



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2026 – 08:21 AM EDT

PDB ID : 9PFU / pdb_00009pfu
EMDB ID : EMD-71614
Title : Cryo-EM structure of the respiratory syncytial virus polymerase (L:P) in post-translocation elongation state
Authors : Cao, D.; Chen, Z.; Gao, Y.; Roesler, C.; Gooneratne, I.; Liang, B.
Deposited on : 2025-07-06
Resolution : 3.54 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:

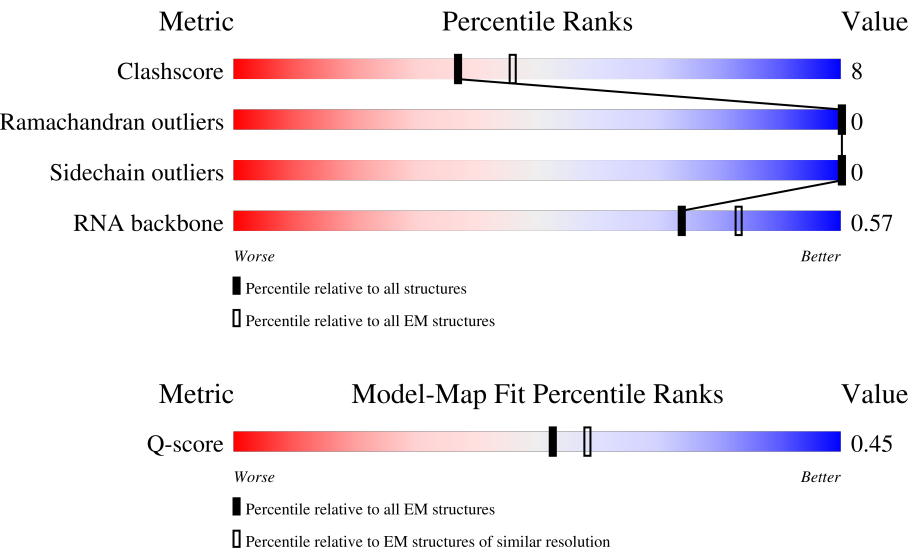
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	2165	58% 16% 26%
2	B	241	19% 5% 76%
2	C	241	20% 77%

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Mol	Chain	Length	Quality of chain
2	D	241	21% 76%
2	E	241	37% 7% 55%
3	P	3	67% 33%
4	T	12	42% 33% 8% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15581 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1604	Total	C	N	O	S	0	0
			13137	8487	2200	2384	66		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	58	Total	C	N	O	S	0	0
			444	273	81	86	4		
2	C	56	Total	C	N	O	S	0	0
			430	262	80	85	3		
2	D	59	Total	C	N	O	S	0	0
			463	284	87	88	4		
2	E	108	Total	C	N	O	S	0	0
			839	508	149	176	6		

- Molecule 3 is a RNA chain called RNA (5'-R(P*AP*CP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	3	Total	C	N	O	P	0	0
			65	29	13	20	3		

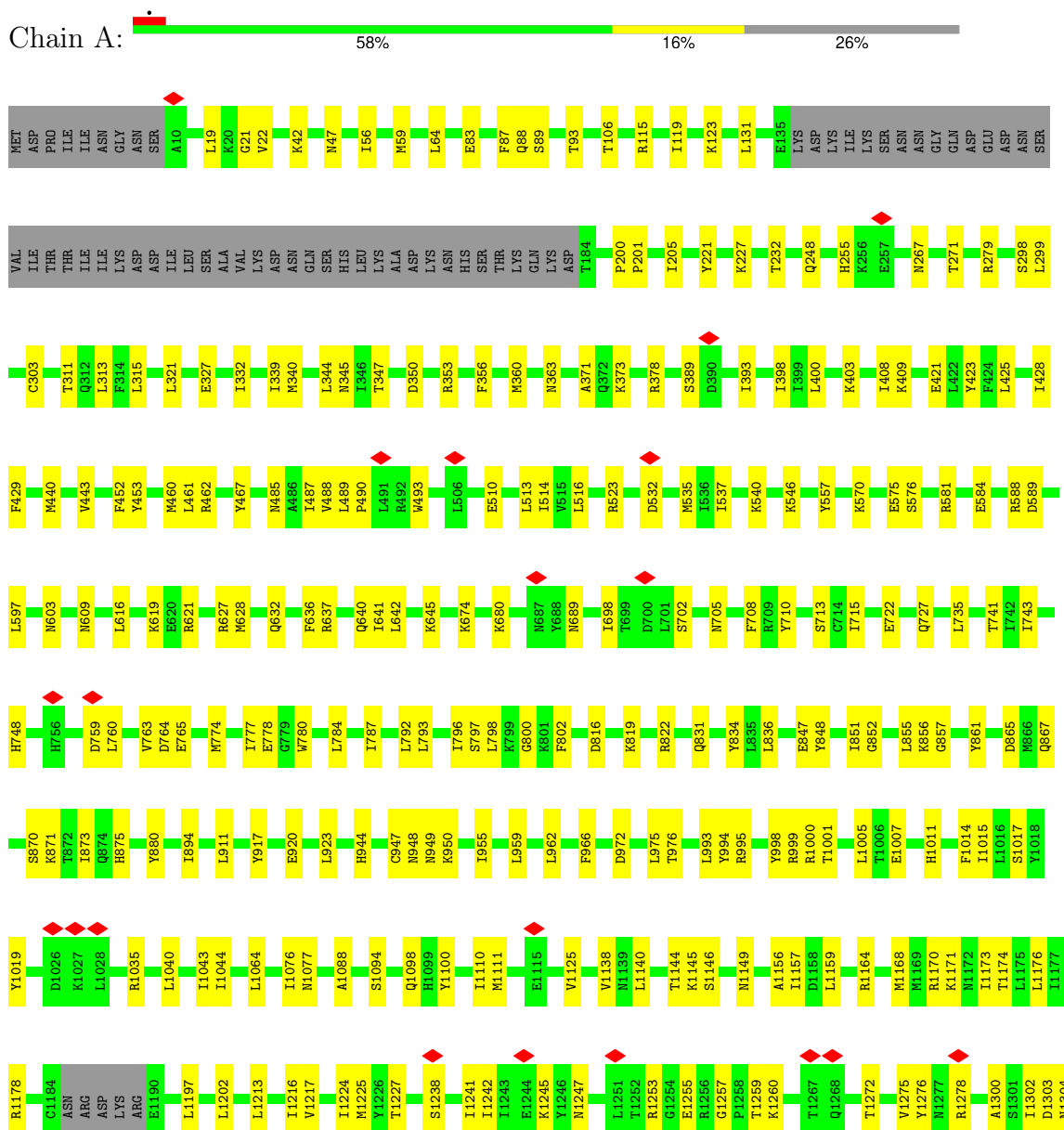
- Molecule 4 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*UP*CP*UP*CP*GP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	10	Total	C	N	O	P	0	0
			203	91	25	77	10		

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: RNA-directed RNA polymerase L





