



wwPDB EM Validation Summary Report ⓘ

Aug 23, 2026 – 12:16 AM JST

PDB ID : 27QB / pdb_000027qb
EMDB ID : EMD-81338
Title : Dictyostelium discoideum cytoplasmic dynein motor domain in the absence of nucleotide (Apo state 2)
Authors : Shimo-Kon, R.; Tokita, H.; Imai, H.; Maeshima, T.; Kon, T.
Deposited on : 2026-06-09
Resolution : 2.66 Å(reported)
Based on initial model : 3VKG

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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.50

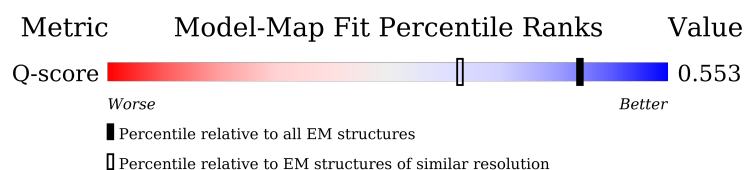
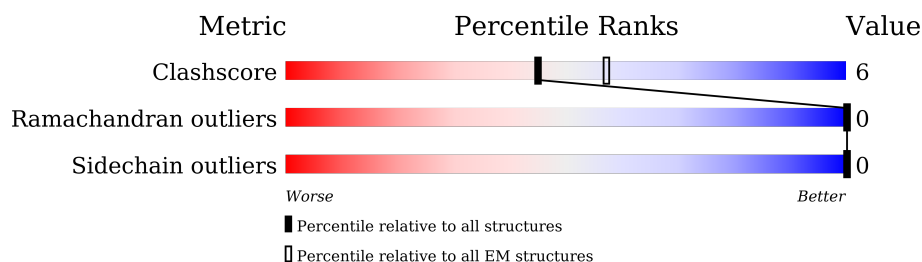
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.66 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	9119 (2.16 - 3.16)

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	3367	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24394 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.

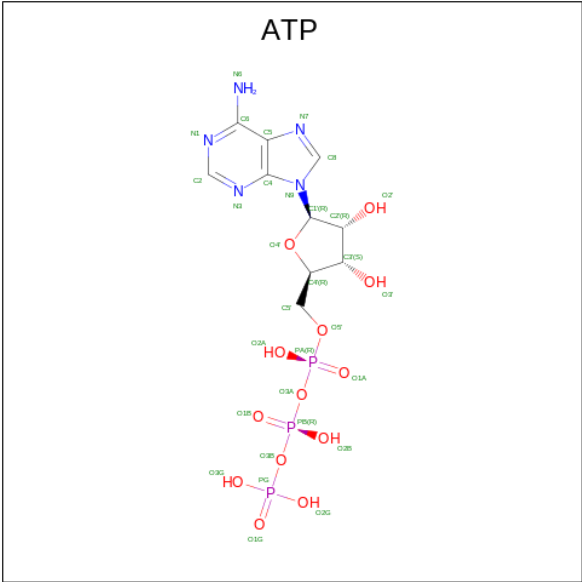
- Molecule 1 is a protein called Dynein heavy chain, cytoplasmic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3027	Total	C	N	O	S	0	0
			24362	15550	4153	4561	98		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1364	MET	-	initiating methionine	UNP P34036
A	1365	THR	-	expression tag	UNP P34036
A	1366	ARG	-	expression tag	UNP P34036
A	1367	HIS	-	expression tag	UNP P34036
A	1368	HIS	-	expression tag	UNP P34036
A	1369	HIS	-	expression tag	UNP P34036
A	1370	HIS	-	expression tag	UNP P34036
A	1371	HIS	-	expression tag	UNP P34036
A	1372	HIS	-	expression tag	UNP P34036
A	1373	GLY	-	expression tag	UNP P34036
A	1374	GLY	-	expression tag	UNP P34036
A	1375	GLY	-	expression tag	UNP P34036
A	1376	ASP	-	expression tag	UNP P34036
A	1377	TYR	-	expression tag	UNP P34036
A	1378	LYS	-	expression tag	UNP P34036
A	1379	ASP	-	expression tag	UNP P34036
A	1380	ASP	-	expression tag	UNP P34036
A	1381	ASP	-	expression tag	UNP P34036
A	1382	ASP	-	expression tag	UNP P34036
A	1383	LYS	-	expression tag	UNP P34036
A	1384	GLY	-	expression tag	UNP P34036
A	1385	GLY	-	expression tag	UNP P34036
A	1386	GLY	-	expression tag	UNP P34036
A	1387	LYS	-	expression tag	UNP P34036

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

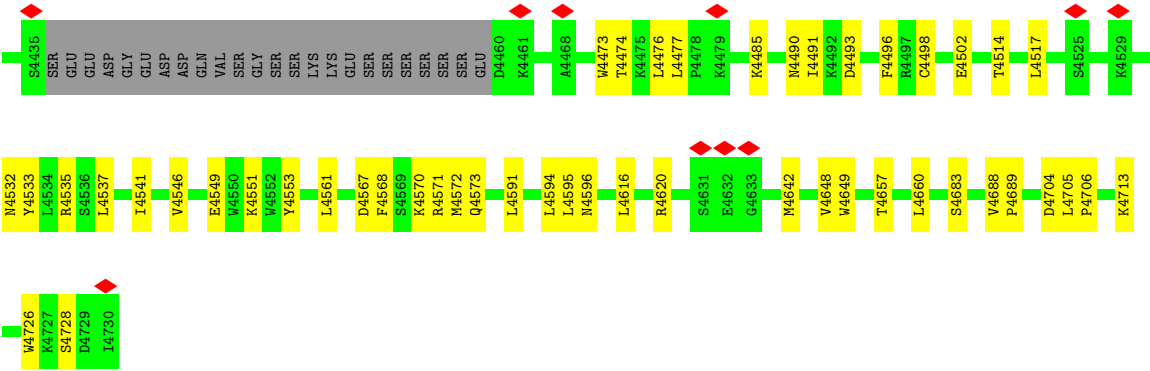
3 Residue-property plots

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: Dynein heavy chain, cytoplasmic



