



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 12:39 AM UTC

PDB ID : 9K4B / pdb_00009k4b
EMDB ID : EMD-62052
Title : Cryo-EM structure of depolymerase S2-4 from Klebsiella phage K64-1
Authors : Zhao, R.; Du, T.; Ren, Z.; Gu, J.; Ru, H.
Deposited on : 2024-10-21
Resolution : 2.18 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

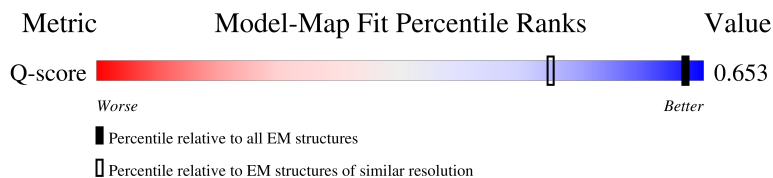
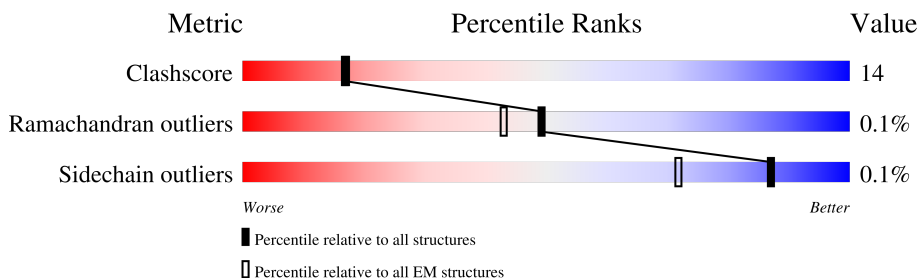
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.18 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	2701 (1.70 - 2.68)

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	922	 50% 22% 28%
1	B	922	 50% 23% 28%
1	C	922	 50% 22% 28%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15447 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 Depolymerase, capsule K1-specific.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	668	Total	C	N	O	S	0	0
			5149	3220	858	1046	25		
1	B	668	Total	C	N	O	S	0	0
			5149	3220	858	1046	25		
1	C	668	Total	C	N	O	S	0	0
			5149	3220	858	1046	25		

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	initiating methionine	UNP A0A0A8J8T2
A	-32	GLY	-	expression tag	UNP A0A0A8J8T2
A	-31	SER	-	expression tag	UNP A0A0A8J8T2
A	-30	SER	-	expression tag	UNP A0A0A8J8T2
A	-29	HIS	-	expression tag	UNP A0A0A8J8T2
A	-28	HIS	-	expression tag	UNP A0A0A8J8T2
A	-27	HIS	-	expression tag	UNP A0A0A8J8T2
A	-26	HIS	-	expression tag	UNP A0A0A8J8T2
A	-25	HIS	-	expression tag	UNP A0A0A8J8T2
A	-24	HIS	-	expression tag	UNP A0A0A8J8T2
A	-23	SER	-	expression tag	UNP A0A0A8J8T2
A	-22	SER	-	expression tag	UNP A0A0A8J8T2
A	-21	GLY	-	expression tag	UNP A0A0A8J8T2
A	-20	LEU	-	expression tag	UNP A0A0A8J8T2
A	-19	VAL	-	expression tag	UNP A0A0A8J8T2
A	-18	PRO	-	expression tag	UNP A0A0A8J8T2
A	-17	ARG	-	expression tag	UNP A0A0A8J8T2
A	-16	GLY	-	expression tag	UNP A0A0A8J8T2
A	-15	SER	-	expression tag	UNP A0A0A8J8T2
A	-14	HIS	-	expression tag	UNP A0A0A8J8T2
A	-13	MET	-	expression tag	UNP A0A0A8J8T2
A	-12	ALA	-	expression tag	UNP A0A0A8J8T2
A	-11	SER	-	expression tag	UNP A0A0A8J8T2
A	-10	MET	-	expression tag	UNP A0A0A8J8T2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	THR	-	expression tag	UNP A0A0A8J8T2
A	-8	GLY	-	expression tag	UNP A0A0A8J8T2
A	-7	GLY	-	expression tag	UNP A0A0A8J8T2
A	-6	GLN	-	expression tag	UNP A0A0A8J8T2
A	-5	GLN	-	expression tag	UNP A0A0A8J8T2
A	-4	MET	-	expression tag	UNP A0A0A8J8T2
A	-3	GLY	-	expression tag	UNP A0A0A8J8T2
A	-2	ARG	-	expression tag	UNP A0A0A8J8T2
A	-1	GLY	-	expression tag	UNP A0A0A8J8T2
A	0	SER	-	expression tag	UNP A0A0A8J8T2
B	-33	MET	-	initiating methionine	UNP A0A0A8J8T2
B	-32	GLY	-	expression tag	UNP A0A0A8J8T2
B	-31	SER	-	expression tag	UNP A0A0A8J8T2
B	-30	SER	-	expression tag	UNP A0A0A8J8T2
B	-29	HIS	-	expression tag	UNP A0A0A8J8T2
B	-28	HIS	-	expression tag	UNP A0A0A8J8T2
B	-27	HIS	-	expression tag	UNP A0A0A8J8T2
B	-26	HIS	-	expression tag	UNP A0A0A8J8T2
B	-25	HIS	-	expression tag	UNP A0A0A8J8T2
B	-24	HIS	-	expression tag	UNP A0A0A8J8T2
B	-23	SER	-	expression tag	UNP A0A0A8J8T2
B	-22	SER	-	expression tag	UNP A0A0A8J8T2
B	-21	GLY	-	expression tag	UNP A0A0A8J8T2
B	-20	LEU	-	expression tag	UNP A0A0A8J8T2
B	-19	VAL	-	expression tag	UNP A0A0A8J8T2
B	-18	PRO	-	expression tag	UNP A0A0A8J8T2
B	-17	ARG	-	expression tag	UNP A0A0A8J8T2
B	-16	GLY	-	expression tag	UNP A0A0A8J8T2
B	-15	SER	-	expression tag	UNP A0A0A8J8T2
B	-14	HIS	-	expression tag	UNP A0A0A8J8T2
B	-13	MET	-	expression tag	UNP A0A0A8J8T2
B	-12	ALA	-	expression tag	UNP A0A0A8J8T2
B	-11	SER	-	expression tag	UNP A0A0A8J8T2
B	-10	MET	-	expression tag	UNP A0A0A8J8T2
B	-9	THR	-	expression tag	UNP A0A0A8J8T2
B	-8	GLY	-	expression tag	UNP A0A0A8J8T2
B	-7	GLY	-	expression tag	UNP A0A0A8J8T2
B	-6	GLN	-	expression tag	UNP A0A0A8J8T2
B	-5	GLN	-	expression tag	UNP A0A0A8J8T2
B	-4	MET	-	expression tag	UNP A0A0A8J8T2
B	-3	GLY	-	expression tag	UNP A0A0A8J8T2
B	-2	ARG	-	expression tag	UNP A0A0A8J8T2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP A0A0A8J8T2
B	0	SER	-	expression tag	UNP A0A0A8J8T2
C	-33	MET	-	initiating methionine	UNP A0A0A8J8T2
C	-32	GLY	-	expression tag	UNP A0A0A8J8T2
C	-31	SER	-	expression tag	UNP A0A0A8J8T2
C	-30	SER	-	expression tag	UNP A0A0A8J8T2
C	-29	HIS	-	expression tag	UNP A0A0A8J8T2
C	-28	HIS	-	expression tag	UNP A0A0A8J8T2
C	-27	HIS	-	expression tag	UNP A0A0A8J8T2
C	-26	HIS	-	expression tag	UNP A0A0A8J8T2
C	-25	HIS	-	expression tag	UNP A0A0A8J8T2
C	-24	HIS	-	expression tag	UNP A0A0A8J8T2
C	-23	SER	-	expression tag	UNP A0A0A8J8T2
C	-22	SER	-	expression tag	UNP A0A0A8J8T2
C	-21	GLY	-	expression tag	UNP A0A0A8J8T2
C	-20	LEU	-	expression tag	UNP A0A0A8J8T2
C	-19	VAL	-	expression tag	UNP A0A0A8J8T2
C	-18	PRO	-	expression tag	UNP A0A0A8J8T2
C	-17	ARG	-	expression tag	UNP A0A0A8J8T2
C	-16	GLY	-	expression tag	UNP A0A0A8J8T2
C	-15	SER	-	expression tag	UNP A0A0A8J8T2
C	-14	HIS	-	expression tag	UNP A0A0A8J8T2
C	-13	MET	-	expression tag	UNP A0A0A8J8T2
C	-12	ALA	-	expression tag	UNP A0A0A8J8T2
C	-11	SER	-	expression tag	UNP A0A0A8J8T2
C	-10	MET	-	expression tag	UNP A0A0A8J8T2
C	-9	THR	-	expression tag	UNP A0A0A8J8T2
C	-8	GLY	-	expression tag	UNP A0A0A8J8T2
C	-7	GLY	-	expression tag	UNP A0A0A8J8T2
C	-6	GLN	-	expression tag	UNP A0A0A8J8T2
C	-5	GLN	-	expression tag	UNP A0A0A8J8T2
C	-4	MET	-	expression tag	UNP A0A0A8J8T2
C	-3	GLY	-	expression tag	UNP A0A0A8J8T2
C	-2	ARG	-	expression tag	UNP A0A0A8J8T2
C	-1	GLY	-	expression tag	UNP A0A0A8J8T2
C	0	SER	-	expression tag	UNP A0A0A8J8T2



