



wwPDB EM Validation Summary Report ⓘ

Jan 9, 2023 – 02:22 PM JST

PDB ID : 7YE1
EMDB ID : EMD-33761
Title : The cryo-EM structure of *C. crescentus* GcrA-TACup
Authors : Wu, X.X.; Zhang, Y.
Deposited on : 2022-07-05
Resolution : 3.70 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:

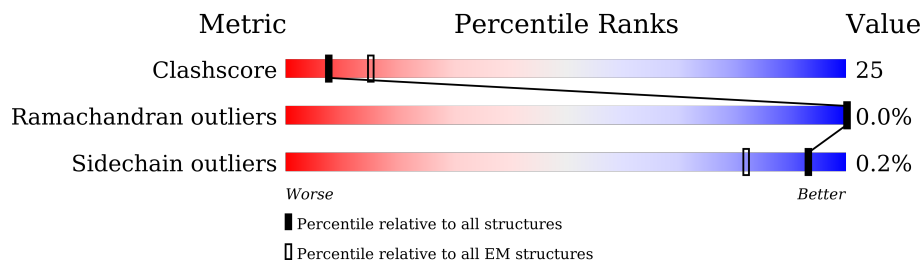
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.70 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	338	52% 38% 9%
1	B	338	30% 37% 33%
2	C	1356	59% 38% .
3	D	1396	46% 36% 18%
4	E	119	39% 19% 42%
5	F	652	40% 36% 24%
6	G	173	5% 32% 27% 40%
7	H	57	23% 75% .

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Mol	Chain	Length	Quality of chain
8	I	57	 16% 82%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 29964 atoms, of which 12 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 alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	307	Total	C	N	O	S	0	0
			2208	1413	369	421	5		
1	B	225	Total	C	N	O	S	0	0
			1675	1068	284	319	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	C	1312	Total	C	H	N	O	S	0	0
			9879	6312	12	1637	1878	40		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1144	Total	C	N	O	S	0	0
			8723	5603	1443	1635	42		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	69	Total	C	N	O	S	0	0
			518	328	87	101	2		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	497	Total	C	N	O	S	0	0
			3851	2465	637	734	15		

- Molecule 6 is a protein called Cell cycle regulatory protein GcrA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	103	Total	C	N	O	S	3	0
			754	476	133	141	4		

- Molecule 7 is a DNA chain called DNA (57-MER)-non template.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	57	Total	C	N	O	P	0	0
			1178	558	229	334	57		

- Molecule 8 is a DNA chain called DNA (57-MER)-template.

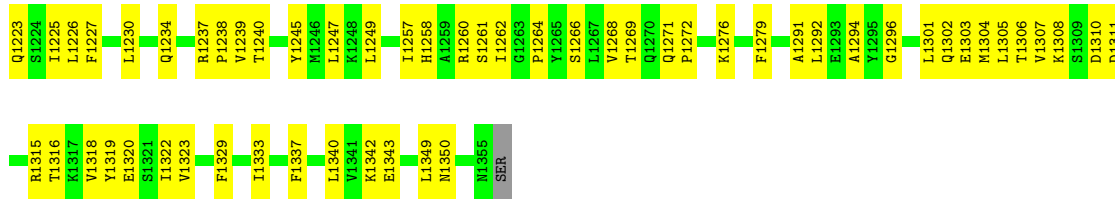
Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	57	Total	C	N	O	P	0	0
			1174	559	210	348	57		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

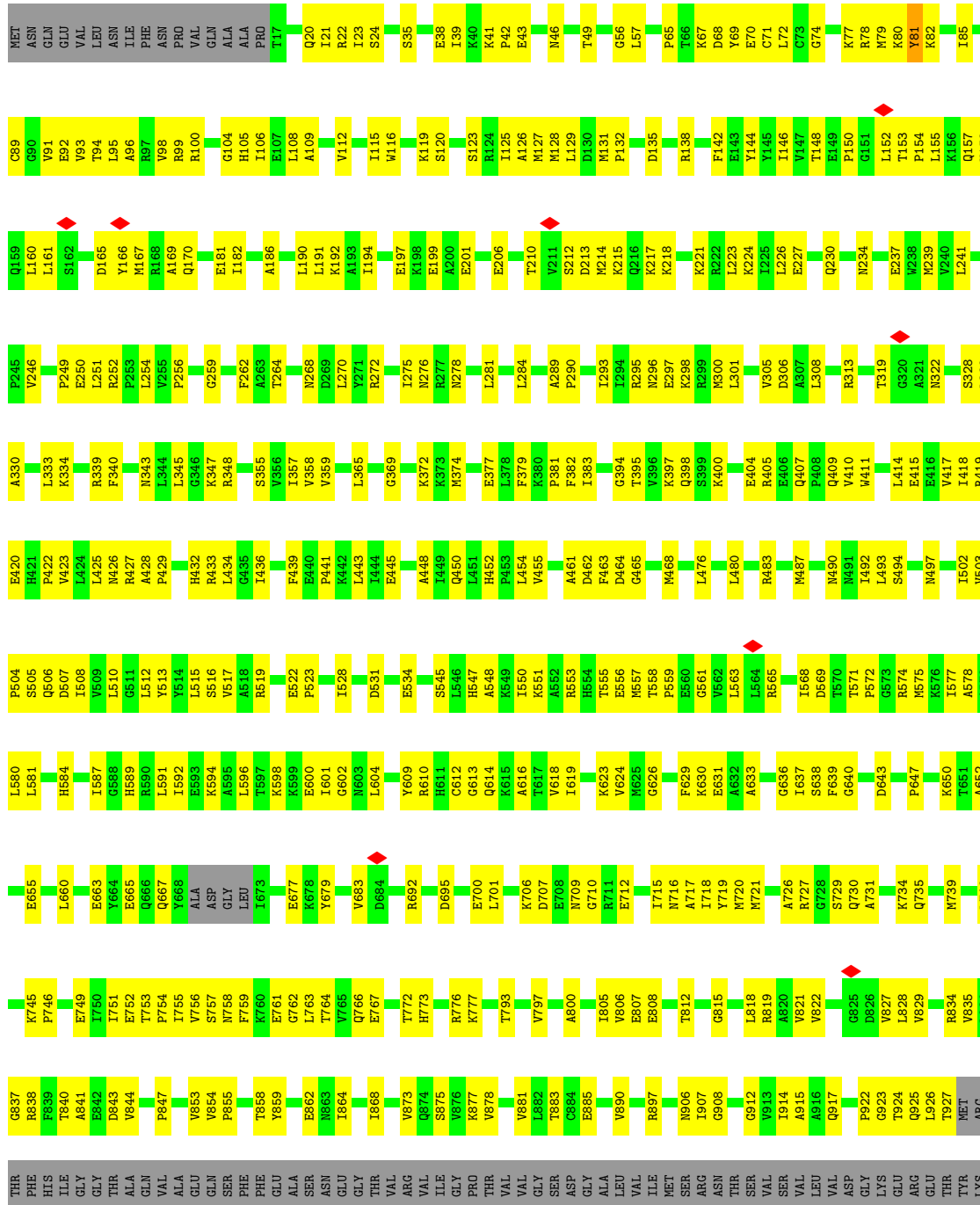
Mol	Chain	Residues	Atoms		AltConf
9	D	1	Total	Mg	0
			1	1	