SER	ASP	GLU	VAL	ASN	SER	LEU	ASN	PRO	THR	THR	GLU	LYS	LEU	ASN	ASN	LEU	GLY	ASN	ASP	SER	ASP	ASP	ASN	ASP	LEU	SER	GLU	ASP	PHE
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• Molecule 2: Phosphoprotein



MET	GLU	LYS	PHE	ALA	PRO	THR	ASN	GLU	PHE	HIS	GLY	ASP	GLU	ASP	ALA	ASN	ASN	ARG	LYS	ALA	THR	LYS	PHE	LEU	GLU	SER	PRO	THR	GLU	LYS	THR	ASN	SER
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THR	ILE	ILE	ASN	PRO	THR	ASN	GLU	THR	GLU	THR	ASP	THR	ALA	GLY	ASN	ASN	PRO	ALA	ASN	THR	LYS	GLN	ARG	LEU	GLU	LYS	PRO	THR	VAL	SER	PHE	LYS	THR
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GLU	GLU	ILE	ASN	ASP	GLN	THR	N128	D129	N130	I131	D139	E140	K141	I145	L146	H150	P159	D168	I181	R182	T183	ALA	ALA	MET	THR	ASP	ASN	ASP	ARG	LEU	GLU	ALA	MET	ALA	ARG	LEU	ASN	GLU	THR	PHE	ASP	VAL	TYR
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LEU	ASN	PRO	THR	THR	GLU	LYS	LEU	ASN	GLY	GLY	ASN	ASP	SER	ASP	ASN	ASP	LEU	SER	GLU	ASP	PHE
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• Molecule 2: Phosphoprotein



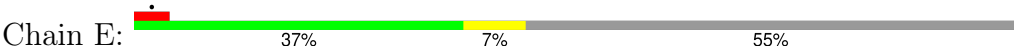
MET	GLU	LYS	PHE	ALA	PRO	THR	ASN	GLU	PHE	HIS	GLY	ASP	THR	ALA	ASN	ASN	ARG	LYS	ALA	THR	LYS	PHE	LEU	GLU	SER	PRO	THR	VAL	SER	GLY	LYS	THR	ASN	SER
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THR	ILE	ILE	ASN	PRO	THR	ASN	GLU	THR	GLU	THR	ASP	THR	ALA	GLY	ASN	ASN	PRO	ALA	ASN	THR	LYS	GLN	ARG	LEU	GLU	LYS	PRO	THR	VAL	SER	PHE	LYS	GLU	THR	ASP	PRO	THR	PRO	ASP	ASN	ASP	ASN	PRO	PHE
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GLU	GLU	ILE	ASN	ASP	GLN	THR	ASN	ASP	N130	I131	T132	A133	R134	L135	D136	R137	I138	D139	E140	I145	G158	PRO	THR	THR	ALA	ARG	ASP	GLY	ILE	ARG	ASP	ALA	ALA	MET	V171	G172	L173	R174	E175	E176	E184	M189	A194	R197	L198	R199	N200	GLU	GLU	GLU	LYS	MET	ALA
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LYS	ASP	THR	SER	GLU	VAL	SER	LEU	ASN	PRO	THR	THR	SER	GLU	LYS	LEU	ASN	ASN	LEU	GLY	ASN	SER	ASP	ASP	ASN	ASN	LEU	LEU	LEU	ASP	GLU	ASP	PHE
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• Molecule 2: Phosphoprotein



MET	GLU	LYS	PHE	ALA	PRO	THR	ASN	GLU	PHE	HIS	GLY	ASP	THR	ALA	ASN	ASN	ARG	LYS	ALA	THR	LYS	PHE	LEU	GLU	SER	PRO	THR	VAL	SER	GLY	LYS	THR	ASN	SER
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THR	ILE	ILE	ASN	PRO	THR	ASN	GLU	THR	GLU	THR	ASP	THR	ALA	GLY	ASN	ASN	PRO	ALA	ASN	THR	LYS	GLN	ARG	LEU	GLU	LYS	PRO	THR	VAL	SER	PHE	LYS	GLU	THR	ASP	PRO	THR	PRO	ASP	ASN	ASP	ASN	PRO	PHE	SER	LYS	ILE	ILE	SER	TYR	LYS	VAL	ASN	SER	THR	ILE	ILE	ASP	THR	PHE	GLU	VAL	ASP	ASN	ASN	LYS	GLU	GLU	GLU	ASN	PRO	ASP	THR	ILE	THR	SER	TYR	SER	ASN	SER	THR	TYR
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GLU	GLU	ILE	ASN	ASP	GLM	THR	ASN	ASP	D129	N130	I131	R134	L135	D136	R137	I138	D139	E140	G158	R163	D168	R174	I178	E179	N189	D190	R191	L192	M195	A196	R197	K208	D209	L223	L227	N230	ASP	SER	ASP	ASN	ASN	ASP	ASP	L236	E239	D240	F241
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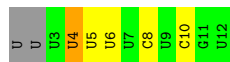
• Molecule 3: RNA (5'-R(P*AP*CP*G)-3')



A1	C2	G3
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- Molecule 4: RNA (5'-R(P*UP*UP*UP*UP*UP*CP*UP*CP*GP*U)-3')

Chain T: 42% 33% 8% 17%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18356	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 ($e^-/\text{\AA}^2$)	54.86	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.070	Depositor
Minimum map value	-0.703	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.175	Depositor
Map size ($\text{\AA}$)	217.77602, 217.77602, 217.77602	wwPDB
Map dimensions	208, 208, 208	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.047, 1.047, 1.047	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	0.14	0/13424	0.36	0/18167
2	B	0.12	0/445	0.34	0/596
2	C	0.16	0/431	0.37	0/578
2	D	0.14	0/462	0.33	0/616
2	E	0.19	0/841	0.42	0/1127
3	P	0.06	0/72	0.12	0/110
4	T	0.06	0/223	0.14	0/343
All	All	0.14	0/15898	0.36	0/21537

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	13137	0	13339	219	0
2	B	444	0	466	11	0
2	C	430	0	445	7	0
2	D	463	0	488	7	0
2	E	839	0	842	15	0
3	P	65	0	34	1	0
4	T	203	0	104	5	0
All	All	15581	0	15718	237	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 8.