I761	D633	T534	Y296	ASP
R762	Q636	A535	GLU	ILE
P763	I637	I538	ILE	ILE
E764	R638	C541	ILE	ILE
L765	Y644	R542	MET	LEU
V768	I645	E547	GLY	ASP
K769	L648	N548	ASP	ILE
N770	A649	C549	ILE	ILE
T771	D650	N550	ILE	ILE
N772	L654	A551	GLN	GLN
N778	D655	Q554	SER	
L779	Q659	W556	D221	D221
W780	G660	V559	E222	E222
Y781	A663	E560	Y223	Y223
L791	R667	E566	V224	V224
S792	G670	D571	L225	L225
P793	K672	K572	K226	K226
P794	A673	F575	Q227	Q227
L795	T674	R579	E228	E228
N796	R678	H580	L229	L229
N797	W685	G581	L230	L230
N798	E691	S583	D231	D231
N799	D692	I584	V232	V232
L800	A695	N585	N233	N233
D801	L696	W586	A234	A234
K828	R708	S587	S235	S235
Y840	I709	Y590	S236	S236
D845	N710	G591	Y237	Y237
L846	I711	E592	L238	L238
L850	G714	P593	N239	N239
S851	I715	N594	T240	T240
N854	G725	M506	K241	K241
I855	S726	V507	N244	N244
L858	D739	Y508	S245	S245
S861	N740	C509	I246	I246
N862	C741	D510	Q247	Q247
I863	T752	K515	E248	E248
T872	L753	T517	E249	E249
N875	C752	Q518	F250	F250
R876	Y754	L519	L253	L253
L877	L755	S522	Y254	Y254
N881	F755	R618	N255	N255
I882	R756	S623	S256	S256
Y883	L888	N624	N257	N257
W884		D632	K268	K268
S887			N269	N269
L888			D273	D273
			V280	V280
			G290	G290
			A291	A291

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	4015926	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.554	Depositor
Minimum map value	-2.460	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	273.92, 273.92, 273.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.37	0/5235	0.59	1/7109 (0.0%)
1	B	0.36	0/5235	0.59	2/7109 (0.0%)
1	C	0.36	0/5235	0.59	0/7109
All	All	0.36	0/15705	0.59	3/21327 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	502	ILE	N-CA-C	-5.37	98.18	109.34
1	A	849	ILE	N-CA-C	-5.35	107.39	111.62
1	B	849	ILE	N-CA-C	-5.17	107.12	111.56

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	5149	0	5016	146	0
1	B	5149	0	5016	158	0
1	C	5149	0	5016	150	0
All	All	15447	0	15048	424	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 14.

The worst 5 of 424 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:306:ASP:OD2	1:B:340:PHE:HB2	1.75	0.85
1:B:851:SER:HB3	1:B:855:ILE:HD11	1.61	0.82
1:B:501:PRO:O	1:B:533:ARG:HA	1.78	0.82
1:A:509:CYS:HB3	1:A:512:ILE:HD11	1.63	0.81
1:A:851:SER:HB3	1:A:855:ILE:HD11	1.61	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	666/922 (72%)	638 (96%)	27 (4%)	1 (0%)	43	49
1	B	666/922 (72%)	638 (96%)	28 (4%)	0	100	100
1	C	666/922 (72%)	637 (96%)	28 (4%)	1 (0%)	43	49
All	All	1998/2766 (72%)	1913 (96%)	83 (4%)	2 (0%)	49	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	501	PRO
1	C	501	PRO

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	588/804 (73%)	588 (100%)	0	100	100
1	B	588/804 (73%)	587 (100%)	1 (0%)	87	94
1	C	588/804 (73%)	588 (100%)	0	100	100
All	All	1764/2412 (73%)	1763 (100%)	1 (0%)	87	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	502	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	485	ASN
1	C	585	ASN
1	C	580	HIS
1	C	697	ASN
1	A	699	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

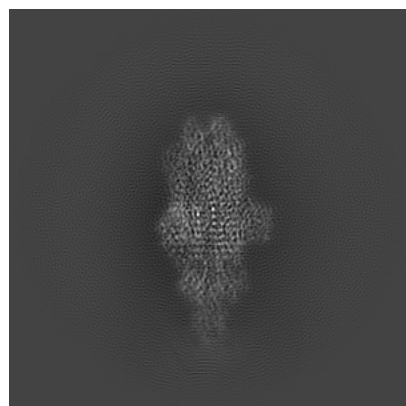
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62052. These allow visual inspection of the internal detail of the map and identification of artifacts.