L3992	L4187	L3846	R3748	I3561	VAL	LYS	SER	ASN	R3006	P2876	K2663
G3995	K4188	D3847	D3753	A3562	GLU	LYS	THR	GLN	R3007	R2876	L2670
S4000	M4189	D3848	D3753	L3563	GLN	MET	ILE	LYS	P3008	R2884	G2674
I4001	I4190	D3849	P3758	L3564	GLU	THR	LYS	LYS	Q3009	L2887	
K4002	L4197	S3850	F3765	D3565	ASN	PRO	LYS	GLN	A3012	E2889	K2680
Q4007	E4201	V3851	T3766	N3566	ALA	ILE	HIS	MET	L3013		
K4018	H4205	L3852	D3768	L3567	ASN	GLU	ASP	GLN	L3014		
W4019	W4201	S3853	R3767	N3568	GLU	ARG	ASP	GLN	L3015		
L4020	W4217	L3855	D3768	S3569	LEU	ALA	ILE	GLN	G3016		
F4030	L4229	E3856	A3771	E3570	LYS	THR	SER	ALA	K3022		
L4033	W4232	T3857	S3779	R3571	LEU	THR	SER	ALA	S3023		
V4034	T4251	L3858	R3780	E3574	LYS	GLY	PRO	ALA	V3024		
Q4038	R4269	K3859	N3785	E3575	GLU	TYR	LYS	ILE	N3045		
D4051	Y4287	L3860	L3798	Q3576	ILE	GLU	PRO	GLN	D3053		
Q4052	G4291	T3862	L3798	Q3577	VAL	ASP	THR	LYS	R3056		
V4053	T4293	THR	L3798	Q3577	ALA	PRO	VAL	ALA	K3057		
W4062	T4293	THR	L3798	Q3577	ALA	PRO	VAL	ALA	L3058		
N4071	D4302	L3861	L3798	Q3577	ALA	PRO	VAL	ALA	L3059		
I4076	L4303	T3862	L3798	Q3577	ALA	PRO	VAL	ALA	L3059		
N4079	W4313	E3864	L3802	N3580	ALA	TYR	ALA	LEU	H2937		
I4083	S4318	L3865	P3807	Q3584	LEU	GLU	MET	GLN	I3069		
L4084	K4319	A3866	D3808	Q3584	GLU	THR	ALA	VAL	D3074		
M4086	L4324	L3867	T3809	V3588	LYS	VAL	VAL	GLN	E3075		
H4090	V4334	K3868	K3812	V3592	ILE	ASN	VAL	LEU	ASN		
L4095	R4346	V3869	R3813	A3595	ALA	ARG	CYS	ASP	S3076		
F4101	F4351	E3870	S3814	F3598	THR	SER	MET	ARG	S3077		
S4136	N4370	E3871	D3815	F3598	TYR	LYS	LEU	ASN	V3078		
Y4140	D4372	T3872	L3816	I3602	GLU	ALA	GLY	LYS	L3079		
S4143	P4371	F3873	L3816	D3606	GLU	GLY	GLY	GLU	E3080		
I4162	L4417	T3874	L3816	D3606	TYR	GLY	ILE	ILE	S3081		
E4169	L4418	V3875	L3816	D3606	THR	PRO	LYS	LYS	K2958		
I4175	L4418	M3876	L3816	D3606	ALA	LEU	LEU	VAL	D2959		
S4178	K4422	A3899	L3816	D3606	THR	VAL	TRP	GLN	L2968		
E4385	P4384	T3919	L3816	D3606	ILE	LYS	ALA	LYS	Y2971		
W4395	E4385	L3919	L3816	D3606	ARG	ALA	ASP	VAL	L3091		
L4417	L4418	L3923	L3816	D3606	GLU	THR	ILE	ALA	G3094		
L4418	L4418	D3932	L3816	D3606	GLU	GLN	LYS	ALA	L3099		
K4422	Q4431	K3933	L3816	D3606	ILE	TYR	ILE	LEU	F3100		
		K3934	L3816	D3606	LYS	THR	MET	GLU	E3101		
		I3947	L3816	D3606	THR	SER	GLU	LYS	G3102		
		L3947	L3816	D3606	GLU	GLU	PRO	ALA	E3103		
		R3954	L3816	D3606	SER	ILE	ASN	GLU	E3104		
		L3960	L3816	D3606	SER	ILE	PHE	PRO	F3105		
		K3964	L3816	D3606	LYS	ASP	LEU	ALA	T3106		
		L3965	L3816	D3606	VAL	ARG	THR	ILE	A3107		
		I3974	L3816	D3606	LYS	ILE	SER	GLU	L3108		
		T3979	L3816	D3606	ASN	PRO	ILE	LYS	M3109		
		S3980	L3816	D3606	LYS	THR	ILE	ALA	H3110		
		N3981	L3816	D3606	VAL	LEU	ASN	GLN	A3111		
		E3987	L3816	D3606	V3557	ARG	TYR	GLU	C3112		
		W3988	L3816	D3606	D3558	GLU	ASP	ALA	G3112		
			L3816	D3606	R3559	GLU	GLU	VAL	K3113		
			L3816	D3606	S3560	ASP	THR	VAL	E3114		
			L3816	D3606		GLU	THR	VAL	T3115		
			L3816	D3606		THR	THR	VAL	A3116		
			L3816	D3606		GLU	THR	VAL	Q3117		
			L3816	D3606		GLU	THR	VAL			



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	910656	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF parameters were estimated using Patch CTF estimation in cryoSPARC and further refined by global and local CTF refinement.	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.606	Depositor
Minimum map value	-1.550	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	261.9, 261.9, 261.9	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87299997, 0.87299997, 0.87299997	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, ATP

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	0.11	0/24882	0.27	0/33708

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	24362	0	24425	307	0
2	A	31	0	12	0	0
3	A	1	0	0	0	0
All	All	24394	0	24437	307	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 6.

The worst 5 of 307 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:2642:ALA:HB3	1:A:2884:ARG:HG3	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3919:ILE:HD11	1:A:3954:ARG:HD2	1.67	0.76
1:A:3053:ASP:OD1	1:A:3056:ARG:NH2	2.20	0.74
1:A:3271:ILE:HG13	1:A:3592:VAL:HG11	1.69	0.74
1:A:3238:ILE:HD11	1:A:3617:TRP:HZ2	1.54	0.73

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	3017/3367 (90%)	2964 (98%)	53 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2727/3028 (90%)	2727 (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 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2907	HIS
1	A	4282	GLN
1	A	3214	ASN
1	A	4638	ASN
1	A	4099	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	ATP	A	5001	3	29,33,33	0.65	0	44,52,52	0.55	0

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	ATP	A	5001	3	-	2/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