The worst 5 of 237 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)
2:C:181:ILE:HD11	2:D:189:ASN:HD21	1.54	0.72
1:A:1304:ASN:ND2	1:A:1431:VAL:O	2.24	0.70
2:B:146:LEU:HD22	2:C:145:ILE:HD11	1.73	0.69
2:E:178:ILE:HG23	2:E:195:MET:HE1	1.74	0.69
1:A:1300:ALA:HA	1:A:1305:LYS:HE2	1.75	0.68

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	1594/2165 (74%)	1585 (99%)	9 (1%)	0	100	100
2	B	56/241 (23%)	56 (100%)	0	0	100	100
2	C	54/241 (22%)	54 (100%)	0	0	100	100
2	D	55/241 (23%)	55 (100%)	0	0	100	100
2	E	104/241 (43%)	104 (100%)	0	0	100	100
All	All	1863/3129 (60%)	1854 (100%)	9 (0%)	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	1490/2012 (74%)	1490 (100%)	0	100	100
2	B	48/220 (22%)	48 (100%)	0	100	100
2	C	47/220 (21%)	47 (100%)	0	100	100
2	D	50/220 (23%)	50 (100%)	0	100	100
2	E	94/220 (43%)	94 (100%)	0	100	100
All	All	1729/2892 (60%)	1729 (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 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1099	HIS
1	A	1268	GLN
2	D	189	ASN
1	A	1632	HIS
1	A	1683	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	P	2/3 (66%)	0	0
4	T	9/12 (75%)	2 (22%)	0
All	All	11/15 (73%)	2 (18%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	T	4	U
4	T	6	U

There are no RNA pucker outliers to report.

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 [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.

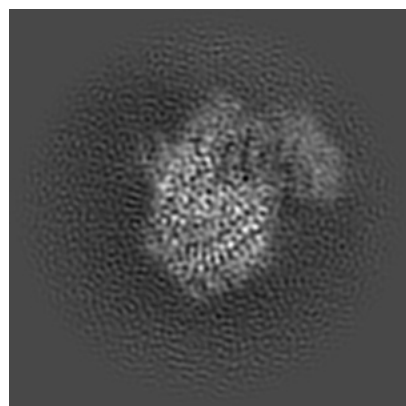
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71614. These allow visual inspection of the internal detail of the map and identification of artifacts.

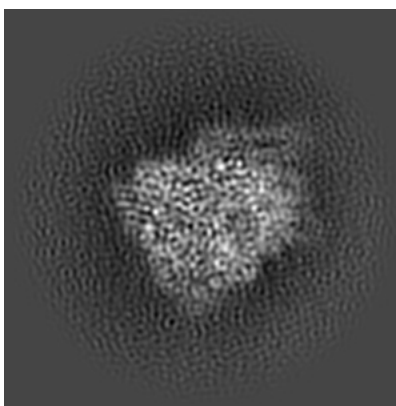
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

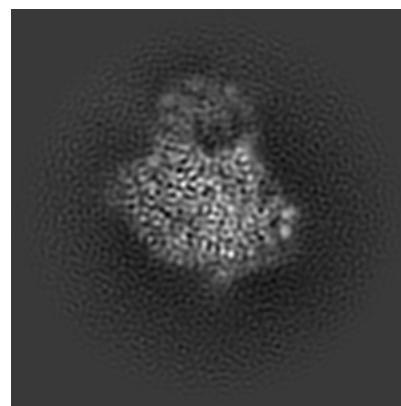
6.1.1 Primary map



X

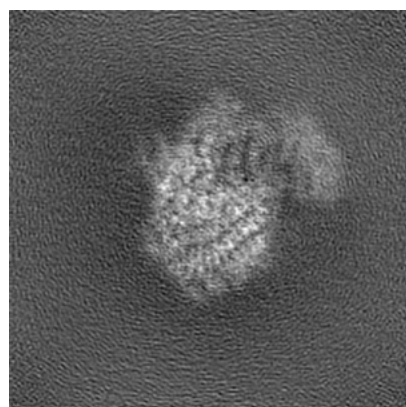


Y

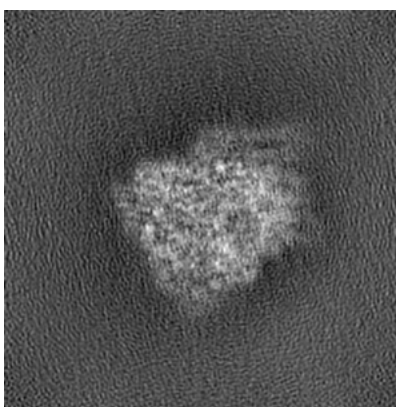


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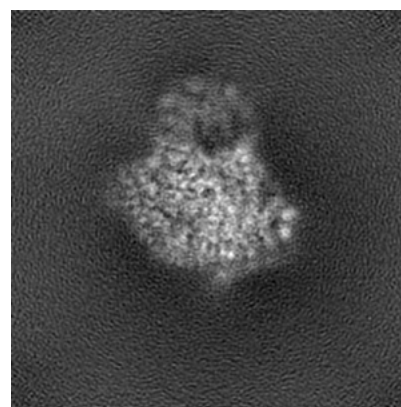
6.1.2 Raw map



X



Y

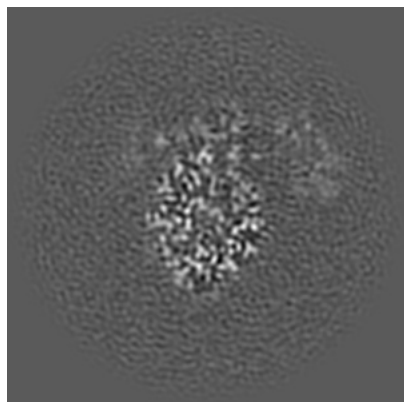


Z

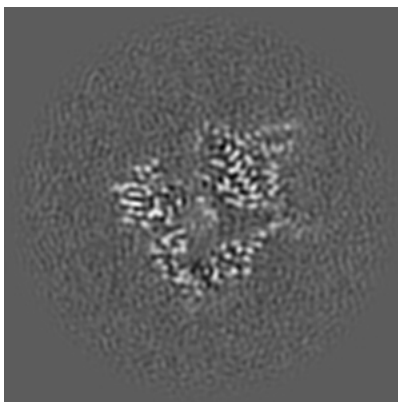
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

