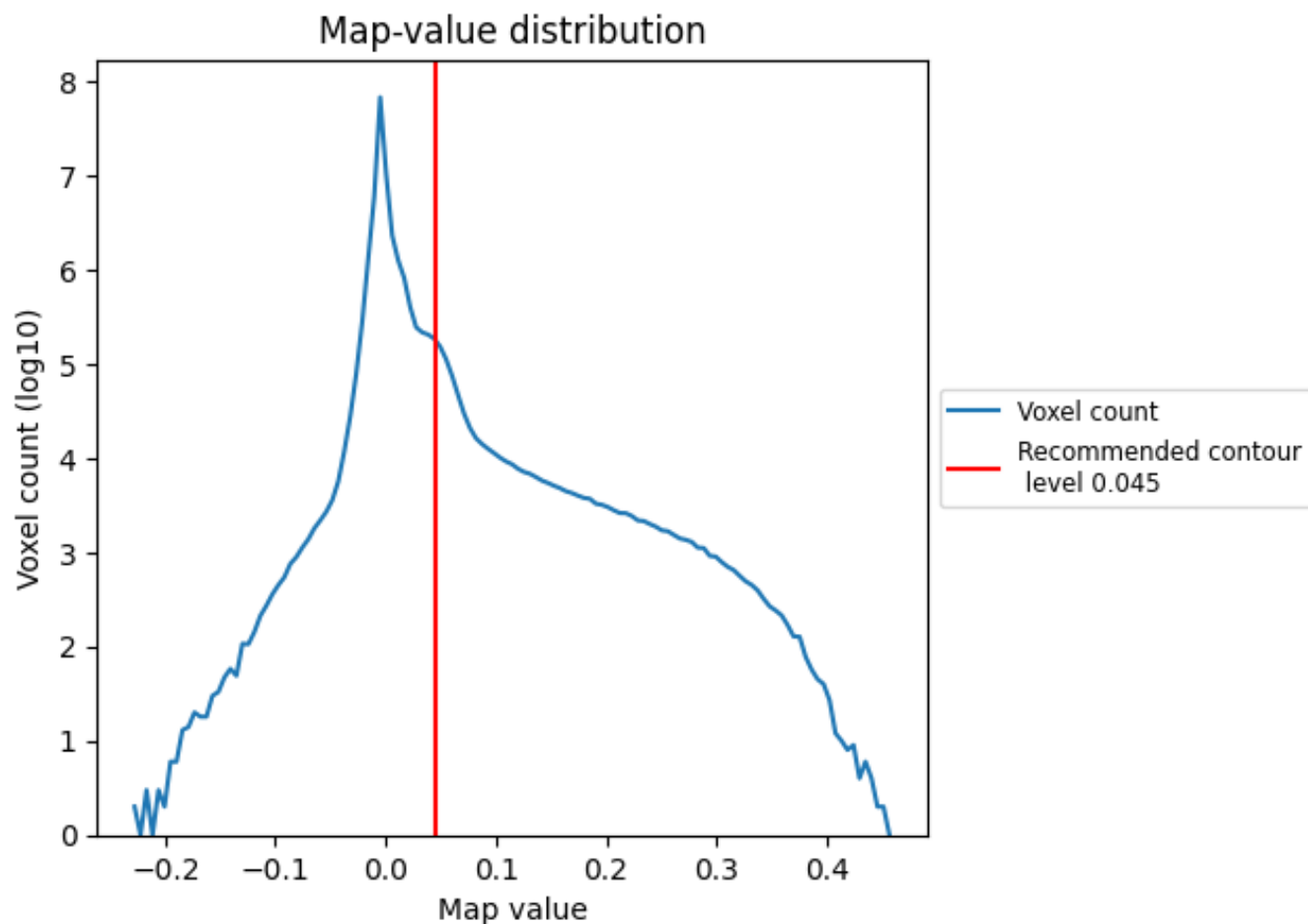
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

