



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2025 – 06:28 PM EDT

PDB ID : 9E0Z / pdb_00009e0z
EMDB ID : EMD-47378
Title : Dimeric motor domains from phi-like dynein-1 bound to a Lis1 dimer under Nde1-Lis1 condition
Authors : Yang, J.; Zhang, K.
Deposited on : 2024-10-21
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.dev126
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

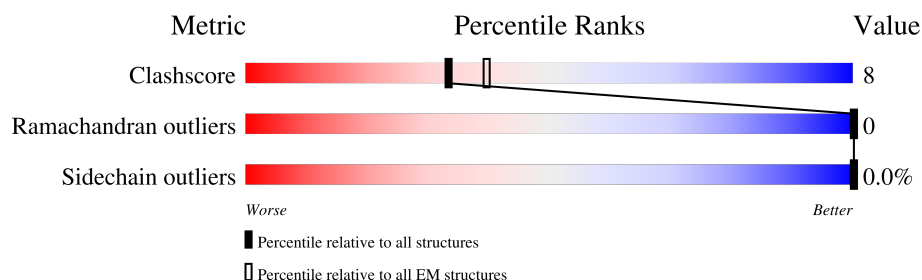
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	<div> <div>15%</div> <div>50%</div> <div>13%</div> <div>37%</div> </div>
1	B	4646	<div> <div>10%</div> <div>51%</div> <div>12%</div> <div>37%</div> </div>
2	C	410	<div> <div>62%</div> <div>16%</div> <div>21%</div> </div>
2	D	410	<div> <div>20%</div> <div>48%</div> <div>29%</div> <div>22%</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 52502 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.

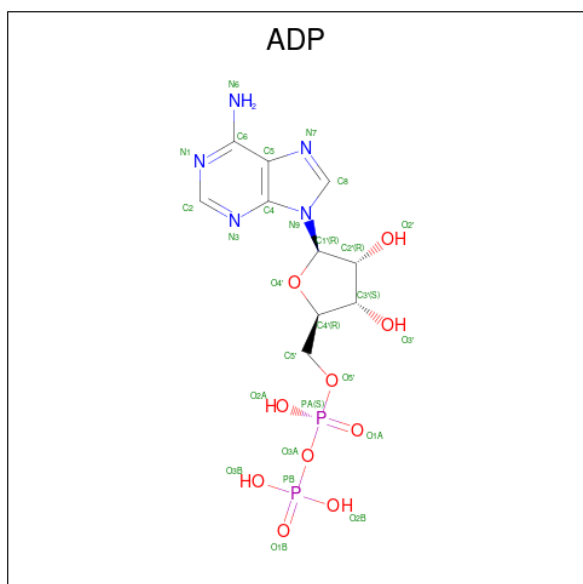
- Molecule 1 is a protein called Cytoplasmic dynein 1 heavy chain 1.

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 a protein called Platelet-activating factor acetylhydrolase IB subunit beta.

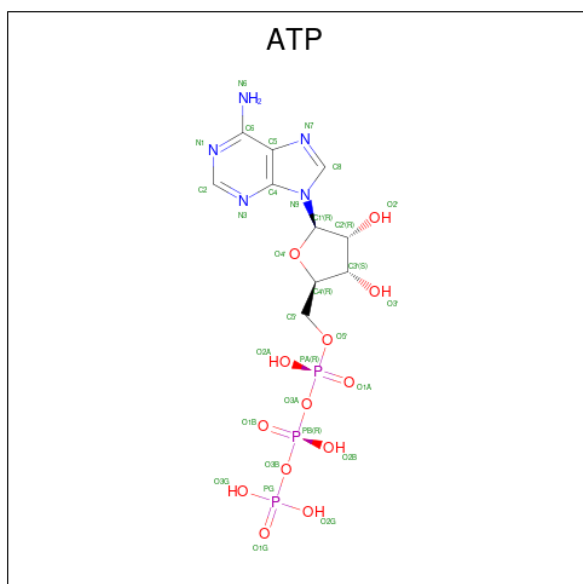
Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	322	Total	C	N	O	S	0	0
			2557	1608	452	477	20		
2	D	319	Total	C	N	O	S	0	0
			2531	1593	446	472	20		

- Molecule 3 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
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 4 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
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	B	1	Total	C	N	O	P	0
			31	10	5	13	3	

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

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

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
5	B	2	2	2	0



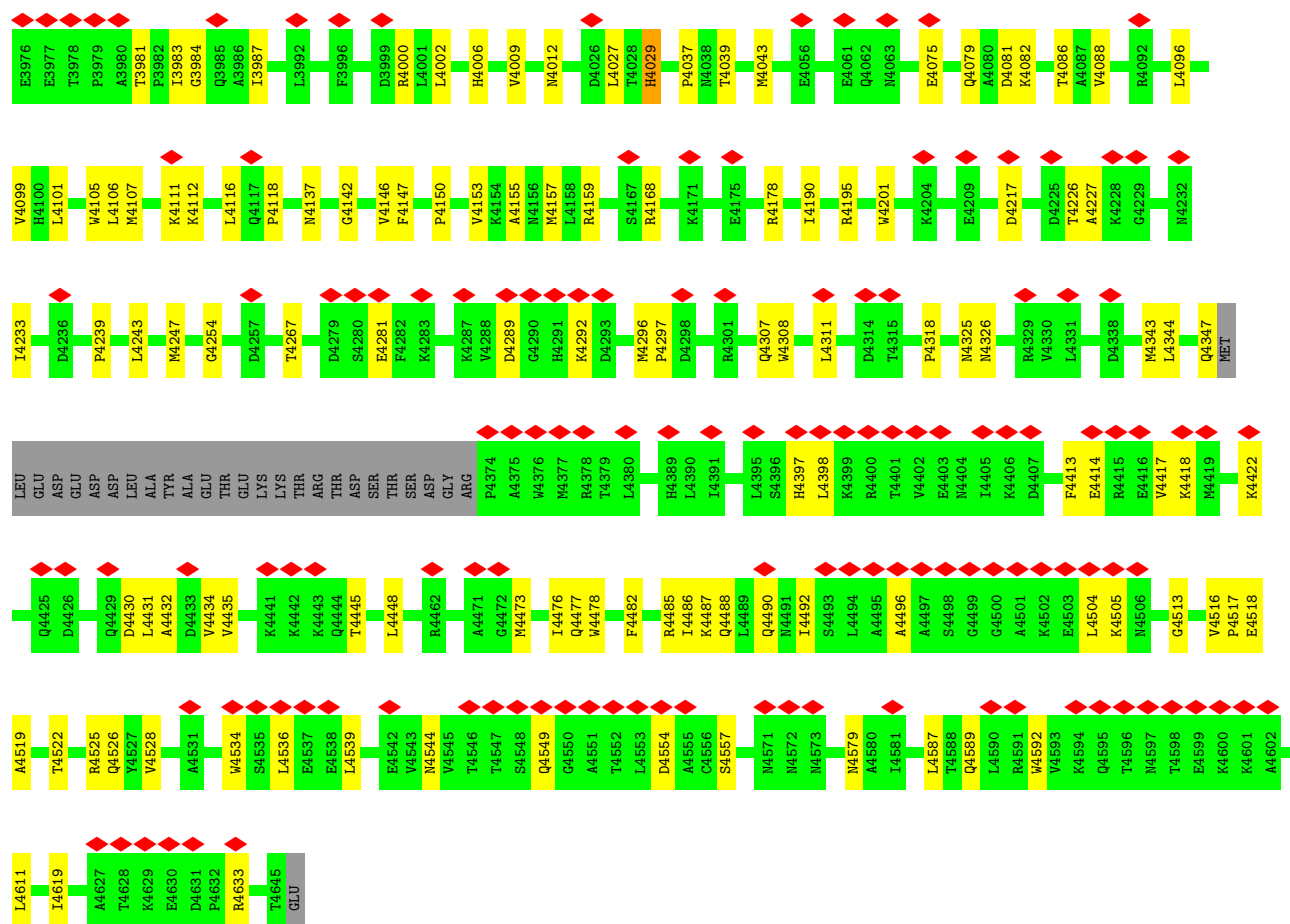
ALA	F3094	E2996	D2885	Y2792	L2661	I2555	S2457	M2361	G2224	E2120	D2011
ASP	T3099	S2997	Q2886	I2793	E2665	E2557	H2463	L2369	S2231	A2121	A2023
GLN	E3100	N2998	E2887	Y2794	E2668	V2558	Q2464	S2370	W2234	V2122	G2024
MET	T3110	L3000	E2888	R2801	F2682	T2559	R2467	T2371	E2242	D2123	R2025
VAL	S3111	D3001	D2889	R2804	F2686	H2560	N2468	F2378	E2248	E2124	S2026
LEU	K3112	S3002	V2890	G2805	M2686	K2561	Q2471	S2384	L2268	G2125	D2030
ASP	K3113	M3008	V2891	F2807	G2691	V2562	Y2472	I2385	E2249	I2126	D2030
ASP	L3114	L3011	V2892	E2808	G2694	A2563	N2475	P2386	K2257	I2127	L2039
LYS	L3115	L3012	Y2901	R2811	R2694	A2564	H2476	L2387	E2249	A2128	D2045
VAL	E3116	A3013	E2902	P2812	D2697	A2564	Y2472	D2388	K2257	E2129	R2046
GLY	K3117	N3014	E2903	L2813	D2697	P2565	N2475	E2389	L2268	N2130	Q2047
PRO	P3118	G3015	E2904	L2814	D2697	D2566	H2476	GLY	L2268	L2131	
ALA	K3119	E3016	L2905	E2815	V2701	D2573	P2477	ASP	D2269	P2132	R2060
ALA	D3124	E3022	D2906	T2816	K2702	V2574	D2478	GLU	N2270	E2133	T2061
VAL	Y3125	G3023	F2912	L2816	K2702	T2575	F2479	ALA	W2275	Q2134	
GLY	K3126	D3024	N2913	P2817	E2704	R2576	P2480	GLN	W2276	E2135	A2066
ASN	V3129	M3030	E2914	V2818	Q2707	E2577	M2481	ARG	D2277	I2136	
ALA	Y3130		E2914	E2819	Q2707	E2578	Q2482	ARG	R2285	I2138	I2069
VAL	D3131	C3033	L2920	G2820	P2714	L2581	L2483	LYS	D2289	P2132	P2071
LYS	K3132	K3034	R2924	L2821	P2714	K2584	E2484	GLY	S2290	E2143	F2072
ILE	Q3135	E3035	R2927	R2823	L2723	H2588	L2486	GLU	L2295	K2148	F2073
LYS	P3136	G3036	L2934	E2828	R2726	K2589	E2487	ASP	V2302	A2151	K2074
GLN	F3137	A3037	L2934	R2836	R2729	P2590	R2492	GLY	F2303	E2152	L2075
HIS	R3140	Q3038	K2943	L2837	H2731	L2591	Y2493	GLU	D2304	L2156	D2077
LEU	E3141	K3039	K2943	V2838	P2732	V2592	L2494	GLU	E2309		E2078
VAL	V3148	E3040	A2951	E2839	P2732	P2596	I2498	ALA	E2310		L2080
GLY	F3149	G3041	L2956	D2840	Y2738	T2604	L2499	ALA	G2305	F2165	
ARG	Q3152	L3042	L2956	L2841	P2739	L2605	D2505		D2306	P2166	D2087
ALA	T3153	M3043	L2961	E2842	G2740	F2606	S2506		V2307	G2167	F2088
VAL	L3154	L3044	K2962	R2843	M2755	S2607	R2507		D2308	P2168	
ASN	R3160	D3045	H2964	R2844	L2756		L2508		E2314	Q2169	R2091
PRO	L3161	H3047	K2965	D2847	R2757	R2610	L2514		M2314	H2171	K2094
ALA	A3162	E3048	K2966	L2855	L2758	E2616	G2615		D2320	R2172	S2095
VAL	K3163	L3050	Y2967	L2855	I2759	G2619	T2522		E2321	G2173	V2096
LEU	R3164	Y3051	E2970	F2858	L2762	L2620	T2523		L2324	E2174	N2102
LEU	T3172	W3053	E2974	N2859	R2763	F2635	T2528		E2331	M2175	V2103
GLY	P3173	F3054	E2974	N2860	T2764	Y2641	A2529		S2334	L2176	K2104
SER	R3174	R3060	L2980	T2861	Y2765	R2642	P2530		E2331	A2177	E2106
ILE	H3175	S3067	L2980	R2862	E2767	T2643	N2531		S2334	L2179	R2107
LEU	D3178	T3067	S3067	E2864	A2772	T2645	T2532		Q2346	E2181	I2108
LEU	H3182	S3072	K2986	K2865	F2784	R2645	L2534		D2347	K2184	K2112
GLY	L3205	E3073	N2987	S2868	T2785	N2646	T2533		T2355	Q2187	R2113
GLY	K3206	D3077	E2988	R2869	Q2786	L2646	P2533		V2356	E2188	E2114
SER	K3207	R3078	L2990	R2869	Q2786	G2647	T2533		M2189	M2189	K2115
	T3208	L3085	L2990	L2872	P2790	V2649	L2534		S2357	Y2190	E2116
	T3211	R3088	M2994	L2872	H2791	L2650	S2540			E2198	E2117
			D2995	L2877		L2655	I2541			T2214	R2118
				S2878		K2657	S2542			L2220	G2119
				K2879			Q2554			M2221	



