



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:26 AM UTC

PDB ID : 7YJJ / pdb_00007yjj
EMDB ID : EMD-33872
Title : Human Cytosolic 10-formyltetrahydrofolate dehydrogenase and Gossypol complex
Authors : Han, C.W.; Lee, H.N.; Jeong, M.S.; Jang, S.B.
Deposited on : 2022-07-20
Resolution : 6.31 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

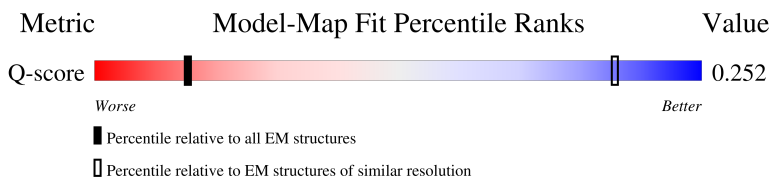
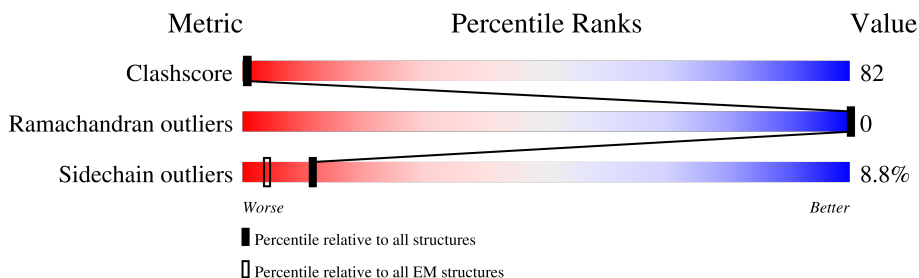
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.31 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	512 (5.82 - 6.81)

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	B	498	21% 73% 6%
1	C	498	21% 73% 6%
1	D	498	22% 72% 6%
1	E	498	20% 73% 6%

2 Entry composition [i](#)

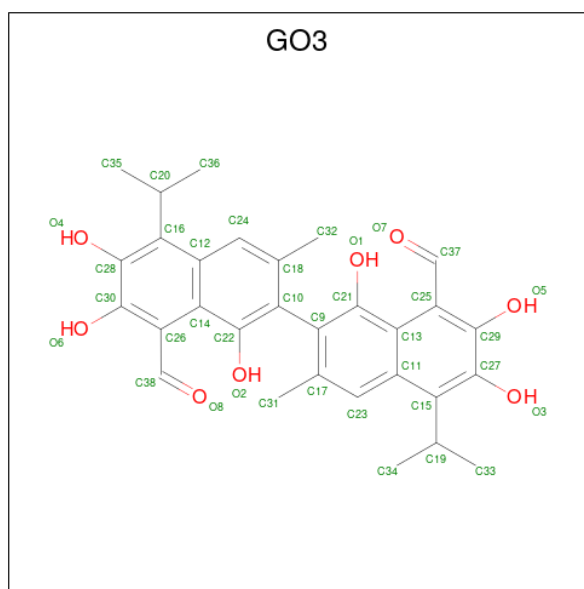
There are 2 unique types of molecules in this entry. The entry contains 15348 atoms, of which 30 are hydrogens and 0 are deuteriums.

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 Cytosolic 10-formyltetrahydrofolate dehydrogenase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	498	Total	C	N	O	S	0	0
			3820	2420	664	713	23		
1	C	498	Total	C	N	O	S	0	0
			3820	2420	664	713	23		
1	D	498	Total	C	N	O	S	0	0
			3820	2420	664	713	23		
1	E	498	Total	C	N	O	S	0	0
			3820	2420	664	713	23		

- Molecule 2 is Gossypol (CCD ID: GO3) (formula: C₃₀H₃₀O₈).

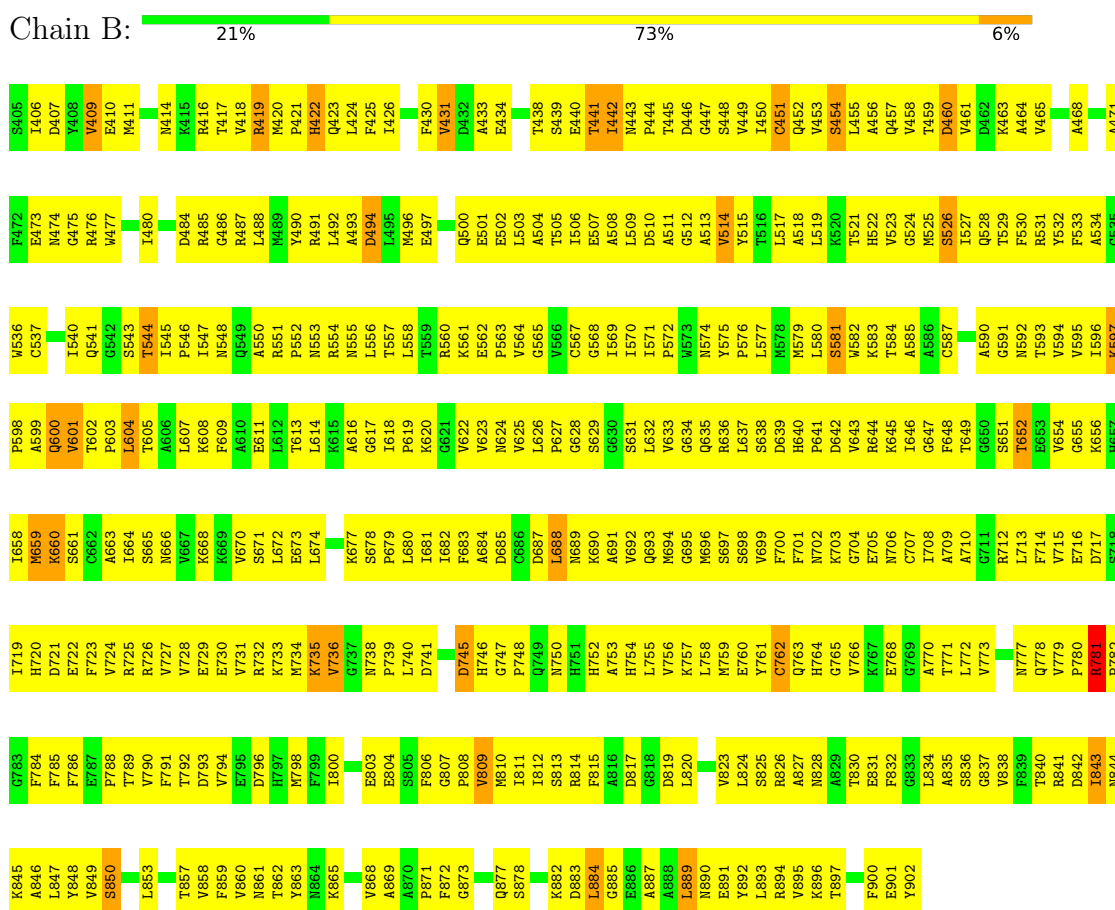


Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	H	O	0
			68	30	30	8	

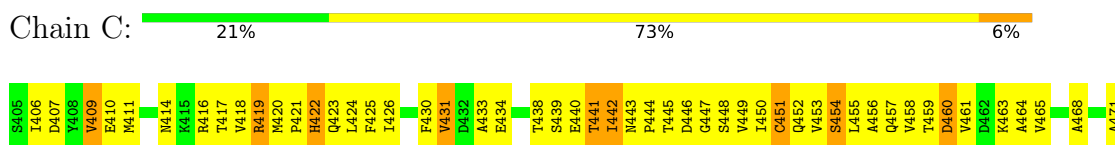
3 Residue-property plots

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: Cytosolic 10-formyltetrahydrofolate dehydrogenase



