



## wwPDB EM Validation Summary Report ⓘ

Jun 2, 2025 – 04:38 PM JST

PDB ID : 8YQV / pdb\_00008yqv  
EMDB ID : EMD-39507  
Title : African swine fever virus RNA Polymerase core  
Authors : Feng, X.Y.  
Deposited on : 2024-03-20  
Resolution : 2.67 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

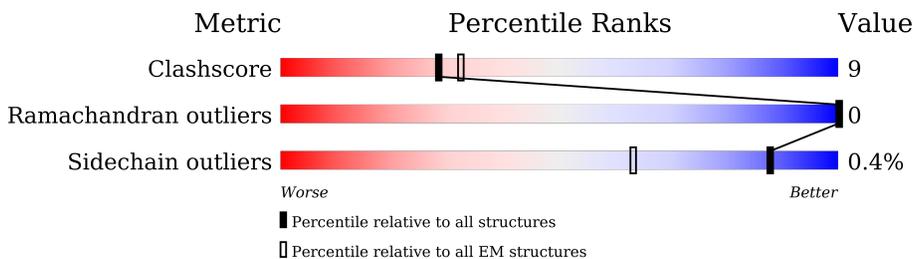
EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

# 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 2.67 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	1450	
2	E	147	
3	B	1242	
4	C	359	
5	D	205	
6	H	80	
7	G	105	
8	F	339	

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 29637 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1375	10954	6958	1906	2030	60	0	0

- Molecule 2 is a protein called C147L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	106	829	528	143	153	5	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	1196	9459	5983	1653	1773	50	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase RPB3-11 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	357	2897	1880	480	525	12	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase RPB5 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	205	1668	1088	278	294	8	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerase RPB10 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	80	630	411	102	110	7	0	0

- Molecule 7 is a protein called C122R.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	59	468	295	80	85	8	0	0

- Molecule 8 is a protein called D339L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	F	339	2727	1753	451	509	14	0	0

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
9	A	1	1	1	0

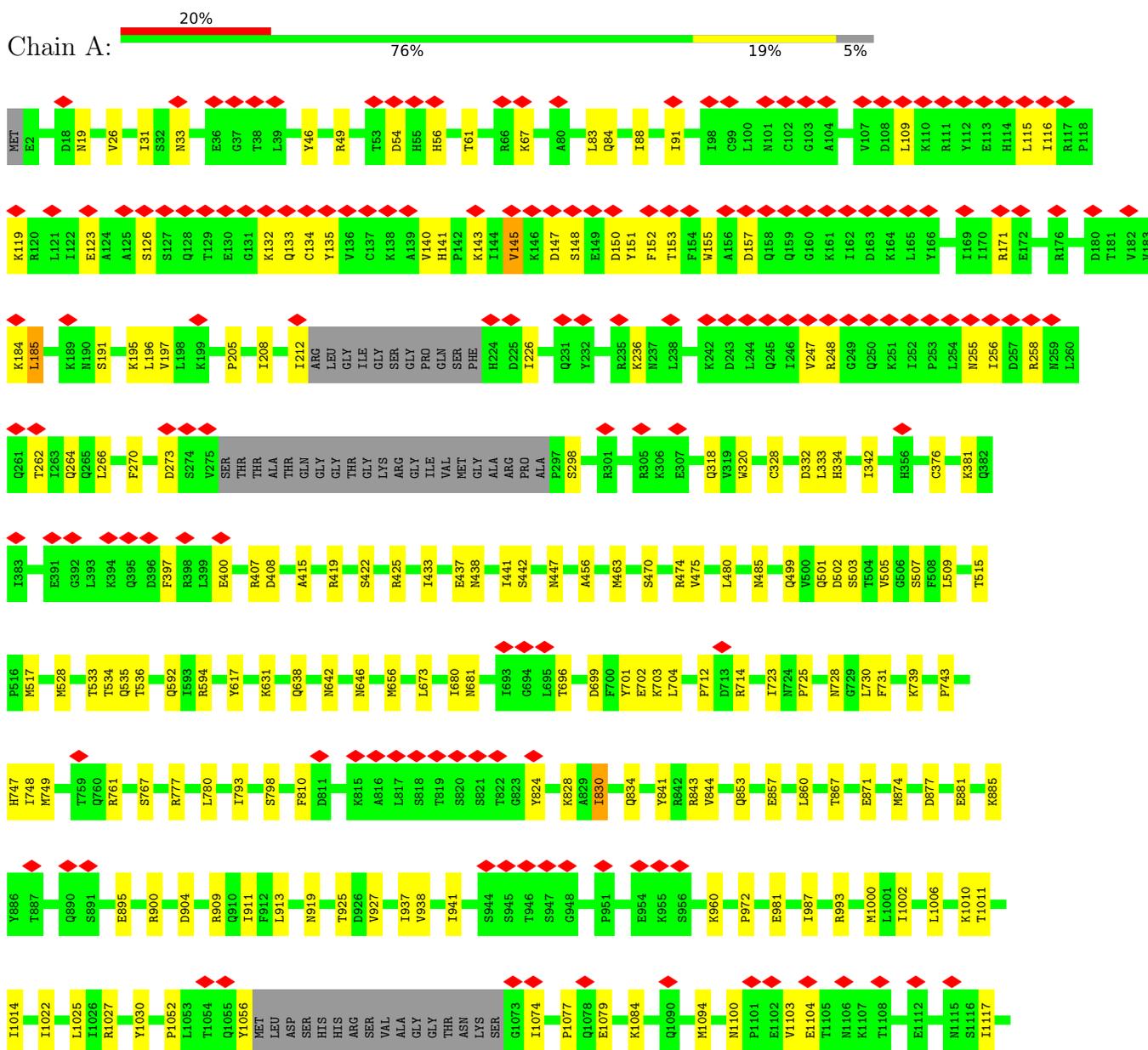
- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

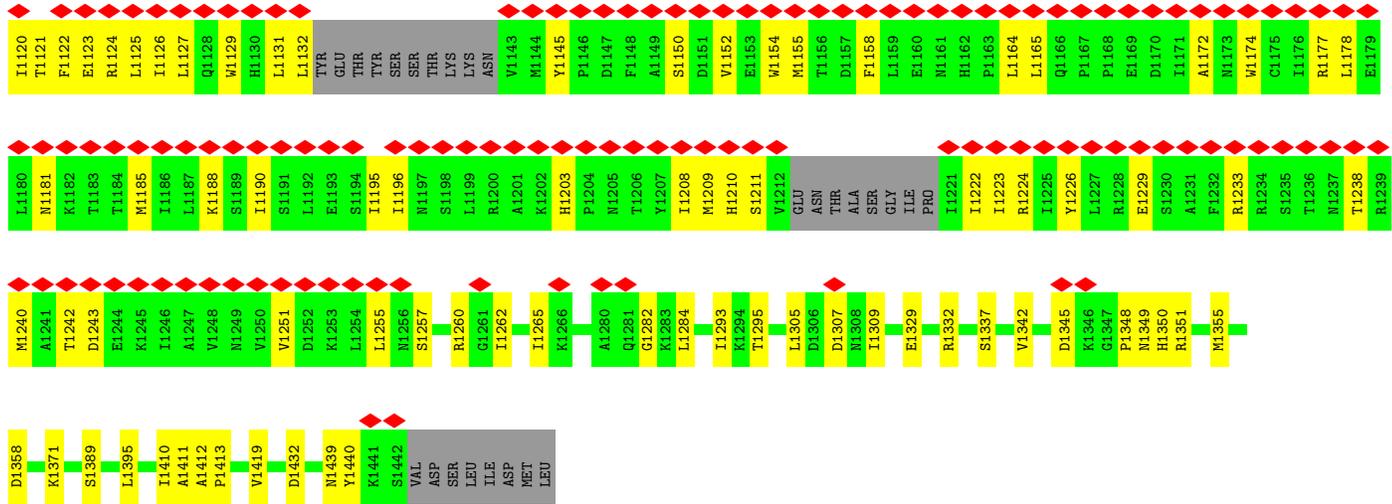
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
10	A	1	1	1	0
10	B	1	1	1	0
10	H	1	1	1	0
10	G	1	1	1	0

