



## wwPDB EM Validation Summary Report ⓘ

Oct 20, 2025 – 12:26 PM EDT

PDB ID : 9DGP / pdb\_00009dgp  
EMDB ID : EMD-46843  
Title : Motor domain of dynein-1 complex on microtubules  
Authors : Rao, Q.; Chai, P.; Zhang, K.  
Deposited on : 2024-09-03  
Resolution : 3.50 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev129  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

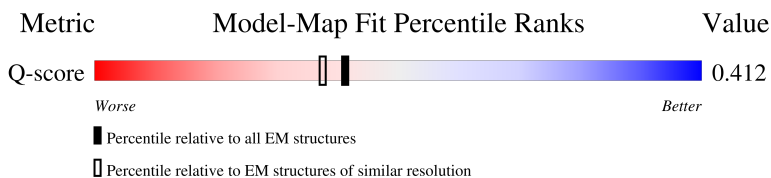
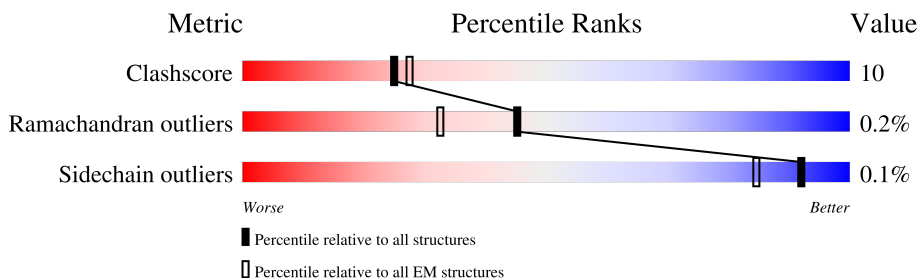
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13950 ( 3.00 - 4.00 )

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  $\geq 3$ , 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 5 unique types of molecules in this entry. The entry contains 24585 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	3037	24461	15582	4227	4533	119	1	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).



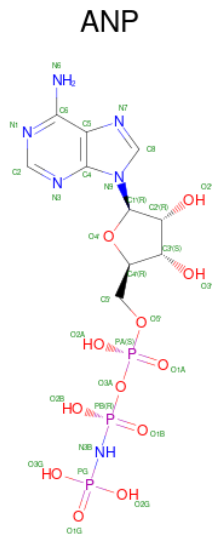
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	27	10	5	10	2	0

- 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 31	C 10	N 5	O 13	P 3	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula:  $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{12}\text{P}_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total 31	C 10	N 6	O 12	P 3	0
4	A	1	Total 31	C 10	N 6	O 12	P 3	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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





R3607	K3491	LEU	ALA	P3127	D3024	V2915	E2775	T2694	Y2493	A2408	D2321
R3620	Q3499	GLU	ASN	D3131	T3028	H2918	F2776	L2605	L2494	R2322	R2322
E3624	M3500	LEU	LYS	L3133	T3028	V2919	T2777	L2620	L2495	R2323	R2323
R3628	L3503	ASP	LYS	P3137	C3033	R2921	T2778	T2634	L2499	L2413	L2324
F3629	L3508	ALA	GLN	R3140	L3042	L2922	E2782	R2643	L2502	Q2414	R2332
V3638	L3509	ARG	VAL	R3140	M3043	R2923	D2787	T2644	L2502	I2415	L2333
D3642	S3510	LYS	GLU	A3142	L3044	L2925	T2788	G2647	S2503	Q2416	S2334
P3643	G3518	VAL	GLN	I3143	F2926	F2926	G2797	V2648	G2504	R2417	L2335
V3644	Y3519	LYS	GLN	V3144	R2927	R2927	R2797	F2682	D2505	A2419	N2338
L3646	F3520	SER	ALA	V3148	E3049	Q2928	K2799	I2666	S2506	A2420	V2339
N3646	Q3523	ASN	ALA	A3157	W3053	L2933	T2800	N2667	N2510	Q2424	R2340
V3648	M3524	LYS	GLU	A3157	Q3057	L2935	E2798	N2668	R2511	P2425	L2341
L3649	M3524	LYS	GLU	N3158	E3061	L2936	K2799	L2668	L2514	F2342	F2343
R3659	L3536	PRO	VAL	T3168	N3061	V2938	E2808	M2671	L2518	V2345	V2345
V3660	Q3537	SER	ALA	T3172	V3064	K2943	R2811	D2672	T2522	L2432	V2347
L3661	Q3538	TYR	VAL	T3172	V3065	K2943	R2811	K2673	T2522	V2433	L2348
I3662	A3539	ASN	GLN	D3178	F3066	L2946	R2823	Y2674	V2524	T2428	F2343
T3663	N3540	TYR	LEU	A3184	T3067	S2947	E2828	G2675	T2524	P2429	V2345
L3664	I3541	GLU	ILE	A3184	M3068	R2948	A2829	R2694	P2527	L2437	L2369
D3668	E3551	VAL	GLU	R3191	N3069	F2949	A2829	V2701	K2528	H2438	C2359
L3671	Y3552	ASN	GLN	S3192	P3070	V2950	R2836	R2701	A2529	H2439	V2360
V3679	L3560	ALA	GLN	L3194	GLU	M2953	T2846	F2708	P2532	A2440	R2361
S3680	R3561	LEU	LEU	E3195	GLY	L2956	L2855	C2712	P2532	L2442	V2362
T3681	L3561	ALA	LEU	E3195	LEU	L2956	R2856	R2713	P2532	K2443	L2369
R3682	P3568	GLY	GLY	E3196	ASP	R2965	H2857	P2714	L2534	H2445	S2370
D3691	C3573	PRO	SER	M3199	ARG	R2966	K2863	G2719	L2535	I2446	T2371
L3692	T3574	VAL	THR	R3206	ALA	T2967	E2864	R2720	L2541	D2446	D2372
C3693	E3575	LEU	ASP	K3207	T3081	G2969	E2864	R2720	G2543	L2449	M2373
S3694	L3578	LYS	ASP	E3210	R3088	E2970	M2867	L2723	E2544	R2451	L2374
V3696	M3579	ALA	LYS	T3211	C3089	E2970	S2868	R2726	L2545	L2452	L2382
N3700	L3580	ALA	ILE	E3217	L3091	D2973	R2869	F2727	T2571	R2453	L2385
S3706	K3581	GLN	VAL	R3220	N3092	R2982	L2872	L2728	T2574	C2464	P2386
F3707	R3582	LEU	ASP	D3221	W3093	K2986	V2884	V2731	T2574	S2460	L2387
L3708	N3584	ALA	ASP	LEU	T3099	K2989	L2889	V2734	L2581	A2465	D2388
V3716	D3591	ASP	ARG	ARG	T3099	E2996	V2893	V2734	L2581	A2465	E2389
V3724	F3592	LEU	VAL	ILE	Y3103	E2996	R2894	I2747	E2587	Q2471	R2396
Q3739	A3596	LYS	PRO	SER	E3108	S2997	A2895	Y2748	R2588	Y2472	R2397
L3740	T3597	ARG	ILE	GLN	E3108	N2998	R2896	G2749	P2590	N2473	R2398
R3743	L3600	PRO	THR	GLU	M3113	V2999	V2899	T2750	L2591	M2481	R2399
N3749	M3601	LEU	ILE	LEU	D3114	L3005	V2899	R2757	V2592	L2486	G2400
L3749	N3602	VAL	GLU	GLU	L3115	M3008	L2905	L2762	L2593	E2487	R2401
	E3603	ARG	ALA	VAL	L3115	M3008	V2910	L2762	L2593	R2488	E2402
		ASN	ASN	LYS	P3123	M3008	V2910	L2762	L2593	Y2489	D2403
		ALA	ALA	ALA	M3126	L3011	E2914	Y2765	M2603	I2490	E2404
						L3012					G2405
						A3013					E2406
											E2407