• Molecule 1: Cytosolic 10-formyltetrahydrofolate dehydrogenase





● Molecule 1: Cytosolic 10-formyltetrahydrofolate dehydrogenase

Chain E:  20% 73% 6%

K845	G783	I719	I658	P598	W536	F472	S405
L847	F784	H720	M659	A599	C537	E473	I406
L846	F785	D721	K660	Q600		M474	D407
Y848	F786	E722	S661	T601	I540	G475	Y408
V849	F787	F723	C662	T602	Q541	R476	V409
S850	F788	V724	A663	P603	G542	W477	E410
	F789	R725	I664	T604	S543		M411
L853	V790	R726	S665	T605	T544	I480	
	F791	V727	N666	A606	I545		N414
T857	T792	V728	V667	L607	P546	D484	K415
V858	D793	E729	K668	K608	I547	R485	R416
F859	V794	E730	A669	F609	N548	G486	T417
V860	E795	V731	V670	A610	Q549	R487	V418
N861	D796	R732	S671	E611	R550	L488	R419
T862	H797	K733	L672	L612	R551	M489	M420
Y863	M798	M734	E673	T613	R552	Y490	P421
N864	F799	K735	L674	L614	N553	R491	H422
K865	I800	V736		K615	R554	L492	Q423
		G737	K677	G621	R560	E497	F430
V868	E803	N738	S678	A616	N555	L424	V431
A869	S804	P739	P679	L618	L556	D494	D432
A870	S805	L740	L680	P619	T557	L495	A433
P871	F806	D741	I681	K620	L558	M496	I426
F872	G807		I682	G621	T559	E497	
G873	P808	D745	F683	V622	R560		F430
G874	V809	H746	A684	E623	K561	Q500	V431
	M810	G747	D685	N624	E562	E501	A433
Q877	F806	P748	C686	V625	P564	E502	A434
S878	I812	Q749	D687	L626	G565	A504	
	S813	N750	L688	P627	V566	L505	T438
K882	R814	H751	N689	G628	C567	T505	S439
D883	F815	V752	K690	S629	G568	I506	E440
L884	A816	A753	V692	G630	E507	E507	T441
G885	D817	H754	V692	S631	I569	A508	I442
F886	G818	L755	C693	L632	I570	L509	N443
A887	D819	V756	M694	V633	I571	P444	P444
	L820	K757	G695	G634	P572	A511	T445
L889	V823	L758	M696	Q635	H573	G512	D446
N890	L824	M759	S697	R636	N574	A513	G447
E891	S825	E760	S698	L637	Y575	V514	S448
Y892	R826	V761	V699	S638	P576	V449	V449
L893	A827	C762	F700	D639	L577	T516	I450
	N828	Q763	F701	H640	R578	L517	C451
K896	A829	H764	N702	P641	M579	A518	Q452
T897	T830	G765	K703	D642	L580	L519	V453
	E831	V766	G704	V643	S581	K520	S454
	F832	K767	E705	R644	H582	T521	L455
F900	F833	E768	N706	K645	K583	H522	A456
E901	G853	G769	C707	I646	L584	V523	Q457
Y902	A835	L770	I708	G647	A585	G524	V458
	S836	A770	A709	F648	A586	S525	T459
	G837	L772	A710	T649	C587	S526	D460
	V838	V773	G711	T649		I527	V461
			R712	G650	A590	Q528	D462
	F839	N777	L713	S651	C591	T529	K463
	T840	Q778	F714	T652	N592	F530	A464
	R841	V779	V715	E653	T593	R531	V465
	D842	P780	E716	V654	V594	Y532	
				G655	V595	F533	A468
	I843	R761	D717	K656	I596	A534	
	N844	F762	E716	V597	C526	F526	A471

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	396292	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39.55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.959	Depositor
Minimum map value	-1.779	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.141	Depositor
Map size (Å)	503.3728, 503.3728, 503.3728	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.9663, 1.9663, 1.9663	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: GO3

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	B	0.30	0/3895	0.62	3/5267 (0.1%)
1	C	0.30	0/3895	0.62	3/5267 (0.1%)
1	D	0.30	0/3895	0.62	3/5267 (0.1%)
1	E	0.30	0/3895	0.62	3/5267 (0.1%)
All	All	0.30	0/15580	0.62	12/21068 (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	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	419	ARG	CA-C-N	-12.01	104.91	121.61
1	D	419	ARG	C-N-CA	-12.01	104.91	121.61
1	B	419	ARG	CA-C-N	-11.97	104.97	121.61
1	B	419	ARG	C-N-CA	-11.97	104.97	121.61
1	E	419	ARG	CA-C-N	-11.96	104.99	121.61

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	544	THR	Peptide
1	B	843	ILE	Peptide
1	C	544	THR	Peptide
1	C	843	ILE	Peptide
1	D	544	THR	Peptide

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	B	3820	0	3826	662	0
1	C	3820	0	3826	646	0
1	D	3820	0	3826	624	0
1	E	3820	0	3826	642	0
2	C	38	30	0	3	0
All	All	15318	30	15304	2512	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 82.

The worst 5 of 2512 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:457:GLN:HB2	1:B:459:THR:HG22	1.34	1.09
1:B:660:LYS:HE2	1:C:664:ILE:HD11	1.31	1.09
1:B:664:ILE:HD11	1:C:660:LYS:HE2	1.33	1.08
1:C:843:ILE:HD13	1:D:843:ILE:HD13	1.36	1.07
1:D:457:GLN:HB2	1:D:459:THR:HG22	1.34	1.07

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	B	496/498 (100%)	407 (82%)	89 (18%)	0	100	100
1	C	496/498 (100%)	407 (82%)	89 (18%)	0	100	100
1	D	496/498 (100%)	406 (82%)	90 (18%)	0	100	100
1	E	496/498 (100%)	407 (82%)	89 (18%)	0	100	100
All	All	1984/1992 (100%)	1627 (82%)	357 (18%)	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	B	409/409 (100%)	373 (91%)	36 (9%)	9	28
1	C	409/409 (100%)	373 (91%)	36 (9%)	9	28
1	D	409/409 (100%)	373 (91%)	36 (9%)	9	28
1	E	409/409 (100%)	373 (91%)	36 (9%)	9	28
All	All	1636/1636 (100%)	1492 (91%)	144 (9%)	11	28

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	454	SER
1	E	891	GLU
1	E	502	GLU
1	E	659	MET
1	C	514	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	751	HIS
1	E	764	HIS
1	C	749	GLN
1	C	706	ASN
1	E	844	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](#)

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](#)

1 ligand is 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	$\# Z > 2$
2	GO3	C	1001	-	41,41,41	1.73	8 (19%)	64,64,64	1.71	12 (18%)

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
2	GO3	C	1001	-	-	4/16/16/16	0/4/4/4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	GO3	C10-C9	5.18	1.60	1.50
2	C	1001	GO3	C25-C37	3.72	1.53	1.45
2	C	1001	GO3	C16-C20	3.22	1.59	1.52
2	C	1001	GO3	C26-C38	3.21	1.52	1.45
2	C	1001	GO3	C9-C17	-2.56	1.37	1.40

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	GO3	C35-C20-C16	5.28	124.81	112.95
2	C	1001	GO3	O2-C22-C10	-4.00	111.92	120.24
2	C	1001	GO3	C26-C14-C12	-3.46	115.74	119.23
2	C	1001	GO3	C30-C26-C14	3.33	122.26	117.86
2	C	1001	GO3	C29-C25-C37	-3.27	112.94	116.50

