



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:56 AM UTC

PDB ID : 9E10 / pdb_00009e10
EMDB ID : EMD-47379
Title : Dimeric motor domains from phi dynein-1 under Lis1 condition
Authors : Yang, J.; Zhang, K.
Deposited on : 2024-10-21
Resolution : 2.71 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

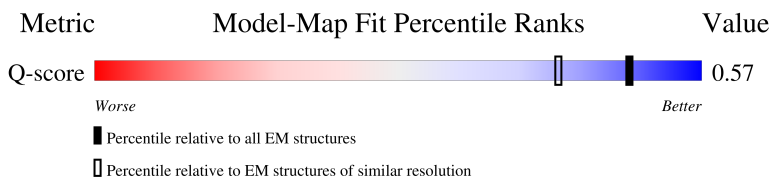
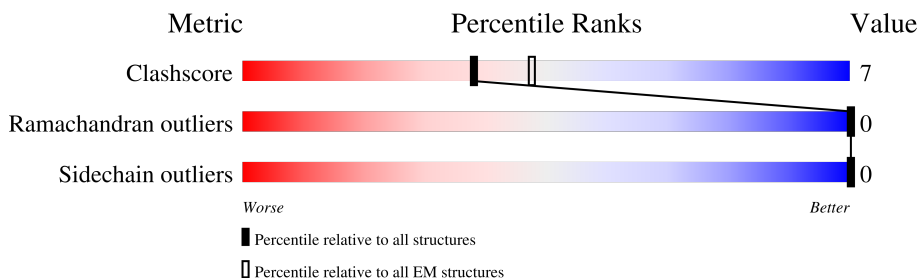
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.71 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	10297 (2.21 - 3.21)

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	 51% 12% 37%
1	B	4646	 51% 12% 37%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 47414 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
1	A	2937	Total	C	N	O	S	0	0
			23593	15028	4070	4378	117		
1	B	2937	Total	C	N	O	S	0	0
			23593	15028	4070	4378	117		

- 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).



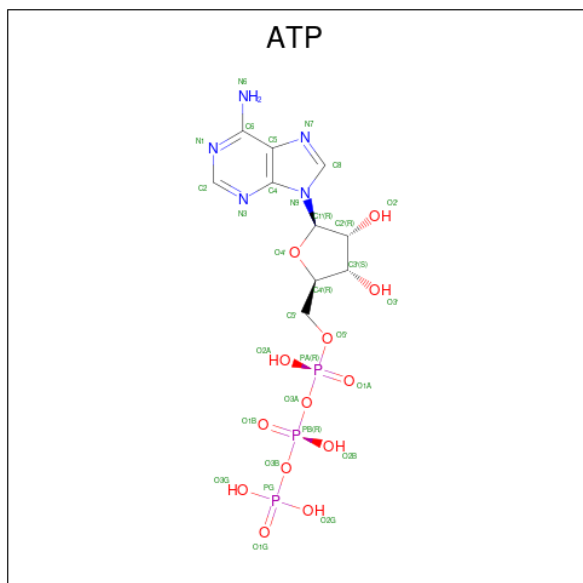
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

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

- 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).

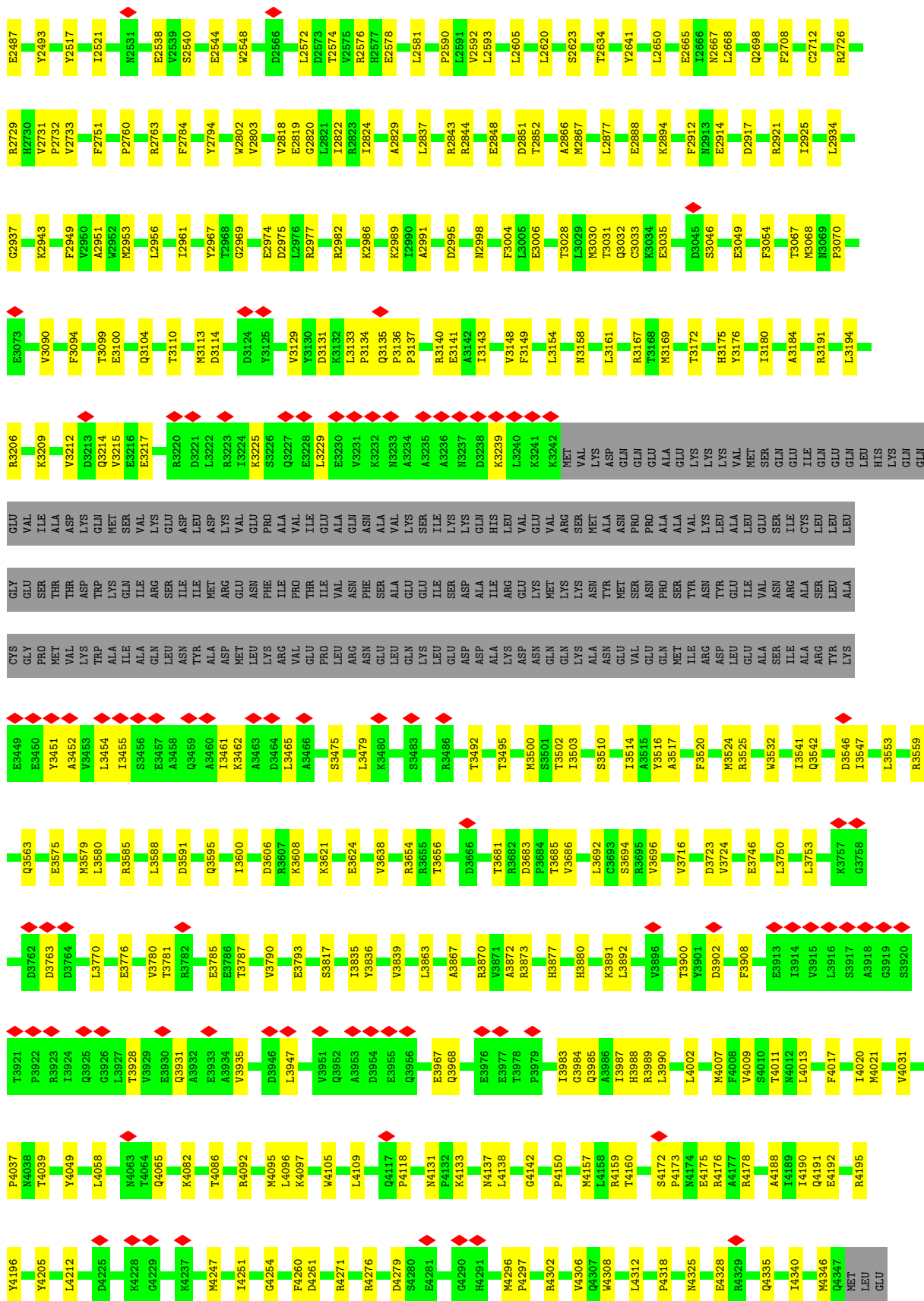


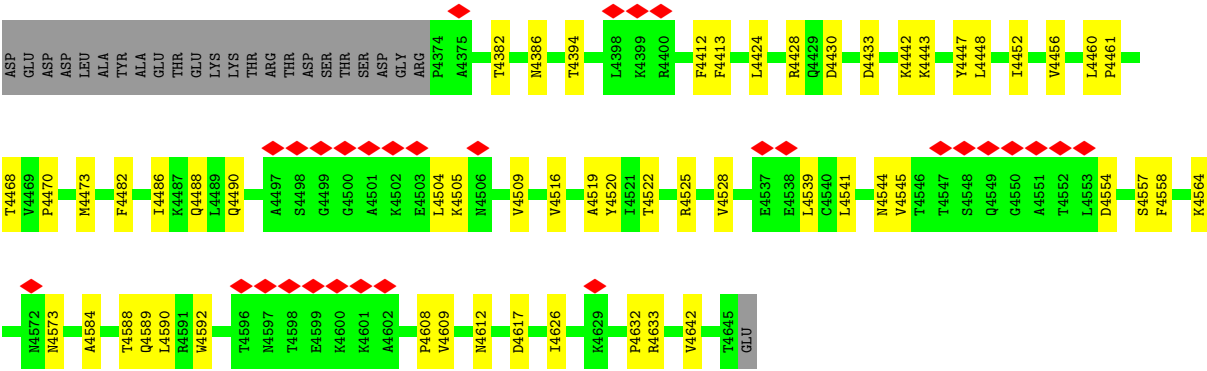
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	B	1	Total	C	N	O	P	0
			31	10	5	13	3	

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

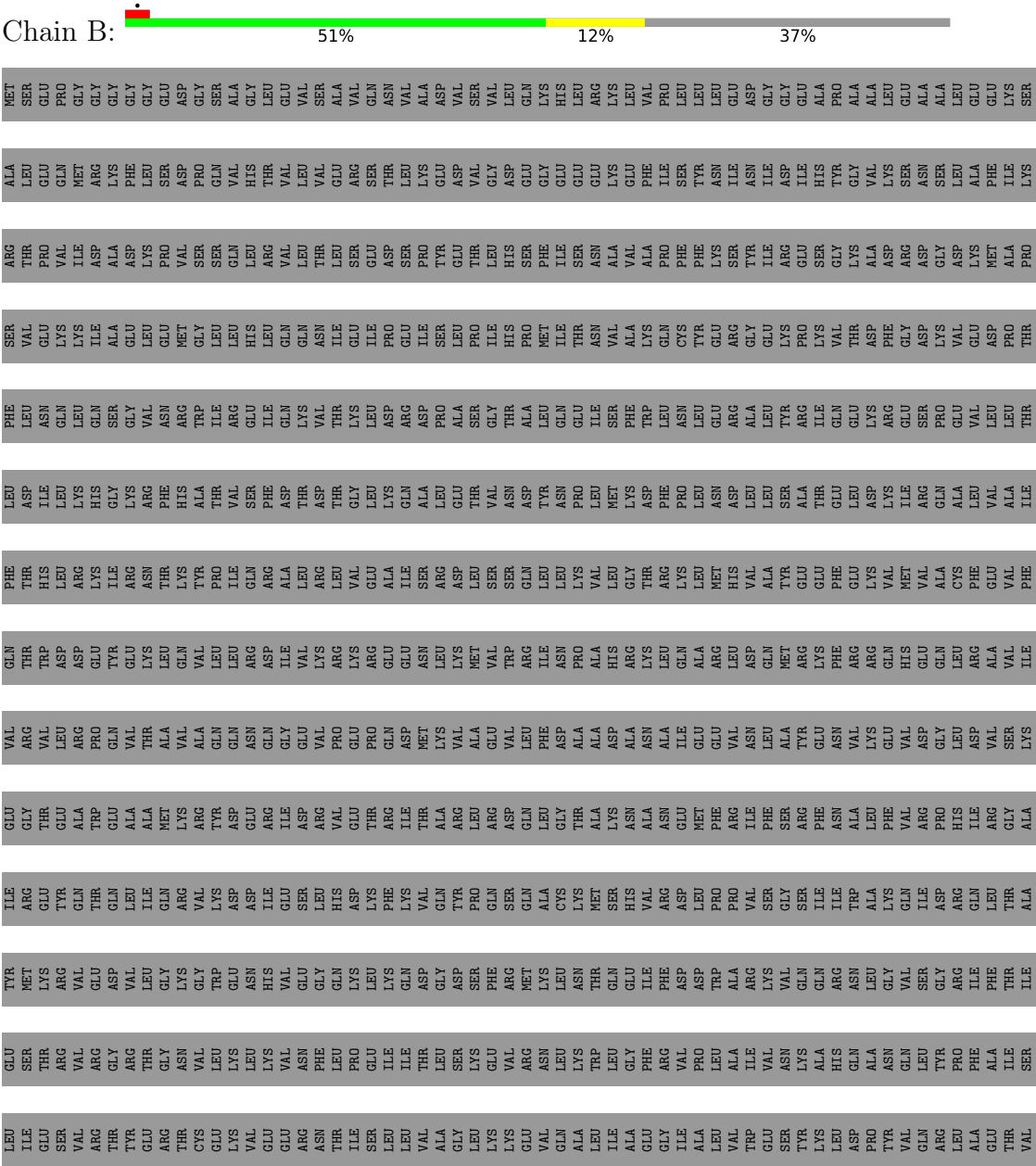
Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Mg	0
			2	2	
4	B	2	Total	Mg	0
			2	2	





