



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 10:34 AM UTC

PDB ID : 9BMY / pdb_00009bmy
EMDB ID : EMD-44715
Title : State-1 of motor domain from full-length human dynein-1 in apo condition
Authors : Chai, P.; Zhang, K.
Deposited on : 2024-05-02
Resolution : 2.86 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

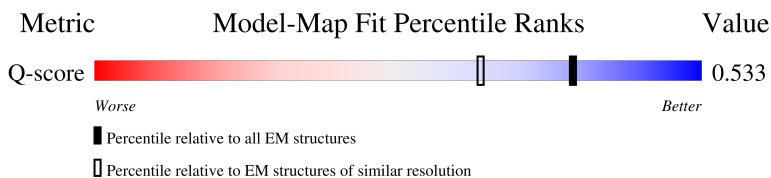
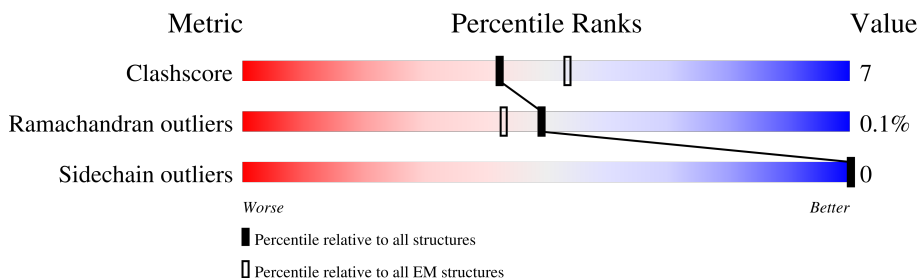
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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	12017 (2.36 - 3.36)

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	4646	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 23707 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 Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2937	23593	15028	4070	4378	117	0	0

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	27	10	5	10	2	0
2	A	1	27	10	5	10	2	0
2	A	1	27	10	5	10	2	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



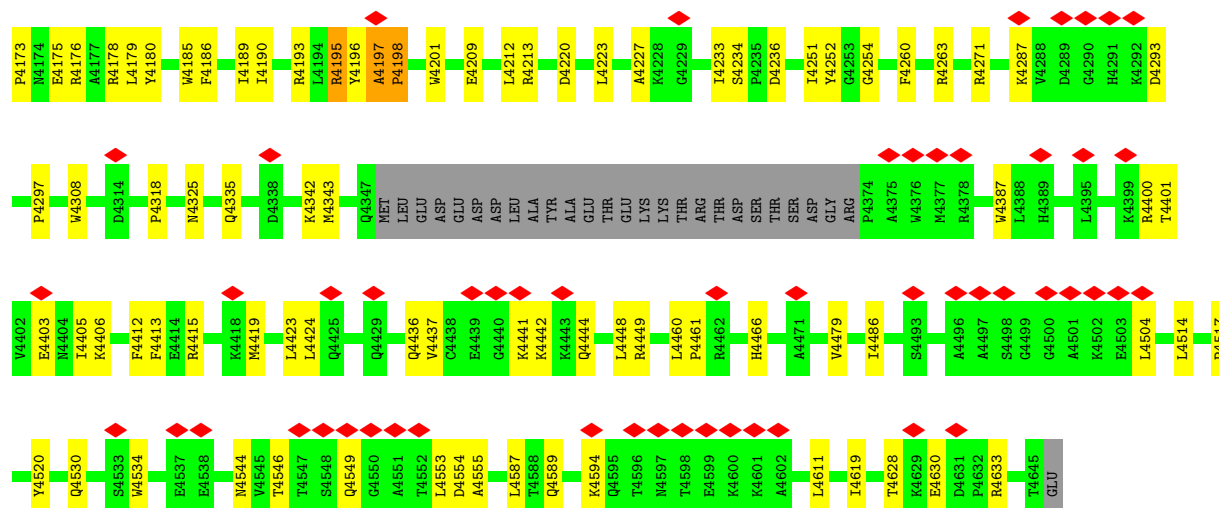
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Mg	0
			2	2	



F3979	H3880	L3692	F3520	ILE	TYR	VAL	SER	R3167	M3030	D2851	R2694	E2513	GLU
A3980	K3891	C3693	M3524	ARG	ASN	LYS	GLN	Q3038	Q3038	A2854	D2697	N2531	ASP
Q3985	T3895	S3694	D3546	LEU	TYR	ALA	ILE	M3043	M3043	H2857	Q2698	D2536	ALA
R3989	T3898	V3703	I3547	GLU	ILE	GLU	GLN	L3044	L3044	E2864	C2712	Y2537	GLN
R3997	E3898	V3716	L3553	SER	ASN	SER	GLN	D3045	D3045	M2867	R2720	E2538	ARG
L4001	D3902	L3731	D3557	ILE	ARG	ILE	LEU	E3049	E3049	S2868	R2729	W2548	ARG
L4002	F3908	L3740	E3558	ALA	ALA	LEU	GLN	I3059	I3059	R2869	W2730	V2557	LYS
V4009	L3909	R3741	W3562	TYR	LEU	GLY	GLN	F3066	F3066	T2882	V2731	V2562	GLU
L4013	R3910	L3742	R3743	LYS	CYS	GLU	VAL	R3206	R3206	P2883	P2732	A2563	ASP
M4021	N3912	Q3744	Q3745	PRO	PRO	SER	ILE	T3211	T3211	L2905	Y2738	A2564	GLY
E4034	E3913	L3750	L3750	VAL	VAL	THR	ASP	V3212	V3212	D2906	F2751	P2565	GLU
P4037	I3914	R3754	R3582	TRP	TRP	ASP	LYS	D3213	D3213	F2912	M2755	V2566	ALA
M4043	V3915	K3757	F3583	ALA	ALA	GLN	GLN	E3216	E3216	M2913	L2756	V2567	ALA
A4051	L3916	G3758	R3584	ILE	ILE	ALA	VAL	E3217	E3217	E2914	R2757	D2573	ALA
I4071	S3917	R3759	R3585	ARG	ARG	LEU	LYS	L3218	L3218	D2917	R2763	R2576	ALA
A4087	A3918	I3760	L3588	ASN	ASN	ILE	ASP	R3219	R3219	R2921	M2773	L2581	ALA
V4088	G3919	I3761	T3597	TYR	TYR	ILE	LEU	R3220	R3220	T3110	E2774	Y2582	ALA
R4092	S3920	D3762	I3600	ALA	ALA	MET	ASP	D3221	D3221	T2925	V2775	P2590	ALA
L4096	T3921	P3763	M3601	MET	MET	GLU	LYS	L3222	L3222	Q2930	F2776	L2591	ALA
K4097	P3922	D3764	K3608	LEU	LEU	ASN	GLU	R3223	R3223	L2933	P2784	V2592	ALA
N4098	R3923	T3765	K3611	LYS	LYS	PHE	PRO	T3224	T3224	T2961	T2788	L2443	ALA
H4100	I3924	I3766	R3617	ARG	ARG	ILE	ALA	K3225	K3225	V2963	Q2789	E2444	ALA
G4104	Q3925	I3767	D3617	VAL	VAL	PRO	VAL	S3226	S3226	D2973	P2790	H2445	ALA
W4105	G3926	K3774	E3624	GLU	GLU	THR	ILE	Q3227	Q3227	E2974	H2791	H2446	ALA
L4106	R3927	R3775	L3634	LEU	LEU	ILE	ALA	E3228	E3228	D2975	L2612	L2449	ALA
M4107	L3928	A3777	V3638	ASN	ASN	GLU	GLN	L3229	L3229	V2979	W2802	T2450	ALA
L4116	S3939	R3782	P3643	GLU	GLU	ILE	LYS	E3230	E3230	M2994	R2803	R2451	ALA
Q4117	F3944	I3789	R3651	ASP	ASP	SER	SER	V3231	V3231	P3134	R2804	L2452	ALA
P4118	K3945	V3790	E3652	ALA	ALA	ILE	GLN	K3232	K3232	R2807	L2630	C2454	ALA
T4127	D3946	I3821	R3655	LYS	LYS	GLU	VAL	N3233	N3233	R2811	N2621	S2457	ALA
M4128	V3950	L3829	V3660	ASP	ASP	LEU	VAL	A3234	A3234	W2825	E2629	H2461	ALA
R4143	Q3952	I3835	L3661	ASN	ASN	GLN	GLU	A3235	A3235	D2835	L2631	Q2471	ALA
P4150	A3953	Y3836	D3666	ALA	ALA	LYS	VAL	A3236	A3236	D2840	L2632	F2479	ALA
T4160	D3954	V3839	Q3667	ASN	ASN	TYR	VAL	H3139	H3139	E2841	K2633	E2487	ALA
T4160	E3955	D3862	I3669	GLU	GLU	MET	PRO	R3140	R3140	E2841	Y2638	R2488	ALA
R4168	Q3956	L3863	T3681	VAL	VAL	SER	ASN	E3141	E3141	R2844	N2667	D2505	ALA
S4172	P3966	V3866	D3691	GLN	GLN	ASP	ALA	A3157	A3157	T2846	L2688	D2510	ALA
L3973	L3973	R3870		GLN	GLN	VAL	ALA	R3160	R3160	L3020	E2688	H2689	ALA
H3974	H3974			ALA	ALA	GLU	GLU	K3163	K3163				ALA
S3975	S3975			LYS	LYS	GLU	GLU	R3164	R3164				ALA
E3976	E3976			LYS	LYS	VAL	VAL						ALA
E3977	E3977			VAL	VAL								ALA
T3978	T3978			MET	MET	SER	ALA						ALA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136324	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.445	Depositor
Minimum map value	-1.410	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	444.4032, 444.4032, 444.4032	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1573, 1.1573, 1.1573	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, ADP, 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	0.18	0/24093	0.32	0/32651

