



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:51 AM UTC

PDB ID : 8P3P / pdb_00008p3p
EMDB ID : EMD-17389
Title : Full-length bacterial polysaccharide co-polymerase WzzE mutant R267E from E. coli. C4 symmetry
Authors : Wiseman, B.; Hogbom, M.
Deposited on : 2023-05-18
Resolution : 2.50 Å(reported)
Based on initial model : 8BHW

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

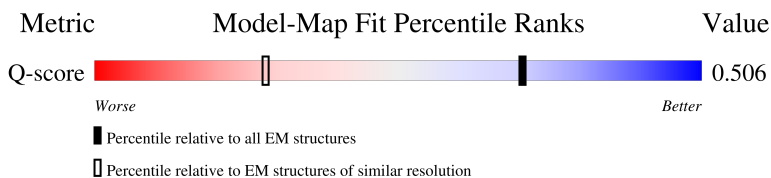
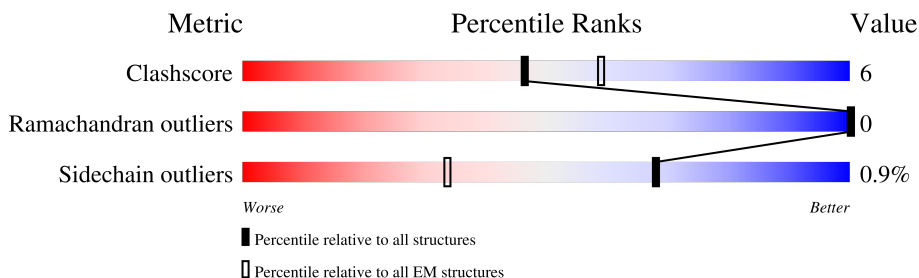
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

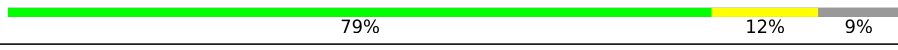
The reported resolution of this entry is 2.50 Å.

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	7115 (2.00 - 3.00)

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	363	
1	B	363	
1	C	363	
1	D	363	

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Mol	Chain	Length	Quality of chain
1	E	363	 78%13%9%
1	F	363	 76%16%9%
1	G	363	 79%12%9%
1	H	363	 79%12%9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21224 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 ECA polysaccharide chain length modulation protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	H	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	A	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	B	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	D	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	E	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	F	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		
1	G	332	Total	C	N	O	S	0	0
			2653	1676	472	490	15		

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	267	GLU	ARG	conflict	UNP P0AG00
C	349	GLU	-	expression tag	UNP P0AG00
C	350	PHE	-	expression tag	UNP P0AG00
C	351	ARG	-	expression tag	UNP P0AG00
C	352	VAL	-	expression tag	UNP P0AG00
C	353	PRO	-	expression tag	UNP P0AG00
C	354	GLY	-	expression tag	UNP P0AG00
C	355	SER	-	expression tag	UNP P0AG00
C	356	HIS	-	expression tag	UNP P0AG00
C	357	HIS	-	expression tag	UNP P0AG00
C	358	HIS	-	expression tag	UNP P0AG00
C	359	HIS	-	expression tag	UNP P0AG00
C	360	HIS	-	expression tag	UNP P0AG00
C	361	HIS	-	expression tag	UNP P0AG00

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Chain	Residue	Modelled	Actual	Comment	Reference
C	362	HIS	-	expression tag	UNP P0AG00
C	363	HIS	-	expression tag	UNP P0AG00
H	267	GLU	ARG	conflict	UNP P0AG00
H	349	GLU	-	expression tag	UNP P0AG00
H	350	PHE	-	expression tag	UNP P0AG00
H	351	ARG	-	expression tag	UNP P0AG00
H	352	VAL	-	expression tag	UNP P0AG00
H	353	PRO	-	expression tag	UNP P0AG00
H	354	GLY	-	expression tag	UNP P0AG00
H	355	SER	-	expression tag	UNP P0AG00
H	356	HIS	-	expression tag	UNP P0AG00
H	357	HIS	-	expression tag	UNP P0AG00
H	358	HIS	-	expression tag	UNP P0AG00
H	359	HIS	-	expression tag	UNP P0AG00
H	360	HIS	-	expression tag	UNP P0AG00
H	361	HIS	-	expression tag	UNP P0AG00
H	362	HIS	-	expression tag	UNP P0AG00
H	363	HIS	-	expression tag	UNP P0AG00
A	267	GLU	ARG	conflict	UNP P0AG00
A	349	GLU	-	expression tag	UNP P0AG00
A	350	PHE	-	expression tag	UNP P0AG00
A	351	ARG	-	expression tag	UNP P0AG00
A	352	VAL	-	expression tag	UNP P0AG00
A	353	PRO	-	expression tag	UNP P0AG00
A	354	GLY	-	expression tag	UNP P0AG00
A	355	SER	-	expression tag	UNP P0AG00
A	356	HIS	-	expression tag	UNP P0AG00
A	357	HIS	-	expression tag	UNP P0AG00
A	358	HIS	-	expression tag	UNP P0AG00
A	359	HIS	-	expression tag	UNP P0AG00
A	360	HIS	-	expression tag	UNP P0AG00
A	361	HIS	-	expression tag	UNP P0AG00
A	362	HIS	-	expression tag	UNP P0AG00
A	363	HIS	-	expression tag	UNP P0AG00
B	267	GLU	ARG	conflict	UNP P0AG00
B	349	GLU	-	expression tag	UNP P0AG00
B	350	PHE	-	expression tag	UNP P0AG00
B	351	ARG	-	expression tag	UNP P0AG00
B	352	VAL	-	expression tag	UNP P0AG00
B	353	PRO	-	expression tag	UNP P0AG00
B	354	GLY	-	expression tag	UNP P0AG00
B	355	SER	-	expression tag	UNP P0AG00