### 3 Residue-property plots

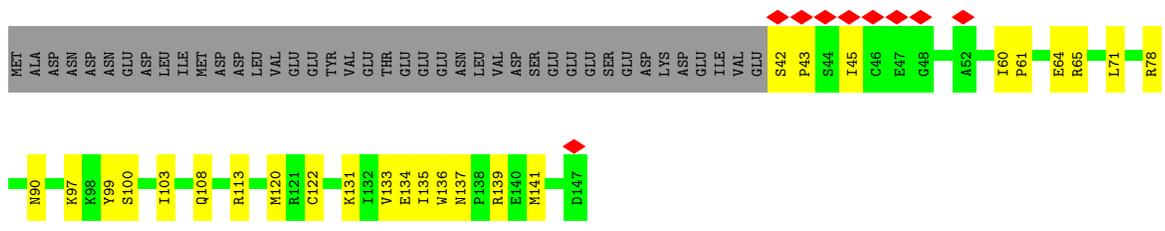
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-directed RNA polymerase subunit

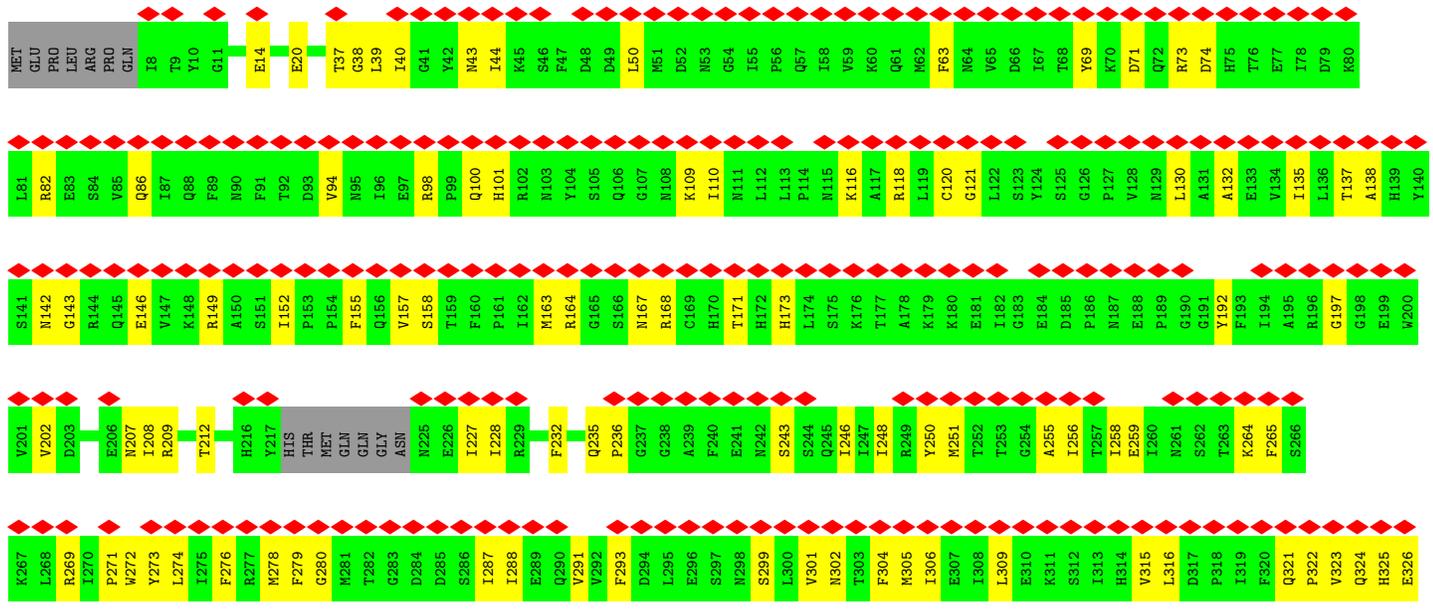


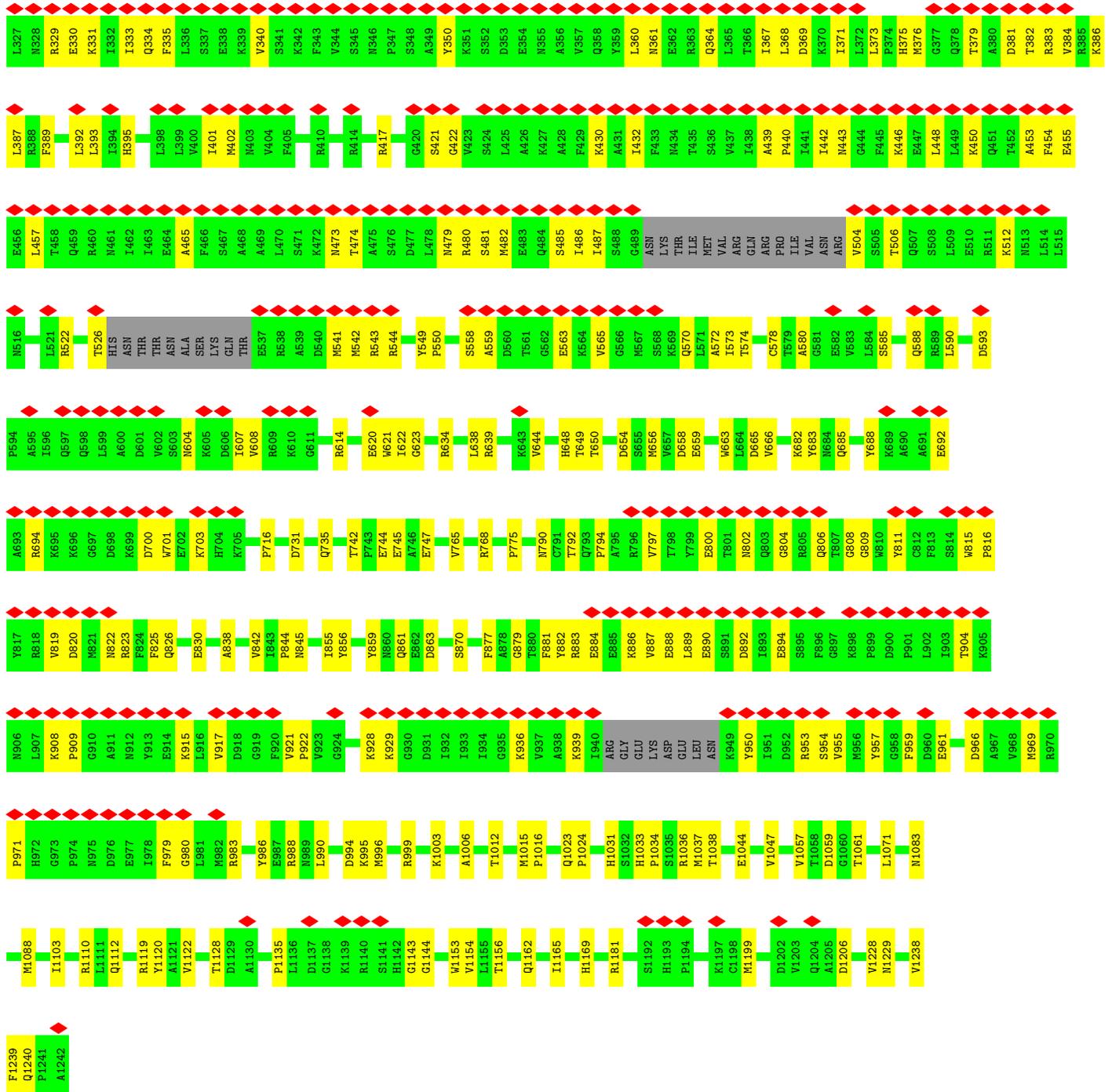


• Molecule 2: C147L

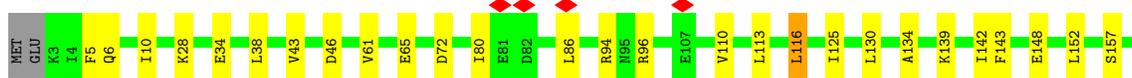
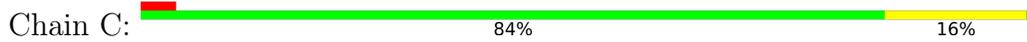


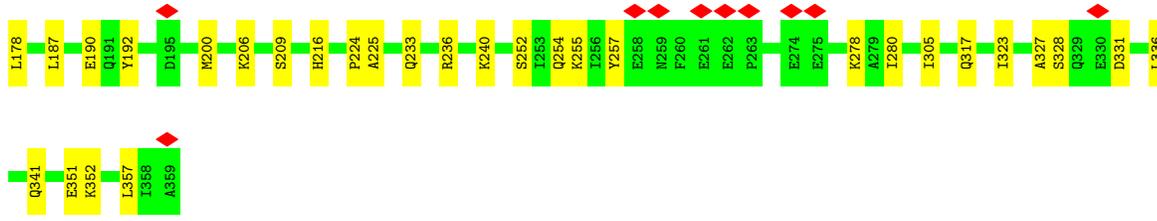
• Molecule 3: DNA-directed RNA polymerase subunit beta