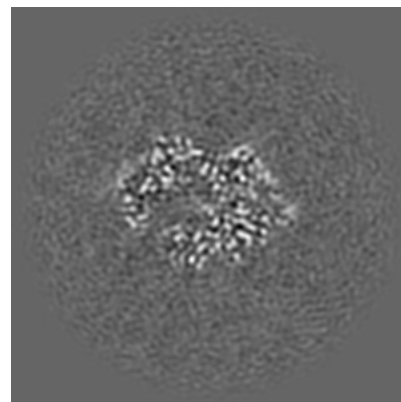
6.2.1 Primary map



X Index: 104

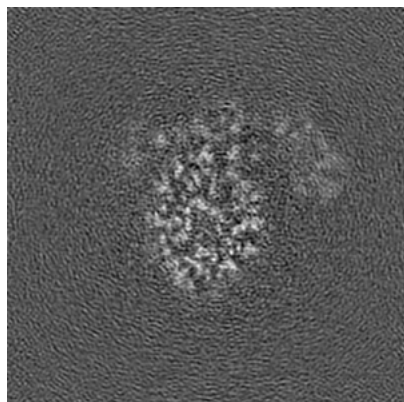


Y Index: 104

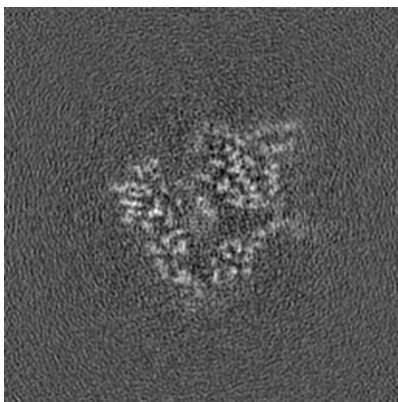


Z Index: 104

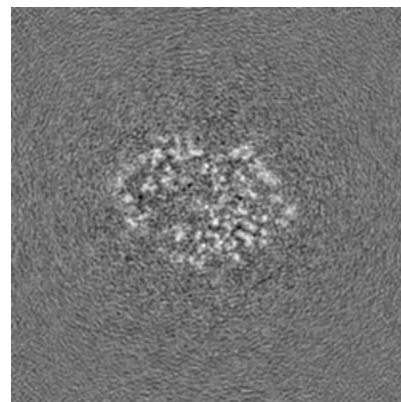
6.2.2 Raw map



X Index: 104



Y Index: 104

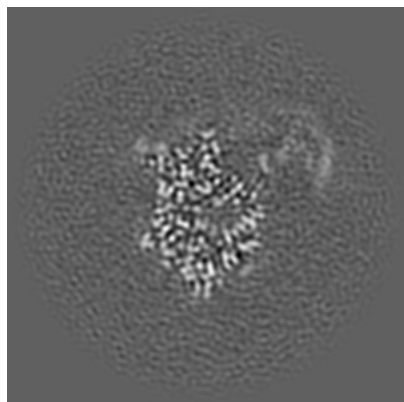


Z Index: 104

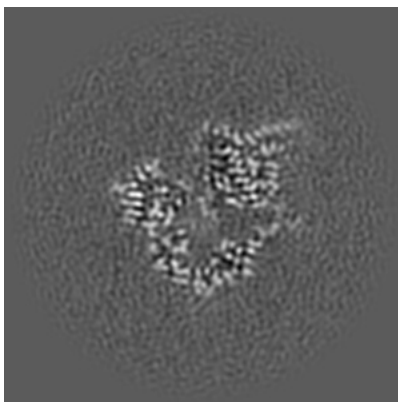
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

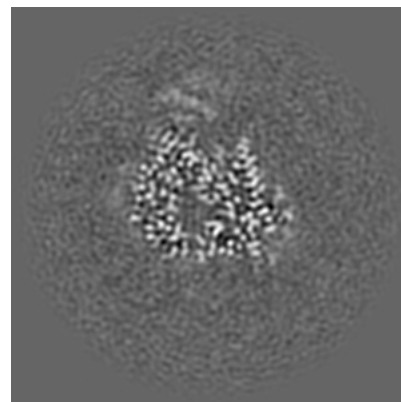
6.3.1 Primary map



X Index: 114

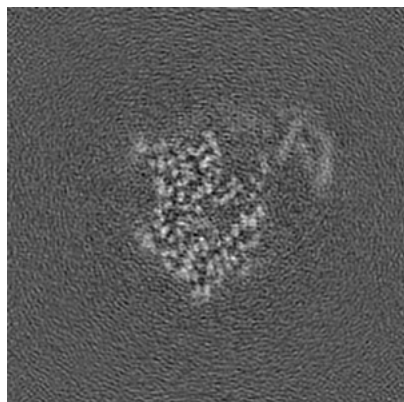


Y Index: 103

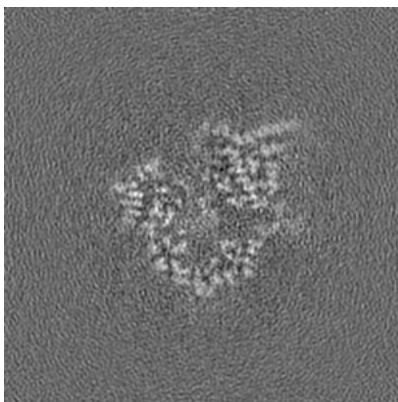


Z Index: 113

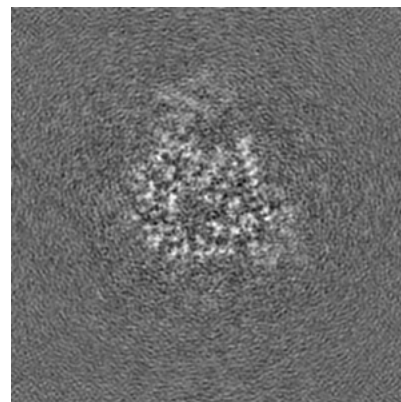
6.3.2 Raw map



X Index: 113



Y Index: 103

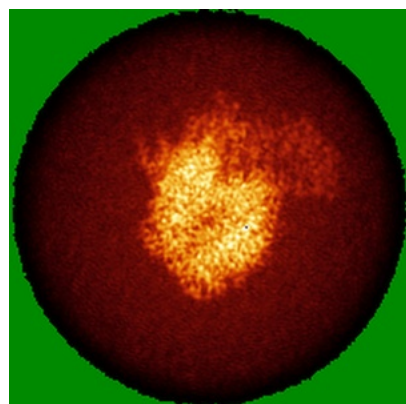


Z Index: 114

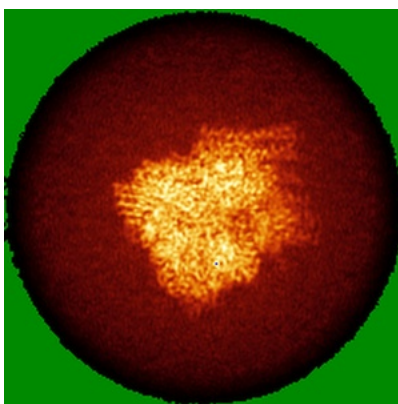
The images above show the largest variance slices of the map in three orthogonal directions.