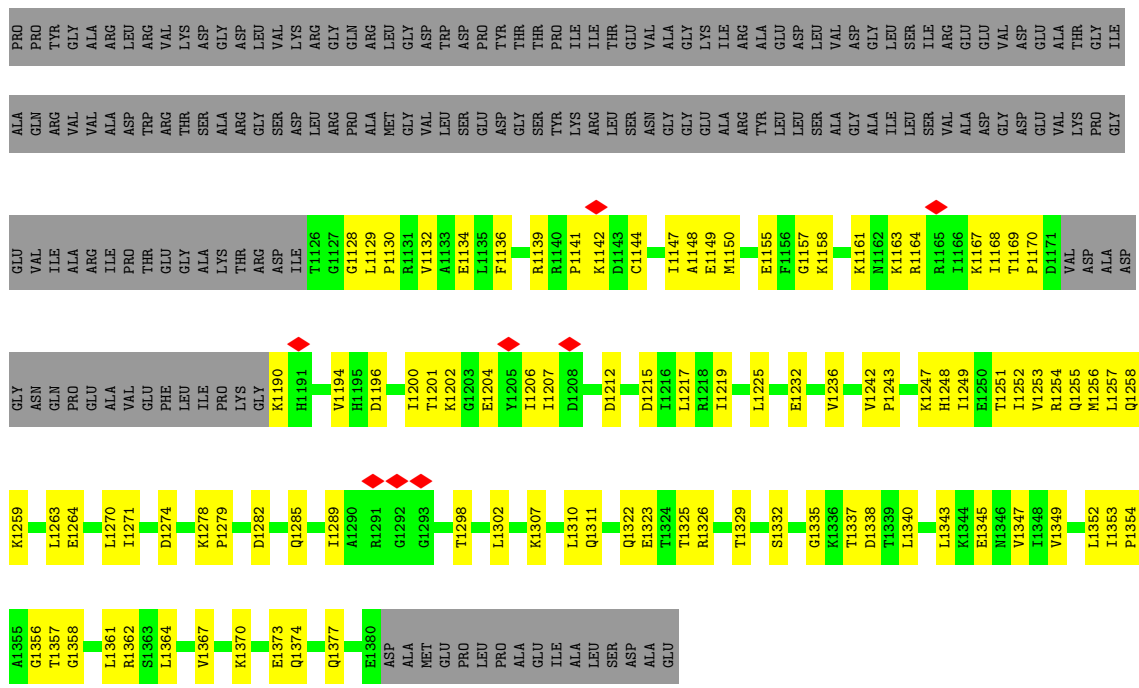
- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
10	D	2	Total	Zn	0
			2	2	
10	G	1	Total	Zn	0
			1	1	

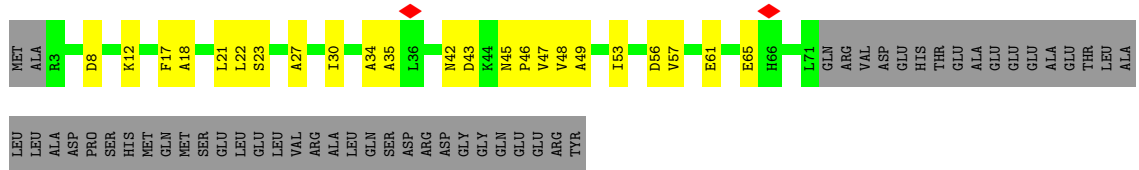


• Molecule 3: DNA-directed RNA polymerase subunit beta'

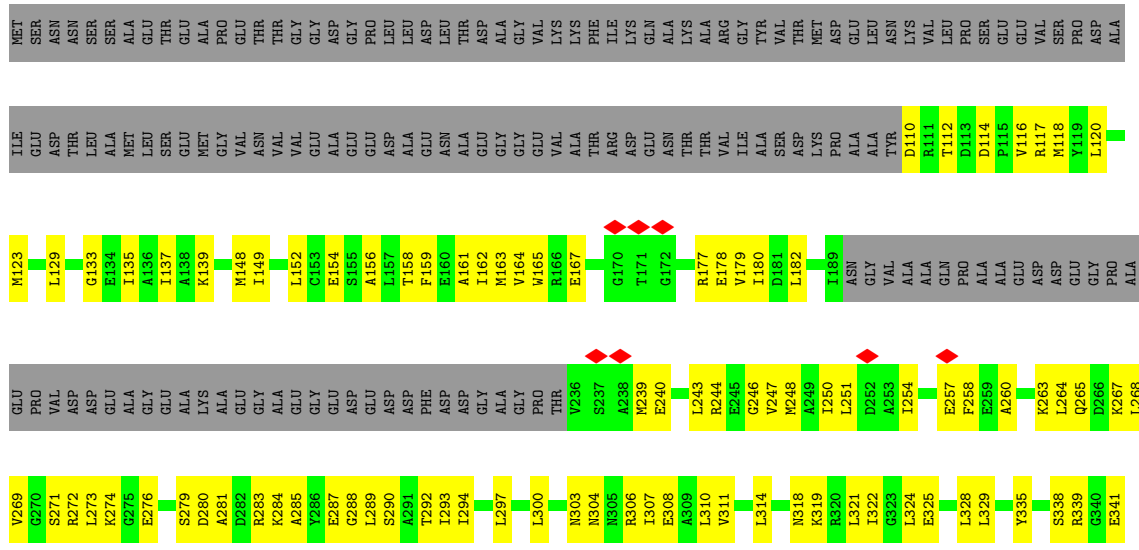


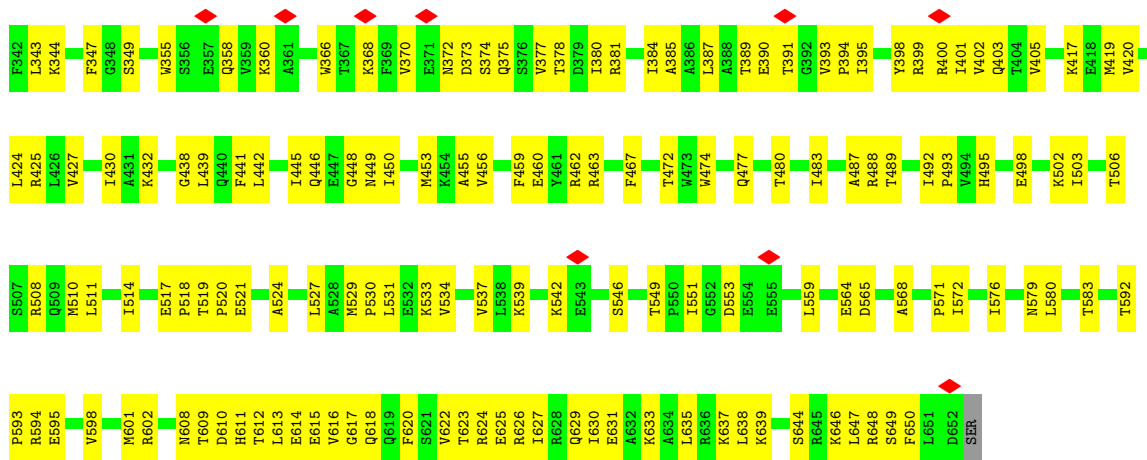


• Molecule 4: DNA-directed RNA polymerase subunit omega

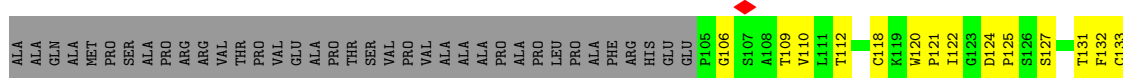
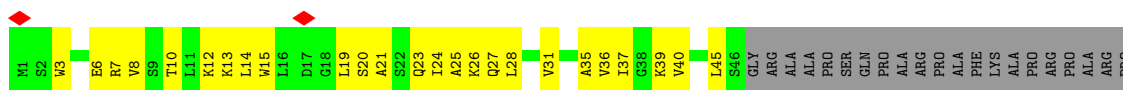
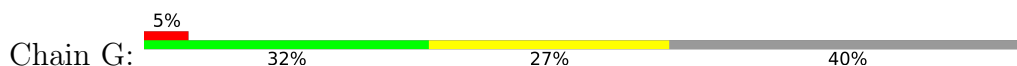


