



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 11:36 PM UTC

PDB ID : 7OIM / pdb_00007oim
EMDB ID : EMD-12932
Title : Mouse RNF213, with mixed nucleotides bound
Authors : Grabarczyk, D.; Ahel, J.; Clausen, T.
Deposited on : 2021-05-11
Resolution : 4.00 Å(reported)
Based on initial model : 6TAX

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

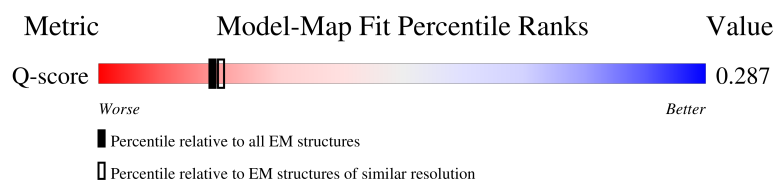
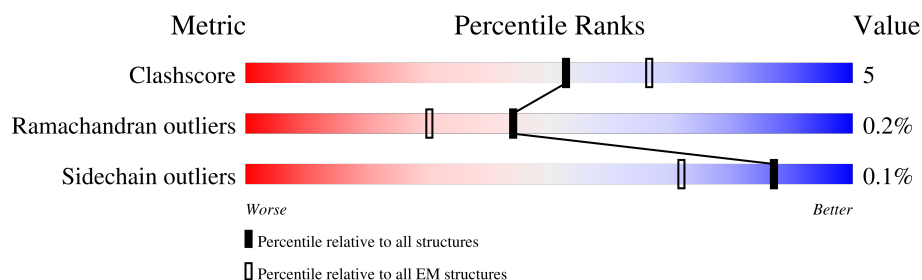
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	4836	 78% 14% 8%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 35597 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 E3 ubiquitin-protein ligase RNF213.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4426	Total	C	N	O	S	0	0
			35505	22641	6093	6561	210		

There are 30 discrepancies between the modelled and reference sequences:

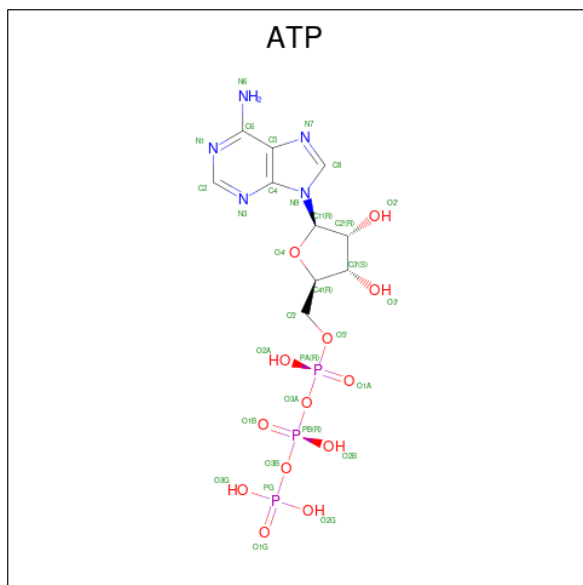
Chain	Residue	Modelled	Actual	Comment	Reference
A	326	MET	-	initiating methionine	UNP E9Q555
A	327	ALA	-	expression tag	UNP E9Q555
A	328	SER	-	expression tag	UNP E9Q555
A	329	TRP	-	expression tag	UNP E9Q555
A	330	SER	-	expression tag	UNP E9Q555
A	331	HIS	-	expression tag	UNP E9Q555
A	332	PRO	-	expression tag	UNP E9Q555
A	333	GLN	-	expression tag	UNP E9Q555
A	334	PHE	-	expression tag	UNP E9Q555
A	335	GLU	-	expression tag	UNP E9Q555
A	336	LYS	-	expression tag	UNP E9Q555
A	337	GLY	-	expression tag	UNP E9Q555
A	338	SER	-	expression tag	UNP E9Q555
A	?	-	VAL	deletion	UNP E9Q555
A	?	-	ARG	deletion	UNP E9Q555
A	?	-	ASN	deletion	UNP E9Q555
A	?	-	ARG	deletion	UNP E9Q555
A	5149	GLY	-	expression tag	UNP E9Q555
A	5150	GLY	-	expression tag	UNP E9Q555
A	5151	GLY	-	expression tag	UNP E9Q555
A	5152	HIS	-	expression tag	UNP E9Q555
A	5153	HIS	-	expression tag	UNP E9Q555
A	5154	HIS	-	expression tag	UNP E9Q555
A	5155	HIS	-	expression tag	UNP E9Q555
A	5156	HIS	-	expression tag	UNP E9Q555
A	5157	HIS	-	expression tag	UNP E9Q555
A	5158	HIS	-	expression tag	UNP E9Q555
A	5159	HIS	-	expression tag	UNP E9Q555

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Chain	Residue	Modelled	Actual	Comment	Reference
A	5160	HIS	-	expression tag	UNP E9Q555
A	5161	HIS	-	expression tag	UNP E9Q555

- Molecule 2 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
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

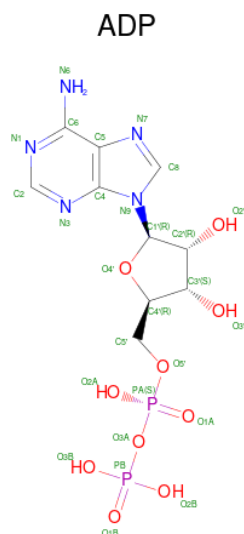
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

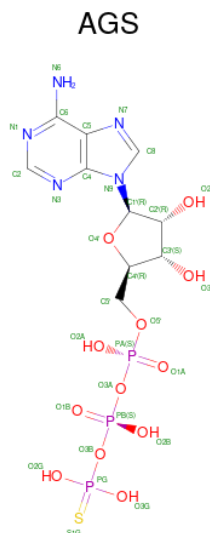
Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Zn	0
			2	2	

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

- Molecule 6 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{12}\text{P}_3\text{S}$) (labeled as "Ligand of Interest" by depositor).

