



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 10:13 AM UTC

PDB ID : 6KF3 / pdb_00006kf3
EMDB ID : EMD-9960
Title : Cryo-EM structure of Thermococcus kodakarensis RNA polymerase
Authors : Jun, S.-H.; Hyun, J.; Jeong, H.; Cha, J.S.; Kim, H.; Bartlett, M.S.; Cho, H.-S.;
Murakami, K.S.
Deposited on : 2019-07-06
Resolution : 3.90 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:

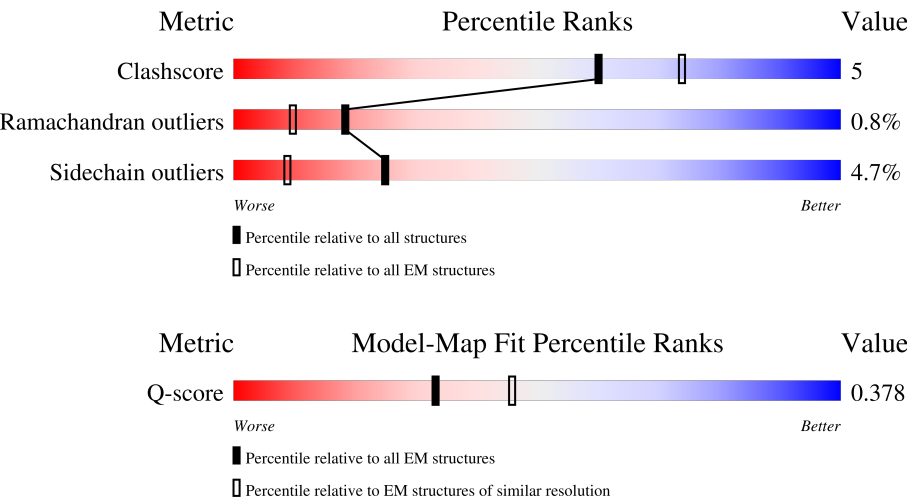
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	906	18% 84% 14% ..
2	B	1123	17% 80% 16% ..
3	C	391	31% 82% 16% ..
4	D	259	85% 14% ..

Continued on next page...

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Mol	Chain	Length	Quality of chain
5	E	190	
6	F	122	
7	H	82	
8	K	57	
9	L	94	
10	N	65	
11	P	49	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 26375 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
1	A	900	Total	C	N	O	S	0	0
			7181	4535	1277	1330	39		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1114	Total	C	N	O	S	0	0
			8892	5616	1587	1652	37		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	388	Total	C	N	O	S	0	0
			3037	1920	525	582	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	257	Total	C	N	O	S	0	0
			2058	1325	340	389	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase, subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	181	Total	C	N	O	S	0	0
			1465	939	250	267	9		

- Molecule 6 is a protein called DNA-directed RNA polymerase, subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	122	Total	C	N	O	S	0	0
			1020	654	169	193	4		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	115	ILE	-	expression tag	UNP Q5JI52
F	116	ASP	-	expression tag	UNP Q5JI52
F	117	GLU	-	expression tag	UNP Q5JI52
F	118	TYR	-	expression tag	UNP Q5JI52
F	119	ARG	-	expression tag	UNP Q5JI52
F	120	PRO	-	expression tag	UNP Q5JI52
F	121	LEU	-	expression tag	UNP Q5JI52
F	122	GLU	-	expression tag	UNP Q5JI52

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	76	Total	C	N	O	0	0
			627	408	105	114		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	56	Total	C	N	O	S	0	0
			433	284	75	73	1		

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	94	Total	C	N	O	S	0	0
			775	493	134	146	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	65	Total	C	N	O	S	0	0
			529	340	89	94	6		

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

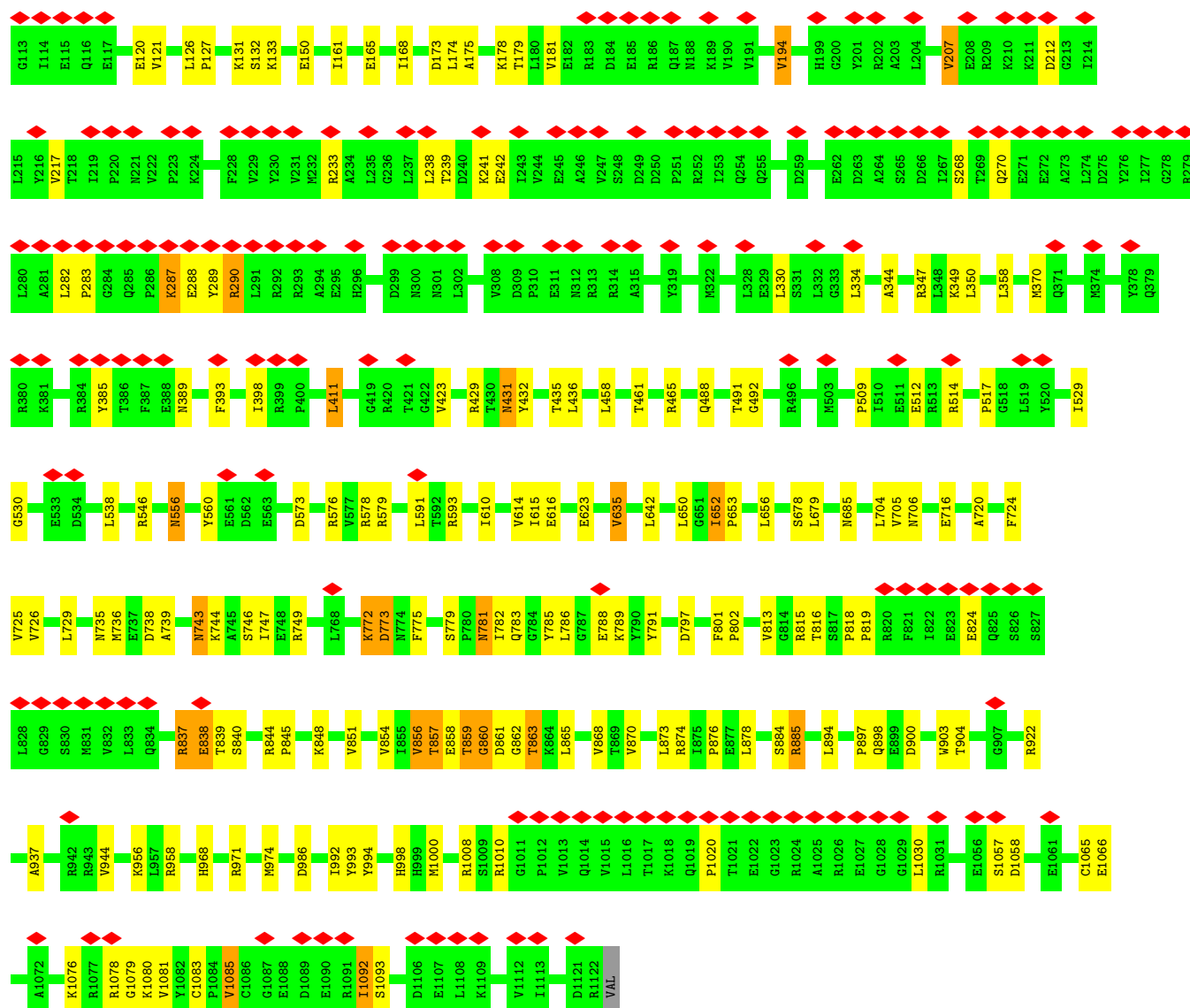
Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	44	Total	C	N	O	S	0	0
			352	221	70	57	4		