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Chain	Residue	Modelled	Actual	Comment	Reference
B	356	HIS	-	expression tag	UNP P0AG00
B	357	HIS	-	expression tag	UNP P0AG00
B	358	HIS	-	expression tag	UNP P0AG00
B	359	HIS	-	expression tag	UNP P0AG00
B	360	HIS	-	expression tag	UNP P0AG00
B	361	HIS	-	expression tag	UNP P0AG00
B	362	HIS	-	expression tag	UNP P0AG00
B	363	HIS	-	expression tag	UNP P0AG00
D	267	GLU	ARG	conflict	UNP P0AG00
D	349	GLU	-	expression tag	UNP P0AG00
D	350	PHE	-	expression tag	UNP P0AG00
D	351	ARG	-	expression tag	UNP P0AG00
D	352	VAL	-	expression tag	UNP P0AG00
D	353	PRO	-	expression tag	UNP P0AG00
D	354	GLY	-	expression tag	UNP P0AG00
D	355	SER	-	expression tag	UNP P0AG00
D	356	HIS	-	expression tag	UNP P0AG00
D	357	HIS	-	expression tag	UNP P0AG00
D	358	HIS	-	expression tag	UNP P0AG00
D	359	HIS	-	expression tag	UNP P0AG00
D	360	HIS	-	expression tag	UNP P0AG00
D	361	HIS	-	expression tag	UNP P0AG00
D	362	HIS	-	expression tag	UNP P0AG00
D	363	HIS	-	expression tag	UNP P0AG00
E	267	GLU	ARG	conflict	UNP P0AG00
E	349	GLU	-	expression tag	UNP P0AG00
E	350	PHE	-	expression tag	UNP P0AG00
E	351	ARG	-	expression tag	UNP P0AG00
E	352	VAL	-	expression tag	UNP P0AG00
E	353	PRO	-	expression tag	UNP P0AG00
E	354	GLY	-	expression tag	UNP P0AG00
E	355	SER	-	expression tag	UNP P0AG00
E	356	HIS	-	expression tag	UNP P0AG00
E	357	HIS	-	expression tag	UNP P0AG00
E	358	HIS	-	expression tag	UNP P0AG00
E	359	HIS	-	expression tag	UNP P0AG00
E	360	HIS	-	expression tag	UNP P0AG00
E	361	HIS	-	expression tag	UNP P0AG00
E	362	HIS	-	expression tag	UNP P0AG00
E	363	HIS	-	expression tag	UNP P0AG00
F	267	GLU	ARG	conflict	UNP P0AG00
F	349	GLU	-	expression tag	UNP P0AG00

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Chain	Residue	Modelled	Actual	Comment	Reference
F	350	PHE	-	expression tag	UNP P0AG00
F	351	ARG	-	expression tag	UNP P0AG00
F	352	VAL	-	expression tag	UNP P0AG00
F	353	PRO	-	expression tag	UNP P0AG00
F	354	GLY	-	expression tag	UNP P0AG00
F	355	SER	-	expression tag	UNP P0AG00
F	356	HIS	-	expression tag	UNP P0AG00
F	357	HIS	-	expression tag	UNP P0AG00
F	358	HIS	-	expression tag	UNP P0AG00
F	359	HIS	-	expression tag	UNP P0AG00
F	360	HIS	-	expression tag	UNP P0AG00
F	361	HIS	-	expression tag	UNP P0AG00
F	362	HIS	-	expression tag	UNP P0AG00
F	363	HIS	-	expression tag	UNP P0AG00
G	267	GLU	ARG	conflict	UNP P0AG00
G	349	GLU	-	expression tag	UNP P0AG00
G	350	PHE	-	expression tag	UNP P0AG00
G	351	ARG	-	expression tag	UNP P0AG00
G	352	VAL	-	expression tag	UNP P0AG00
G	353	PRO	-	expression tag	UNP P0AG00
G	354	GLY	-	expression tag	UNP P0AG00
G	355	SER	-	expression tag	UNP P0AG00
G	356	HIS	-	expression tag	UNP P0AG00
G	357	HIS	-	expression tag	UNP P0AG00
G	358	HIS	-	expression tag	UNP P0AG00
G	359	HIS	-	expression tag	UNP P0AG00
G	360	HIS	-	expression tag	UNP P0AG00
G	361	HIS	-	expression tag	UNP P0AG00
G	362	HIS	-	expression tag	UNP P0AG00
G	363	HIS	-	expression tag	UNP P0AG00

PHE
ARG
VAL
PRO
GLY
SER
HIS
HIS
HIS
HIS
HIS
HIS

- Molecule 1: ECA polysaccharide chain length modulation protein

Chain B: 

MET THR GLN PRO MET PRO GLY LYS PRO ALA GLU ASP GLU ASN GLU L17 G21 G21 T25 S56 A59 R63 P64 T65 V66 N67 M68 V84 R85 S86 N87 M88 S110 W111 D112 T113 R114 R115 E116 F117 W118 L119 Q120 Y124 K125 M142 I146 D152

V157 L163 T167 A168 P169 L175 K210 M224 N225 S226 R241 D245 V246 P247 D279 Y282 R286 Q303 T304 Y305 P311 M328 W329 G330 I331 A338 R345 K348

GLU PHE ARG VAL PRO GLY SER HIS HIS HIS HIS HIS HIS HIS HIS

- Molecule 1: ECA polysaccharide chain length modulation protein

Chain D: 

MET THR GLN PRO MET PRO GLY LYS PRO ALA GLU ASP GLU ASN GLU L17 L26 I33 M36 L45 Q53 E54 A59 N81 L82 V84 M83 A89 S90 M97 L108 W118 T121 D122 Y123 Y124 K133 M142 D152 F153 T154 R155

L163 P169 N173 L174 L175 Y178 E193 L194 K195 R201 K232 E235 Q236 H237 D245 V246 P247 A248 E249 E250 L251 P252 D253 S254 E255 M256 F257 D279 L298 D299 P300 R301 P311 R317 D318 S319 P320 R321 F324 L325 M326 G334 L336 K348

GLU PHE ARG VAL PRO GLY SER HIS HIS HIS HIS HIS HIS HIS HIS

- Molecule 1: ECA polysaccharide chain length modulation protein

Chain E: 

MET THR GLN PRO MET PRO GLY LYS PRO ALA GLU ASP GLU ASN GLU L17 G21 G21 T25 S56 A59 R63 P64 T65 V66 N67 M68 L69 V84 R85 S86 N87 M88 M97 S110 W111 D112 T113 R114 E116 F117 W118 L119 Q120 Y124 K125 M142 I146

D152 V157 L163 T167 A168 P169 L175 M224 N225 S226 R241 S242 D245 V246 P247 G260 D279 Y282 R286 Q303 T304 Y305 P311 M328 W329 G330 I331 A338 R345 K348

GLU PHE ARG VAL PRO GLY SER HIS HIS HIS HIS HIS HIS HIS HIS

- Molecule 1: ECA polysaccharide chain length modulation protein

Chain F: 

MET THR GLN PRO MET PRO GLY LYS PRO ALA GLU ASP GLU ASN GLU L17 L26 I33 M36 L45 Q53 E54 A59 N81 L82 V84 M88 A89 S90 M97 L108 W118 T121 D122 Y123 Y124 K133 M142 D152 R155 L163

P169 N173 L174 L175 Y178 E193 L194 K195 W198 R201 M224 K232 E235 Q236 H237 D245 V246 P247 A248 E249 E250 L251 P252 D253 S254 E255 M256 F257 D279 T291 V294 G295 P296 T297 L298 P300 R301 P311 R317 D318 S319 P320 R321

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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	308817	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.600	Depositor
Minimum map value	-0.227	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	414.0, 414.0, 414.0	wwPDB
Map dimensions	500, 500, 500	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	0.13	0/2706	0.30	0/3662
1	B	0.14	0/2706	0.33	0/3662
1	C	0.13	0/2706	0.30	0/3662
1	D	0.13	0/2706	0.29	0/3662
1	E	0.14	0/2706	0.32	0/3662
1	F	0.13	0/2706	0.30	0/3662
1	G	0.14	0/2706	0.33	0/3662
1	H	0.14	0/2706	0.33	0/3662
All	All	0.13	0/21648	0.31	0/29296