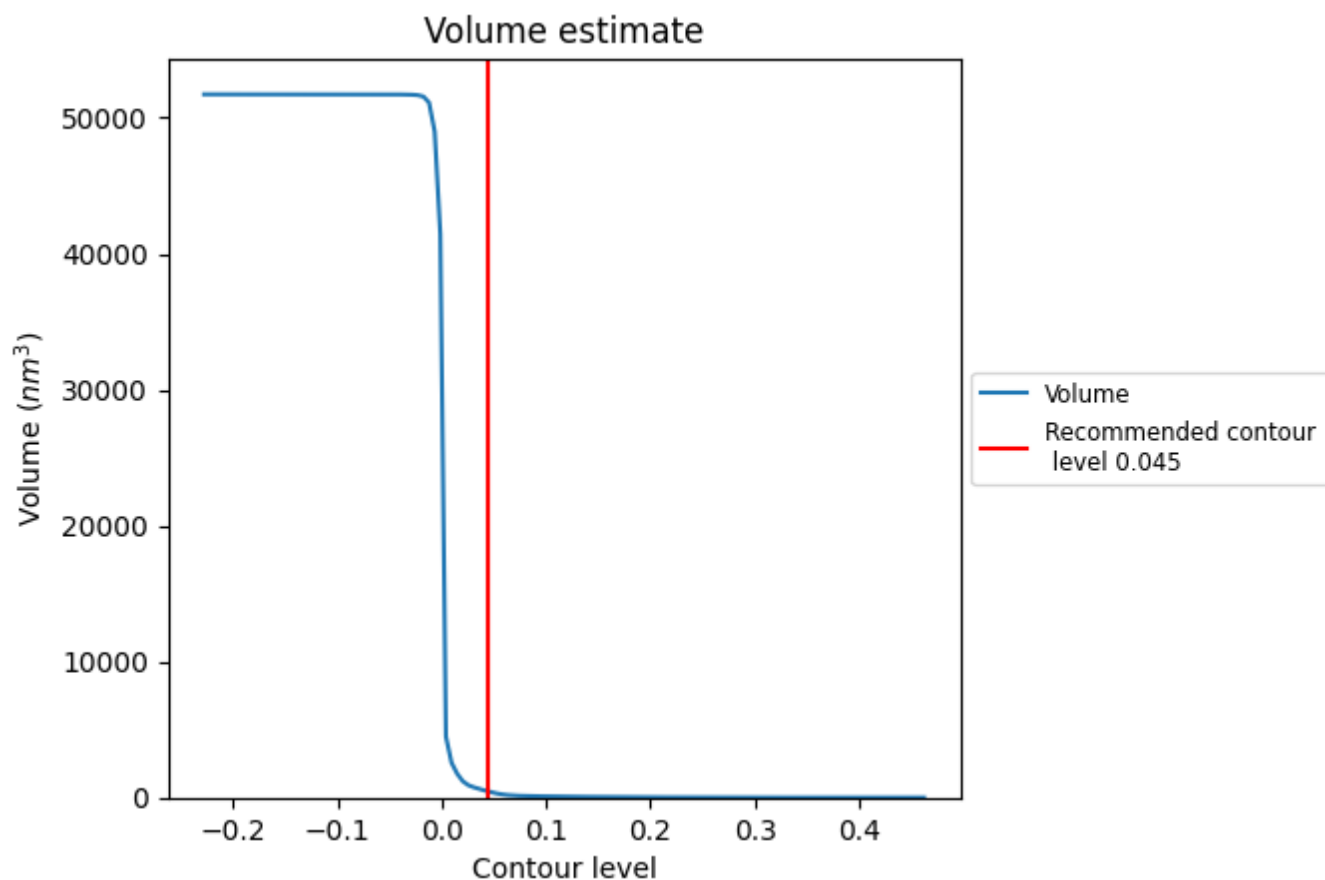
This section contains the results of statistical analysis of the map.

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.