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1001	GO3	C13-C25-C37-O7
2	C	1001	GO3	C29-C25-C37-O7
2	C	1001	GO3	C14-C26-C38-O8
2	C	1001	GO3	C30-C26-C38-O8

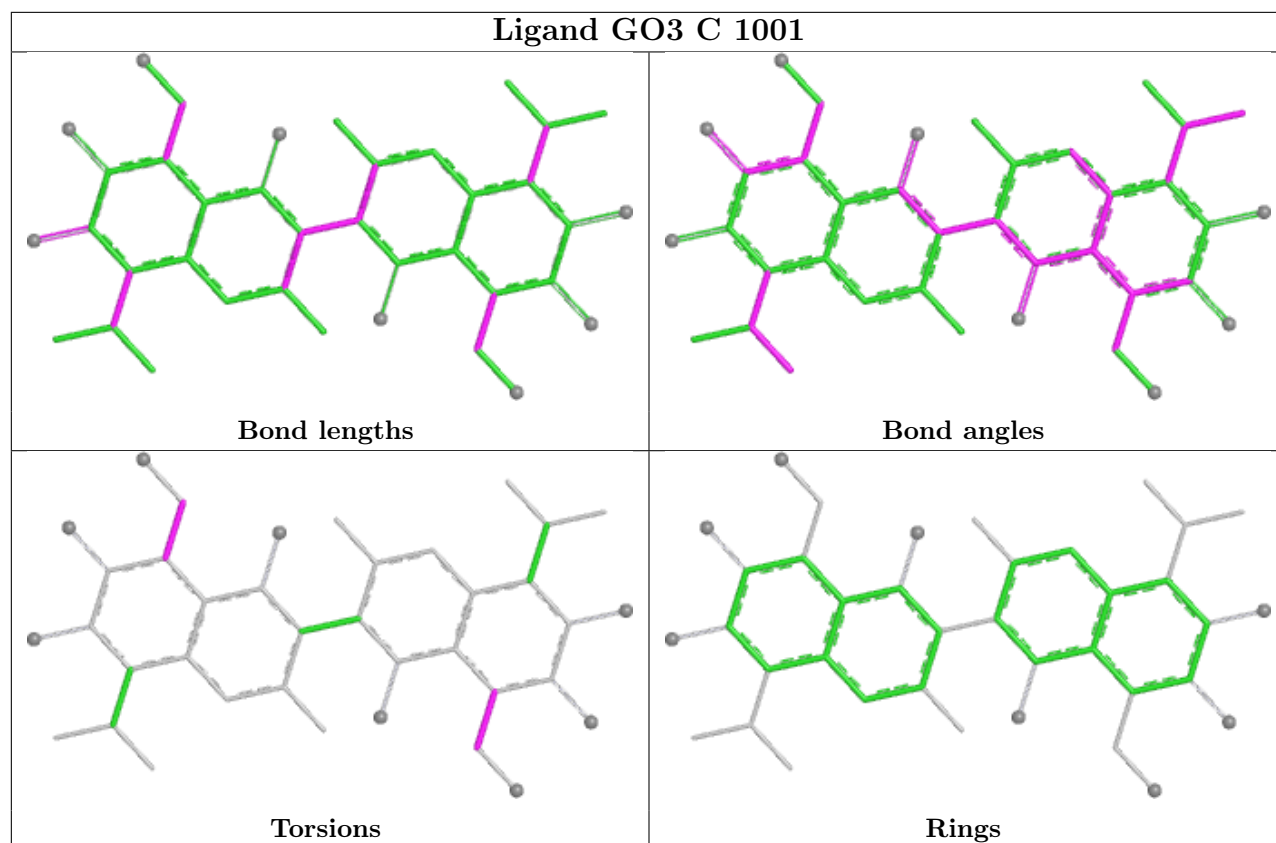
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	GO3	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



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.

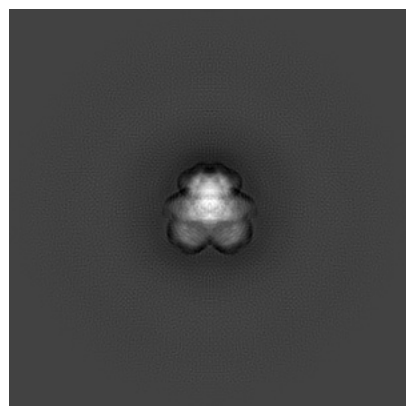
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33872. These allow visual inspection of the internal detail of the map and identification of artifacts.

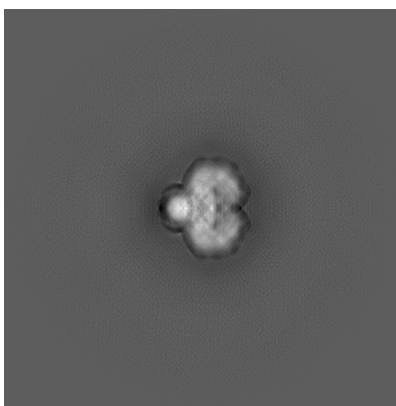
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

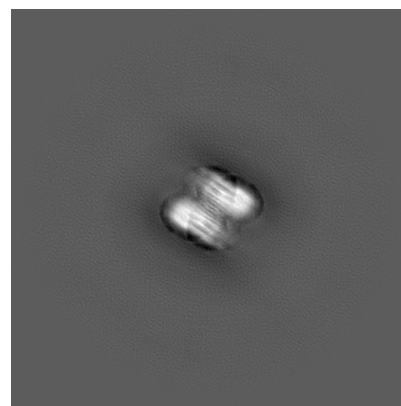
6.1.1 Primary map



X

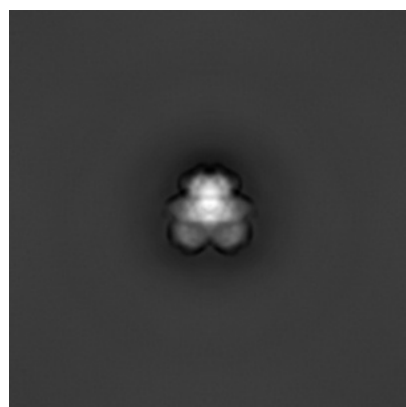


Y

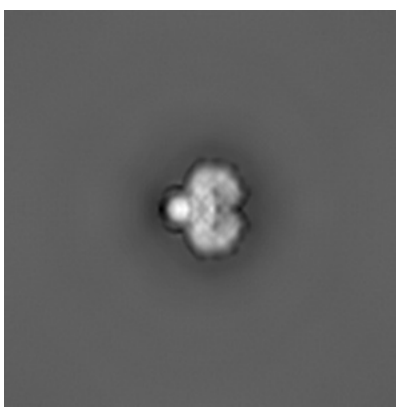


Z

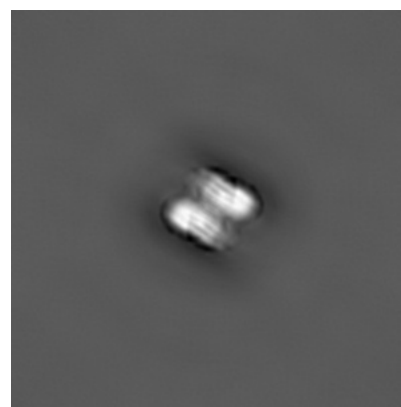
6.1.2 Raw map



X



Y

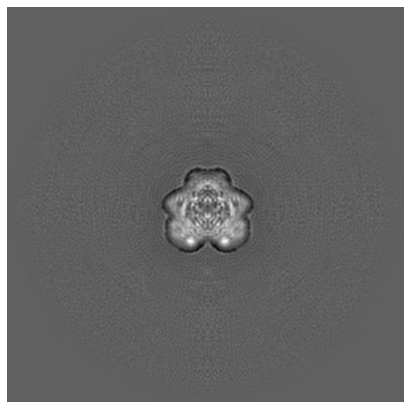


Z

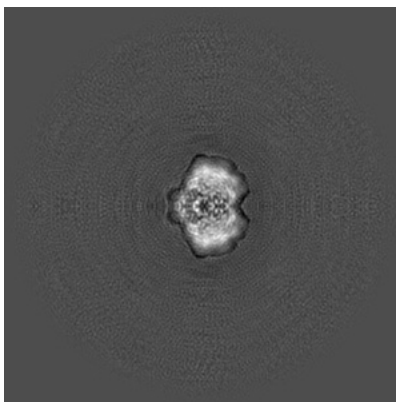
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