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	2653	0	2633	33	0
1	B	2653	0	2633	30	0
1	C	2653	0	2633	35	0
1	D	2653	0	2633	34	0
1	E	2653	0	2633	32	0
1	F	2653	0	2633	37	0
1	G	2653	0	2633	31	0
1	H	2653	0	2633	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	21224	0	21064	258	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 258 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:C:124:TYR:HB2	1:C:142:MET:HE1	1.59	0.84
1:D:124:TYR:HB2	1:D:142:MET:HE1	1.59	0.84
1:A:124:TYR:HB2	1:A:142:MET:HE1	1.59	0.83
1:F:124:TYR:HB2	1:F:142:MET:HE1	1.59	0.82
1:G:84:VAL:HG23	1:G:85:ARG:HE	1.47	0.80

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	330/363 (91%)	313 (95%)	17 (5%)	0	100	100
1	B	330/363 (91%)	320 (97%)	10 (3%)	0	100	100
1	C	330/363 (91%)	313 (95%)	17 (5%)	0	100	100
1	D	330/363 (91%)	313 (95%)	17 (5%)	0	100	100
1	E	330/363 (91%)	320 (97%)	10 (3%)	0	100	100
1	F	330/363 (91%)	313 (95%)	17 (5%)	0	100	100
1	G	330/363 (91%)	320 (97%)	10 (3%)	0	100	100
1	H	330/363 (91%)	320 (97%)	10 (3%)	0	100	100
All	All	2640/2904 (91%)	2532 (96%)	108 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	276/303 (91%)	275 (100%)	1 (0%)	84	93
1	B	276/303 (91%)	272 (99%)	4 (1%)	59	81
1	C	276/303 (91%)	274 (99%)	2 (1%)	76	89
1	D	276/303 (91%)	275 (100%)	1 (0%)	84	93
1	E	276/303 (91%)	272 (99%)	4 (1%)	59	81
1	F	276/303 (91%)	275 (100%)	1 (0%)	84	93
1	G	276/303 (91%)	273 (99%)	3 (1%)	65	84
1	H	276/303 (91%)	273 (99%)	3 (1%)	65	84
All	All	2208/2424 (91%)	2189 (99%)	19 (1%)	68	87

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	328	MET
1	G	226	SER
1	G	328	MET
1	G	56	SER
1	B	226	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	272	GLN
1	G	144	ASN
1	G	272	GLN
1	G	158	ASN
1	B	144	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.

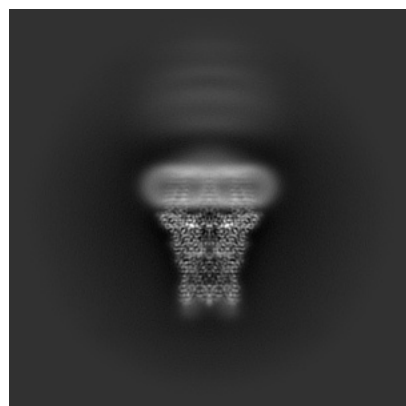
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17389. These allow visual inspection of the internal detail of the map and identification of artifacts.

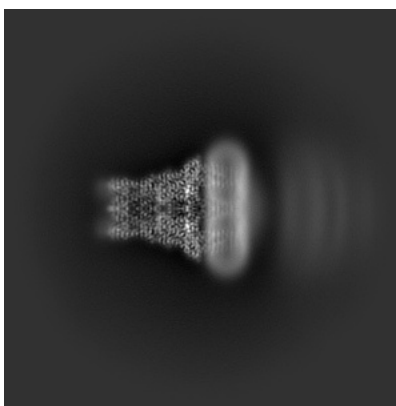
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

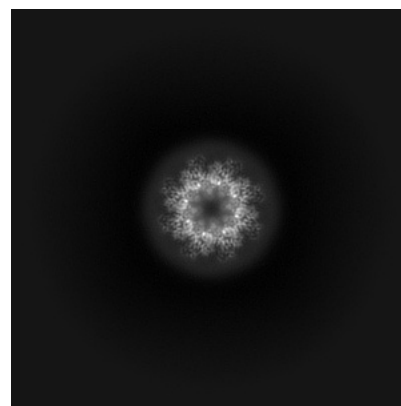
6.1.1 Primary map



X

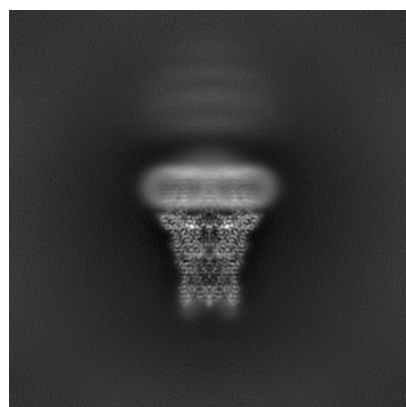


Y

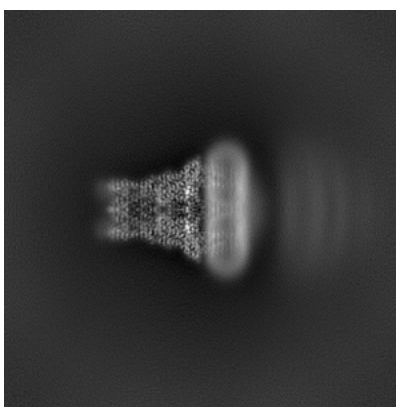


Z

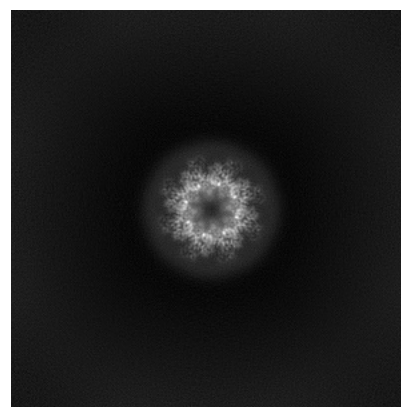
6.1.2 Raw map



X



Y

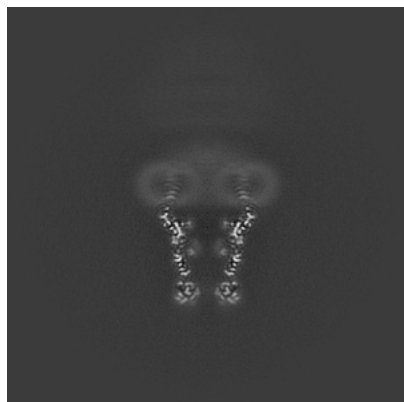


Z

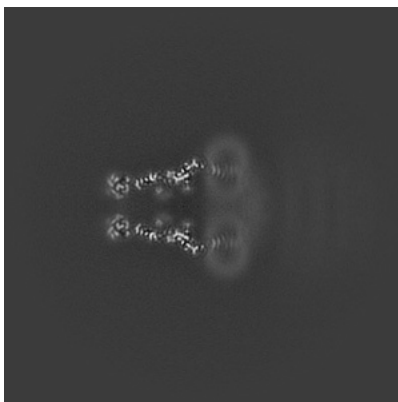
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