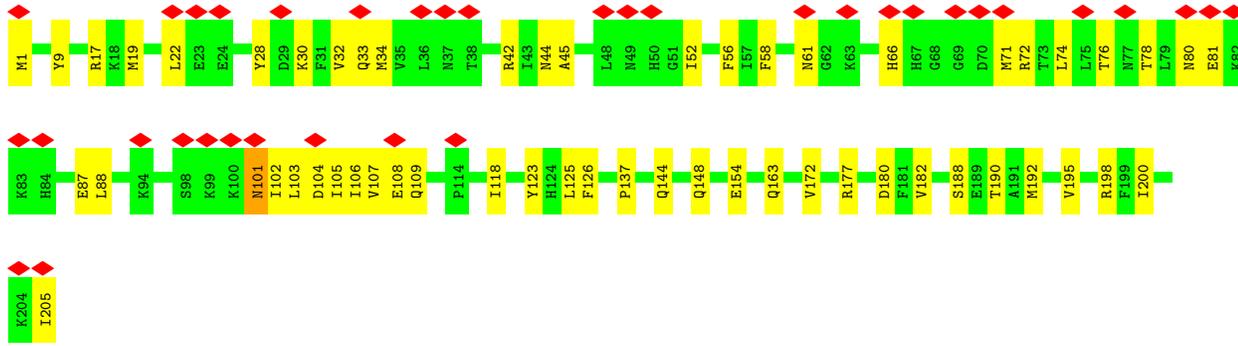
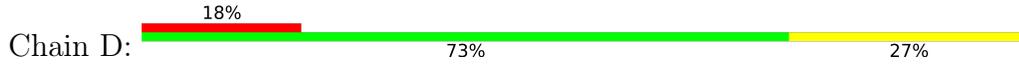


● Molecule 4: DNA-directed RNA polymerase RPB3-11 homolog

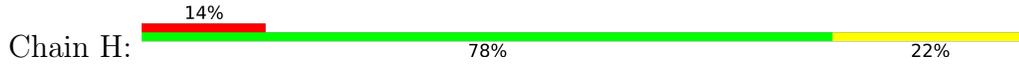




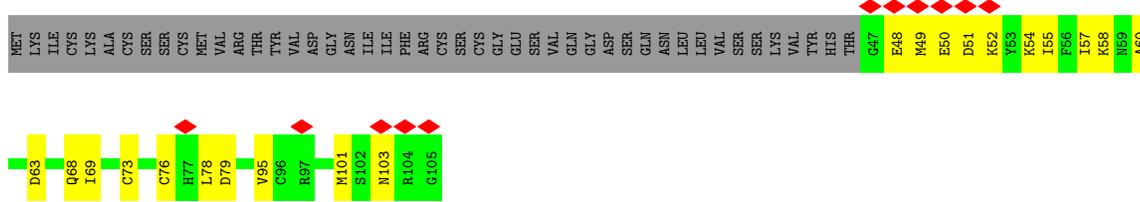
• Molecule 5: DNA-directed RNA polymerase RPB5 homolog



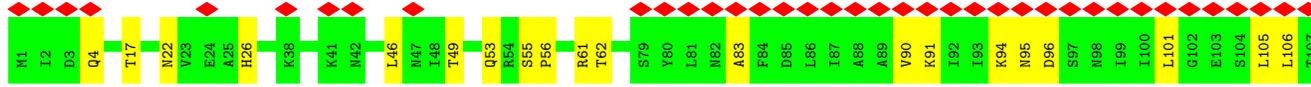
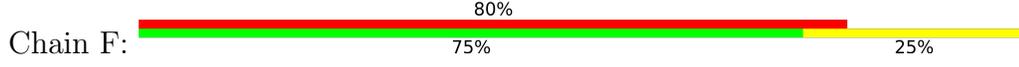
• Molecule 6: DNA-directed RNA polymerase RPB10 homolog



• Molecule 7: C122R



• Molecule 8: D339L



E108	E169	G228	S288
P109	E169	K229	A289
V110	L170	E230	E290
T111	T171	M231	V291
I112	Q172	S232	M292
V113	E173	R233	F293
I114	Q174	L234	V294
P115	A175	K235	T295
S116	L176	P236	L296
S117	M177	C237	L297
E118	L178	N238	K298
S119	T179	V239	E299
Q120	K180	L240	I300
N121	L181	S241	I301
N122	V182	F242	N302
V123	M183	L243	Y303
A124	I184	Y244	L304
E125	I185	D245	Q305
V126	E186	A246	F306
G127	M187	L247	I307
Q128	L188	K248	N308
I129	L189	N249	D309
V130	E190	K250	L310
P131	S191	N251	C311
V132	R192	S252	D312
Q133	S193	S253	T313
L134	K194	L254	F314
A135	K195	G255	N315
M136	D196	F256	N316
S137	F197	W257	E317
S138	K198	A258	Q318
V139	Q199	R259	L319
Y140	I200	P260	I320
Y141	C201	P261	K321
I142	F202	N262	R322
P143	F203	L263	H323
G144	E204	L264	E324
R145	K205	K265	N325
Q146	L206	S266	I326
Q147	Y207	S267	W327
A148	Y208	P268	M328
S149	T209	L269	L329
A150	Y210	A270	I330
T151	S211	Y271	E331
G152	I212	Q272	Q332
S153	S213	Q273	R333
I154	S214	D274	K334
F155	D215	Q275	I335
I156	E216	N276	G336
P157	I217	S277	H337
K158	L218	F278	D338
H159	D219	N279	F339
T160	L220	A280	
F161	K221	T281	
S162	I222	E282	
V163	W223	L283	
Y164	K224	P284	
H165	G225	I285	
V166	P226	I286	
Q167	K227	C287	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	354548	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 ( $e^-/\text{\AA}^2$ )	1.25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.260	Depositor
Minimum map value	-1.946	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.488	Depositor
Map size ( $\text{\AA}$ )	290.88, 290.88, 290.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.808, 0.808, 0.808	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.28	0/11163	0.39	1/15116 (0.0%)
2	E	0.30	0/841	0.43	0/1139
3	B	0.24	0/9648	0.38	0/13055
4	C	0.29	0/2959	0.39	0/4000
5	D	0.27	0/1707	0.43	0/2311
6	H	0.37	0/643	0.43	0/872
7	G	0.23	0/476	0.40	0/638
8	F	0.17	0/2782	0.35	0/3767
All	All	0.26	0/30219	0.39	1/40898 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	185	LEU	CA-CB-CG	5.10	134.16	116.30

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	10954	0	11085	188	0
2	E	829	0	877	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	9459	0	9413	227	0
4	C	2897	0	2976	35	0
5	D	1668	0	1713	44	0
6	H	630	0	659	12	0
7	G	468	0	467	13	0
8	F	2727	0	2755	62	0
9	A	1	0	0	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
10	G	1	0	0	0	0
10	H	1	0	0	0	0
All	All	29637	0	29945	555	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 9.

The worst 5 of 555 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:A:1123:GLU:O	1:A:1126:ILE:HG13	1.62	0.97
3:B:522:ARG:HB2	3:B:570:GLN:HE22	1.35	0.89
2:E:42:SER:OG	2:E:43:PRO:HD3	1.72	0.88
6:H:37:LEU:HD12	6:H:38:PRO:HD2	1.59	0.85
4:C:139:LYS:HE3	4:C:139:LYS:HA	1.61	0.83

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	1363/1450 (94%)	1307 (96%)	56 (4%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	104/147 (71%)	102 (98%)	2 (2%)	0	100	100
3	B	1186/1242 (96%)	1138 (96%)	48 (4%)	0	100	100
4	C	355/359 (99%)	346 (98%)	9 (2%)	0	100	100
5	D	203/205 (99%)	195 (96%)	8 (4%)	0	100	100
6	H	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
7	G	57/105 (54%)	51 (90%)	6 (10%)	0	100	100
8	F	337/339 (99%)	324 (96%)	13 (4%)	0	100	100
All	All	3683/3927 (94%)	3538 (96%)	145 (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	1219/1279 (95%)	1213 (100%)	6 (0%)	86	95
2	E	96/136 (71%)	96 (100%)	0	100	100
3	B	1038/1081 (96%)	1036 (100%)	2 (0%)	92	98
4	C	326/328 (99%)	325 (100%)	1 (0%)	91	97
5	D	185/185 (100%)	183 (99%)	2 (1%)	70	86
6	H	70/70 (100%)	70 (100%)	0	100	100
7	G	54/96 (56%)	54 (100%)	0	100	100
8	F	312/312 (100%)	311 (100%)	1 (0%)	91	97
All	All	3300/3487 (95%)	3288 (100%)	12 (0%)	88	96

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	1128	THR
4	C	116	LEU

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Mol	Chain	Res	Type
8	F	62	THR
5	D	101	ASN
1	A	400	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	173	HIS
5	D	144	GLN
3	B	419	HIS
5	D	109	GLN
8	F	272	GLN

### 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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

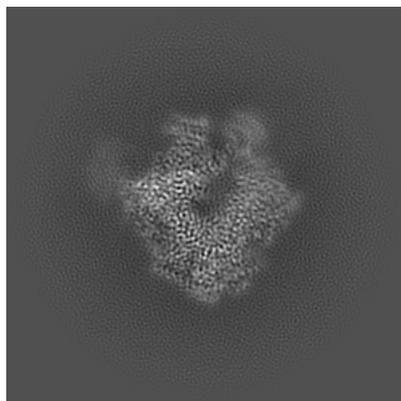
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39507. These allow visual inspection of the internal detail of the map and identification of artifacts.

