



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 07:56 AM EDT

PDB ID : 9MU7 / pdb_00009mu7
EMDB ID : EMD-48622
Title : Structure of a native *Drosophila melanogaster* Pol II Elongation Complex with a well-defined Rpb4/Rpb7 stalk
Authors : Venette-Smith, N.L.; Vishwakarma, R.K.; Dollinger, R.; Schultz, J.; Venkatakrishnan, V.; Babitzke, P.; Anand, G.; Gilmour, D.S.; Armache, J.-P.; Murakami, K.S.
Deposited on : 2025-01-13
Resolution : 3.44 Å (reported)
Based on initial model : .

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

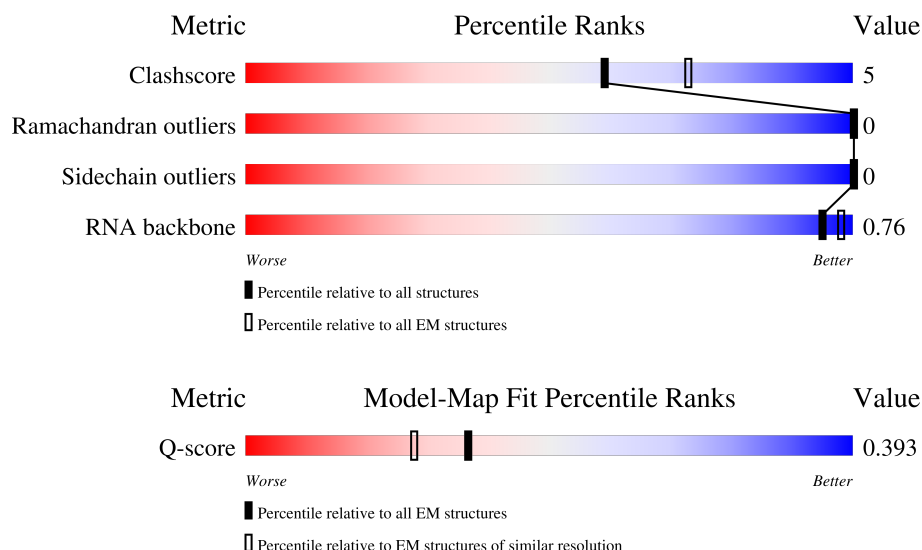
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.44 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	13877 (2.94 - 3.94)

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	1470	5% 86% 14%
2	B	1164	87% 13%
3	C	269	5% 83% 17%

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Mol	Chain	Length	Quality of chain
4	D	130	
5	F	84	
6	G	173	
7	H	147	
8	I	116	
9	J	67	
10	K	116	
11	L	46	
12	R	10	
13	T	50	
14	N	39	
15	E	210	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 33887 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 II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1470	Total	C	N	O	S	0	0
			11634	7310	2067	2168	89		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1164	Total	C	N	O	S	0	0
			9257	5851	1633	1709	64		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	269	Total	C	N	O	S	0	0
			2156	1354	362	432	8		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit Rpb4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	130	Total	C	N	O	S	0	0
			1058	666	175	212	5		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	84	Total	C	N	O	S	0	0
			678	433	116	123	6		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	173	Total	C	N	O	S	0	0
			1344	873	217	246	8		

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	147	Total	C	N	O	S	0	0
			1186	748	200	228	10		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	116	Total	C	N	O	S	0	0
			959	594	170	183	12		

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	67	Total	C	N	O	S	0	0
			530	342	89	93	6		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	116	Total	C	N	O	S	0	0
			935	603	153	176	3		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	46	Total	C	N	O	S	0	0
			390	239	78	66	7		

- Molecule 12 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	10	Total	C	N	O	P	0	0
			220	100	50	60	10		

- Molecule 13 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	50	Total	C	N	O	P	0	0
			998	498	102	348	50		

- Molecule 14 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	39	Total	C	N	O	P	0	0
			819	390	195	195	39		

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	210	Total	C	N	O	S	0	0
			1715	1087	294	322	12		

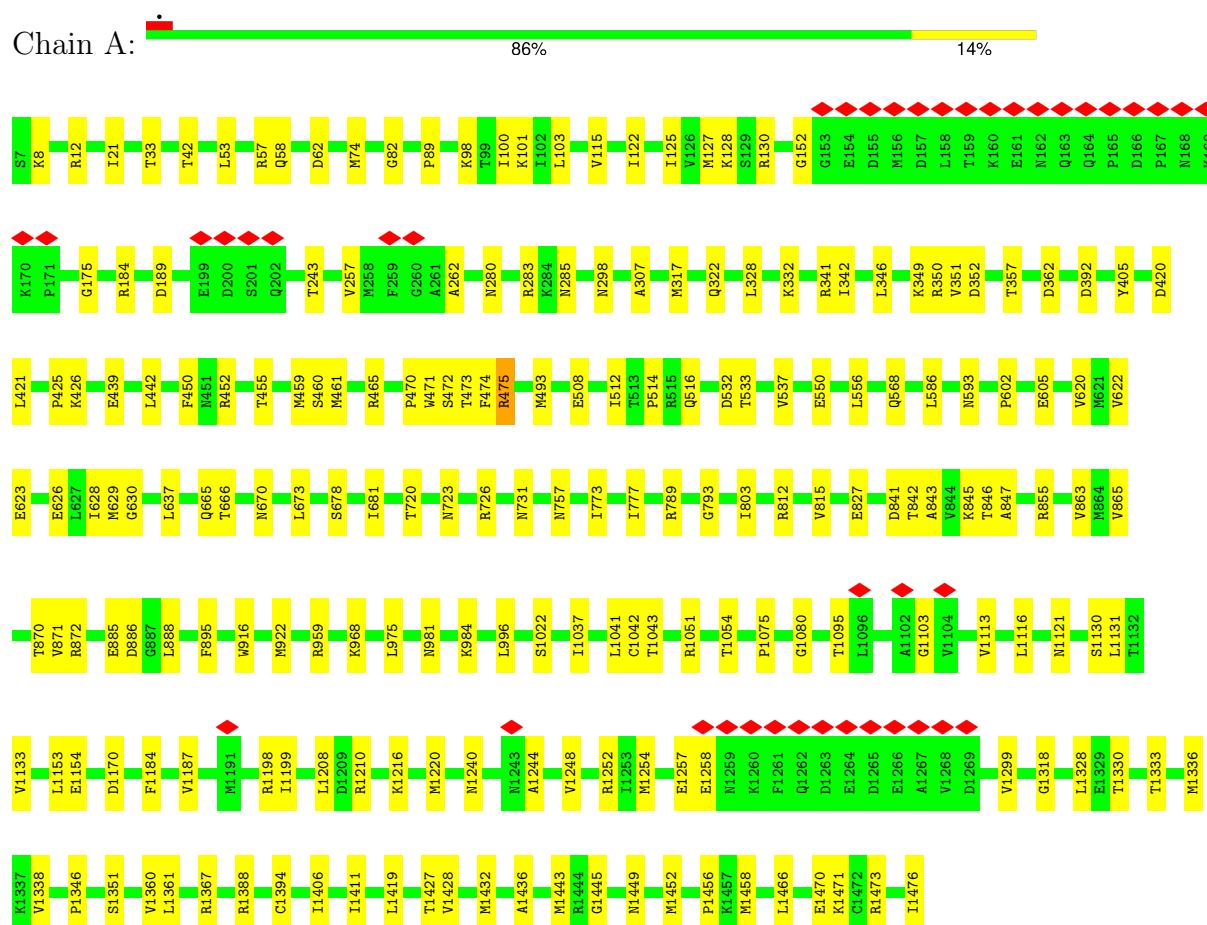
- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
16	A	2	Total	Zn	0
			2	2	
16	B	1	Total	Zn	0
			1	1	
16	C	1	Total	Zn	0
			1	1	
16	I	2	Total	Zn	0
			2	2	
16	J	1	Total	Zn	0
			1	1	
16	L	1	Total	Zn	0
			1	1	