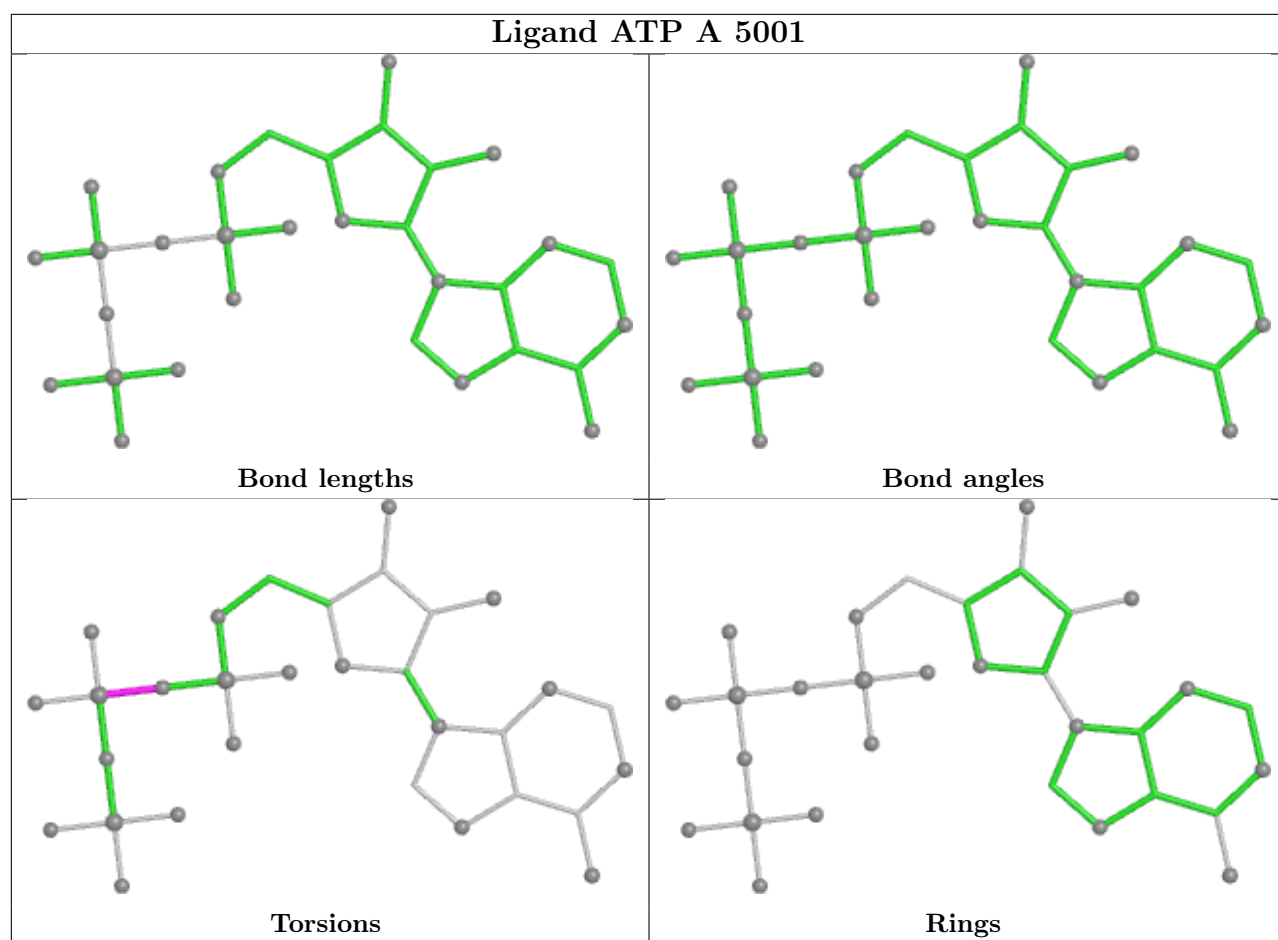
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5001	ATP	PA-O3A-PB-O1B
2	A	5001	ATP	PA-O3A-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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.

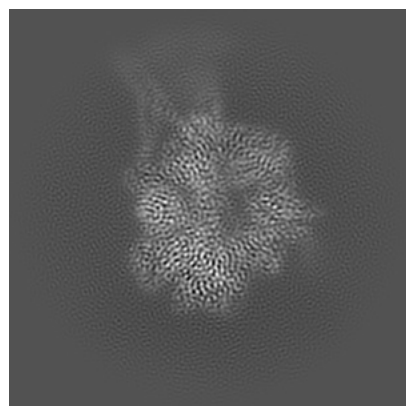
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-81338. These allow visual inspection of the internal detail of the map and identification of artifacts.

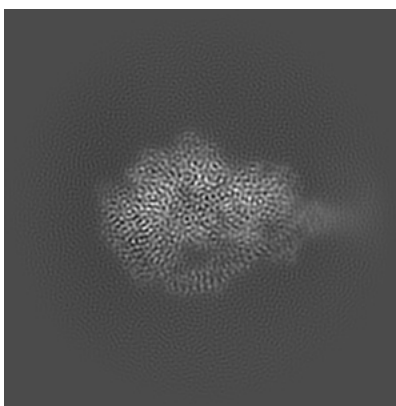
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

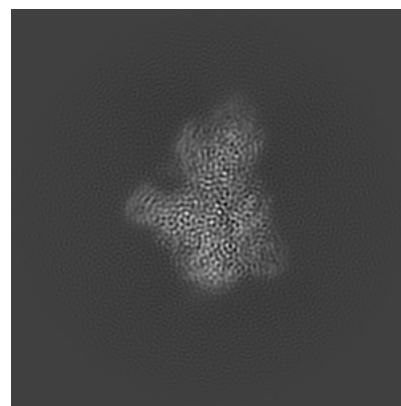
6.1.1 Primary map



X

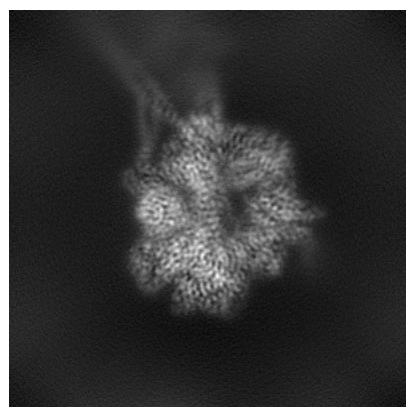


Y

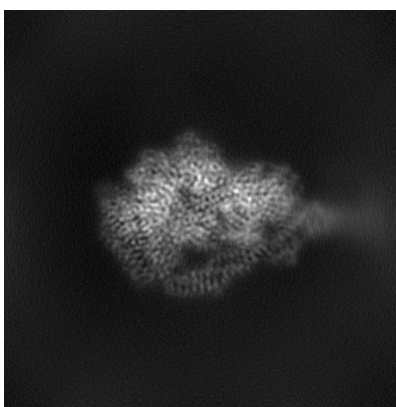


Z

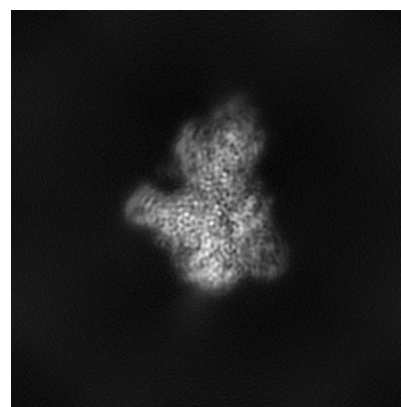
6.1.2 Raw map



X



Y

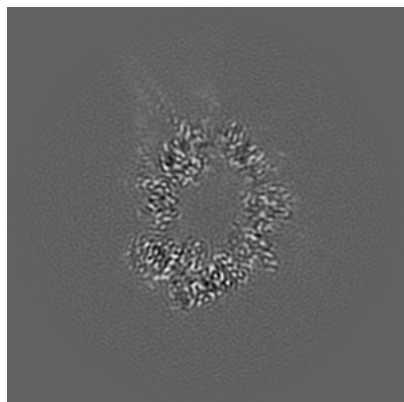


Z

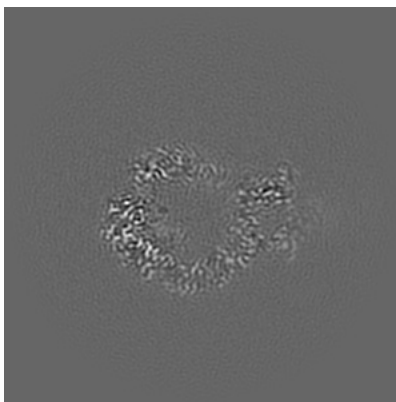
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