[illegible]

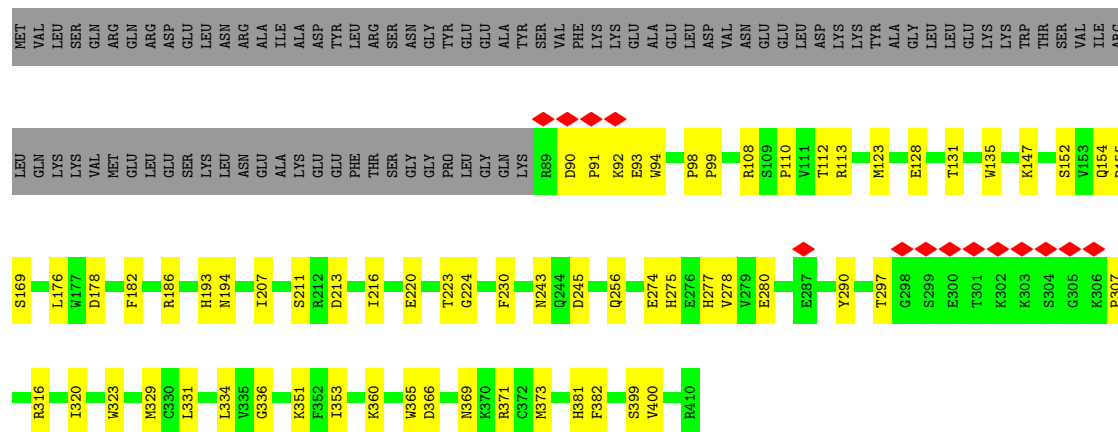






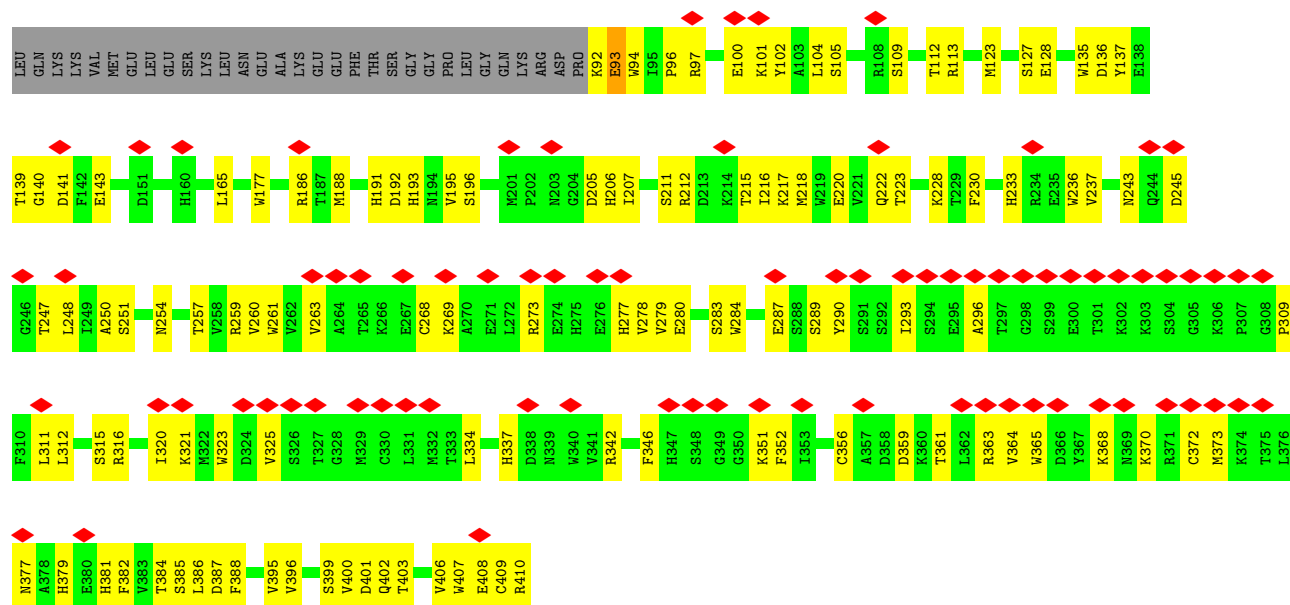
• Molecule 2: Platelet-activating factor acetylhydrolase IB subunit beta

Chain C: 62% 16% 21%



• Molecule 2: Platelet-activating factor acetylhydrolase IB subunit beta

Chain D: 48% 29% 22%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	215049	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	1.498	Depositor
Minimum map value	-0.699	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.3	Depositor
Map size (\AA)	444.4032, 444.4032, 444.4032	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: 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	0.12	0/24093	0.29	0/32651
1	B	0.12	0/24093	0.29	0/32651
2	C	0.12	0/2624	0.32	0/3555
2	D	0.16	0/2597	0.38	1/3518 (0.0%)
All	All	0.12	0/53407	0.30	1/72375 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	93	GLU	N-CA-C	-5.10	106.90	112.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	23593	0	23658	377	0
1	B	23593	0	23658	351	0
2	C	2557	0	2487	42	0
2	D	2531	0	2463	87	0
3	A	81	0	36	2	0
3	B	81	0	36	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	31	0	12	1	0
4	B	31	0	12	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
All	All	52502	0	52362	854	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 8.

The worst 5 of 854 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:2686:MET:HE2	1:A:2703:LEU:HD11	1.65	0.79
1:A:2221:MET:HG2	1:A:2343:PHE:HB2	1.64	0.79
1:A:4234:SER:HB3	1:A:4237:LYS:HG2	1.64	0.79
1:A:2956:LEU:HD23	1:A:2989:LYS:HB3	1.65	0.78
1:A:2644:THR:HG22	1:A:2646:ASN:H	1.49	0.78

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%)	2885 (98%)	44 (2%)	0	100	100
1	B	2929/4646 (63%)	2872 (98%)	57 (2%)	0	100	100
2	C	320/410 (78%)	306 (96%)	14 (4%)	0	100	100
2	D	317/410 (77%)	300 (95%)	17 (5%)	0	100	100
All	All	6495/10112 (64%)	6363 (98%)	132 (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%)	2604 (100%)	1 (0%)	100	100
1	B	2605/4125 (63%)	2604 (100%)	1 (0%)	100	100
2	C	287/364 (79%)	287 (100%)	0	100	100
2	D	284/364 (78%)	284 (100%)	0	100	100
All	All	5781/8978 (64%)	5779 (100%)	2 (0%)	100	100

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

Mol	Chain	Res	Type
1	A	4397	HIS
1	B	4029	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4098	ASN
1	B	4191	GLN
2	C	381	HIS
1	A	4012	ASN
1	A	3985	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 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
3	ADP	A	4701	5	24,29,29	0.89	0	29,45,45	1.22	2 (6%)
3	ADP	B	4704	-	24,29,29	0.86	0	29,45,45	1.19	2 (6%)
3	ADP	B	4701	5	24,29,29	0.87	0	29,45,45	1.24	2 (6%)
3	ADP	A	4703	-	24,29,29	0.89	0	29,45,45	1.23	2 (6%)
3	ADP	A	4704	-	24,29,29	0.88	0	29,45,45	1.20	2 (6%)
4	ATP	A	4702	5	28,33,33	0.66	0	34,52,52	0.58	1 (2%)
4	ATP	B	4702	5	28,33,33	0.67	0	34,52,52	0.59	1 (2%)
3	ADP	B	4703	-	24,29,29	0.88	0	29,45,45	1.23	2 (6%)

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
3	ADP	A	4701	5	-	0/12/32/32	0/3/3/3
3	ADP	B	4704	-	-	1/12/32/32	0/3/3/3
3	ADP	B	4701	5	-	3/12/32/32	0/3/3/3
3	ADP	A	4703	-	-	5/12/32/32	0/3/3/3
3	ADP	A	4704	-	-	1/12/32/32	0/3/3/3
4	ATP	A	4702	5	-	5/18/38/38	0/3/3/3
4	ATP	B	4702	5	-	4/18/38/38	0/3/3/3
3	ADP	B	4703	-	-	5/12/32/32	0/3/3/3

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	4703	ADP	N3-C2-N1	-3.73	123.61	128.67
3	A	4701	ADP	N3-C2-N1	-3.72	123.62	128.67
3	A	4703	ADP	N3-C2-N1	-3.69	123.66	128.67
3	B	4704	ADP	N3-C2-N1	-3.68	123.67	128.67
3	A	4704	ADP	N3-C2-N1	-3.68	123.67	128.67