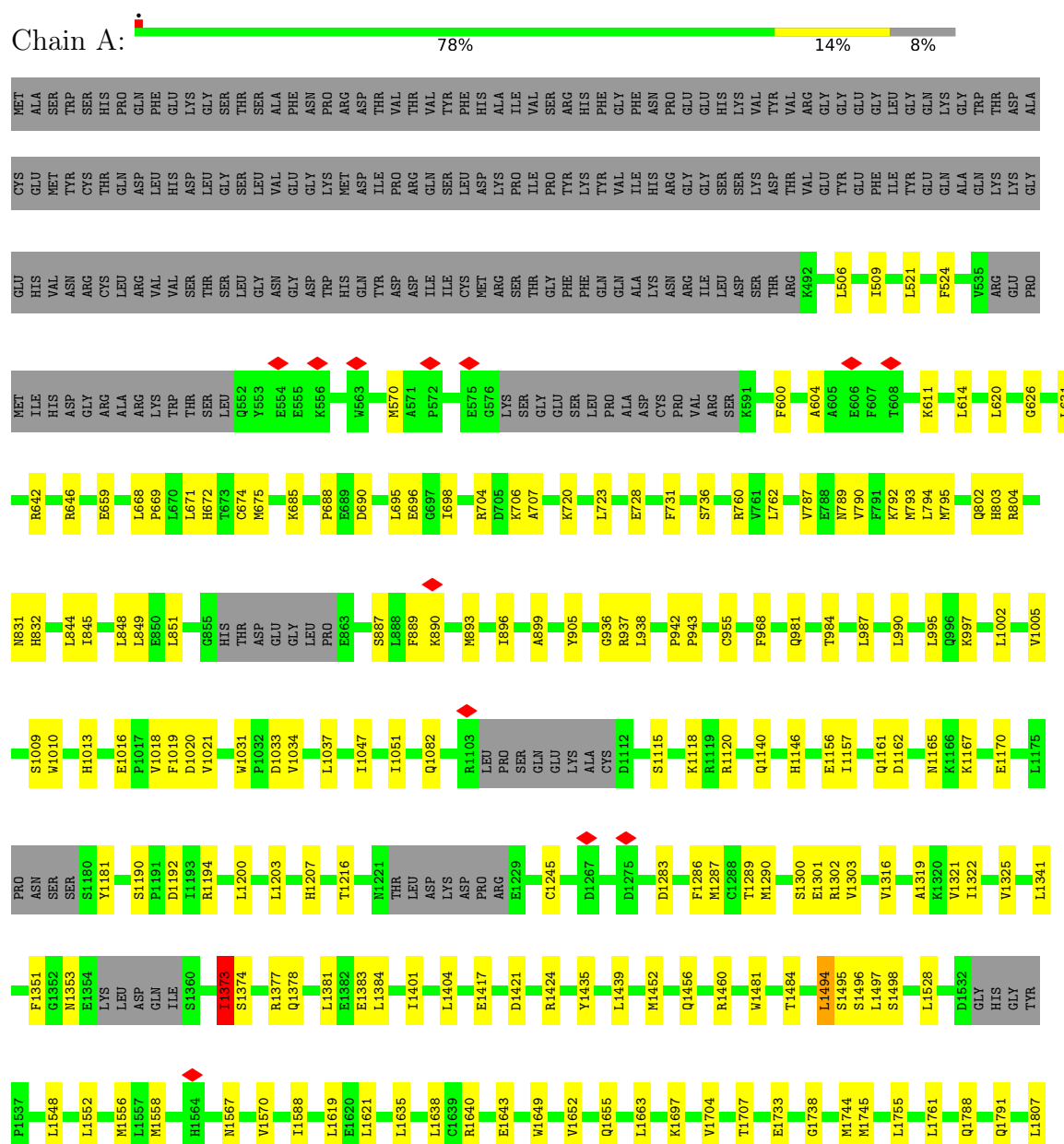


Mol	Chain	Residues	Atoms					AltConf	
6	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

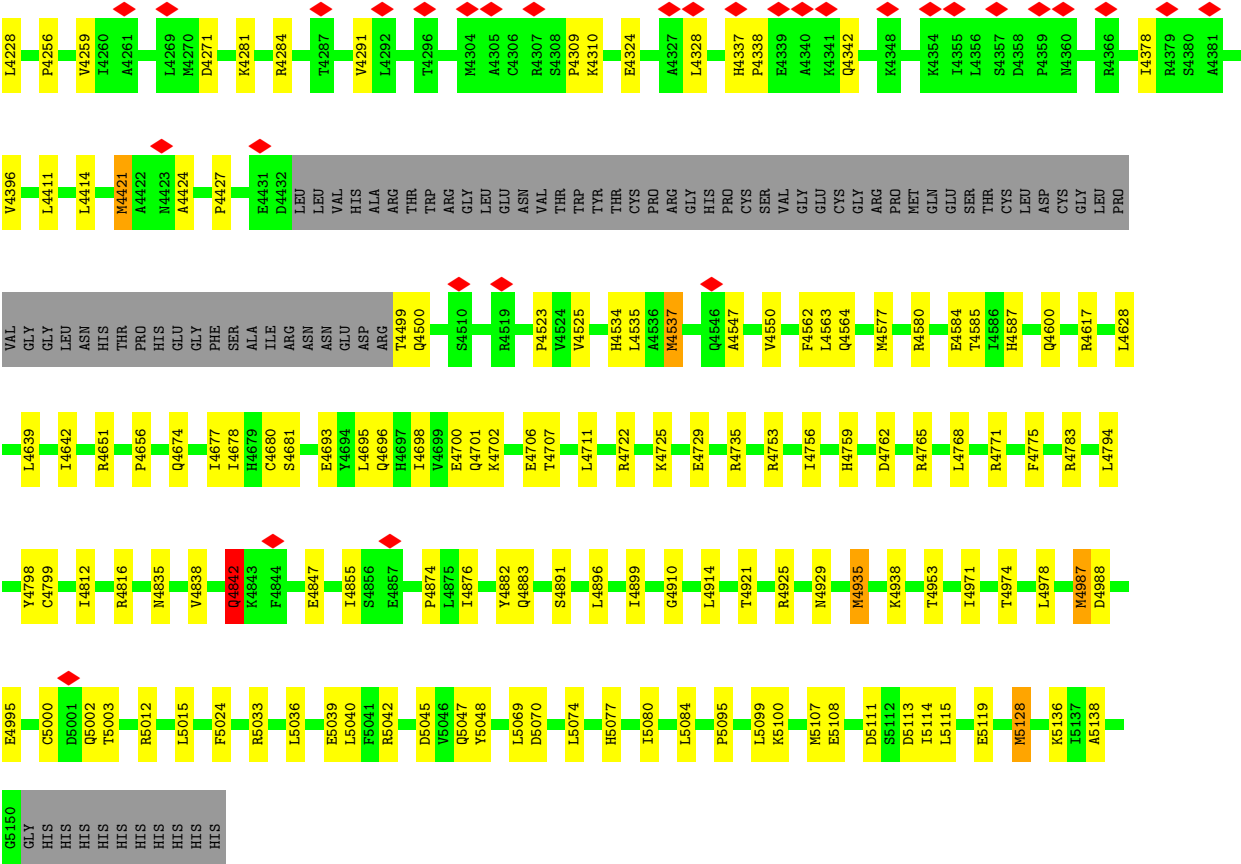
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: E3 ubiquitin-protein ligase RNF213