• Molecule 5: RNA polymerase sigma factor RpoD





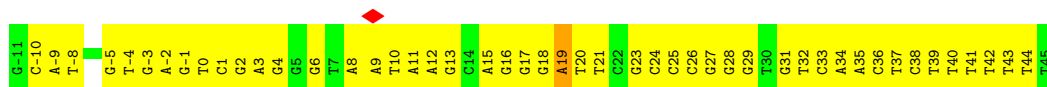
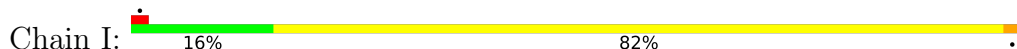
• Molecule 6: Cell cycle regulatory protein GcrA



• Molecule 7: DNA (57-MER)-non template



• Molecule 8: DNA (57-MER)-template



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	287227	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 ($e^-/\text{\AA}^2$)	62.4	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.069	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (\AA)	304.2, 304.2, 304.2	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.014, 1.014, 1.014	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: MG, 6MA, 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	0.23	0/2235	0.43	0/3037
1	B	0.29	0/1700	0.45	0/2307
2	C	0.24	0/10030	0.40	0/13526
3	D	0.23	0/8863	0.39	0/11917
4	E	0.22	0/523	0.38	0/706
5	F	0.23	0/3901	0.37	0/5231
6	G	0.23	0/782	0.41	0/1056
7	H	0.49	0/1299	0.84	0/2001
8	I	0.50	0/1289	0.94	0/1987
All	All	0.27	0/30622	0.47	0/41768

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	2208	0	2143	134	0
1	B	1675	0	1665	140	0
2	C	9867	12	9563	462	0
3	D	8723	0	8765	437	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	518	0	517	24	0
5	F	3851	0	3842	250	0
6	G	754	0	731	47	0
7	H	1178	0	640	54	0
8	I	1174	0	647	73	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
10	G	1	0	0	0	0
All	All	29952	12	28513	1488	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 25.

The worst 5 of 1488 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:ALA:HB3	1:B:129:PRO:HA	1.27	1.09
1:B:49:VAL:HG21	1:B:223:LEU:HD11	1.39	1.04
7:H:-13:DC:H2''	7:H:-12:DT:H5''	1.42	1.01
1:B:113:VAL:CG2	1:B:134:CYS:HB2	1.90	1.00
5:F:257:GLU:HB3	5:F:293:ILE:HG22	1.39	1.00

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	301/338 (89%)	285 (95%)	16 (5%)	0	100 100
1	B	221/338 (65%)	207 (94%)	13 (6%)	1 (0%)	29 66
2	C	1300/1356 (96%)	1240 (95%)	60 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	1136/1396 (81%)	1096 (96%)	40 (4%)	0	100	100
4	E	67/119 (56%)	66 (98%)	1 (2%)	0	100	100
5	F	493/652 (76%)	479 (97%)	14 (3%)	0	100	100
6	G	102/173 (59%)	98 (96%)	4 (4%)	0	100	100
All	All	3620/4372 (83%)	3471 (96%)	148 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	130	ASP

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	218/285 (76%)	217 (100%)	1 (0%)	88	94
1	B	178/285 (62%)	178 (100%)	0	100	100
2	C	1037/1137 (91%)	1035 (100%)	2 (0%)	93	97
3	D	944/1157 (82%)	943 (100%)	1 (0%)	93	98
4	E	58/100 (58%)	58 (100%)	0	100	100
5	F	414/542 (76%)	413 (100%)	1 (0%)	93	97
6	G	79/134 (59%)	79 (100%)	0	100	100
All	All	2928/3640 (80%)	2923 (100%)	5 (0%)	93	97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	ARG
2	C	472	TYR
2	C	738	ARG
3	D	81	TYR
5	F	579	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	440	GLN
5	F	577	GLN
6	G	152	GLN
2	C	1134	HIS
2	C	976	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	6MA	I	19	8	18,24,25	3.11	10 (55%)	15,34,37	2.04	3 (20%)
7	6MA	H	-21	8,7	18,24,25	3.07	10 (55%)	15,34,37	2.03	3 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	6MA	I	19	8	-	5/5/23/24	0/3/3/3
7	6MA	H	-21	8,7	-	5/5/23/24	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	I	19	6MA	O4'-C4'	7.95	1.62	1.45
8	I	19	6MA	C3'-C4'	-7.70	1.31	1.53
7	H	-21	6MA	O4'-C4'	7.62	1.62	1.45
7	H	-21	6MA	C3'-C4'	-7.55	1.32	1.53
7	H	-21	6MA	O4'-C1'	-3.05	1.35	1.42

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	19	6MA	N3-C2-N1	-5.64	119.87	128.68
7	H	-21	6MA	N3-C2-N1	-5.62	119.89	128.68
7	H	-21	6MA	C2-N1-C6	3.72	119.78	116.59
8	I	19	6MA	C2-N1-C6	3.68	119.75	116.59
8	I	19	6MA	C1-N6-C6	-2.91	120.36	122.87

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	H	-21	6MA	O4'-C4'-C5'-O5'
7	H	-21	6MA	N1-C6-N6-C1
8	I	19	6MA	O4'-C4'-C5'-O5'
8	I	19	6MA	C3'-C4'-C5'-O5'
8	I	19	6MA	C5-C6-N6-C1

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	I	19	6MA	3	0
7	H	-21	6MA	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

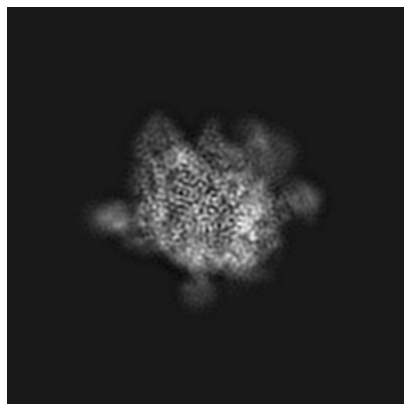
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33761. These allow visual inspection of the internal detail of the map and identification of artifacts.