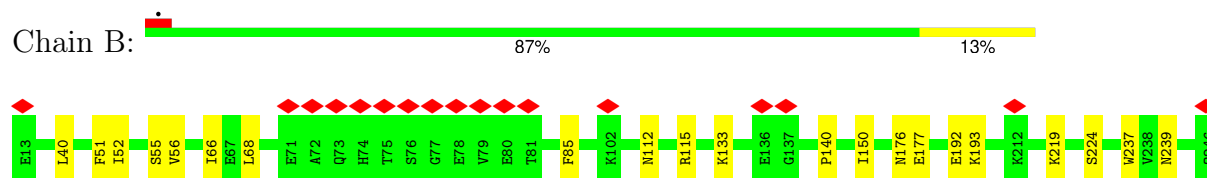
3 Residue-property plots

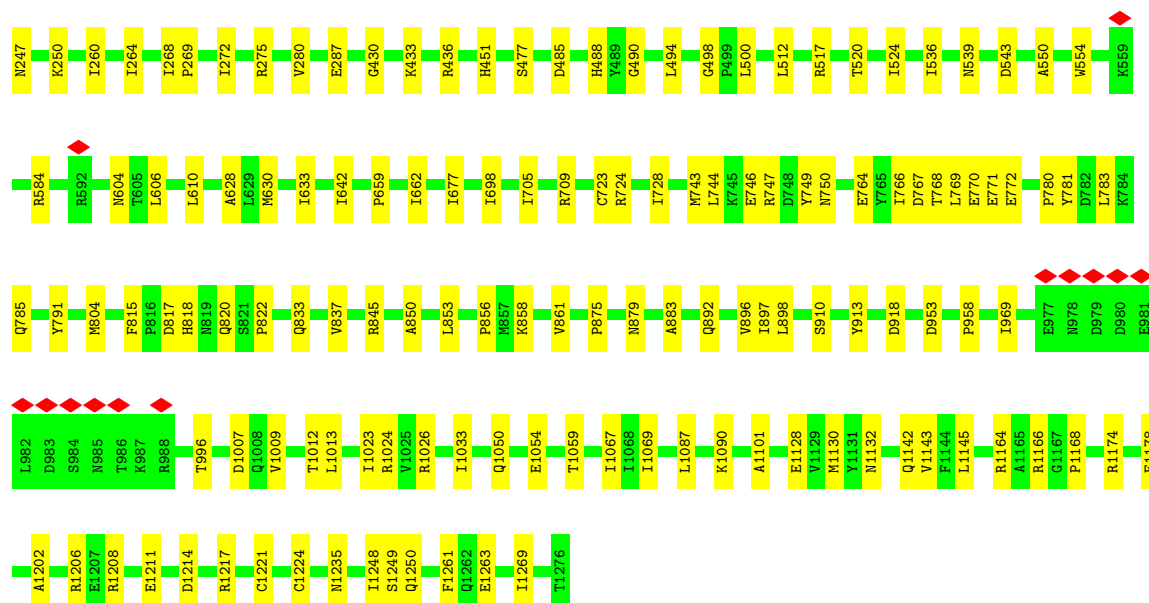
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 II subunit RPB1

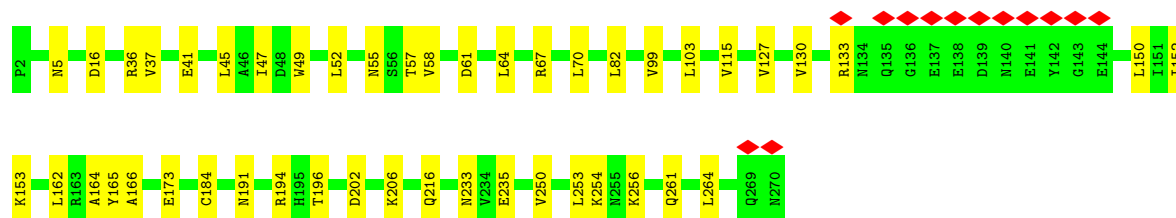
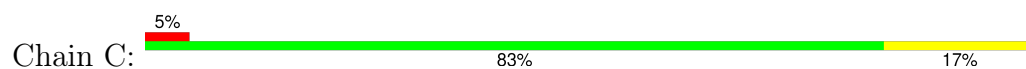


• Molecule 2: DNA-directed RNA polymerase II subunit RPB2

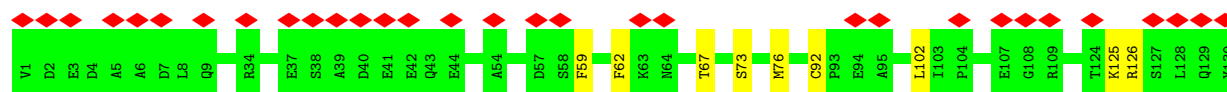
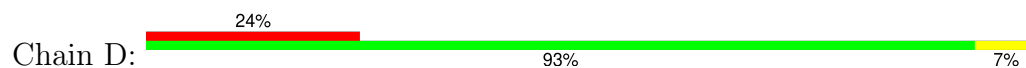




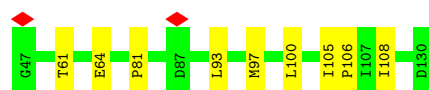
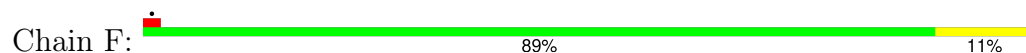
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3



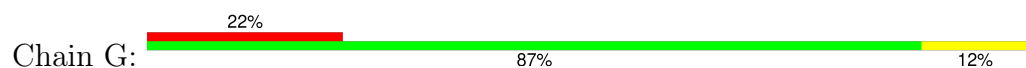
• Molecule 4: DNA-directed RNA polymerase II subunit Rpb4

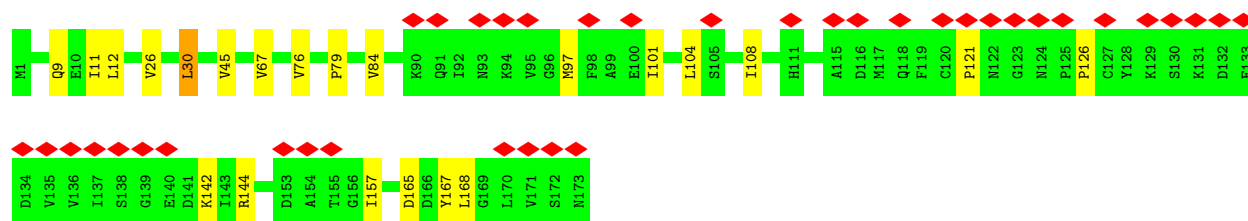


• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2

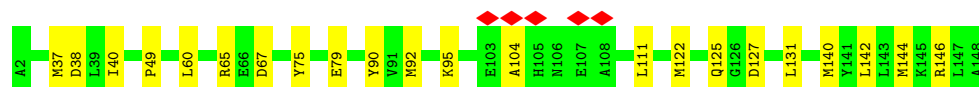
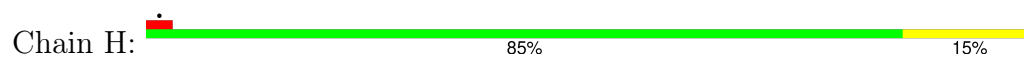


• Molecule 6: DNA-directed RNA polymerase II subunit RPB7

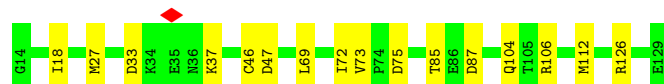
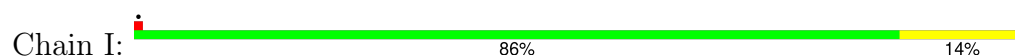




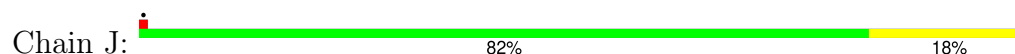
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC3



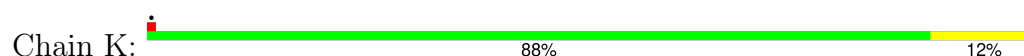
- Molecule 8: DNA-directed RNA polymerase II subunit RPB9