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

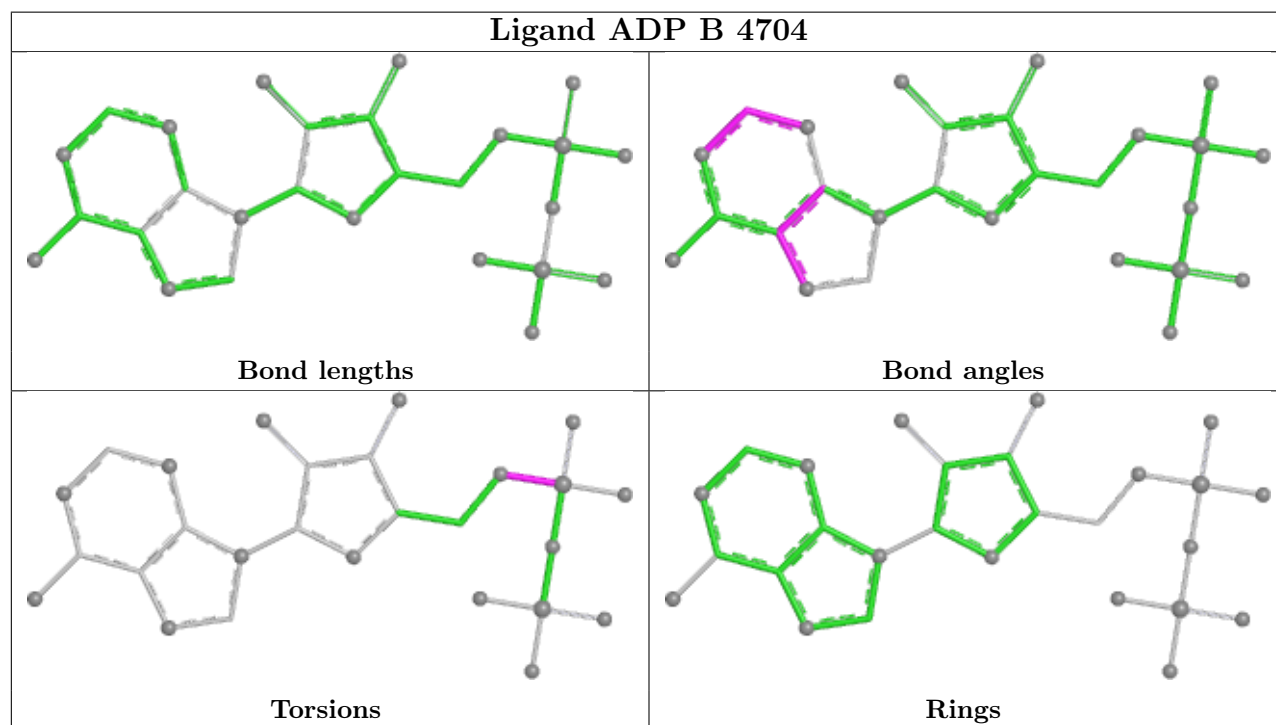
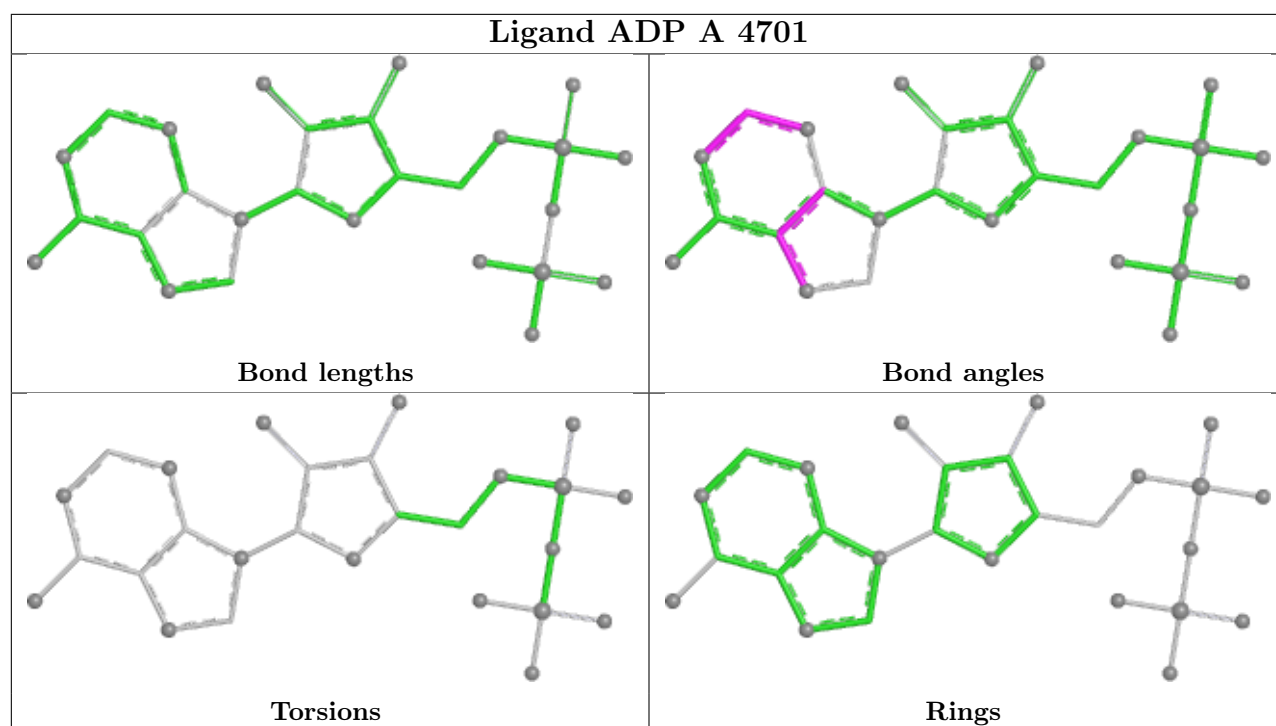
Mol	Chain	Res	Type	Atoms
3	A	4703	ADP	C5'-O5'-PA-O1A
3	A	4703	ADP	C5'-O5'-PA-O3A
3	B	4701	ADP	C5'-O5'-PA-O1A
3	B	4701	ADP	C5'-O5'-PA-O2A
3	B	4701	ADP	C5'-O5'-PA-O3A

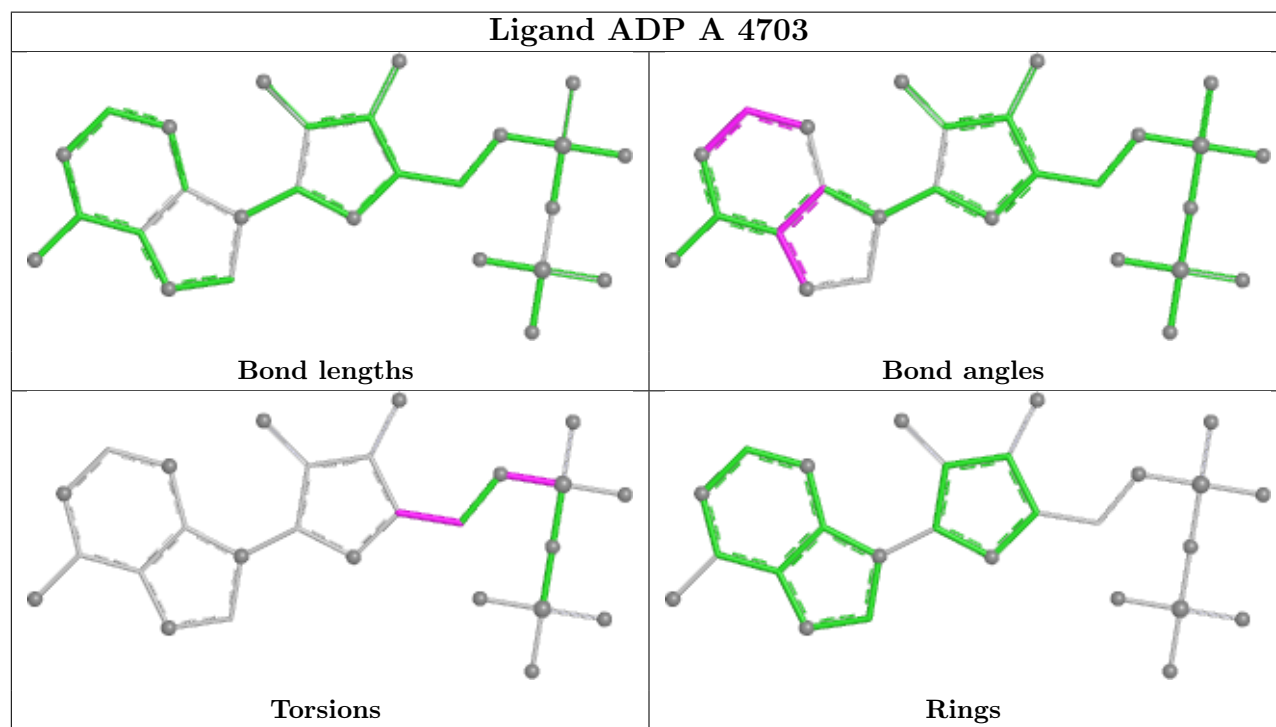
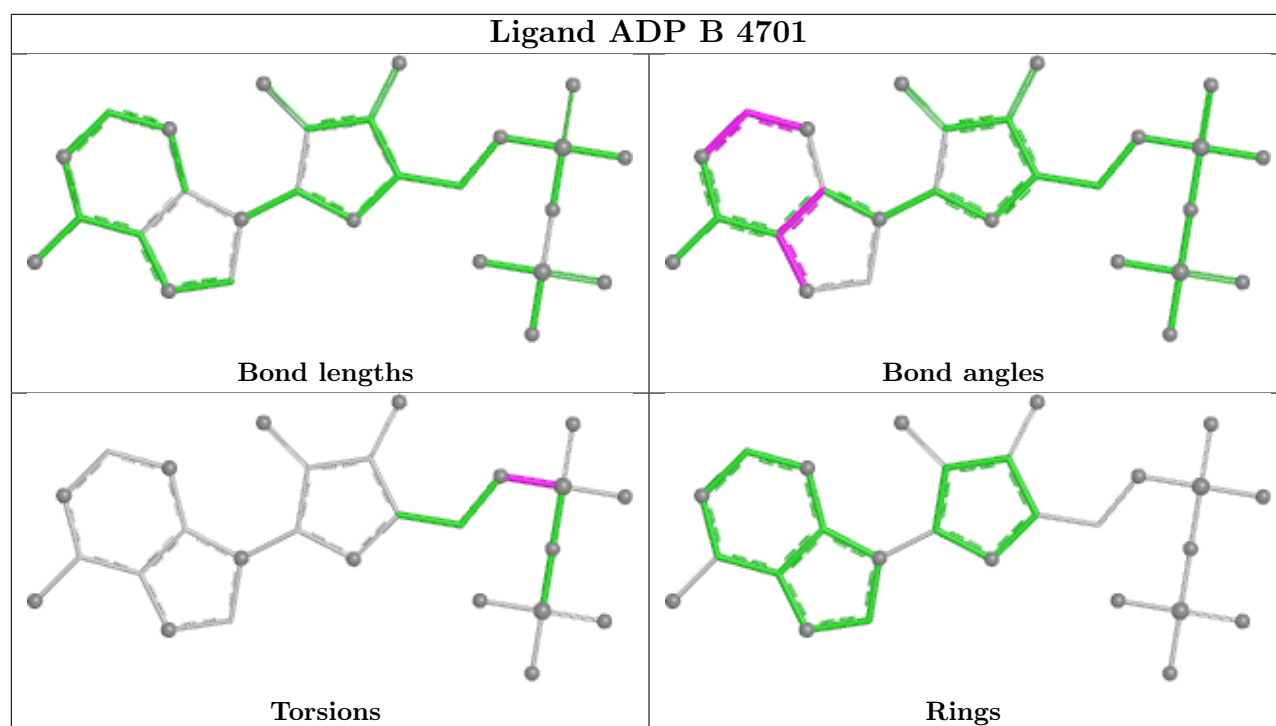
There are no ring outliers.