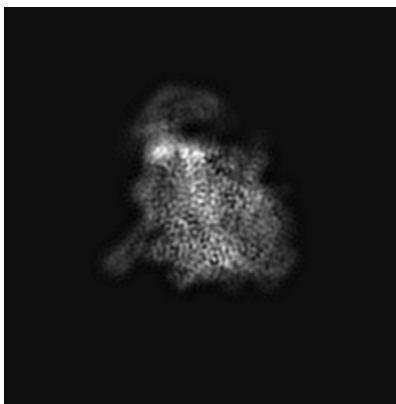
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

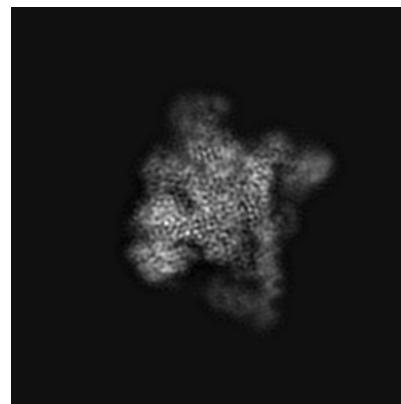
6.1.1 Primary map



X

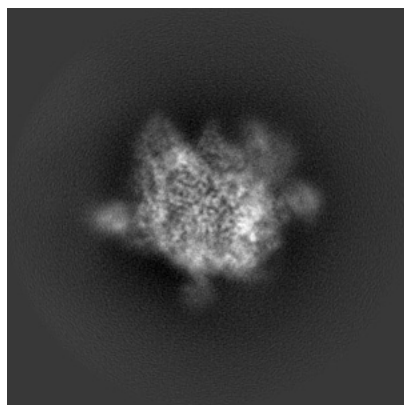


Y

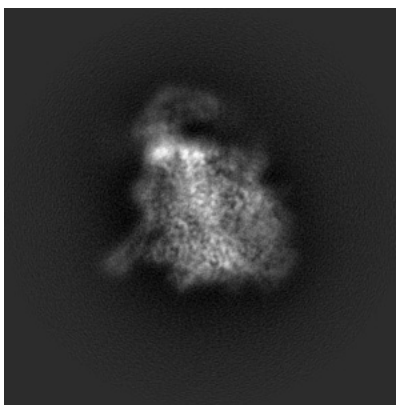


Z

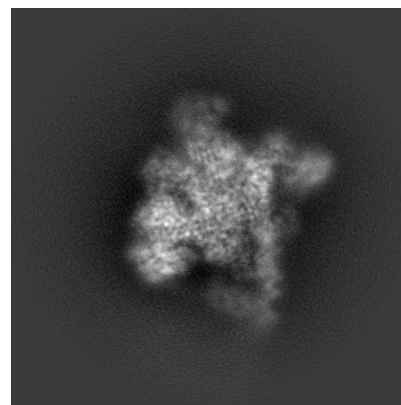
6.1.2 Raw map



X



Y

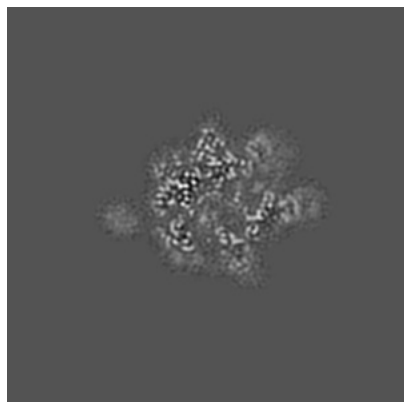


Z

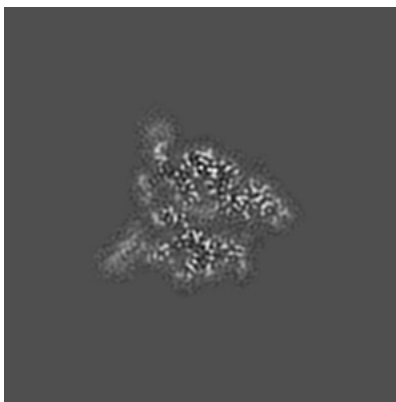
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

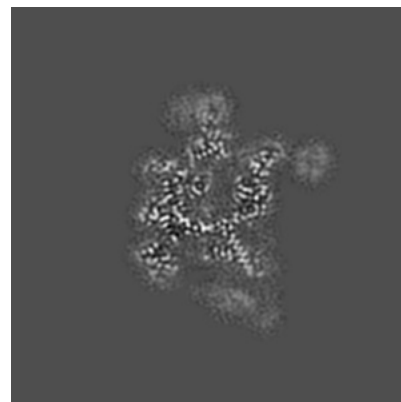
6.2.1 Primary map



X Index: 150

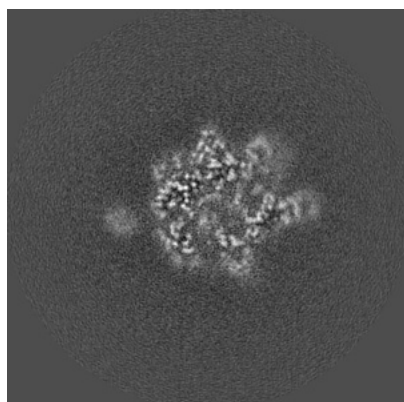


Y Index: 150

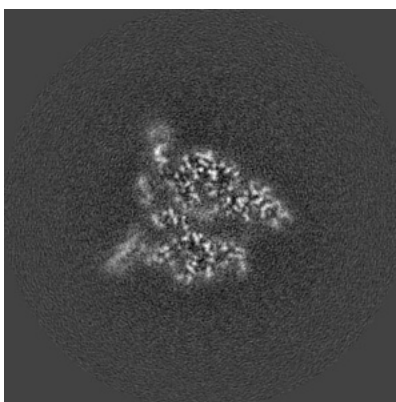


Z Index: 150

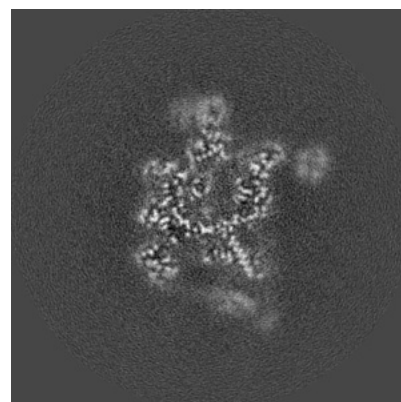
6.2.2 Raw map



X Index: 150



Y Index: 150

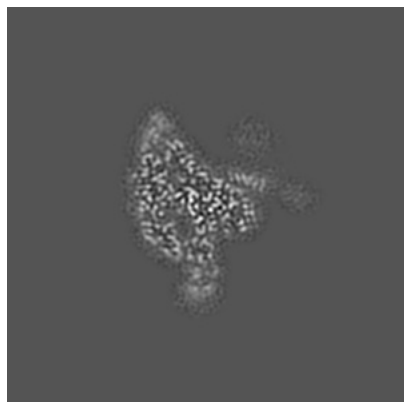


Z Index: 150

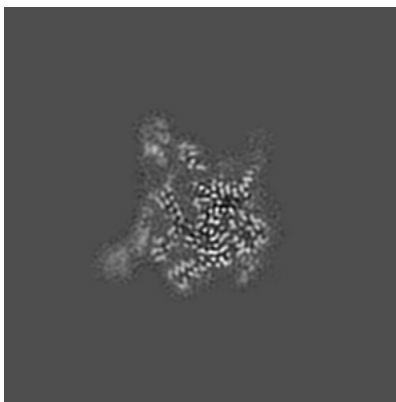
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