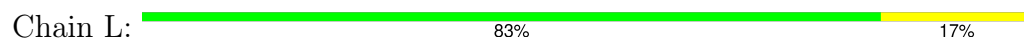
- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 10: DNA-directed RNA polymerase II subunit RPB11



- Molecule 11: DNA-directed RNA polymerase II subunit RPB12

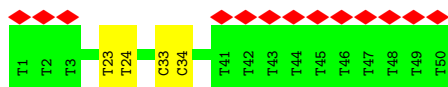
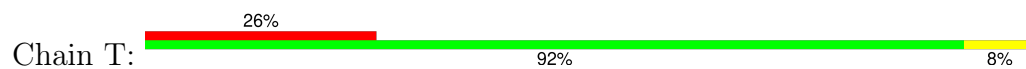


- Molecule 12: RNA

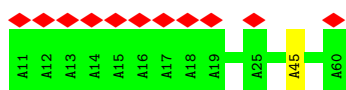




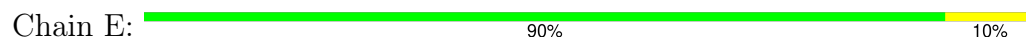
- Molecule 13: Template DNA



- Molecule 14: Non-template DNA



- Molecule 15: DNA-directed RNA polymerase II subunit RPB5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	70116	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; 'Patch CTF Estimation' in cryoSPARC	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.65	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	1.512	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	415.368, 415.368, 415.368	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1538, 1.1538, 1.1538	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.21	0/11849	0.45	5/15988 (0.0%)
2	B	0.19	0/9444	0.41	0/12756
3	C	0.18	0/2201	0.36	0/2989
4	D	0.17	0/1075	0.44	0/1442
5	F	0.19	0/689	0.48	0/927
6	G	0.16	0/1375	0.46	1/1862 (0.1%)
7	H	0.17	0/1211	0.39	0/1627
8	I	0.18	0/980	0.48	0/1325
9	J	0.19	0/539	0.37	0/726
10	K	0.20	0/954	0.41	0/1286
11	L	0.19	0/397	0.47	0/527
12	R	0.14	0/249	0.22	0/386
13	T	0.23	0/1097	0.55	0/1692
14	N	0.17	0/934	0.28	0/1435
15	E	0.16	0/1745	0.40	0/2350
All	All	0.19	0/34739	0.43	6/47318 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	420	ASP	O-C-N	-8.20	113.69	122.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	420	ASP	CA-C-N	8.05	136.18	122.26
1	A	420	ASP	C-N-CA	8.05	136.18	122.26
1	A	470	PRO	N-CA-C	6.36	122.57	113.47
1	A	470	PRO	CB-CA-C	-6.25	103.12	113.06

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	475	ARG	Sidechain

5.2 Too-close contacts

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	11634	0	11724	130	0
2	B	9257	0	9229	100	0
3	C	2156	0	2084	33	0
4	D	1058	0	1033	7	0
5	F	678	0	713	7	0
6	G	1344	0	1361	15	0
7	H	1186	0	1132	13	0
8	I	959	0	900	10	0
9	J	530	0	542	9	0
10	K	935	0	946	12	0
11	L	390	0	386	6	0
12	R	220	0	111	5	0
13	T	998	0	599	3	0
14	N	819	0	431	1	0
15	E	1715	0	1740	14	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
All	All	33887	0	32931	306	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 5.

The worst 5 of 306 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:425:PRO:C	1:A:426:LYS:N	2.14	1.06
2:B:51:PHE:O	2:B:55:SER:HB2	1.85	0.76
2:B:709:ARG:HE	8:I:104:GLN:HE21	1.38	0.71
12:R:39:A:H61	13:T:33:DC:H42	1.36	0.70
1:A:628:ILE:HG22	1:A:629:MET:HG3	1.78	0.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1466/1470 (100%)	1410 (96%)	56 (4%)	0	100	100
2	B	1162/1164 (100%)	1119 (96%)	43 (4%)	0	100	100
3	C	267/269 (99%)	257 (96%)	10 (4%)	0	100	100
4	D	128/130 (98%)	126 (98%)	2 (2%)	0	100	100
5	F	82/84 (98%)	82 (100%)	0	0	100	100
6	G	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
7	H	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
8	I	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
9	J	65/67 (97%)	63 (97%)	2 (3%)	0	100	100
10	K	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
11	L	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
15	E	208/210 (99%)	201 (97%)	7 (3%)	0	100	100
All	All	3966/3992 (99%)	3819 (96%)	147 (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	1289/1290 (100%)	1289 (100%)	0	100	100
2	B	1003/1015 (99%)	1003 (100%)	0	100	100
3	C	244/244 (100%)	244 (100%)	0	100	100
4	D	115/116 (99%)	115 (100%)	0	100	100
5	F	75/75 (100%)	75 (100%)	0	100	100
6	G	149/149 (100%)	149 (100%)	0	100	100
7	H	127/127 (100%)	127 (100%)	0	100	100
8	I	108/108 (100%)	108 (100%)	0	100	100
9	J	56/57 (98%)	56 (100%)	0	100	100
10	K	102/102 (100%)	102 (100%)	0	100	100
11	L	42/42 (100%)	42 (100%)	0	100	100
15	E	192/192 (100%)	192 (100%)	0	100	100
All	All	3502/3517 (100%)	3502 (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 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1250	GLN
4	D	16	ASN
3	C	209	HIS
4	D	117	GLN
1	A	1305	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	R	9/10 (90%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 8 ligands modelled in this entry, 8 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
14	N	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	25:DA	O3'	37:DA	P	23.14
1	A	425:PRO	C	426:LYS	N	2.14

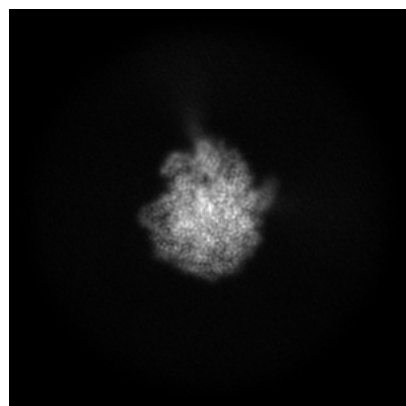
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48622. These allow visual inspection of the internal detail of the map and identification of artifacts.

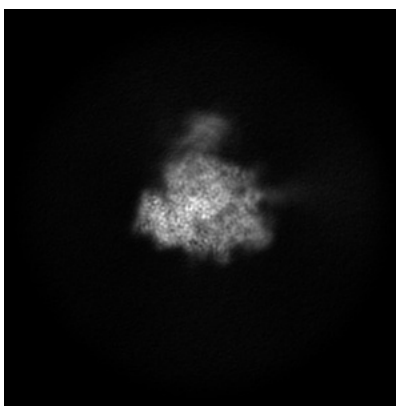
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