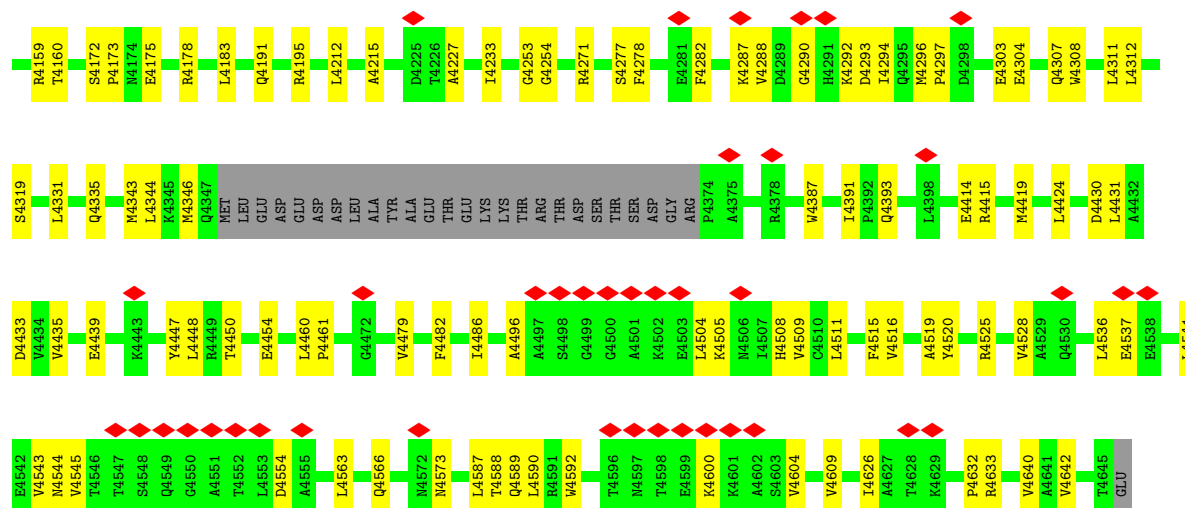


● Molecule 1: Cytoplasmic dynein 1 heavy chain 1





A3986	L3987	D3902	D3762	R3569	S3456	ALA	LYS	MET	T3099	G2937	N2752	P2525	ASP
H3988	H3988	L3909	D3763	Q3563	E3457	ILE	GLN	SER	E3100	K2943	M2755	A2529	GLY
R3989	R3989	L3909	D3764	Q3563	A3458	ALA	ARG	LYS	Q3104	A2951	T2770	P2530	GLY
L3990	L3990	L3909	D3764	Q3563	A3459	LEU	SER	ILE	T3110	L2956	F2784	N2531	GLY
F3996	F3996	E3913	L3770	I3578	A3460	ASN	ILE	ASP	S3111	L2956	F2784	D2536	ALA
M4004	M4004	V3915	K3774	M3579	I3461	ALA	ILE	ASP	K3112	L2956	F2784	S2410	ALA
M4007	M4007	L3916	K3775	L3580	K3462	ASP	MET	ASP	M3113	L2956	F2784	Y2537	S2410
T4011	T4011	S3917	E3776	N3584	A3463	MET	GLY	VAL	D3114	L2956	F2784	E2538	P2411
M4012	M4012	L3918	V3780	L3588	A3466	LEU	ASN	GLY	I3115	L2956	F2784	G2543	L2412
L4013	L4013	G3919	T3781	D3591	A3467	ARG	ILE	PRO	E3116	L2956	F2784	W2548	L2413
F4017	F4017	S3920	K3782	I3600	N3473	VAL	PRO	VAL	D3124	L2956	F2784	K2551	I2415
M4018	M4018	T3921	K3783	I3600	S3474	GLY	ILE	ILE	Y3125	L2956	F2784	R2417	Q2416
S4019	S4019	P3922	V3784	R3606	S3475	LEU	VAL	ALA	M3126	L2956	F2784	H2560	M2412
L4020	L4020	R3923	E3785	R3607	S3476	ARG	ASN	GLN	P3127	L2956	F2784	K2561	L2413
M4021	M4021	T3924	E3786	K3608	L3479	ASN	PHE	ASN	L3133	L2956	F2784	V2562	M2423
P4037	P4037	Q3925	I3789	V3638	K3480	GLY	SER	ALA	P3134	L2956	F2784	L2572	V2433
Y4049	Y4049	G3926	C3808	N3650	S3481	ALA	VAL	ALA	Q3135	L2956	F2784	R2576	L2437
Q4065	Q4065	T3927	S3817	R3651	L3482	GLN	GLY	LYS	P3136	L2956	F2784	L2581	F2441
K4082	K4082	E3930	Y3825	E3652	S3483	LYS	ILE	LYS	Q3137	L2956	F2784	P2590	I2446
T4086	T4086	A3932	F3832	R3654	E3484	ASP	ASP	LYS	R3140	L2956	F2784	L2591	L2449
V4087	V4087	E3933	T3835	E3655	S3485	ASP	ALA	LYS	E3141	L2956	F2784	V2592	L2451
V4088	V4088	Q3931	Y3836	R3656	R3486	ALA	ILE	ALA	A3142	L2956	F2784	L2593	L2452
R4092	R4092	T3656	E3487	T3656	E3487	LYS	ARG	GLY	I3143	L2956	F2784	G2600	S2457
M4095	M4095	D3666	K3491	D3666	K3491	ASN	LYS	GLY	V3148	L2956	F2784	Y2641	M2461
L4096	L4096	Q3667	T3495	Q3667	T3495	GLN	MET	VAL	F3149	L2956	F2784	L2650	L2462
K4097	K4097	D3668	F3496	D3668	F3496	LYS	LYS	ARG	V3150	L2956	F2784	E2685	Q2485
W4105	W4105	T3681	K3497	T3681	K3497	ALA	ASN	ASN	L3154	L2956	F2784	L2666	L2486
M4107	M4107	R3682	Q3499	R3682	Q3499	VAL	MET	PRO	N3158	L2956	F2784	L2668	E2487
L4116	L4116	D3683	T3502	D3683	T3502	GLY	SER	ASN	T2852	L2956	F2784	F2708	R2492
Q4117	Q4117	V3686	T3503	V3686	T3503	ILE	TYR	VAL	A3162	L2956	F2784	C2712	I2498
P4118	P4118	D3691	S3510	D3691	S3510	ARG	ASN	ILE	K3163	L2956	F2784	R2726	L2499
N4131	N4131	L3692	I3514	L3692	I3514	ASP	TYR	GLY	M3169	L2956	F2784	D2505	D2505
P4132	P4132	R3695	A3515	R3695	A3515	LEU	GLY	GLY	R3174	L2956	F2784	H2730	G2515
V4135	V4135	V3716	A3517	V3716	A3517	GLY	ILE	PRO	H3175	L2956	F2784	V2731	E2516
N4137	N4137	D3723	F3520	D3723	F3520	VAL	VAL	THR	Y3176	L2956	F2784	P2732	Y2517
L4138	L4138	L3731	K3524	L3731	K3524	ALA	ARG	THR	I3180	L2956	F2784	V2733	V2517
P4150	P4150	Q3735	R3525	Q3735	R3525	LYS	TYR	ASP	A3184	L2956	F2784	Y2735	I2521
N4156	N4156	L3745	W3532	L3745	W3532	GLY	GLY	TRP	K3190	L2956	F2784		
		K3757	Q3538	K3757	Q3538	THR	THR		R3191	L2956	F2784		
		G3758	T3541	G3758	T3541	VAL	VAL		R3206	L2956	F2784		
		R3759	Q3542	R3759	Q3542	LYS	LYS		K3207	L2956	F2784		
			D3546		D3546	VAL	VAL		I3208	L2956	F2784		
			I3547		I3547	ALA	ALA		T3211	L2956	F2784		
			L3553		L3553	ASP	ASP		V3212	L2956	F2784		
						LYS	LYS			L2956	F2784		
						GLN	GLN			L2956	F2784		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	160539	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 ($e^-/\text{\AA}^2$)	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	2.763	Depositor
Minimum map value	-1.378	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.3	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, 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	0.13	0/24093	0.29	0/32651
1	B	0.13	0/24093	0.30	0/32651
All	All	0.13	0/48186	0.29	0/65302

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

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	23658	333	0
1	B	23593	0	23657	368	0
2	A	81	0	36	3	0
2	B	81	0	36	2	0
3	A	31	0	12	0	0
3	B	31	0	12	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
All	All	47414	0	47411	700	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 700 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:2320:ASP:OD1	1:A:2321:ASP:N	2.12	0.83
1:B:2320:ASP:OD1	1:B:2321:ASP:N	2.13	0.80
1:B:3970:VAL:HB	1:B:3989:ARG:HD3	1.65	0.78
1:B:2452:LEU:HD13	1:B:2729:ARG:HH21	1.52	0.73
1:B:2492:ARG:HE	1:B:2525:PRO:HG2	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	2929/4646 (63%)	2881 (98%)	48 (2%)	0	100	100
1	B	2929/4646 (63%)	2889 (99%)	40 (1%)	0	100	100
All	All	5858/9292 (63%)	5770 (98%)	88 (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	2605/4125 (63%)	2605 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	2605/4125 (63%)	2605 (100%)	0	100	100
All	All	5210/8250 (63%)	5210 (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 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2430	ASN
1	B	3499	GLN
1	B	2464	GLN
1	B	2834	GLN
1	B	3535	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	B	4701	4	28,29,29	1.40	4 (14%)	43,45,45	1.82	9 (20%)
2	ADP	A	4703	-	28,29,29	1.40	4 (14%)	43,45,45	1.87	9 (20%)
3	ATP	A	4702	4	32,33,33	0.34	0	48,52,52	0.28	0
3	ATP	B	4702	4	32,33,33	0.34	0	48,52,52	0.28	0
2	ADP	B	4704	-	28,29,29	1.41	4 (14%)	43,45,45	1.83	9 (20%)
2	ADP	A	4704	-	28,29,29	1.41	4 (14%)	43,45,45	1.83	9 (20%)
2	ADP	A	4701	4	28,29,29	1.40	4 (14%)	43,45,45	1.83	9 (20%)
2	ADP	B	4703	-	28,29,29	1.40	4 (14%)	43,45,45	1.87	9 (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
2	ADP	B	4701	4	-	4/16/32/32	0/3/3/3
2	ADP	A	4703	-	-	0/16/32/32	0/3/3/3
3	ATP	A	4702	4	-	4/22/38/38	0/3/3/3
3	ATP	B	4702	4	-	4/22/38/38	0/3/3/3
2	ADP	B	4704	-	-	3/16/32/32	0/3/3/3
2	ADP	A	4704	-	-	3/16/32/32	0/3/3/3
2	ADP	A	4701	4	-	3/16/32/32	0/3/3/3
2	ADP	B	4703	-	-	1/16/32/32	0/3/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4703	ADP	C5-C4	4.74	1.47	1.39
2	A	4704	ADP	C5-C4	4.66	1.47	1.39
2	A	4703	ADP	C5-C4	4.66	1.47	1.39
2	B	4704	ADP	C5-C4	4.63	1.47	1.39
2	A	4701	ADP	C5-C4	4.60	1.47	1.39