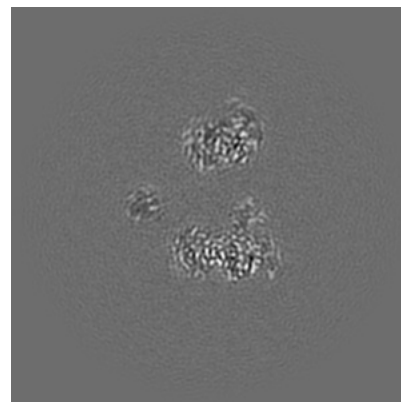
6.2.1 Primary map



X Index: 150

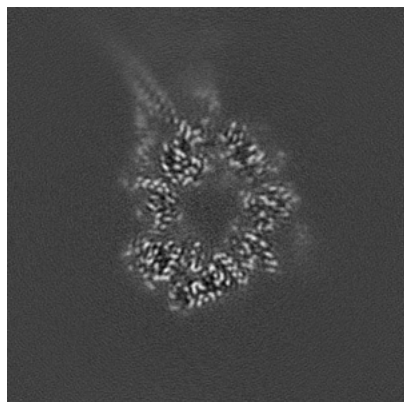


Y Index: 150

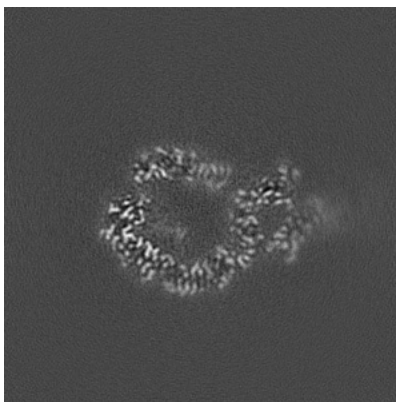


Z Index: 150

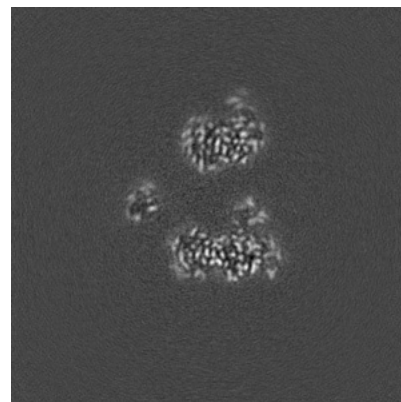
6.2.2 Raw map



X Index: 150



Y Index: 150

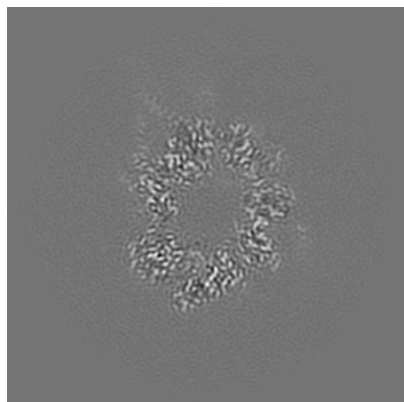


Z Index: 150

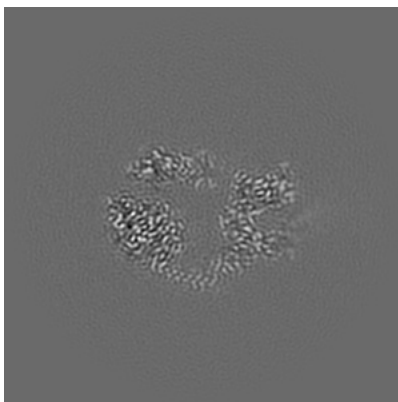
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

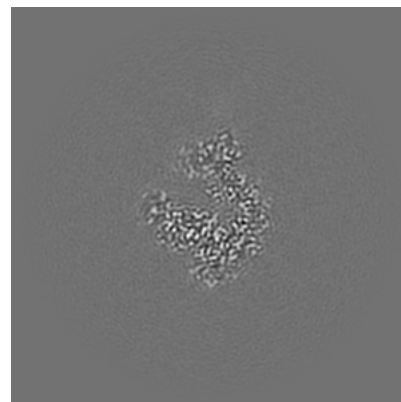
6.3.1 Primary map



X Index: 153

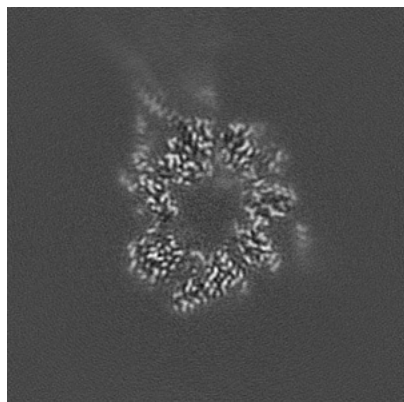


Y Index: 142

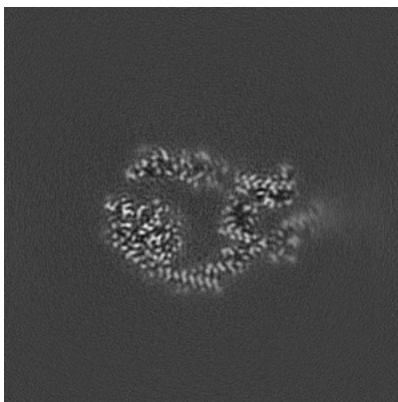


Z Index: 115

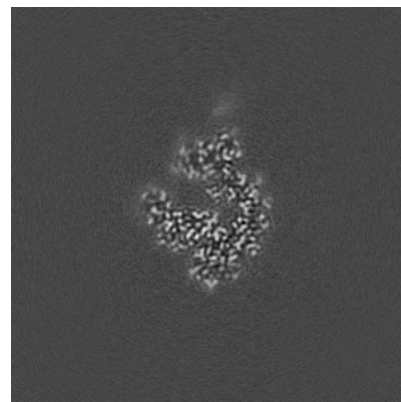
6.3.2 Raw map



X Index: 153



Y Index: 144

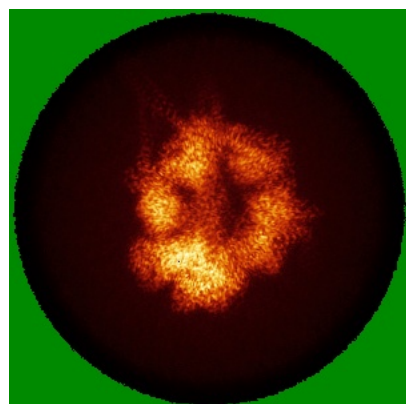


Z Index: 115

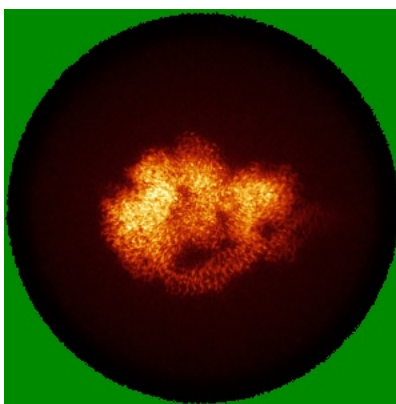
The images above show the largest variance slices of the map in three orthogonal directions.