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	4195	ARG	Sidechain

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	23593	0	23657	315	0
2	A	81	0	36	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	3	0
4	A	2	0	0	0	0
All	All	23707	0	23705	317	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 7.

The worst 5 of 317 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:2221:MET:HG2	1:A:2343:PHE:HB2	1.55	0.89
1:A:2629:GLU:OE2	1:A:2633:LYS:NZ	2.12	0.83
1:A:4271:ARG:HD3	1:A:4633:ARG:HH12	1.43	0.82
1:A:1490:TRP:HH2	1:A:1537:TRP:HD1	1.29	0.79
1:A:4088:VAL:HG11	1:A:4116:LEU:HD21	1.67	0.76

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	2929/4646 (63%)	2882 (98%)	45 (2%)	2 (0%)	48 68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4197	ALA
1	A	4198	PRO

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	2605/4125 (63%)	2605 (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 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3602	ASN
1	A	4054	HIS
1	A	3636	GLN
1	A	3877	HIS
1	A	4425	GLN

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, 2 are monoatomic - leaving 4 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	ADP	A	4704	-	28,29,29	0.47	0	43,45,45	0.47	0
3	ATP	A	4702	4	32,33,33	0.56	0	48,52,52	0.58	0
2	ADP	A	4703	-	28,29,29	0.47	0	43,45,45	0.46	0
2	ADP	A	4701	4	28,29,29	0.45	0	43,45,45	0.49	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	ADP	A	4704	-	-	2/16/32/32	0/3/3/3
3	ATP	A	4702	4	-	2/22/38/38	0/3/3/3
2	ADP	A	4703	-	-	1/16/32/32	0/3/3/3
2	ADP	A	4701	4	-	0/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

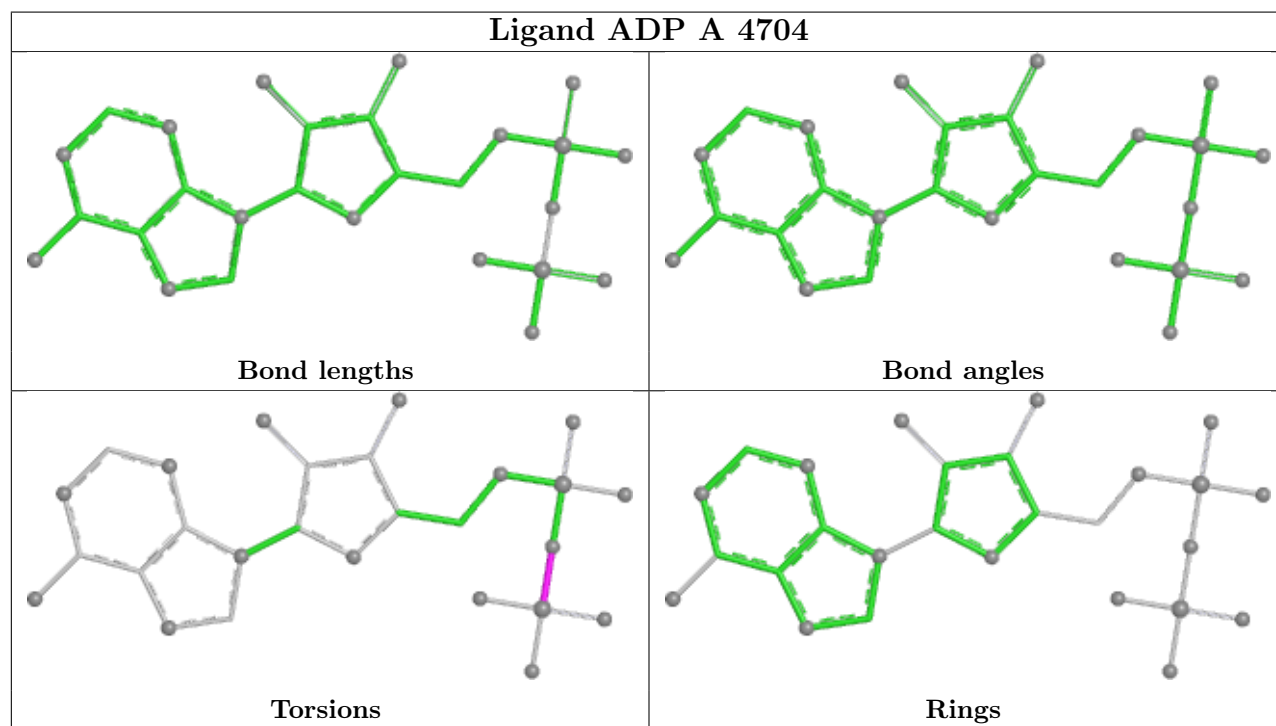
Mol	Chain	Res	Type	Atoms
2	A	4704	ADP	PA-O3A-PB-O2B
3	A	4702	ATP	O4'-C4'-C5'-O5'
2	A	4704	ADP	PA-O3A-PB-O1B
3	A	4702	ATP	C3'-C4'-C5'-O5'
2	A	4703	ADP	PA-O3A-PB-O3B