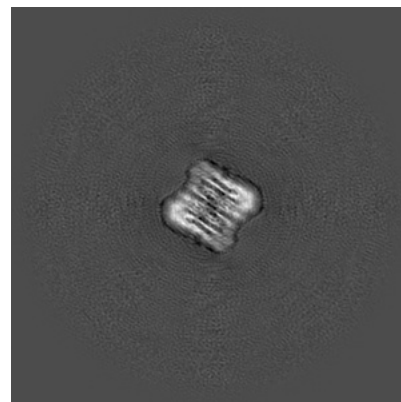
6.2.1 Primary map



X Index: 128

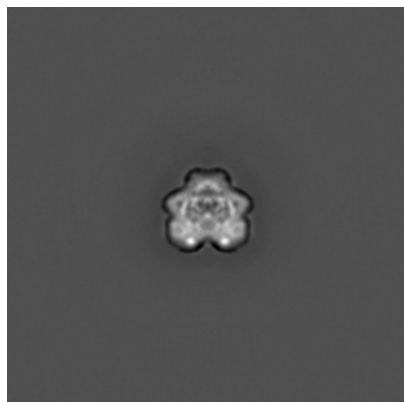


Y Index: 128

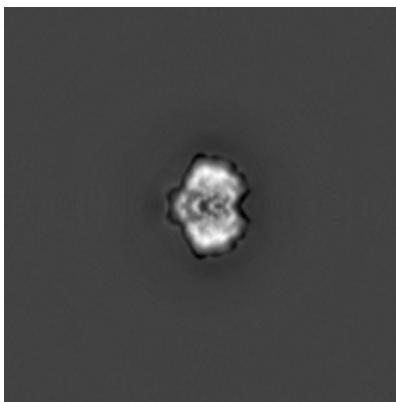


Z Index: 128

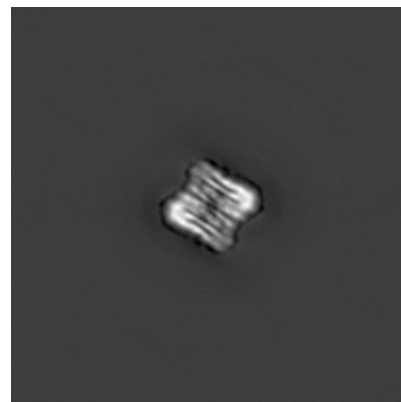
6.2.2 Raw map



X Index: 128



Y Index: 128

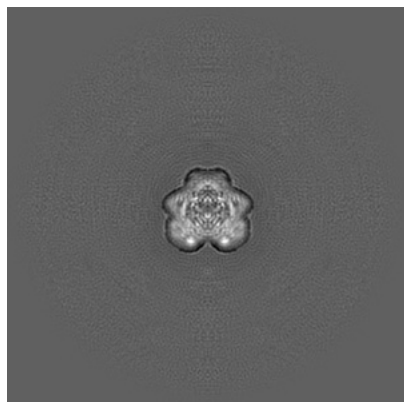


Z Index: 128

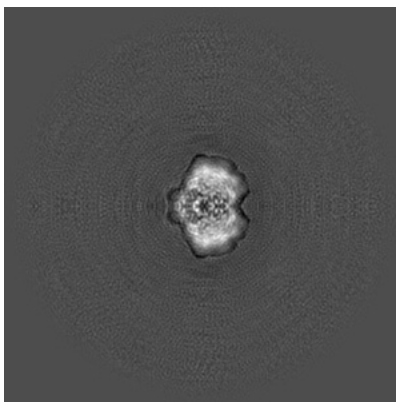
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

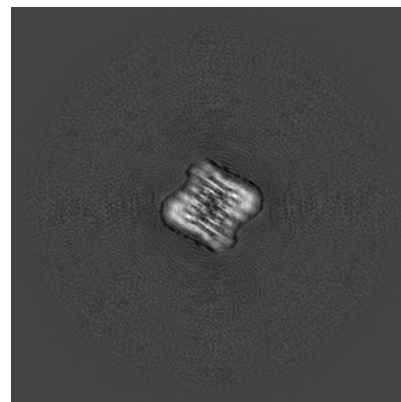
6.3.1 Primary map



X Index: 128

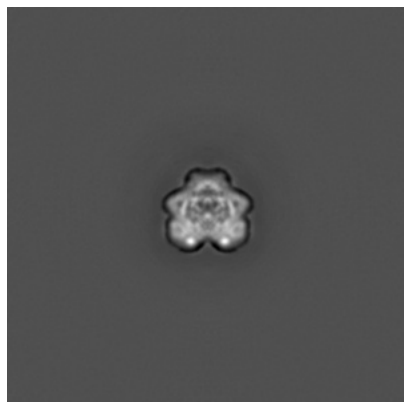


Y Index: 128

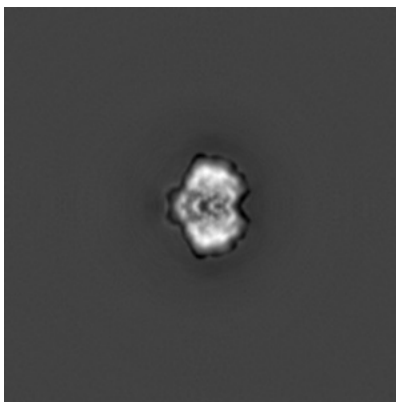


Z Index: 129

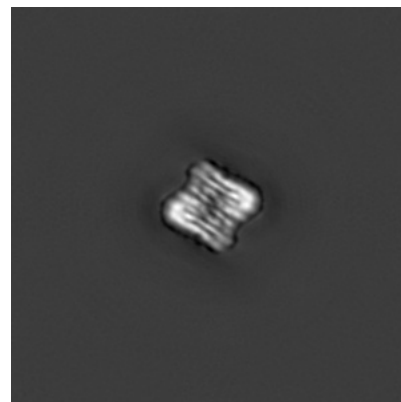
6.3.2 Raw map



X Index: 128



Y Index: 128

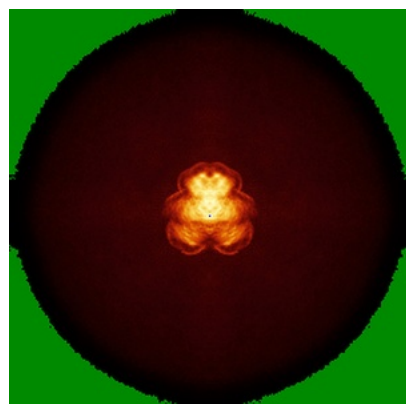


Z Index: 129

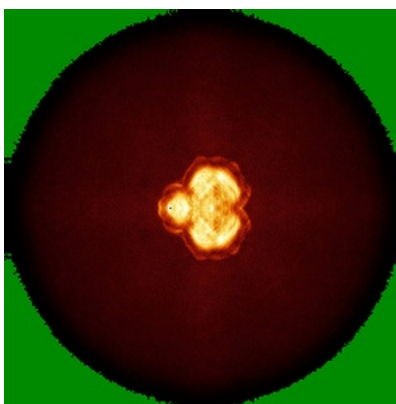
The images above show the largest variance slices of the map in three orthogonal directions.