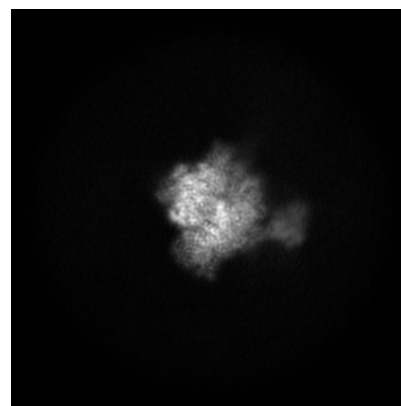
6.1.1 Primary map



X

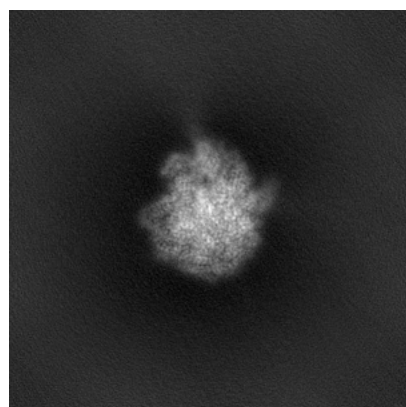


Y

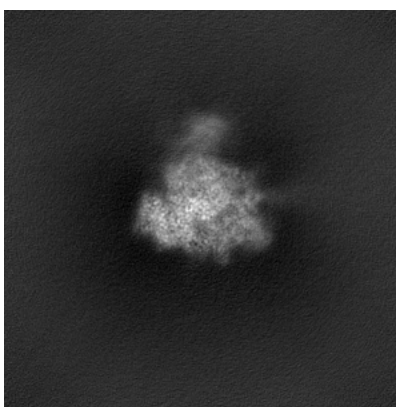


Z

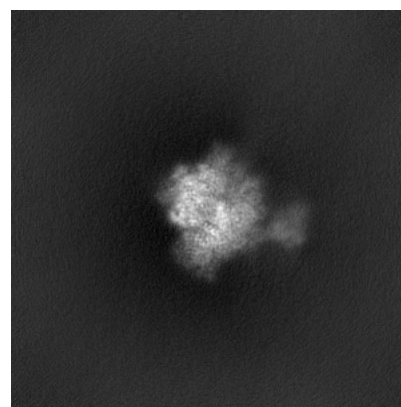
6.1.2 Raw map



X



Y

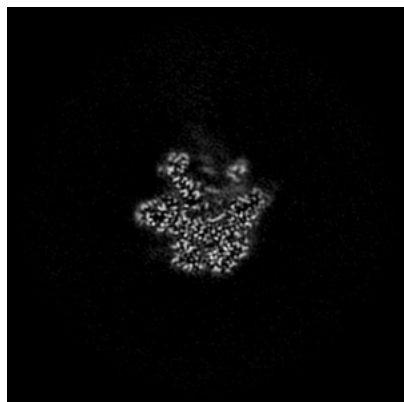


Z

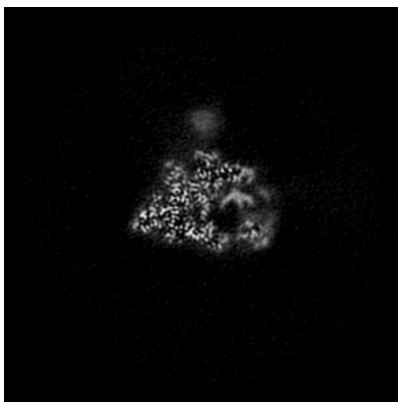
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

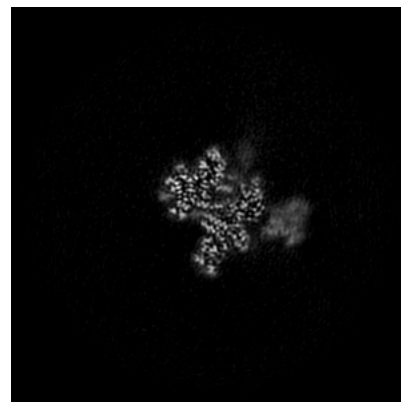
6.2.1 Primary map



X Index: 180

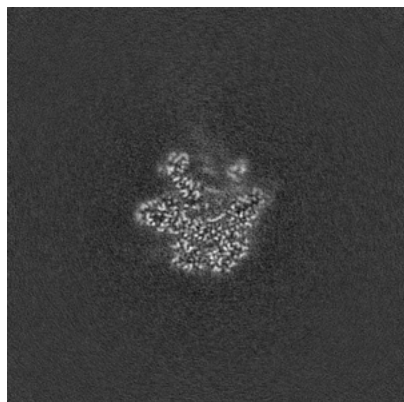


Y Index: 180

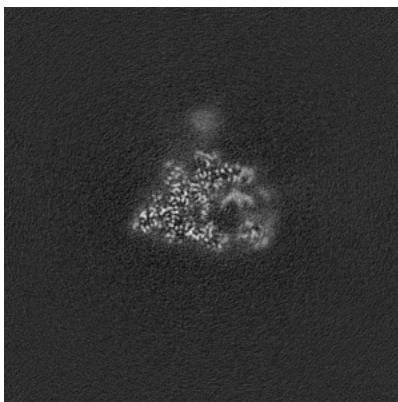


Z Index: 180

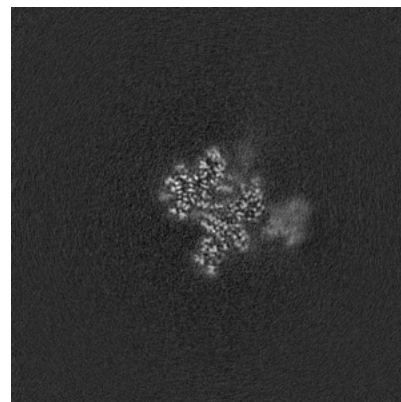
6.2.2 Raw map



X Index: 180



Y Index: 180

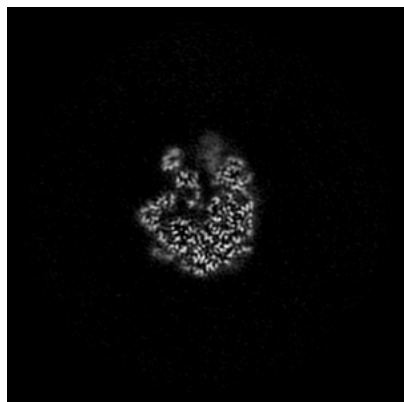


Z Index: 180

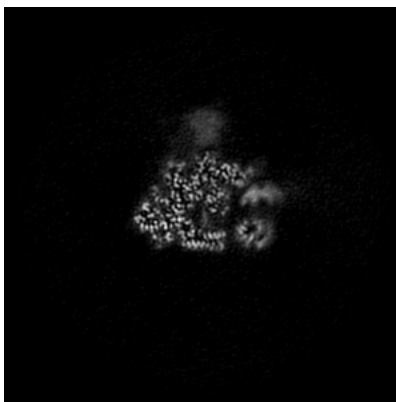
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