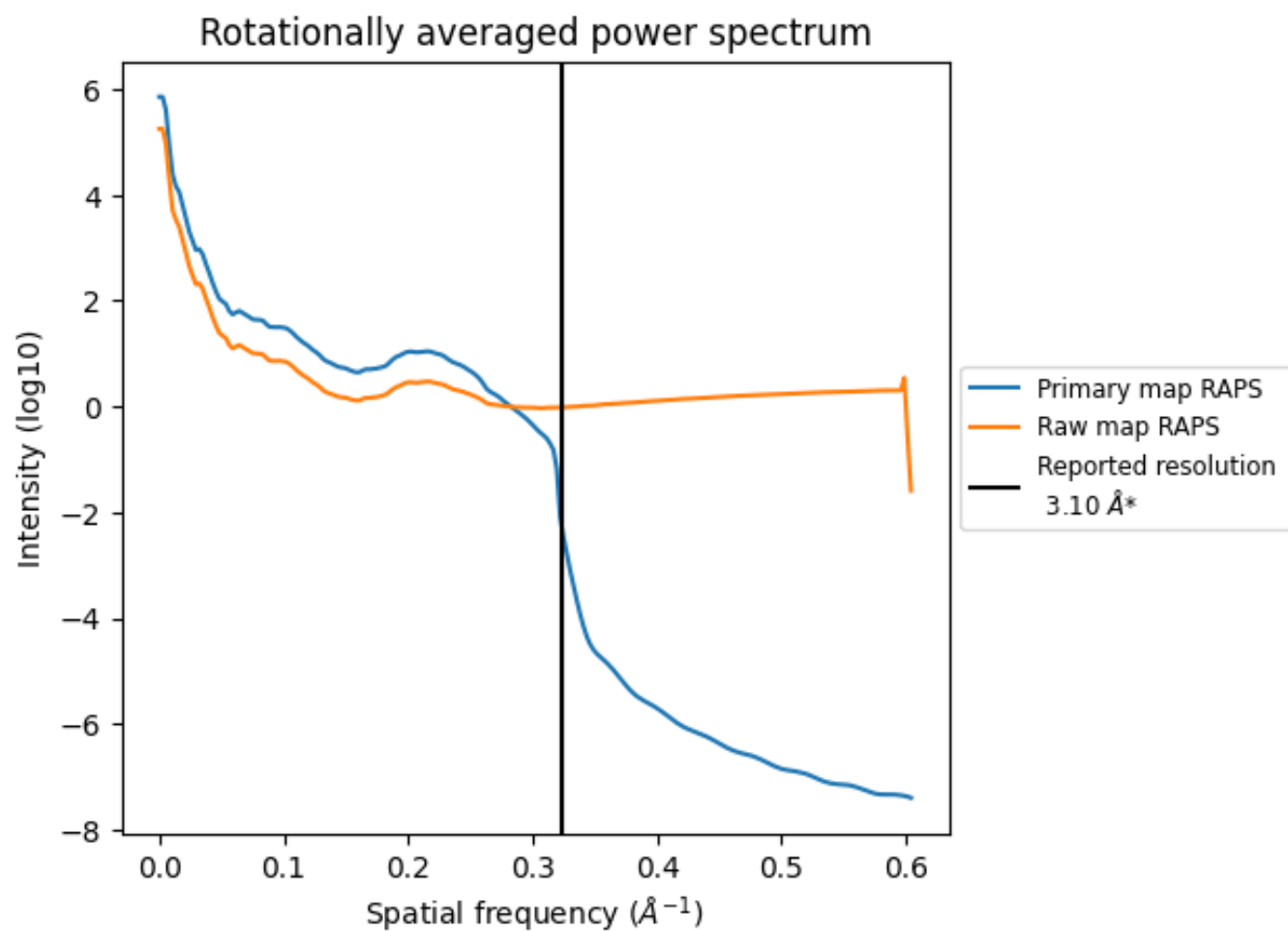
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 444 nm³; this corresponds to an approximate mass of 401 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 ⓘ