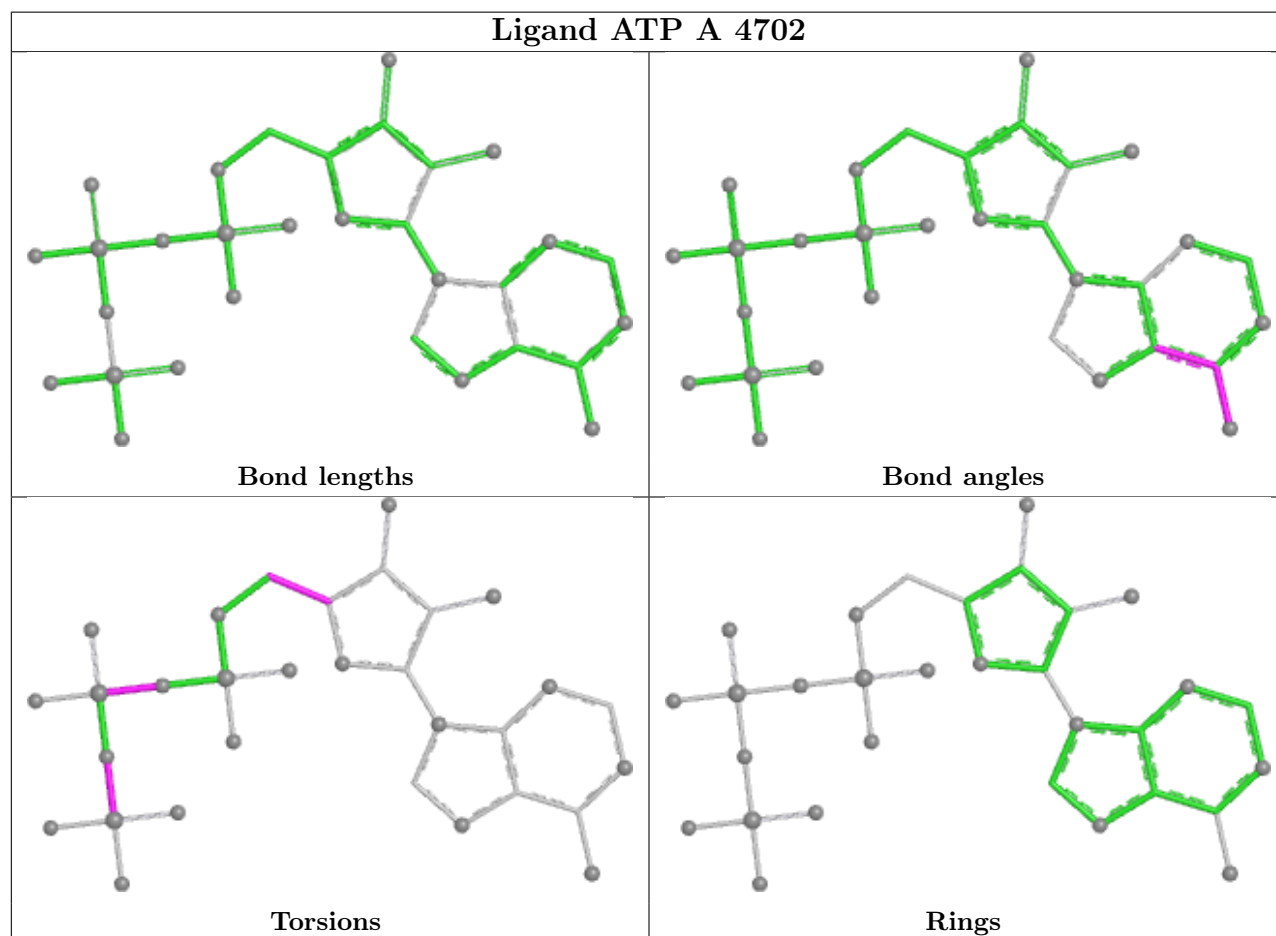
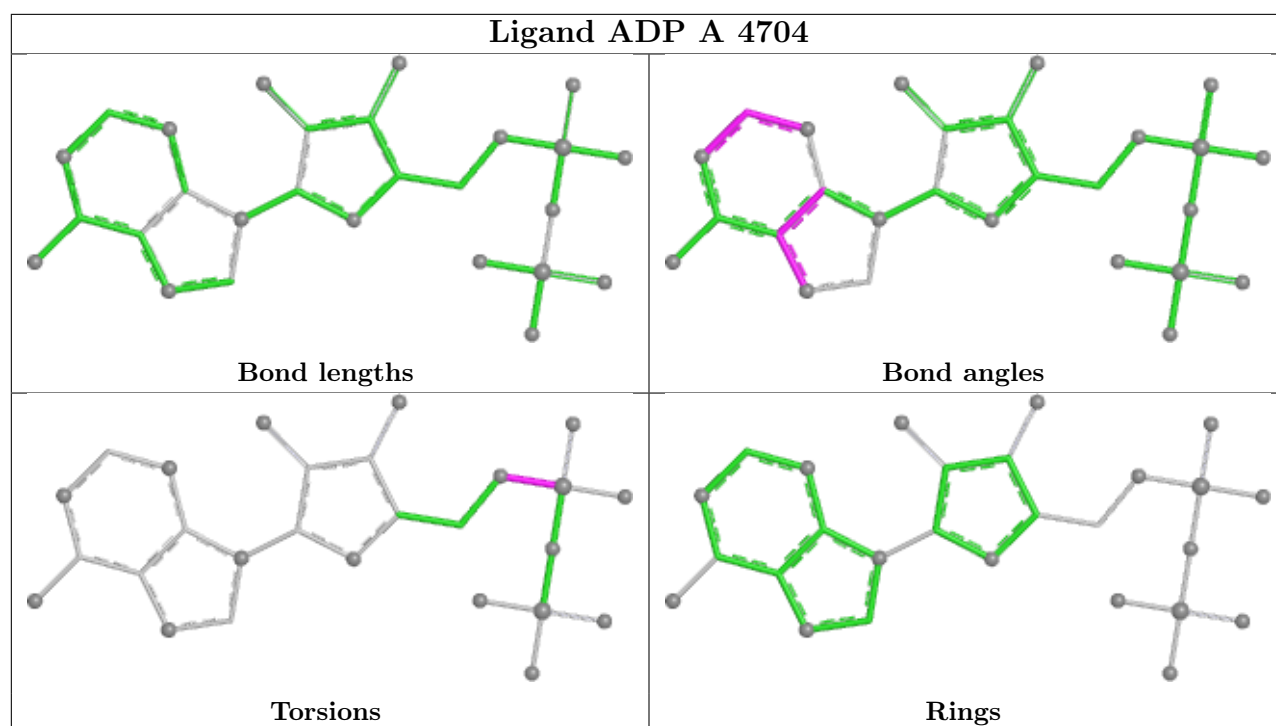
4 monomers are involved in 8 short contacts:

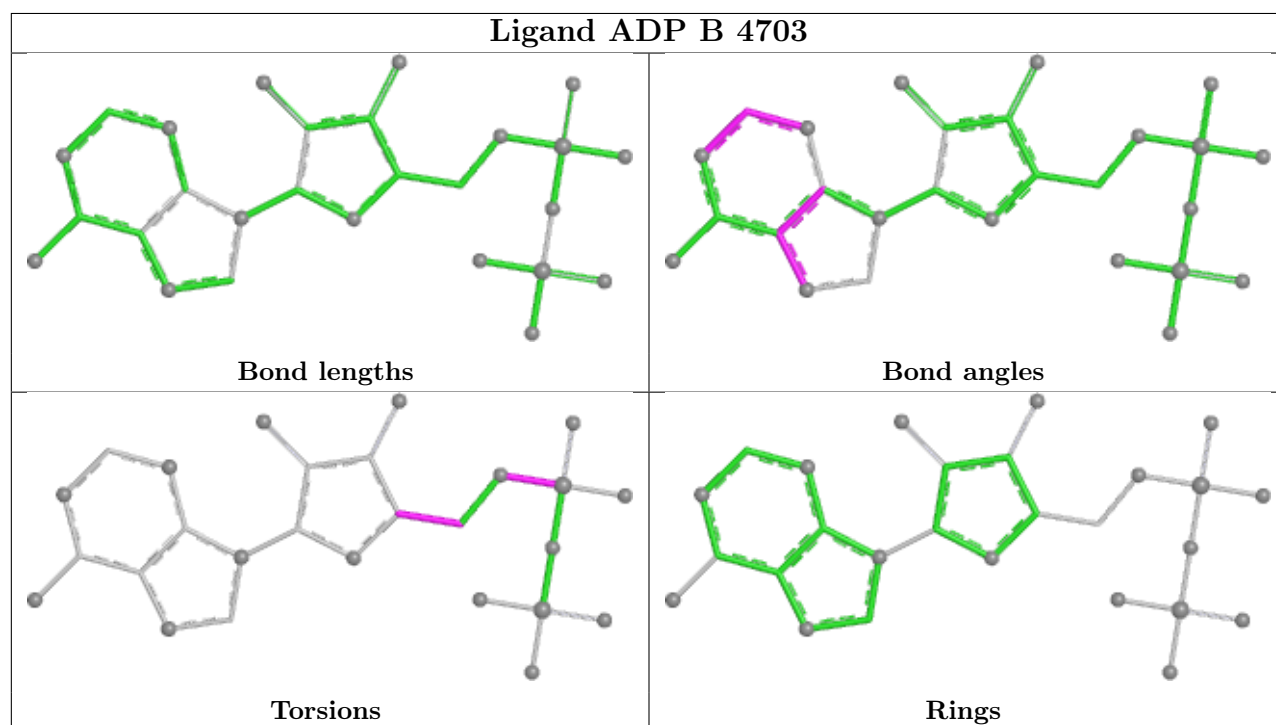
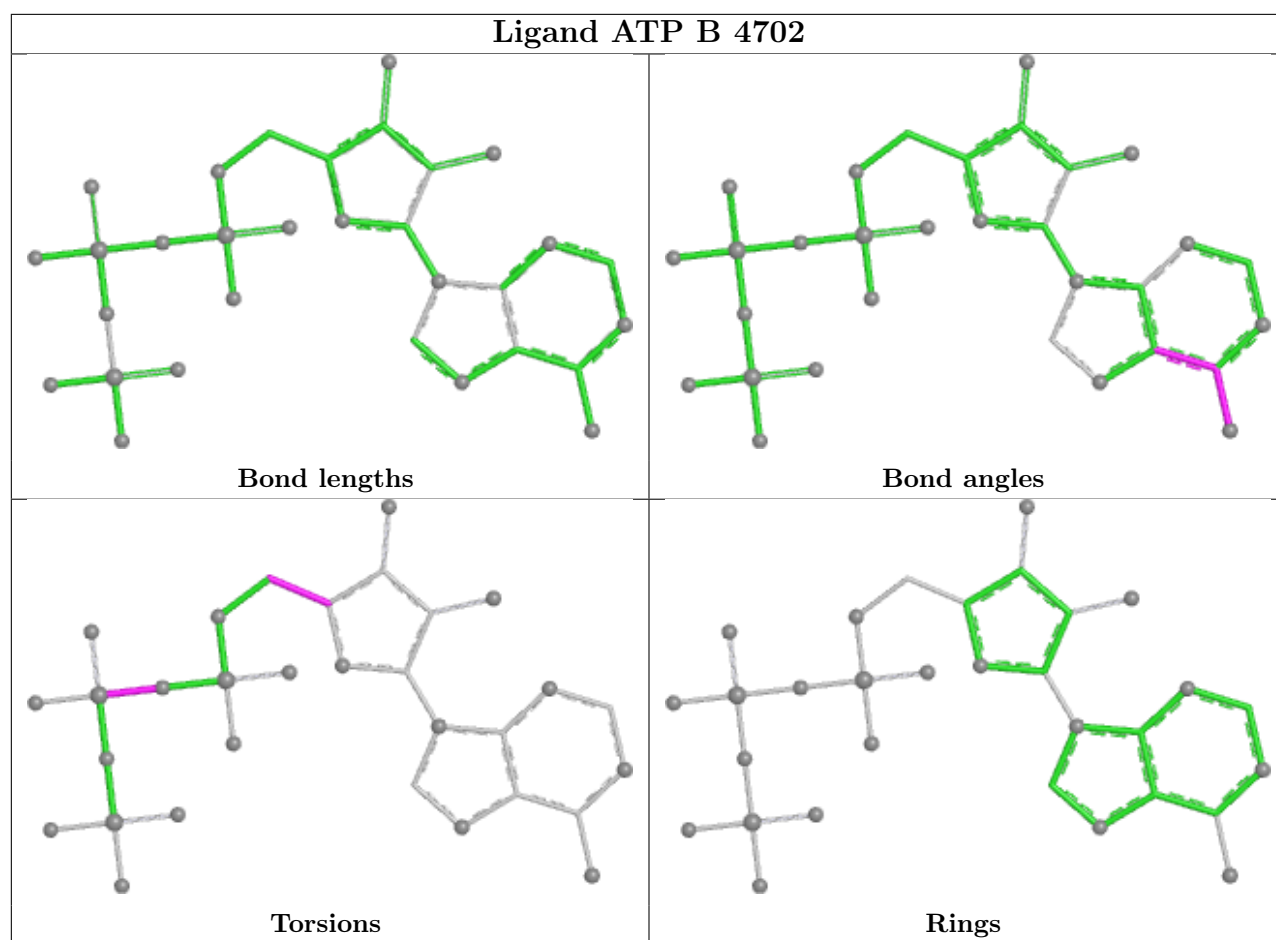
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	4701	ADP	2	0
3	B	4701	ADP	3	0
4	A	4702	ATP	1	0
3	B	4703	ADP	2	0