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

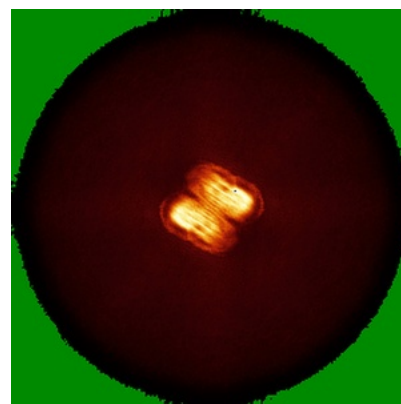
6.4.1 Primary map



X

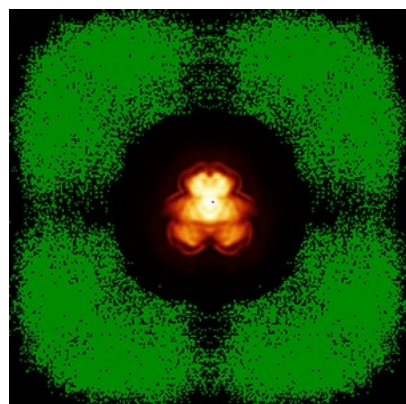


Y

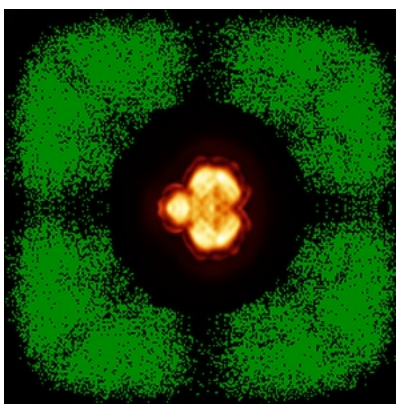


Z

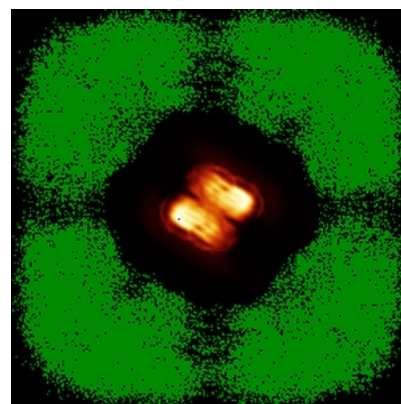
6.4.2 Raw map



X



Y

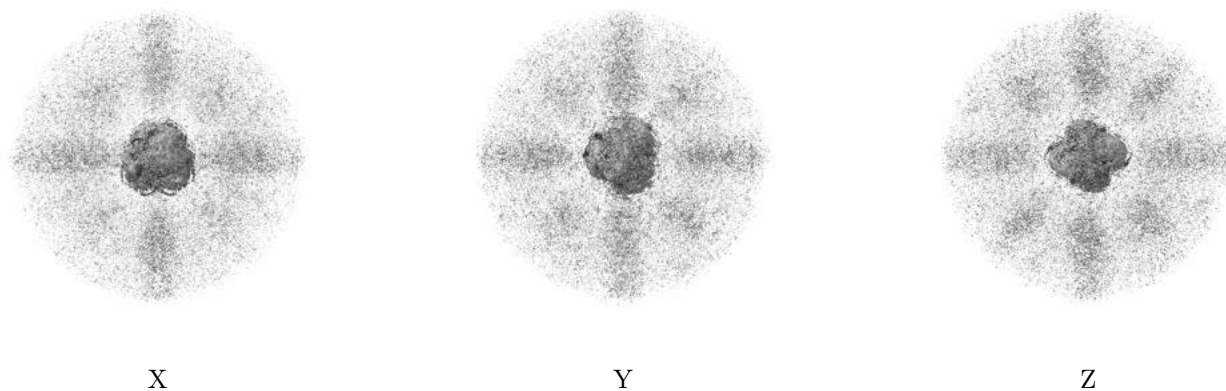


Z

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.

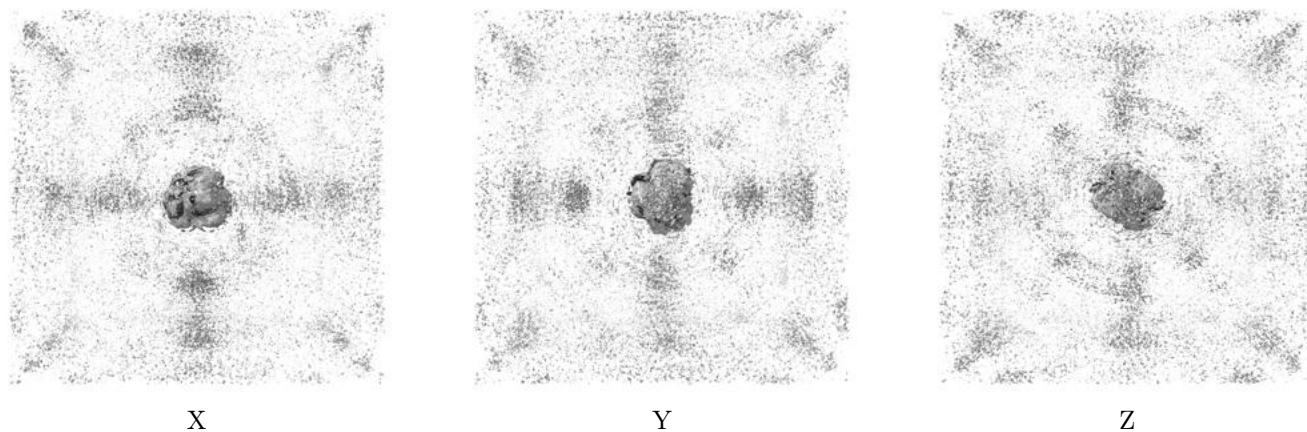
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.141. 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.