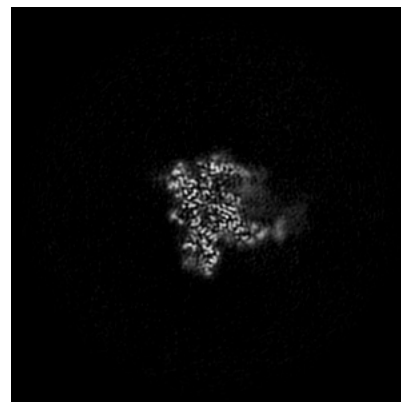
6.3.1 Primary map



X Index: 171

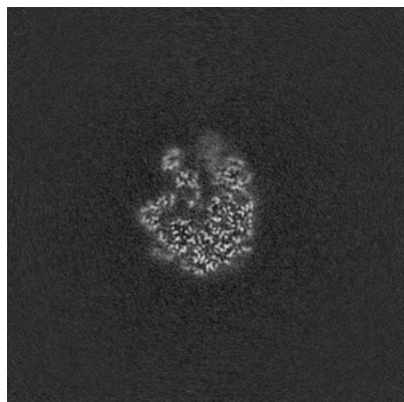


Y Index: 174

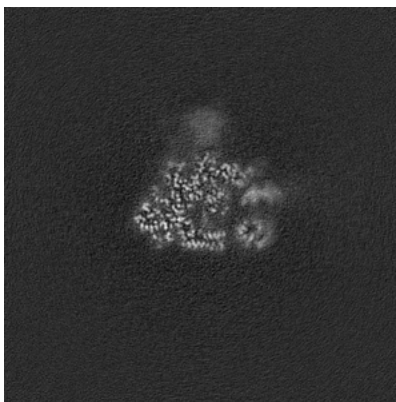


Z Index: 164

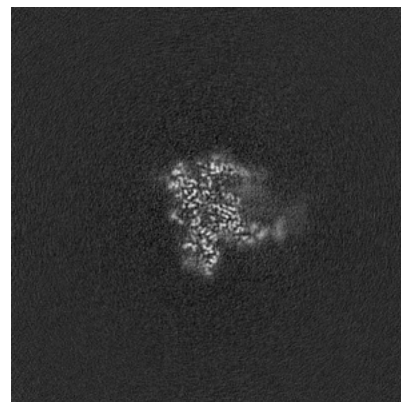
6.3.2 Raw map



X Index: 171



Y Index: 174

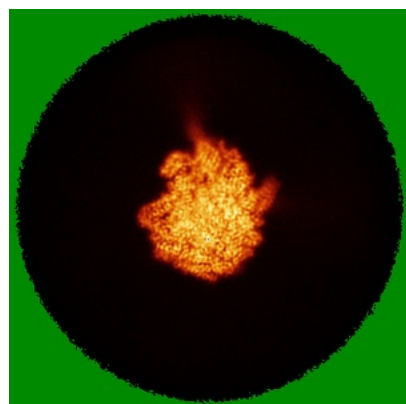


Z Index: 164

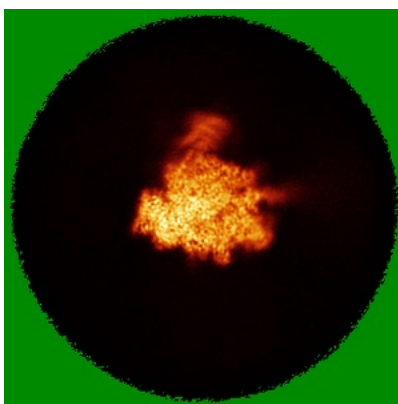
The images above show the largest variance slices of the map in three orthogonal directions.

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

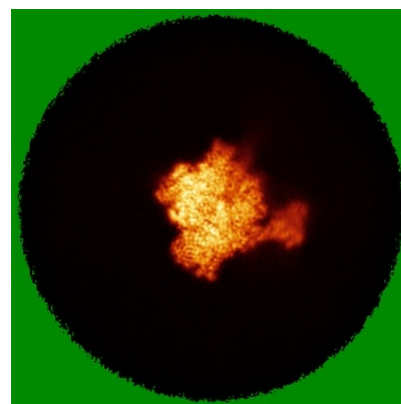
6.4.1 Primary map



X

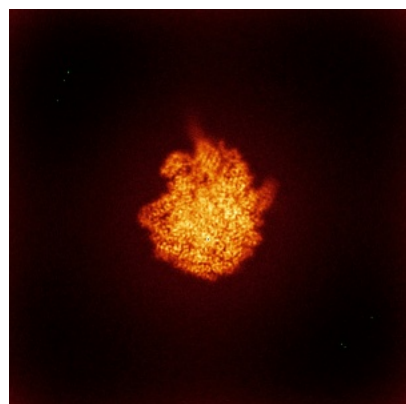


Y

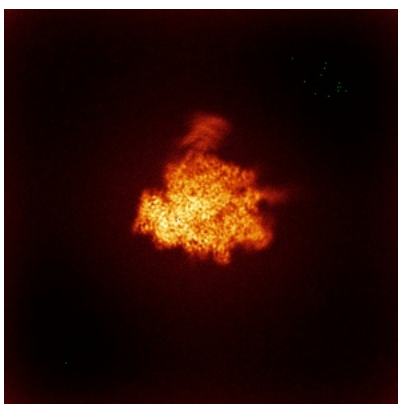


Z

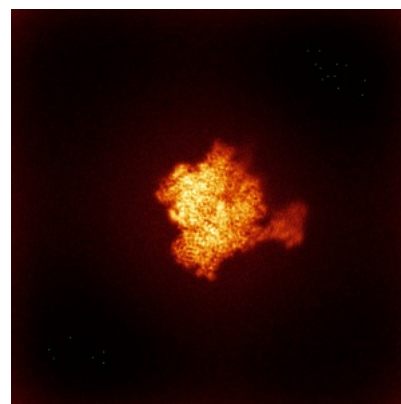
6.4.2 Raw map



X



Y

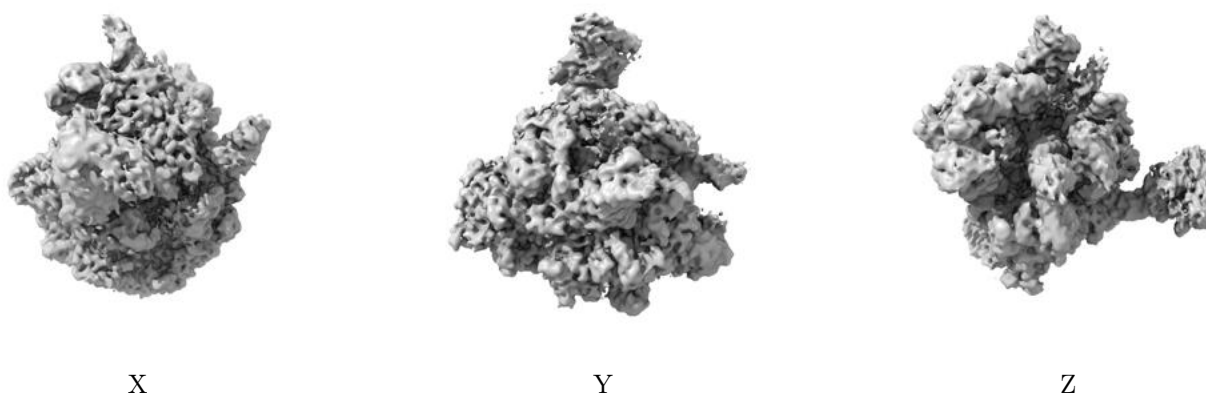


Z

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.

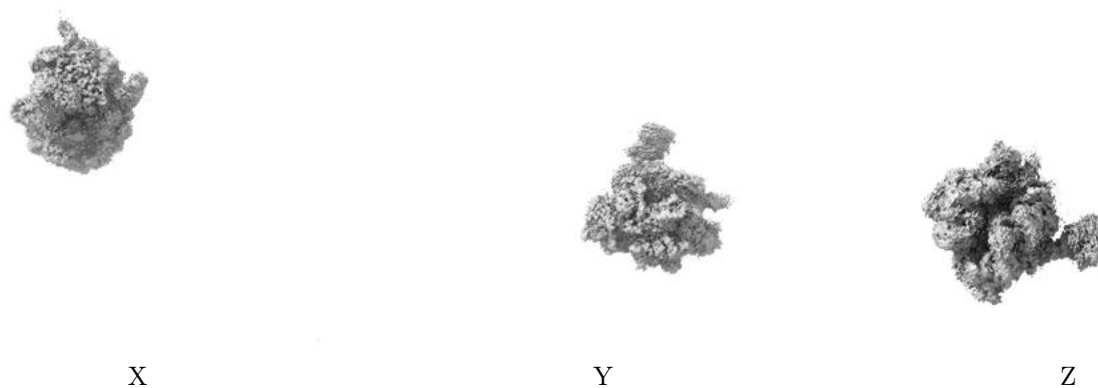
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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.