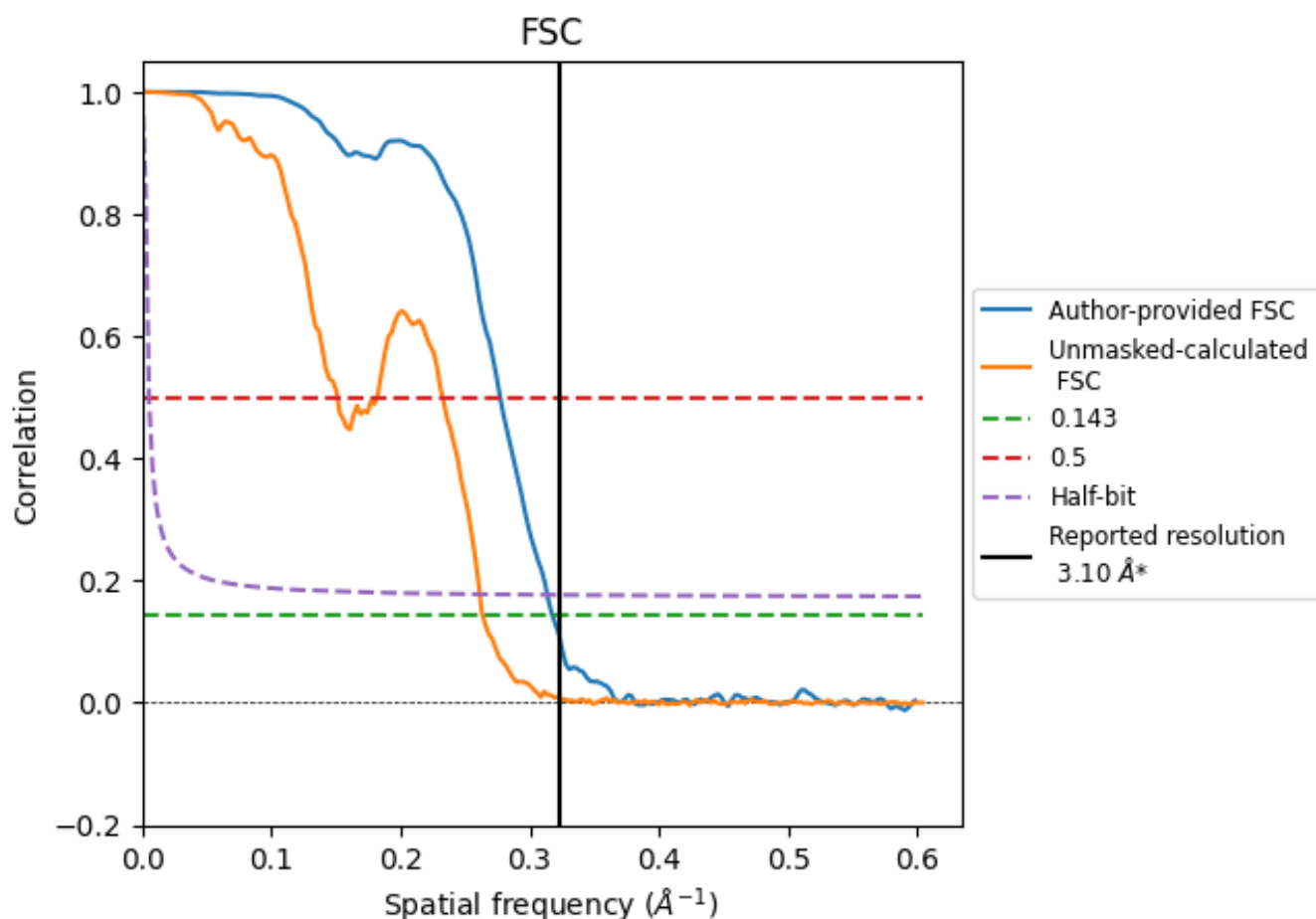


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

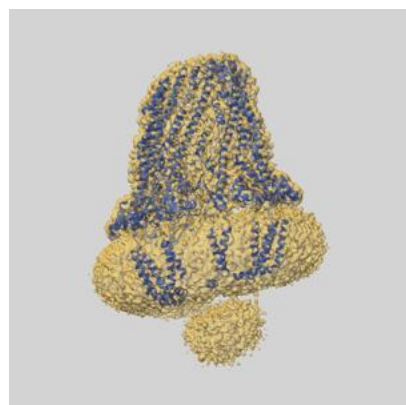
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.15	3.61	3.19
Unmasked-calculated*	3.79	6.62	3.83

*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 3.1 by more than 10 %

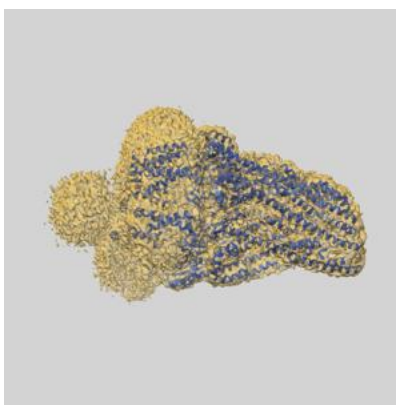
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54965 and PDB model 9SKI. Per-residue inclusion information can be found in section [3](#) on page [8](#).