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

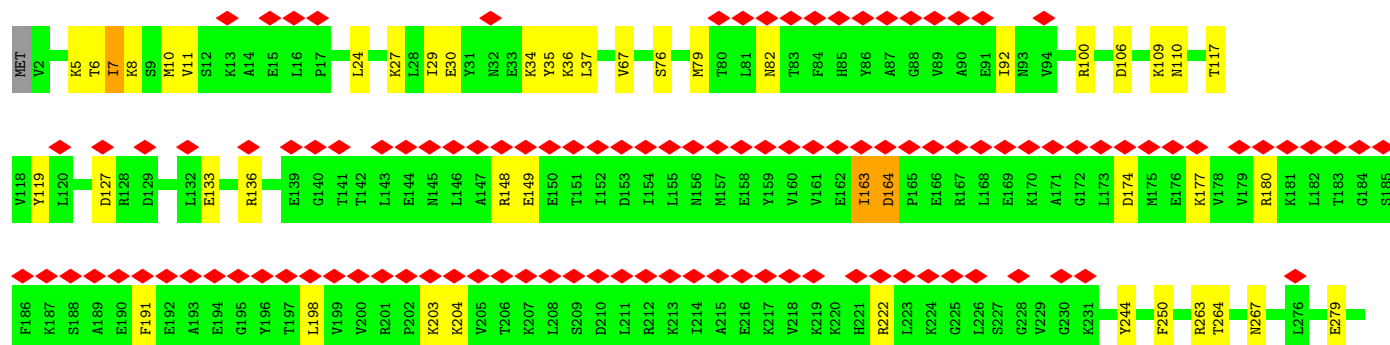
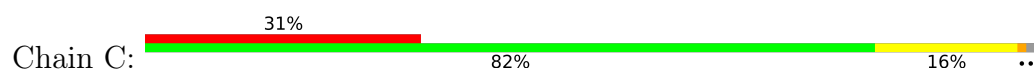
Mol	Chain	Residues	Atoms		AltConf
12	A	1	Total 1	Mg 1	0

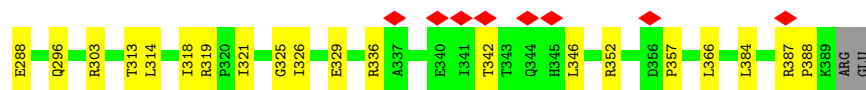
- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	A	2	Total 2	Zn 2	0
13	B	1	Total 1	Zn 1	0
13	N	1	Total 1	Zn 1	0
13	P	1	Total 1	Zn 1	0



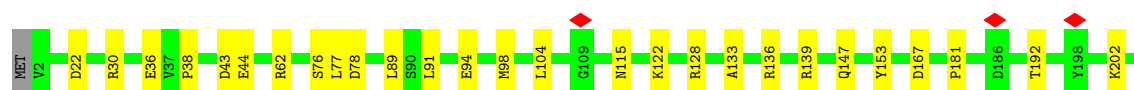
• Molecule 3: DNA-directed RNA polymerase subunit A''





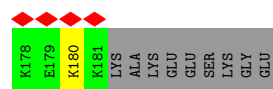
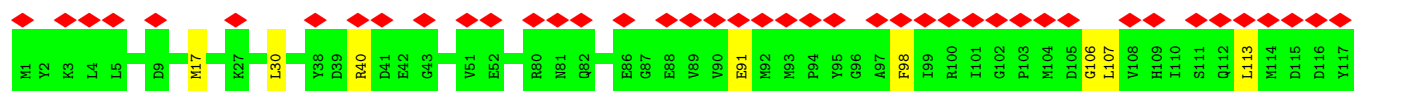
- Molecule 4: DNA-directed RNA polymerase subunit D

Chain D: 85% 14% ..



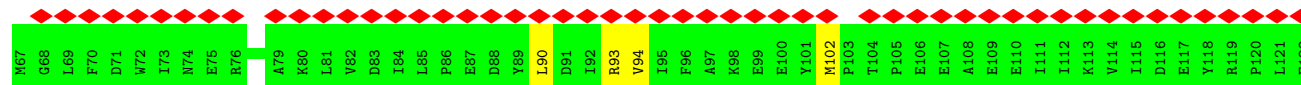
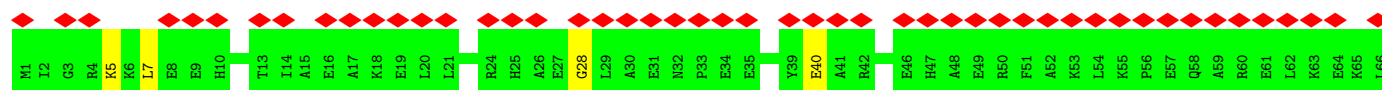
- Molecule 5: DNA-directed RNA polymerase, subunit E

Chain E: 53% 85% 11% 5%



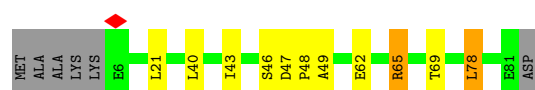
- Molecule 6: DNA-directed RNA polymerase, subunit F

Chain F: 83% 93% 7%

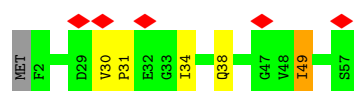
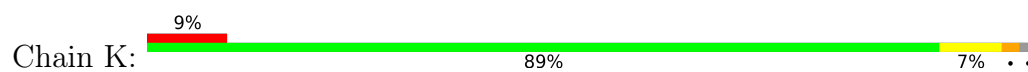


- Molecule 7: DNA-directed RNA polymerase subunit H

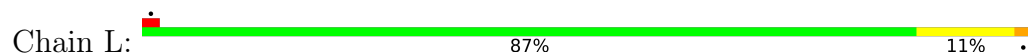
Chain H: 79% 11% 7%



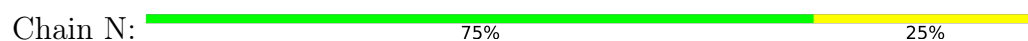
- Molecule 8: DNA-directed RNA polymerase subunit K



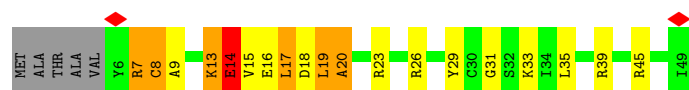
- Molecule 9: DNA-directed RNA polymerase subunit L



- Molecule 10: DNA-directed RNA polymerase subunit N



- Molecule 11: DNA-directed RNA polymerase subunit P



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	139242	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.713	Depositor
Minimum map value	-0.530	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	246.4, 246.4, 246.4	wwPDB
Map dimensions	176, 176, 176	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.4, 1.4, 1.4	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, 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	0.36	0/7324	0.77	0/9885
2	B	0.38	0/9070	0.78	7/12256 (0.1%)
3	C	0.34	0/3077	0.83	0/4156
4	D	0.36	0/2103	0.76	4/2848 (0.1%)
5	E	0.20	0/1491	0.52	0/2008
6	F	0.20	0/1040	0.63	2/1399 (0.1%)
7	H	0.34	0/641	0.77	0/866
8	K	0.37	0/441	0.72	0/598
9	L	0.32	0/790	0.77	0/1066
10	N	0.43	0/538	0.92	3/723 (0.4%)
11	P	0.40	0/357	1.12	5/477 (1.0%)
All	All	0.35	0/26872	0.77	21/36282 (0.1%)

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	4
2	B	0	3
3	C	0	6
8	K	0	2
11	P	0	1
All	All	0	16

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	57	VAL	CA-C-N	7.22	144.33	127.00
2	B	57	VAL	C-N-CA	7.22	144.33	127.00
11	P	13	LYS	CA-C-N	6.92	134.77	121.54
11	P	13	LYS	C-N-CA	6.92	134.77	121.54
2	B	57	VAL	C-N-CD	-6.77	105.70	120.60