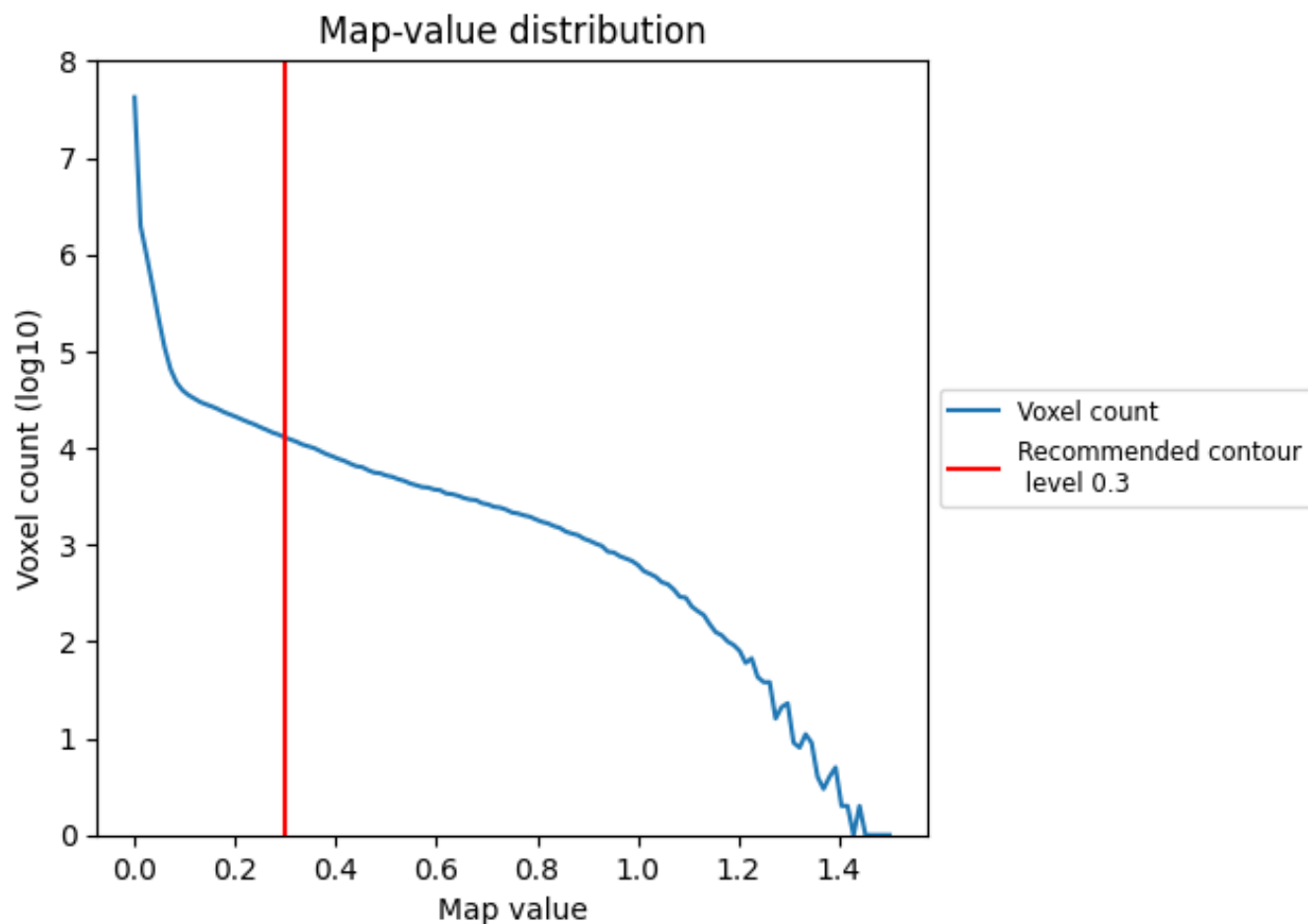
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

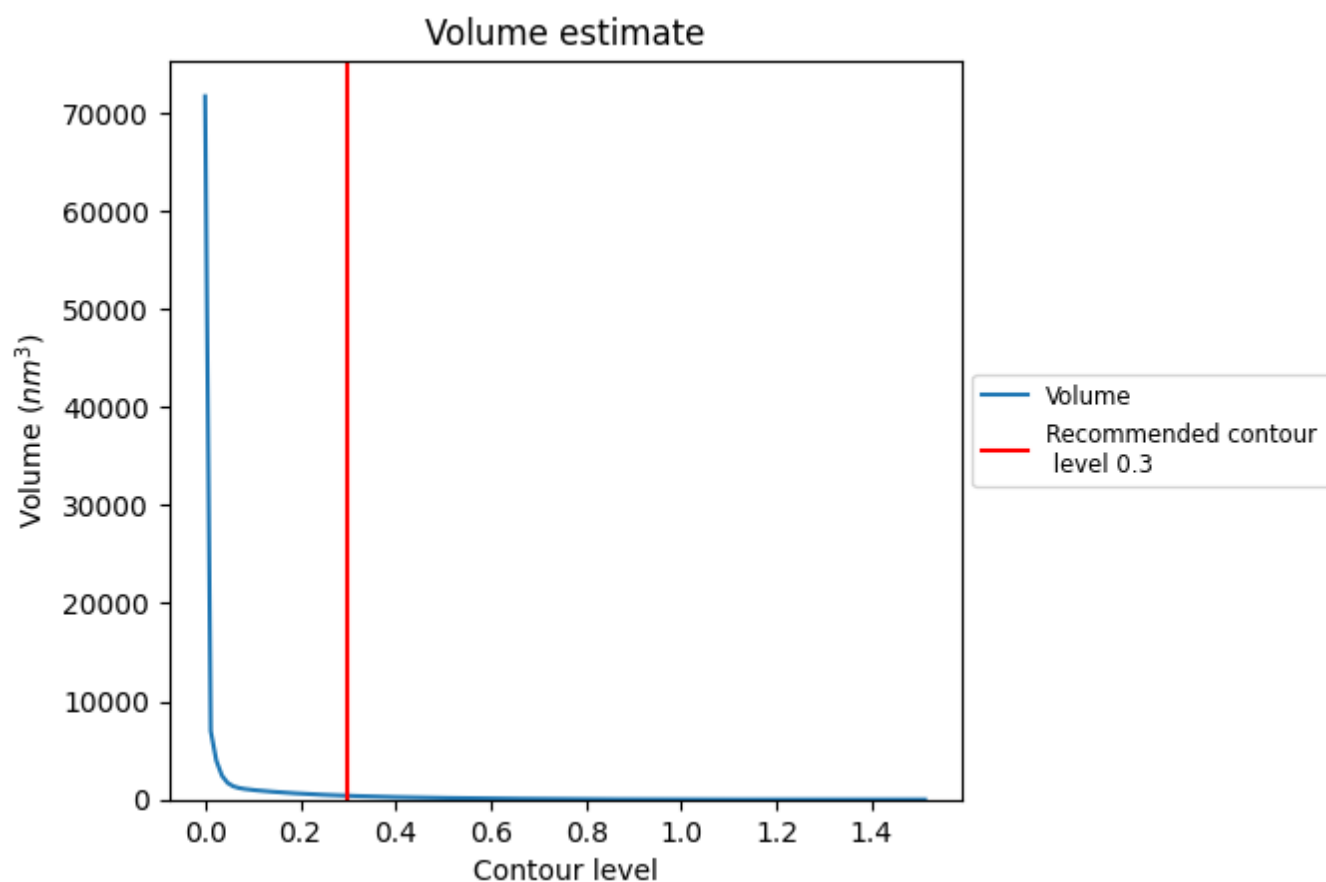
This section contains the results of statistical analysis of the map.

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.