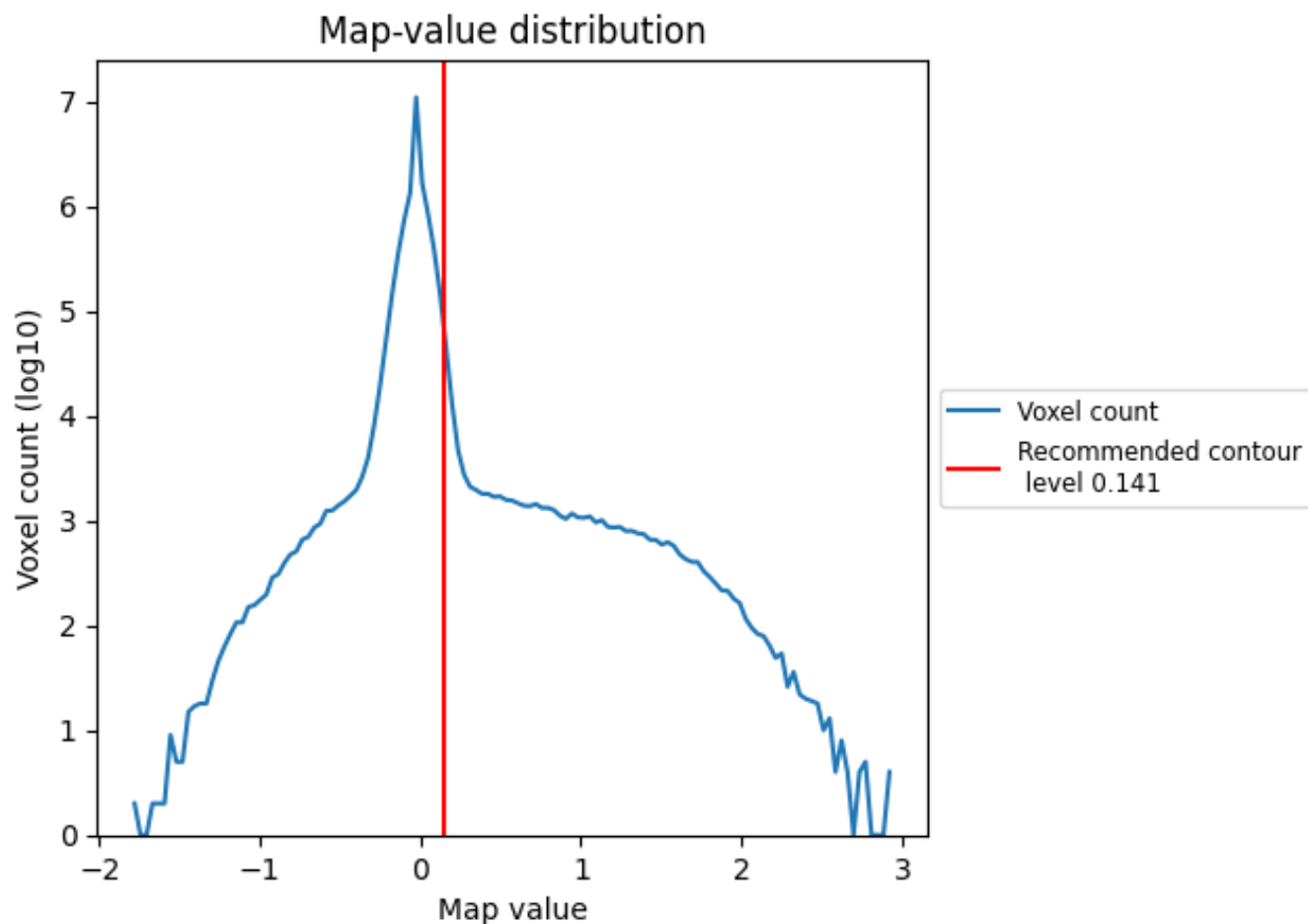
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

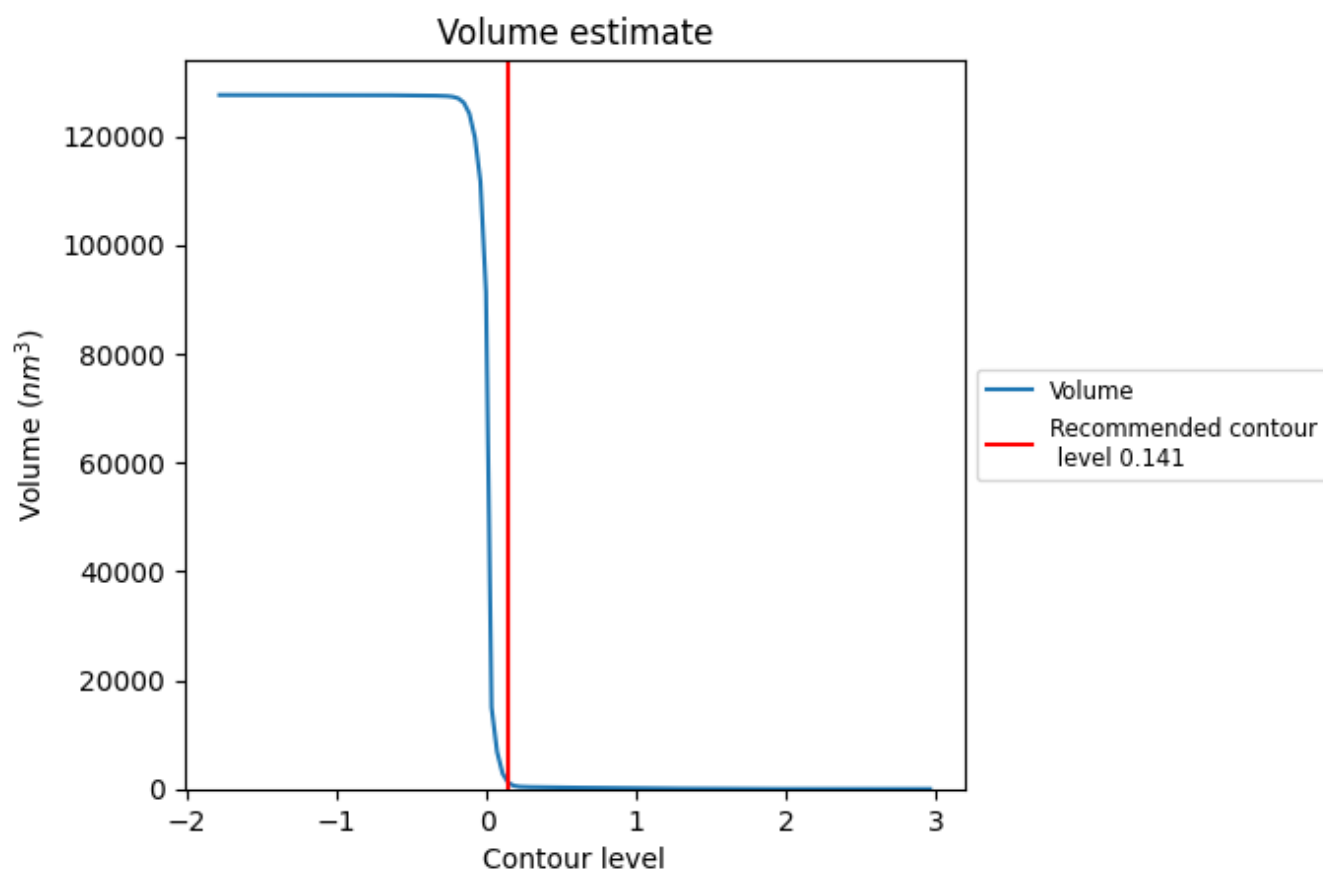
This section contains the results of statistical analysis of the map.

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.