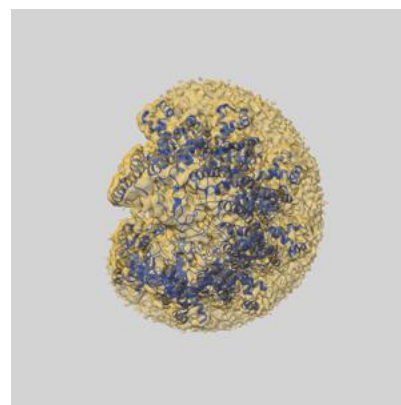
9.1 Map-model overlay [i](#)



X



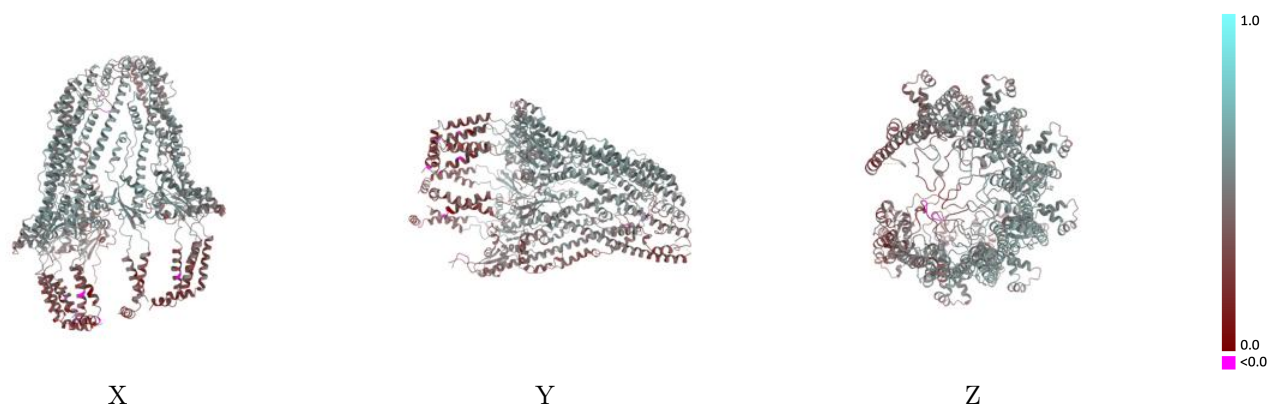
Y



Z

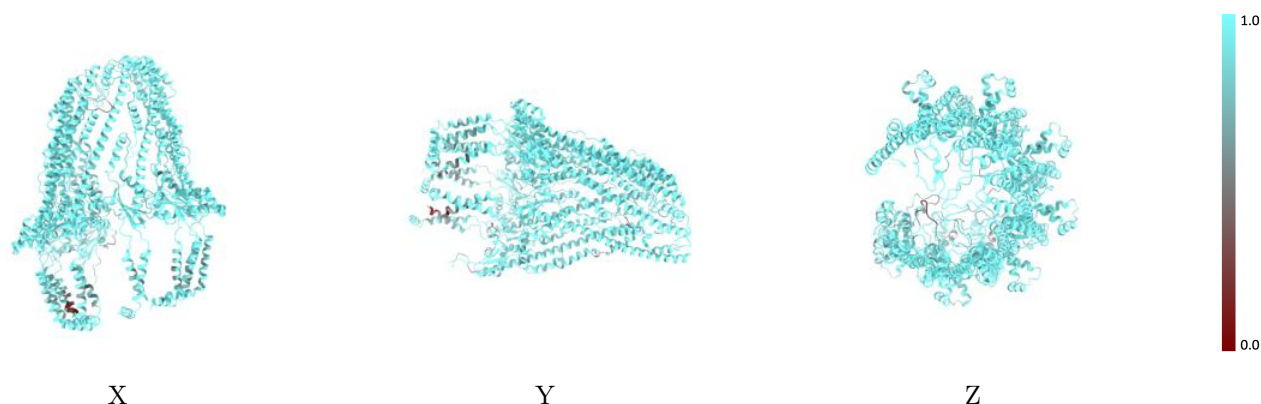
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