E4538	N4404	R4301	F4147	T4028	V3871	A3752
L4539	I4405	R4302	T4160	H4029	M3875	L3753
C4540	P4408	Q4307	R4168	I4030	L3876	N3754
L4541	R4411	L4311	I4169	M4043	H3877	E3755
E4542	F4412	P4324	S4172	C4044	Q3878	V3756
V4543	V4417	M4325	E4175	S4045	D3879	K3757
S4548	L4423	N4326	R4176	Y4049	A3884	K3758
Q4549	L4424	V4330	A4177	V4055	M3885	I3760
S4550	L4424	V4330	A4178	L4058	L3887	L3761
A4551	Q4429	T4333	Q4191	S4068	A3888	D3762
D4554	D4433	K4342	E4192	I4069	R3889	D3763
S4557	C4438	M4343	R4193	A4070	I3890	D3764
F4558	K4564	L4344	L4194	I4071	K3891	T3765
K4564	K4442	K4345	E4209	Q4079	T3900	I3767
T4569	L4448	M4346	L4212	A4080	Y3901	T3768
K4574	L4460	L4349	R4213	A4081	E3902	T3769
S4578	L4460	E4350	S4214	K4082	L3909	L3770
T4583	S4463	D4351	D4217	N4085	K3912	E3771
V4586	E4465	E4352	D4224	T4086	I3914	L3773
L4587	S4465	D4353	P4239	A4087	V3915	K3774
T4588	H4466	ASP	A4242	V4088	L3916	T3787
Q4589	V4475	LEU	A4248	K4089	S3917	M3791
L4590	I4476	ALA	G4091	S4090	A3918	V3794
V4597	Q4477	GLU	R4092	R4092	P3922	V3797
A4598	W4478	THR	A4093	W4093	K3923	Y3801
K4601	V4479	GLU	V4094	L4094	I3924	S3809
V4604	R4485	LYS	I4251	L4096	Q3931	S3817
V4605	I4486	THR	G4253	K4097	A3932	Q3820
V4609	S4493	THR	T4267	N4098	E3933	I3821
I4619	A4504	THR	R4271	V4099	A3934	L3829
F4620	K4505	ASP	R4276	H4100	V3935	L3835
V4622	G4513	GLY	F4278	L4106	V3936	Y3836
I4626	P4517	ARG	D4279	W4105	F3944	V3839
A4627	Y4520	THR	F4282	L4124	P3966	V3849
E4630	Y4521	H4381	K4283	F4125	W3974	L3856
Y4636	T4524	M4386	L4284	L4126	I3983	C3857
E4637	R4525	W4387	T4127	W4128	F3996	I3858
V4642	Q4526	L4390	K4292	E4129	R4000	I3859
E4646	Y4527	L4398	D4293	I4130	V4009	L3863
	L4536	T4401	I4294	L4137	N4012	V3866
	E4537		G4299	L4138	L4013	
			I4300	V4146	L4027	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	106660	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	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.813	Depositor
Minimum map value	-1.093	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.15	Depositor
Map size ( $\text{\AA}$ )	333.312, 333.312, 333.312	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.302, 1.302, 1.302	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, ANP, ADP, MG

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	0.37	0/24982	0.49	0/33848

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	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1360	ARG	Sidechain
1	A	2292	ARG	Sidechain
1	A	2757	ARG	Sidechain
1	A	4123	ARG	Sidechain
1	A	4302	ARG	Sidechain

### 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	24461	0	24528	508	0
2	A	27	0	12	2	0
3	A	31	0	12	2	0
4	A	62	0	26	4	0
5	A	4	0	0	0	0
All	All	24585	0	24578	508	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 10.

The worst 5 of 508 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:2598:GLY:H	4:A:4703:ANP:HNB1	1.23	0.85
1:A:3638:VAL:HG12	1:A:3681:THR:HB	1.64	0.79
1:A:1370:LEU:HD11	1:A:1390:LEU:HD12	1.66	0.77
1:A:2581:LEU:HD21	1:A:2605:LEU:HD23	1.68	0.75
1:A:2506:SER:HB3	1:A:2510:MET:HB2	1.71	0.70

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	3026/4646 (65%)	2968 (98%)	53 (2%)	5 (0%)	44 75

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3914	ILE
1	A	4586	PRO
1	A	4028	THR

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Mol	Chain	Res	Type
1	A	4292	LYS
1	A	4130	ILE

### 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	2704/4122 (66%)	2702 (100%)	2 (0%)	<a href="#">92</a> <a href="#">97</a>

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2295	LEU
1	A	2855	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4078	ASN
1	A	4100	HIS
1	A	4506	ASN
1	A	2282	HIS
1	A	2263	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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 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
4	ANP	A	4704	5	29,33,33	2.51	6 (20%)	31,52,52	1.50	4 (12%)
2	ADP	A	4701	-	24,29,29	0.88	0	29,45,45	1.22	2 (6%)
4	ANP	A	4703	5	29,33,33	2.49	6 (20%)	31,52,52	1.45	3 (9%)
3	ATP	A	4702	5	28,33,33	0.72	0	34,52,52	0.58	1 (2%)

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
4	ANP	A	4704	5	-	8/14/38/38	0/3/3/3
2	ADP	A	4701	-	-	3/12/32/32	0/3/3/3
4	ANP	A	4703	5	-	4/14/38/38	0/3/3/3
3	ATP	A	4702	5	-	3/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4704	ANP	PB-O3A	8.86	1.70	1.59
4	A	4703	ANP	PB-O3A	8.83	1.70	1.59
4	A	4703	ANP	PG-N3B	6.22	1.79	1.63
4	A	4704	ANP	PG-N3B	6.17	1.79	1.63
4	A	4704	ANP	PG-O1G	4.69	1.53	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	4703	ANP	O2B-PB-O1B	4.90	120.38	109.87
4	A	4704	ANP	O2B-PB-O1B	4.81	120.18	109.87
4	A	4704	ANP	O1G-PG-N3B	-4.09	105.75	111.77
4	A	4703	ANP	O1G-PG-N3B	-3.84	106.12	111.77
2	A	4701	ADP	N3-C2-N1	-3.69	123.67	128.67

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	4703	ANP	PB-N3B-PG-O1G
4	A	4703	ANP	PA-O3A-PB-O2B
4	A	4704	ANP	PB-N3B-PG-O1G
4	A	4704	ANP	PG-N3B-PB-O1B
4	A	4704	ANP	C5'-O5'-PA-O2A

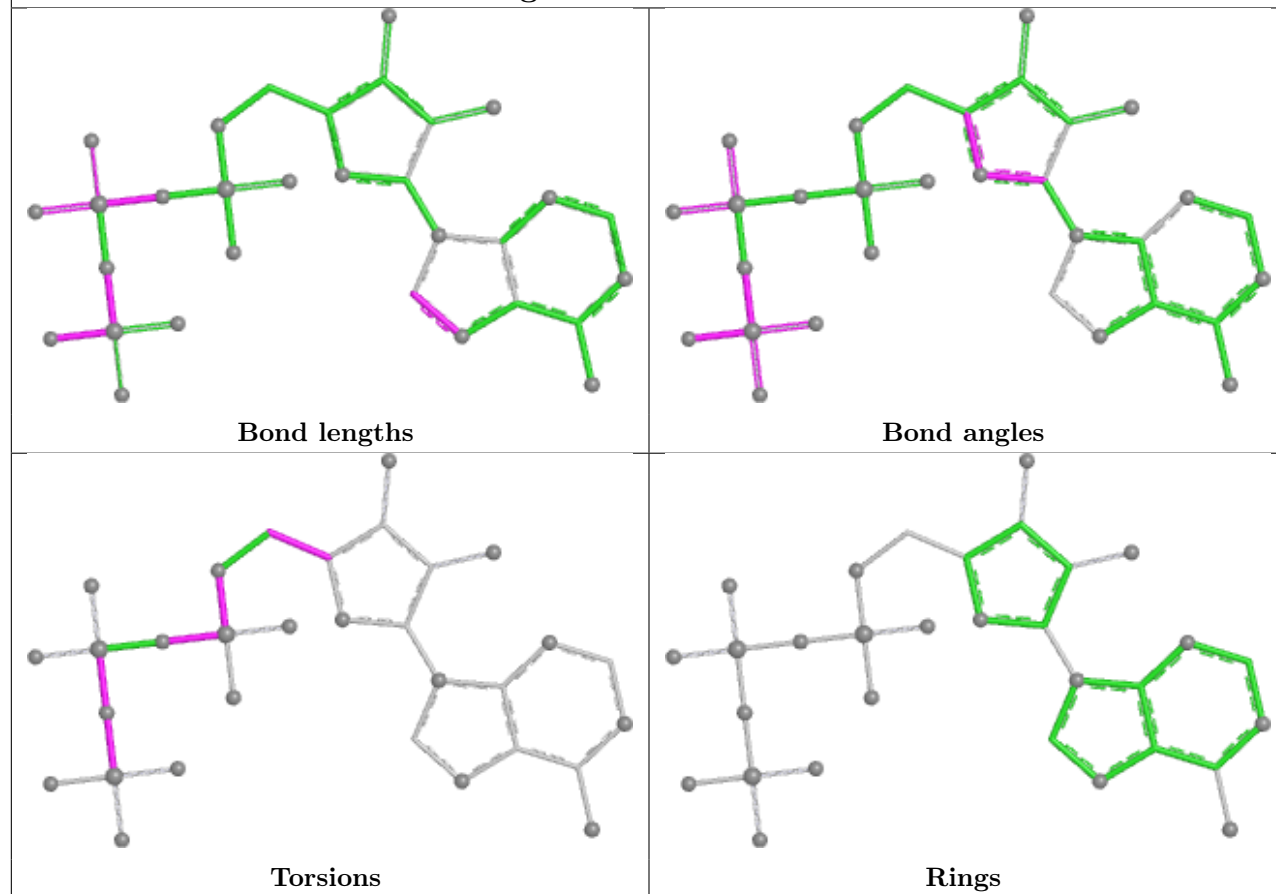
There are no ring outliers.