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4703	ADP	C5-C4-N3	-6.07	118.36	126.72
2	A	4703	ADP	C5-C4-N3	-5.92	118.56	126.72
2	B	4704	ADP	C5-C4-N3	-5.88	118.62	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4704	ADP	C5-C4-N3	-5.83	118.69	126.72
2	A	4701	ADP	C5-C4-N3	-5.71	118.85	126.72

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

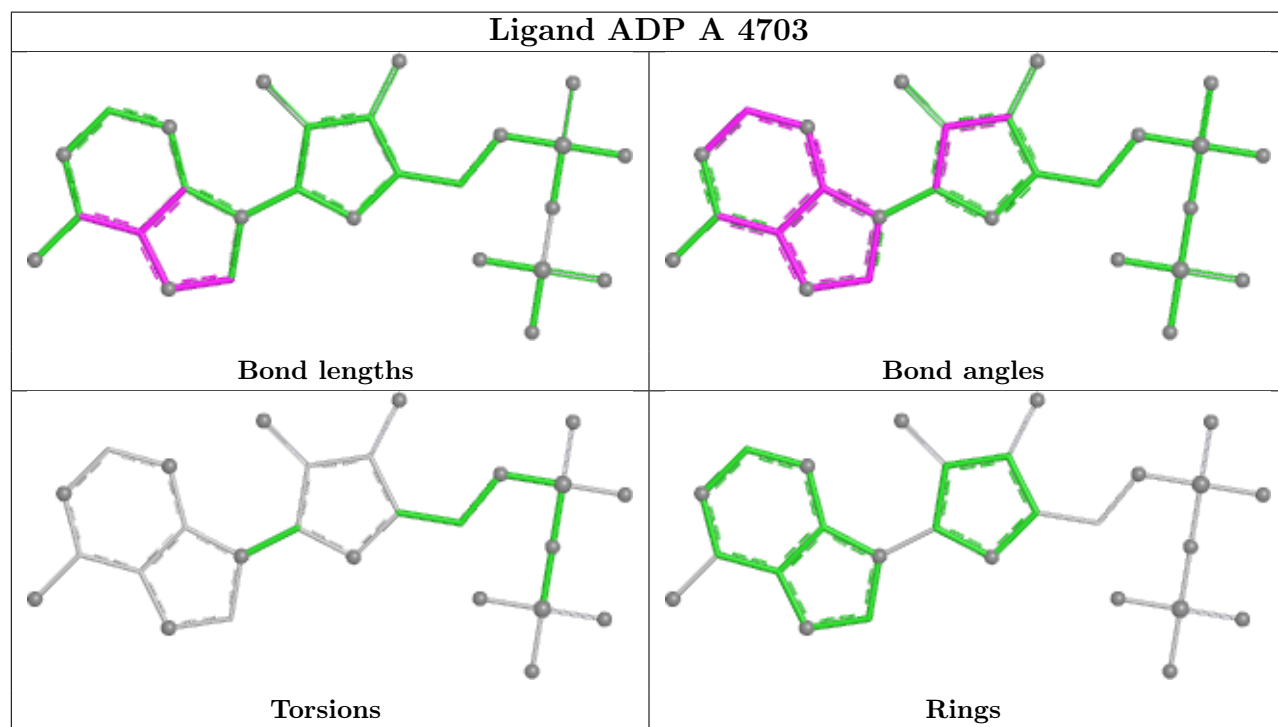
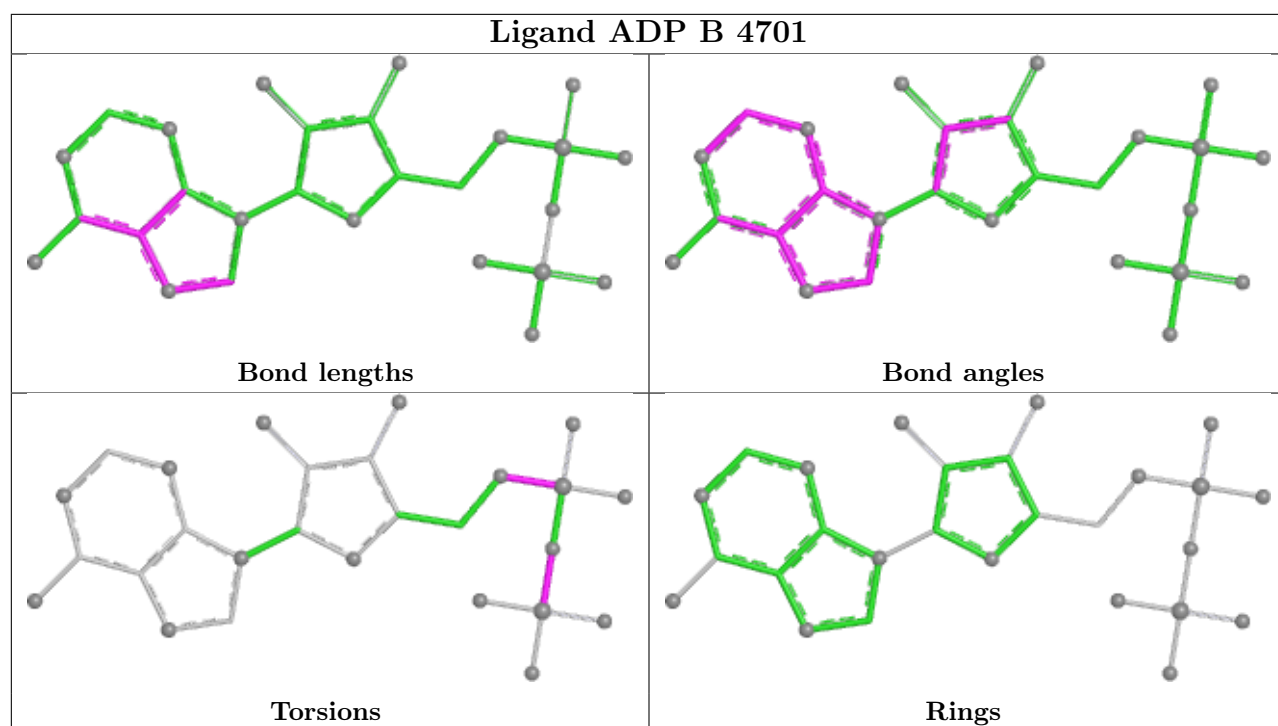
Mol	Chain	Res	Type	Atoms
2	A	4701	ADP	C5'-O5'-PA-O1A
2	A	4701	ADP	C5'-O5'-PA-O2A
2	A	4701	ADP	C5'-O5'-PA-O3A
2	A	4704	ADP	C5'-O5'-PA-O1A
2	B	4701	ADP	C5'-O5'-PA-O1A

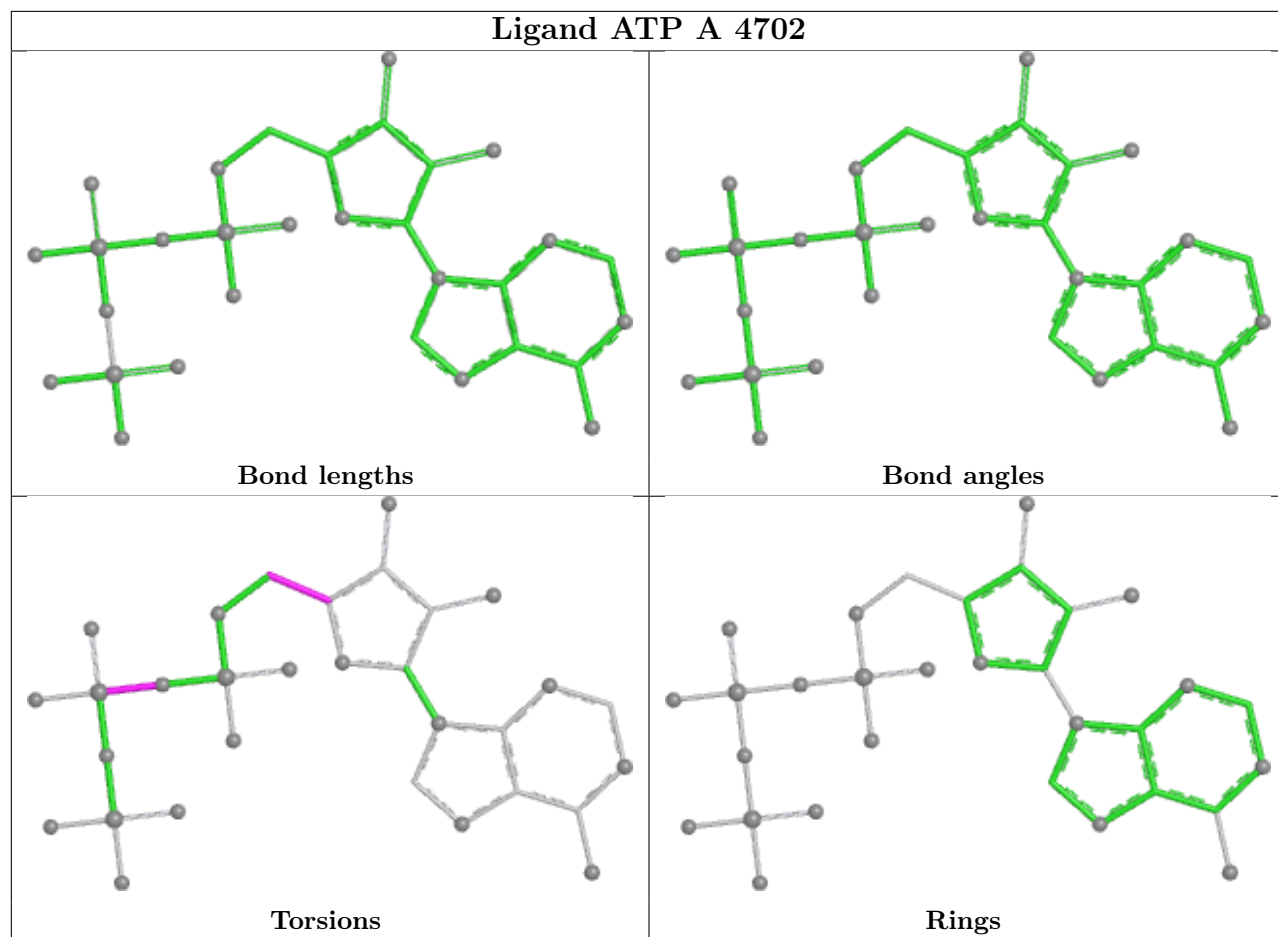
There are no ring outliers.