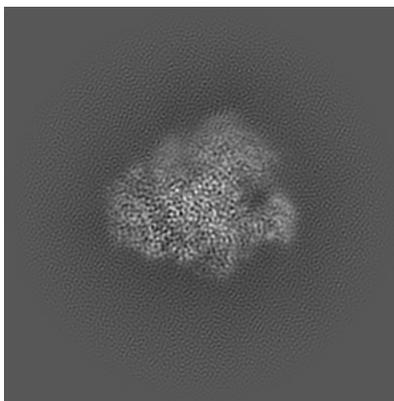
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

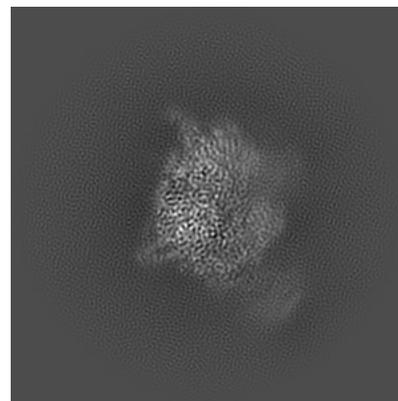
#### 6.1.1 Primary map



X

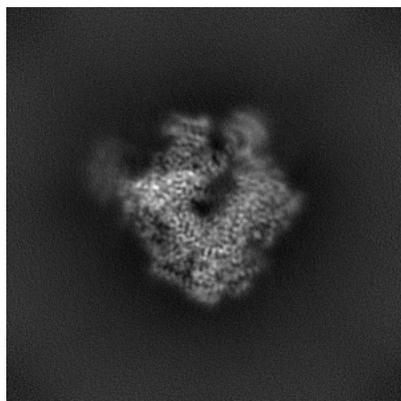


Y

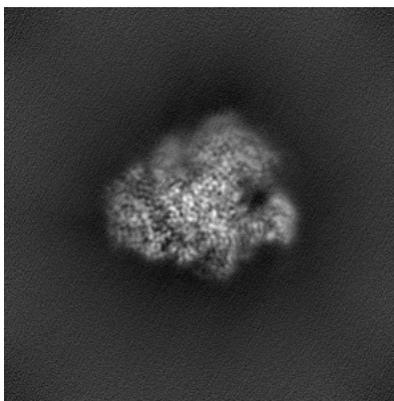


Z

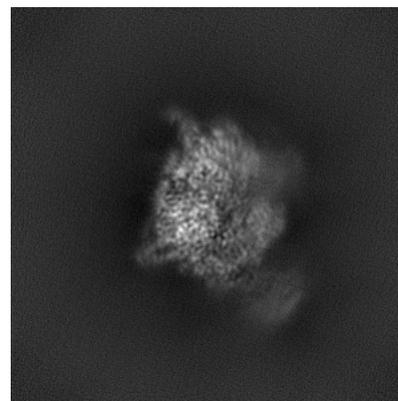
#### 6.1.2 Raw map



X



Y

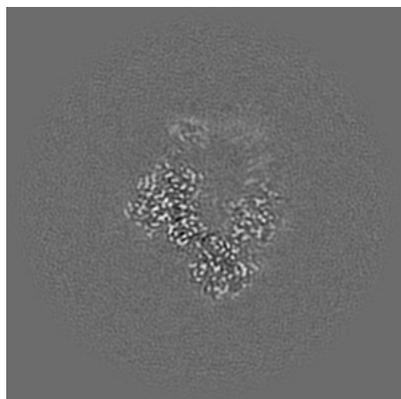


Z

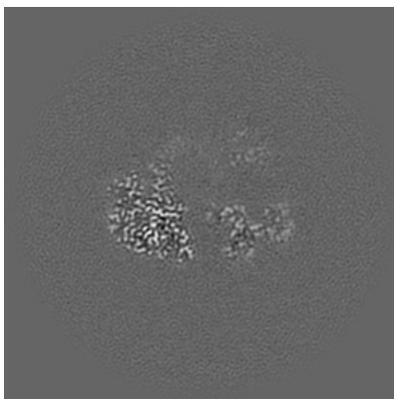
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

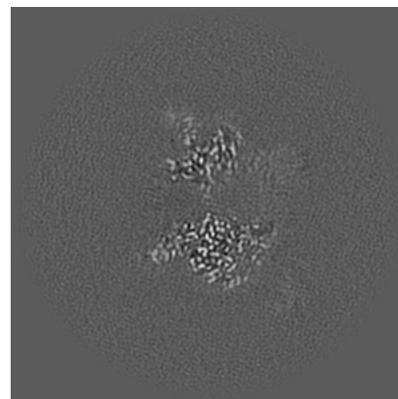
### 6.2.1 Primary map



X Index: 180

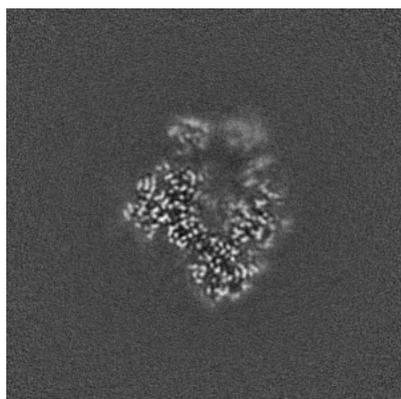


Y Index: 180

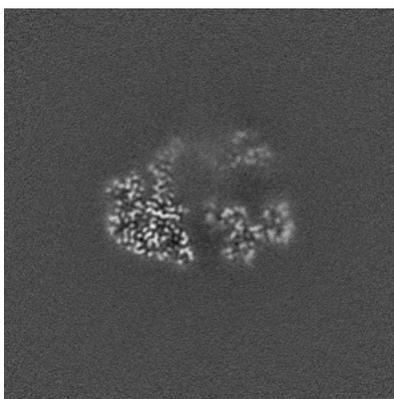


Z Index: 180

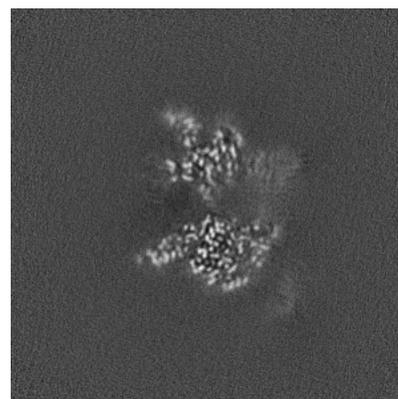
### 6.2.2 Raw map



X Index: 180



Y Index: 180

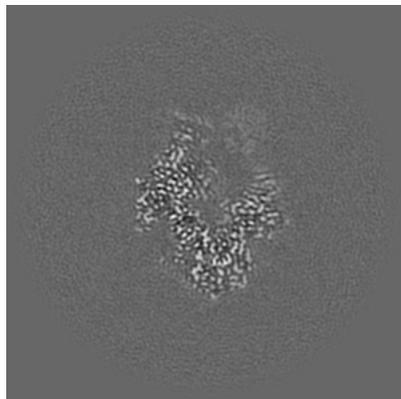


Z Index: 180

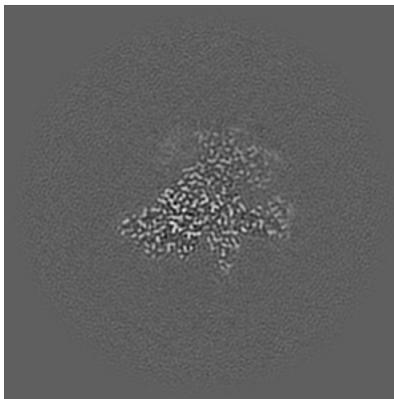
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