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	396	GLU	Peptide
1	A	427	GLN	Peptide
1	A	455	CYS	Peptide
1	A	874	GLU	Peptide
2	B	10	PRO	Peptide

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	7181	0	7253	71	0
2	B	8892	0	8952	100	0
3	C	3037	0	3151	32	0
4	D	2058	0	2068	21	0
5	E	1465	0	1503	13	0
6	F	1020	0	1024	5	0
7	H	627	0	642	6	0
8	K	433	0	466	2	0
9	L	775	0	770	8	0
10	N	529	0	543	8	0
11	P	352	0	376	10	0
12	A	1	0	0	0	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	N	1	0	0	0	0
13	P	1	0	0	0	0
All	All	26375	0	26748	240	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 240 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:445:TYR:HB2	1:A:449:ARG:HH22	1.48	0.76
1:A:597:PRO:HA	1:A:601:ARG:HD2	1.74	0.70
2:B:773:ASP:HB3	2:B:818:PRO:HD3	1.73	0.69
1:A:871:LYS:HB3	1:A:875:ASP:HB3	1.77	0.65
1:A:325:ASN:OD1	2:B:1008:ARG:NH1	2.30	0.64

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	898/906 (99%)	759 (84%)	133 (15%)	6 (1%)	18	53
2	B	1112/1123 (99%)	940 (84%)	160 (14%)	12 (1%)	11	43
3	C	386/391 (99%)	311 (81%)	73 (19%)	2 (0%)	24	59
4	D	255/259 (98%)	242 (95%)	11 (4%)	2 (1%)	16	50
5	E	179/190 (94%)	168 (94%)	11 (6%)	0	100	100
6	F	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
7	H	74/82 (90%)	61 (82%)	11 (15%)	2 (3%)	4	28
8	K	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
9	L	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
10	N	63/65 (97%)	53 (84%)	10 (16%)	0	100	100
11	P	42/49 (86%)	28 (67%)	13 (31%)	1 (2%)	4	29
All	All	3275/3338 (98%)	2801 (86%)	449 (14%)	25 (1%)	18	50

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	593	LEU
2	B	432	TYR
4	D	232	VAL
1	A	604	ALA
1	A	888	VAL

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	774/779 (99%)	745 (96%)	29 (4%)	30	53
2	B	961/969 (99%)	896 (93%)	65 (7%)	14	41
3	C	331/334 (99%)	315 (95%)	16 (5%)	23	48
4	D	226/228 (99%)	223 (99%)	3 (1%)	61	71
5	E	160/167 (96%)	159 (99%)	1 (1%)	78	80
6	F	107/107 (100%)	107 (100%)	0	100	100
7	H	68/72 (94%)	66 (97%)	2 (3%)	37	58
8	K	45/46 (98%)	44 (98%)	1 (2%)	45	64
9	L	81/81 (100%)	78 (96%)	3 (4%)	30	53
10	N	59/59 (100%)	53 (90%)	6 (10%)	7	26
11	P	37/40 (92%)	28 (76%)	9 (24%)	1	4
All	All	2849/2882 (99%)	2714 (95%)	135 (5%)	25	48

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	H	78	LEU
9	L	90	LYS
11	P	16	GLU
2	B	423	VAL
2	B	411	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	162	ASN
6	F	32	ASN
9	L	37	HIS
2	B	254	GLN
1	A	820	HIS

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 6 ligands modelled in this entry, 6 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 ⓘ

There are no chain breaks in this entry.

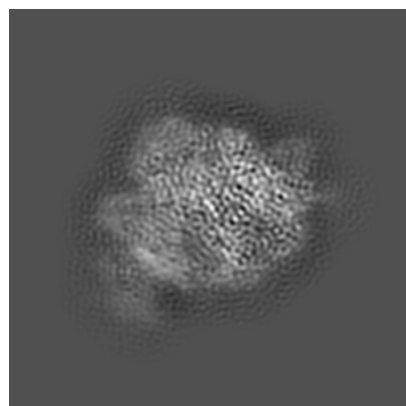
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9960. These allow visual inspection of the internal detail of the map and identification of artifacts.

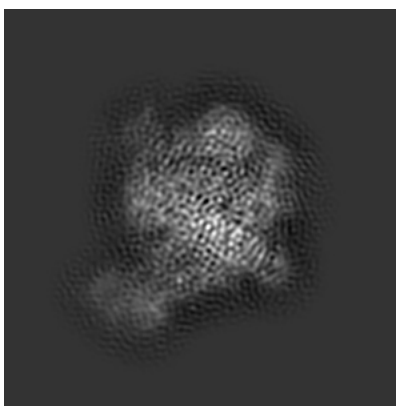
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

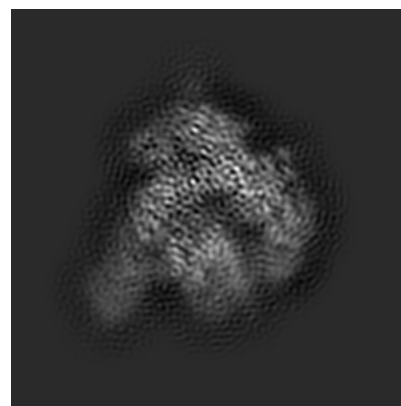
6.1.1 Primary map



X

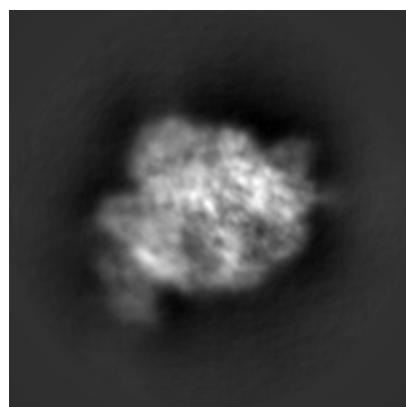


Y

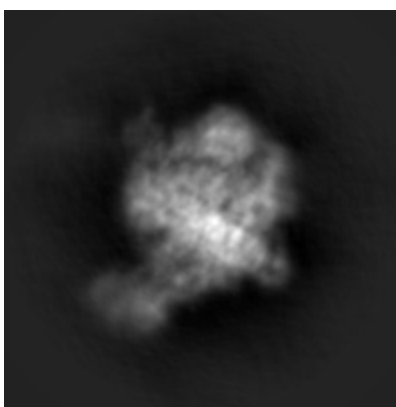


Z

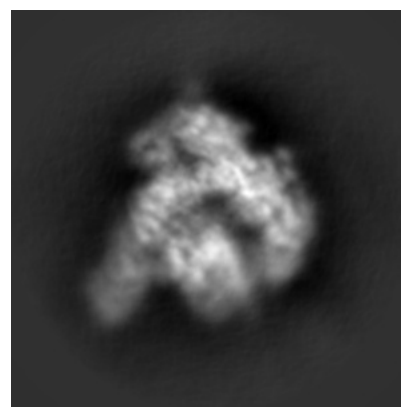
6.1.2 Raw map



X



Y

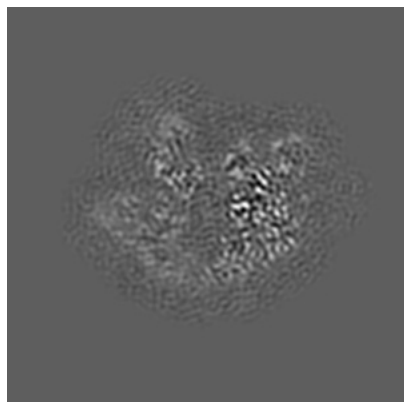


Z

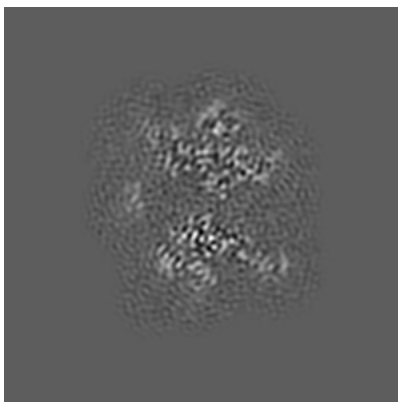
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