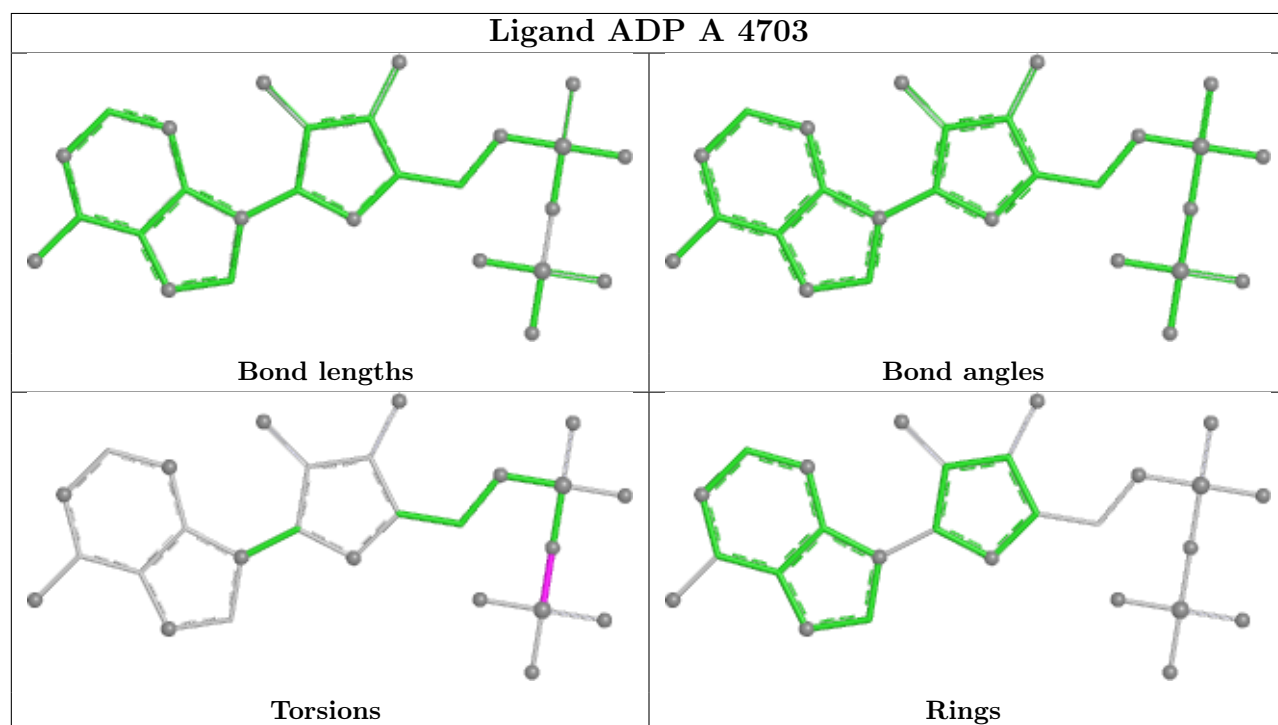
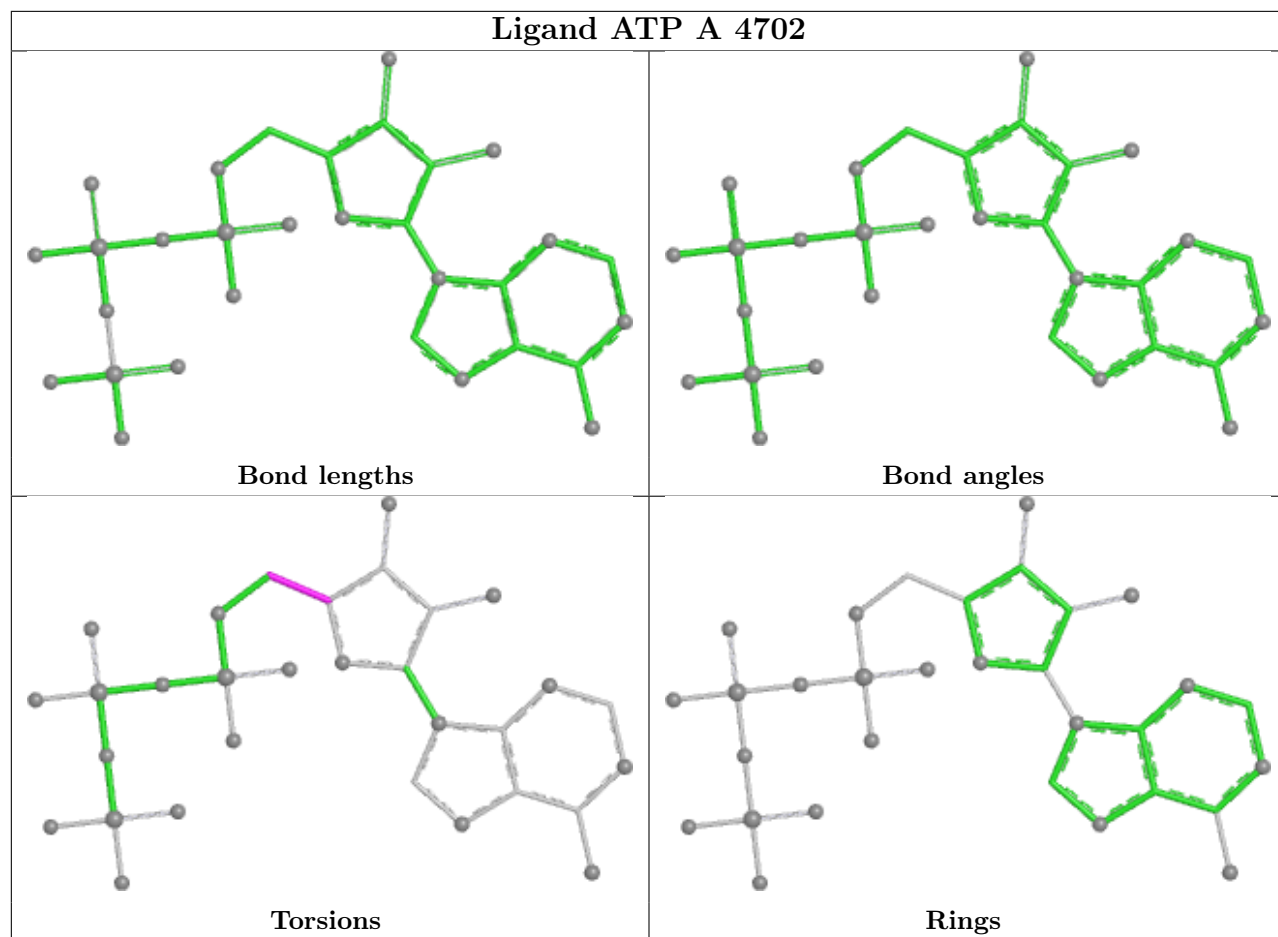
There are no ring outliers.

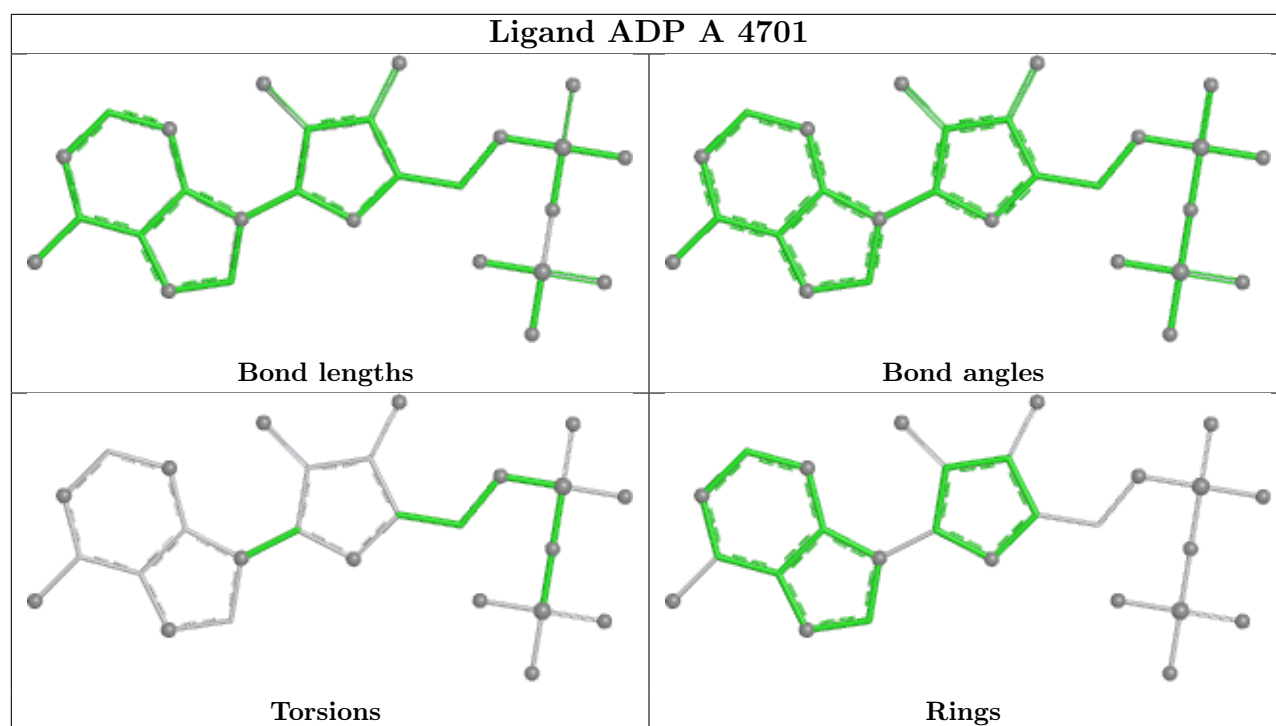
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	4702	ATP	3	0
2	A	4701	ADP	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.