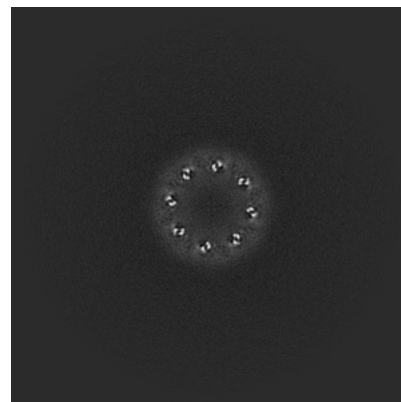
6.2.1 Primary map



X Index: 250

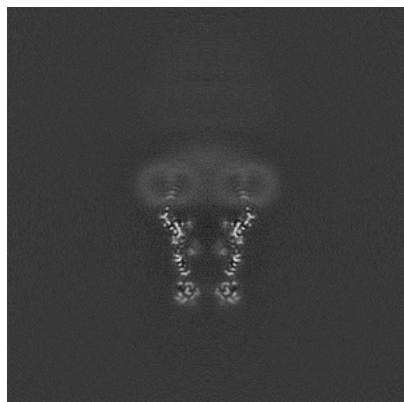


Y Index: 250

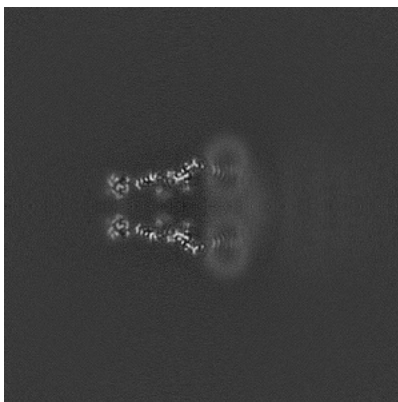


Z Index: 250

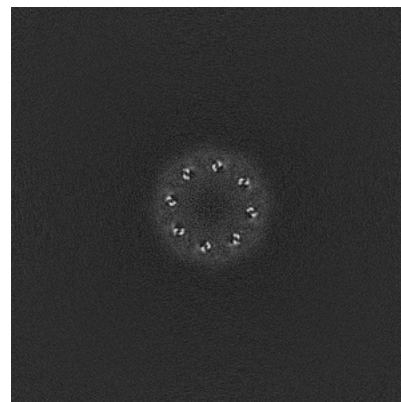
6.2.2 Raw map



X Index: 250



Y Index: 250

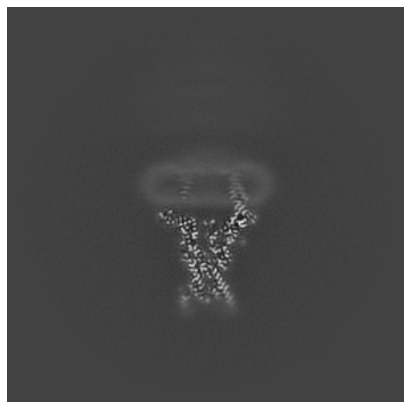


Z Index: 250

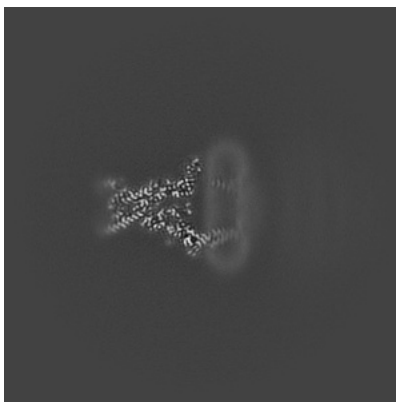
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

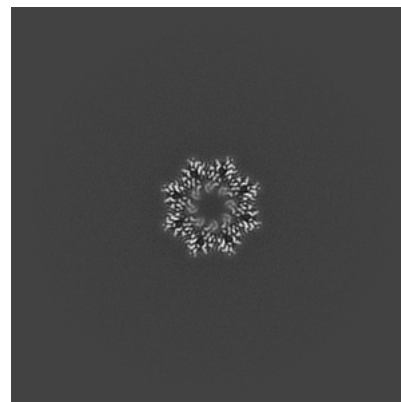
6.3.1 Primary map



X Index: 221

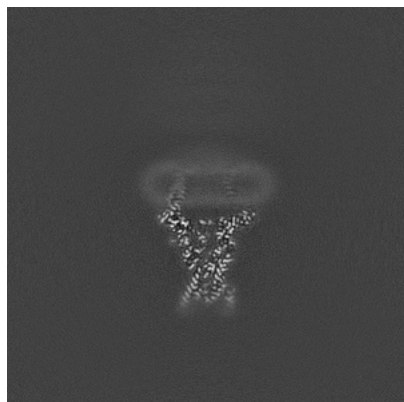


Y Index: 221

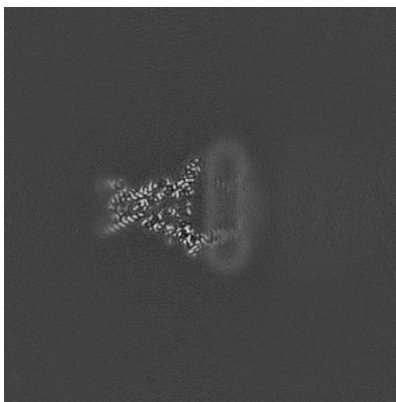


Z Index: 230

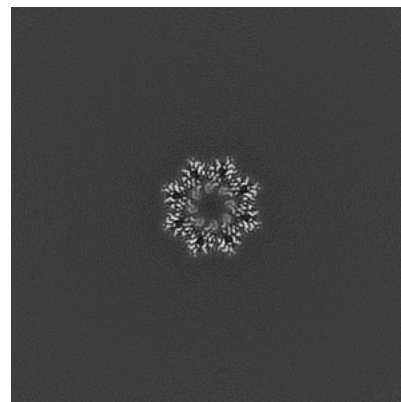
6.3.2 Raw map



X Index: 278



Y Index: 222



Z Index: 230

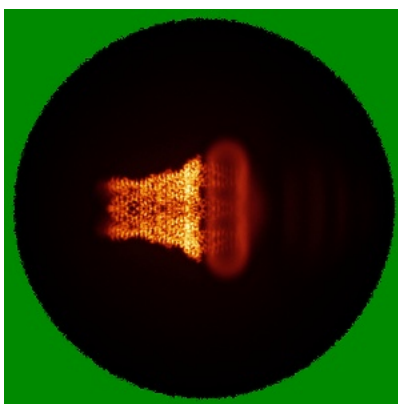
The images above show the largest variance slices of the map in three orthogonal directions.