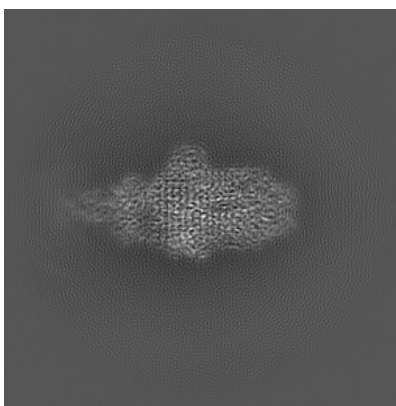
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

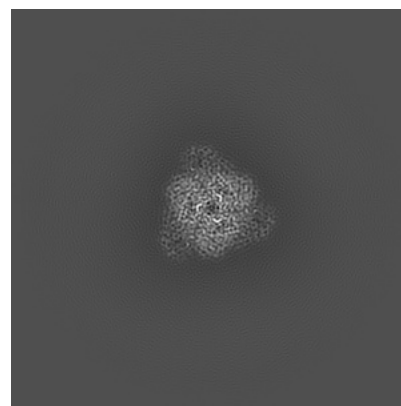
6.1.1 Primary map



X

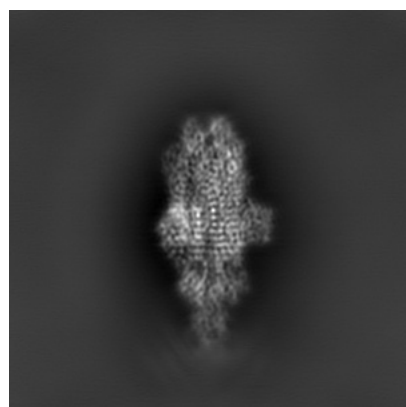


Y

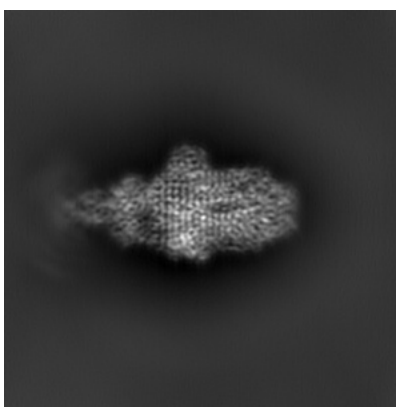


Z

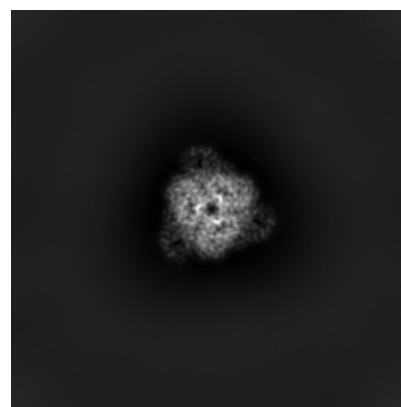
6.1.2 Raw map



X



Y

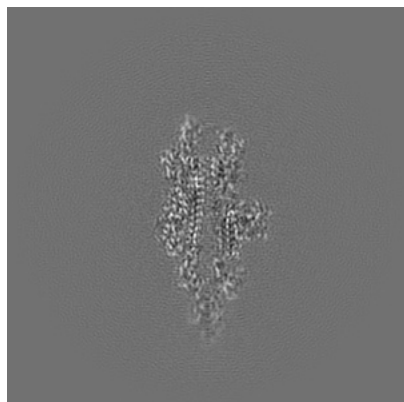


Z

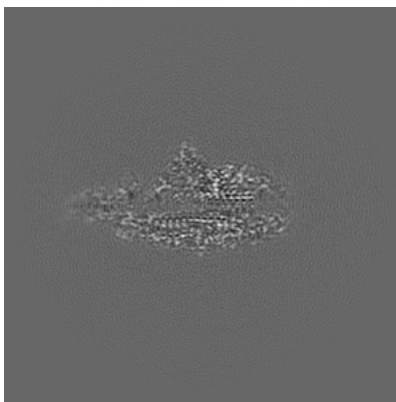
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

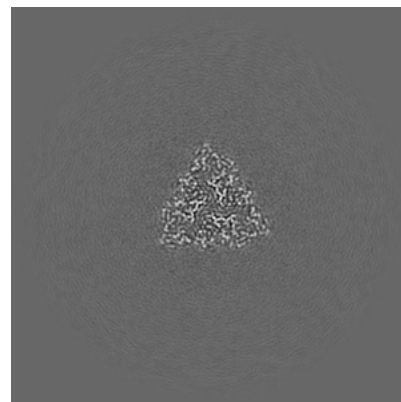
6.2.1 Primary map



X Index: 128



Y Index: 128

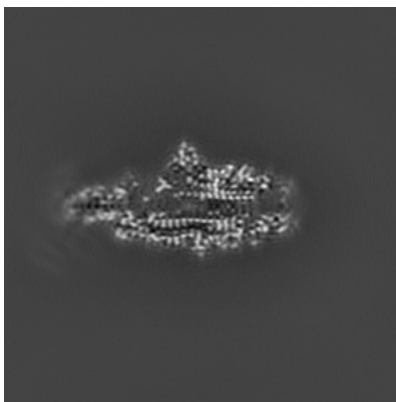


Z Index: 128

6.2.2 Raw map



X Index: 128



Y Index: 128

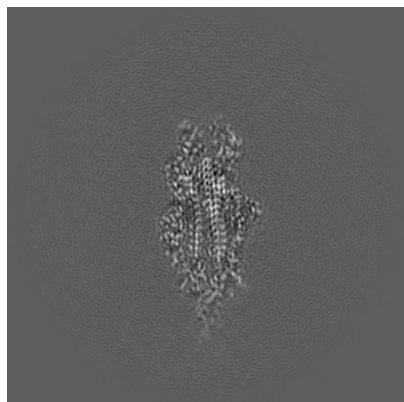


Z Index: 128

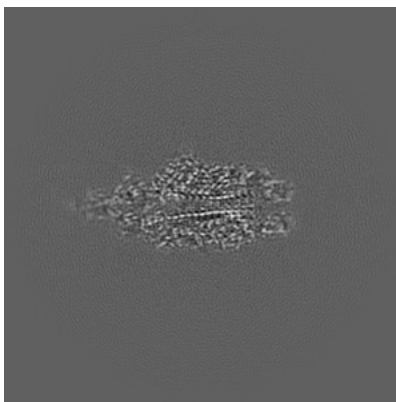
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