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

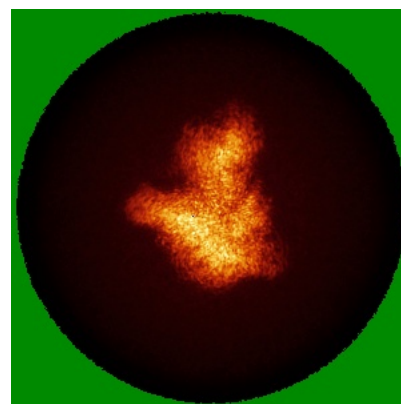
6.4.1 Primary map



X

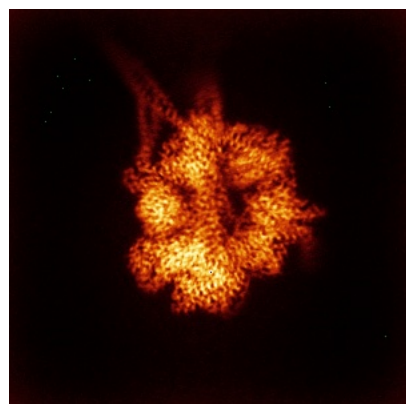


Y

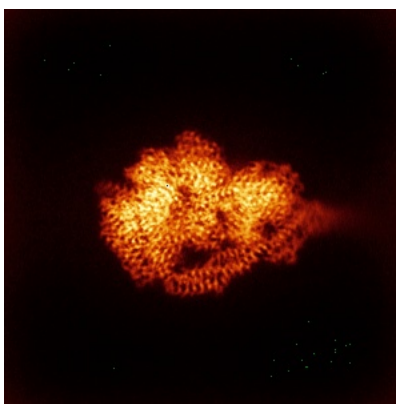


Z

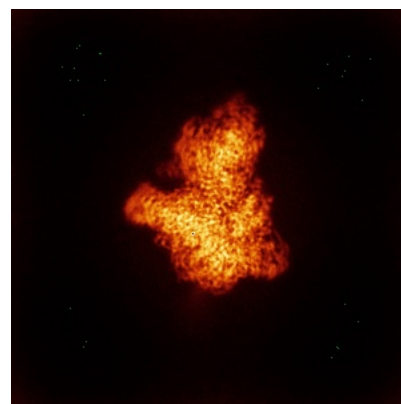
6.4.2 Raw map



X



Y

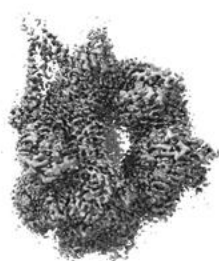


Z

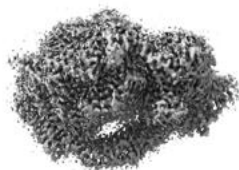
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.14. 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



X



Y



Z

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.

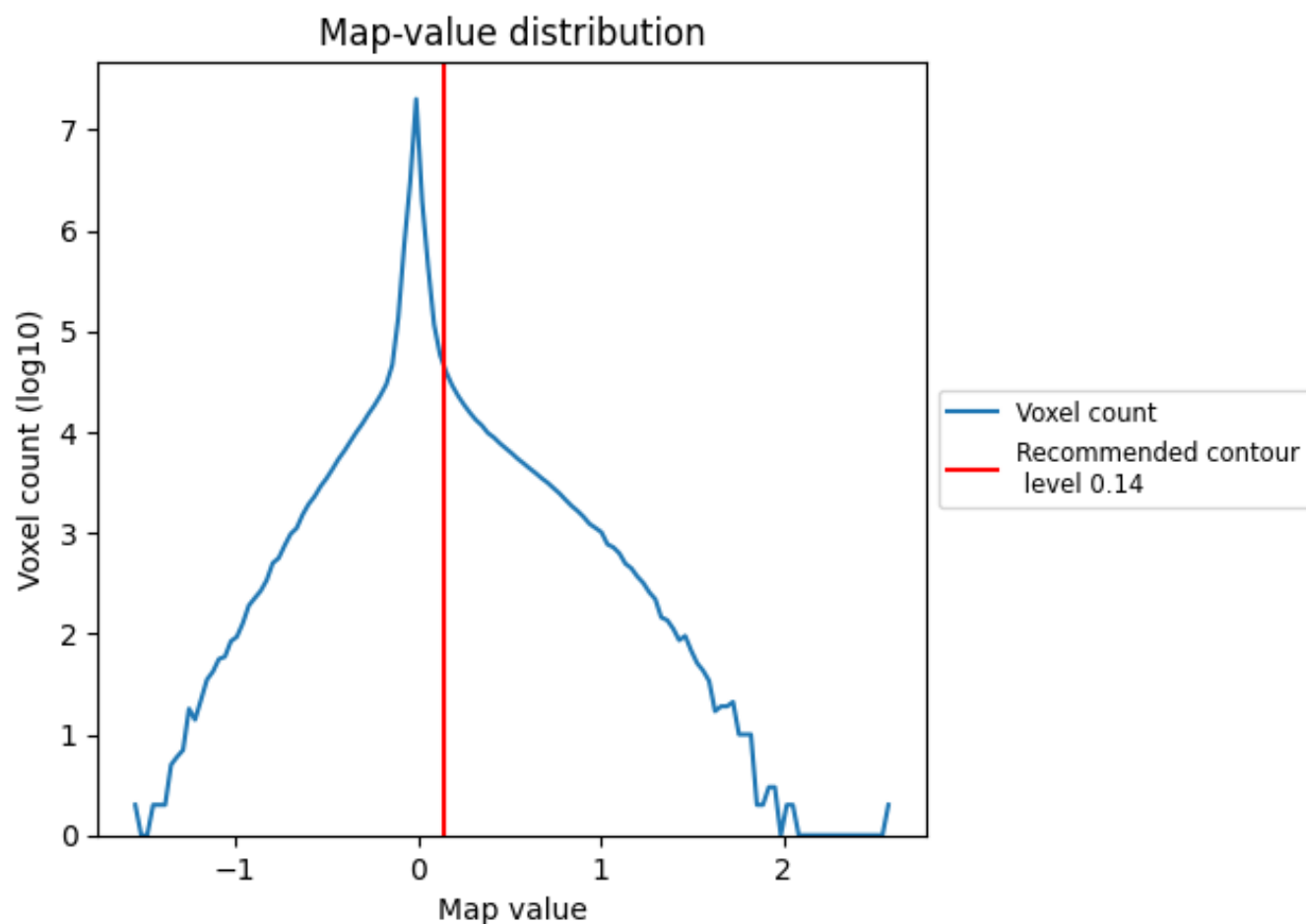
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