3 monomers are involved in 8 short contacts:

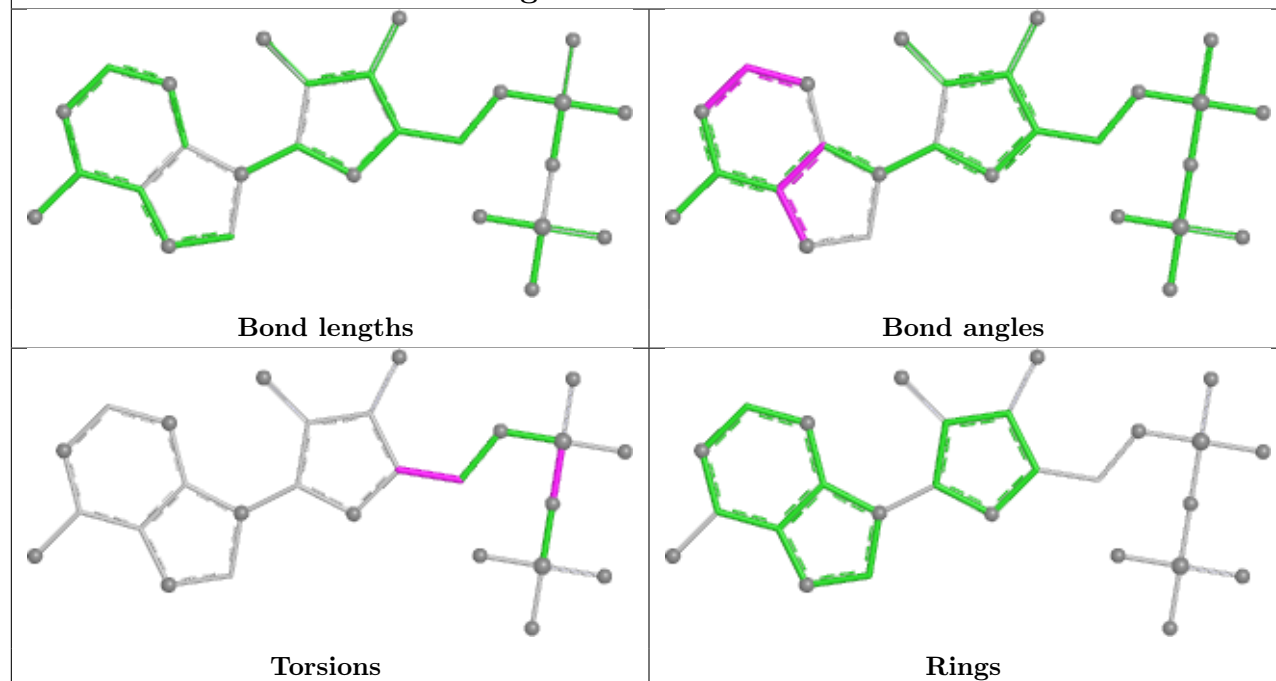
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	4701	ADP	2	0
4	A	4703	ANP	4	0
3	A	4702	ATP	2	0

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.