ASP	ALA	GLN	LYS	H4060	R4061	P4069	D4072	L4084	D4098	L4113	T4114	K4117	S4126	E4129	D4130	S4131	V4132	A4138	L4142	L4143	E4144	Q4164	E4165	P4166	V4167	R4168	I4169	A4170	S4171	L4175	V4178	L4185	E4200	L4201	K4205	R4206	N4221	H4224	R4225	L4053								
K3938	F3942	F3946	V3958	C3959	L3960	H3964	R3969	C3970	I3971	Q3972	T3973	W3974	L3975	L3976	P3977	Q3978	L3982	L3986	T3987	D3988	L3989	P3990	D3991	K3992	F3993	S3994	V3995	R4002	K4007	H4008	A4009	R4012	H4013	D4021	M4026	I4039	L4042	L4046	Q4049	K4050	L4053							
P3786	Q3787	V3788	L3789	S3790	S3793	L3808	D3809	K3821	G3822	K3826	P3827	E3849	G3850	Y3851	S3855	R3860	I3863	Q3864	E3865	V3866	R3867	R3872	A3877	L3878	F3879	V3880	E3881	H3882	L3884	I3891	L3897	L3904	K3907	C3908	L3909	E3910	V3922	M3925	L3928	K3937								
A3605	D3609	L3610	W3611	M3612	Y3615	L3618	V3626	LEU	ASN	ASN	THR	ARG	ASN	ASN	GLU	MET	S3637	K3645	N3646	L3647	P3656	F3657	S3658	R3662	E3687	K3691	T3692	P3693	V3696	Q3700	L3720	S3726	R3727	E3728	M3731	F3732	M3735	A3736	R3780	H3785								
GLU	VAL	ASP	GLU	GLU	MET	LYS	ALA	SER	ASP	PRO	ARG	SER	CYS	ASP	CYS	S3472	R3479	L3480	V3481	V3485	Q3495	N3496	R3501	R3505	I3508	D3516	R3519	R3530	W3549	Y3550	T3551	D3558	R3567	D3590	R3591	D3592	G3593	L3594	L3595	L3598	D3602							
S3254	H3268	F3274	S3281	R3282	L3292	L3296	N3327	P3321	P3322	P3323	L3324	L3325	N3326	R3332	Q3365	D3369	L3379	L3460	V3481	V3485	Q3495	N3496	R3501	R3505	I3508	D3516	R3519	R3530	W3549	Y3550	T3551	D3558	R3567	D3590	R3591	D3592	G3593	L3594	L3595	L3598	D3602							
Q3077	L3090	G3091	R3096	V3109	V3115	Q3119	F3120	P3121	V3122	P3123	L3124	L3125	N3126	R3127	L3133	D3134	M3135	V3138	L3139	Q3140	W3142	Q3143	K3144	V3147	Q3164	C3185	A3186	S3187	V3188	E3194	R3199	D3200	E3203	E3204	Y3206	R3207	P3223	D3224	A3225	V3226	F3237	T3238						
I2845	S2846	N2847	W2848	A2853	R2863	P2866	L2872	I2878	D2887	L2914	L2935	Q2938	D2939	T2940	H2942	Y2984	D2995	G2996	S2999	R3000	T3006	A3011	L3012	I3014	L3015	Q3016	Q3017	E3021	I3028	M3053	V3059	L3062	N3063	L3064	Y3068													
T2513	R2528	V2529	P2534	Q2556	V2559	W2587	R2590	C2594	G2595	D2601	C2605	V2608	D2624	H2628	D2632	L2658	E2659	E2660	A2708	V2717	E2721	L2722	P2725	L2728	G2733	I2742	A2746	G2808	K2815	L2830	E2831	D2832	F2842															
VAL	E2247	K2257	R2258	F2269	D2272	I2294	G2299	K2303	V2306	M2307	L2311	F2312	F2326	L2329	K2334	L2356	M2369	R2370	R2372	V2377	T2406	T2443	F2447	A2450	S2457	C2458	I2459	I2462	L2473	H2474	S2477	N2486	S2509															
ASP	P2113	E2119	P2128	Y2129	Q2130	Q2137	Q2138	Q2139	D2142	V2151	L2159	F2162	W2173	L2176	R2177	F2182	L2183	Q2186	D2189	F2208	M2219	D2222	T2225	T2226	T2227	LEU	HIS	THR	SER	ASP	GLN	SER	PRO	GLY	ARG	GLN	VAL	THR	ILE	ARG	GLY	HIS	THR					
S2021	T2022	Q2025	F2033	K2034	L2035	L2038	Q2039	Y2040	L2041	M2042	I2048	W2049	Y2057	P2062	Q2063	GLY	SER	VAL	GLN	PRO	LYS	ARG	SER	SER	LYS	LEU	ASN	ALA	ARG	ALA	P2080	L2081	L2085	R2094	P2095	P2096	K2097	E2098	V2099	I2100	E2103	LEU	THR	PRO	GLU	SER	HIS	THR
Y1810	T1820	F1821	D1822	L1826	C1827	T1828	T1831	R1841	T1845	V1853	D1860	E1865	Q1869	H1882	R1883	E1884	R1896	L1925	R1934	S1937	A1938	F1942	L1946	A1956	L1975	R1976	D1977	P1981	R1986	L1987	T1988	L1992	V2014	D2019	T2020													



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	336000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45, 40.5	Depositor
Minimum defocus (nm)	-1500	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.034	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	370.656, 370.656, 370.656	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.053, 1.053, 1.053	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, ZN, MG, AGS, ADP

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	0.27	0/36242	0.72	49/49026 (0.1%)

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	6

There are no bond length outliers.