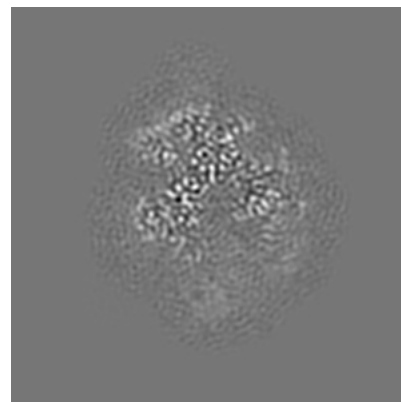
6.2.1 Primary map



X Index: 88

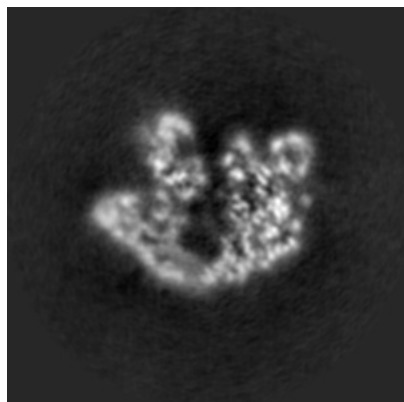


Y Index: 88

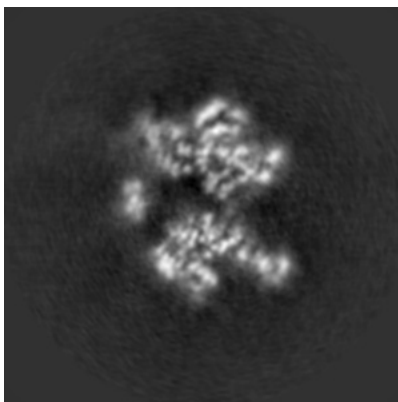


Z Index: 88

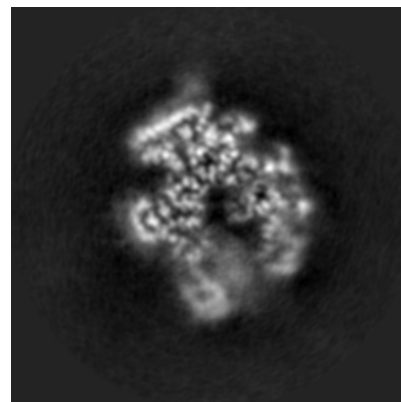
6.2.2 Raw map



X Index: 88



Y Index: 88

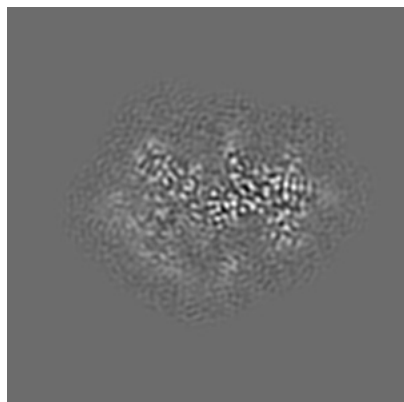


Z Index: 88

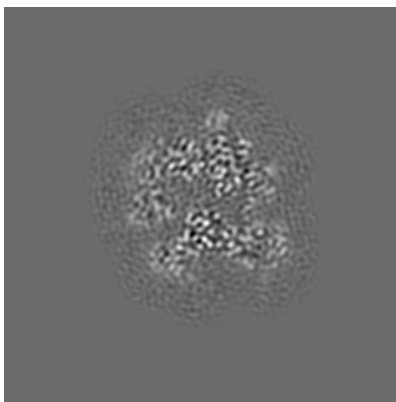
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

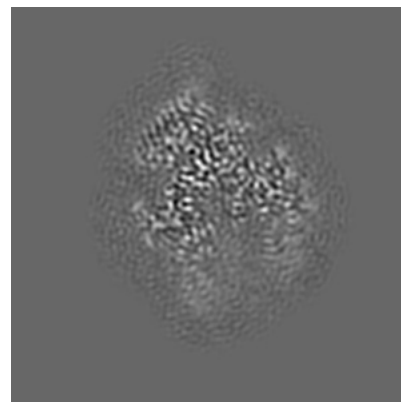
6.3.1 Primary map



X Index: 80

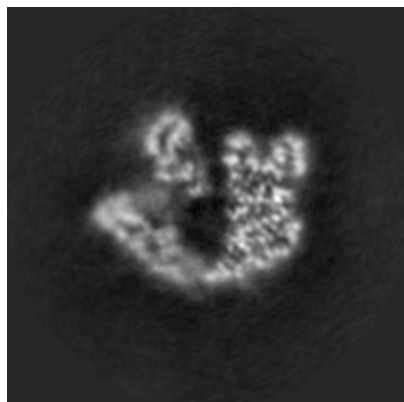


Y Index: 96

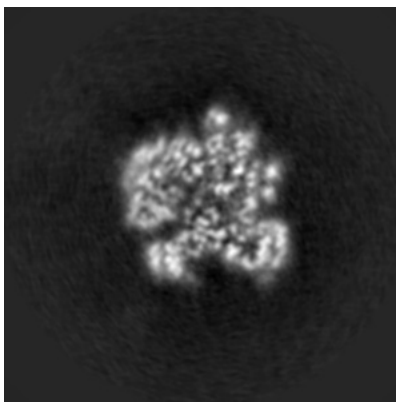


Z Index: 92

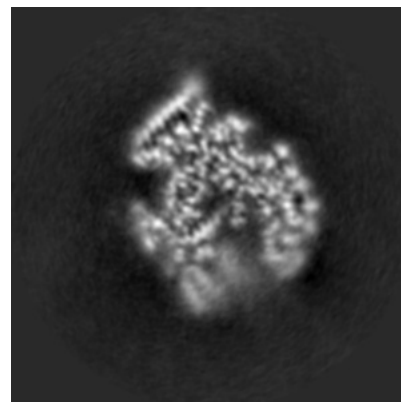
6.3.2 Raw map



X Index: 91



Y Index: 97

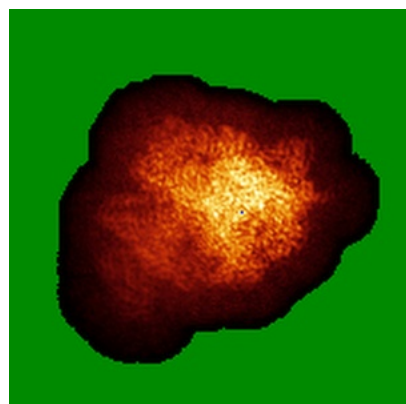


Z Index: 93

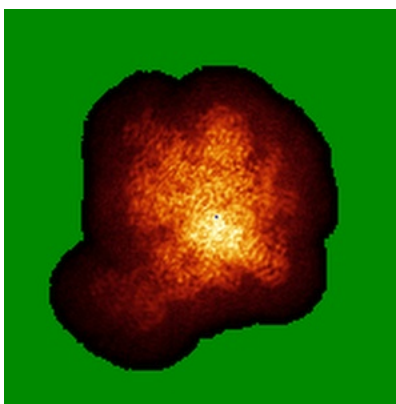
The images above show the largest variance slices of the map in three orthogonal directions.