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

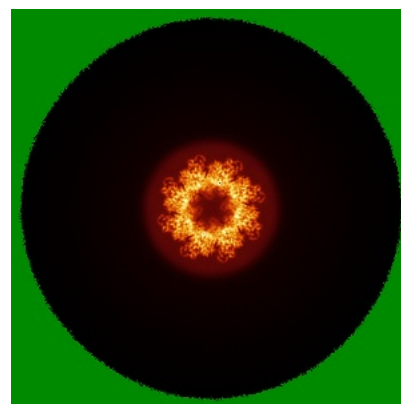
6.4.1 Primary map



X

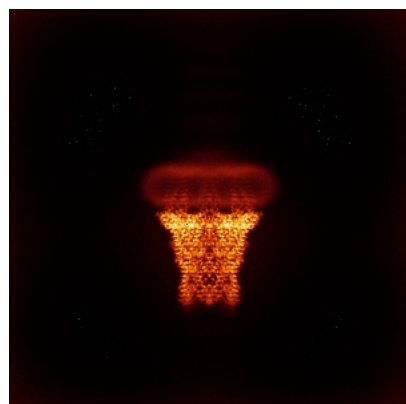


Y

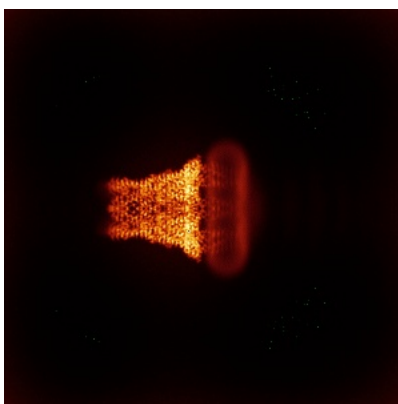


Z

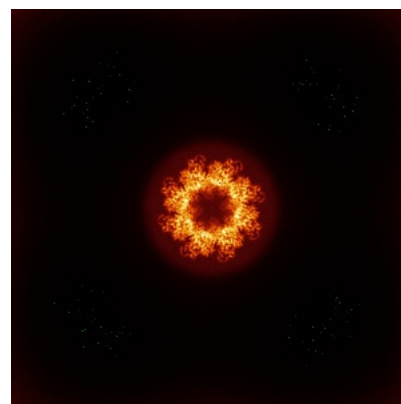
6.4.2 Raw map



X



Y

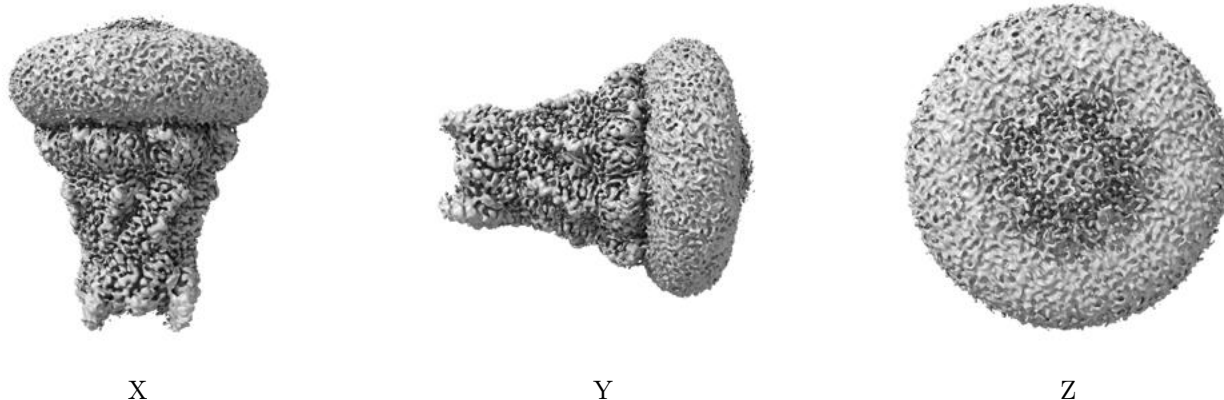


Z

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 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

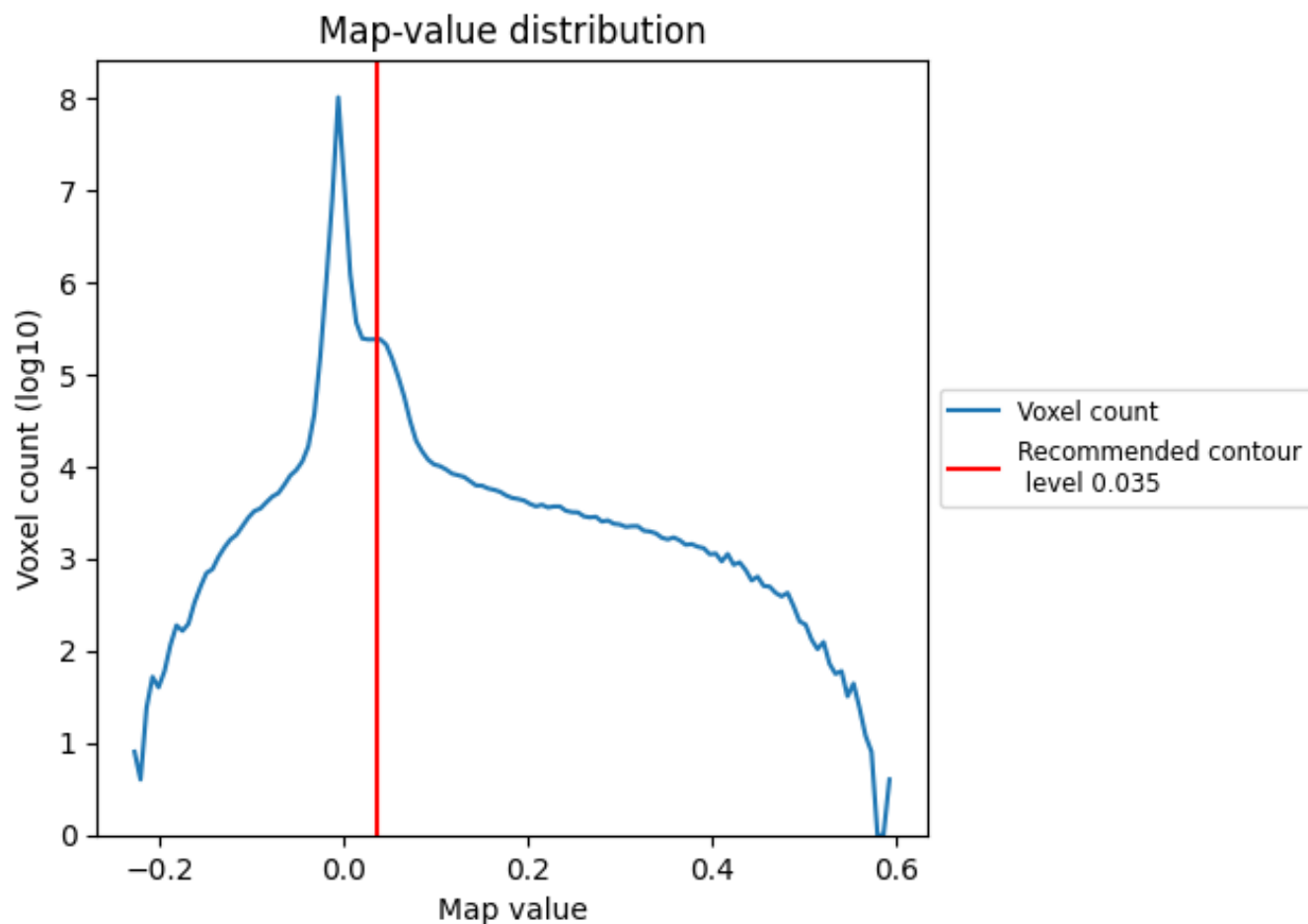
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