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1494	LEU	O-C-N	10.89	137.07	122.59
1	A	4701	GLN	CA-CB-CG	8.97	132.05	114.10
1	A	3121	PRO	CA-C-N	7.73	136.42	122.13
1	A	3121	PRO	C-N-CA	7.73	136.42	122.13
1	A	4701	GLN	N-CA-CB	7.40	121.11	110.16

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1016	GLU	Peptide
1	A	1170	GLU	Peptide
1	A	1373	ILE	Peptide
1	A	659	GLU	Peptide
1	A	688	PRO	Peptide

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	35505	0	35642	378	0
2	A	31	0	12	3	0
3	A	1	0	0	0	0
4	A	2	0	0	0	0
5	A	27	0	12	0	0
6	A	31	0	12	2	0
All	All	35597	0	35678	378	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 5.

The worst 5 of 378 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:731:PHE:HB3	1:A:760:ARG:HH21	1.47	0.78
1:A:4935:MET:SD	1:A:4938:LYS:NZ	2.60	0.74
1:A:942:PRO:HB3	1:A:3207:ARG:HE	1.54	0.72
1:A:3292:LEU:O	1:A:3296:LEU:HB2	1.91	0.70
1:A:942:PRO:HB3	1:A:3207:ARG:HH21	1.56	0.70

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	4394/4836 (91%)	4028 (92%)	358 (8%)	8 (0%)	43 75

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3122	VAL
1	A	4600	GLN
1	A	1374	SER
1	A	3496	ASN
1	A	4166	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	3970/4342 (91%)	3968 (100%)	2 (0%)	88 89

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

Mol	Chain	Res	Type
1	A	4587	HIS
1	A	4842	GLN

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	4560	GLN
1	A	4564	GLN
1	A	4885	GLN
1	A	2677	ASN
1	A	2655	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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
5	ADP	A	5205	-	28,29,29	1.42	4 (14%)	43,45,45	1.90	9 (20%)
6	AGS	A	5206	-	32,33,33	0.51	1 (3%)	45,52,52	0.70	1 (2%)
2	ATP	A	5201	3	32,33,33	0.37	0	48,52,52	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	A	5205	-	-	5/16/32/32	0/3/3/3
6	AGS	A	5206	-	-	8/21/38/38	0/3/3/3
2	ATP	A	5201	3	-	7/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	5205	ADP	C5-C4	4.64	1.47	1.39
5	A	5205	ADP	C5-C6	2.74	1.48	1.41
5	A	5205	ADP	C8-N7	2.42	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	5205	ADP	C5-N7	-2.31	1.34	1.39
6	A	5206	AGS	PG-S1G	2.10	1.95	1.90

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	5205	ADP	C5-C4-N3	-6.15	118.25	126.72
5	A	5205	ADP	N3-C4-N9	4.79	135.31	127.17
5	A	5205	ADP	C2-N3-C4	3.92	121.41	111.83
6	A	5206	AGS	PB-O3B-PG	-3.68	119.72	133.17
5	A	5205	ADP	C4-C5-N7	-3.56	106.51	110.58