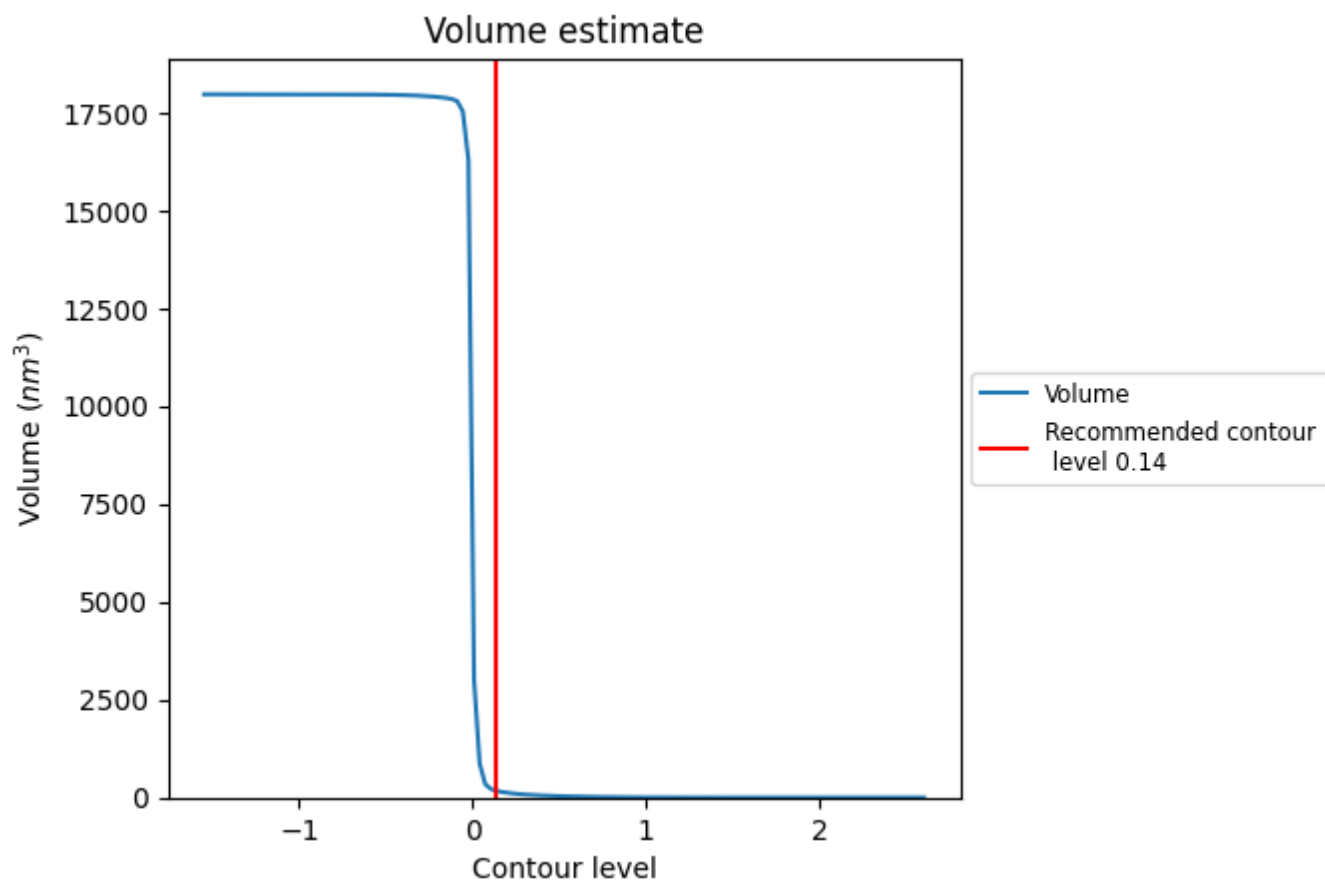
This section contains the results of statistical analysis of the map.

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.

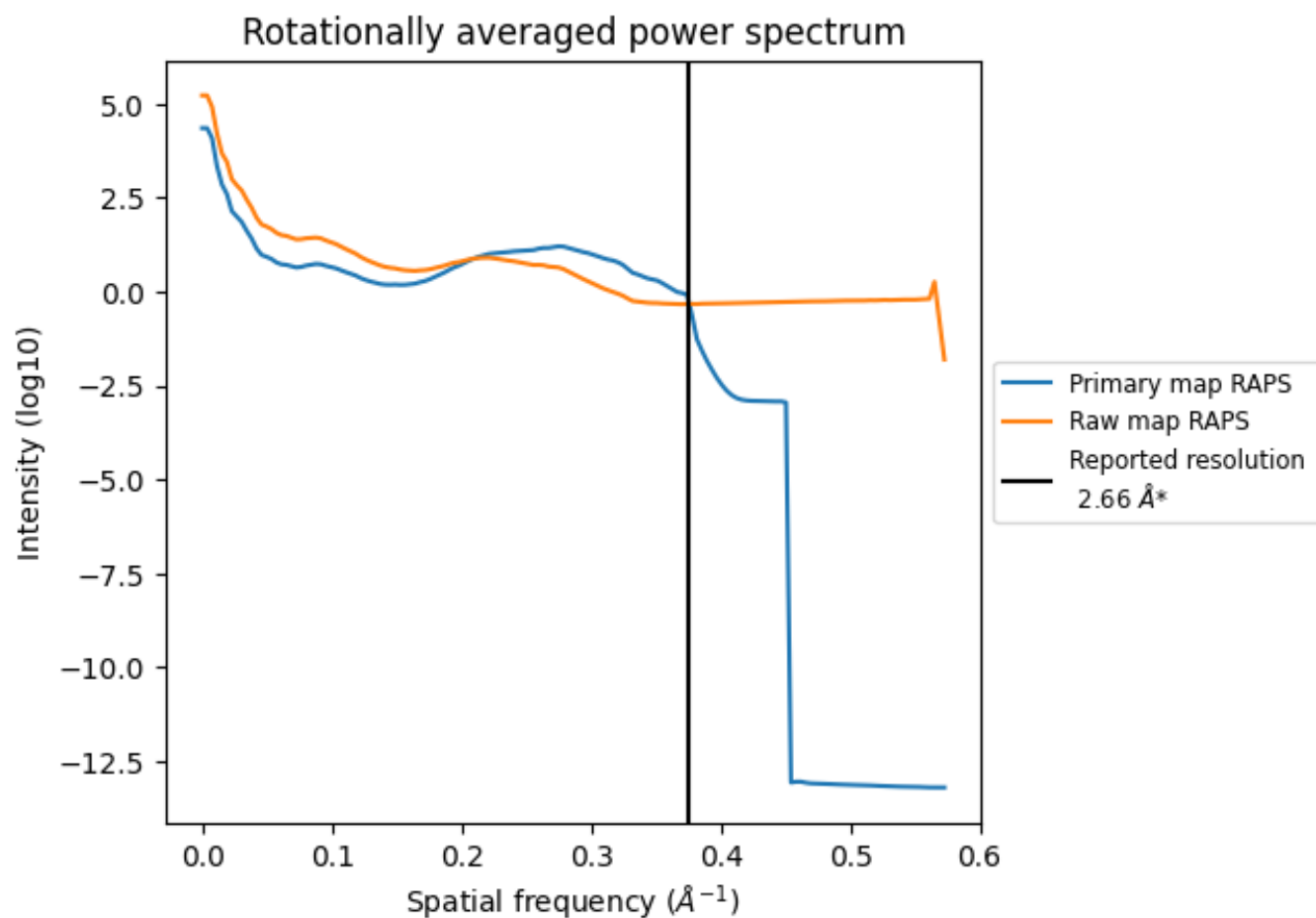
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 169 nm³; this corresponds to an approximate mass of 153 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 ⓘ