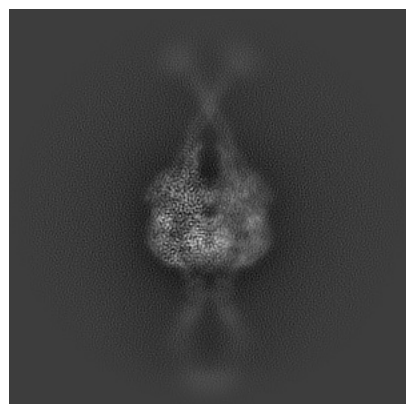
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44715. These allow visual inspection of the internal detail of the map and identification of artifacts.

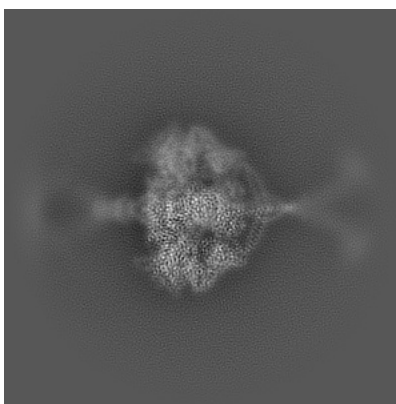
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

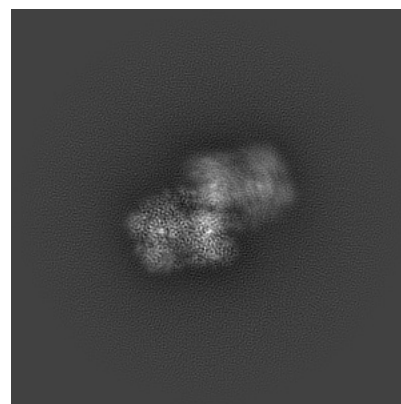
6.1.1 Primary map



X

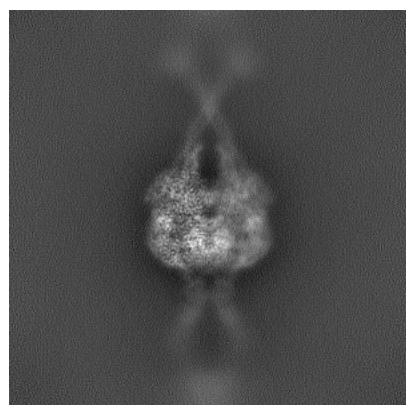


Y

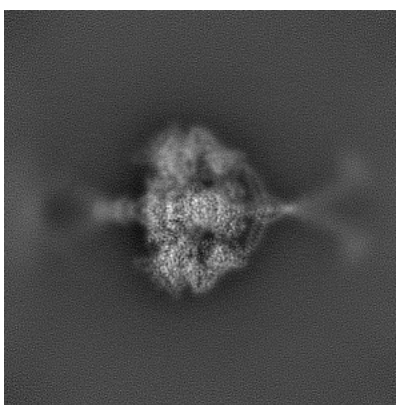


Z

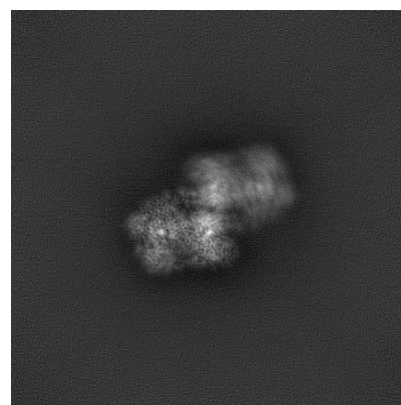
6.1.2 Raw map



X



Y

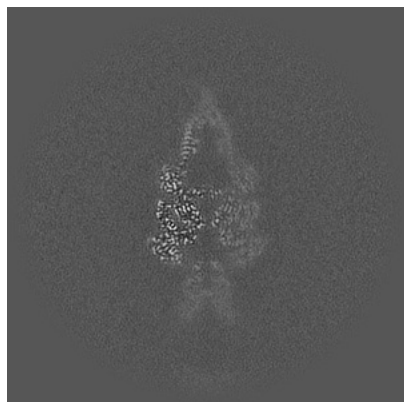


Z

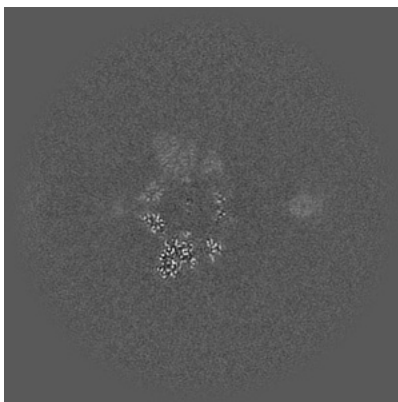
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192

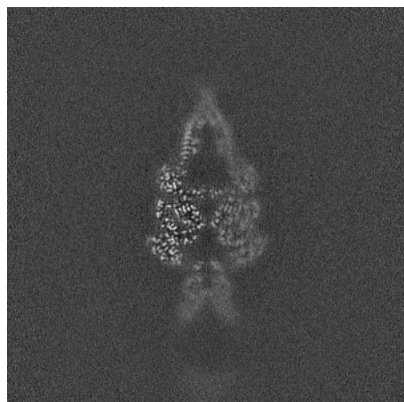


Y Index: 192

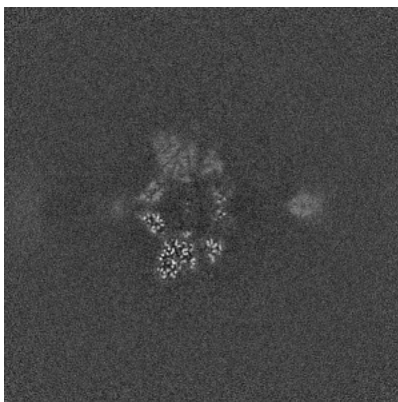


Z Index: 192

6.2.2 Raw map



X Index: 192



Y Index: 192

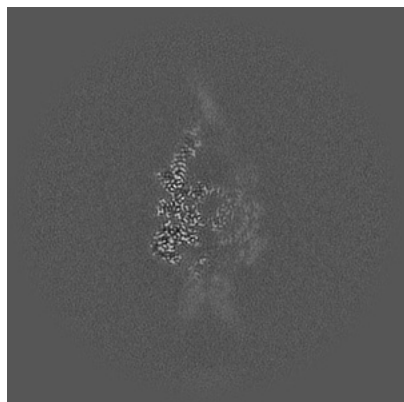


Z Index: 192

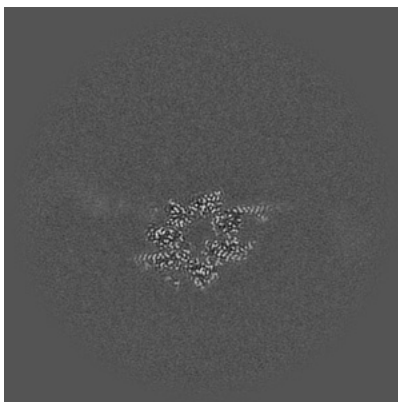
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