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

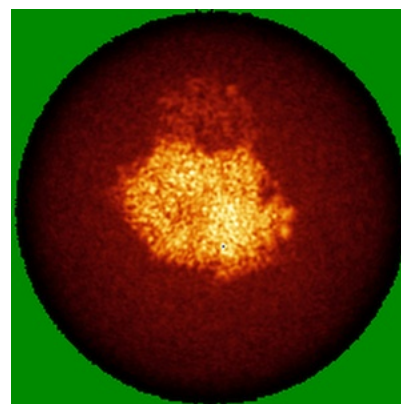
6.4.1 Primary map



X

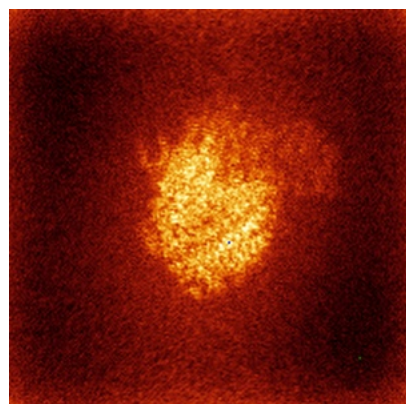


Y

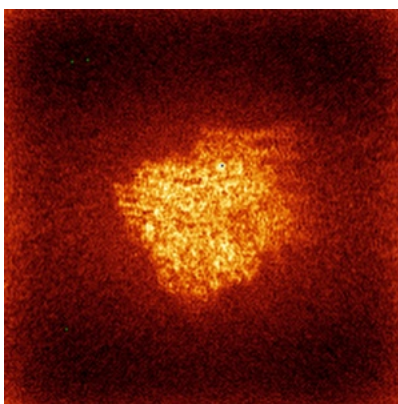


Z

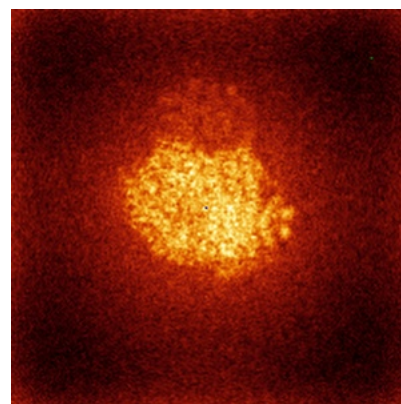
6.4.2 Raw map



X



Y

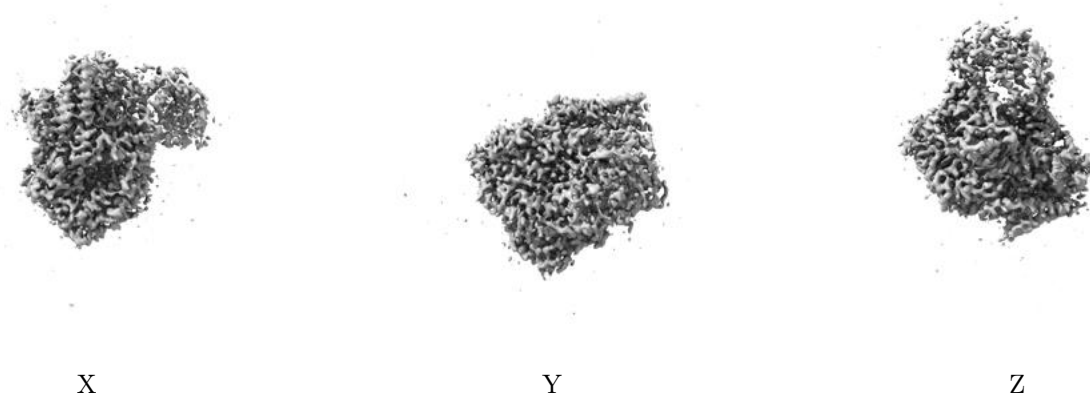


Z

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.

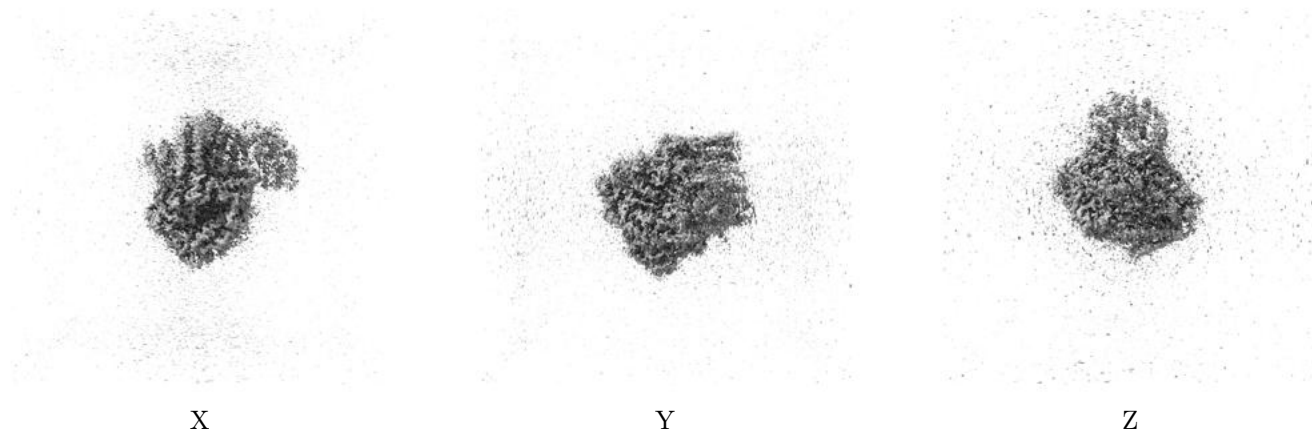
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.175. 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.

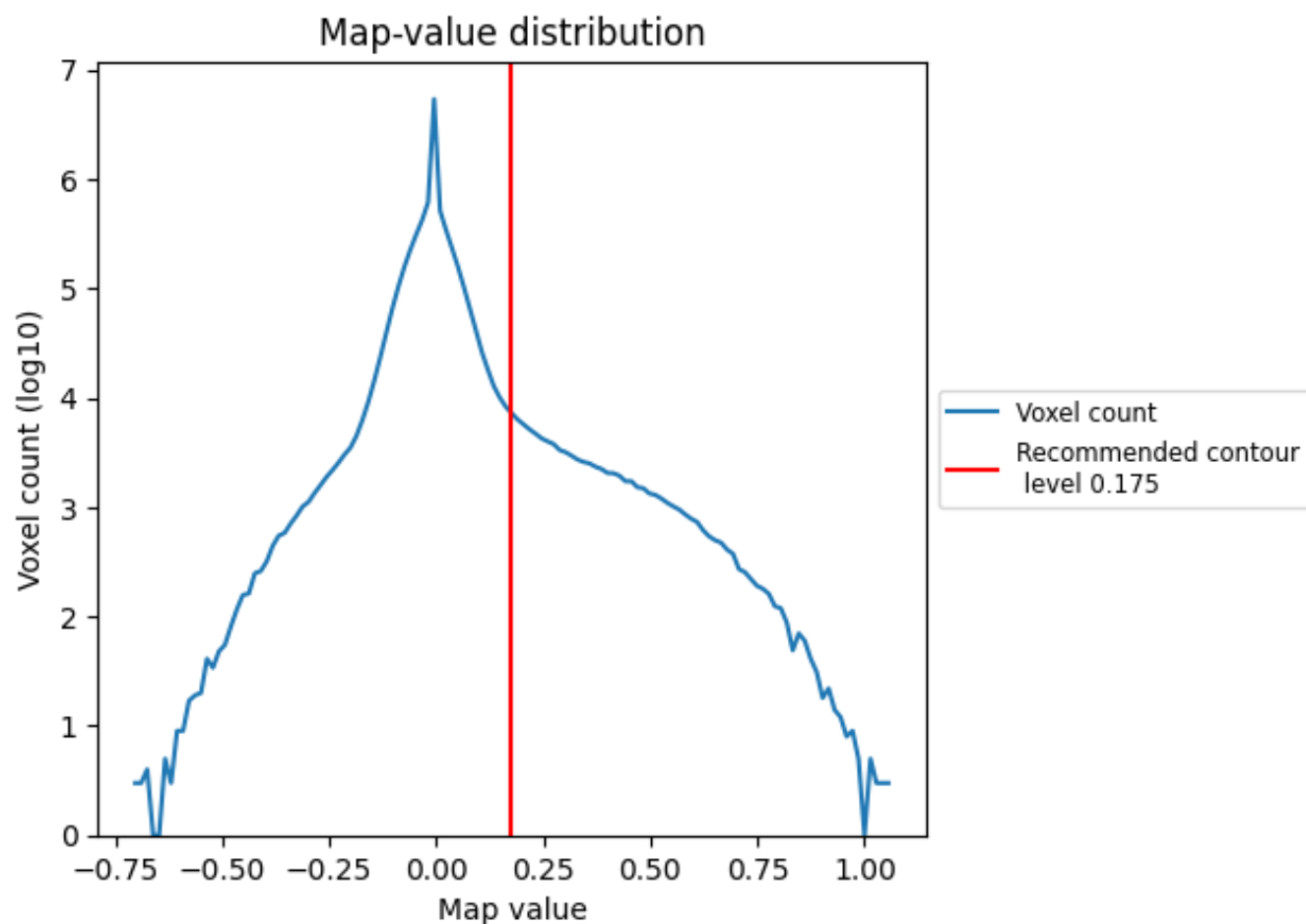
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