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.









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.

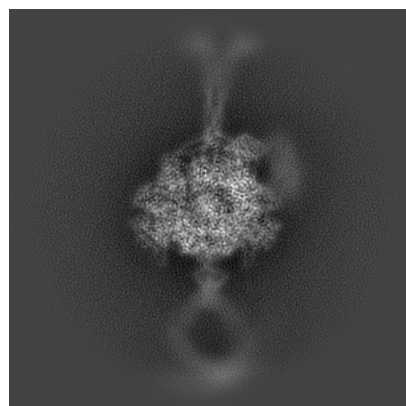
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47378. These allow visual inspection of the internal detail of the map and identification of artifacts.

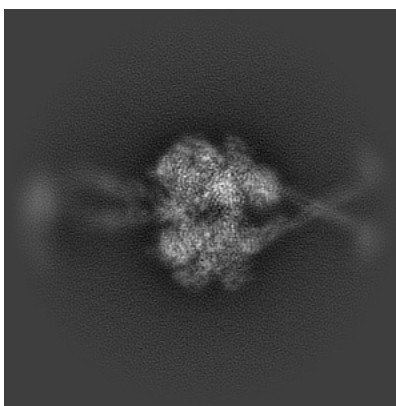
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

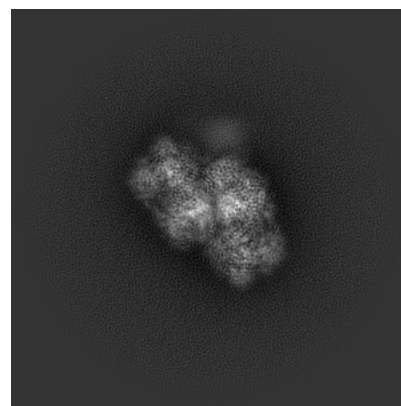
6.1.1 Primary map



X

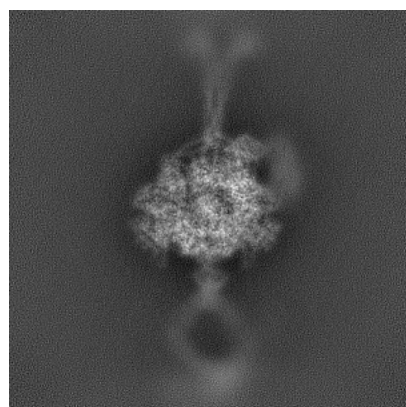


Y

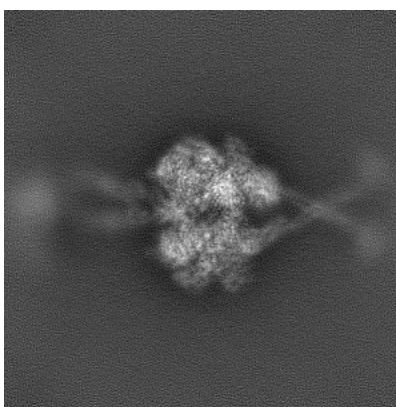


Z

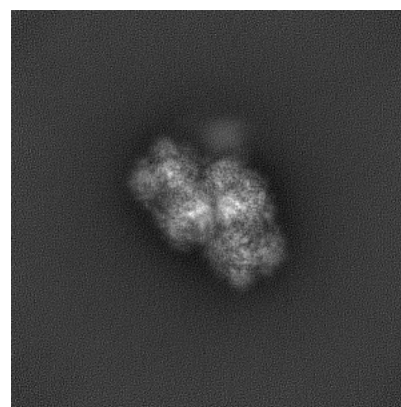
6.1.2 Raw map



X



Y

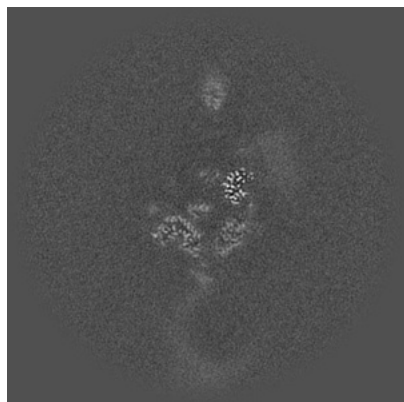


Z

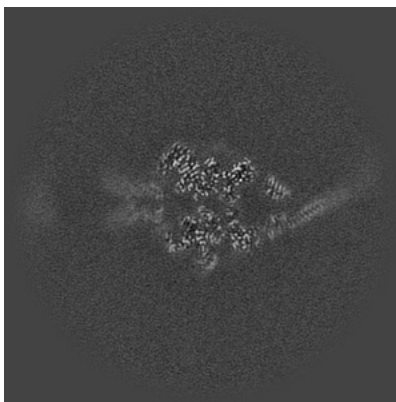
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

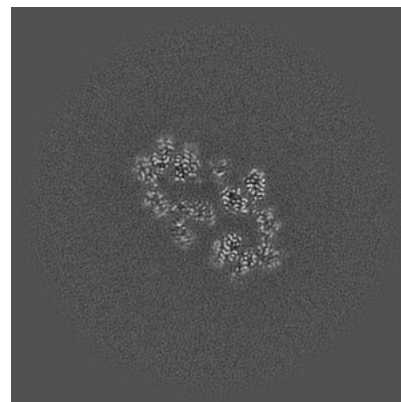
6.2.1 Primary map



X Index: 192

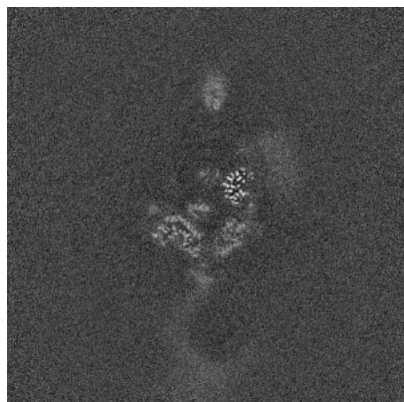


Y Index: 192

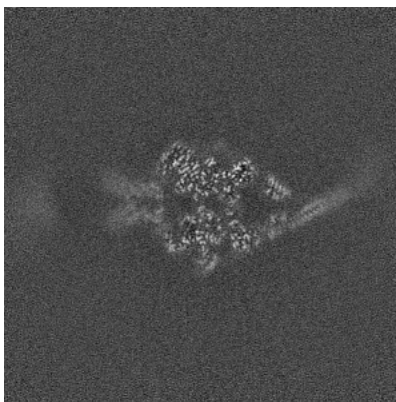


Z Index: 192

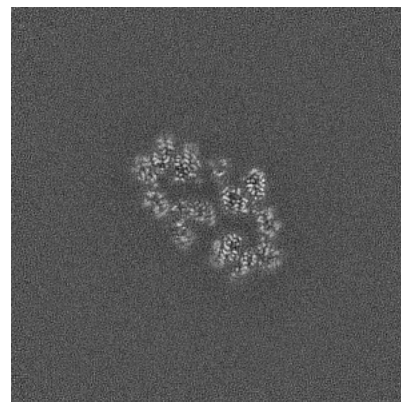
6.2.2 Raw map



X Index: 192



Y Index: 192

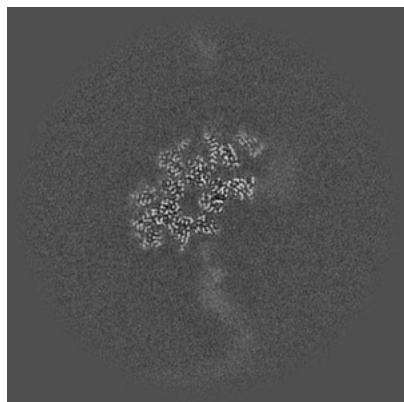


Z Index: 192

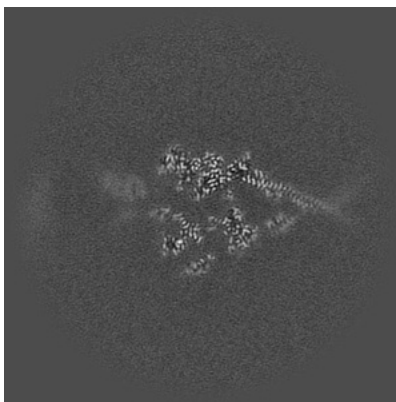
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