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

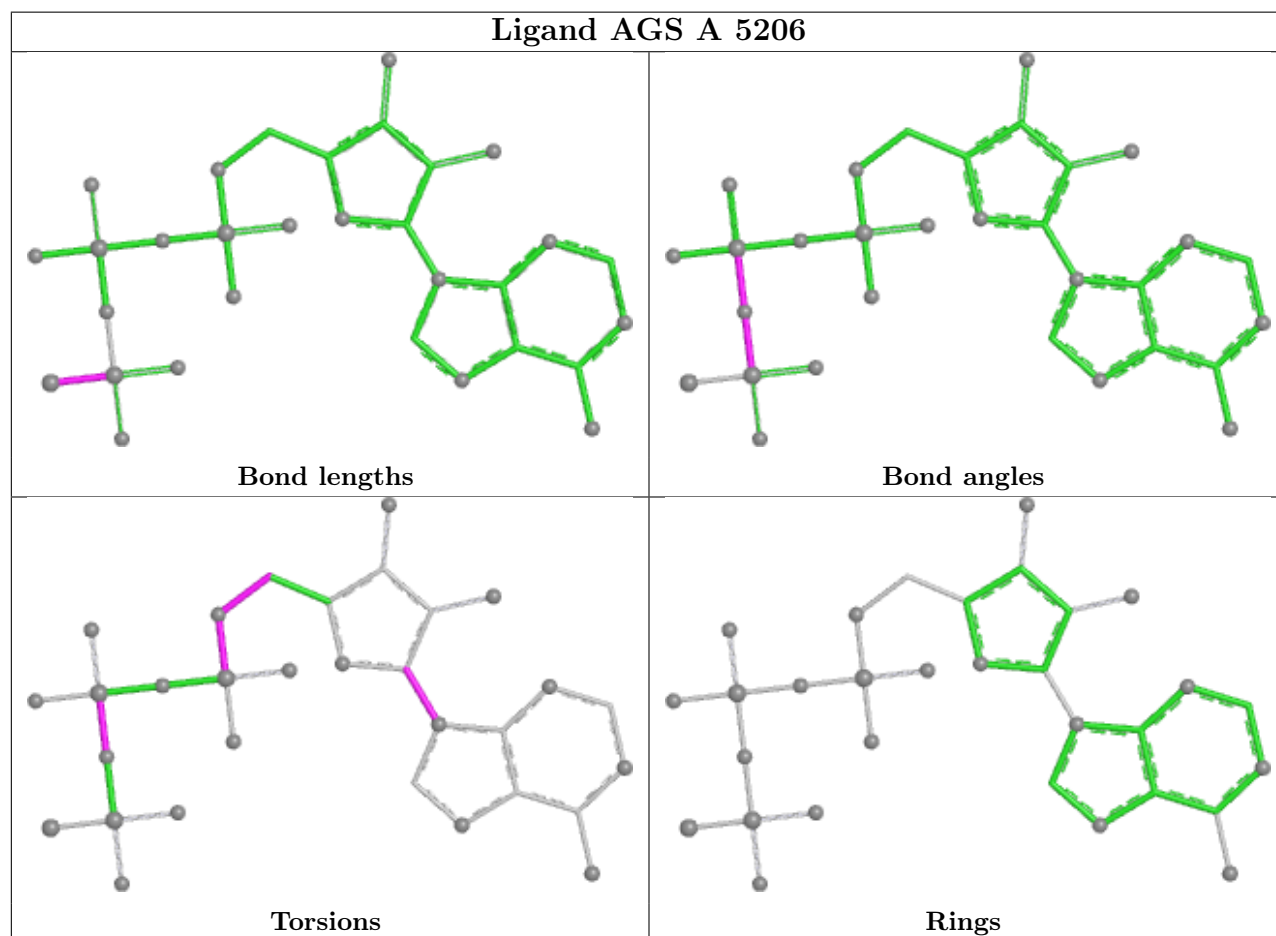
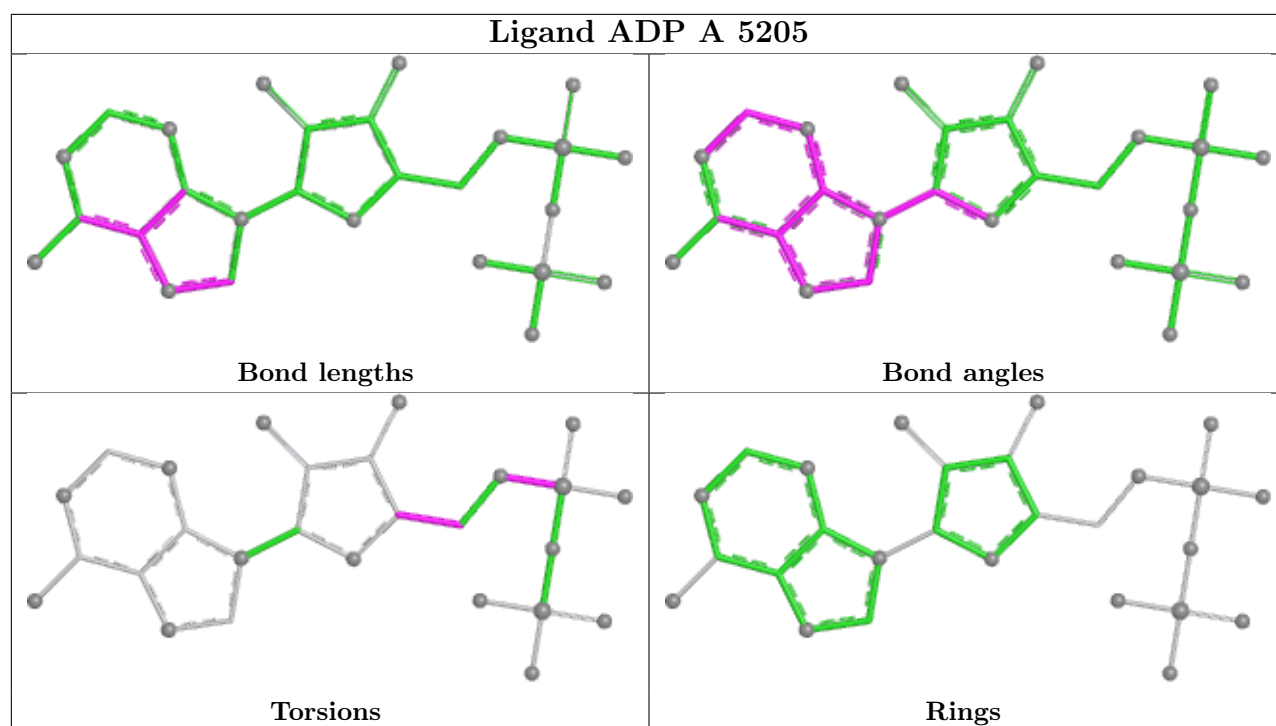
Mol	Chain	Res	Type	Atoms
2	A	5201	ATP	C5'-O5'-PA-O1A
2	A	5201	ATP	C5'-O5'-PA-O2A
2	A	5201	ATP	C5'-O5'-PA-O3A
2	A	5201	ATP	O4'-C4'-C5'-O5'
5	A	5205	ADP	C5'-O5'-PA-O2A

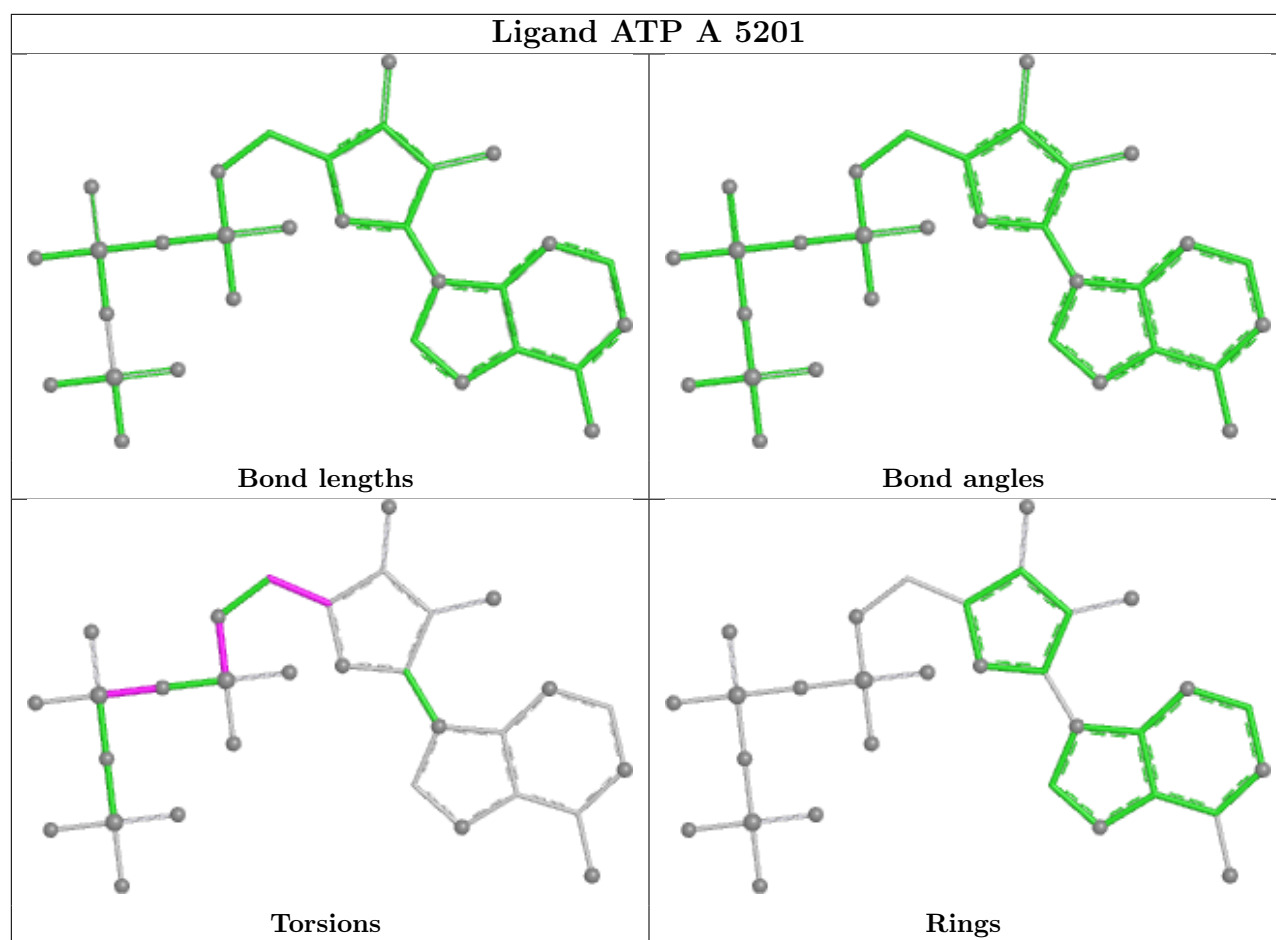
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	5206	AGS	2	0
2	A	5201	ATP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