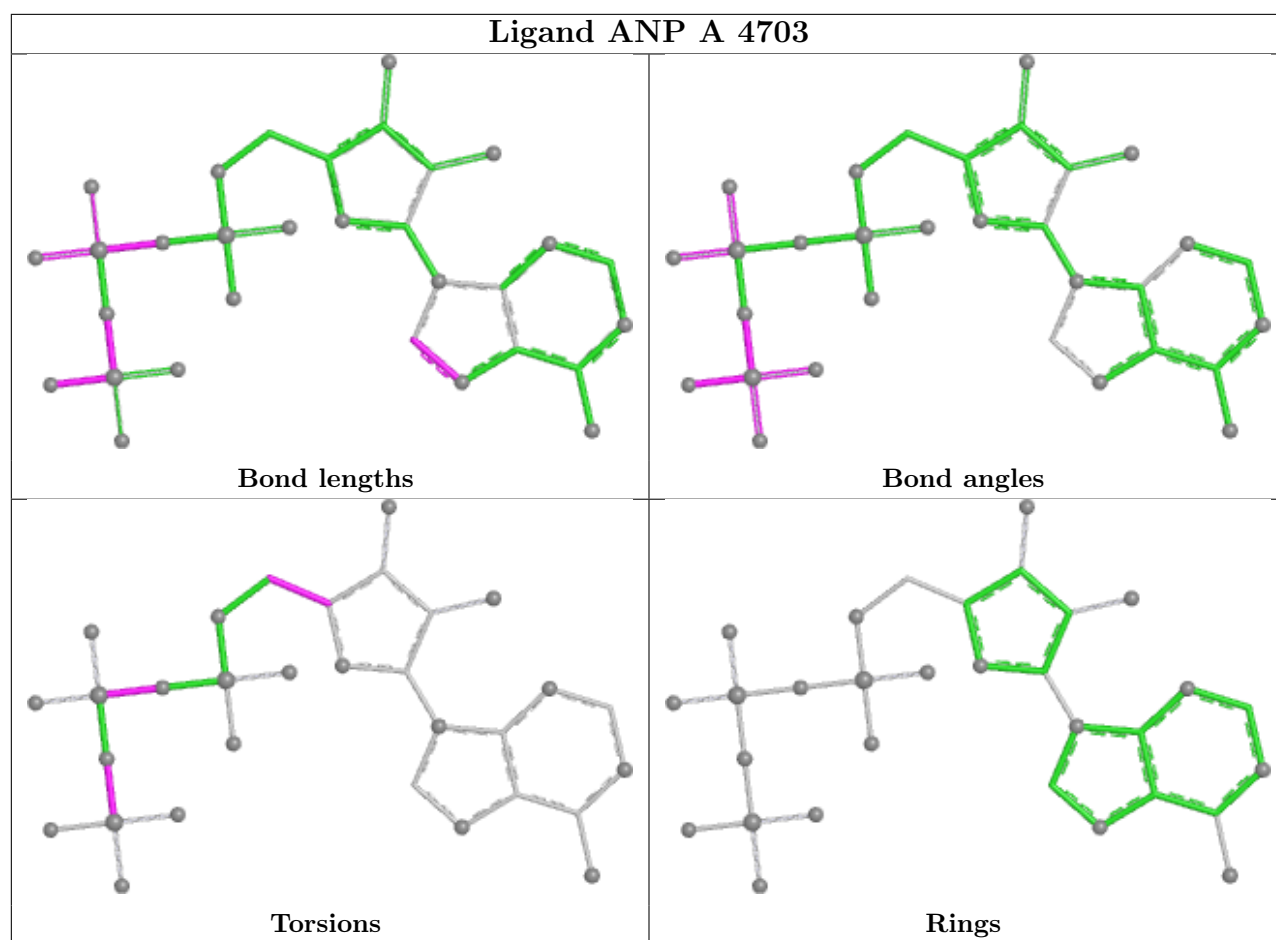
## Ligand ANP A 4704

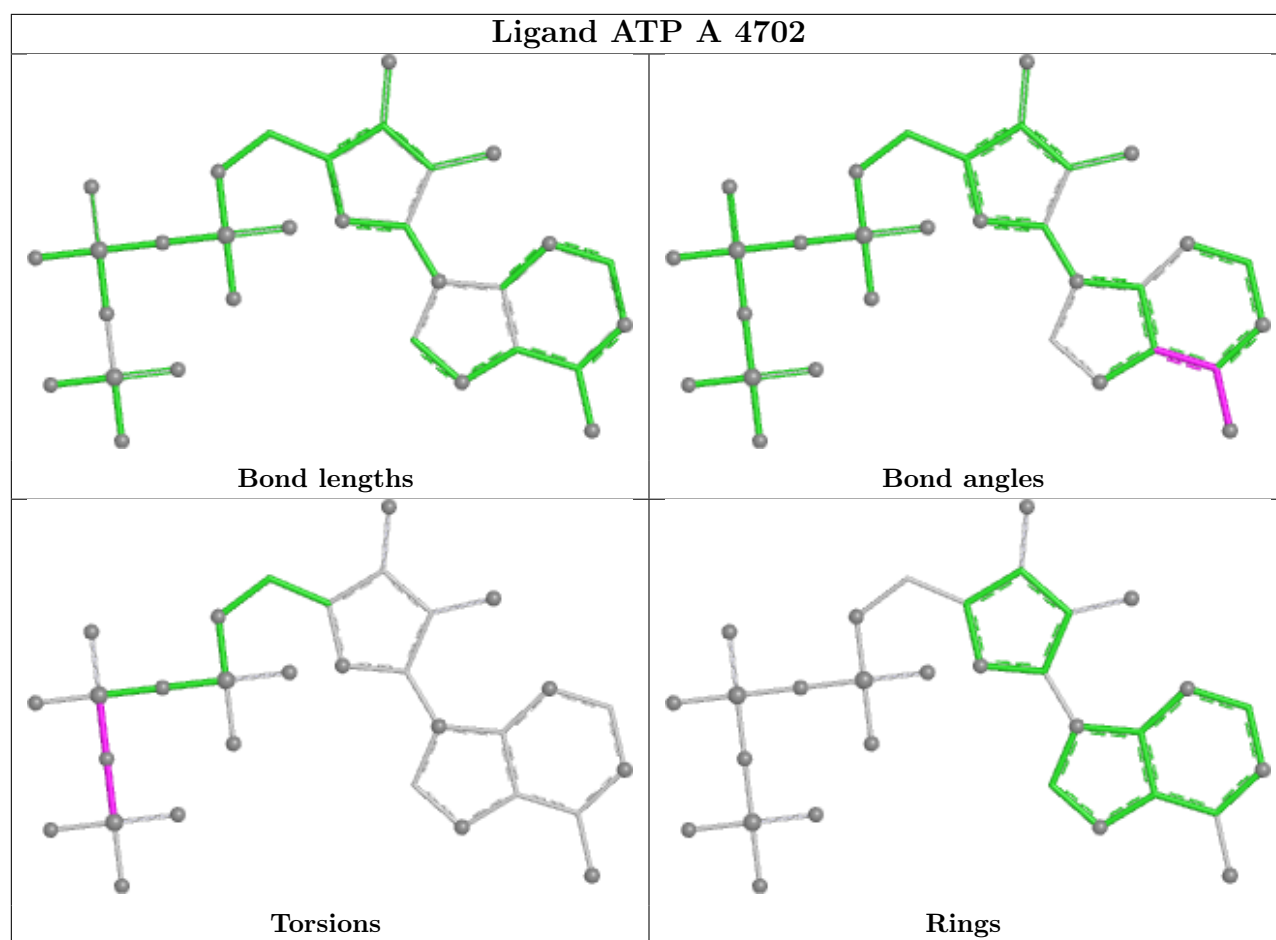


## Ligand ADP A 4701









## 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.

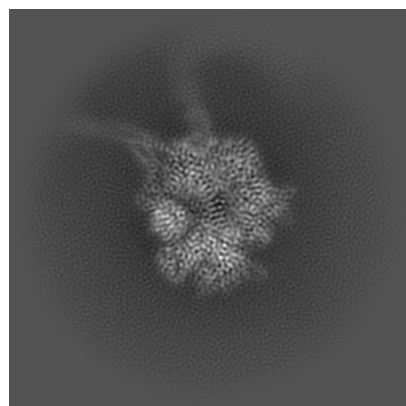
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46843. These allow visual inspection of the internal detail of the map and identification of artifacts.

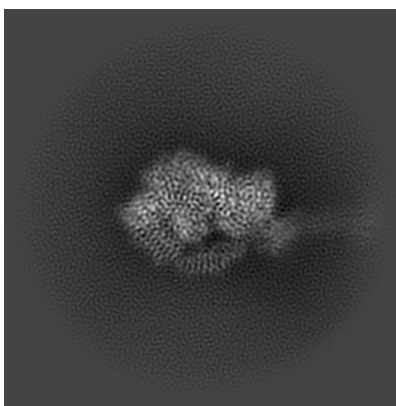
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

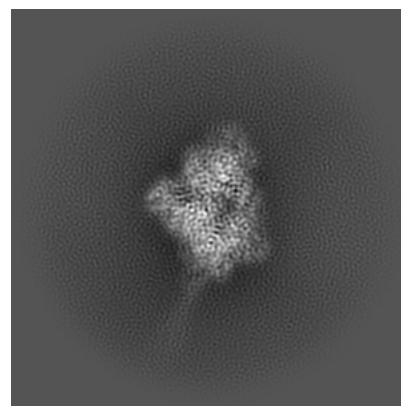
#### 6.1.1 Primary map



X

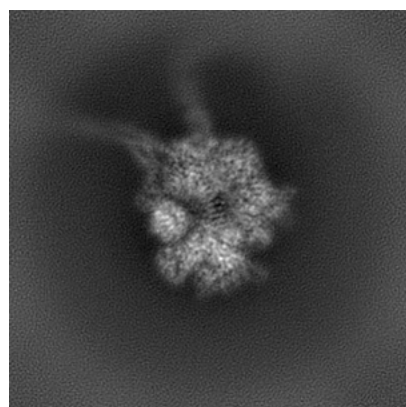


Y

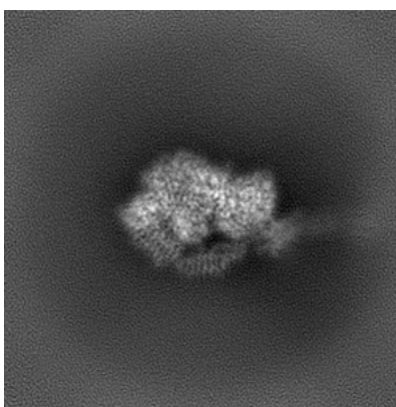


Z

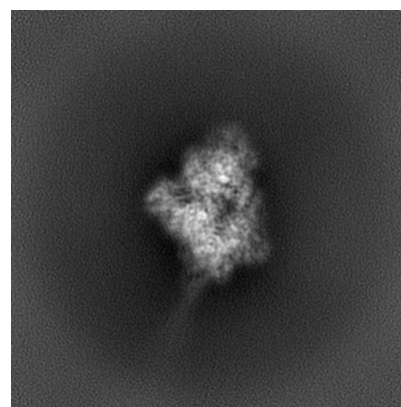
#### 6.1.2 Raw map



X



Y

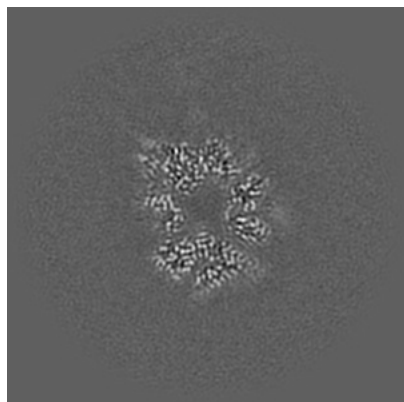


Z

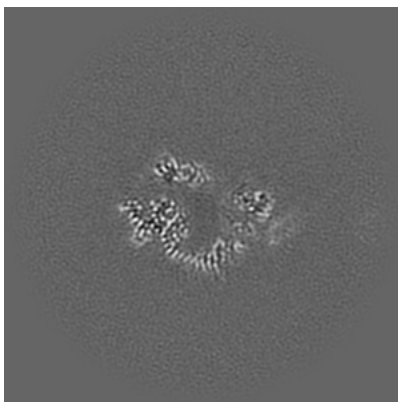
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

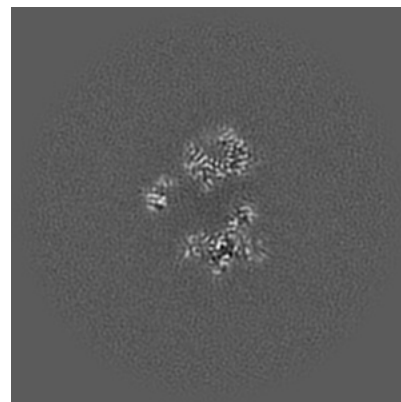
### 6.2.1 Primary map



X Index: 128

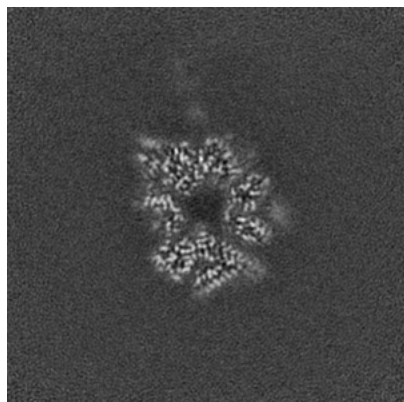


Y Index: 128

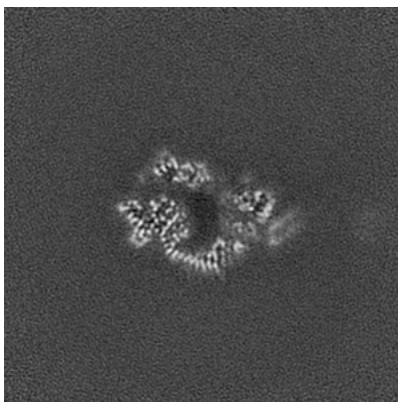


Z Index: 128

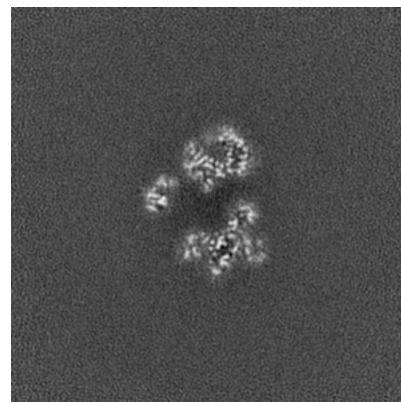
### 6.2.2 Raw map



X Index: 128



Y Index: 128

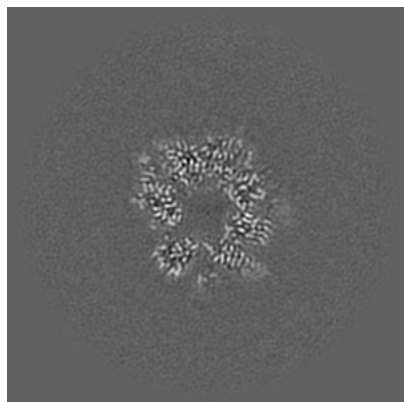


Z Index: 128

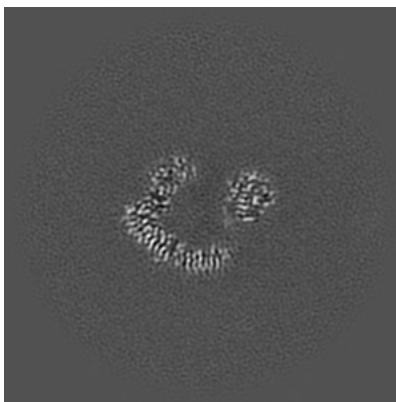
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