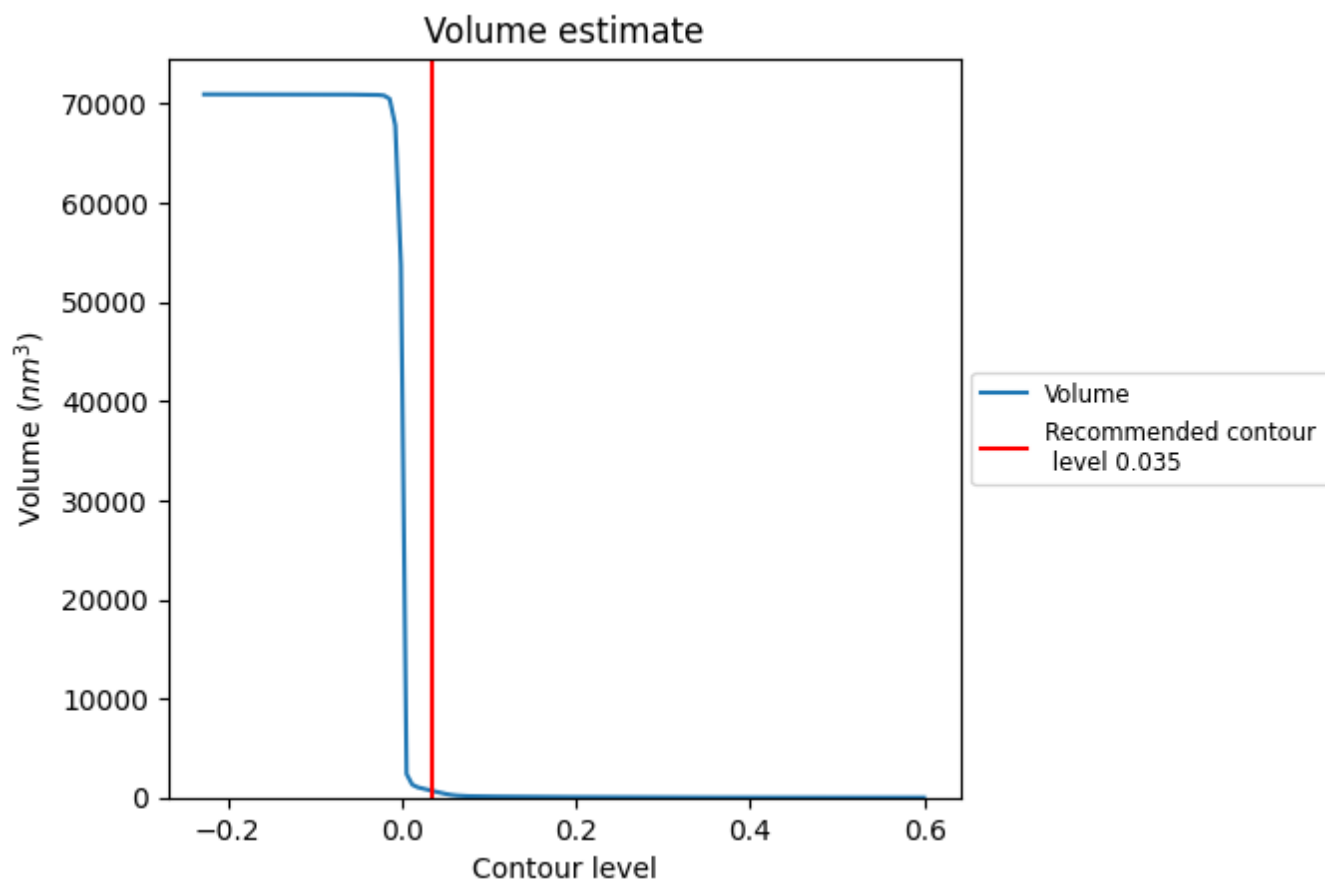
This section contains the results of statistical analysis of the map.

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.

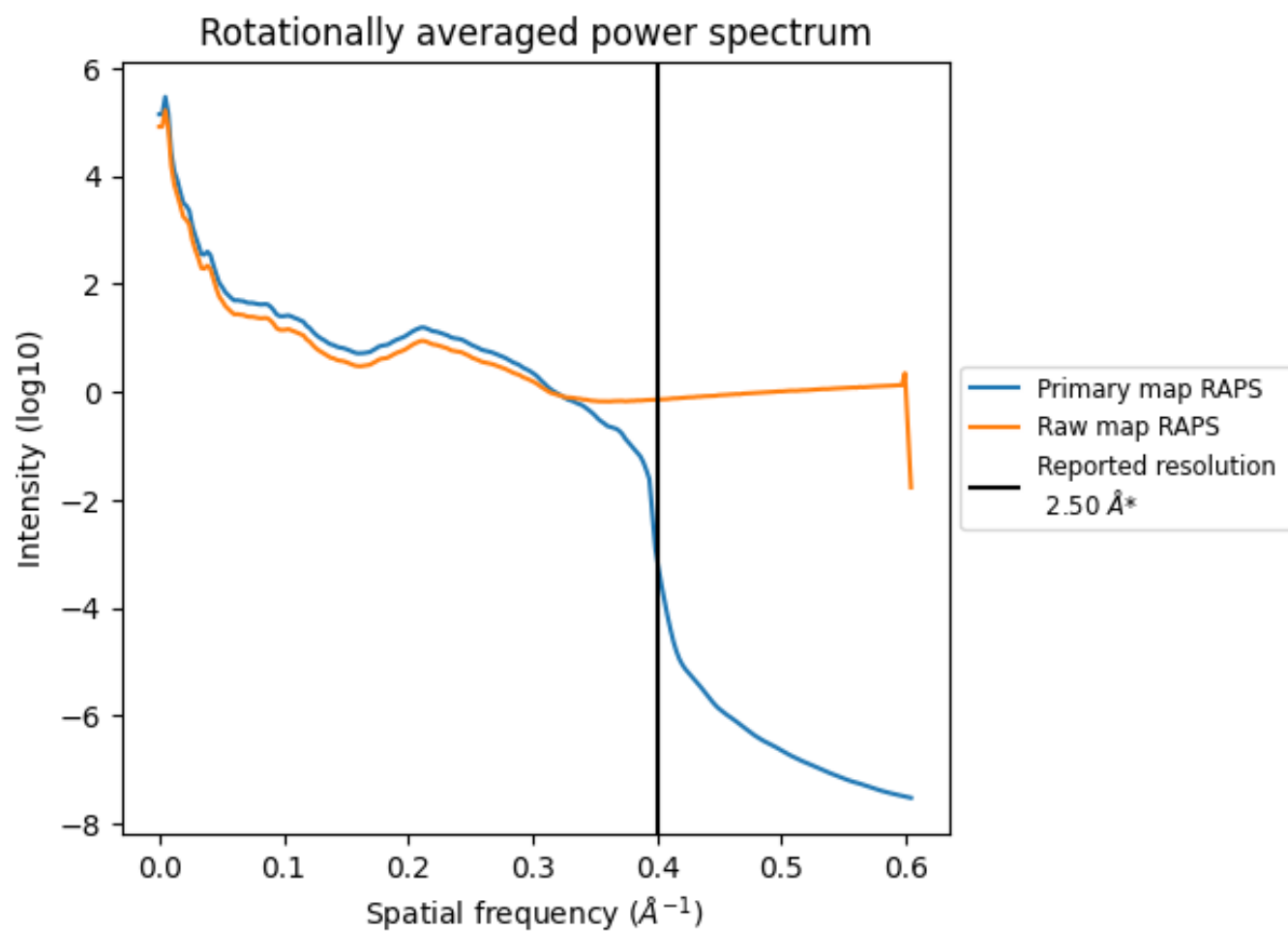
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 674 nm^3 ; this corresponds to an approximate mass of 609 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 ⓘ