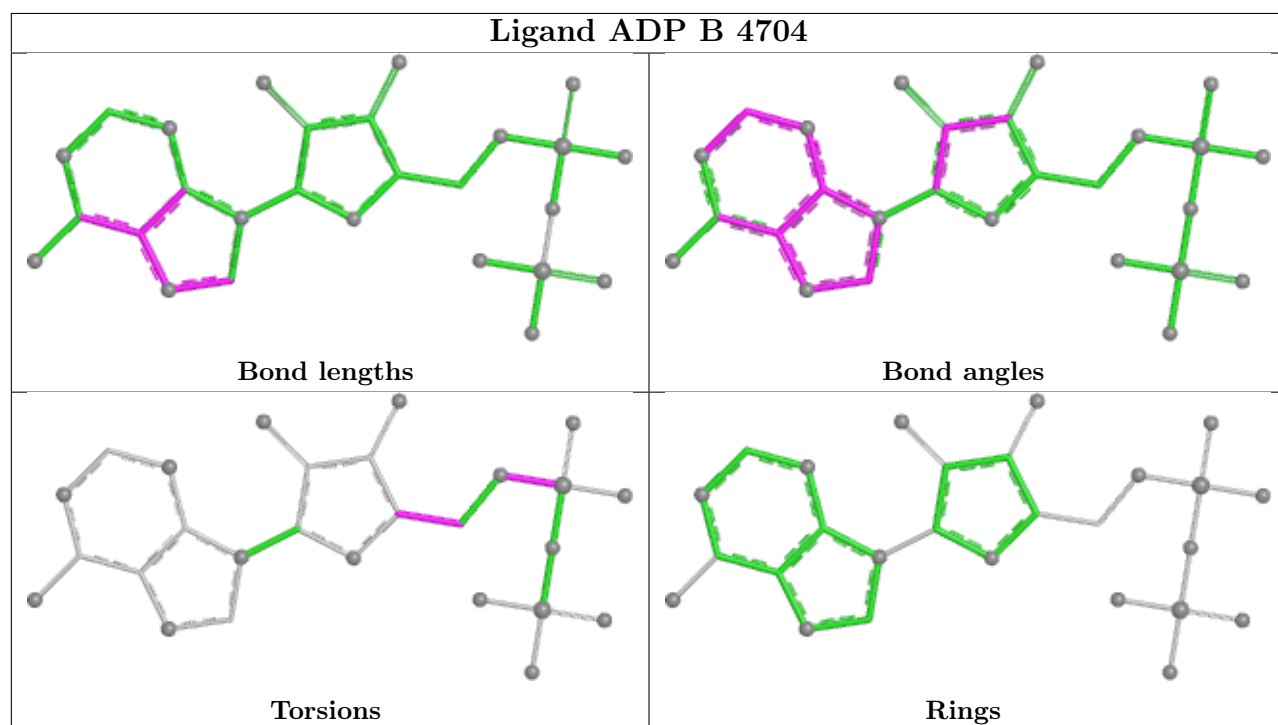
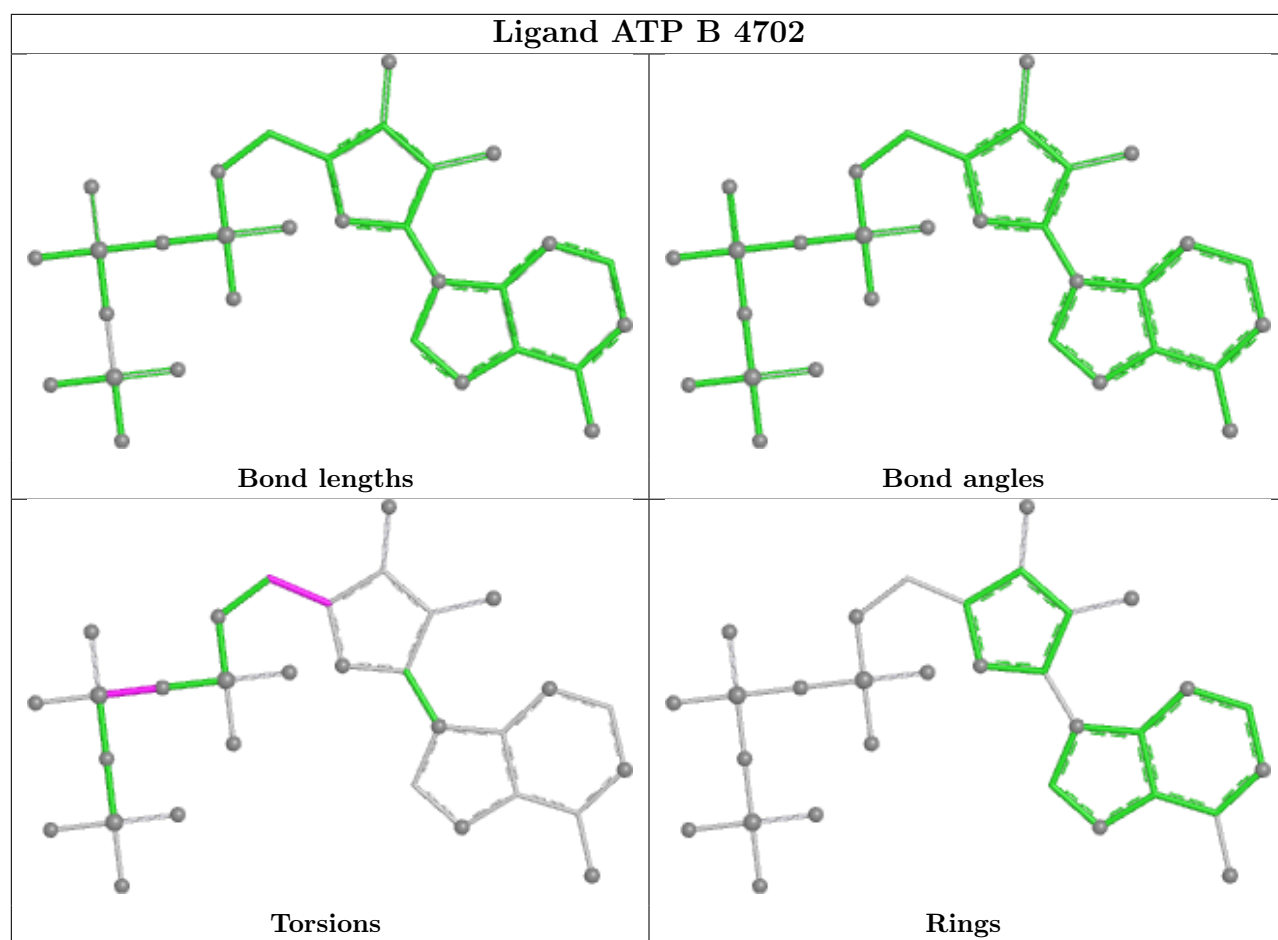
4 monomers are involved in 6 short contacts:

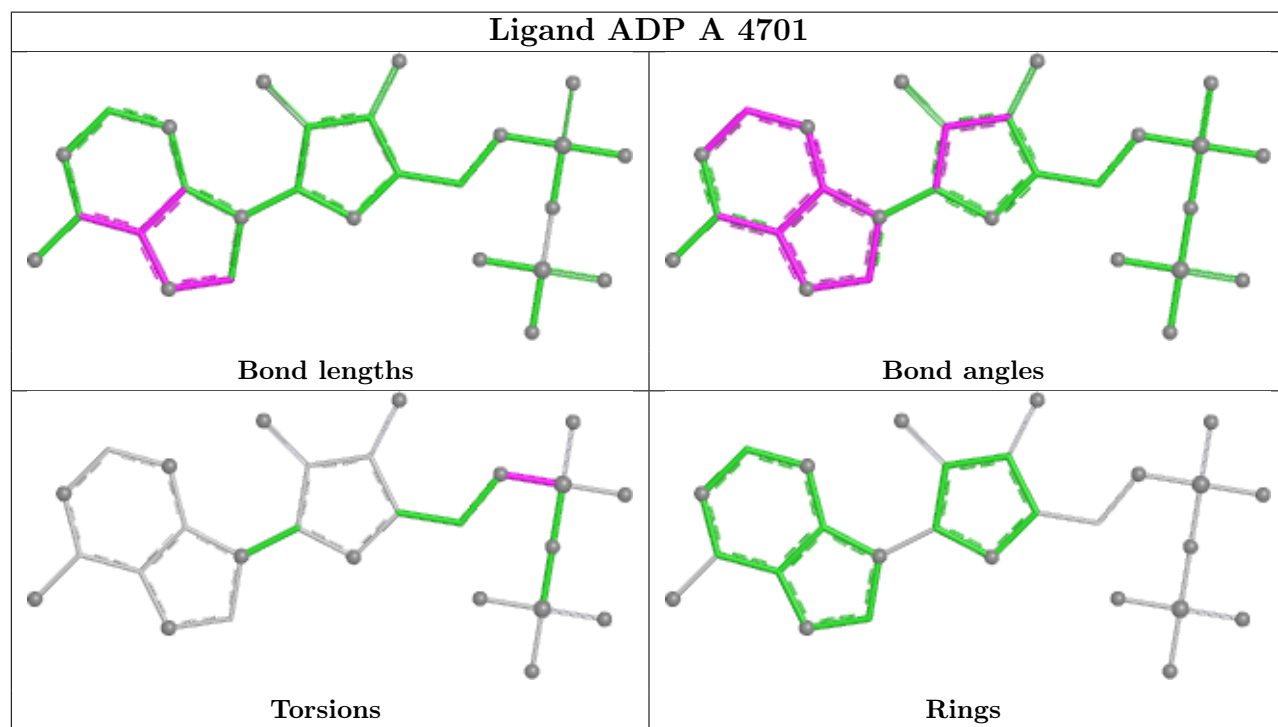
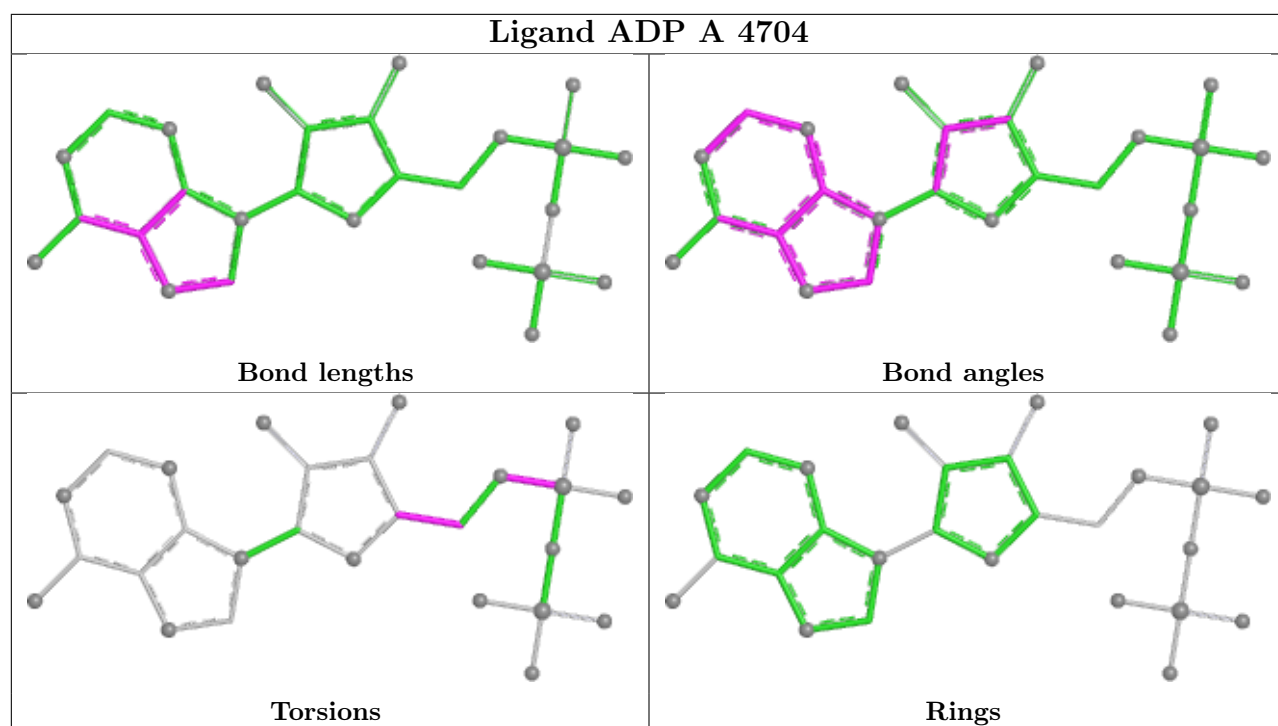
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4701	ADP	1	0
3	B	4702	ATP	1	0
2	A	4701	ADP	3	0
2	B	4703	ADP	1	0