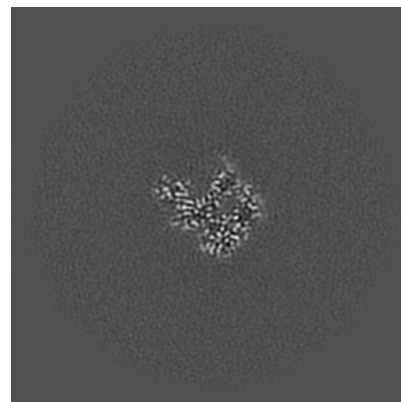
### 6.3.1 Primary map



X Index: 132

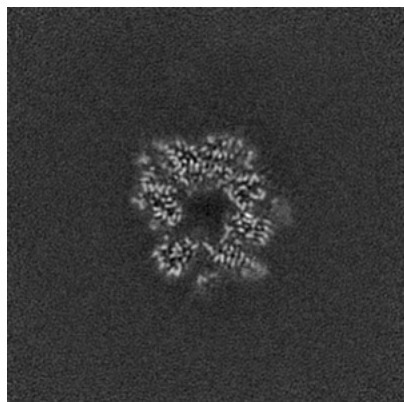


Y Index: 136

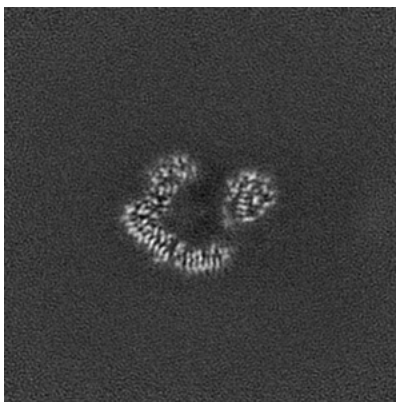


Z Index: 101

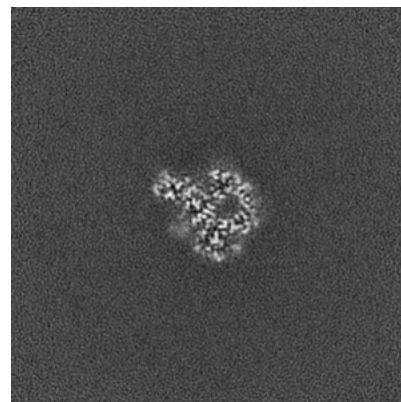
### 6.3.2 Raw map



X Index: 132



Y Index: 136



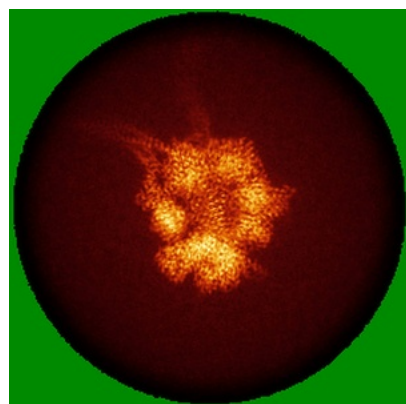
Z Index: 97

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

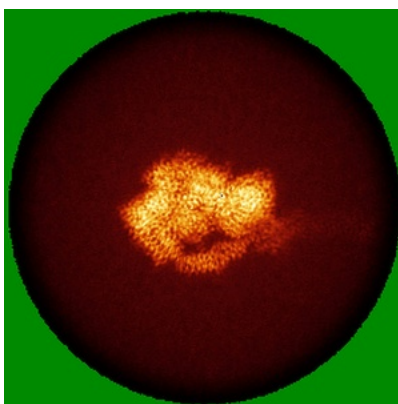


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

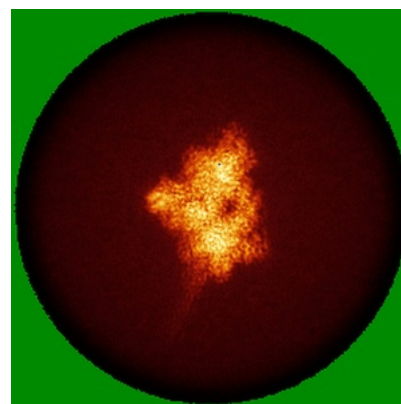
### 6.4.1 Primary map



X

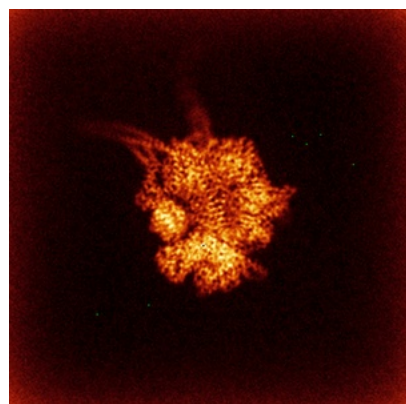


Y

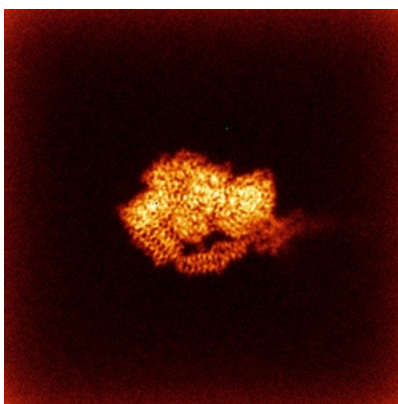


Z

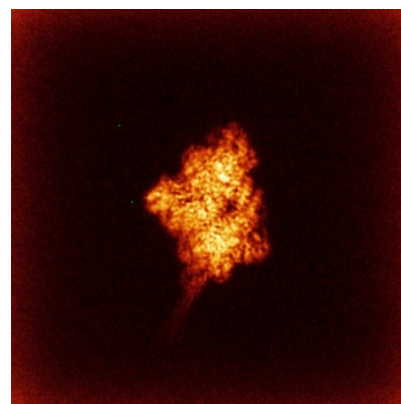
### 6.4.2 Raw map



X



Y

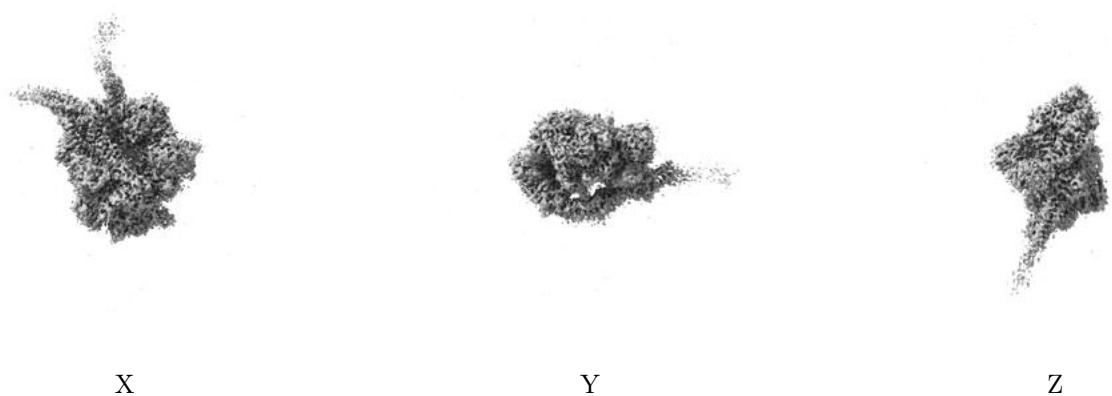


Z

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.