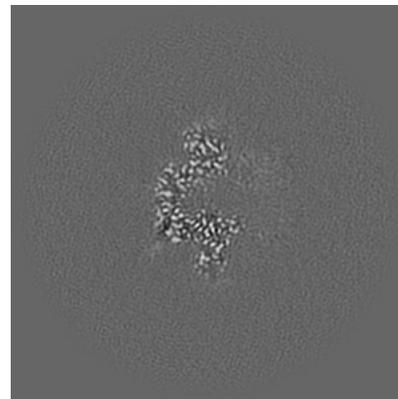
### 6.3.1 Primary map



X Index: 172

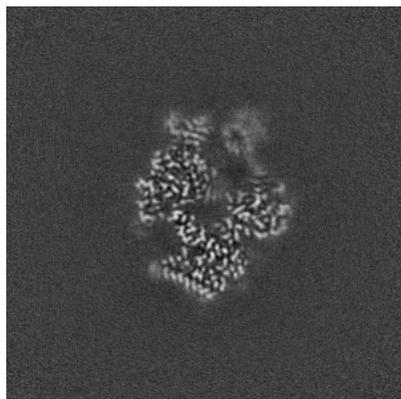


Y Index: 159

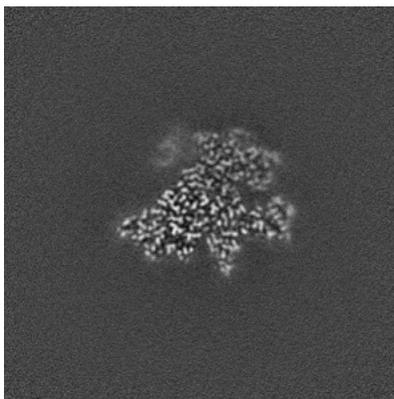


Z Index: 166

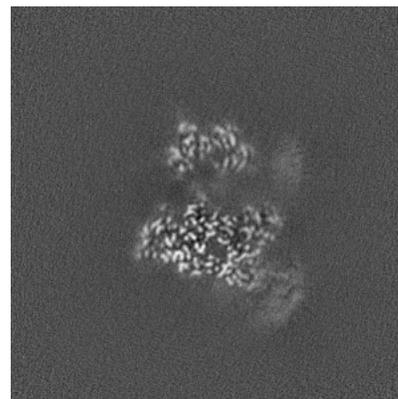
### 6.3.2 Raw map



X Index: 167



Y Index: 159

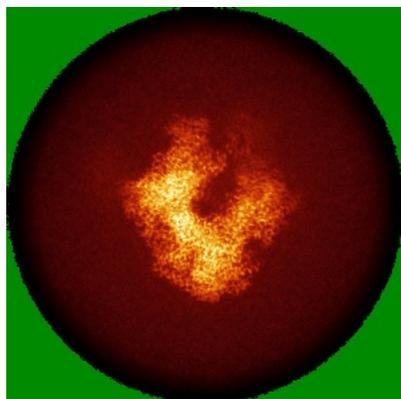


Z Index: 197

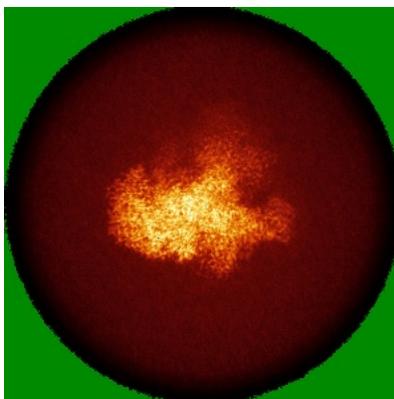
The images above show the largest variance slices of the map in three orthogonal directions.

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

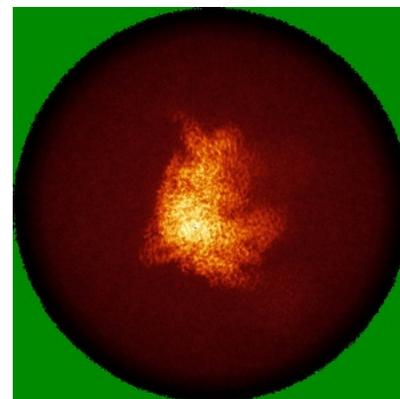
### 6.4.1 Primary map



X

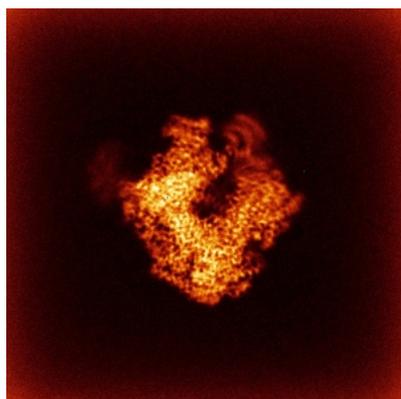


Y

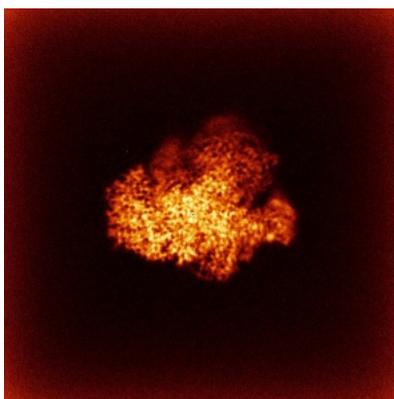


Z

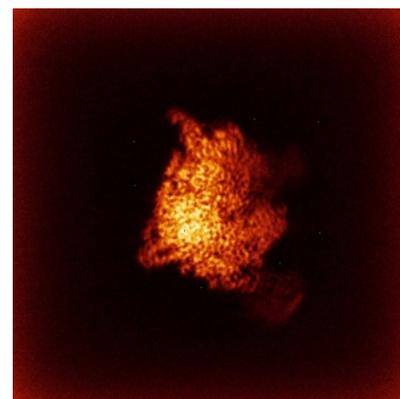
### 6.4.2 Raw map



X



Y

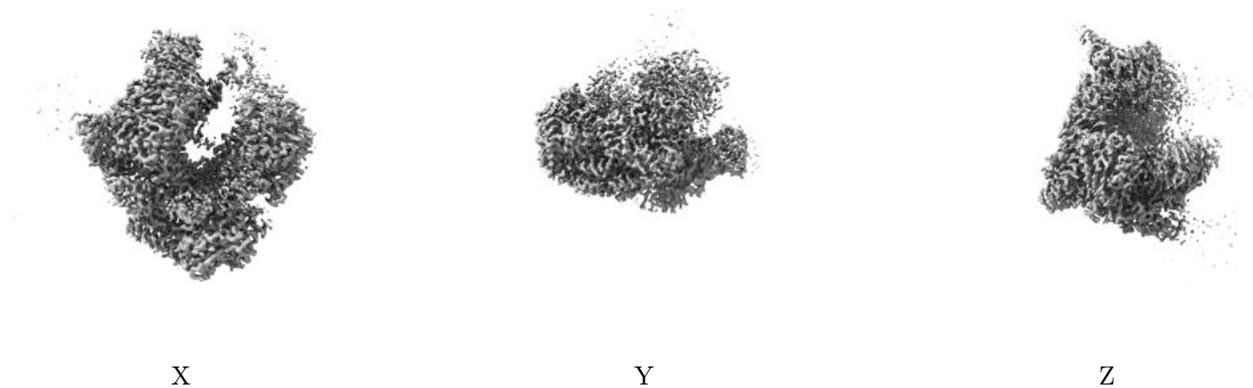


Z

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.

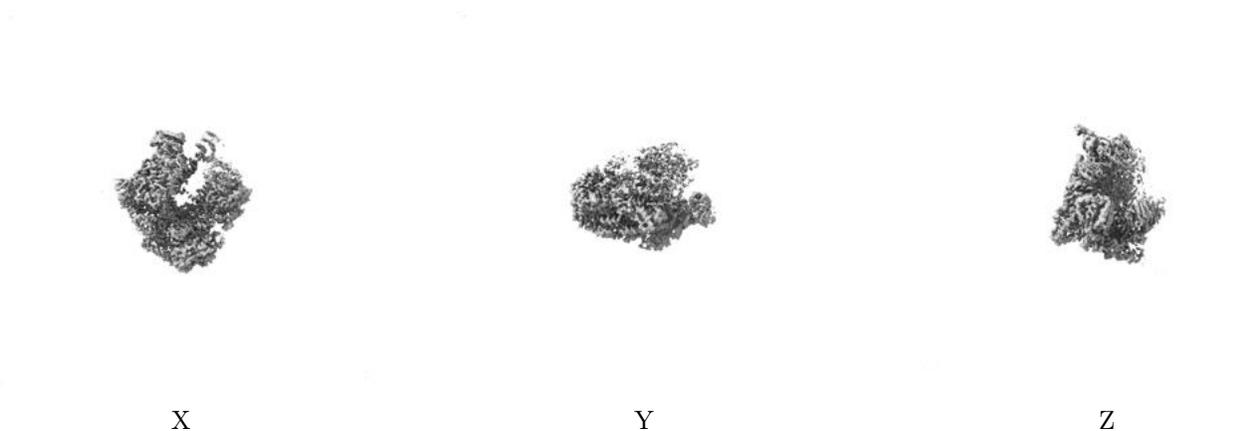
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.488. 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.