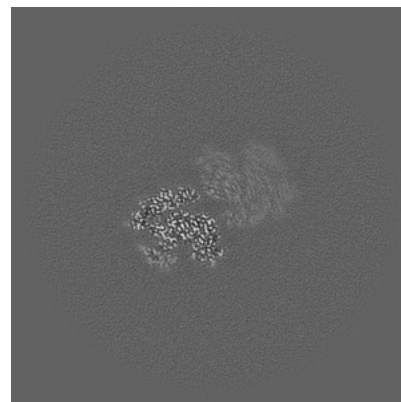
6.3.1 Primary map



X Index: 187

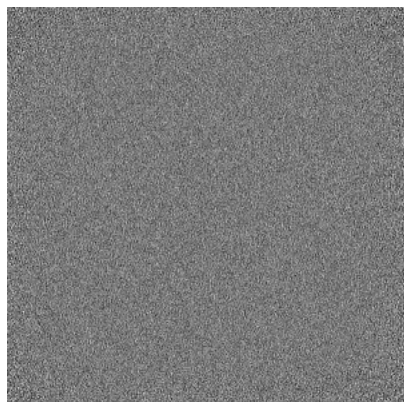


Y Index: 169

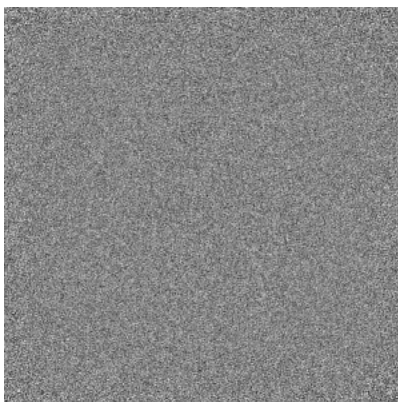


Z Index: 161

6.3.2 Raw map



X Index: 0



Y Index: 0

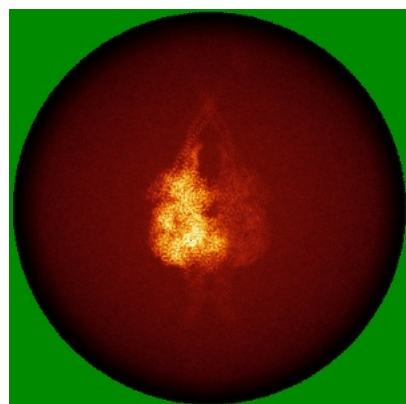


Z Index: 161

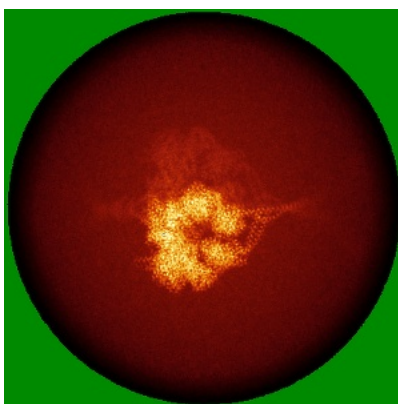
The images above show the largest variance slices of the map in three orthogonal directions.

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

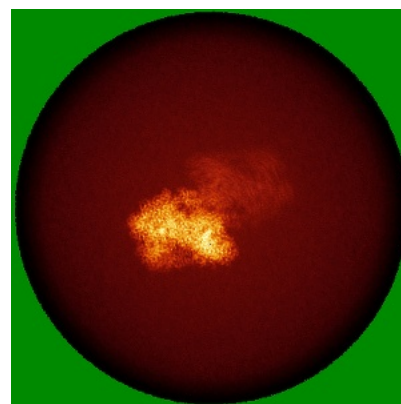
6.4.1 Primary map



X

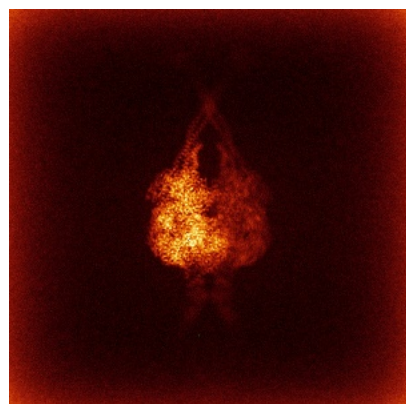


Y

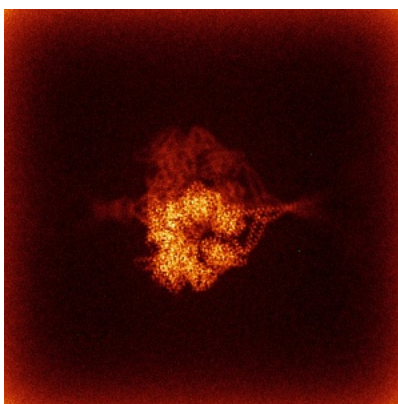


Z

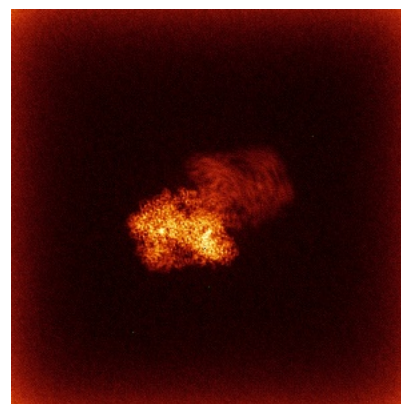
6.4.2 Raw map



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 0.35. 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.

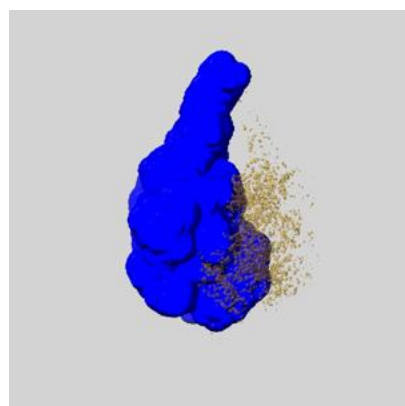
6.6 Mask visualisation [i](#)

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

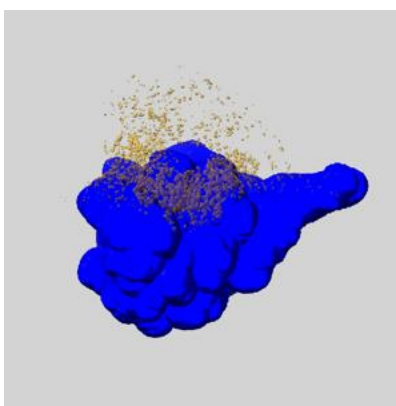
A mask typically either:

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

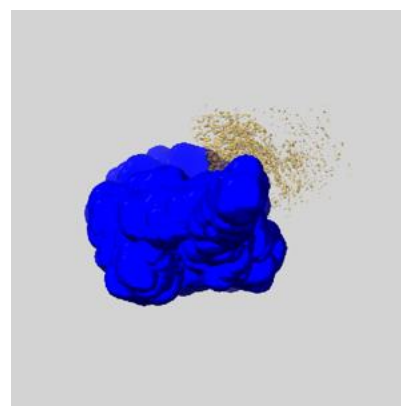
6.6.1 emd_44715_msk_1.map [i](#)