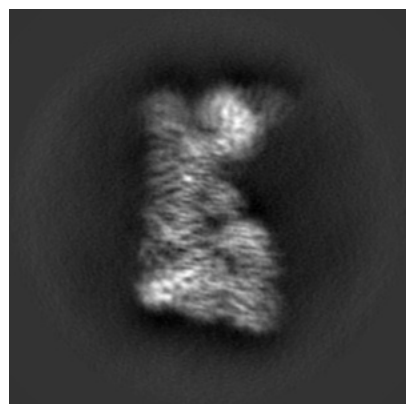
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12932. These allow visual inspection of the internal detail of the map and identification of artifacts.

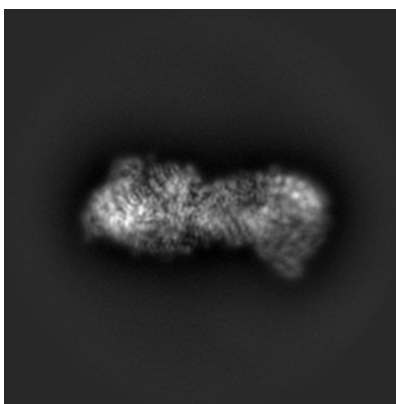
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

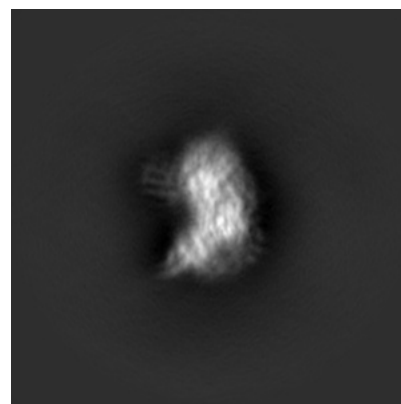
6.1.1 Primary map



X

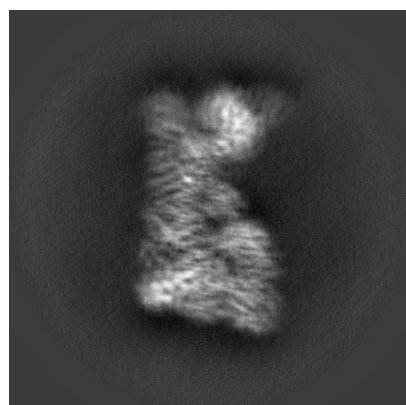


Y

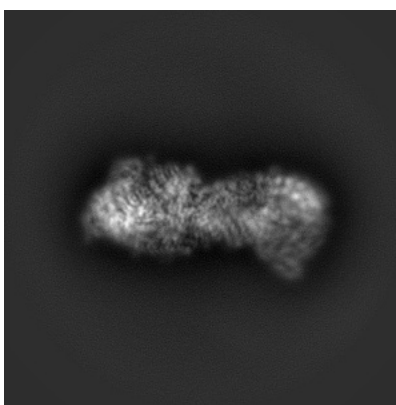


Z

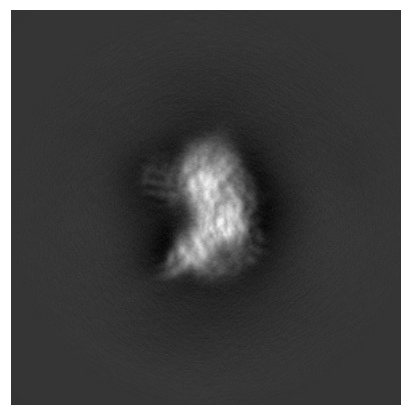
6.1.2 Raw map



X



Y

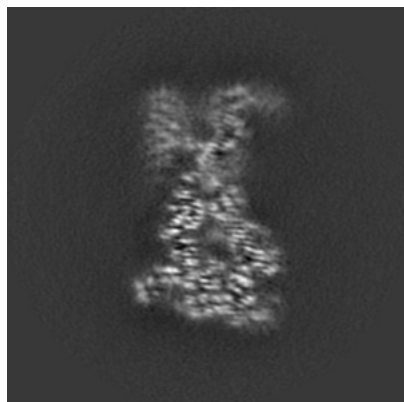


Z

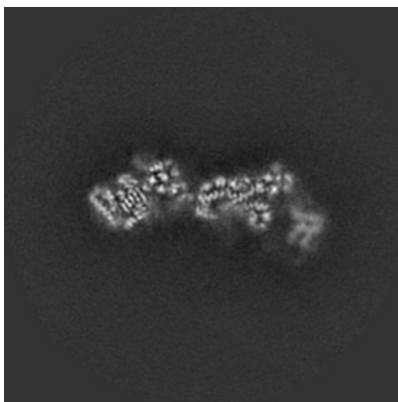
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