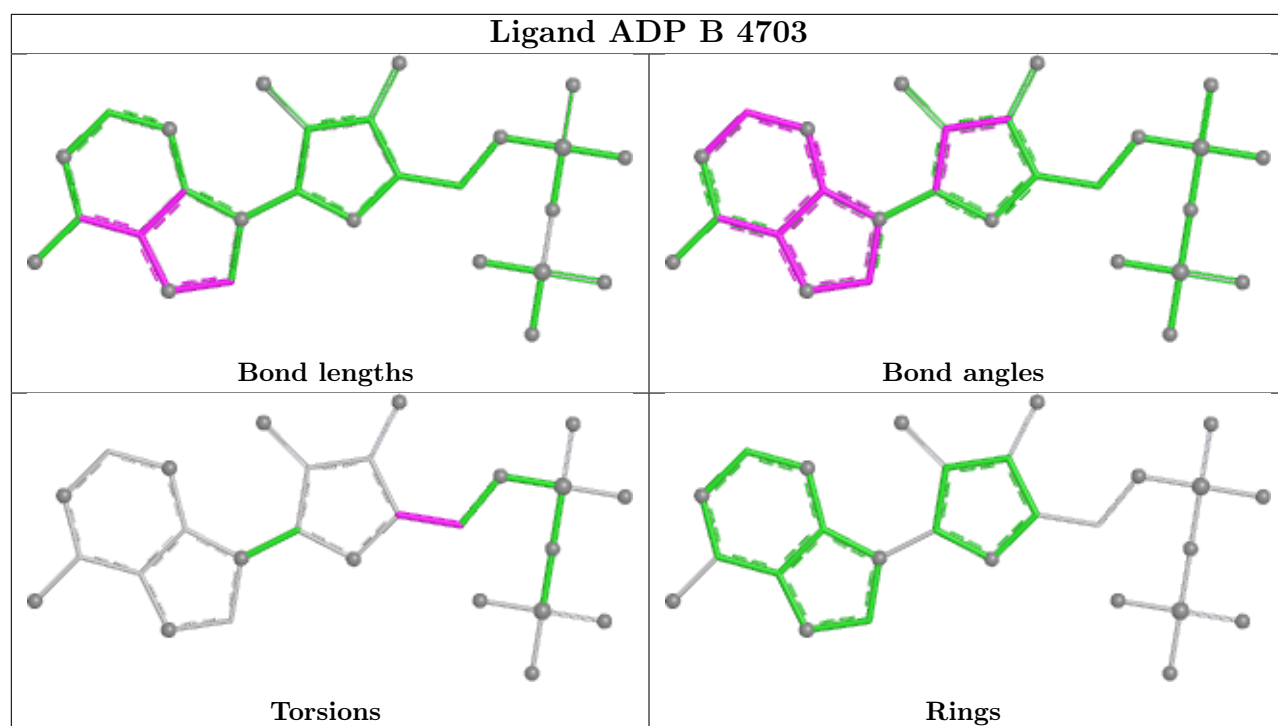
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

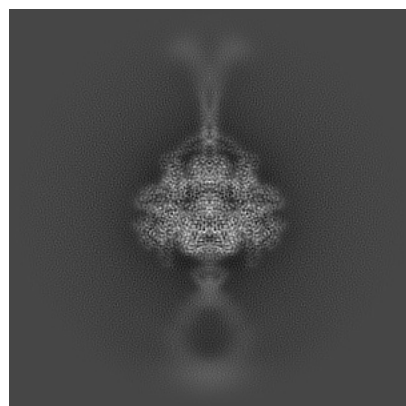
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47379. These allow visual inspection of the internal detail of the map and identification of artifacts.

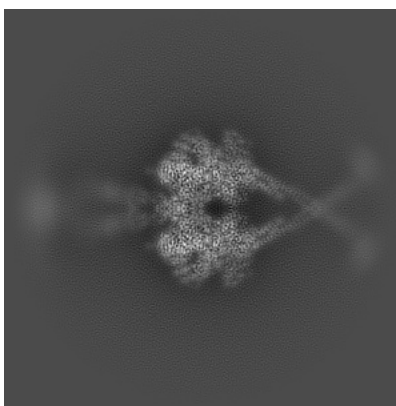
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

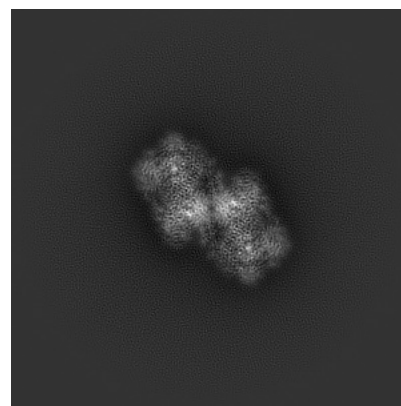
6.1.1 Primary map



X

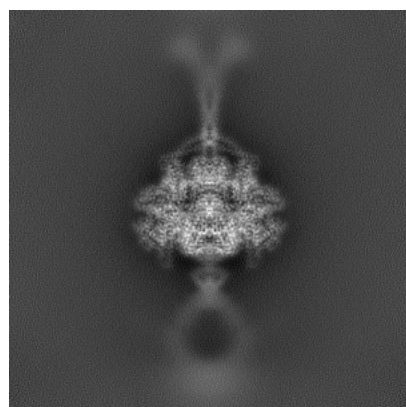


Y

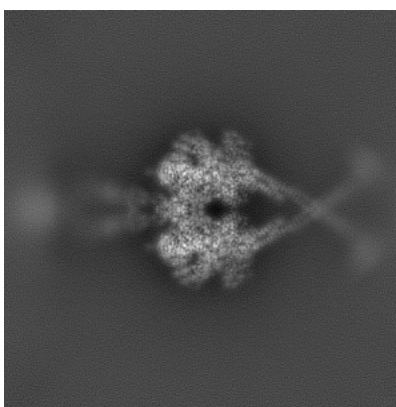


Z

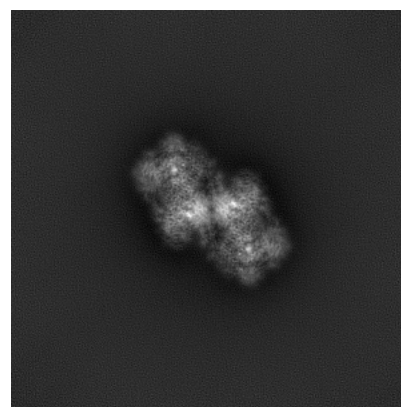
6.1.2 Raw map



X



Y

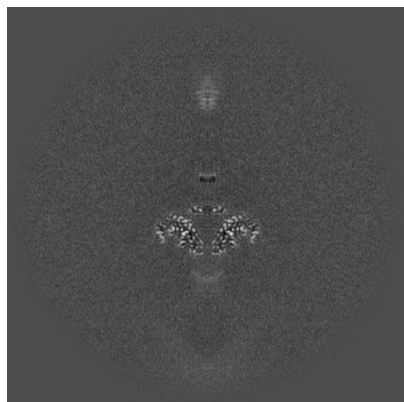


Z

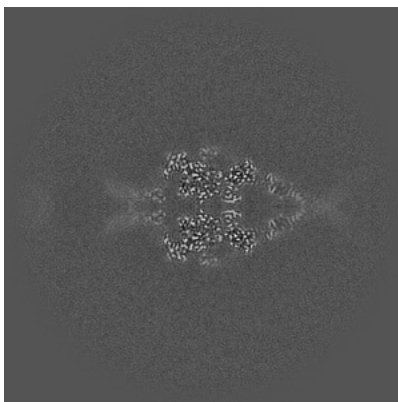
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

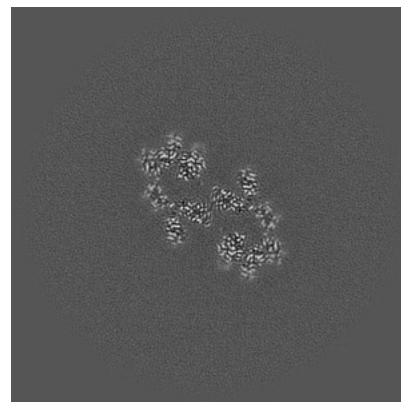
6.2.1 Primary map



X Index: 192

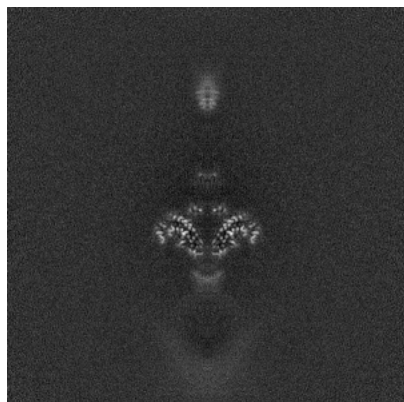


Y Index: 192

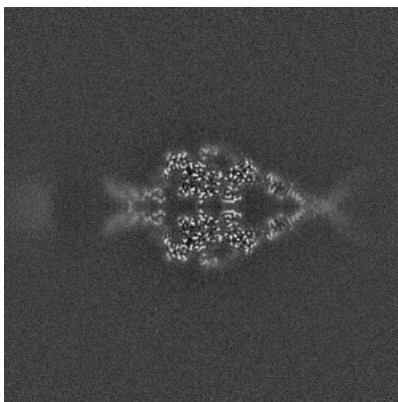


Z Index: 192

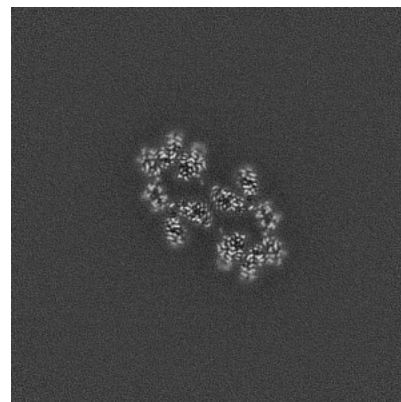
6.2.2 Raw map



X Index: 192



Y Index: 192

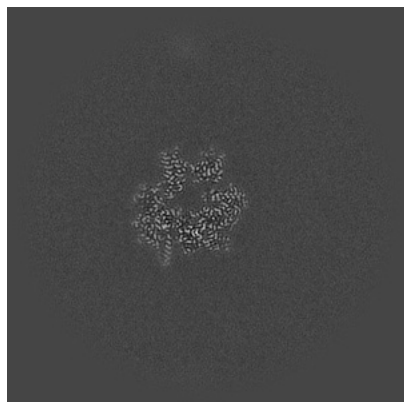


Z Index: 192

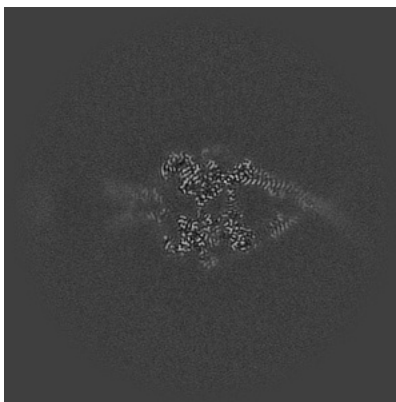
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