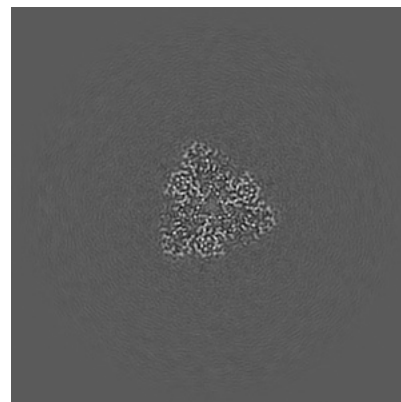
6.3.1 Primary map



X Index: 134



Y Index: 132

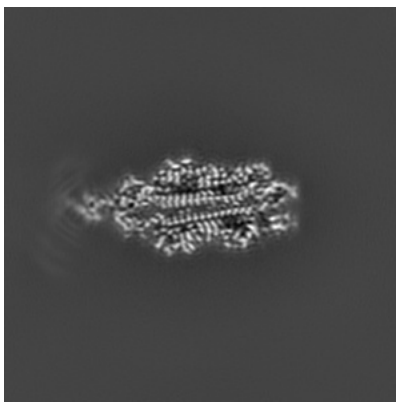


Z Index: 118

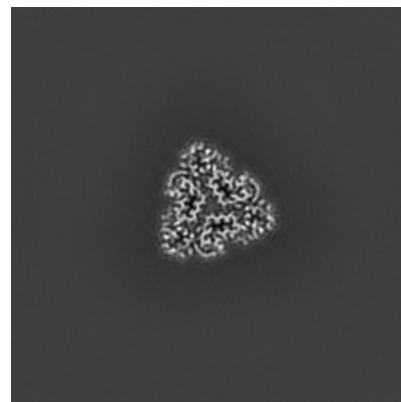
6.3.2 Raw map



X Index: 133



Y Index: 136

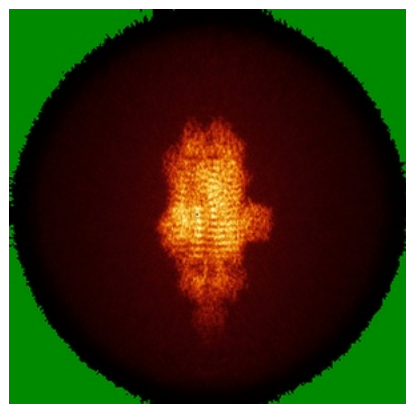


Z Index: 119

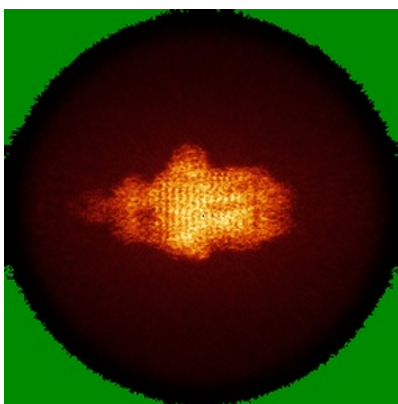
The images above show the largest variance slices of the map in three orthogonal directions.

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

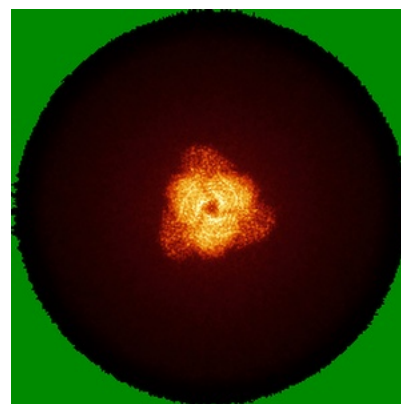
6.4.1 Primary map



X

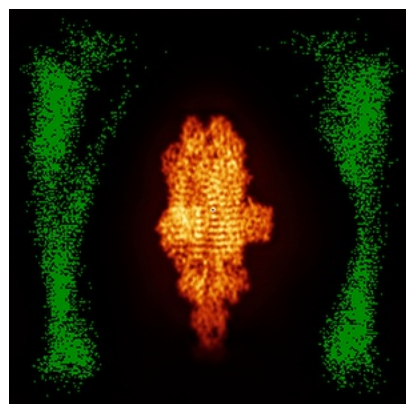


Y

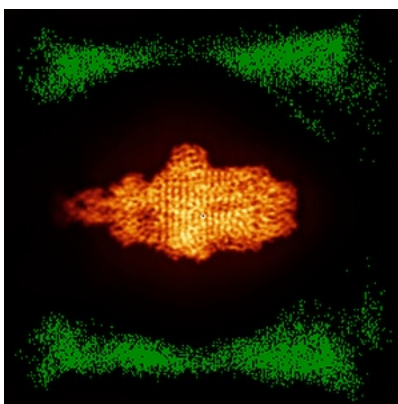


Z

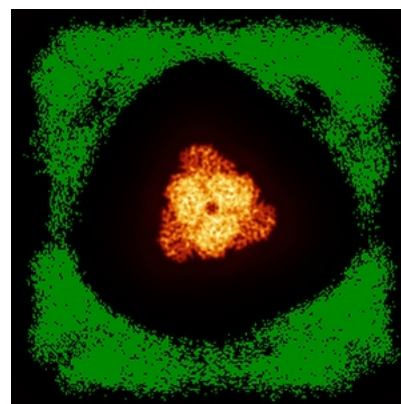
6.4.2 Raw map



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](#)

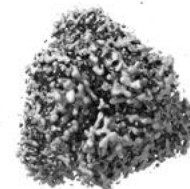
6.5.1 Primary map



X



Y



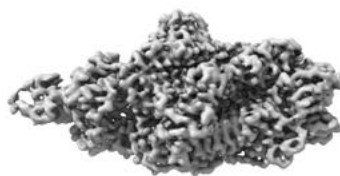
Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

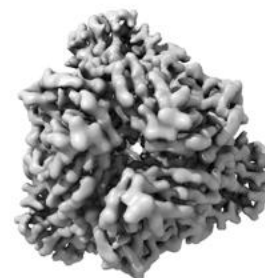
6.5.2 Raw map



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.