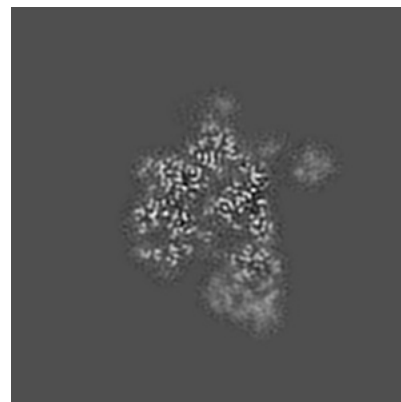
6.3.1 Primary map



X Index: 116

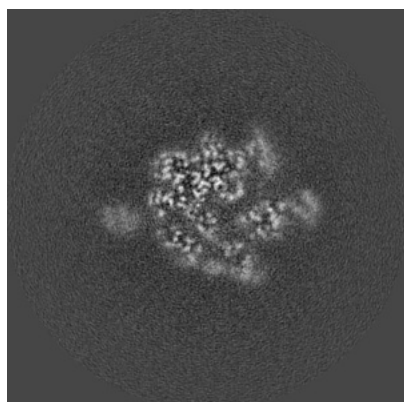


Y Index: 137

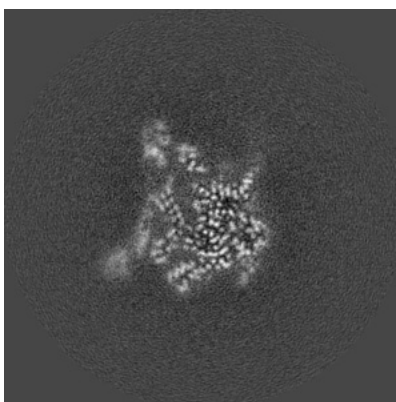


Z Index: 141

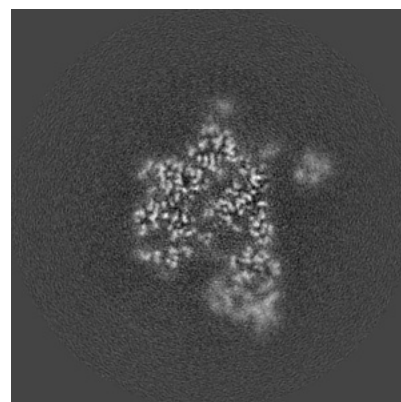
6.3.2 Raw map



X Index: 156



Y Index: 137

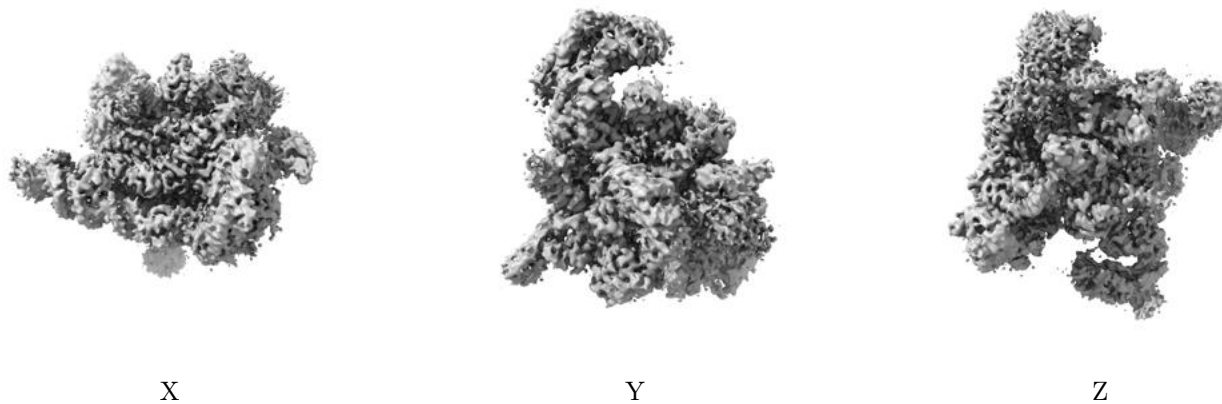


Z Index: 141

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

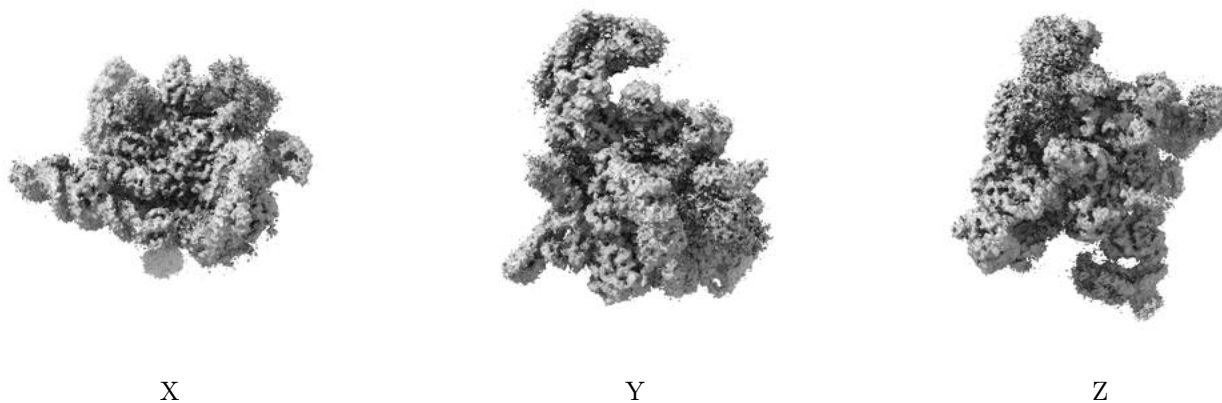
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

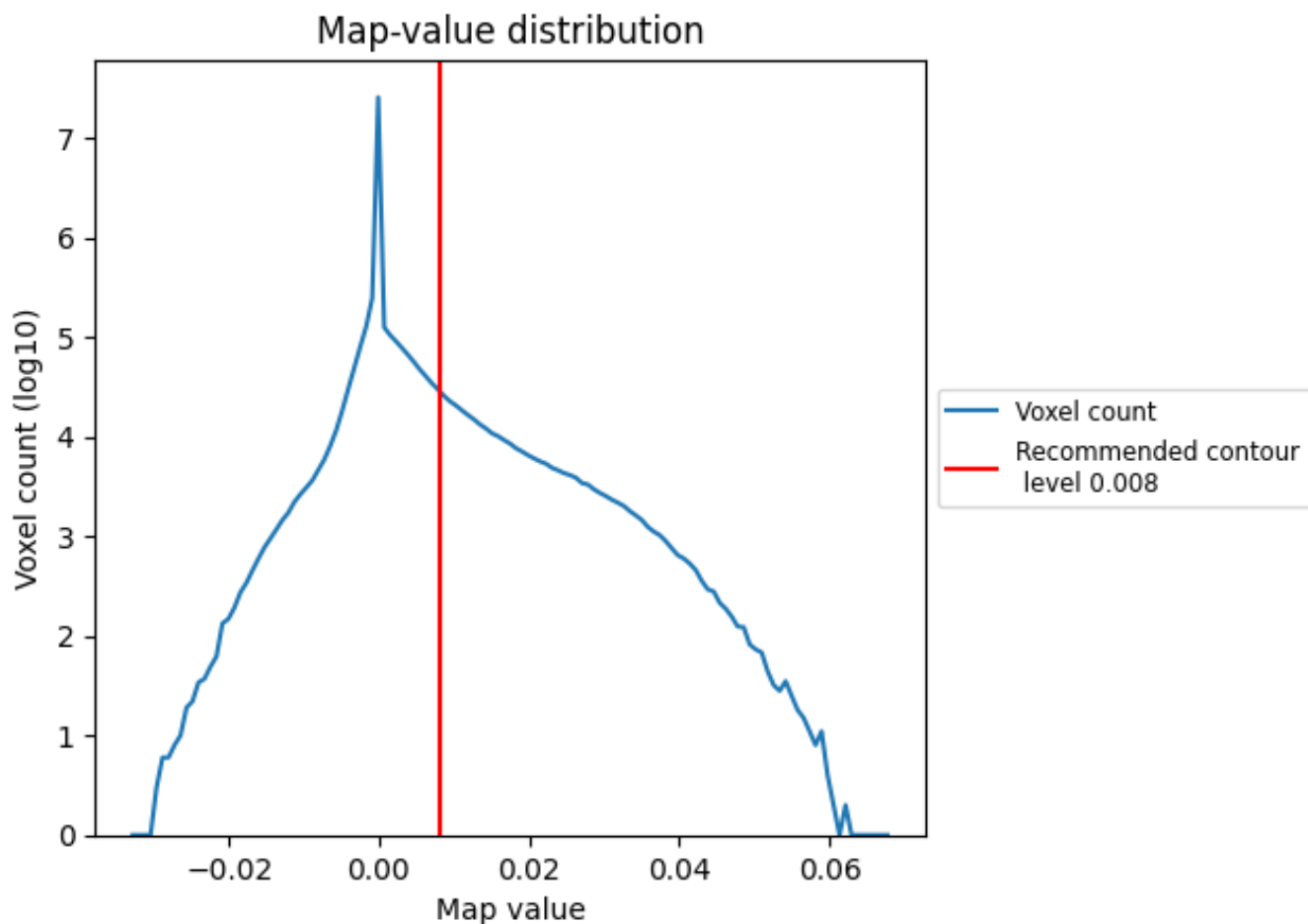
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