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

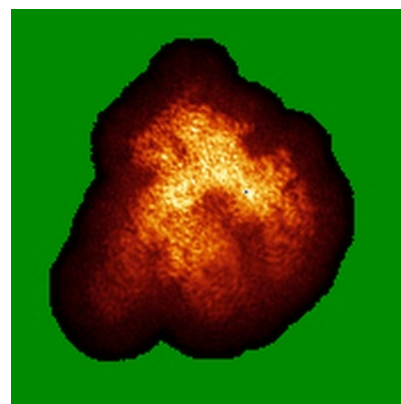
6.4.1 Primary map



X

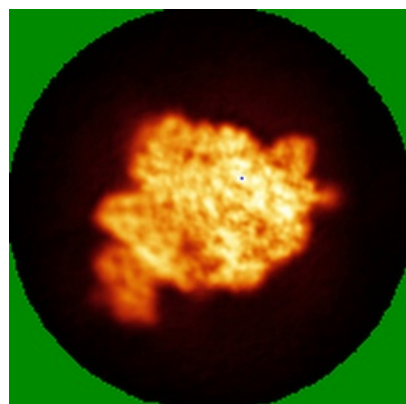


Y

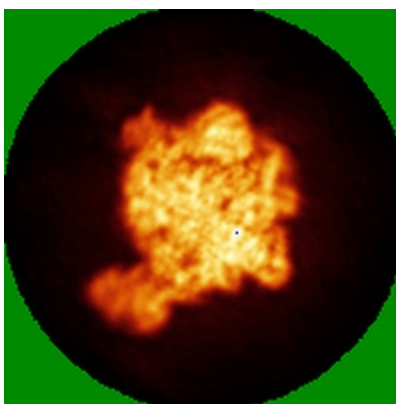


Z

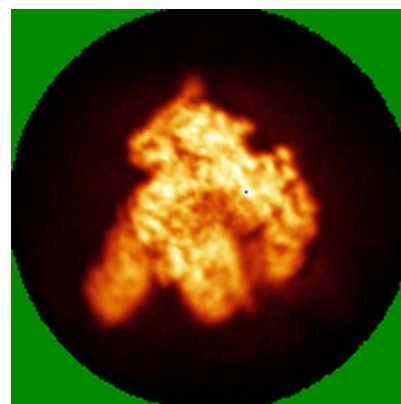
6.4.2 Raw map



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.

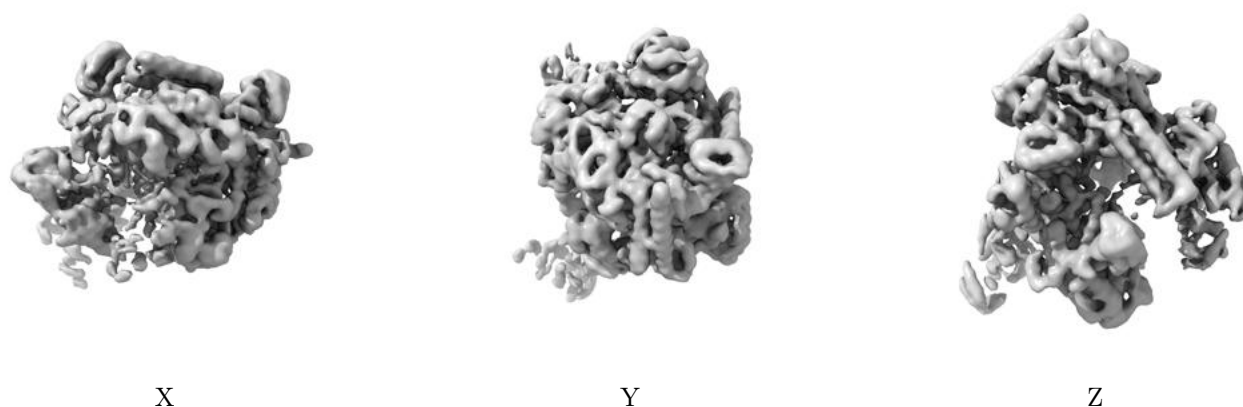
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. 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.

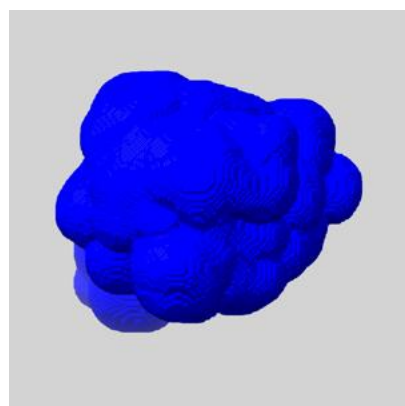
6.6 Mask visualisation [i](#)

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

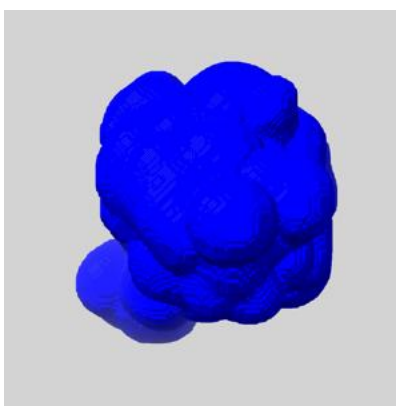
A mask typically either:

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

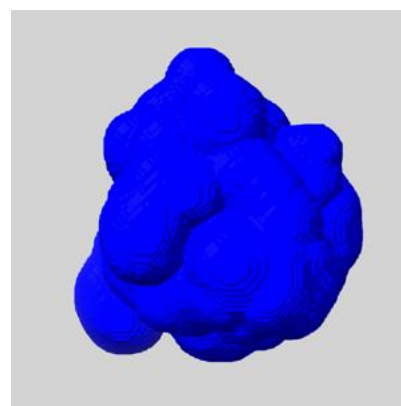
6.6.1 emd_9960_msk_1.map [i](#)