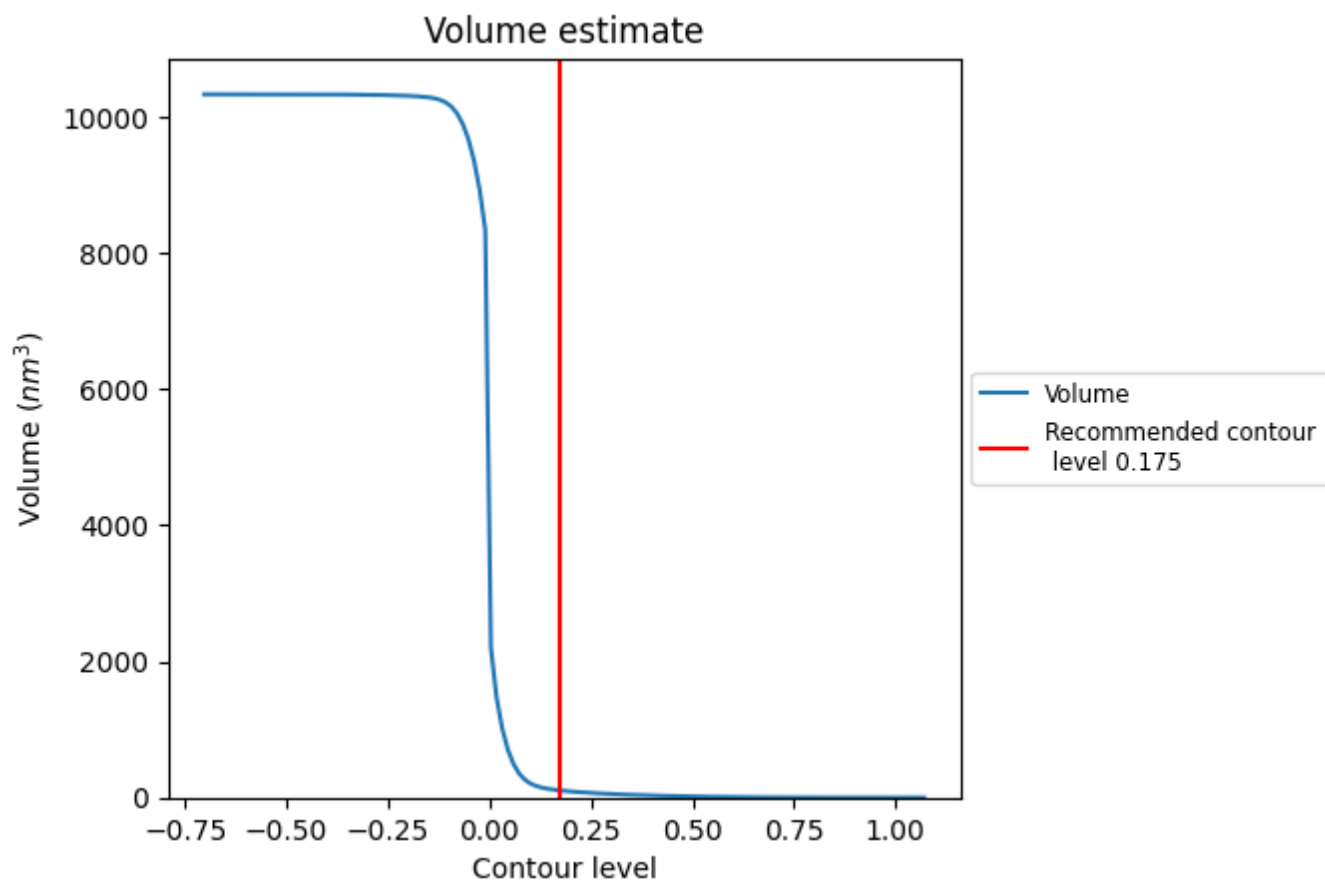
This section contains the results of statistical analysis of the map.

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.