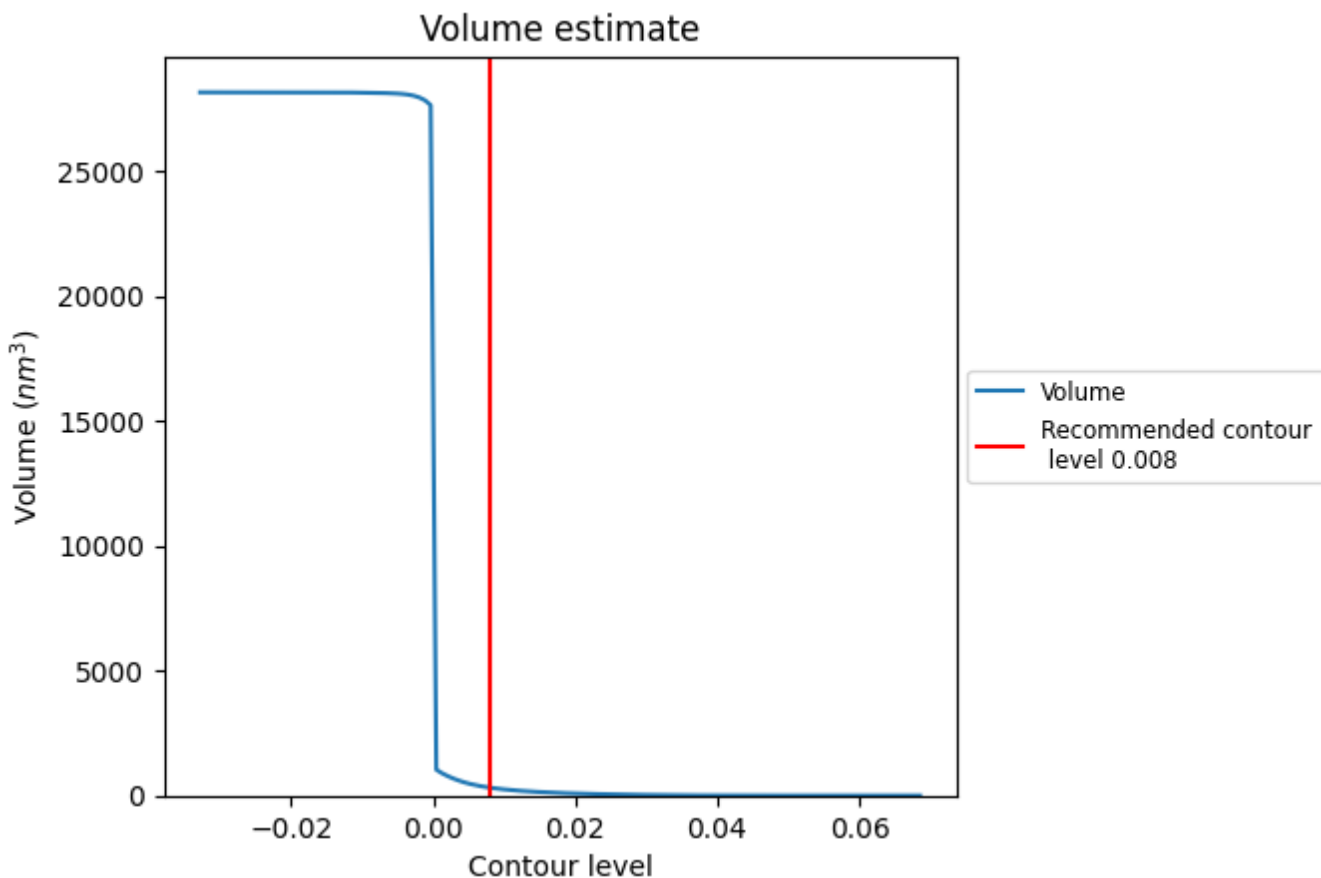
This section contains the results of statistical analysis of the map.

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.

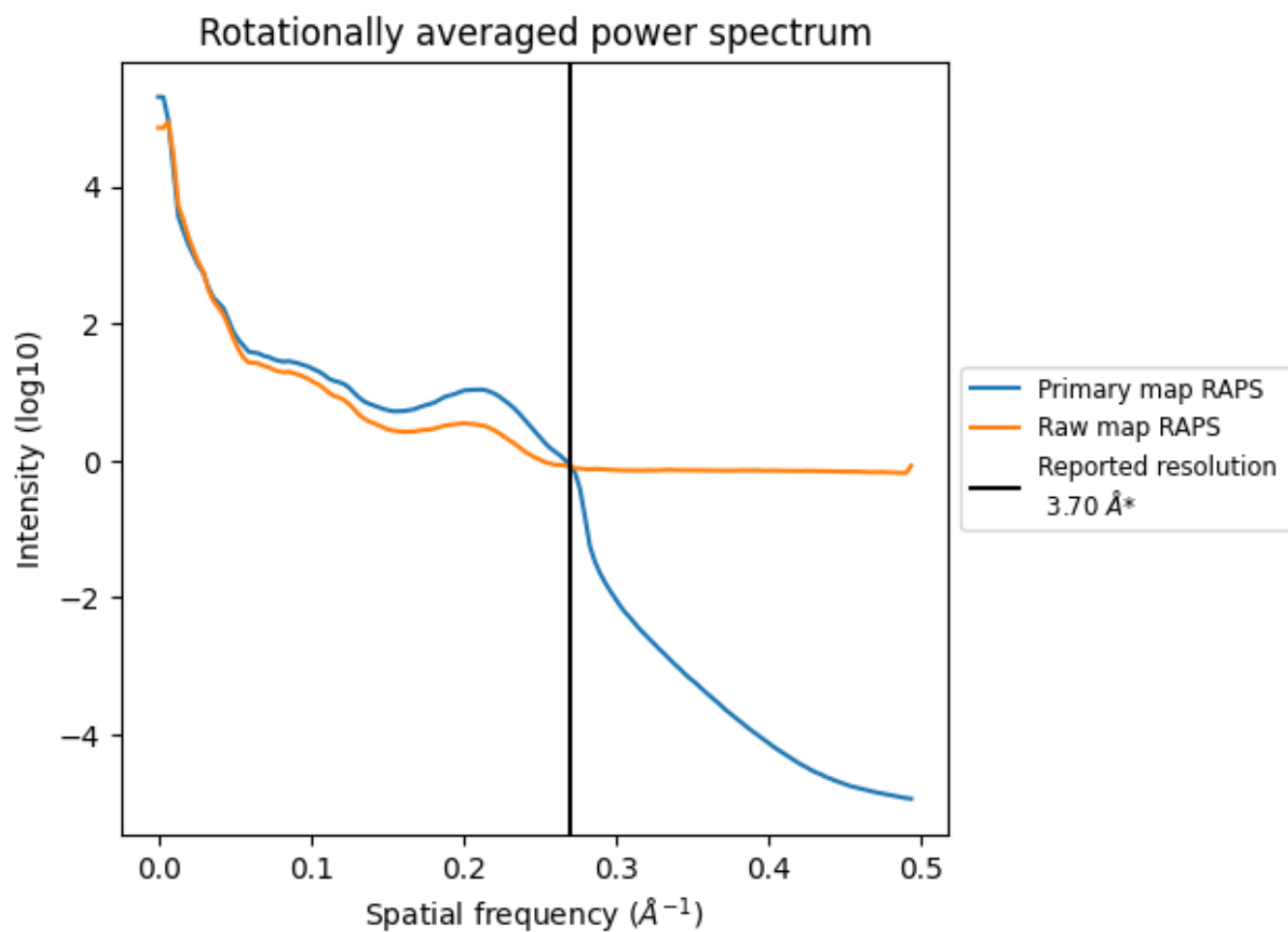
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 316 nm^3 ; this corresponds to an approximate mass of 286 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](#)