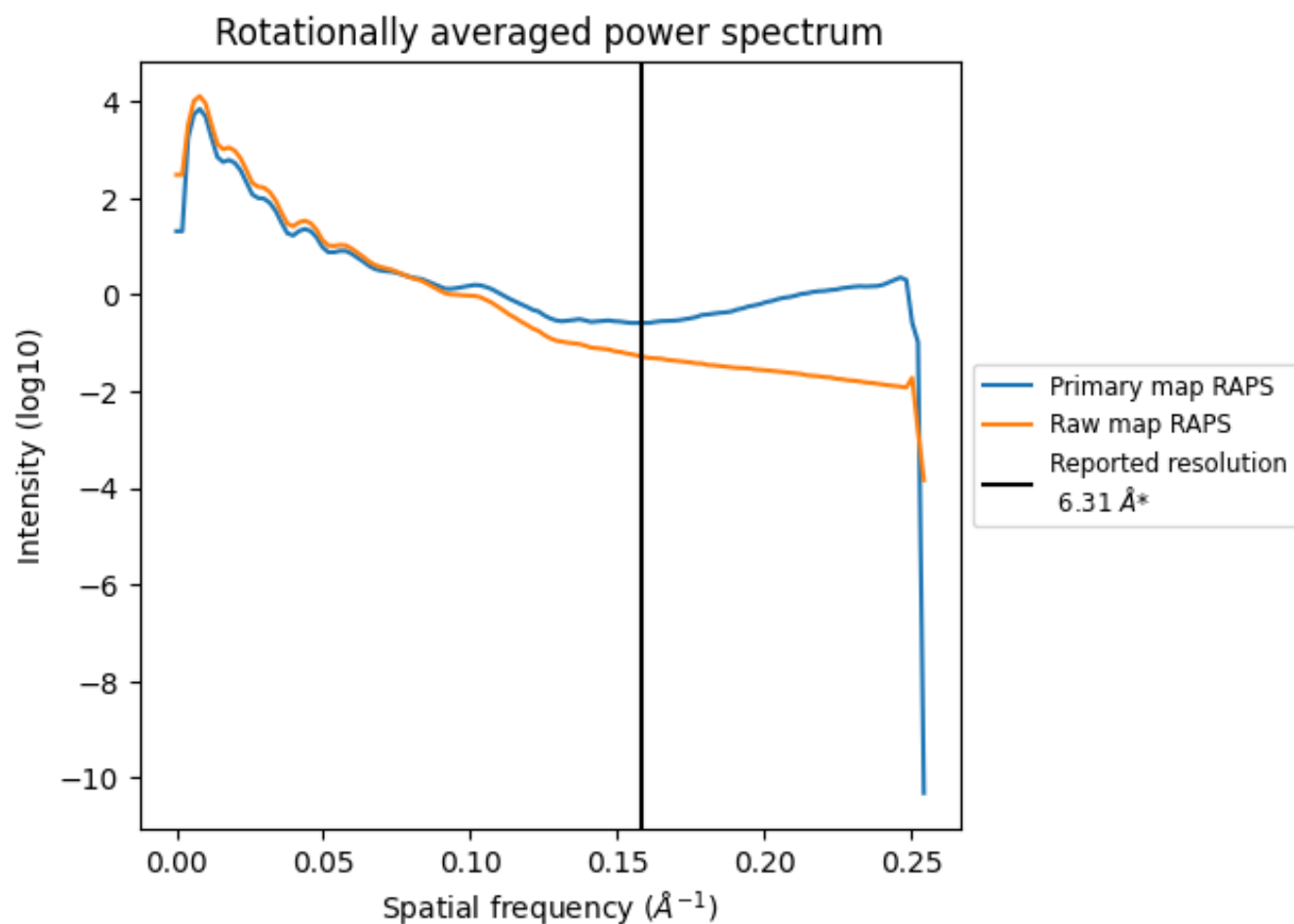
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1355 nm^3 ; this corresponds to an approximate mass of 1224 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 ⓘ