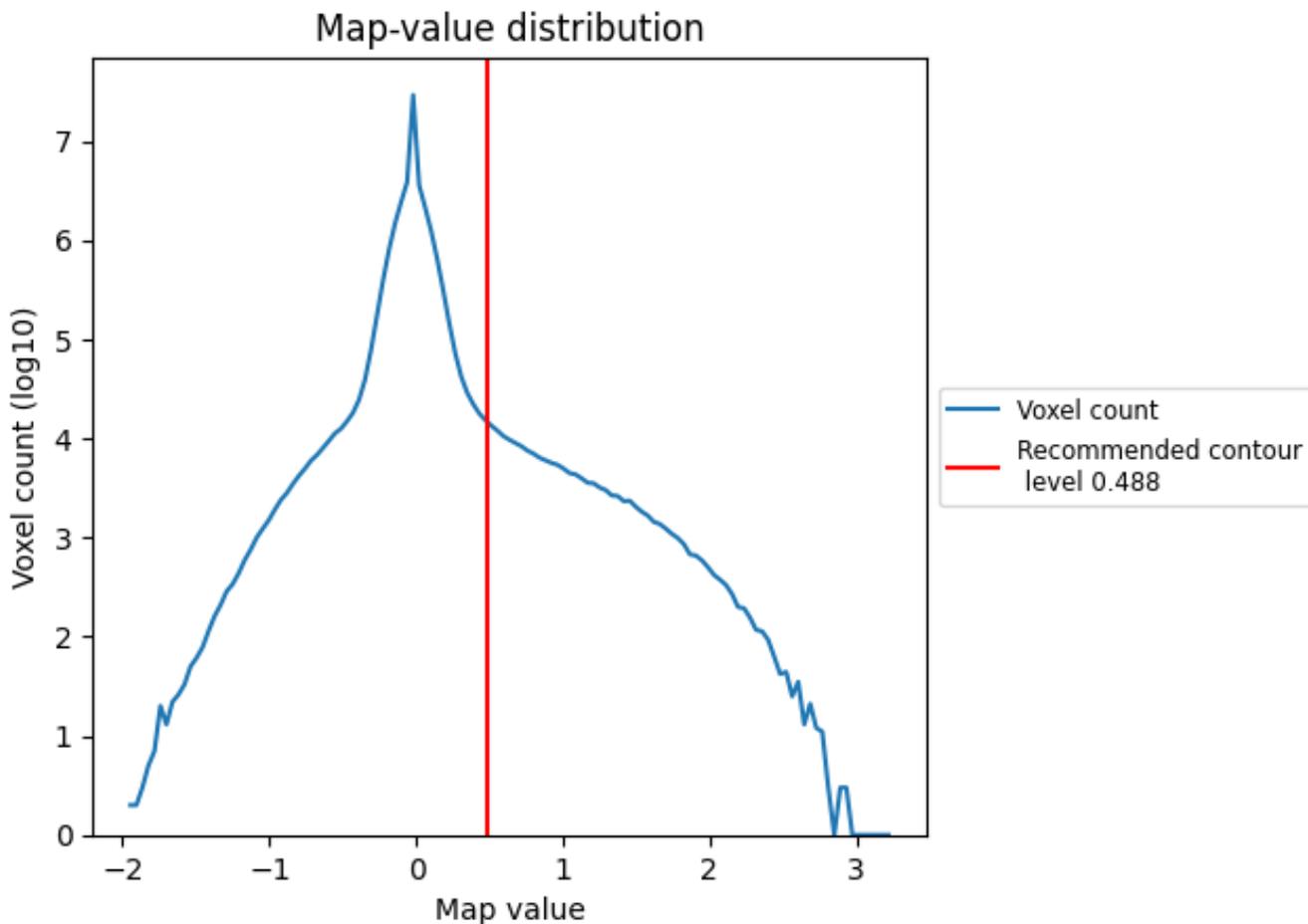
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

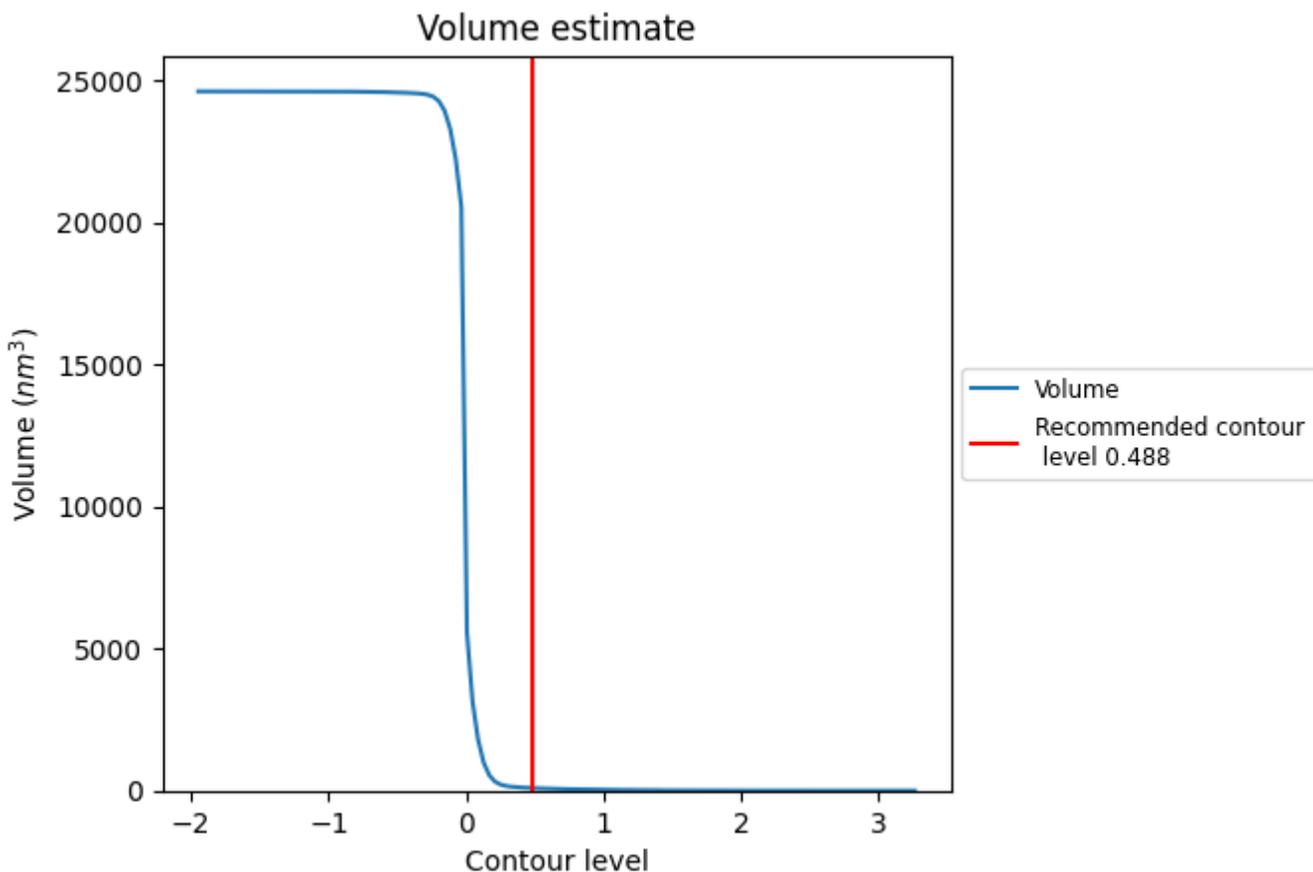
This section contains the results of statistical analysis of the map.