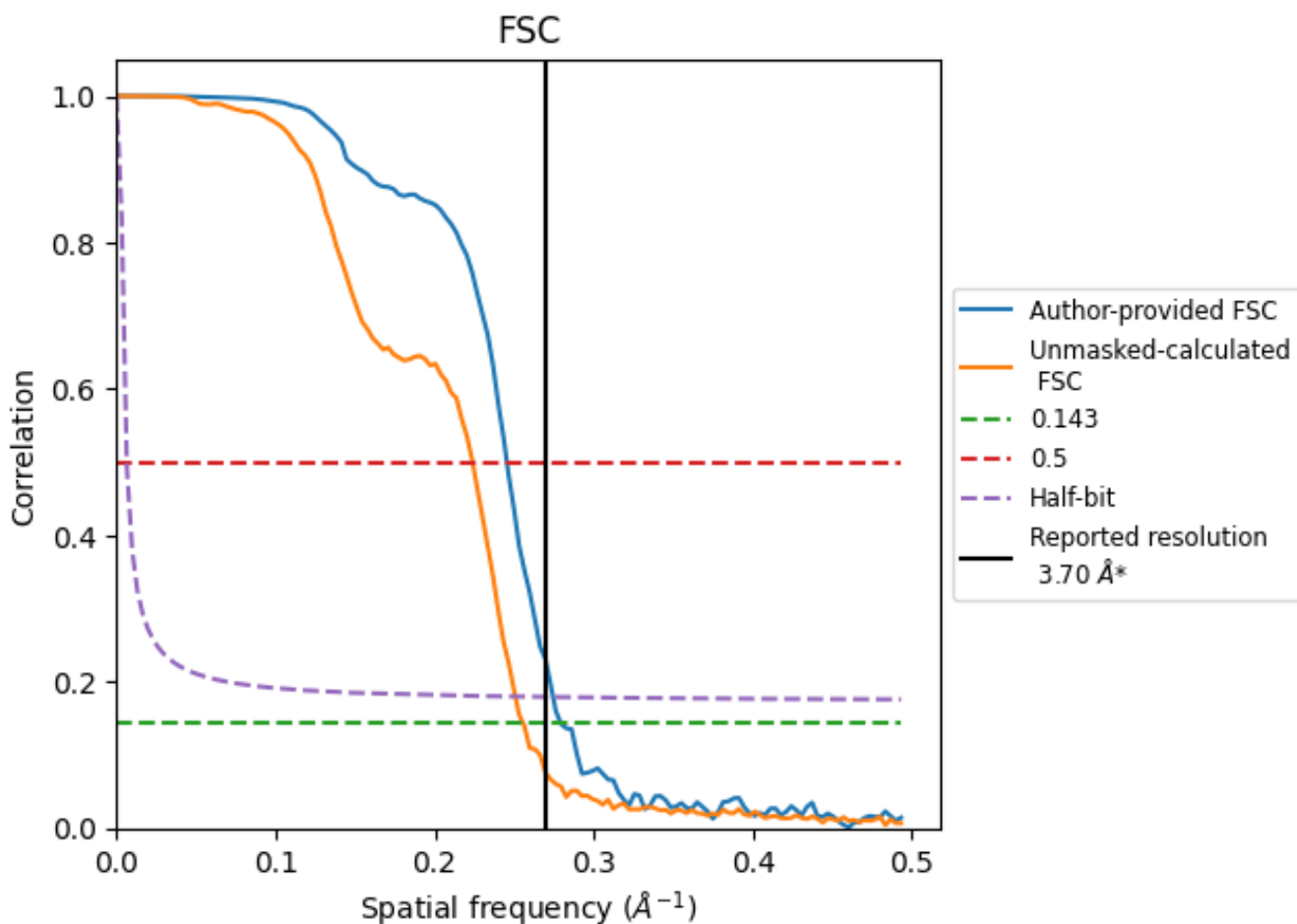


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

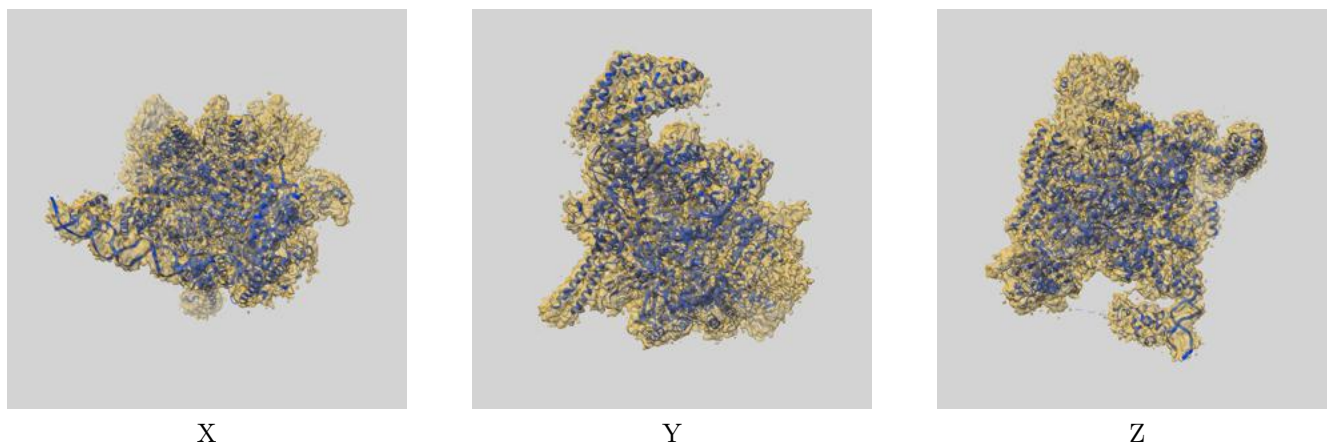
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.58	4.07	3.64
Unmasked-calculated*	3.91	4.47	3.99