X



Y

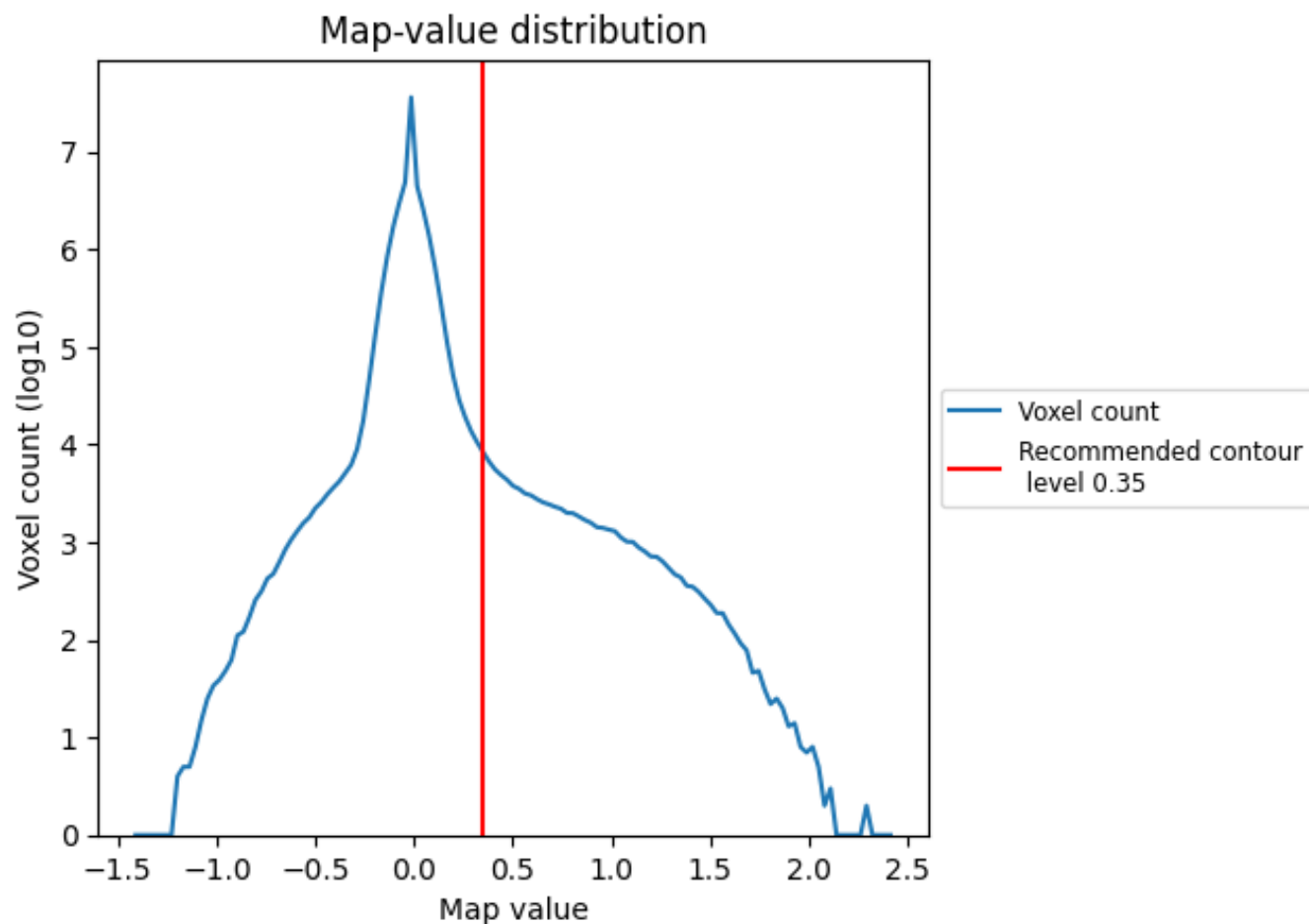


Z

7 Map analysis [i](#)

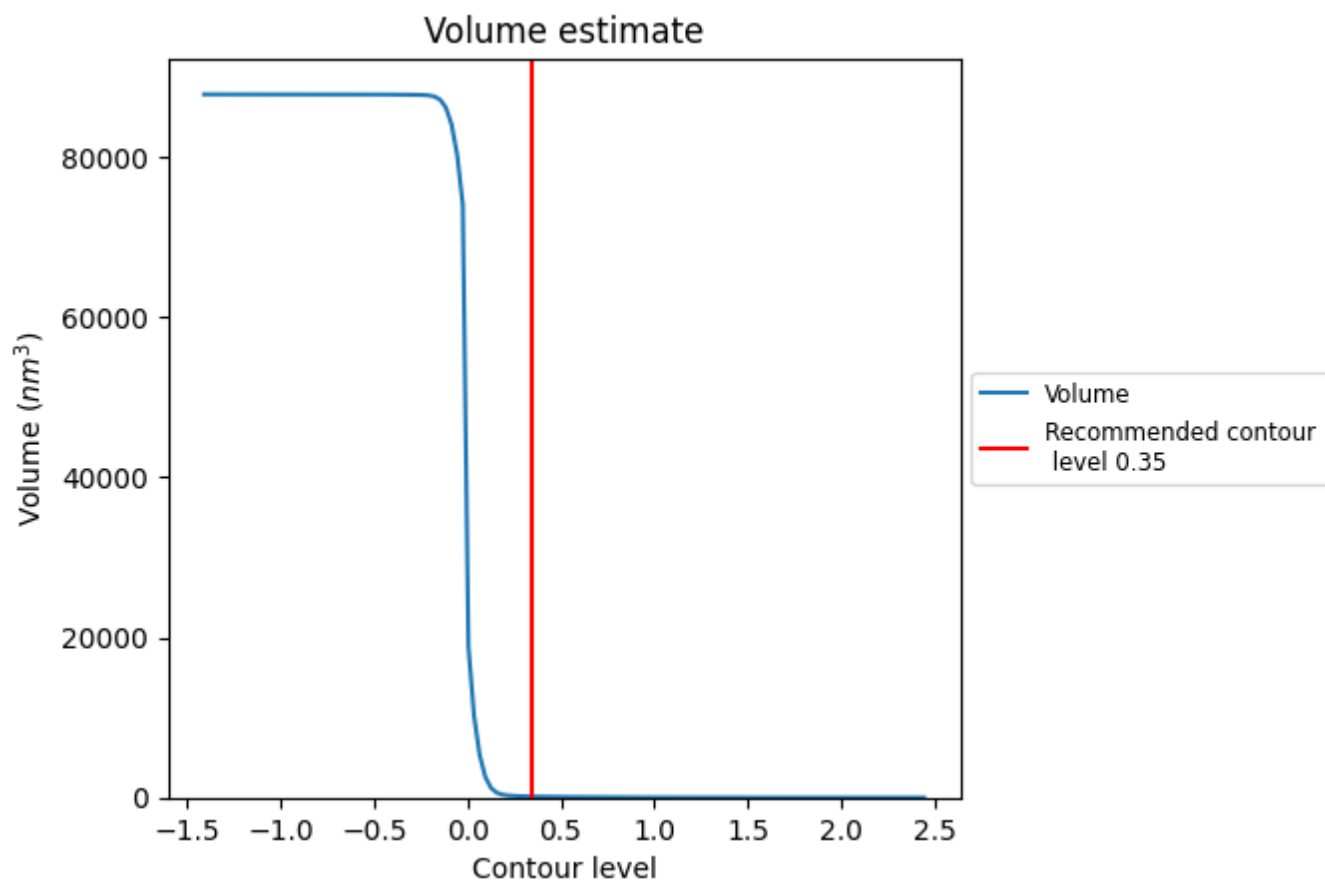
This section contains the results of statistical analysis of the map.

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.