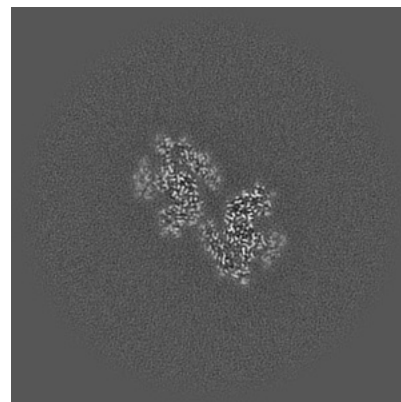
6.3.1 Primary map



X Index: 215

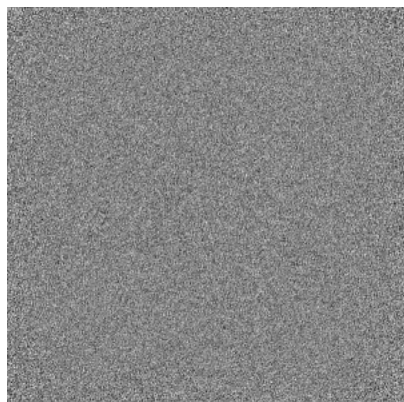


Y Index: 199

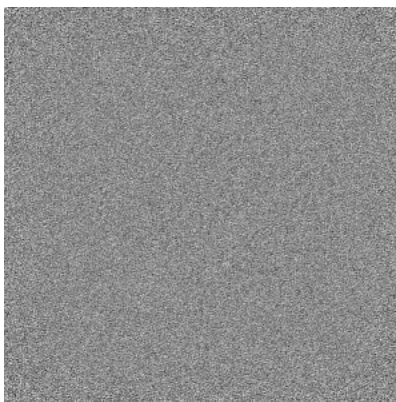


Z Index: 173

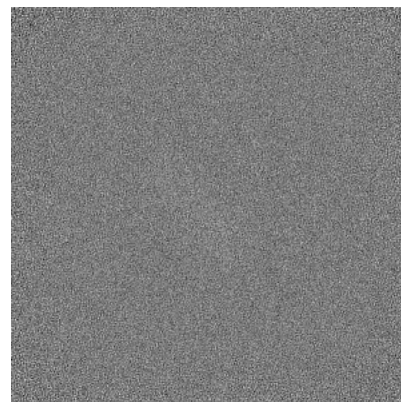
6.3.2 Raw map



X Index: 0



Y Index: 0

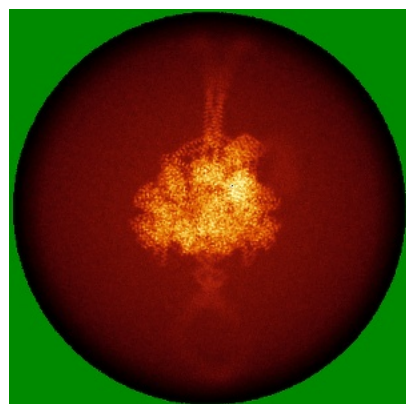


Z Index: 0

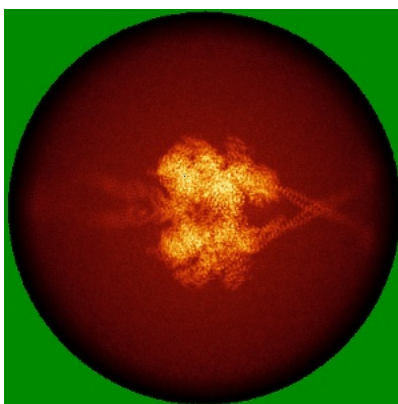
The images above show the largest variance slices of the map in three orthogonal directions.

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

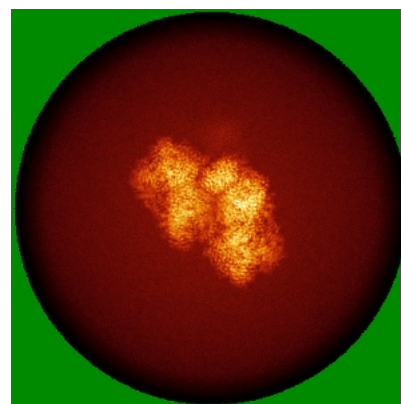
6.4.1 Primary map



X

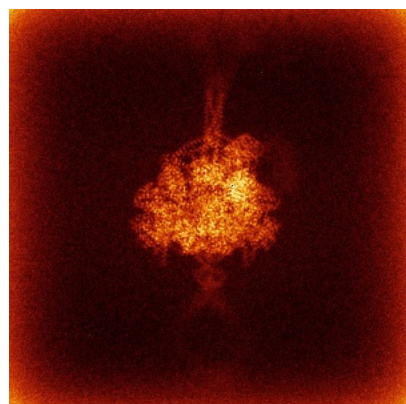


Y

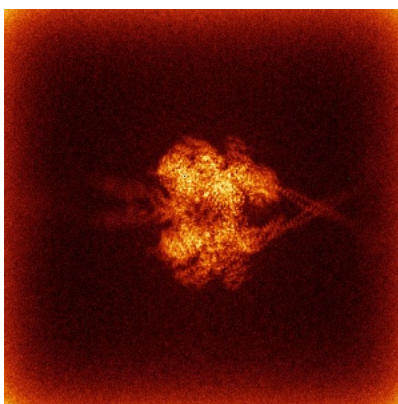


Z

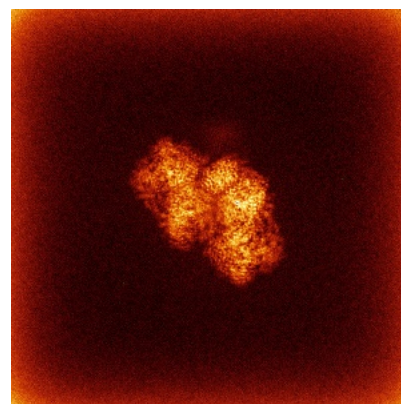
6.4.2 Raw map



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.

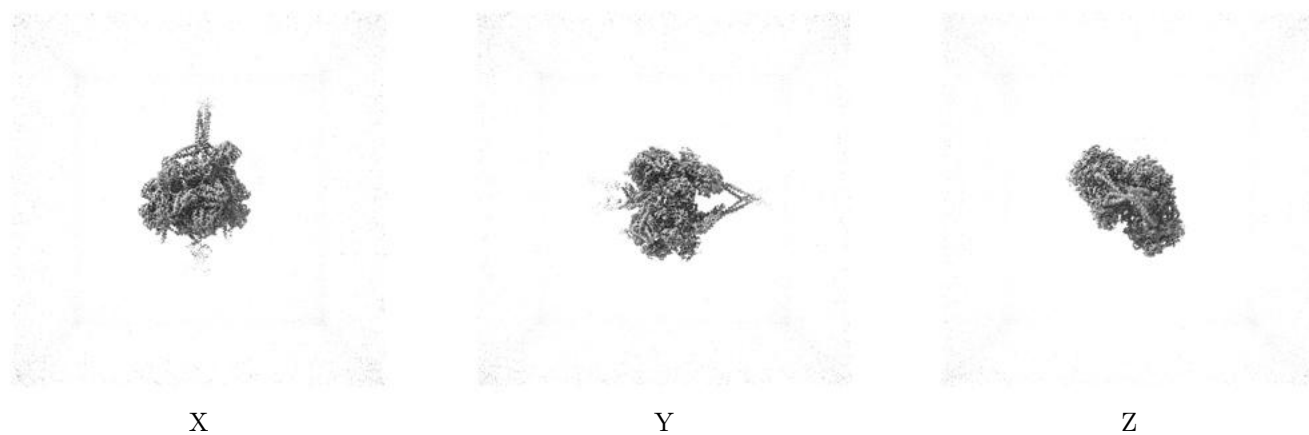
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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



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.

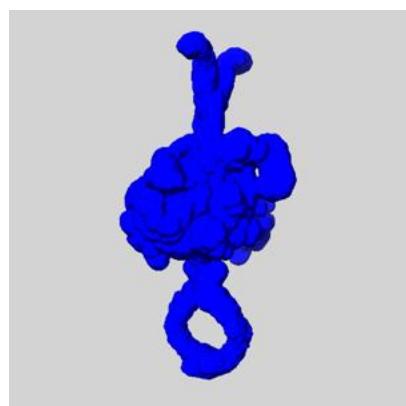
6.6 Mask visualisation [i](#)

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

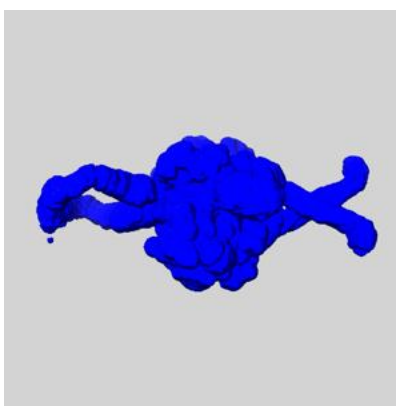
A mask typically either:

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

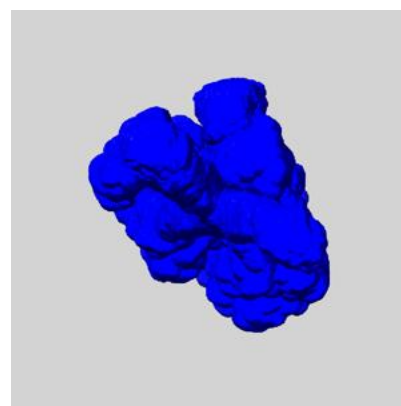
6.6.1 emd_47378_msk_1.map [i](#)