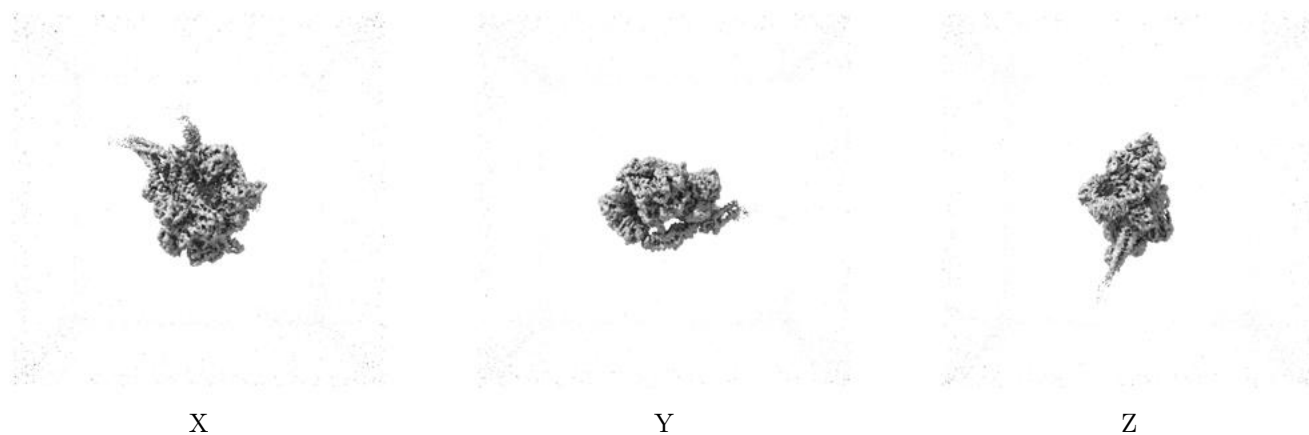
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

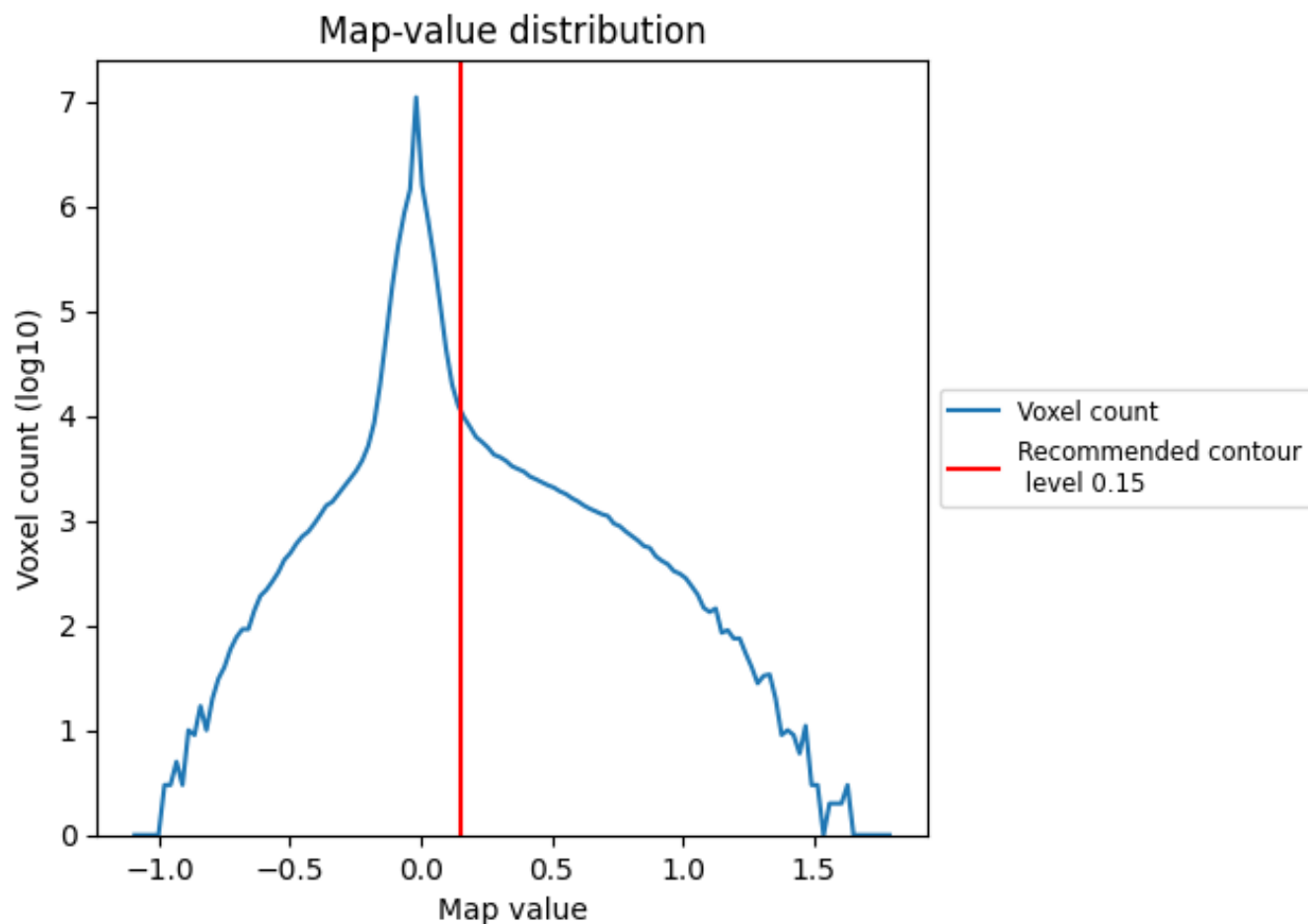
## 6.6 Mask visualisation [i](#)

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.

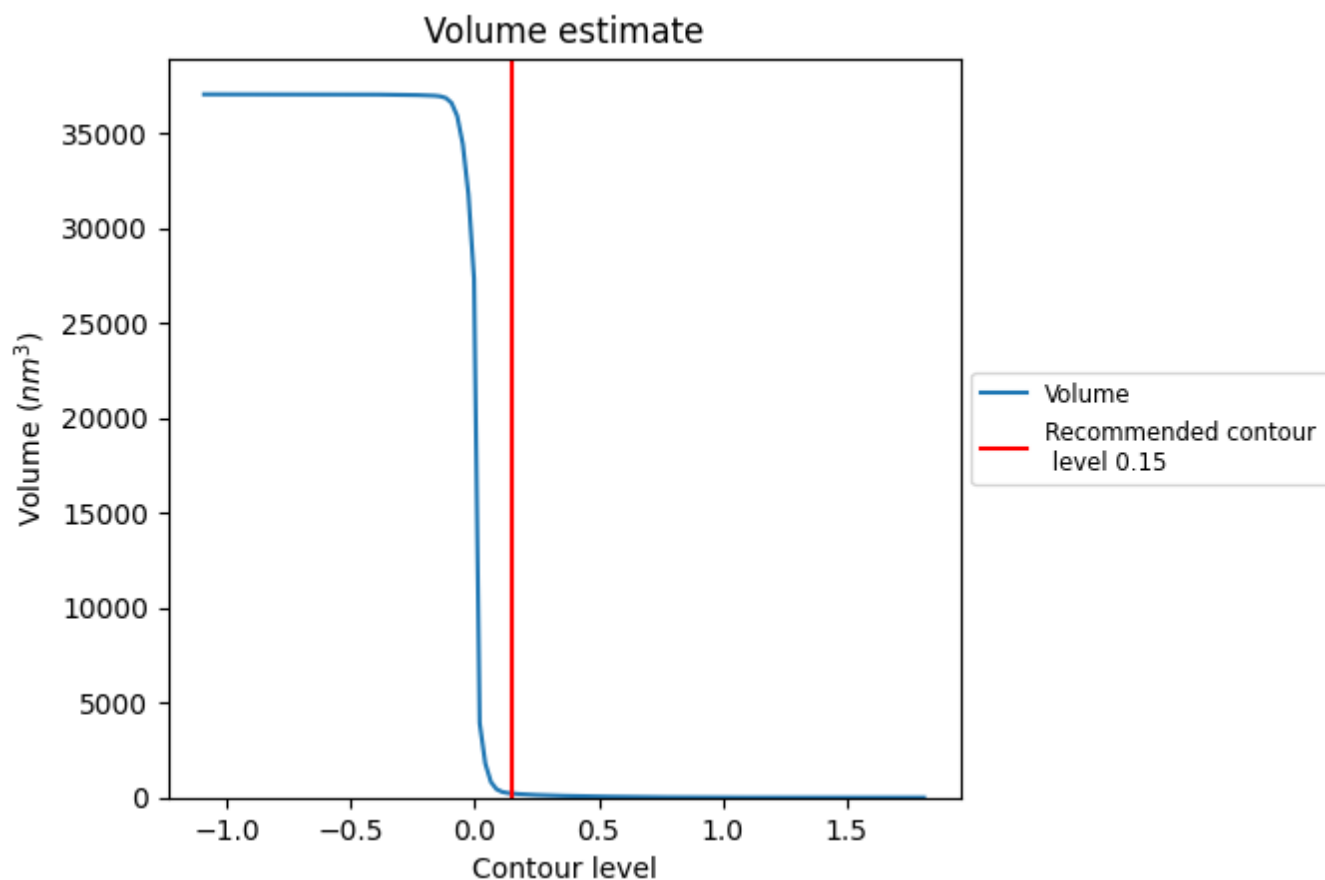
### 7.1 Map-value distribution [i](#)



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.