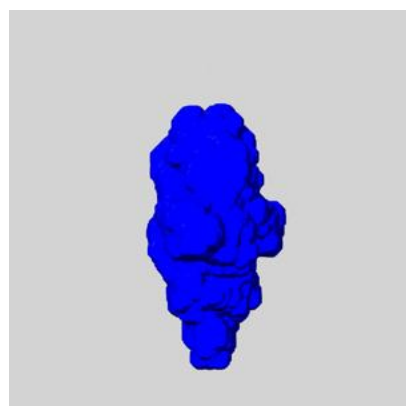
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

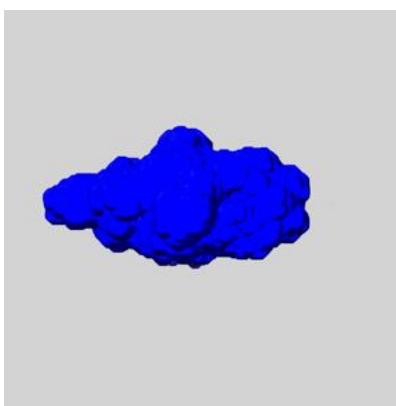
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

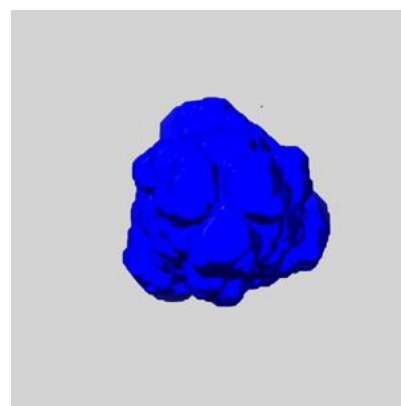
6.6.1 emd_62052_msk_1.map [i](#)