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

9 Map-model fit [i](#)

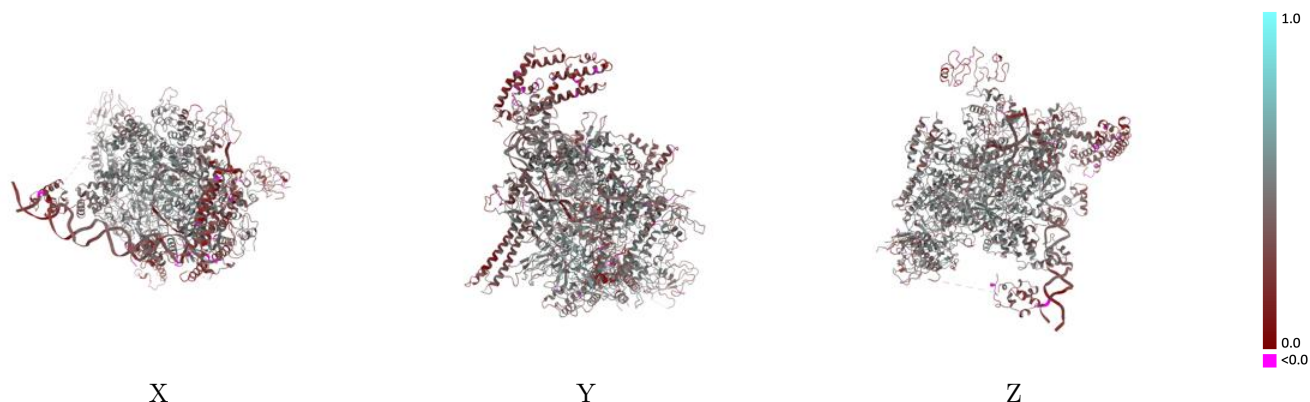
This section contains information regarding the fit between EMDB map EMD-33761 and PDB model 7YE1. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



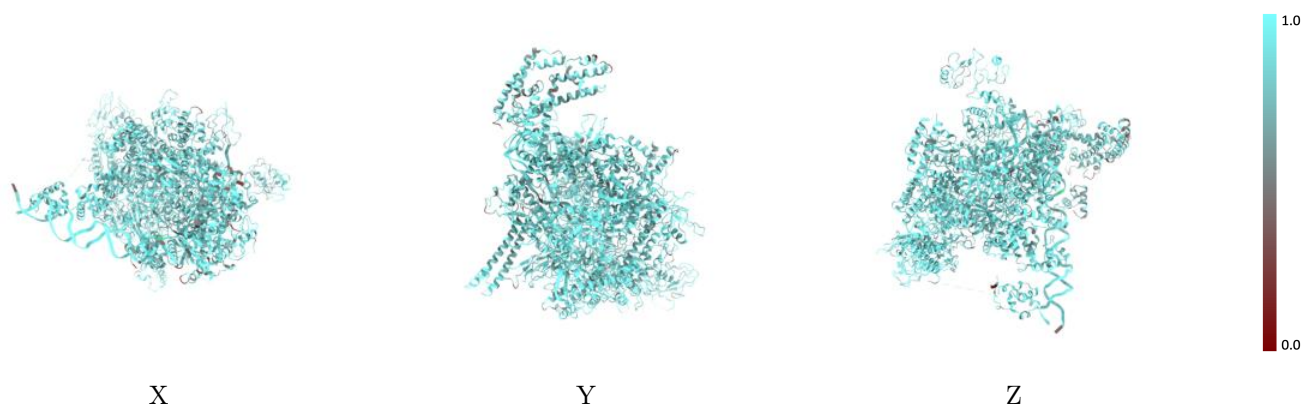
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



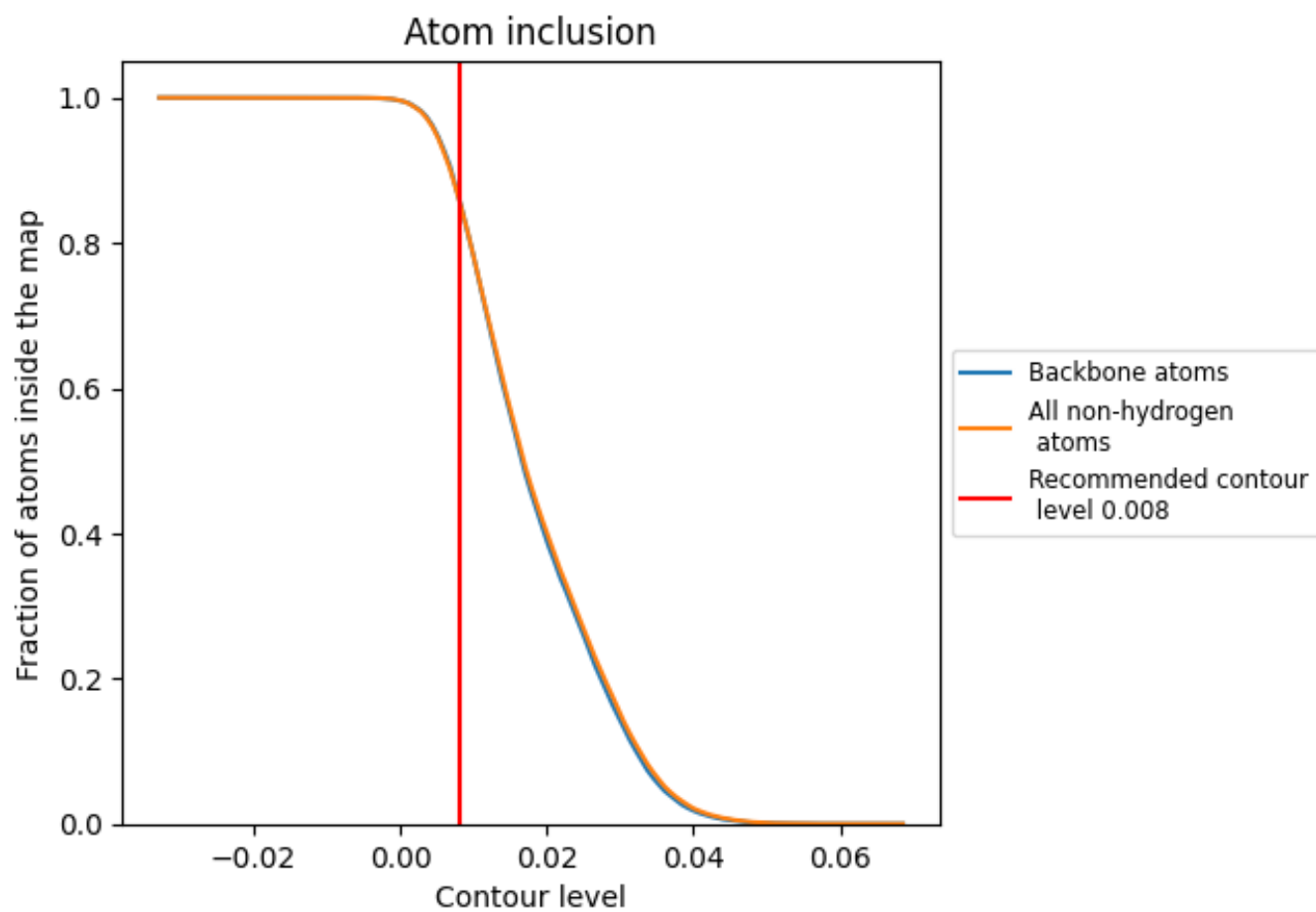
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8616	 0.4070
A	 0.8720	 0.4060
B	 0.8676	 0.3990
C	 0.8667	 0.4290
D	 0.8694	 0.4400
E	 0.8649	 0.4370
F	 0.8197	 0.3390
G	 0.7853	 0.3630
H	 0.9109	 0.3220
I	 0.8969	 0.3020