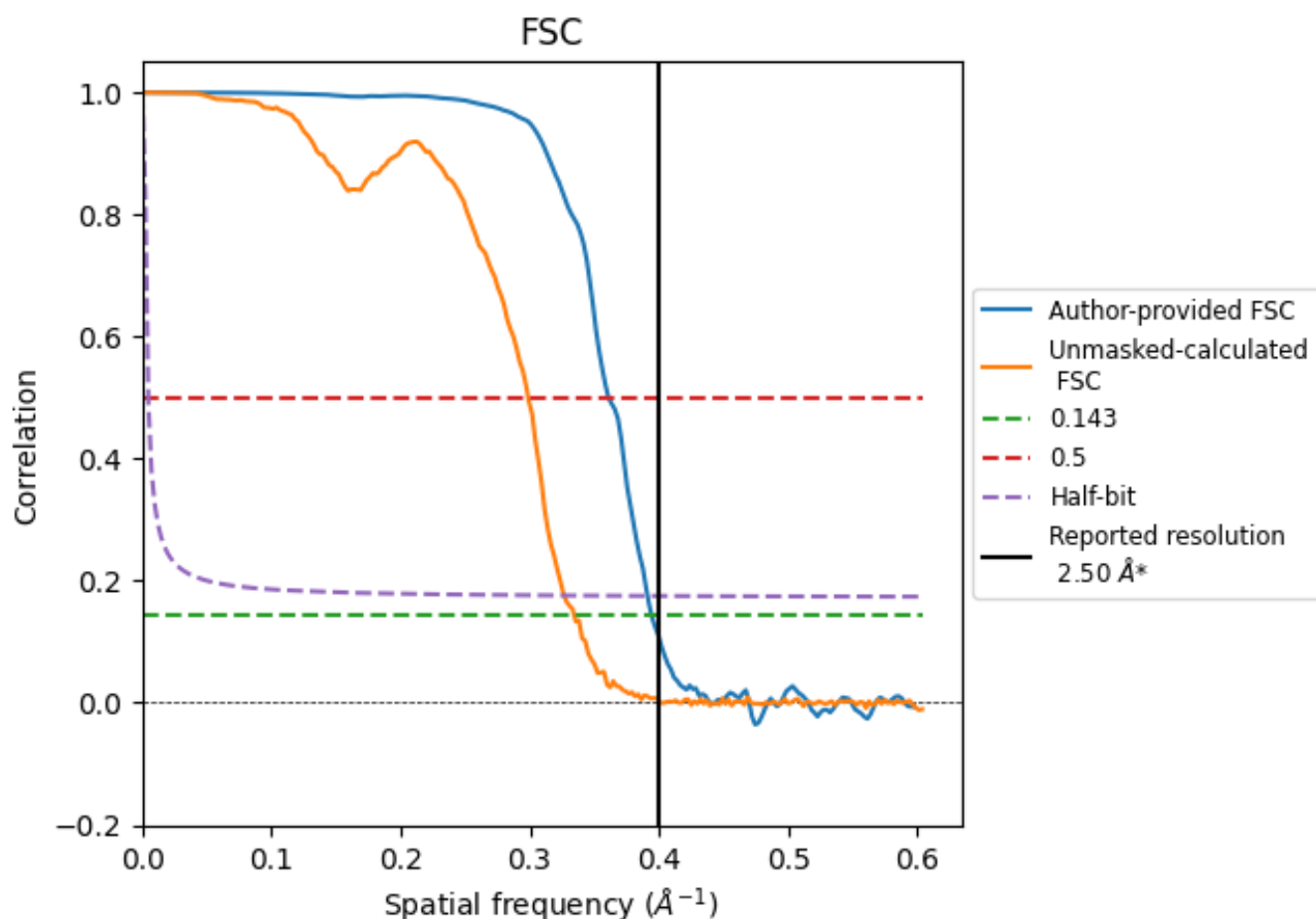


*Reported resolution corresponds to spatial frequency of 0.400 $\text{\AA}^{-1}$

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 0.400 Å⁻¹

8.2 Resolution estimates [i](#)

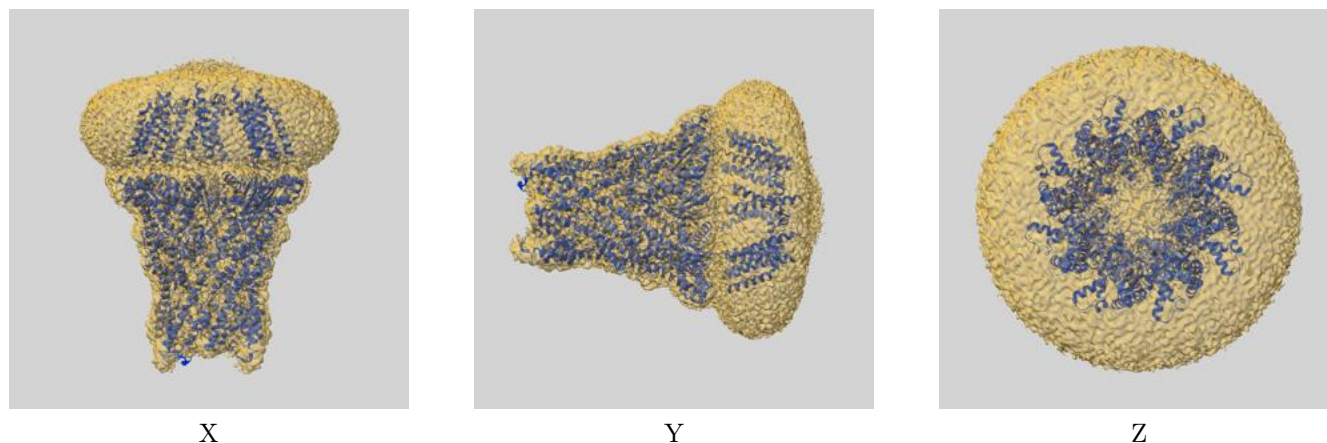
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.53	2.77	2.56
Unmasked-calculated*	2.99	3.35	3.06