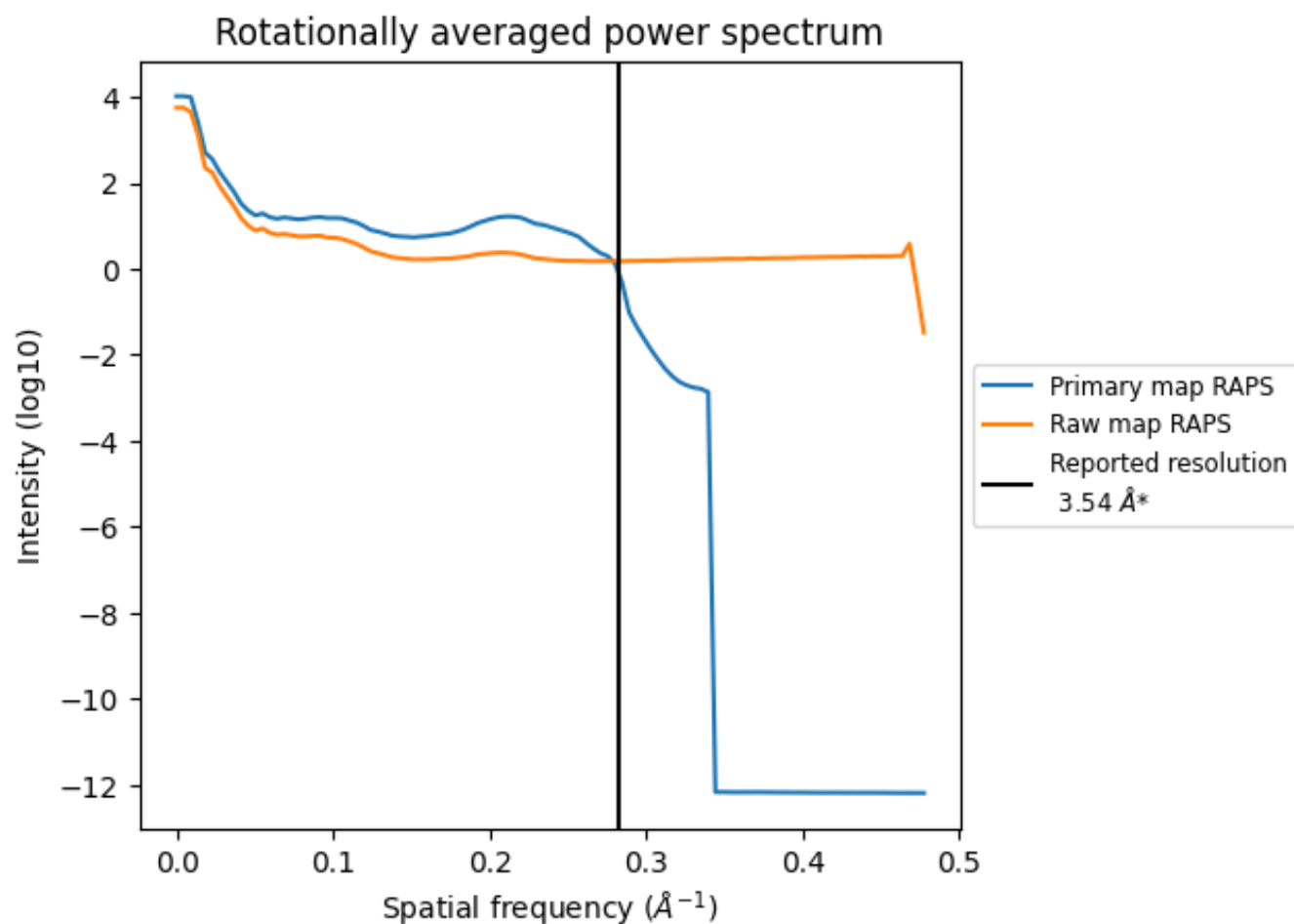
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 104 nm³; this corresponds to an approximate mass of 93 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 ⓘ

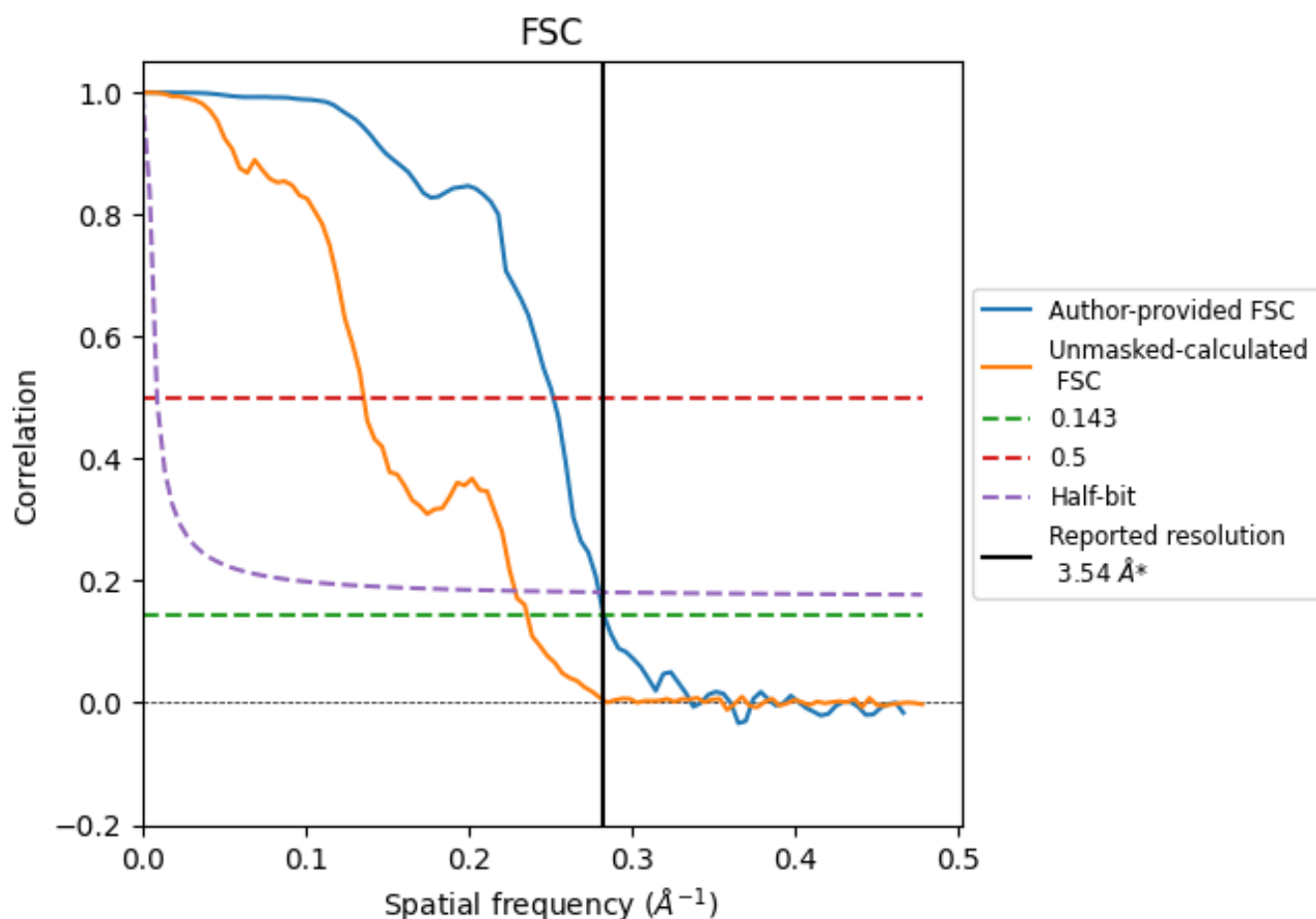


*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

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 $0.282 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