### 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.

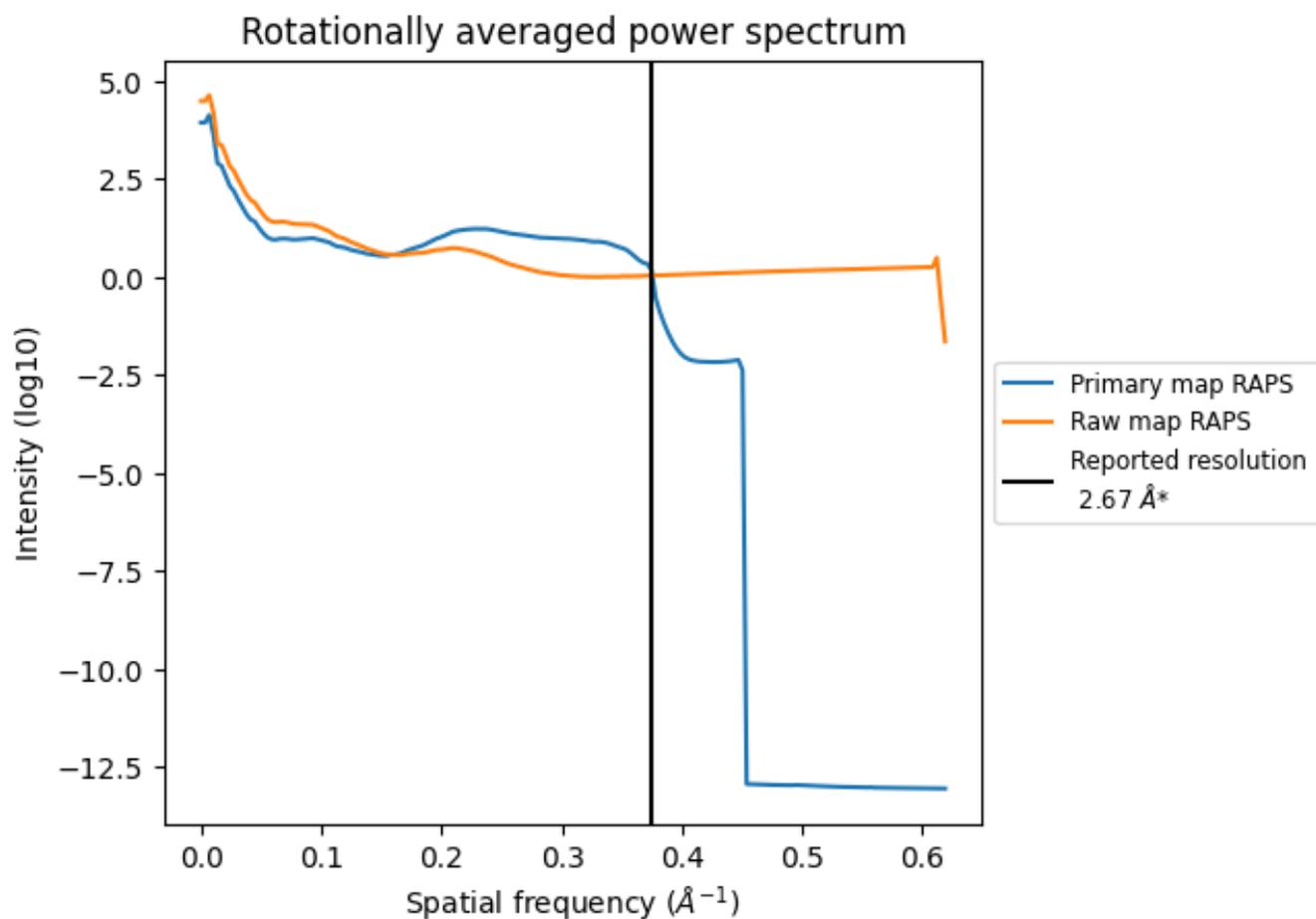
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 89 nm<sup>3</sup>; this corresponds to an approximate mass of 80 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 [i](#)

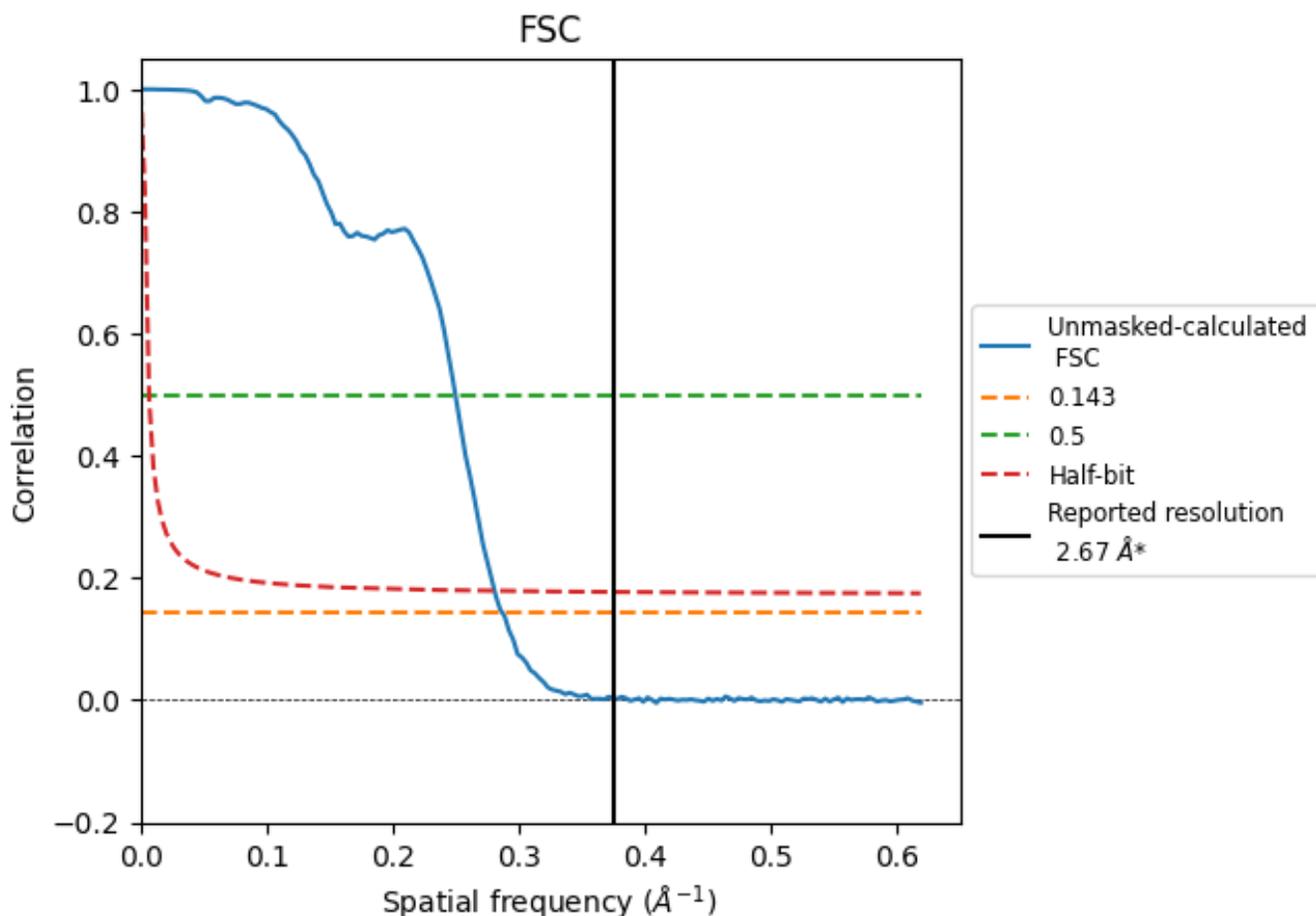


\*Reported resolution corresponds to spatial frequency of 0.375 Å<sup>-1</sup>

## 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 0.375 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

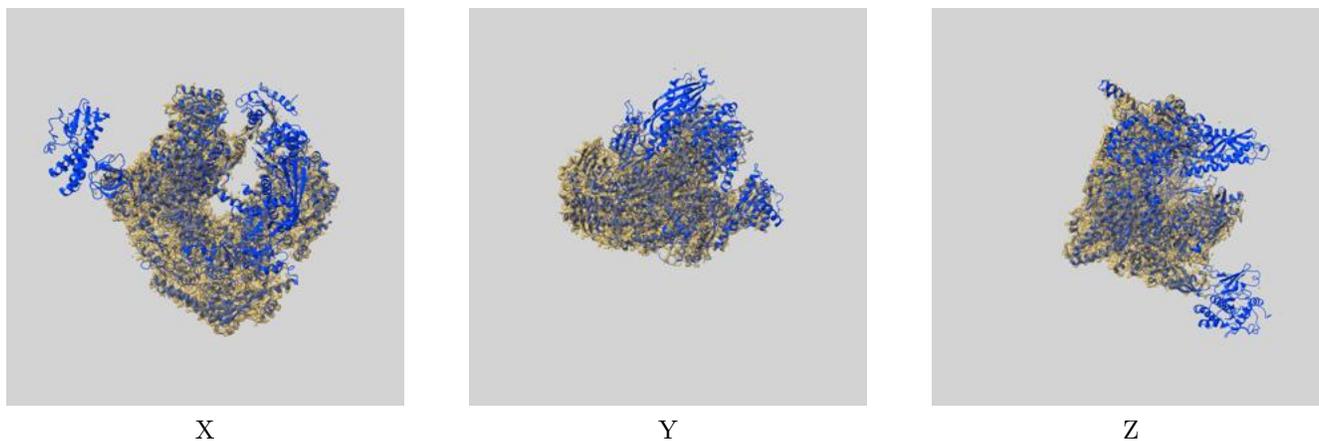
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.48	4.00	3.56