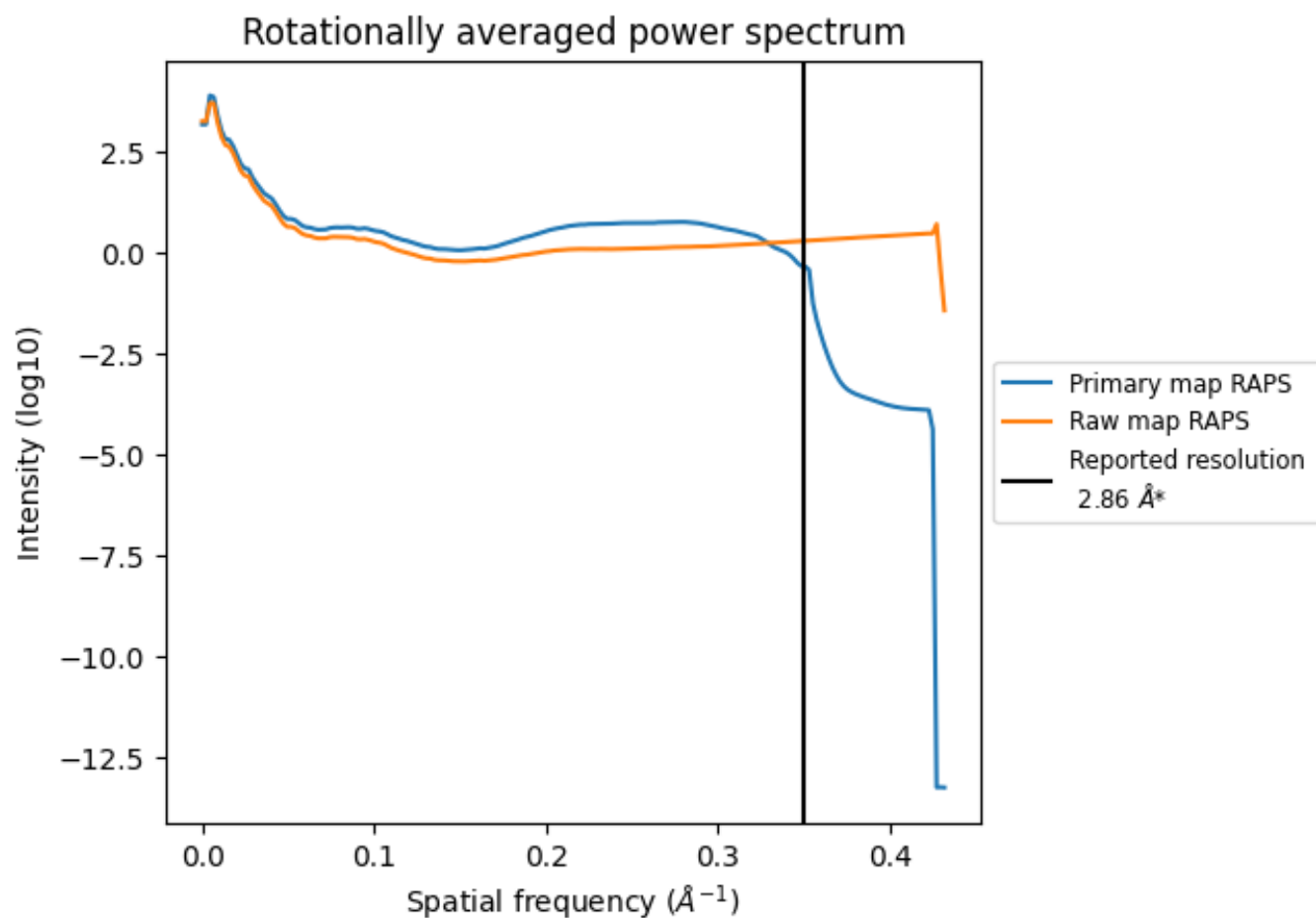
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm^3 ; this corresponds to an approximate mass of 114 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 ⓘ

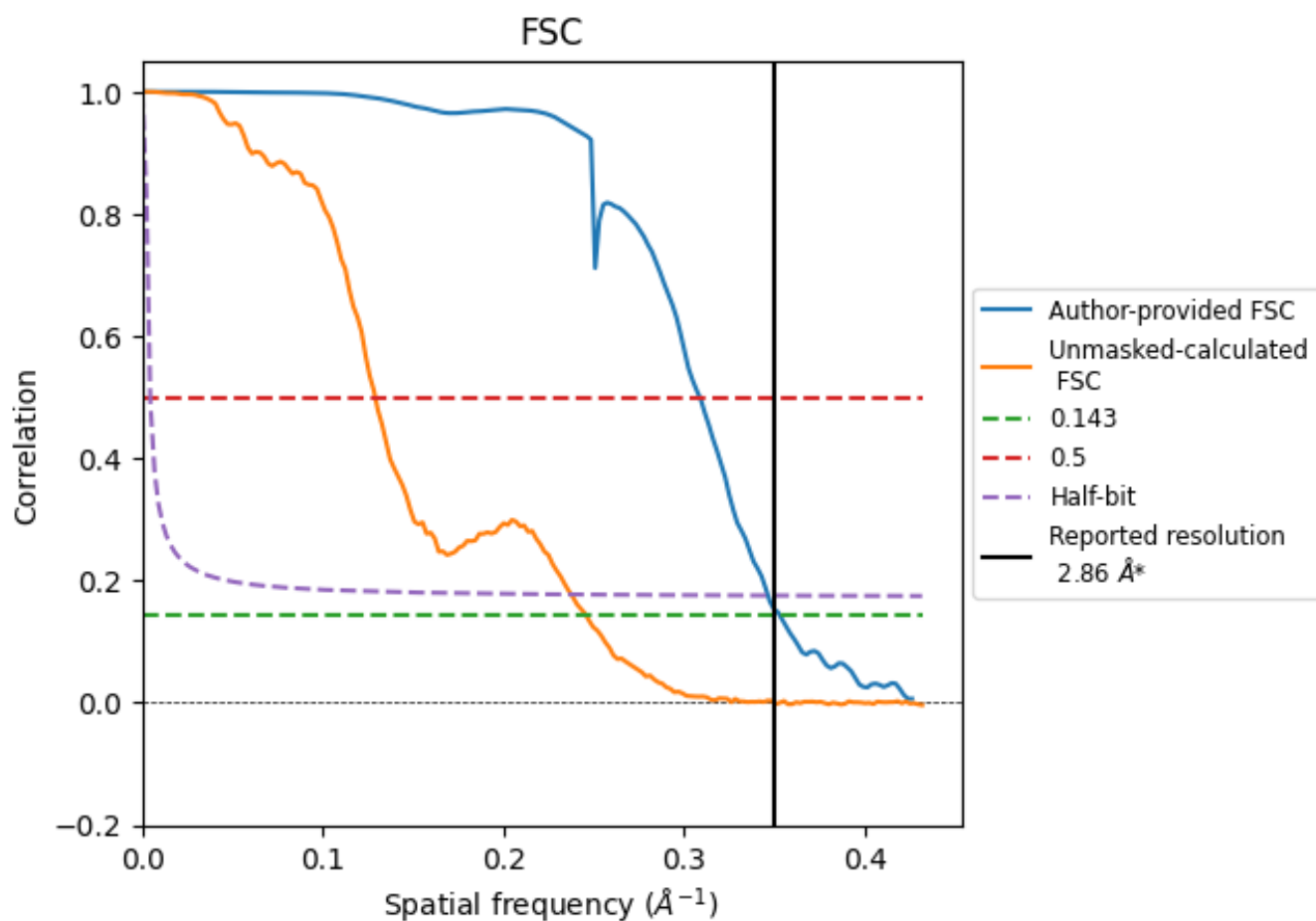


*Reported resolution corresponds to spatial frequency of 0.350 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.350 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

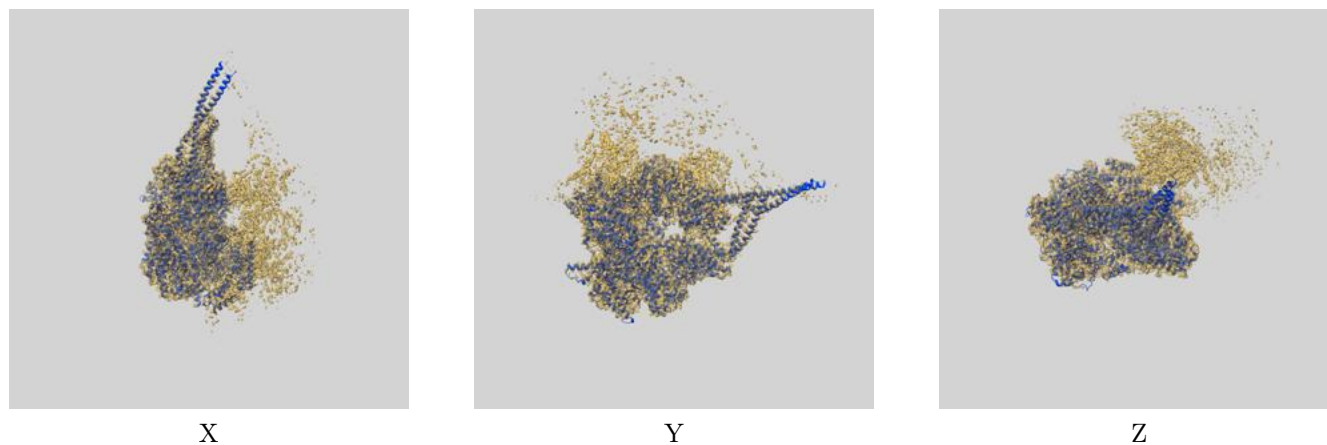
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.83	3.24	2.89
Unmasked-calculated*	4.07	7.75	4.21