X



Y

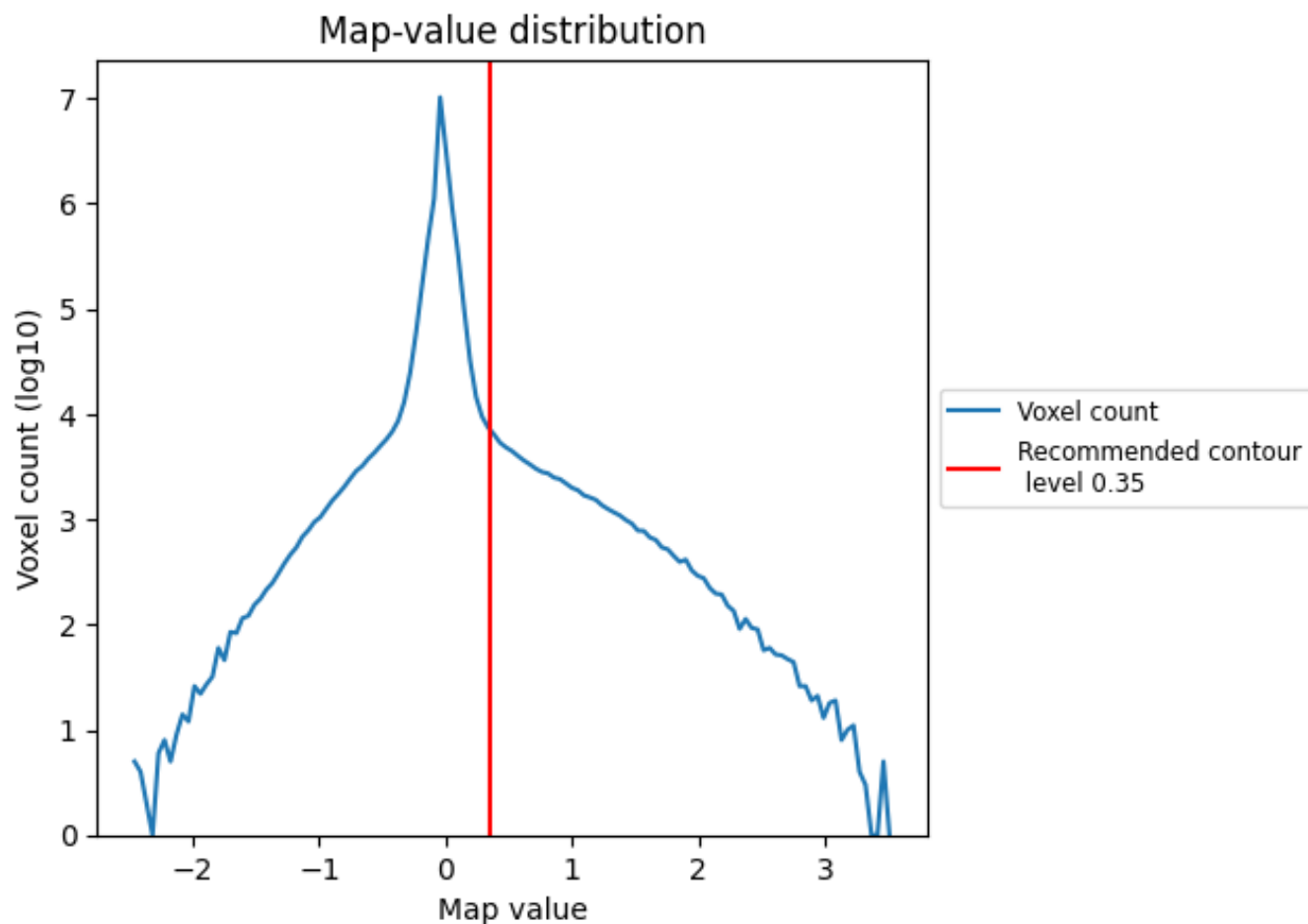


Z

7 Map analysis [i](#)

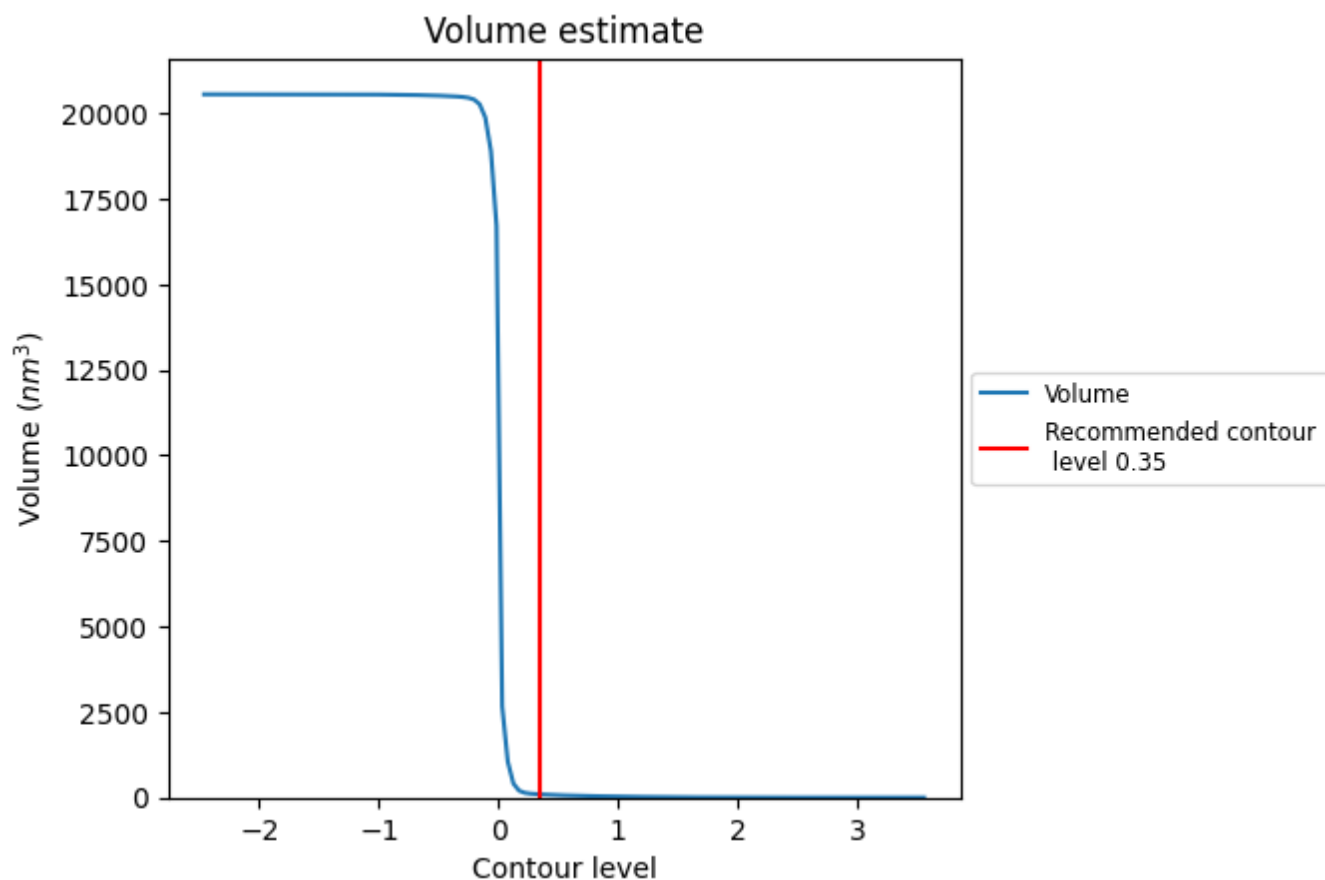
This section contains the results of statistical analysis of the map.

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.

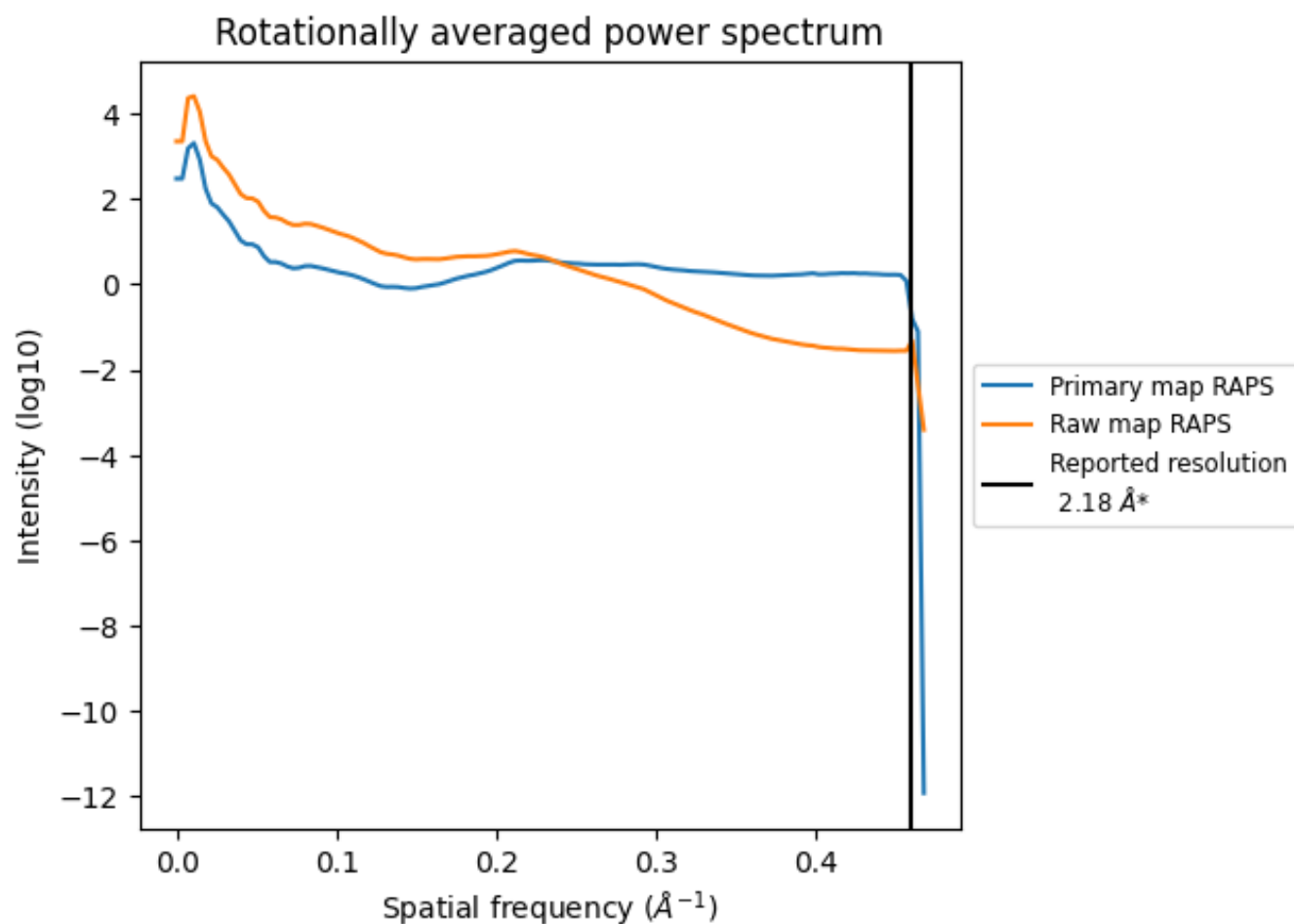
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93 nm³; this corresponds to an approximate mass of 84 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 ⓘ