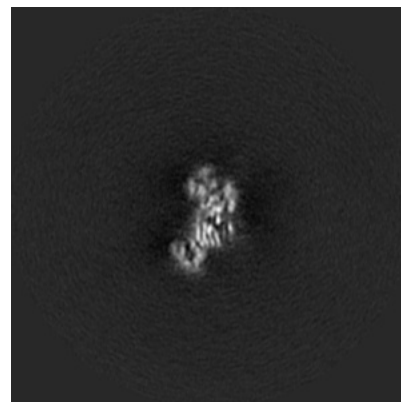
6.2.1 Primary map



X Index: 176

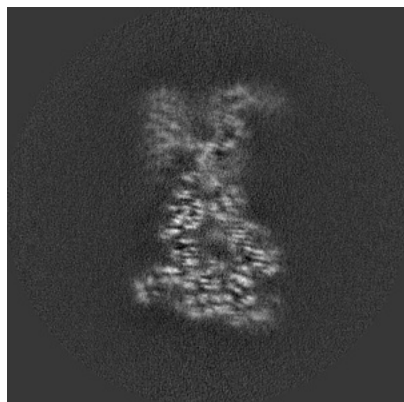


Y Index: 176

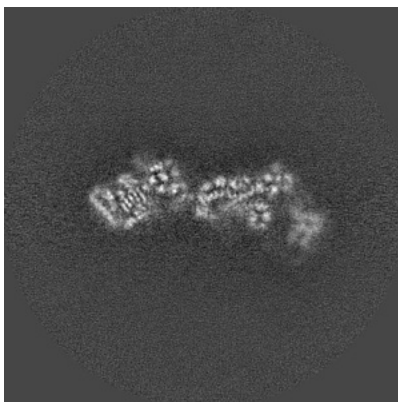


Z Index: 176

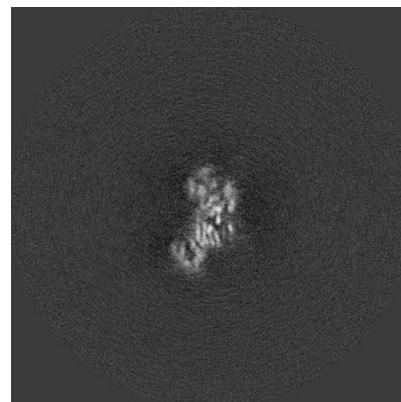
6.2.2 Raw map



X Index: 176



Y Index: 176

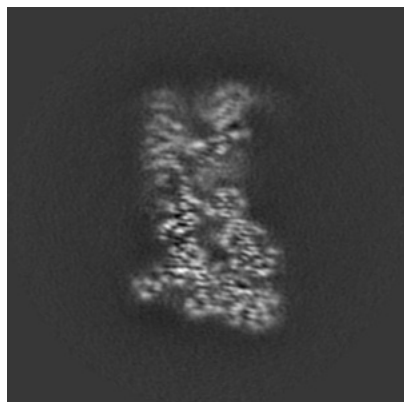


Z Index: 176

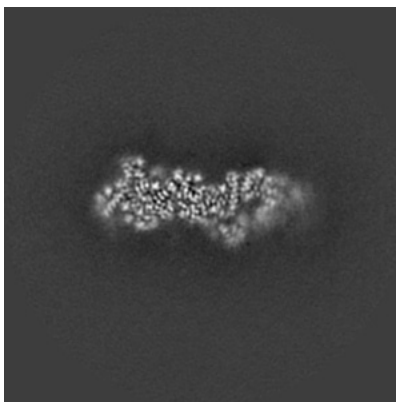
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

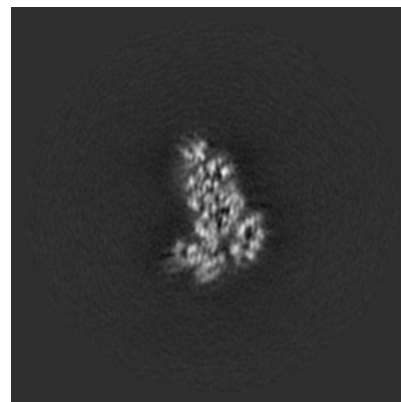
6.3.1 Primary map



X Index: 172

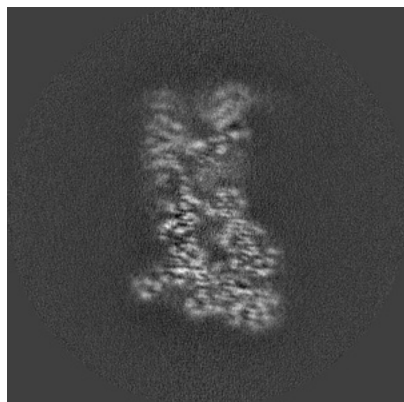


Y Index: 159

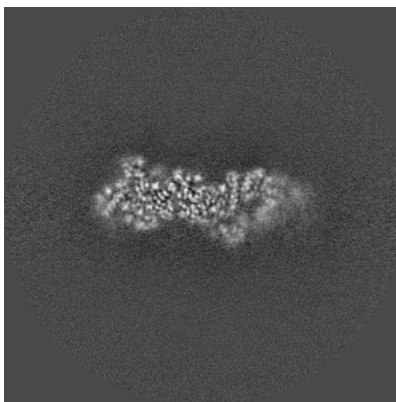


Z Index: 109

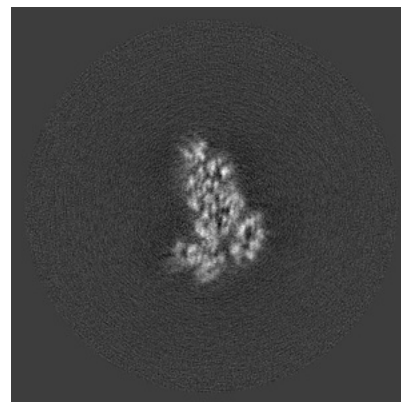
6.3.2 Raw map



X Index: 172



Y Index: 159



Z Index: 109

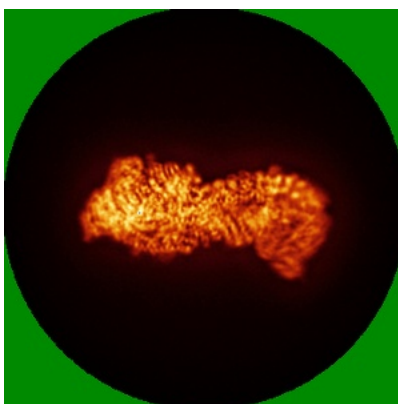
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