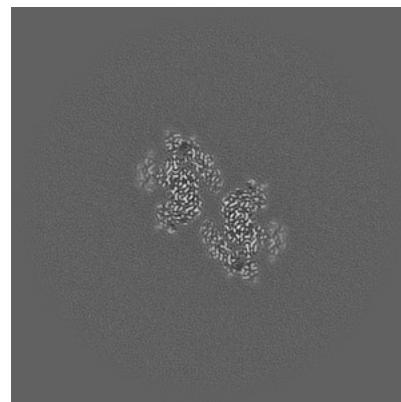
6.3.1 Primary map



X Index: 227

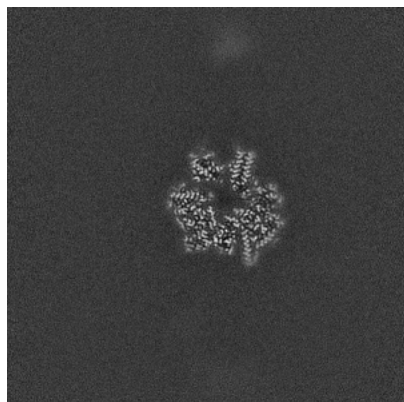


Y Index: 195

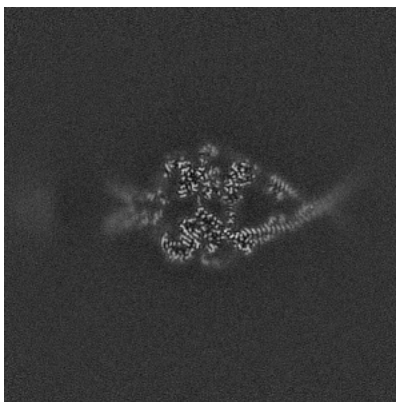


Z Index: 173

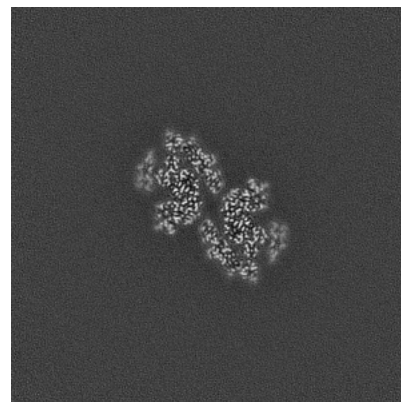
6.3.2 Raw map



X Index: 156



Y Index: 189

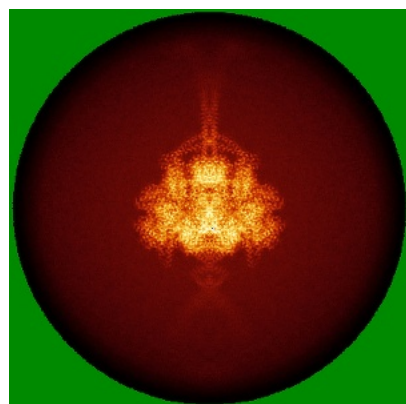


Z Index: 172

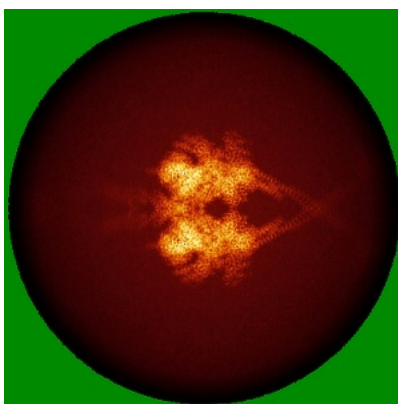
The images above show the largest variance slices of the map in three orthogonal directions.

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

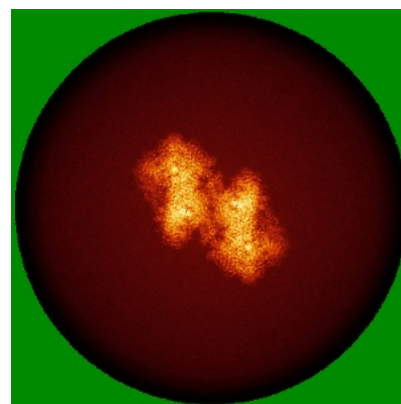
6.4.1 Primary map



X

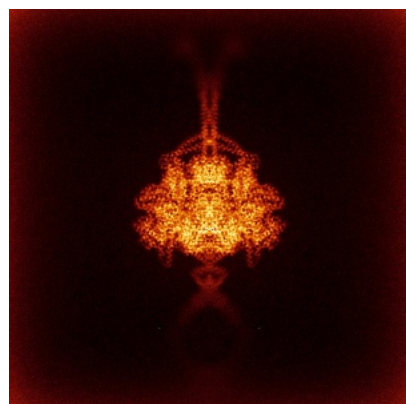


Y

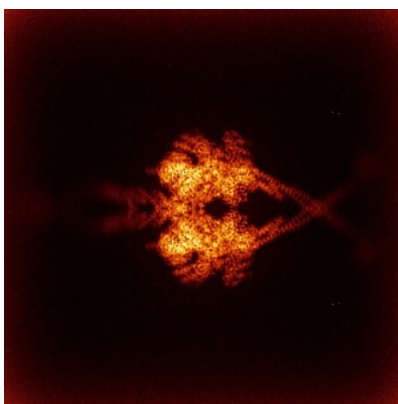


Z

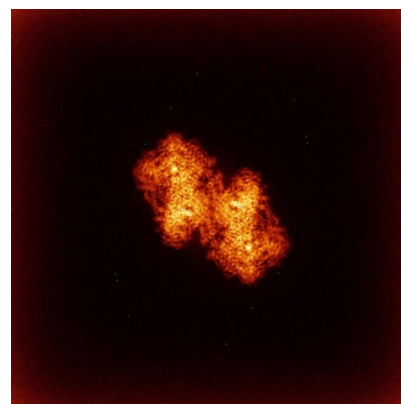
6.4.2 Raw map



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 0.3. 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.

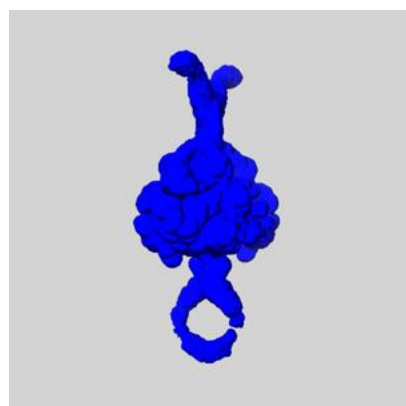
6.6 Mask visualisation [i](#)

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

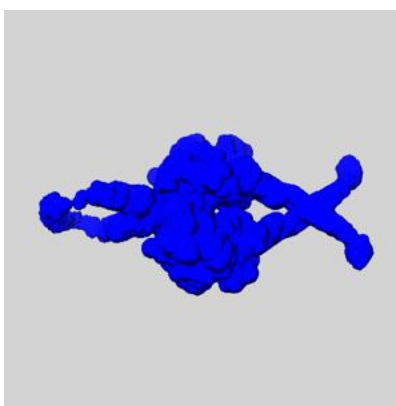
A mask typically either:

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

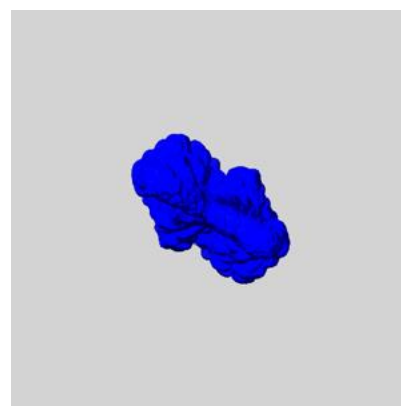
6.6.1 emd_47379_msk_1.map [i](#)