X



Y

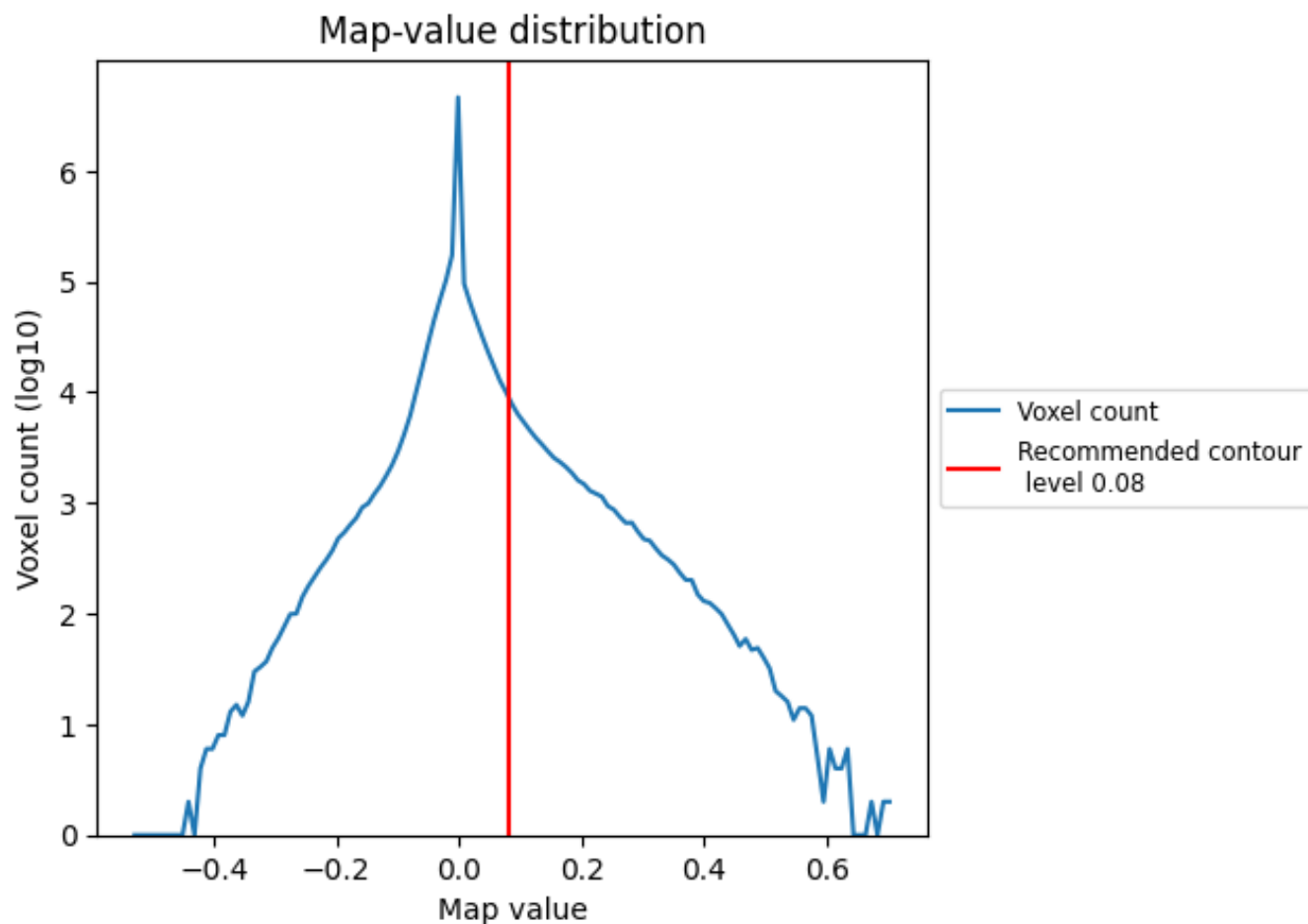


Z

7 Map analysis [i](#)

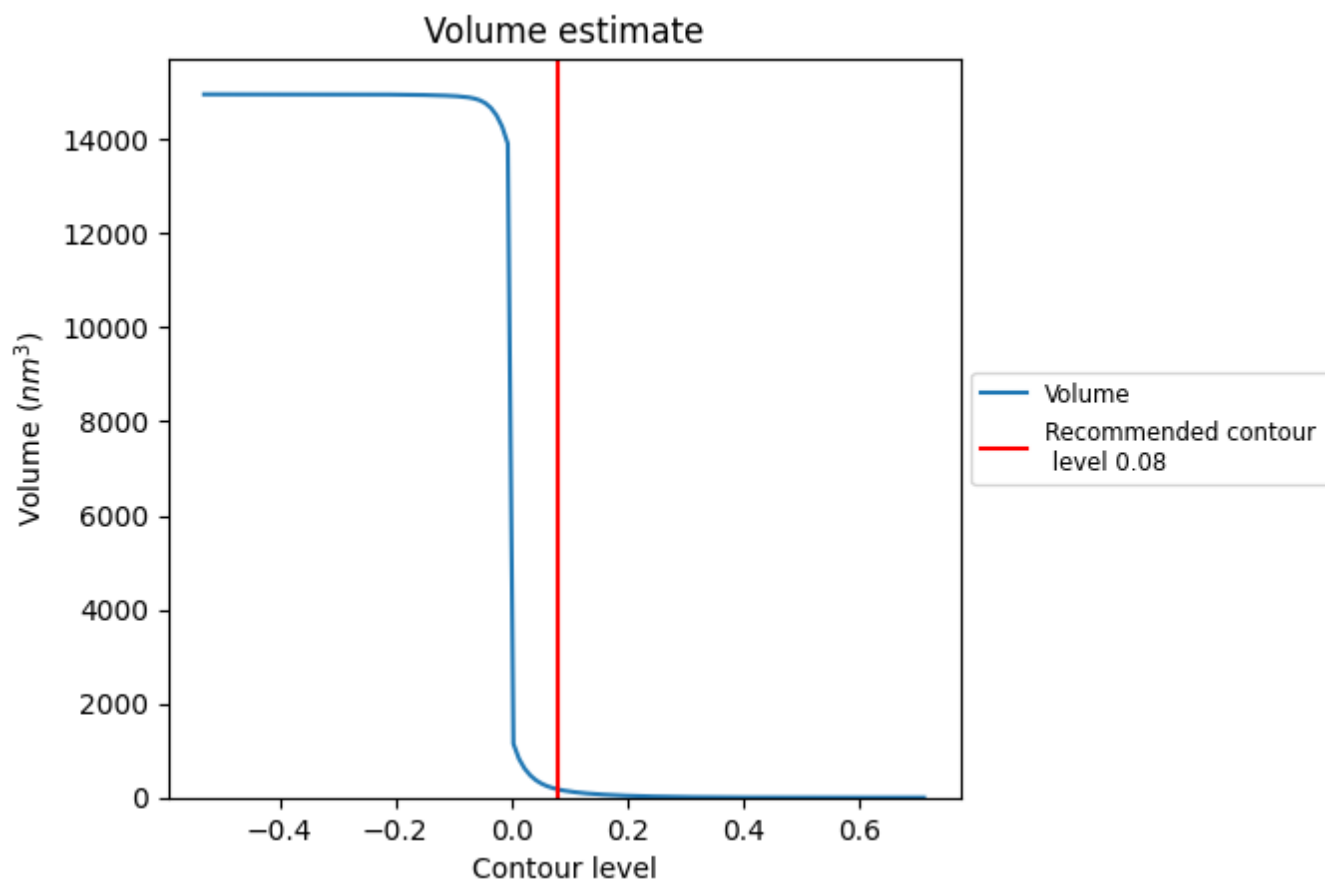
This section contains the results of statistical analysis of the map.

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.

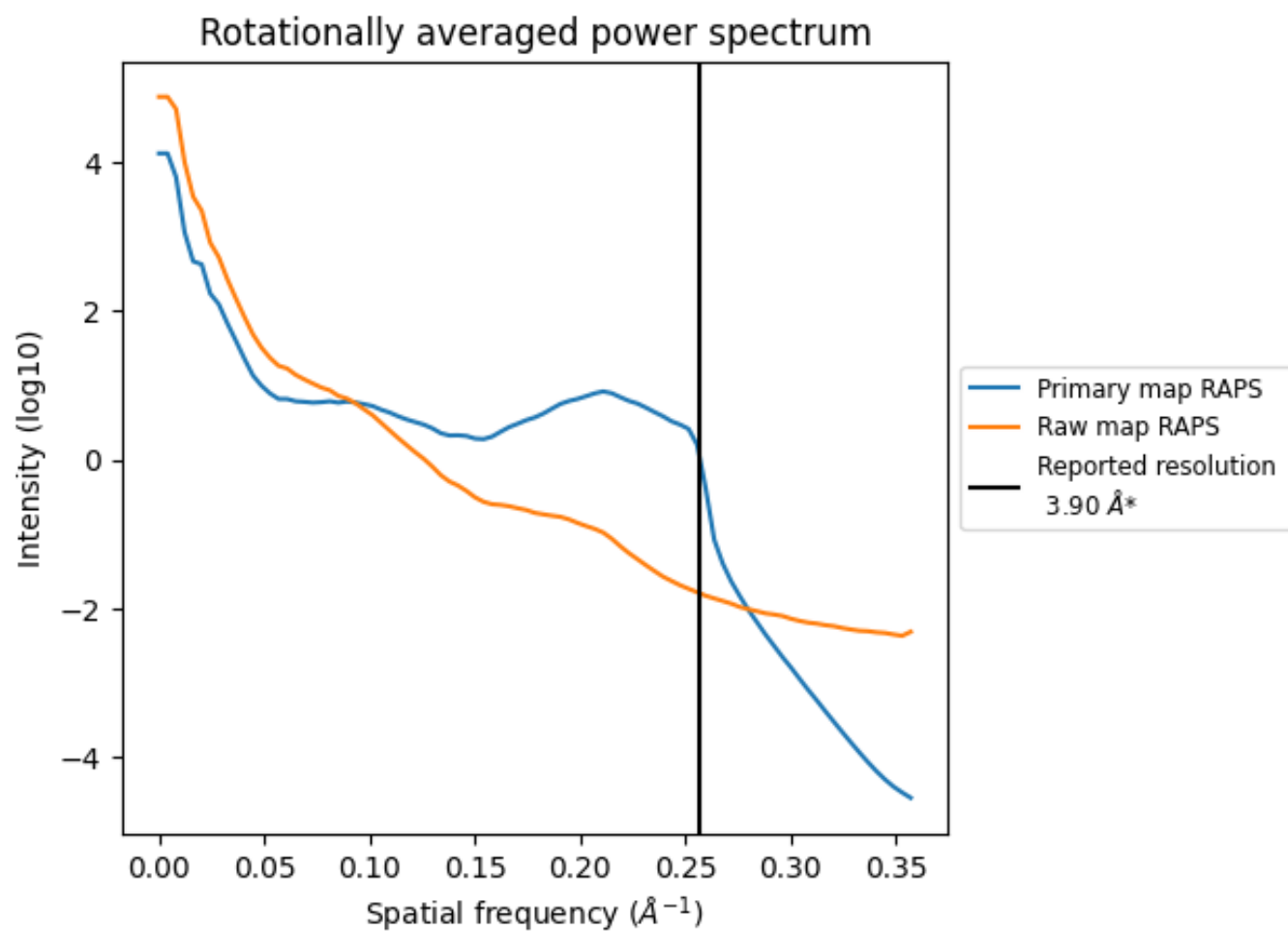
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 178 nm³; this corresponds to an approximate mass of 161 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 ⓘ