*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 2.99 differs from the reported value 2.5 by more than 10 %

9 Map-model fit [i](#)

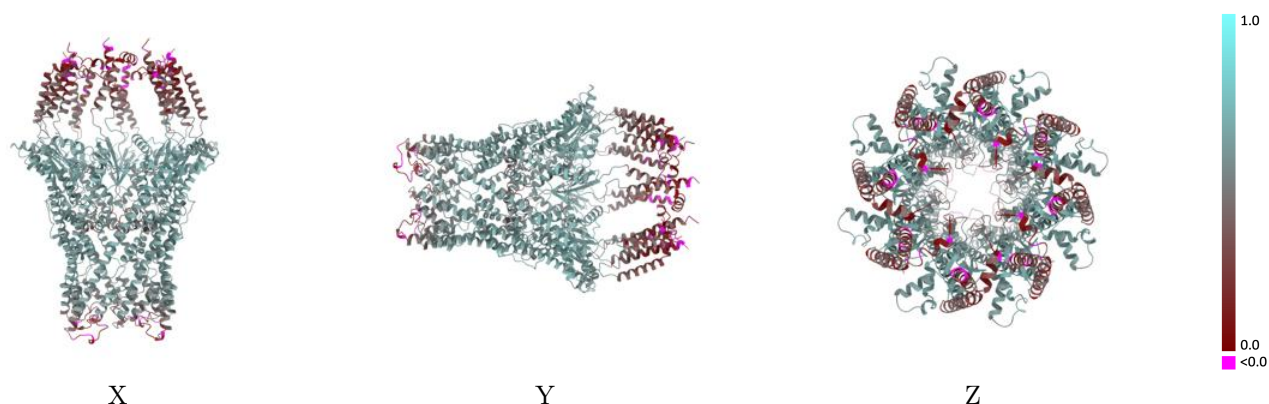
This section contains information regarding the fit between EMDB map EMD-17389 and PDB model 8P3P. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.035 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](#)

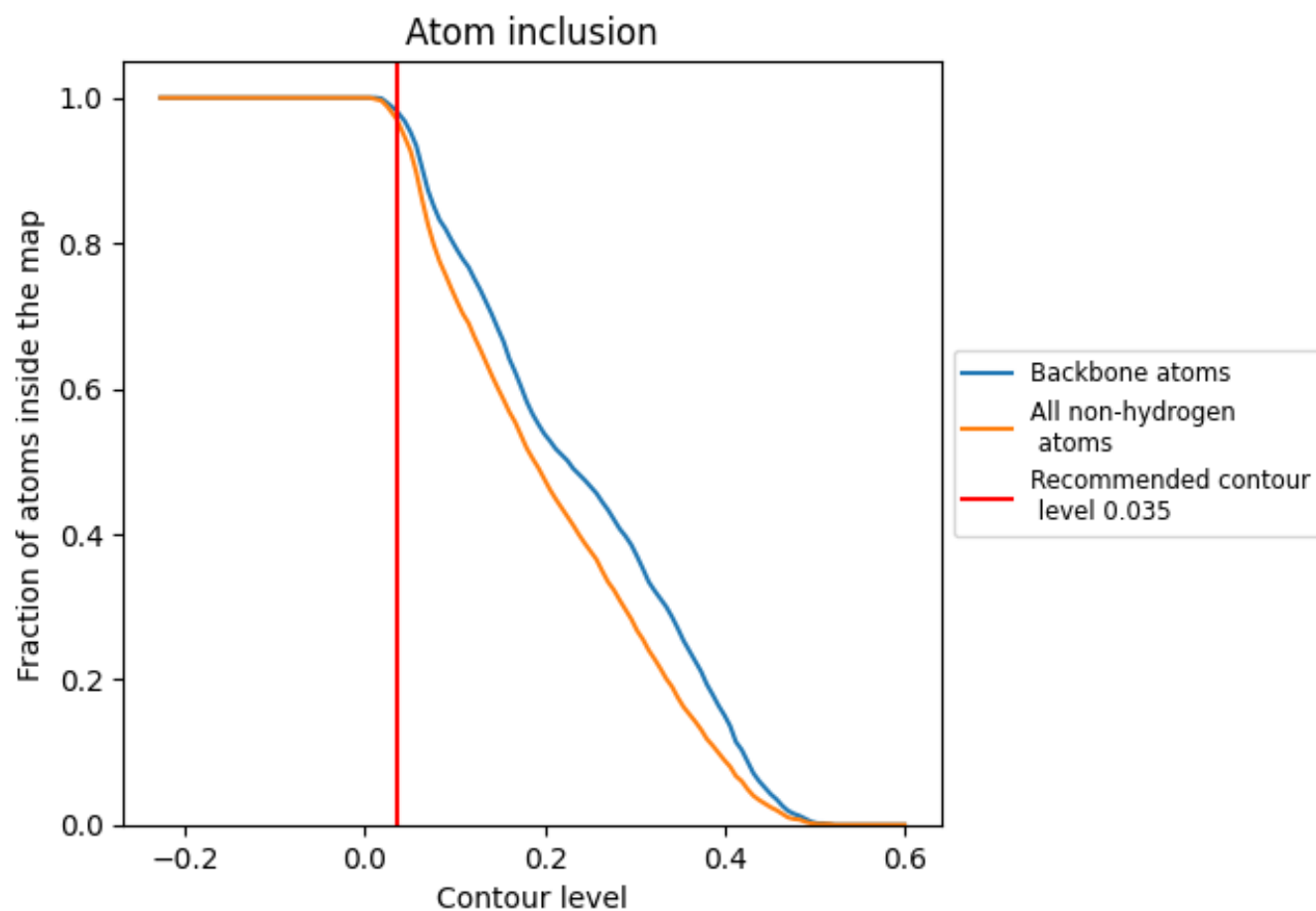


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 98% of all backbone atoms, 97% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9710	0.5060
A	0.9580	0.4940
B	0.9830	0.5180
C	0.9580	0.4950
D	0.9580	0.4940
E	0.9830	0.5170
F	0.9580	0.4970
G	0.9830	0.5170
H	0.9830	0.5180

1.0

0.0

<0.0