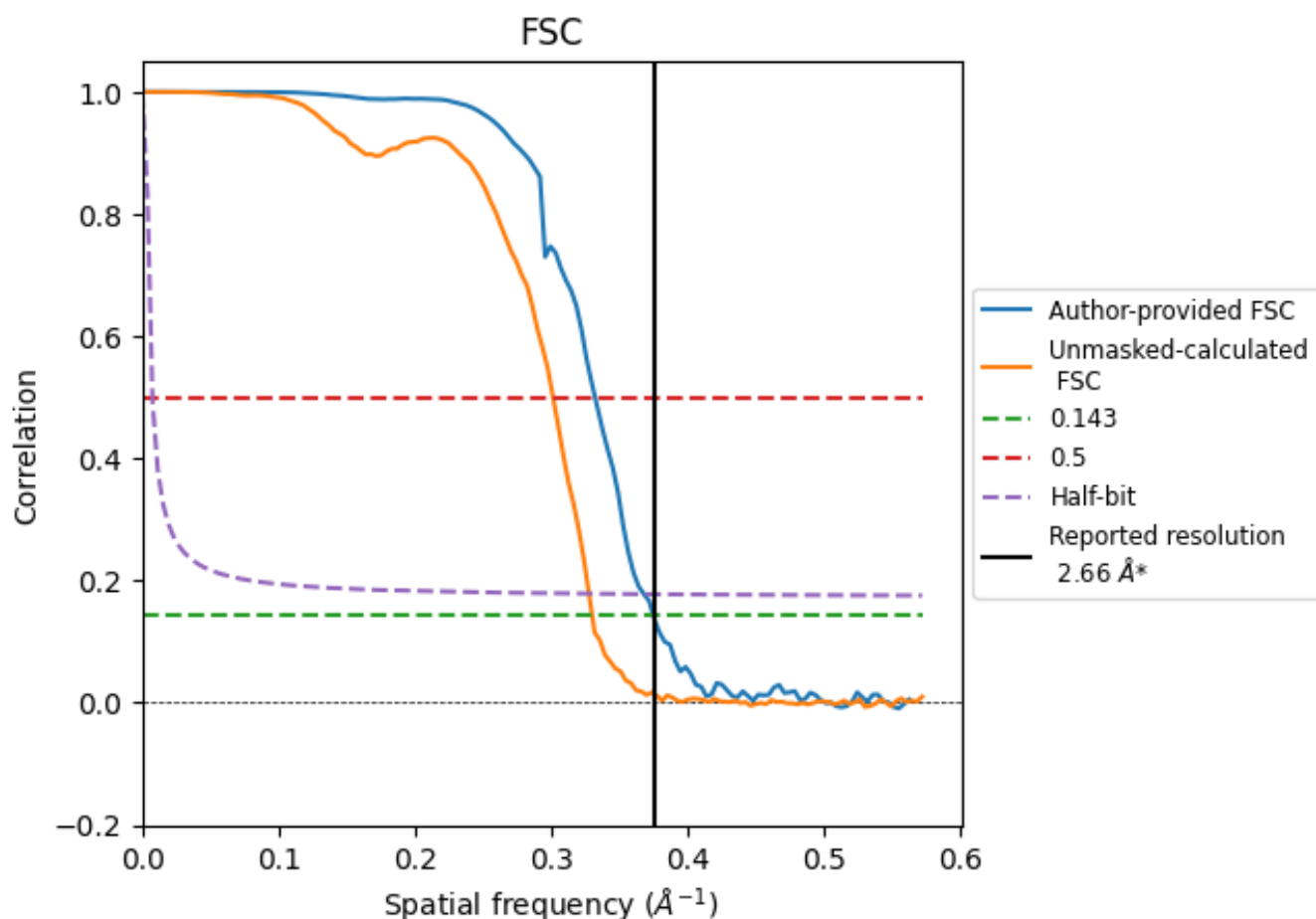


*Reported resolution corresponds to spatial frequency of 0.376 Å⁻¹

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 $0.376 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

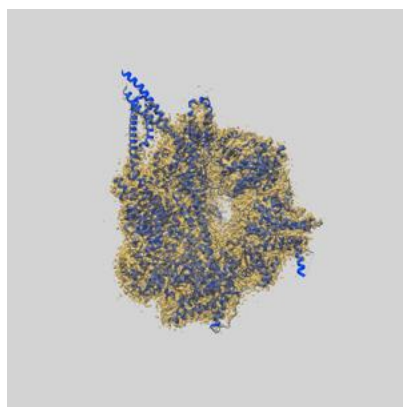
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.66	-	-
Author-provided FSC curve	2.67	3.01	2.71
Unmasked-calculated*	3.03	3.31	3.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.03 differs from the reported value 2.66 by more than 10 %

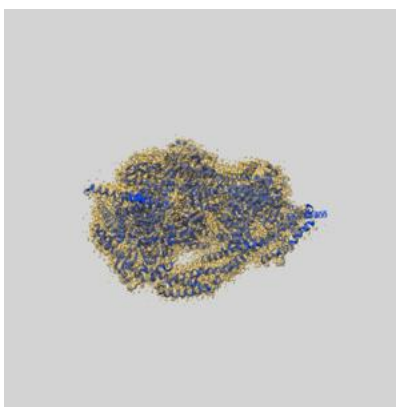
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-81338 and PDB model 27QB. Per-residue inclusion information can be found in section [3](#) on page [5](#).