X



Y

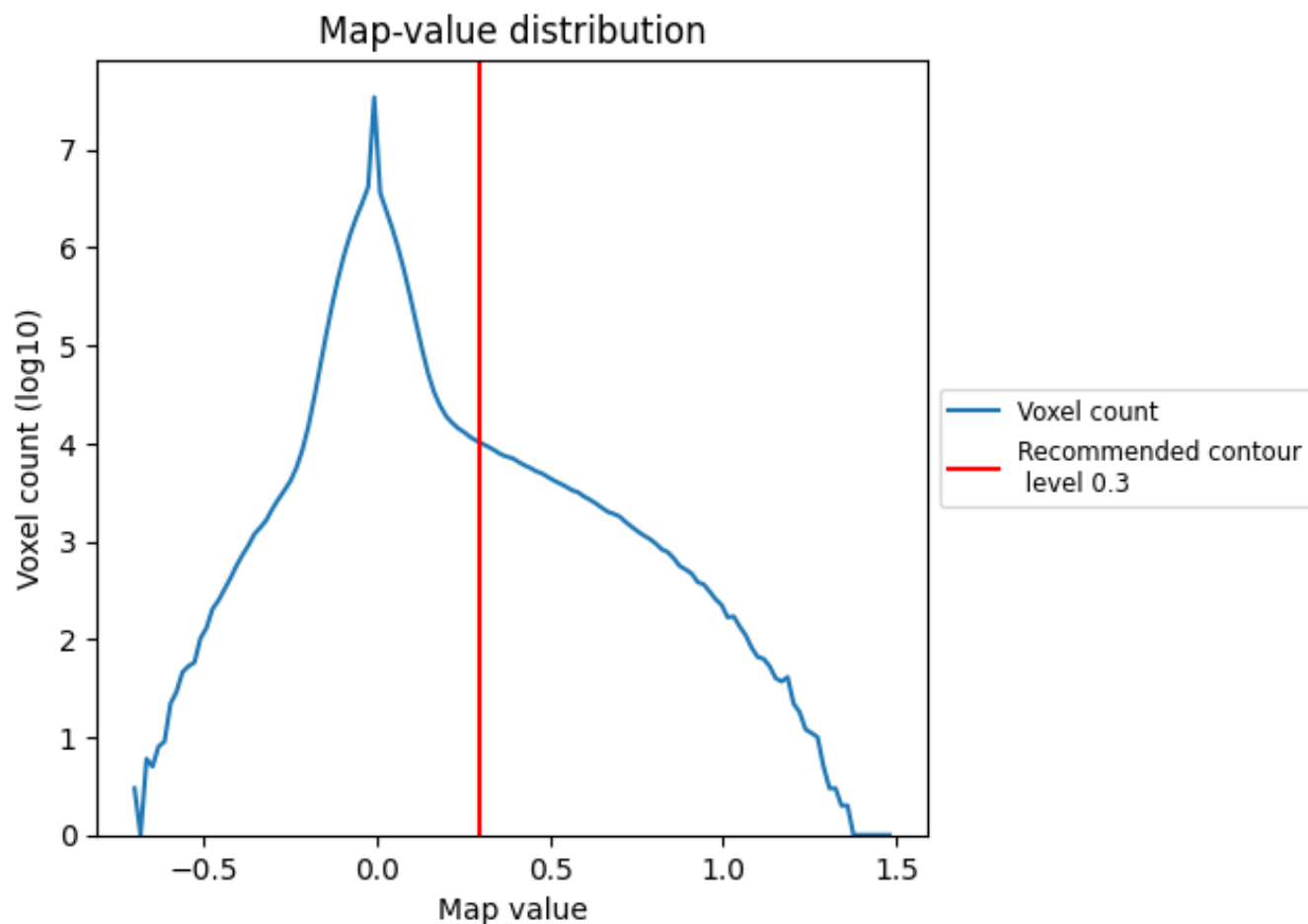


Z

7 Map analysis [i](#)

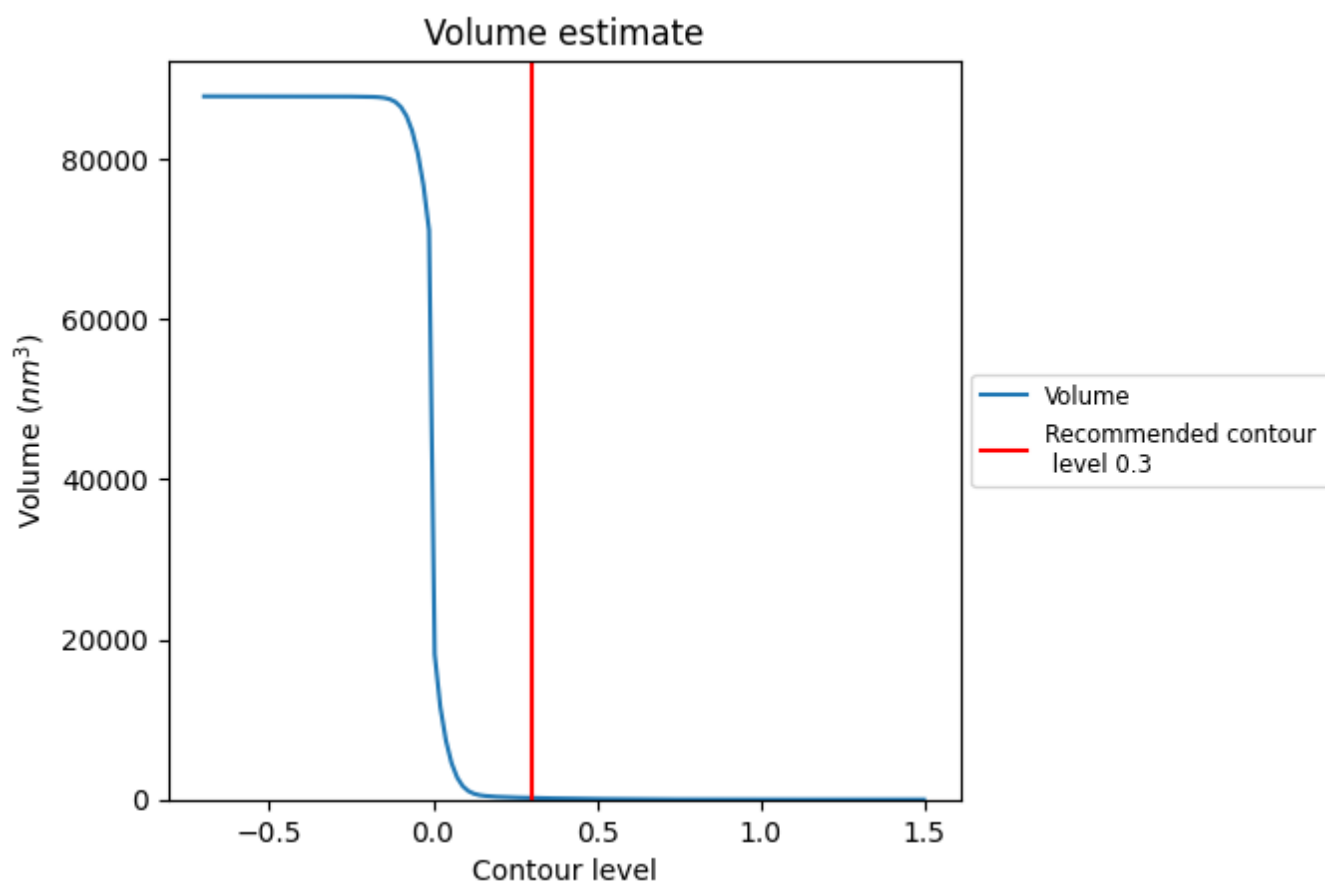
This section contains the results of statistical analysis of the map.

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.

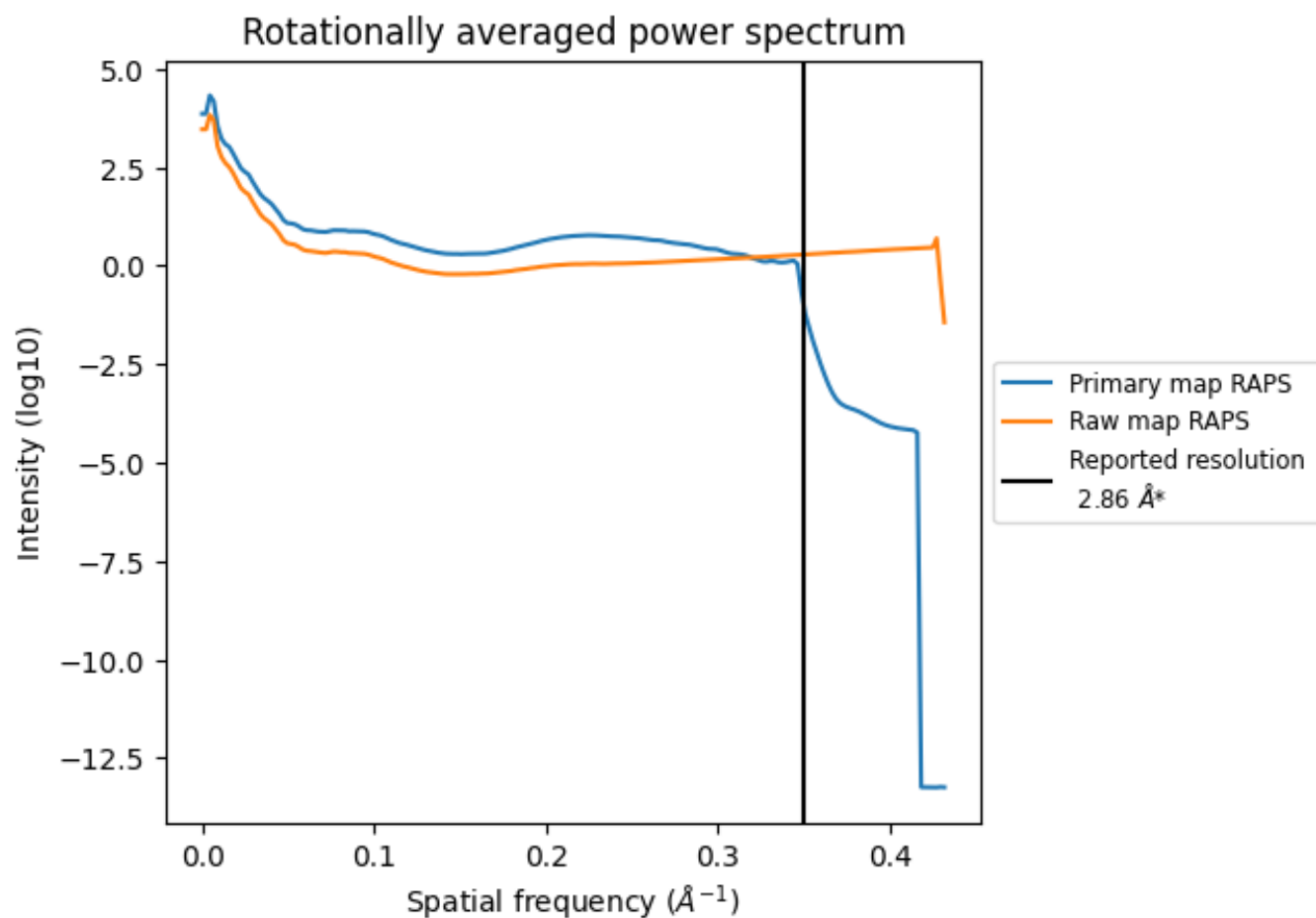
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 207 nm³; this corresponds to an approximate mass of 187 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 ⓘ