\*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 3.48 differs from the reported value 2.67 by more than 10 %

## 9 Map-model fit [i](#)

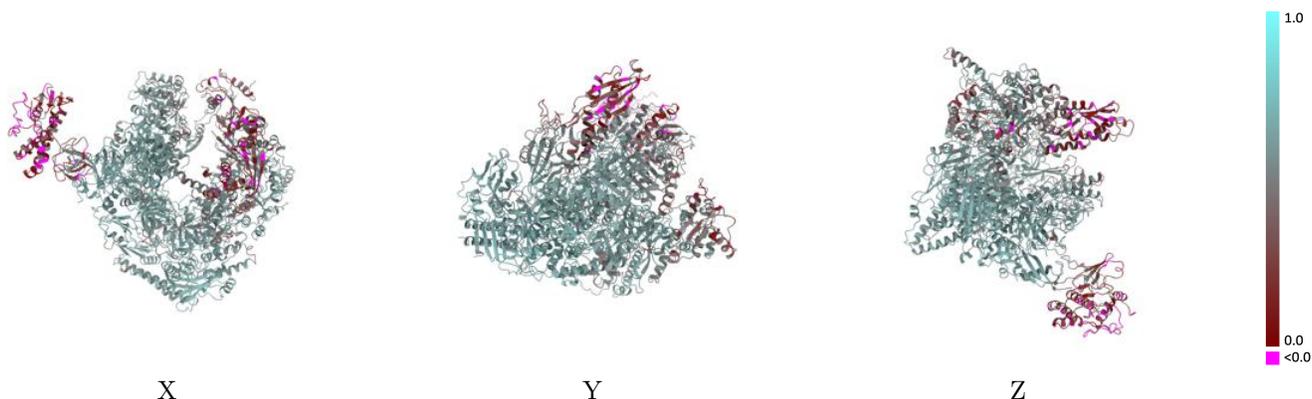
This section contains information regarding the fit between EMDB map EMD-39507 and PDB model 8YQV. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



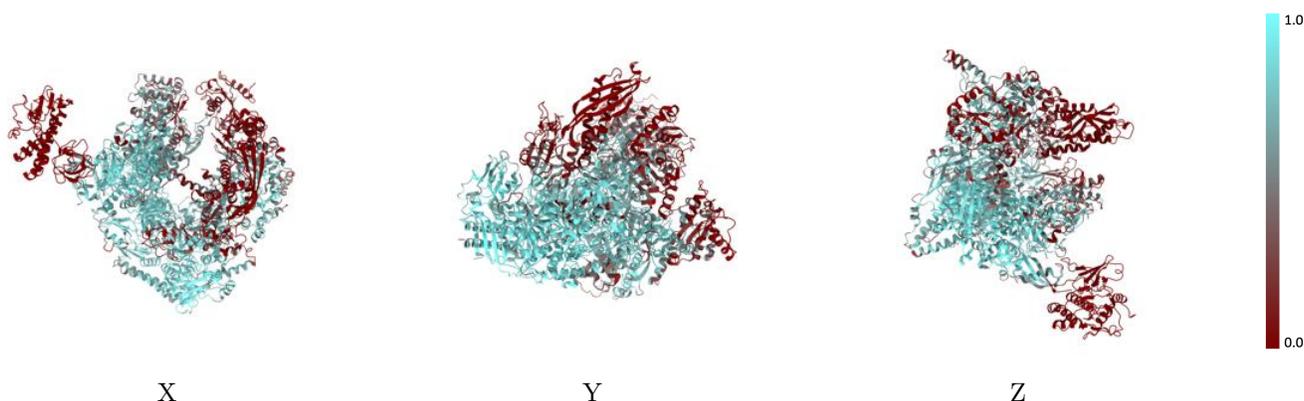
The images above show the 3D surface view of the map at the recommended contour level 0.488 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



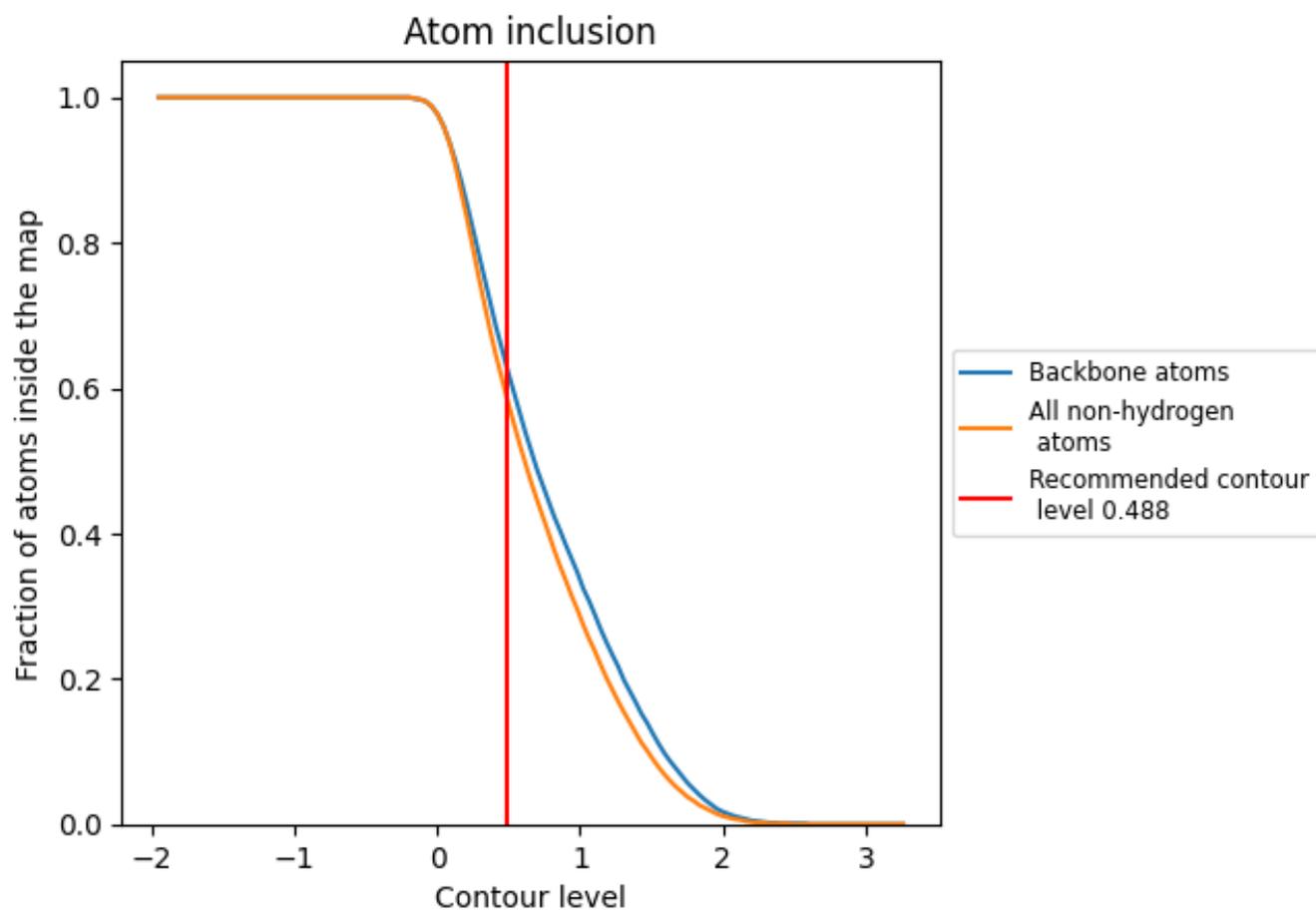
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.488).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 59% 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 (0.488) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5870	 0.5370
A	 0.6880	 0.5840
B	 0.4690	 0.5080
C	 0.8290	 0.6230
D	 0.6960	 0.5940
E	 0.7910	 0.6170
F	 0.1610	 0.2850
G	 0.5950	 0.5490
H	 0.7640	 0.6010