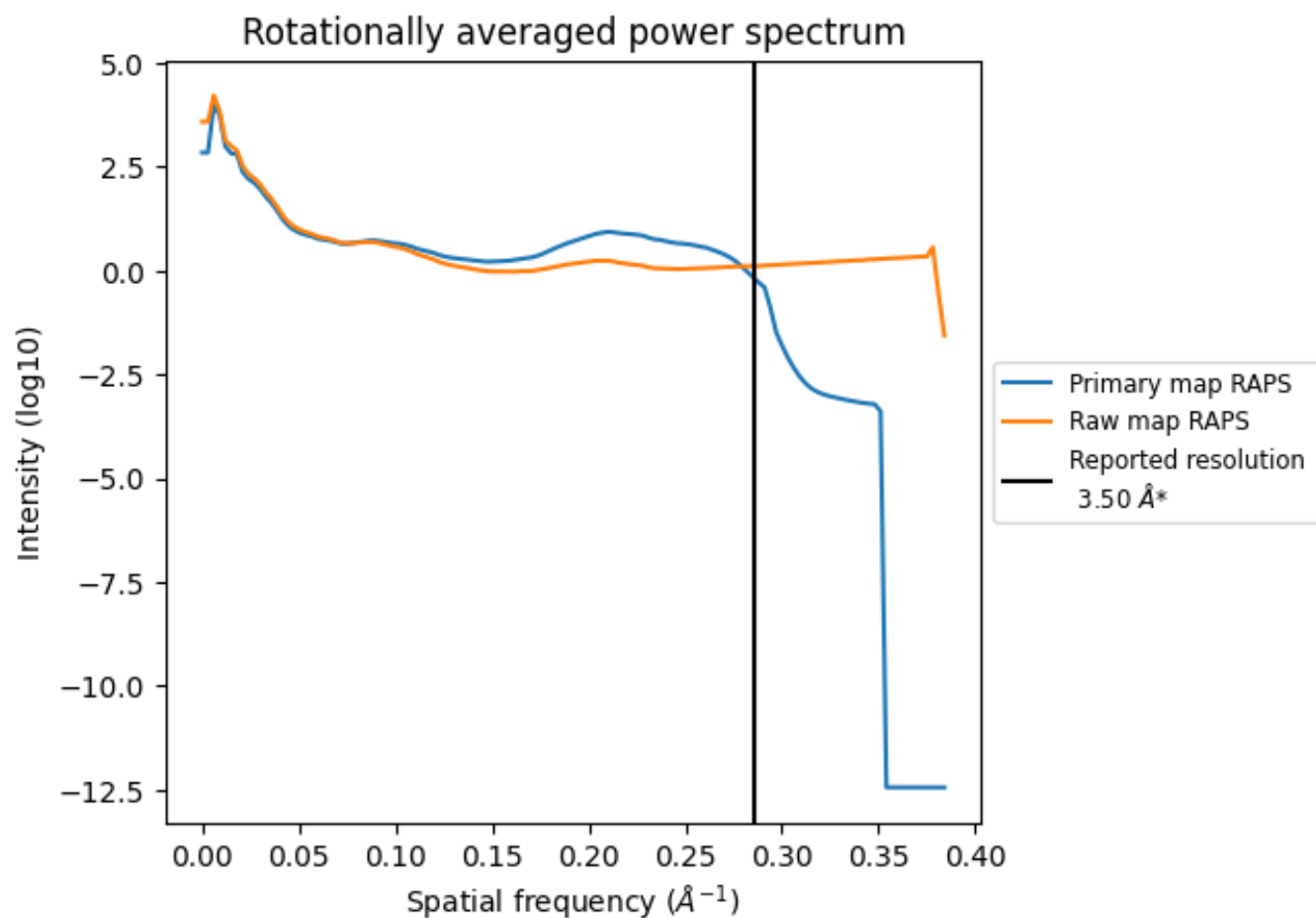
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 215  $\text{nm}^3$ ; this corresponds to an approximate mass of 194 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 ⓘ

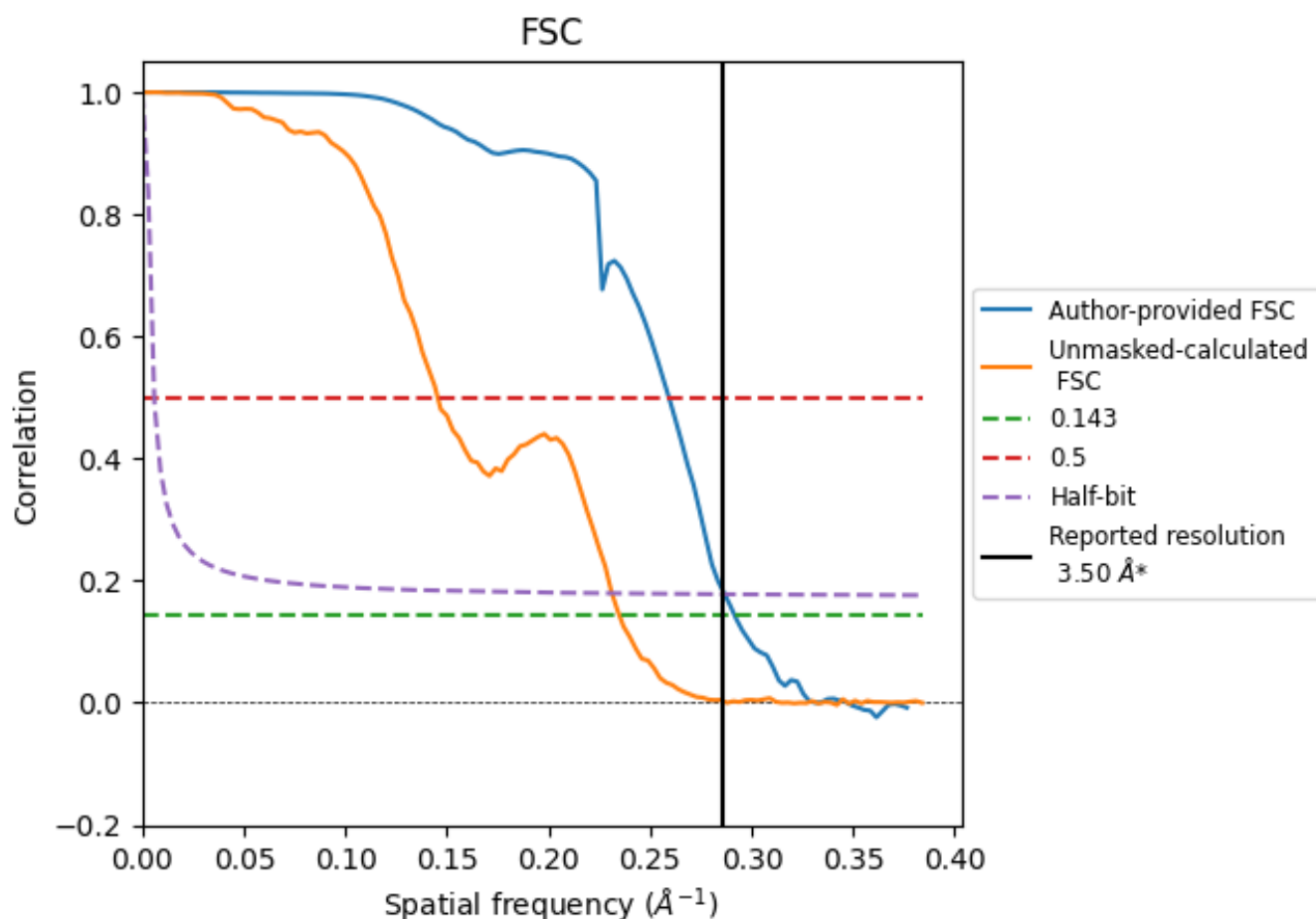


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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  $0.286 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