X



Y

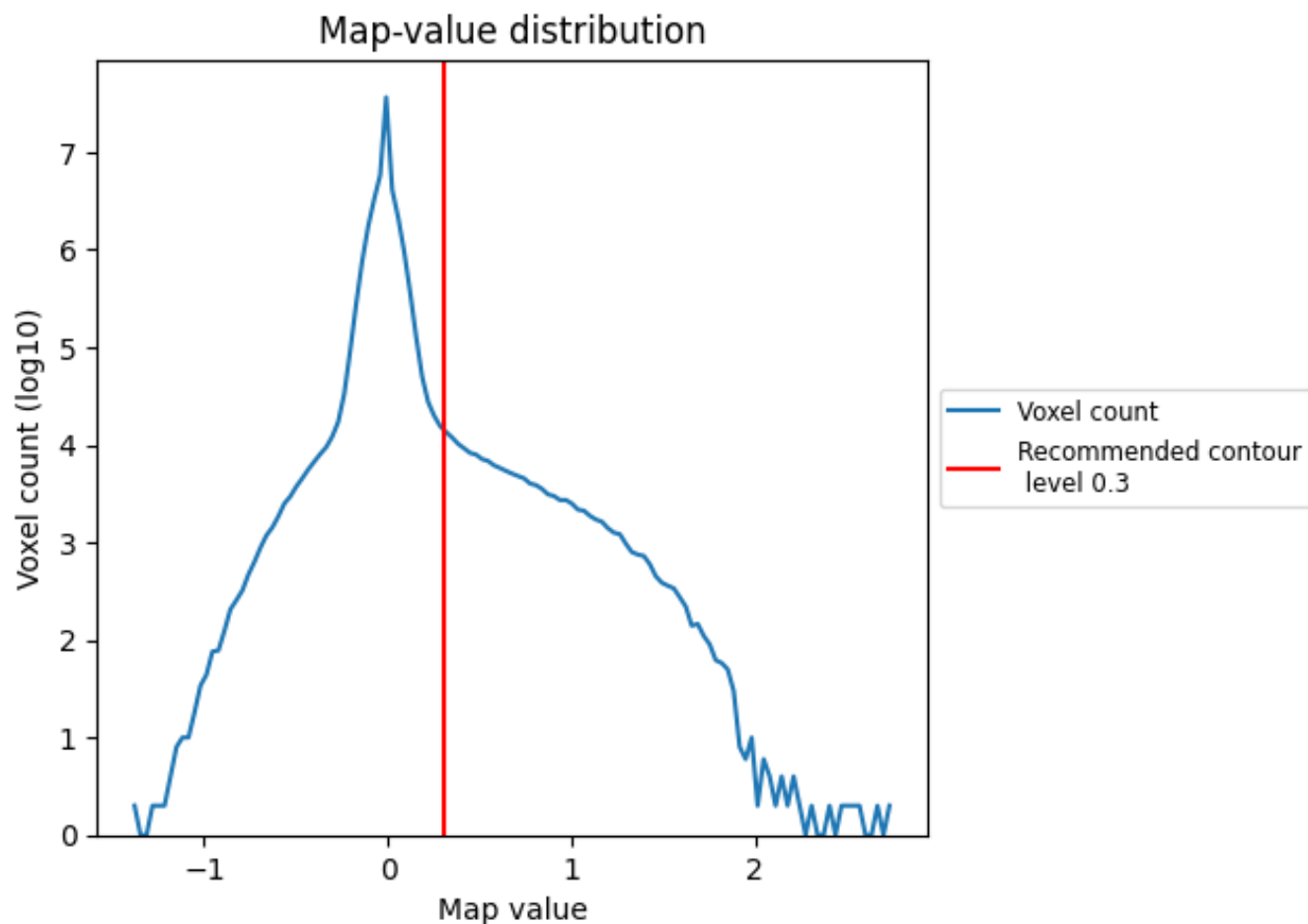


Z

7 Map analysis [i](#)

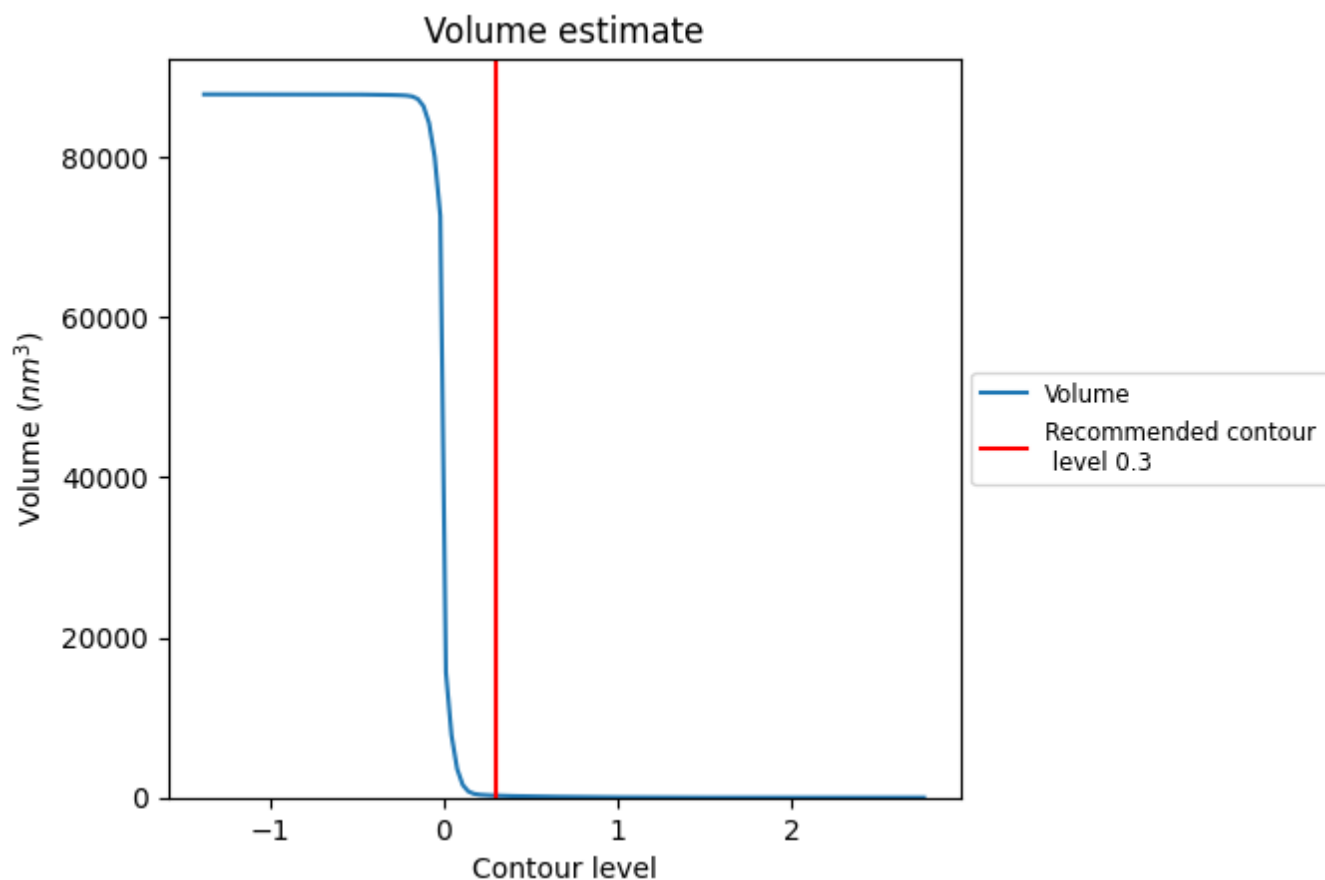
This section contains the results of statistical analysis of the map.

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.

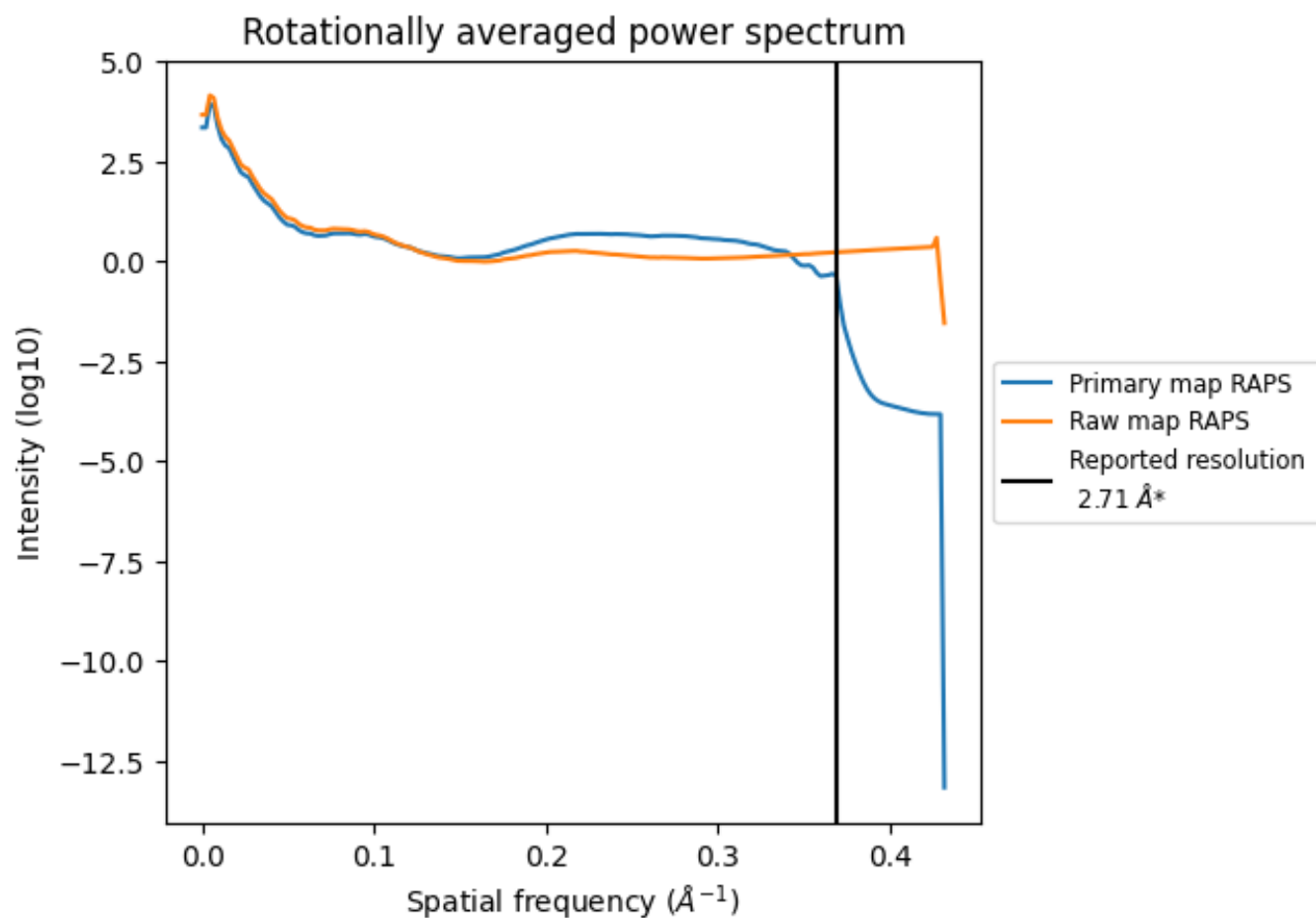
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 249 nm^3 ; this corresponds to an approximate mass of 225 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 ⓘ