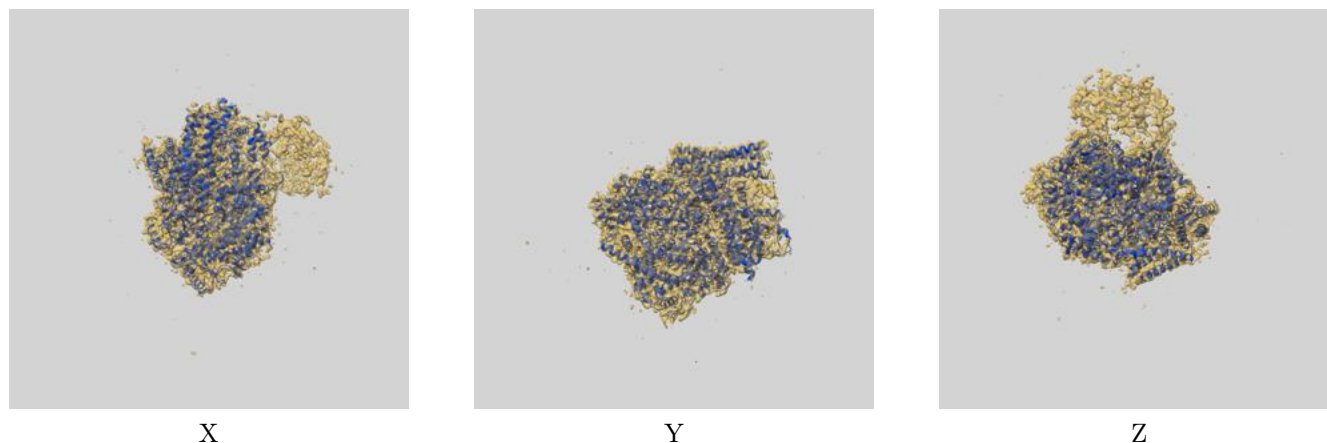
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	3.97	3.58
Unmasked-calculated*	4.24	7.37	4.38

*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 4.24 differs from the reported value 3.54 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-71614 and PDB model 9PFU. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



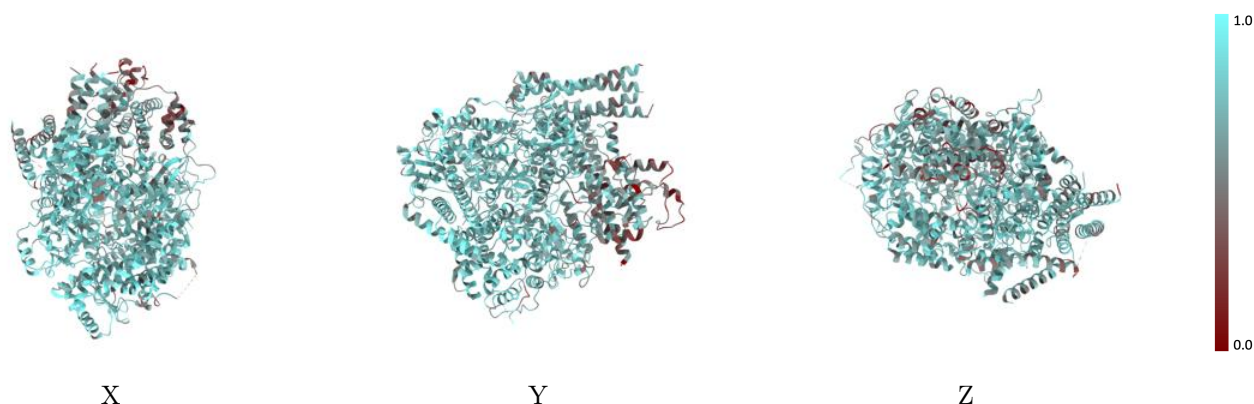
The images above show the 3D surface view of the map at the recommended contour level 0.175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



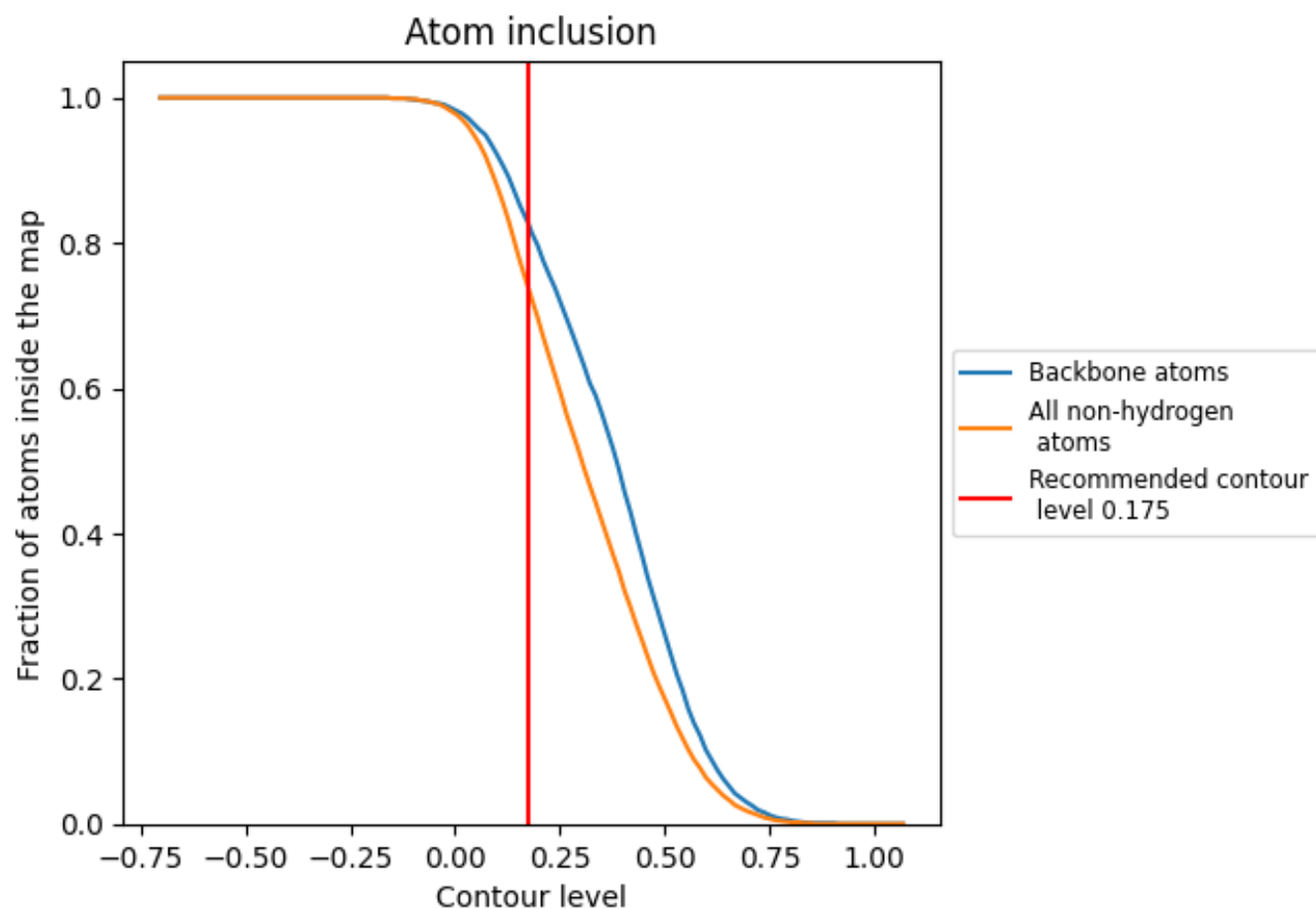
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.175).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 74% 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 (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7380	0.4500
A	0.7460	0.4560
B	0.7200	0.4320
C	0.6530	0.4130
D	0.6480	0.3780
E	0.6840	0.4220
P	0.8150	0.4210
T	0.8420	0.4590

1.0

0.0

<0.0