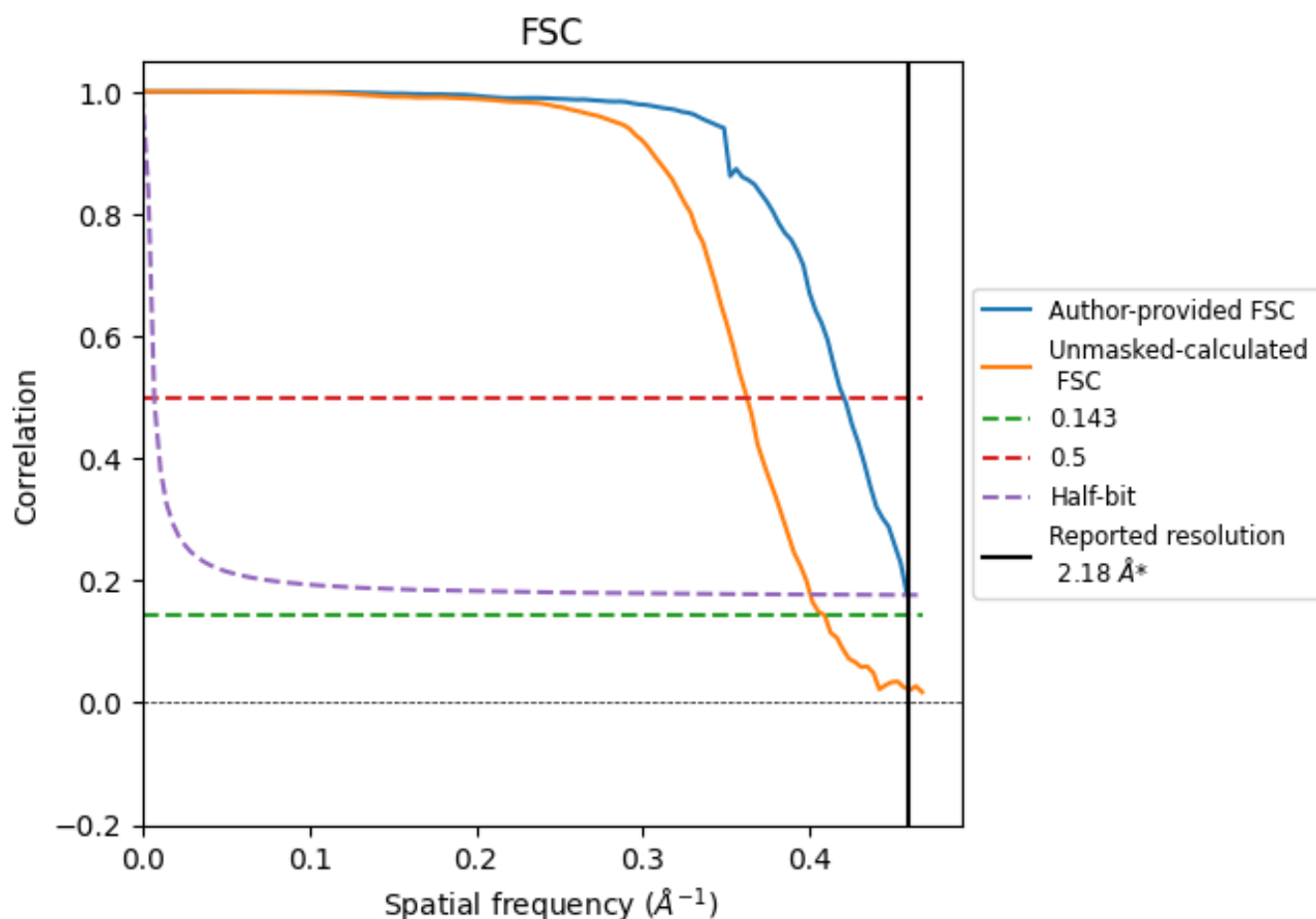


*Reported resolution corresponds to spatial frequency of 0.459 Å⁻¹

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 0.459 \AA^{-1}

8.2 Resolution estimates [i](#)

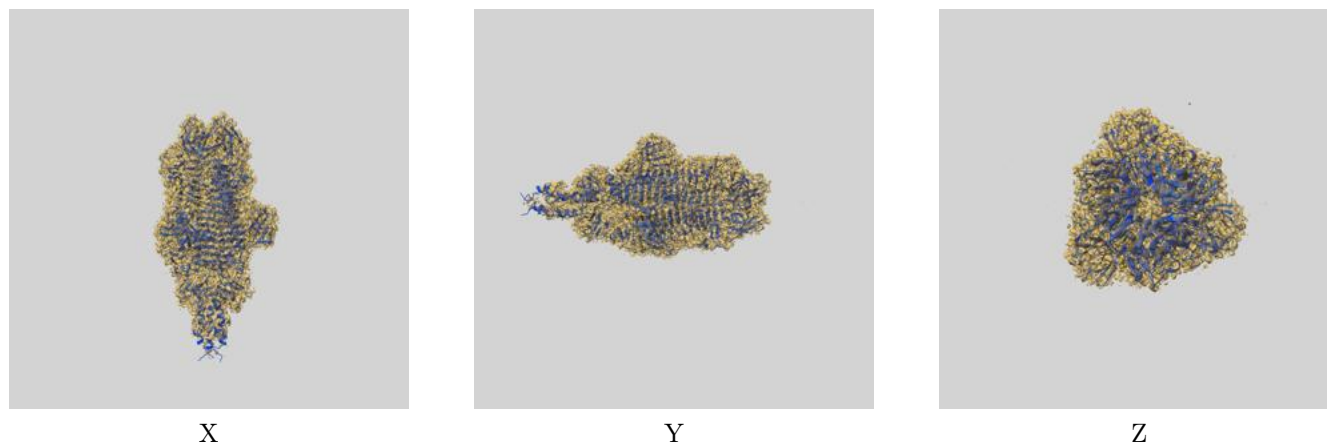
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.18	-	-
Author-provided FSC curve	-	2.38	-
Unmasked-calculated*	2.45	2.76	2.50

*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 2.45 differs from the reported value 2.18 by more than 10 %