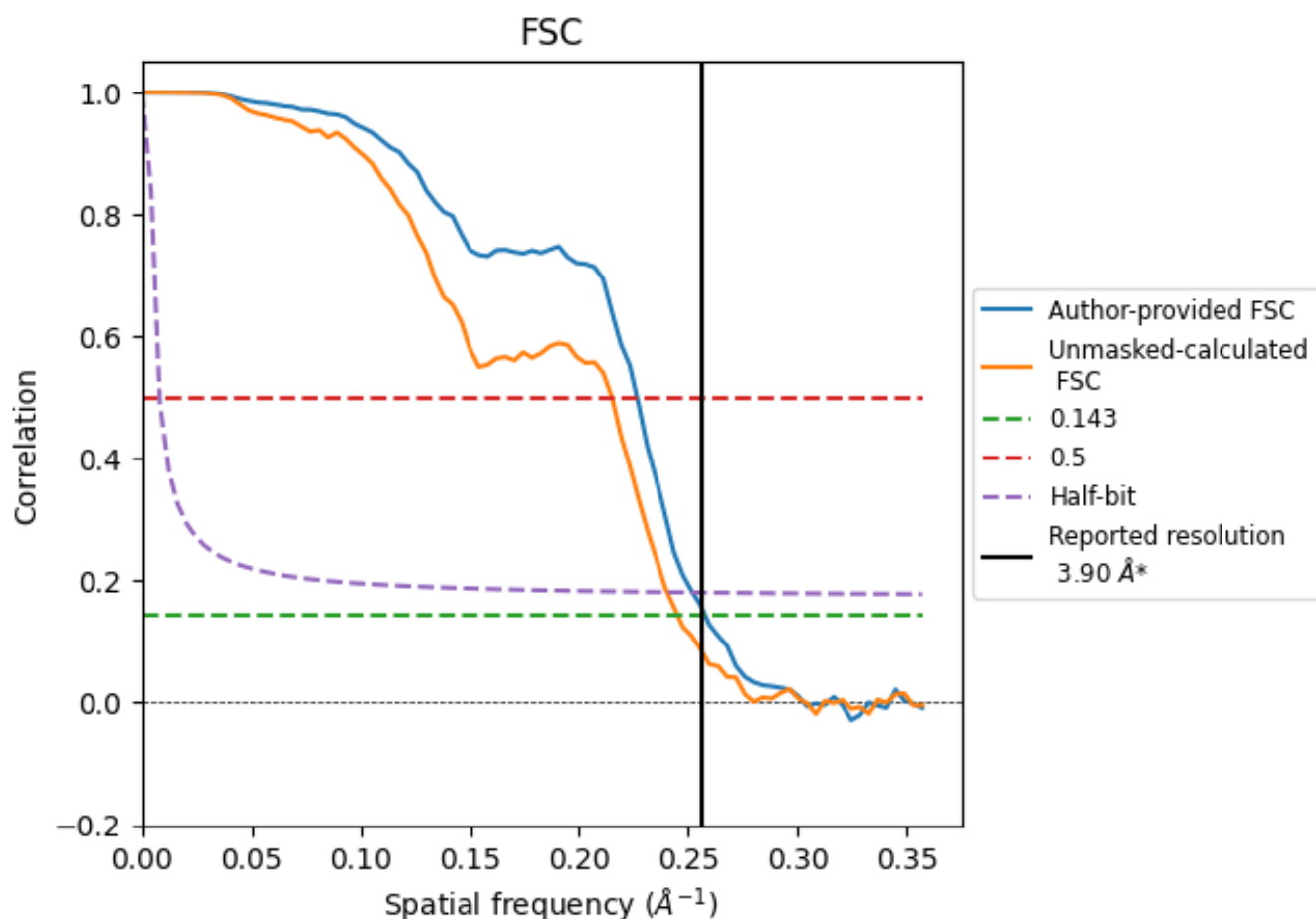


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 $0.256 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

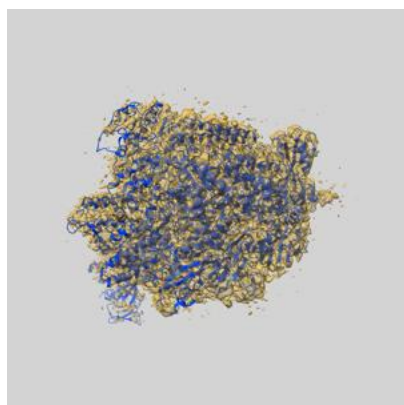
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.88	4.42	3.97
Unmasked-calculated*	4.08	4.65	4.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

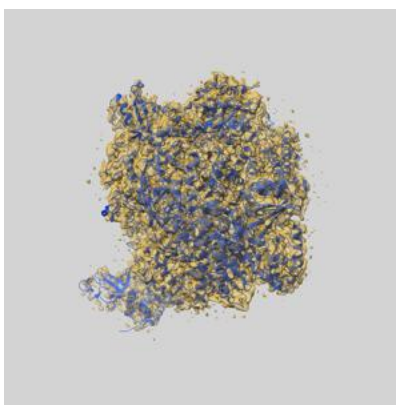
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9960 and PDB model 6KF3. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

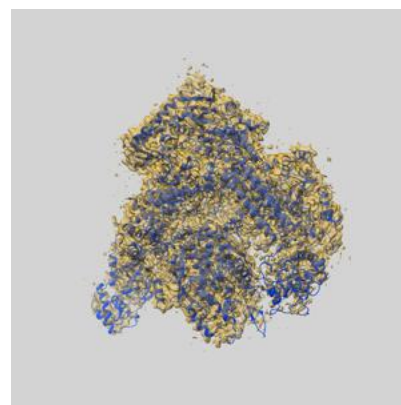
9.1 Map-model overlay [i](#)