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.07 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

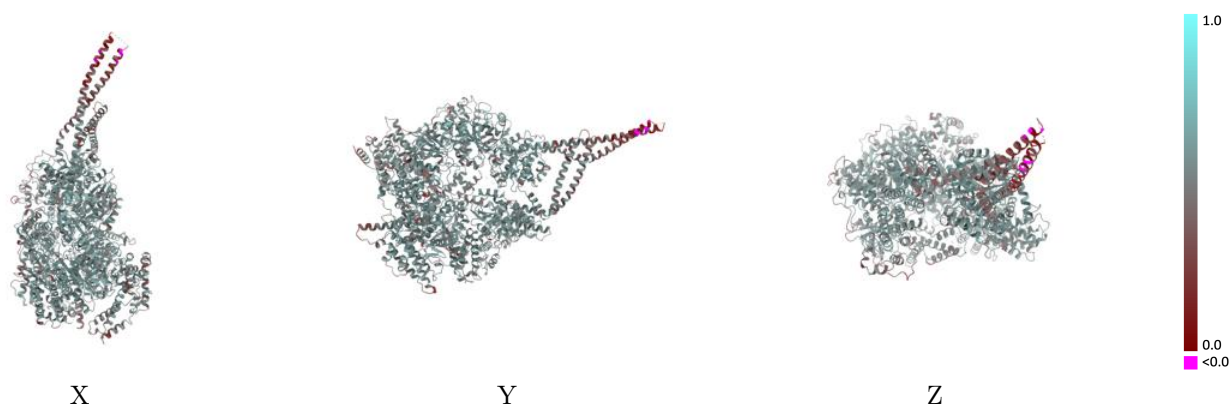
This section contains information regarding the fit between EMDB map EMD-44715 and PDB model 9BMY. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



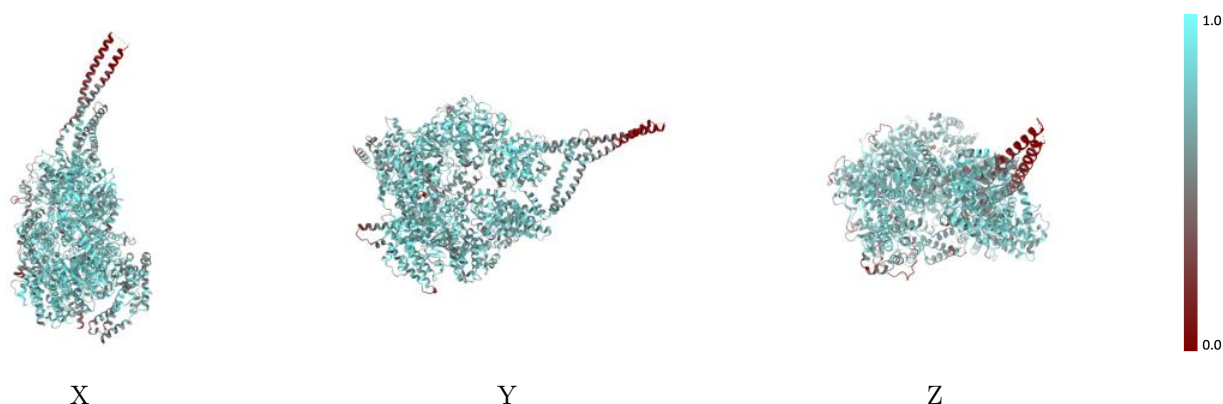
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



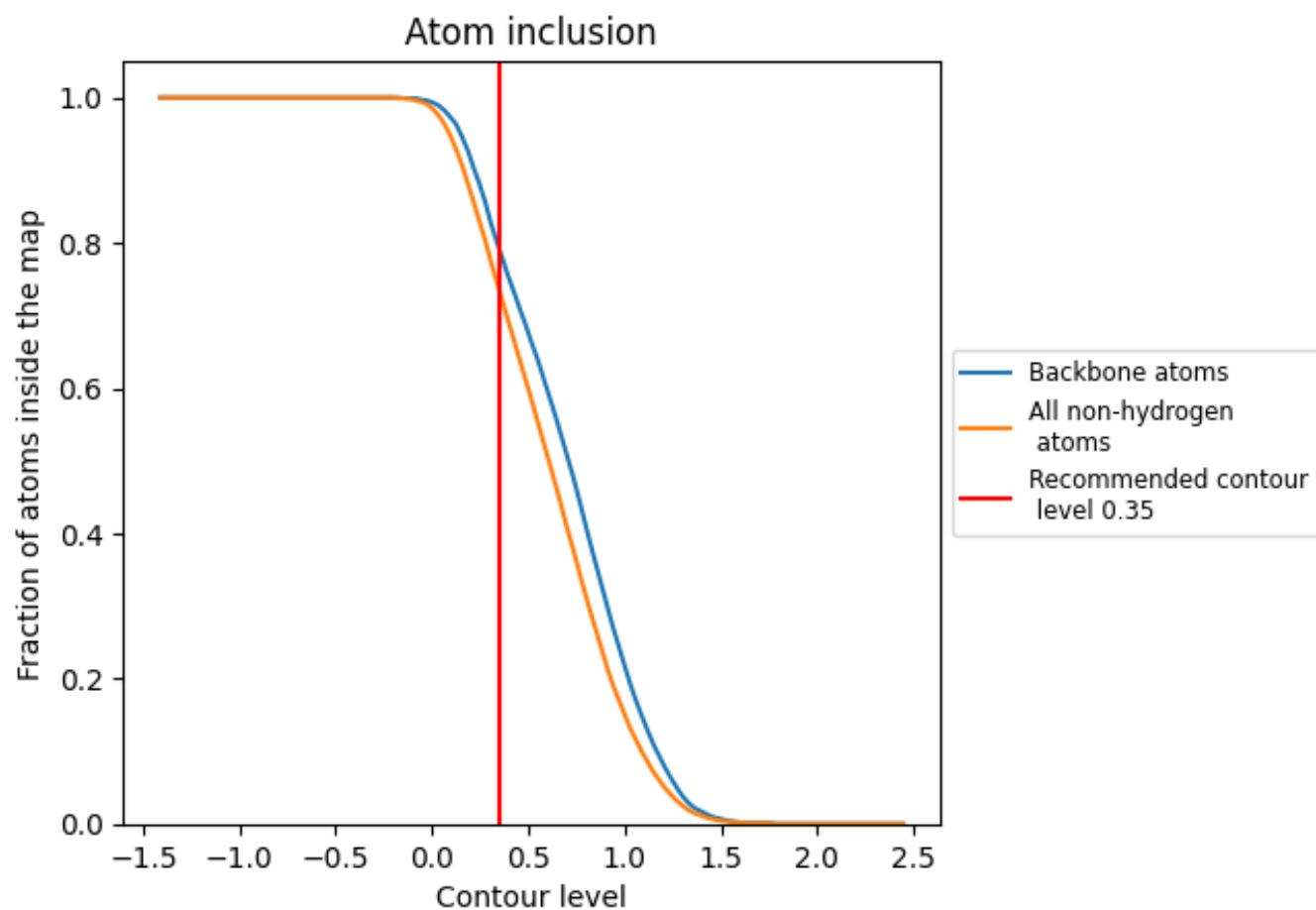
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 73% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7340	0.5330
A	0.7340	0.5330