9 Map-model fit [i](#)

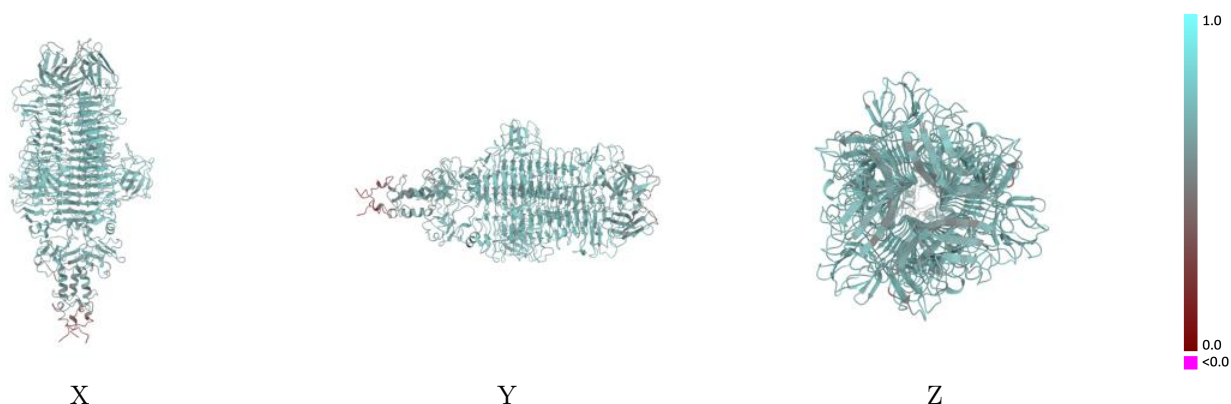
This section contains information regarding the fit between EMDB map EMD-62052 and PDB model 9K4B. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



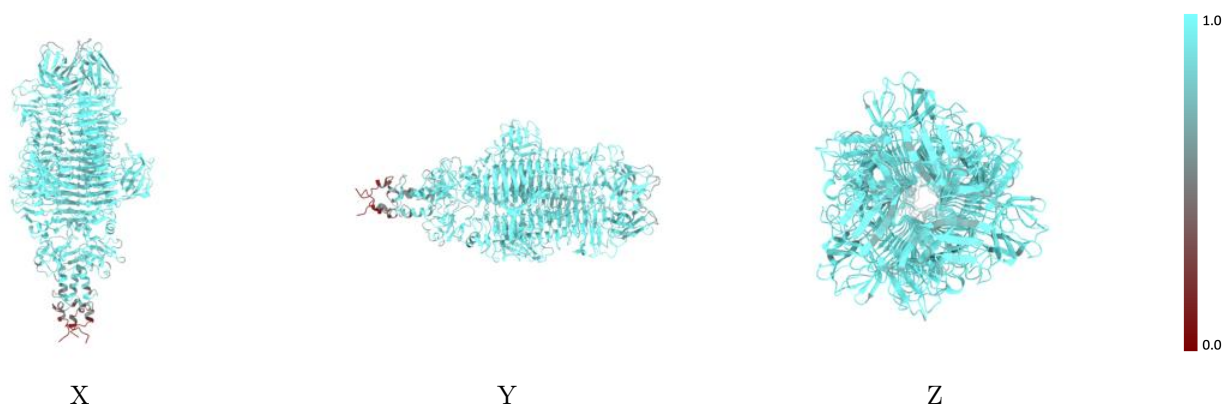
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



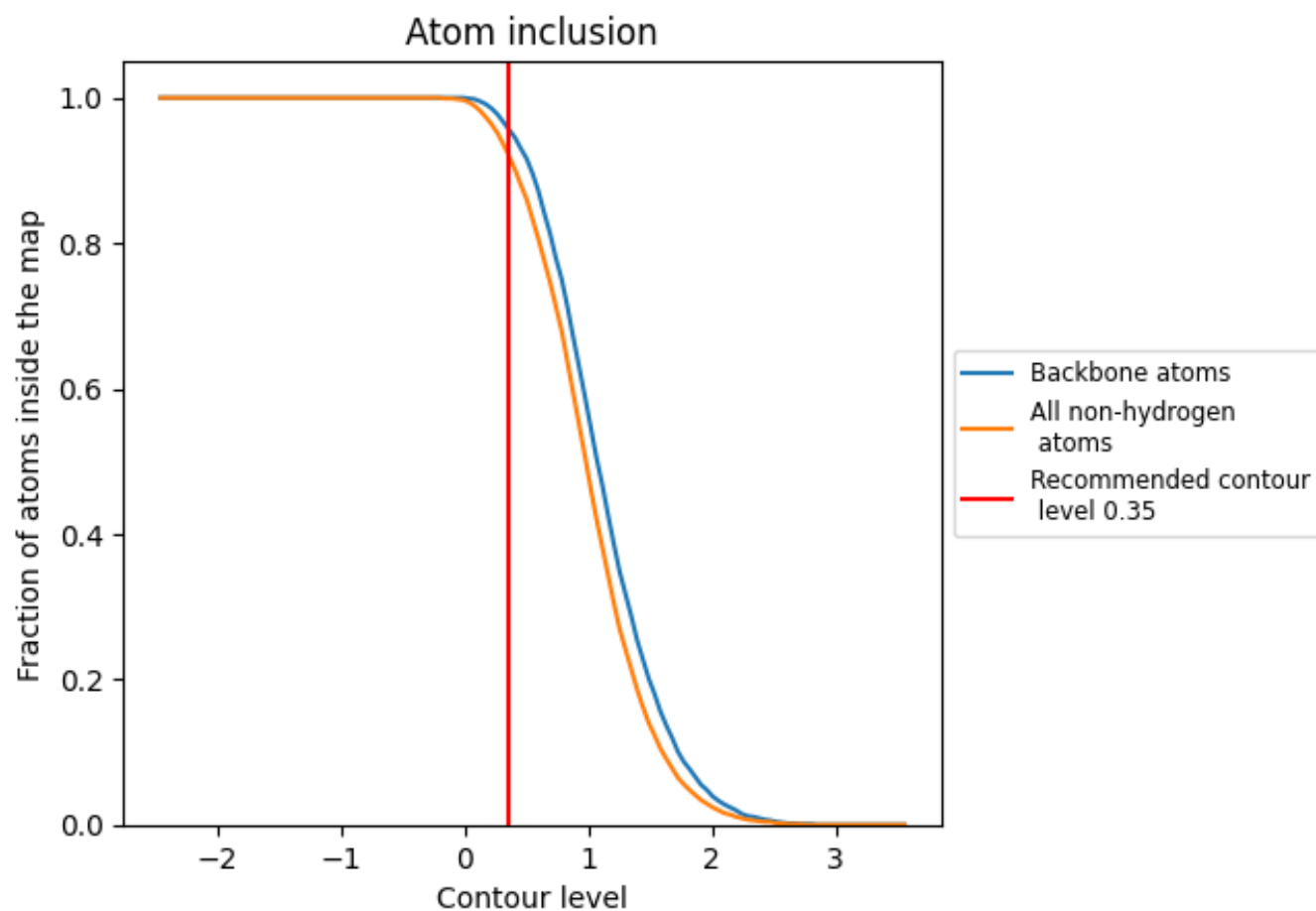
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9230	<div></div> 0.6530
A	<div></div> 0.9240	<div></div> 0.6520
B	<div></div> 0.9230	<div></div> 0.6540
C	<div></div> 0.9210	<div></div> 0.6520