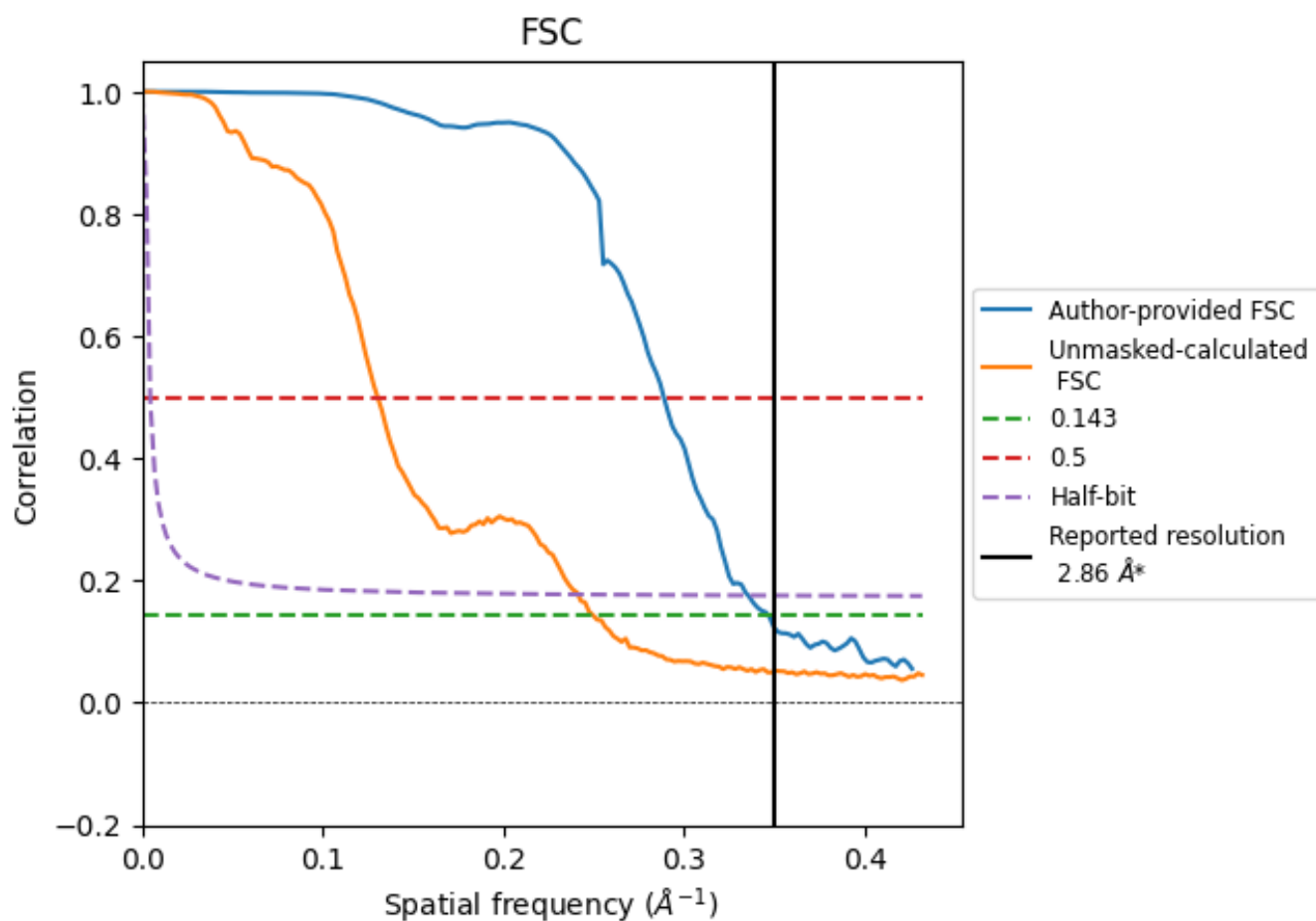


*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

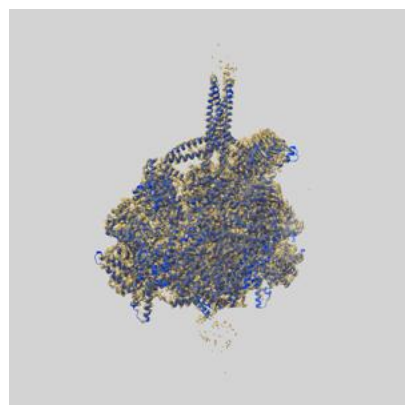
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.88	3.46	2.98
Unmasked-calculated*	4.00	7.67	4.14

*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 4.00 differs from the reported value 2.86 by more than 10 %

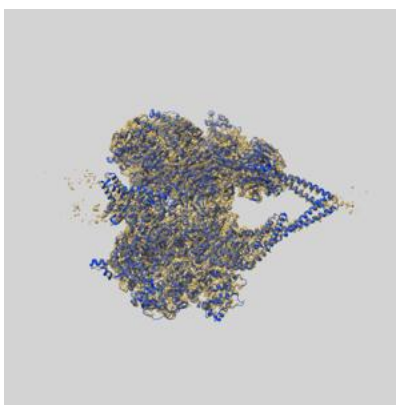
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47378 and PDB model 9E0Z. Per-residue inclusion information can be found in section [3](#) on page [6](#).

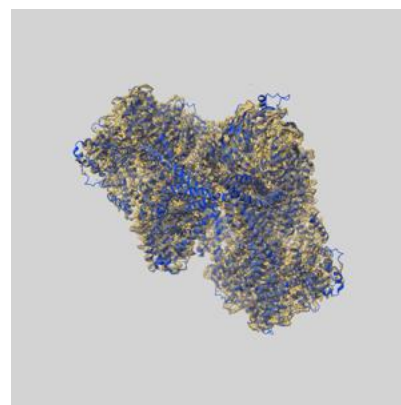
9.1 Map-model overlay [i](#)



X



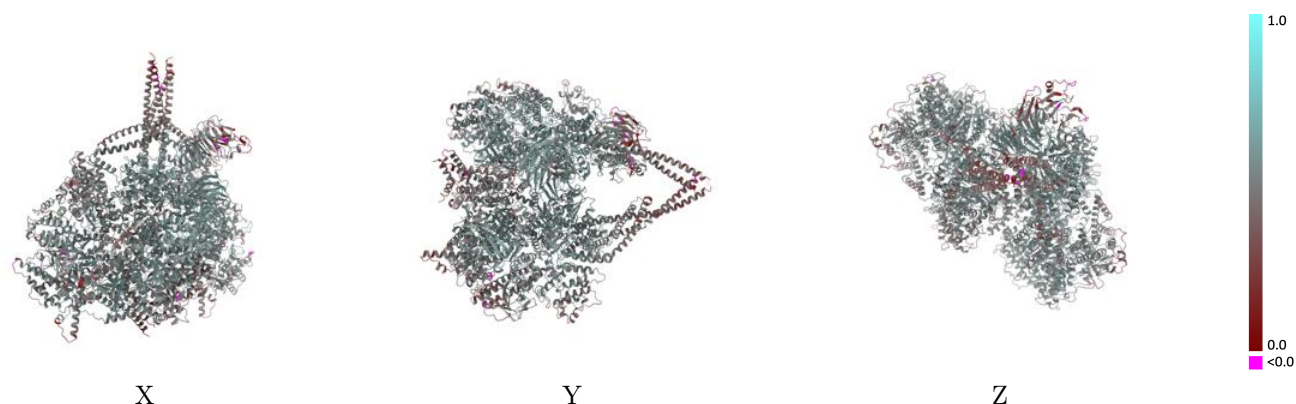
Y



Z

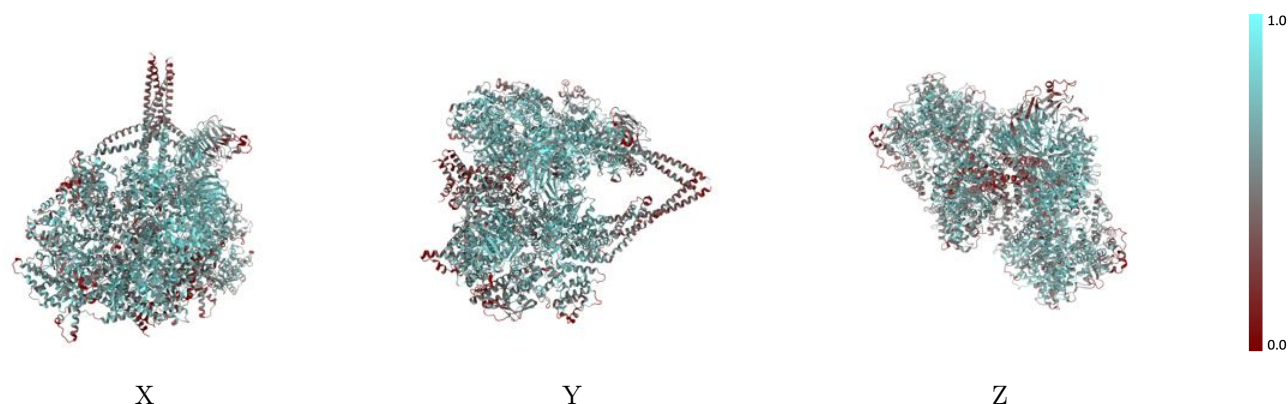
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



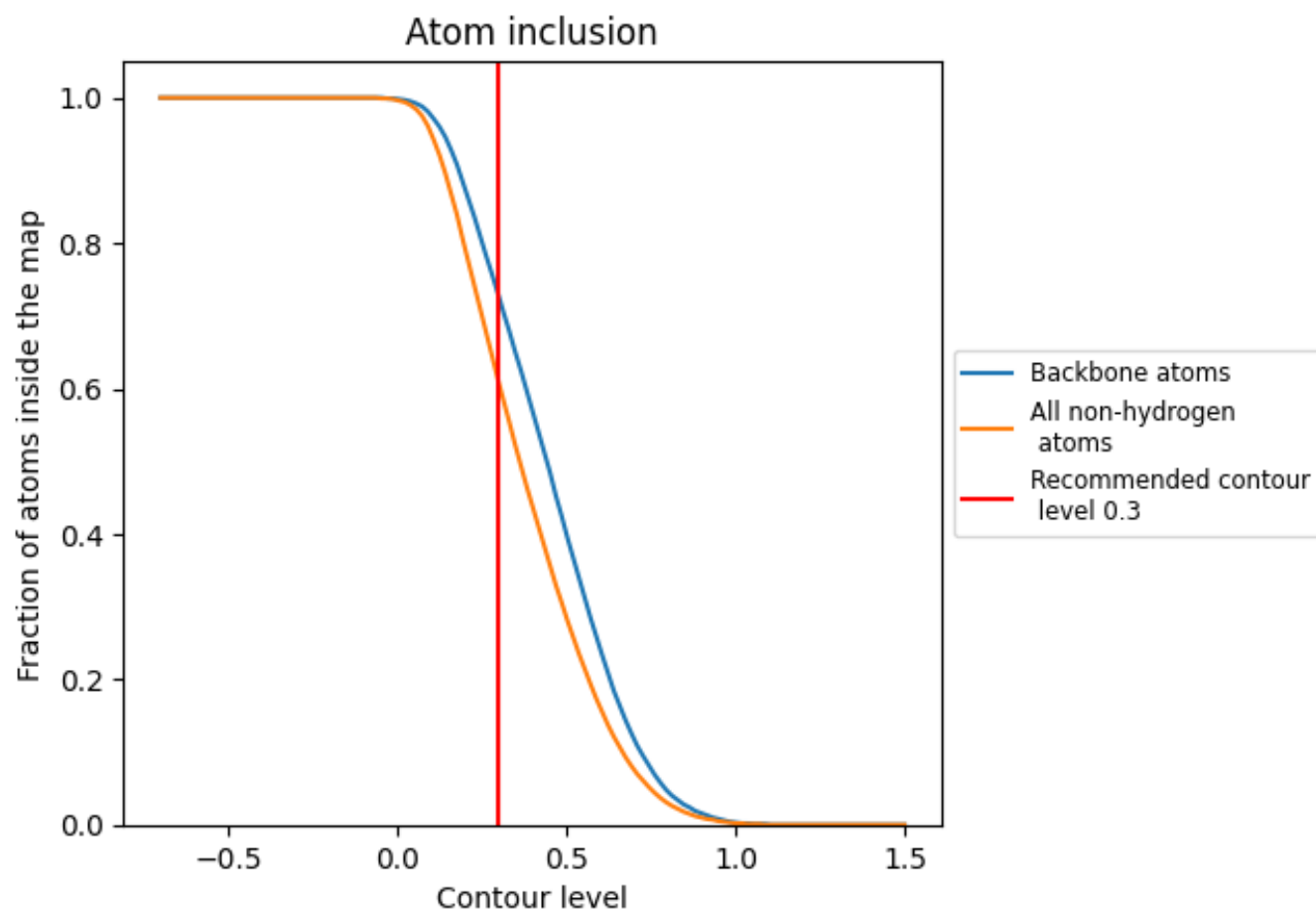
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 73% of all backbone atoms, 61% 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> 0.6080	<div></div> 0.5020
A	<div></div> 0.5740	<div></div> 0.4920
B	<div></div> 0.6360	<div></div> 0.5130
C	<div></div> 0.7400	<div></div> 0.5600
D	<div></div> 0.5350	<div></div> 0.4330