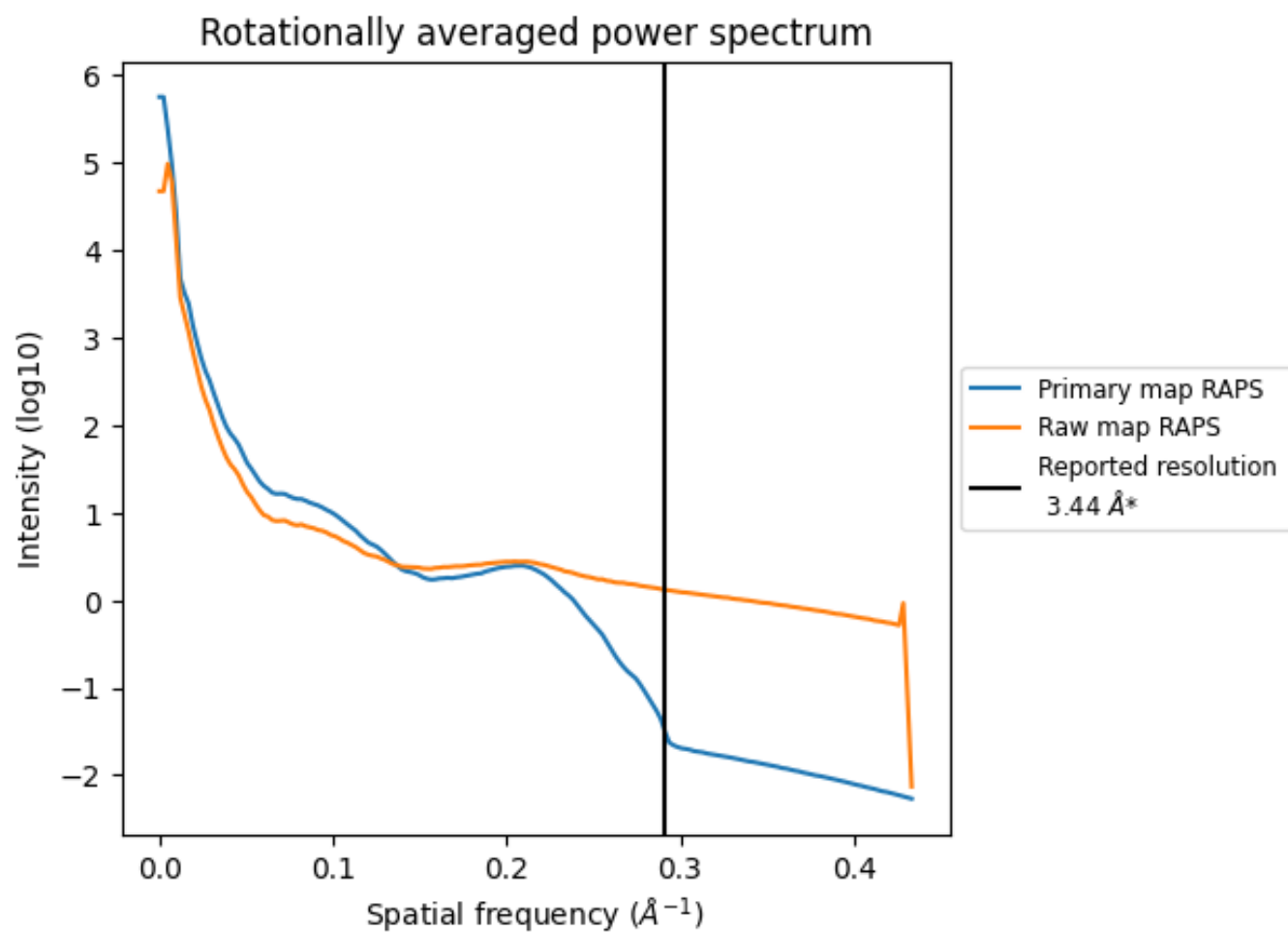
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 387 nm³; this corresponds to an approximate mass of 350 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 ⓘ

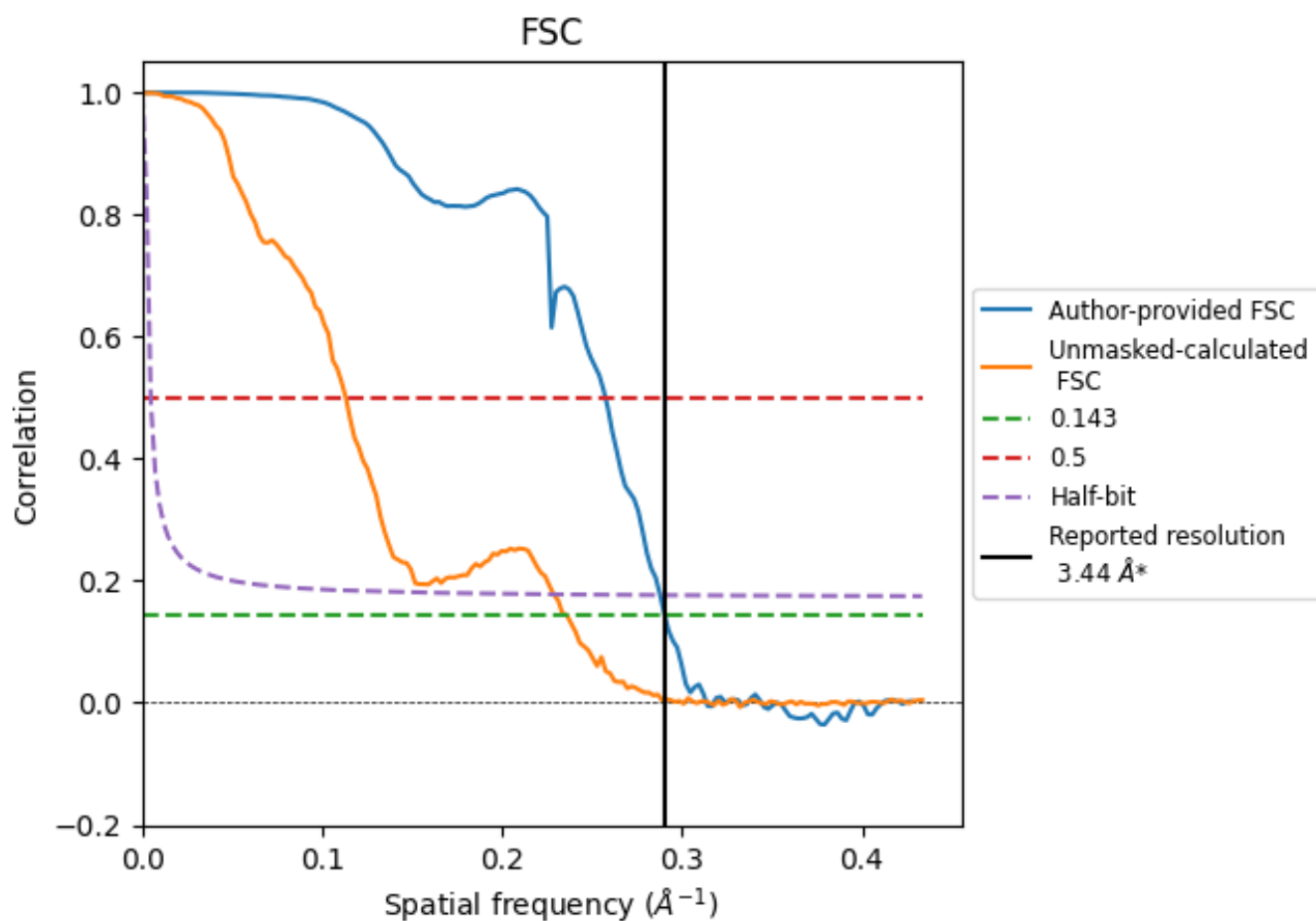


*Reported resolution corresponds to spatial frequency of $0.291 \text{ \AA}^{-1}$

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 $0.291 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

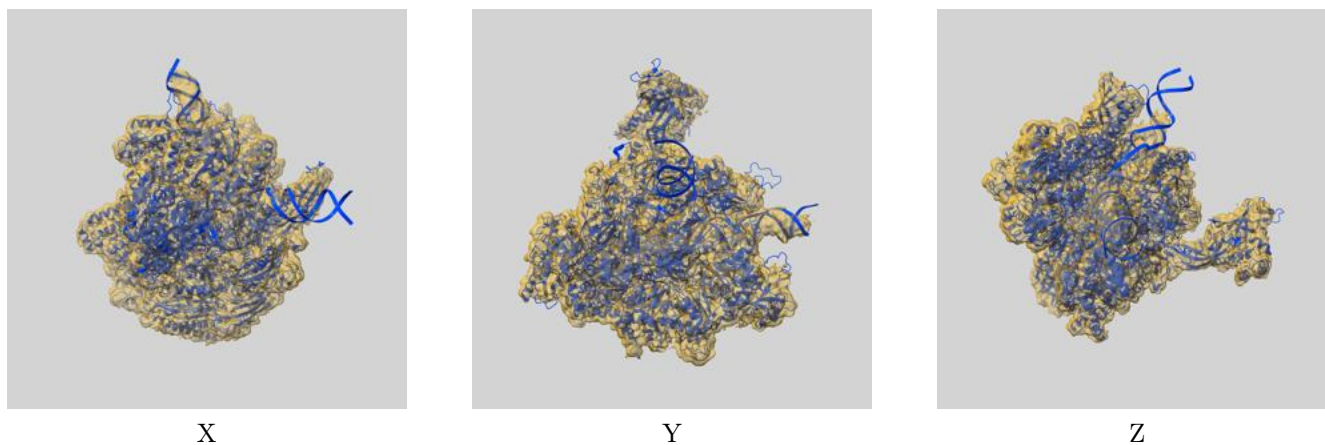
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	3.44	3.89	3.47
Unmasked-calculated*	4.24	8.84	4.37