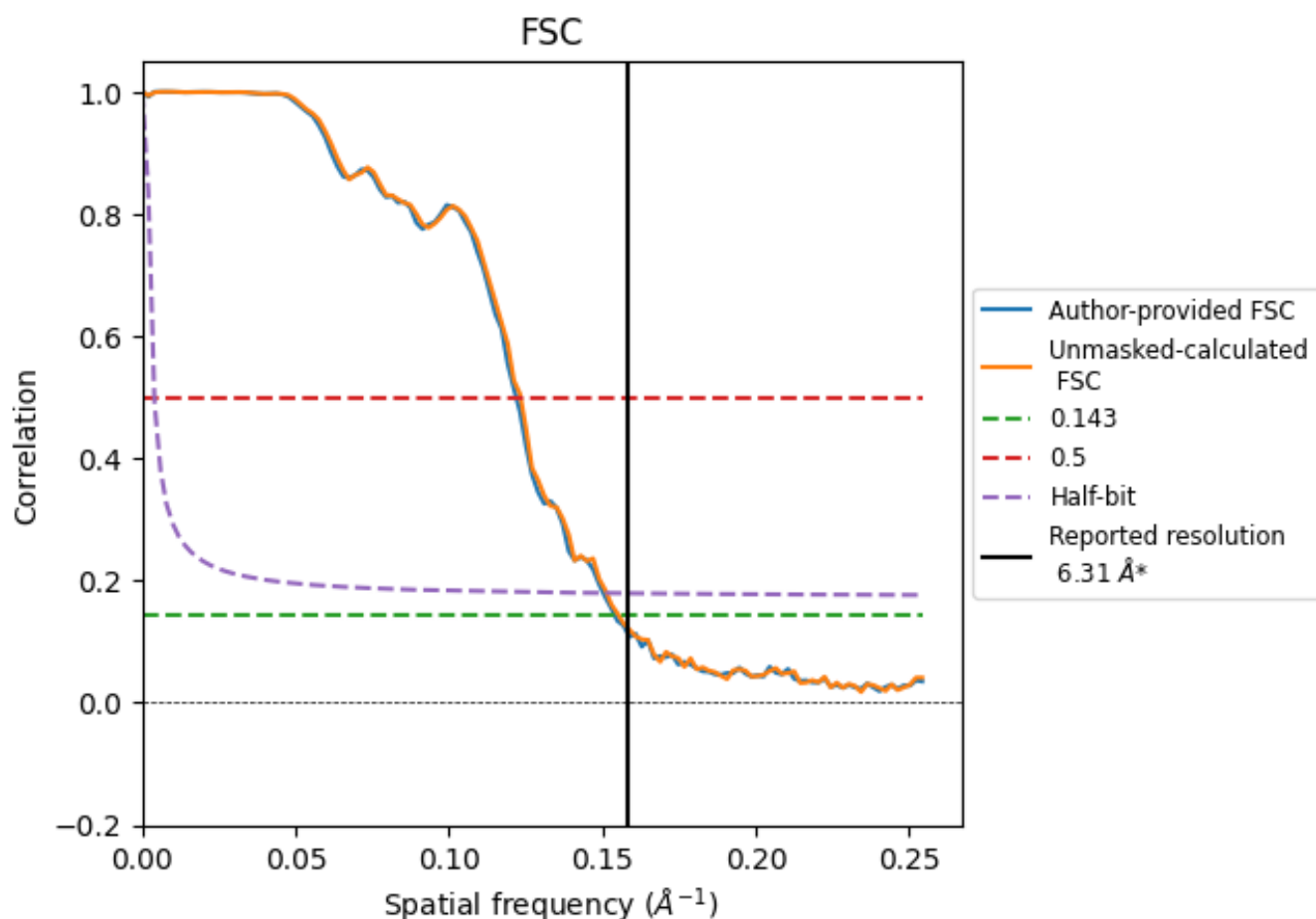


*Reported resolution corresponds to spatial frequency of 0.158 Å⁻¹

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 0.158 Å⁻¹

8.2 Resolution estimates [i](#)

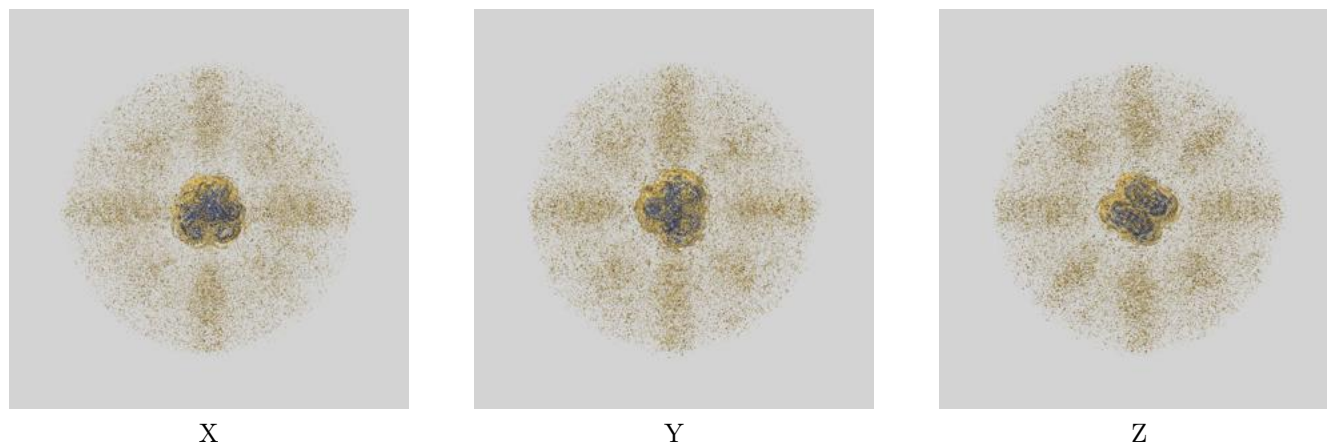
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.31	-	-
Author-provided FSC curve	6.49	8.20	6.65
Unmasked-calculated*	6.44	8.11	6.61

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

9 Map-model fit [i](#)

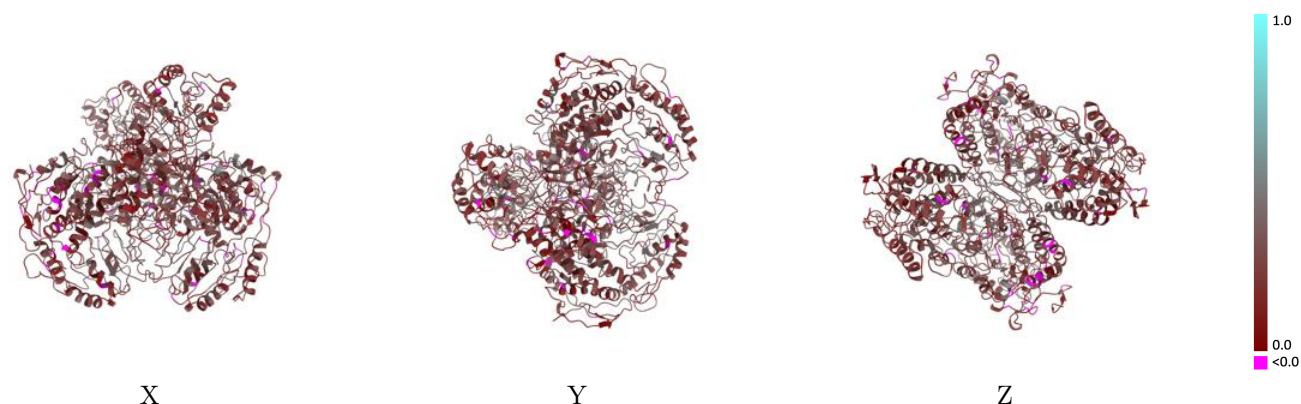
This section contains information regarding the fit between EMDB map EMD-33872 and PDB model 7YJJ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.141 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](#)

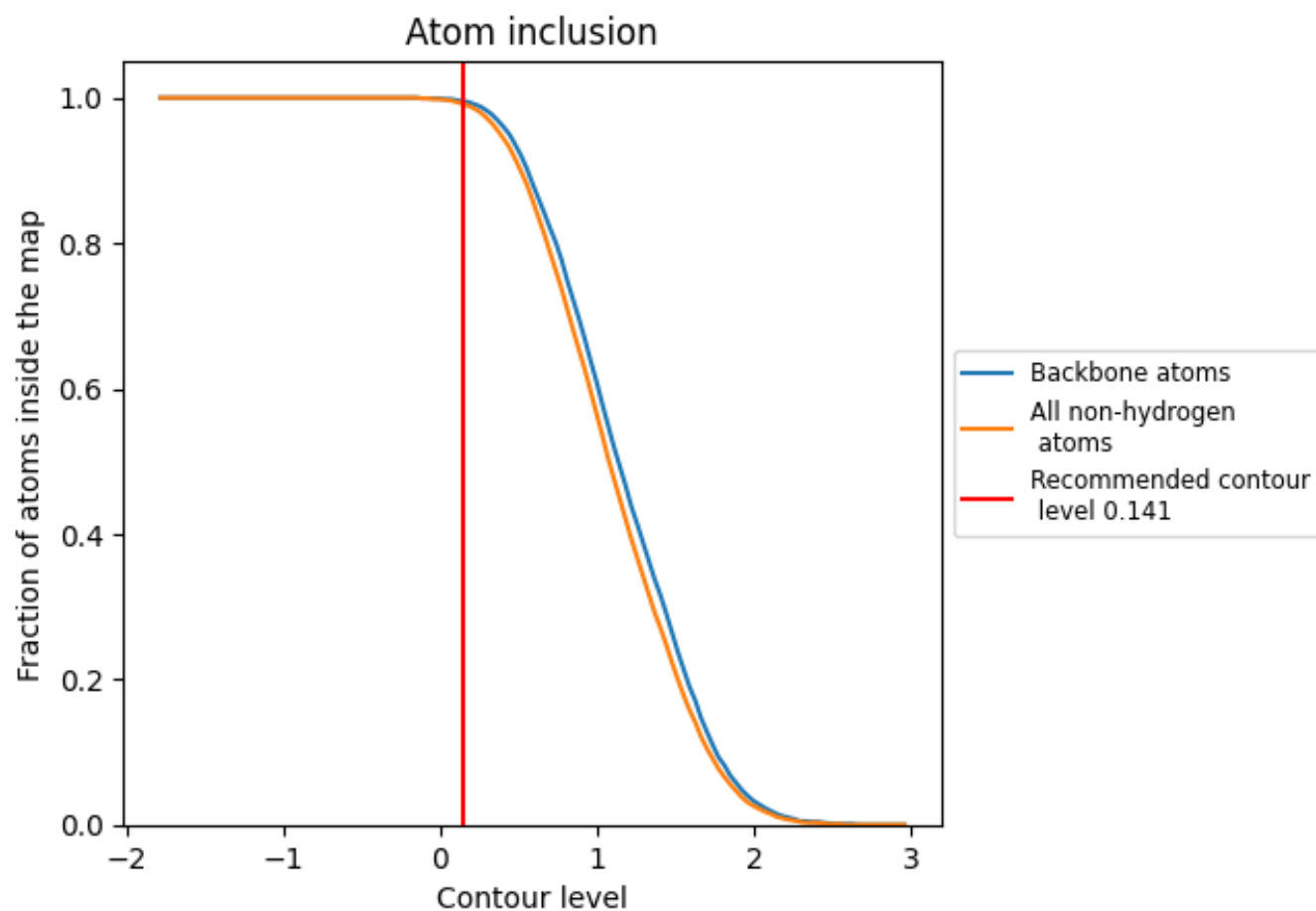


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.141) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9920	0.2520
B	0.9980	0.2580
C	0.9850	0.2460
D	0.9860	0.2510
E	0.9980	0.2550