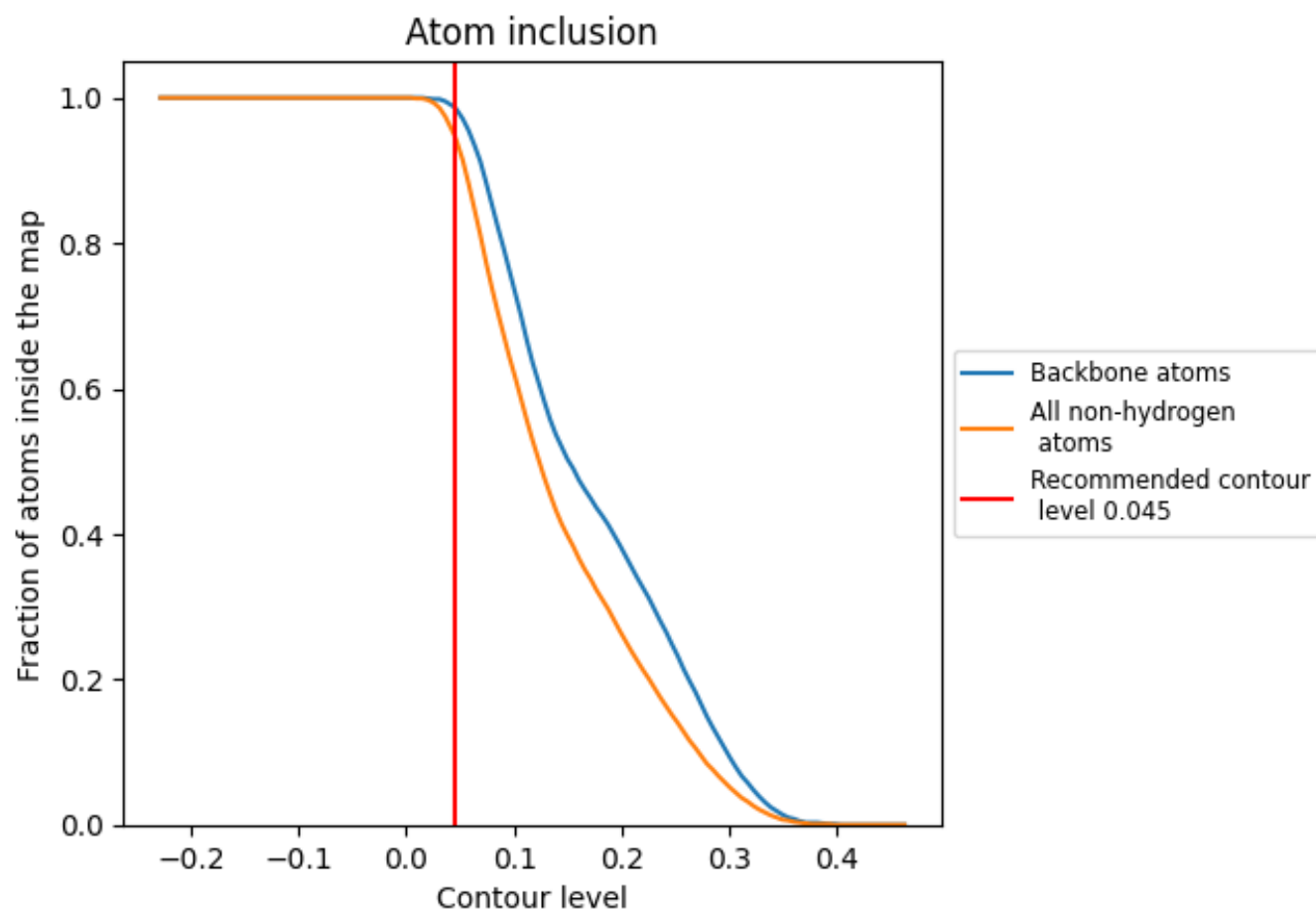
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 95% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9480	<div><div></div></div> 0.4520
A	<div><div></div></div> 0.9380	<div><div></div></div> 0.4060
B	<div><div></div></div> 0.9620	<div><div></div></div> 0.4720
C	<div><div></div></div> 0.9640	<div><div></div></div> 0.4860
D	<div><div></div></div> 0.9600	<div><div></div></div> 0.4860
E	<div><div></div></div> 0.9600	<div><div></div></div> 0.4840
F	<div><div></div></div> 0.9440	<div><div></div></div> 0.4540
G	<div><div></div></div> 0.8980	<div><div></div></div> 0.3590

1.0

0.0

<0.0