*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 3.44 by more than 10 %

9 Map-model fit [i](#)

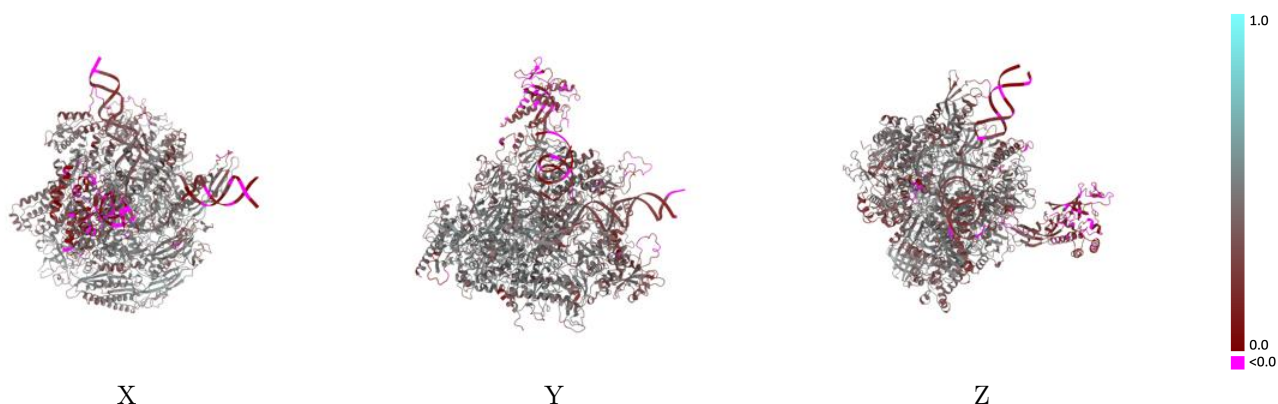
This section contains information regarding the fit between EMDB map EMD-48622 and PDB model 9MU7. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



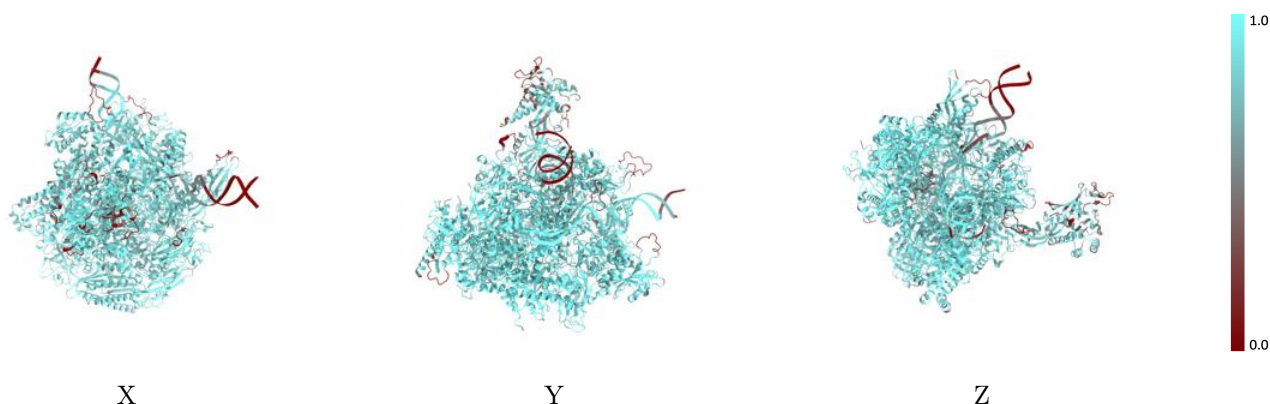
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



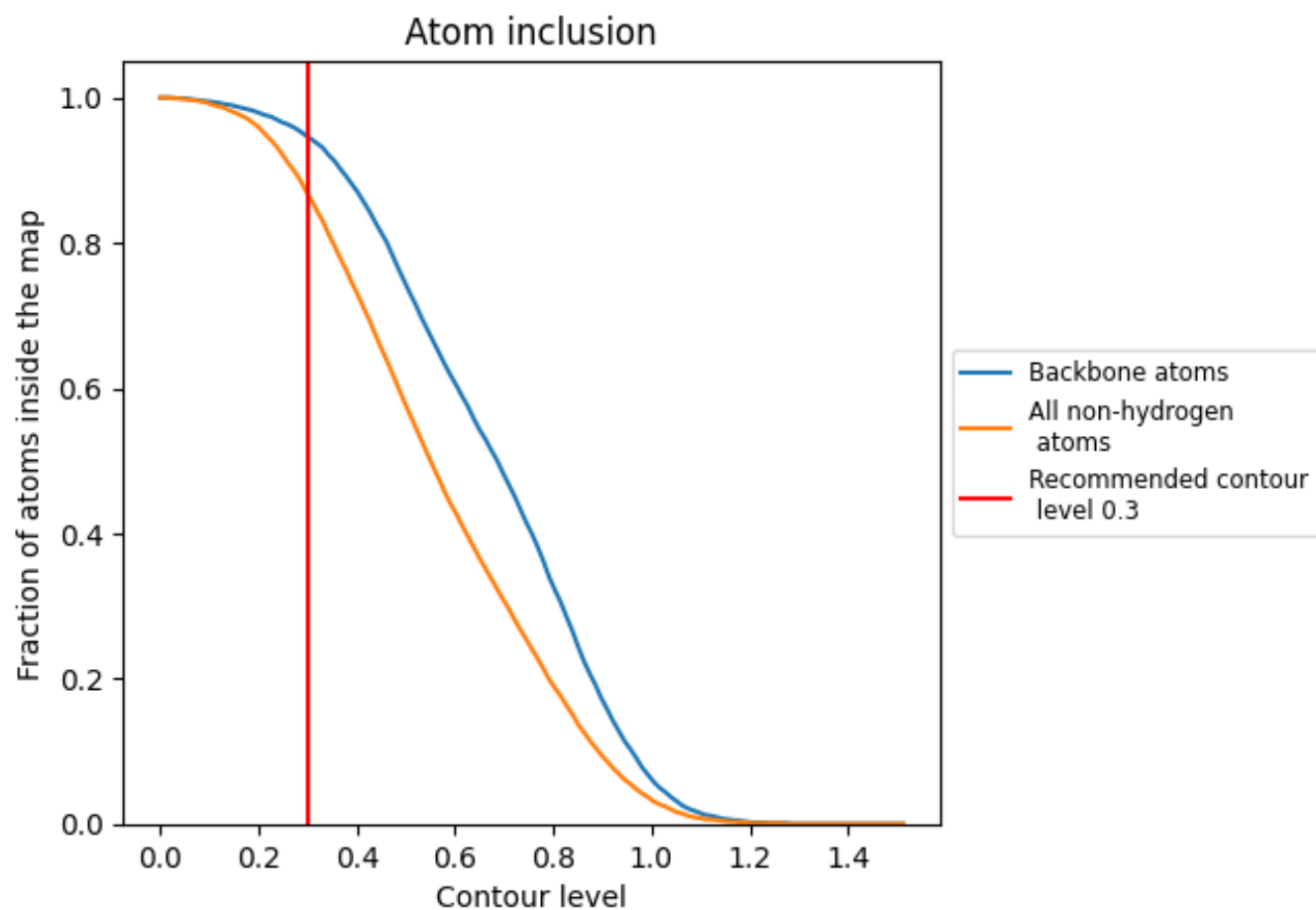
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8670	 0.3930
A	 0.8770	 0.4150
B	 0.9090	 0.4340
C	 0.8950	 0.4410
D	 0.6510	 0.1120
E	 0.8960	 0.4010
F	 0.9080	 0.4220
G	 0.6900	 0.1670
H	 0.9010	 0.4360
I	 0.9200	 0.3830
J	 0.9270	 0.4570
K	 0.9170	 0.4450
L	 0.9350	 0.4190
N	 0.6120	 0.1850
R	 0.9960	 0.4280
T	 0.6880	 0.2470