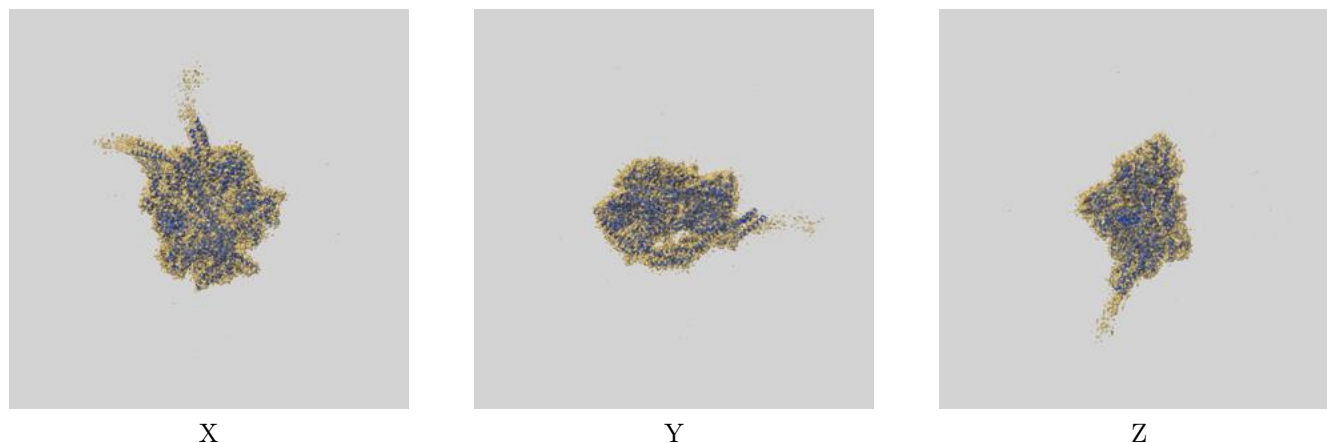
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.43	3.86	3.49
Unmasked-calculated*	4.26	6.87	4.32

\*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 4.26 differs from the reported value 3.5 by more than 10 %

## 9 Map-model fit [i](#)

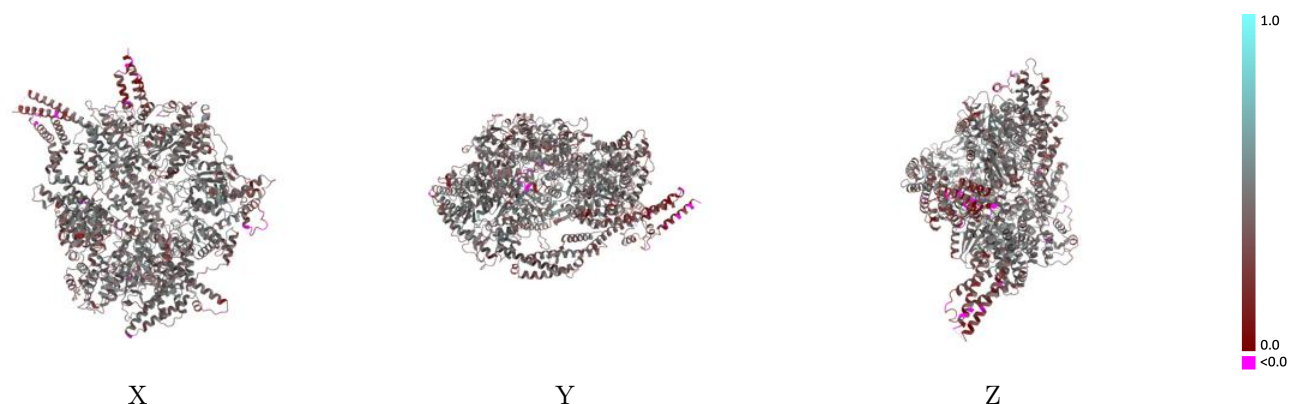
This section contains information regarding the fit between EMDB map EMD-46843 and PDB model 9DGP. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

### 9.1 Map-model overlay [i](#)



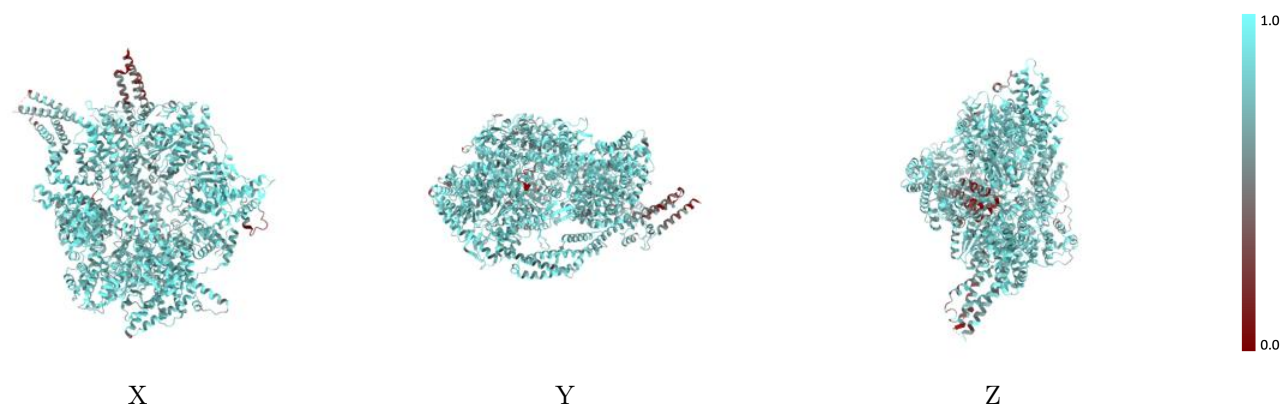
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



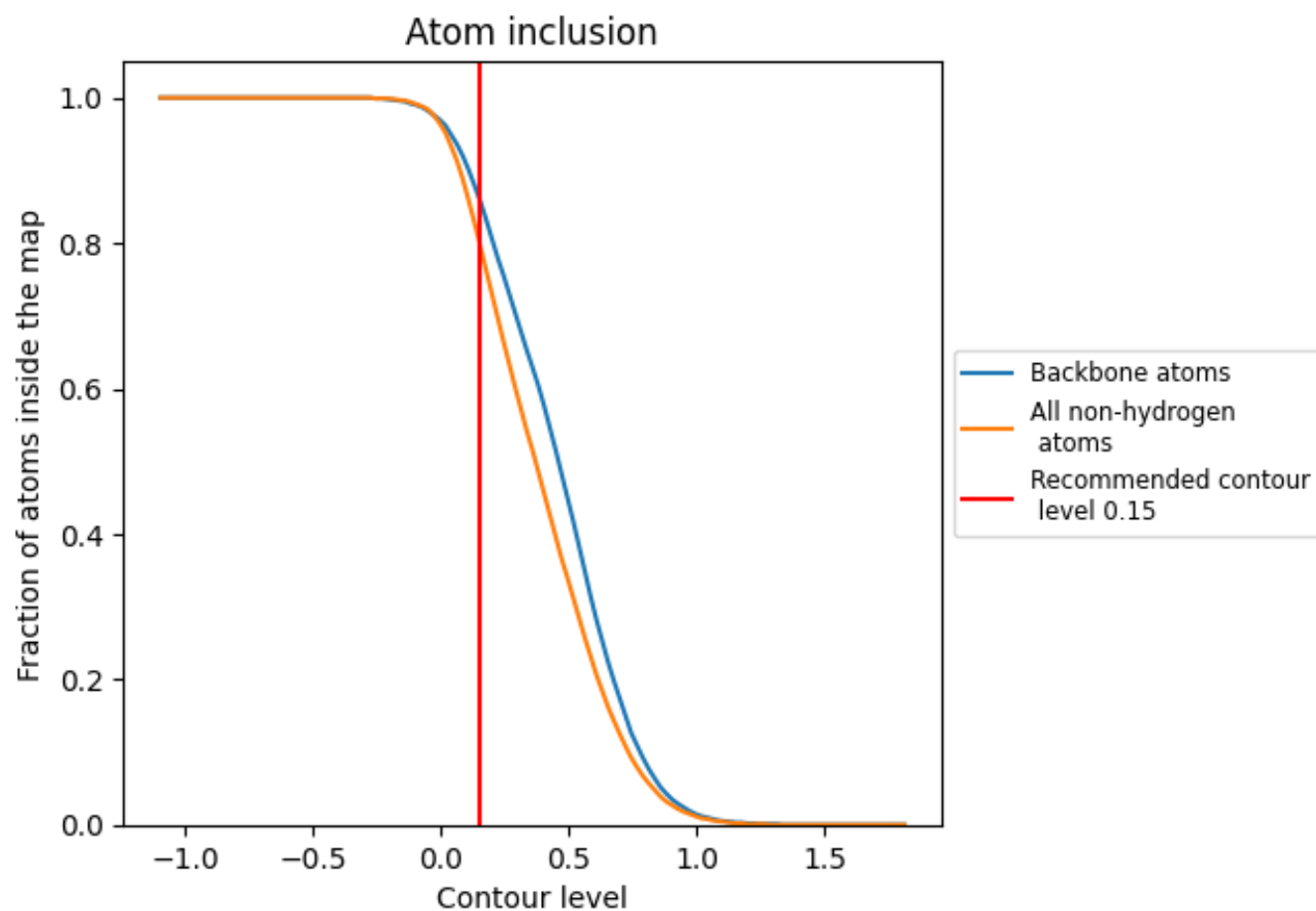
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

## 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8050	<div></div> 0.4120
A	<div></div> 0.8050	<div></div> 0.4120