X



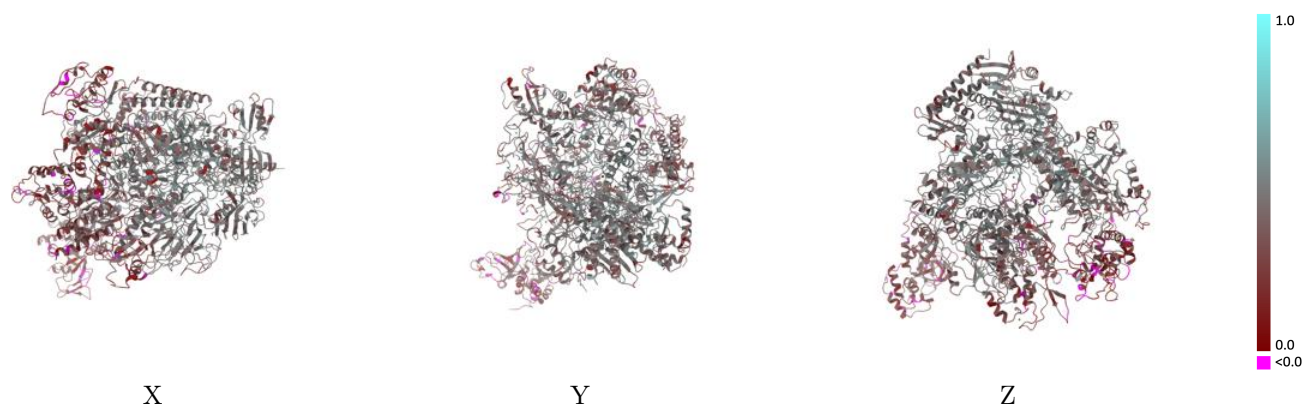
Y



Z

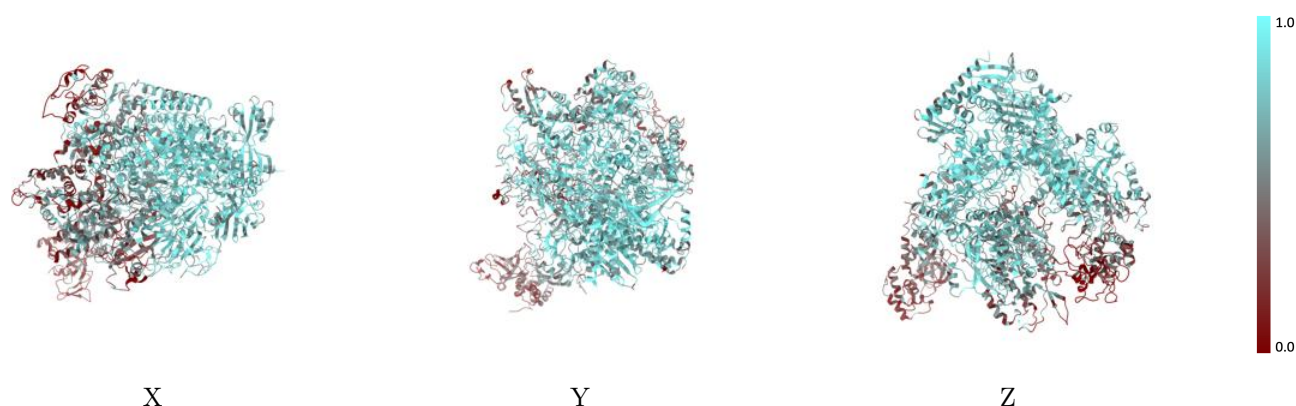
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



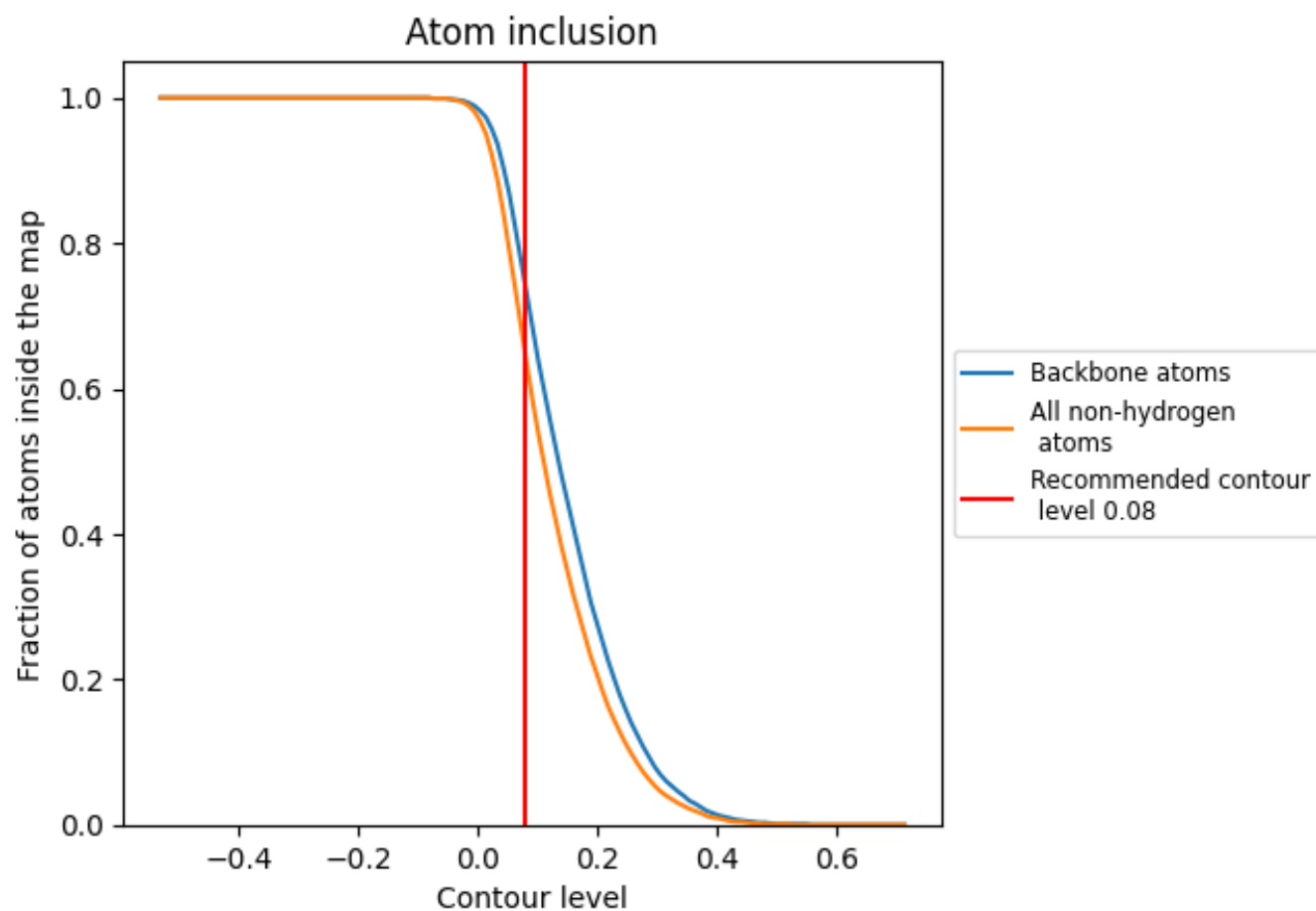
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 64% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6420	0.3780
A	0.6830	0.3860
B	0.6720	0.3970
C	0.5350	0.3320
D	0.7810	0.4340
E	0.3450	0.2730
F	0.2030	0.2040
H	0.7580	0.4230
K	0.7390	0.4080
L	0.7970	0.4340
N	0.8310	0.4630
P	0.7590	0.4020

1.0

0.0

<0.0