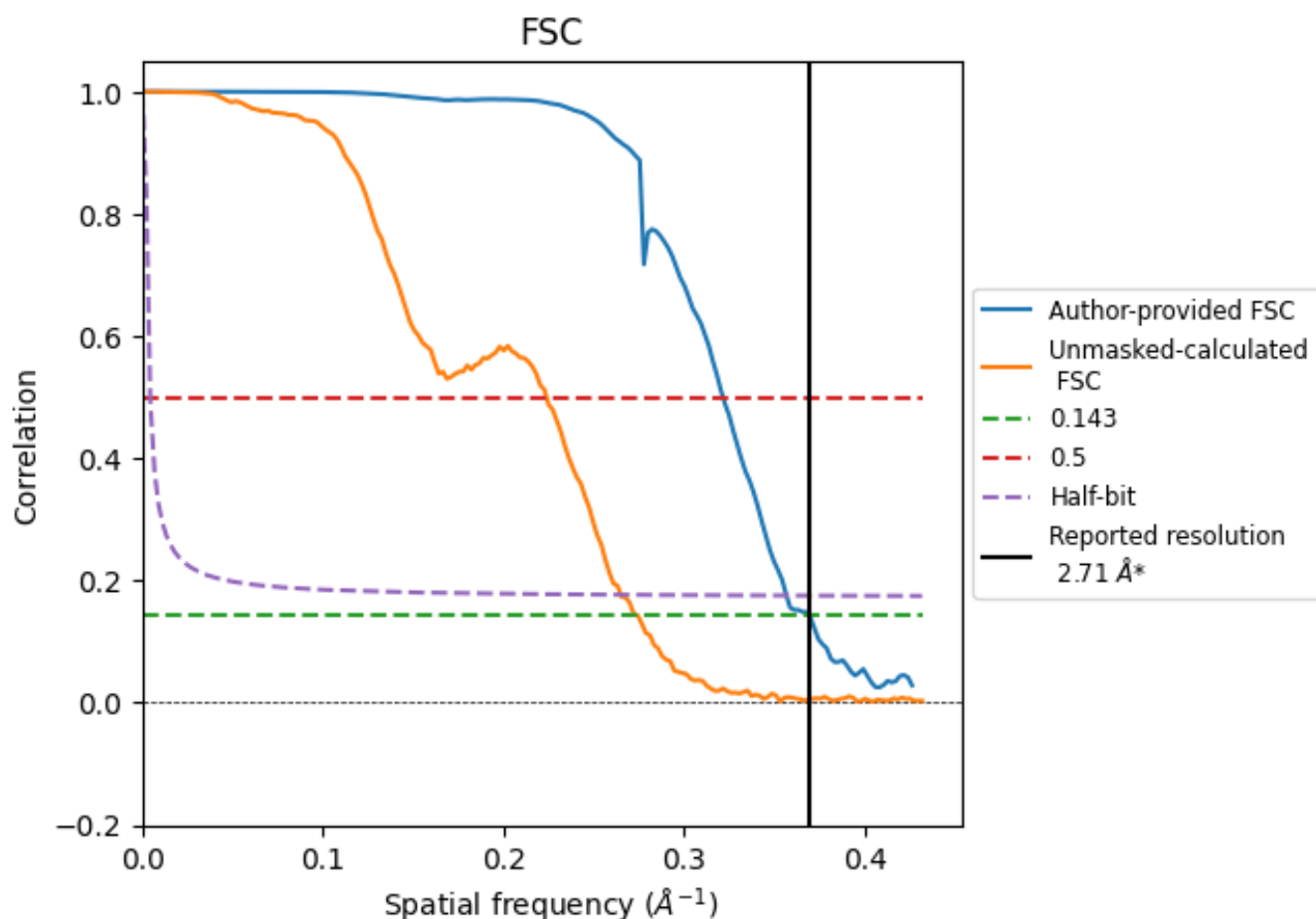


*Reported resolution corresponds to spatial frequency of 0.369 \AA^{-1}

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 0.369 \AA^{-1}

8.2 Resolution estimates [i](#)

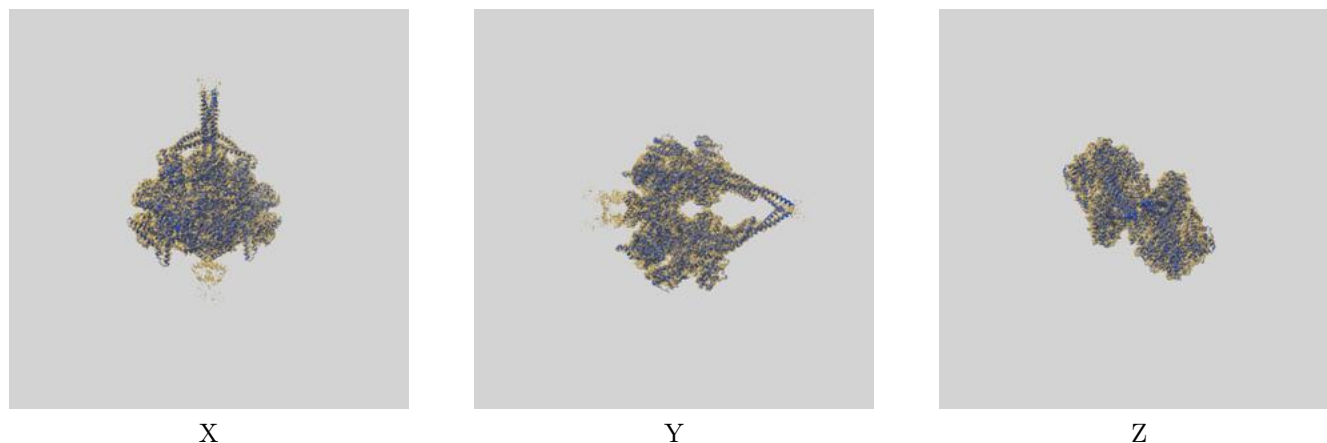
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.71	-	-
Author-provided FSC curve	2.71	3.11	2.80
Unmasked-calculated*	3.65	4.47	3.77

*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 3.65 differs from the reported value 2.71 by more than 10 %

9 Map-model fit [i](#)

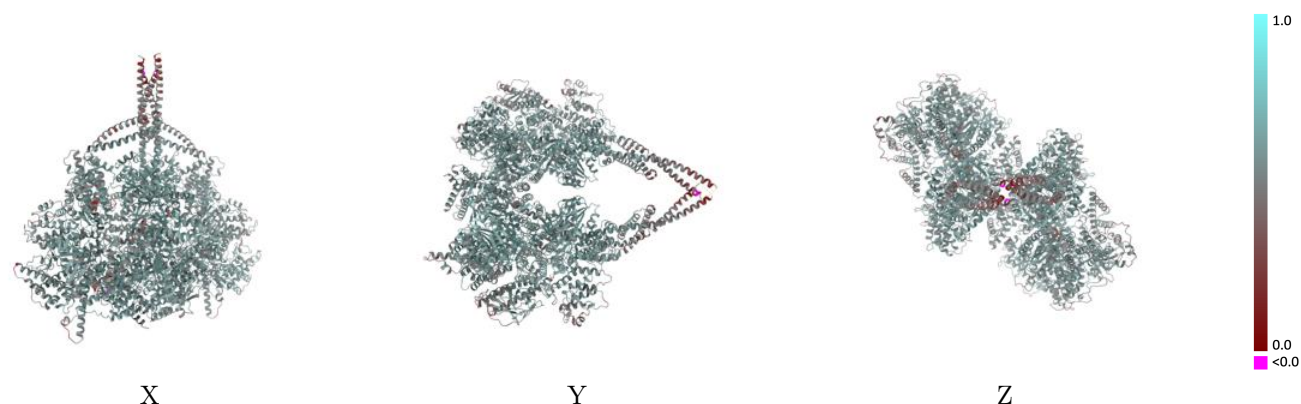
This section contains information regarding the fit between EMDB map EMD-47379 and PDB model 9E10. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



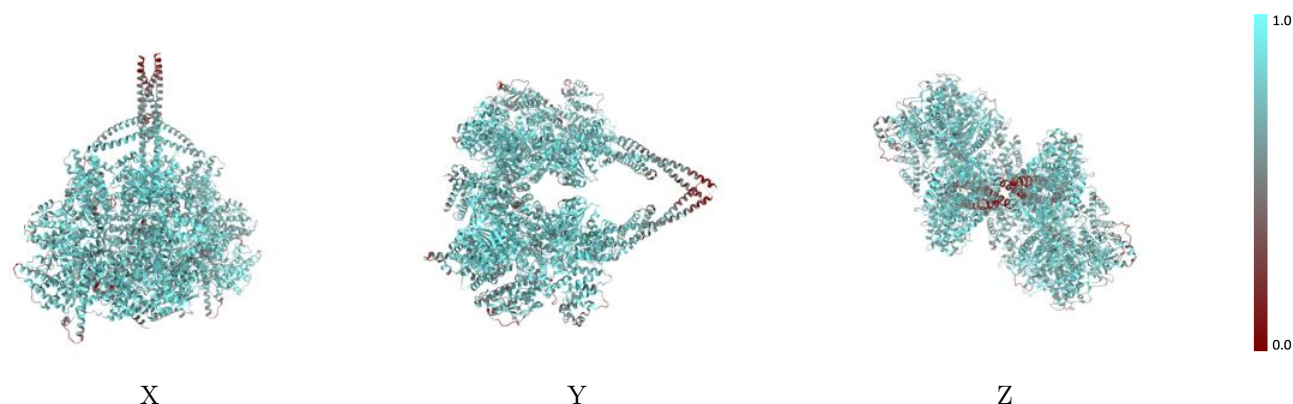
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



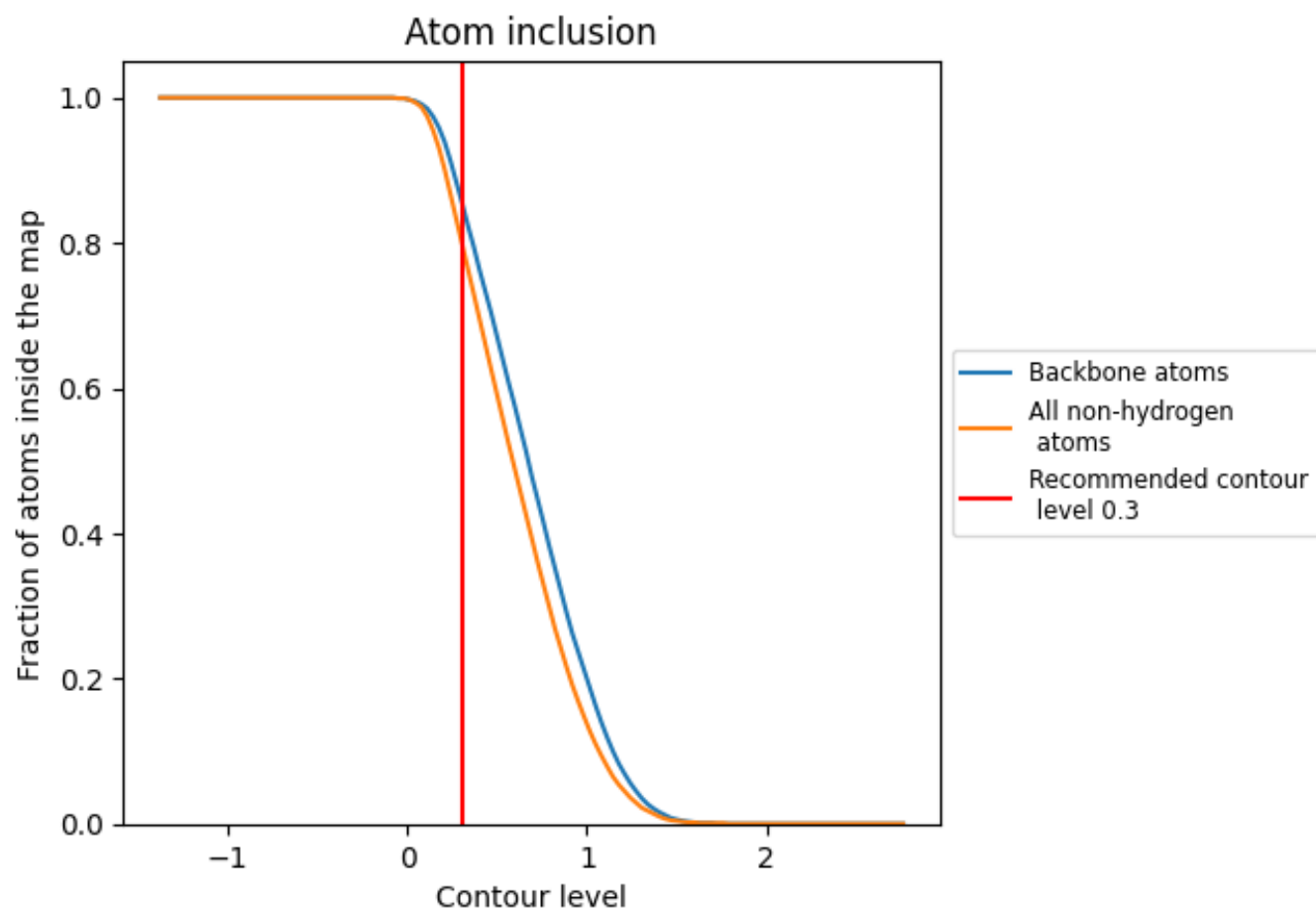
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8040	<div></div> 0.5700
A	<div></div> 0.8050	<div></div> 0.5710
B	<div></div> 0.8040	<div></div> 0.5700