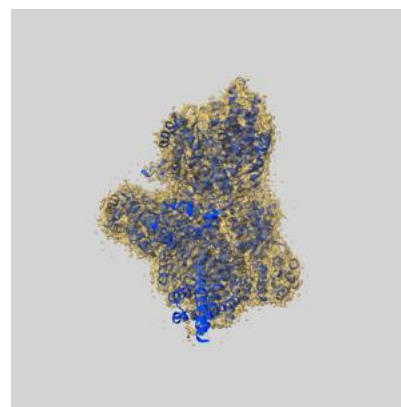
9.1 Map-model overlay [i](#)



X



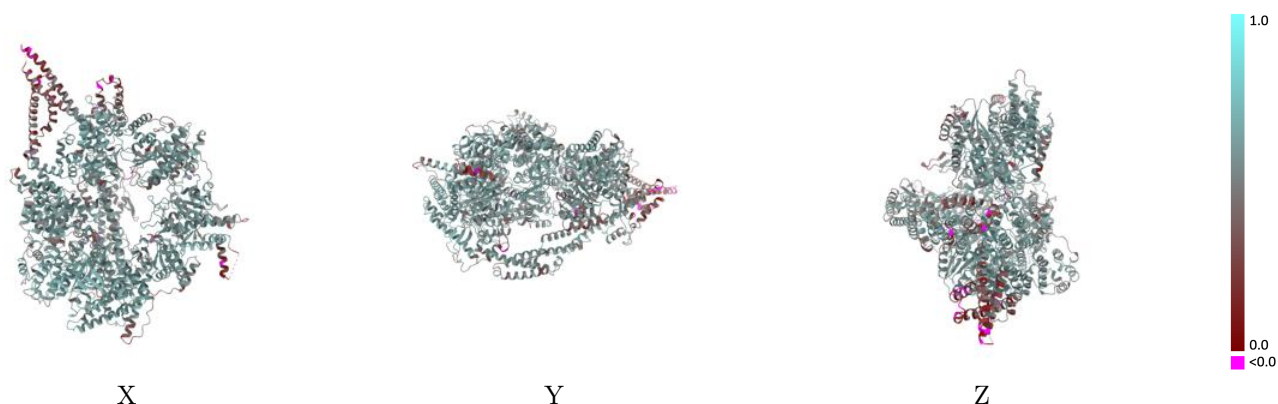
Y



Z

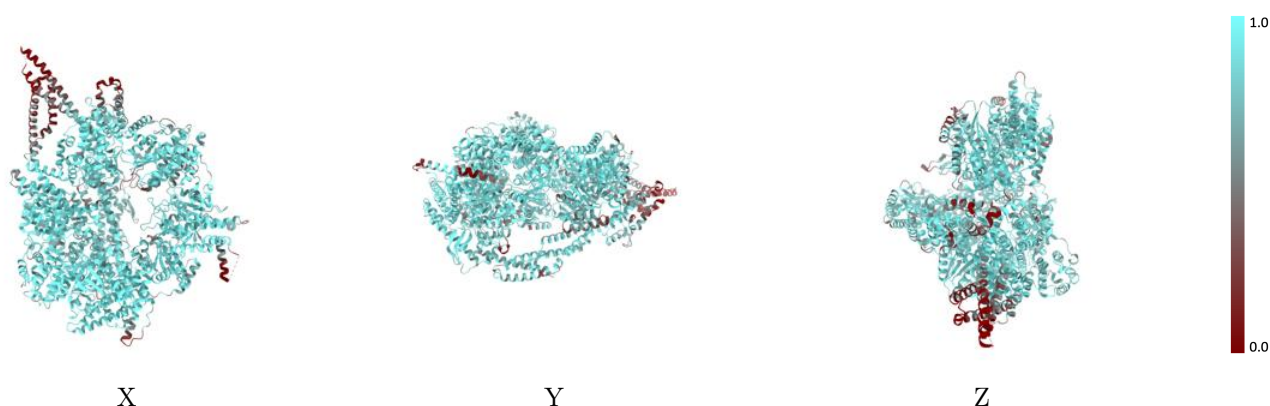
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



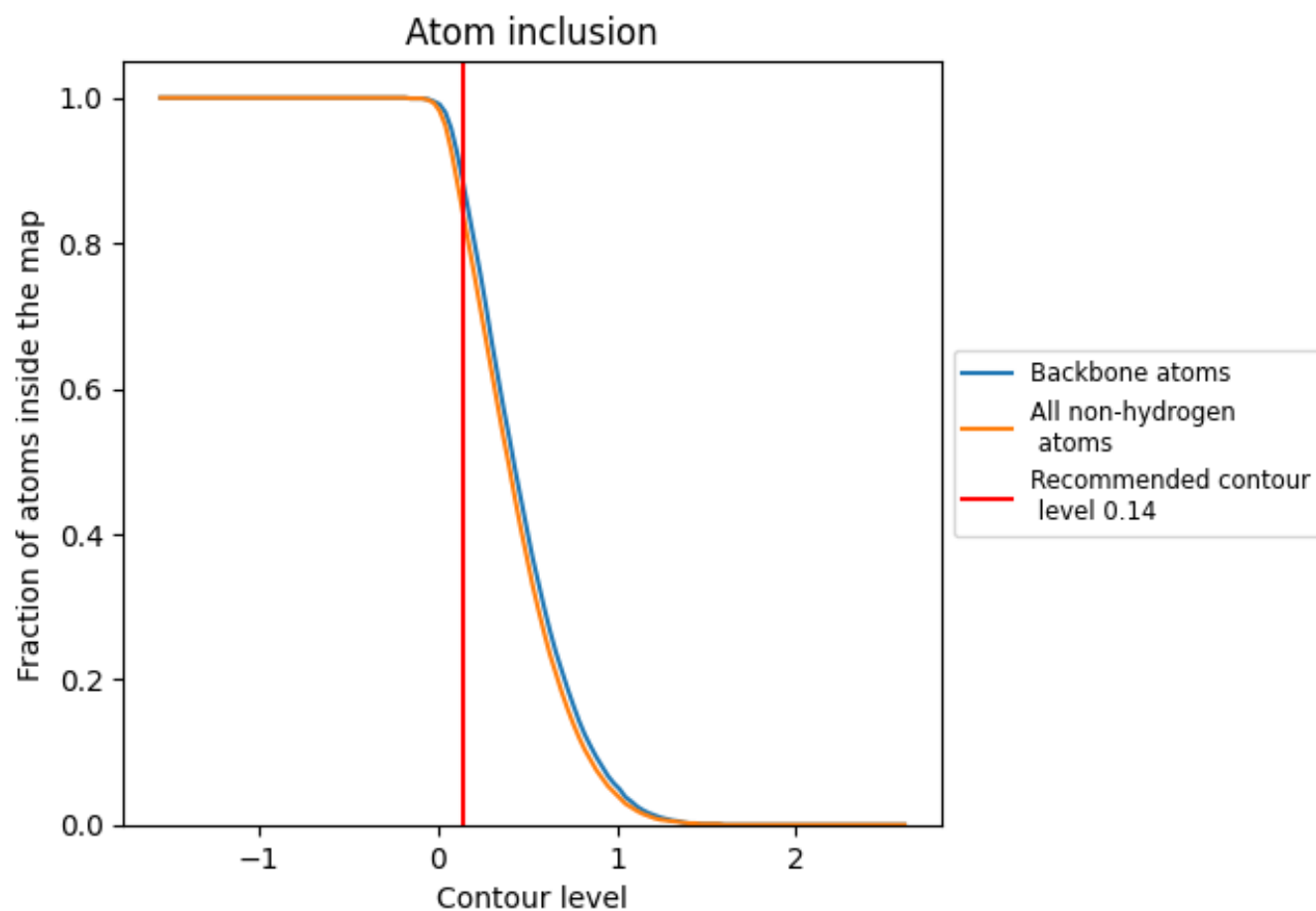
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8410	0.5530
A	0.8410	0.5530