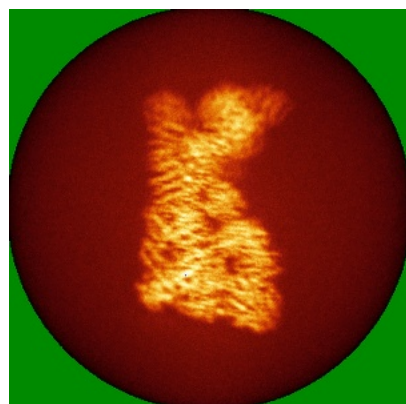


Y

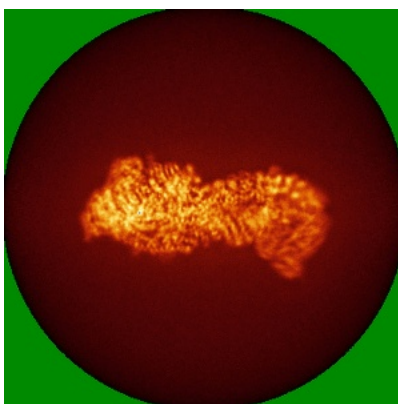


Z

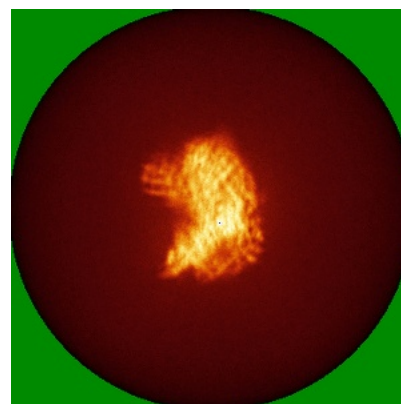
6.4.2 Raw map



X



Y

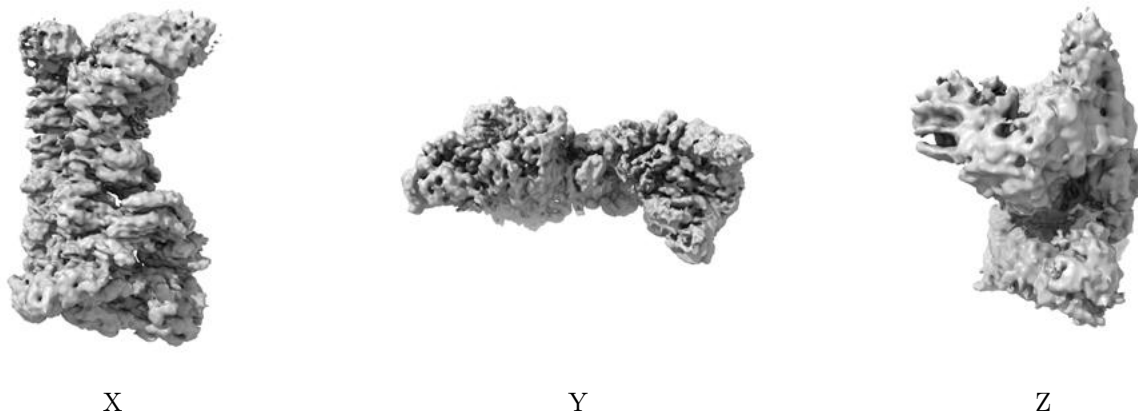


Z

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.

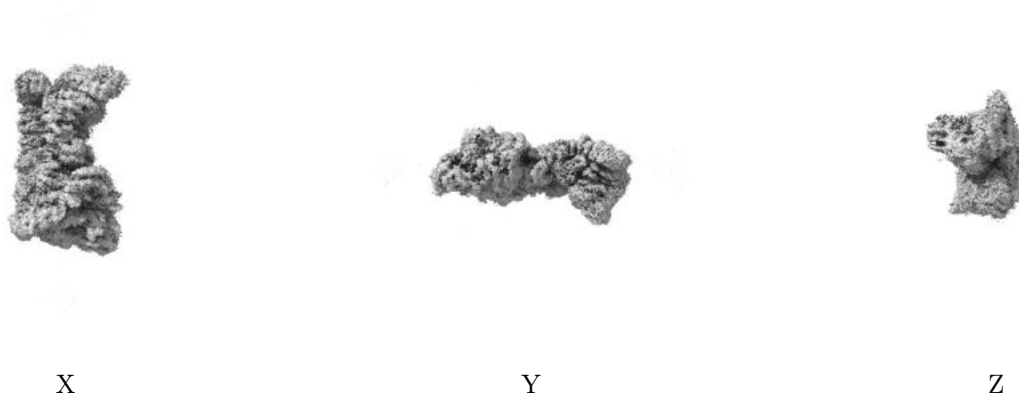
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

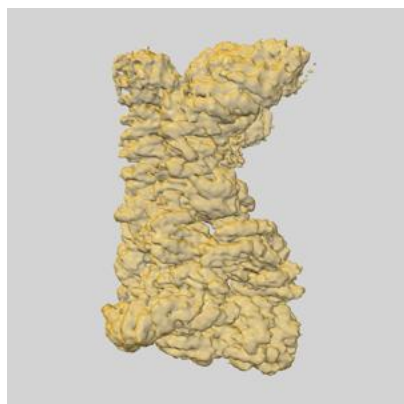
6.6 Mask visualisation [i](#)

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

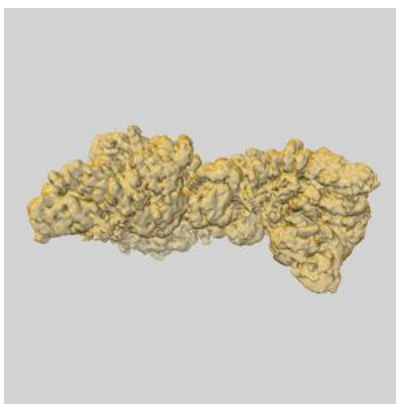
A mask typically either:

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

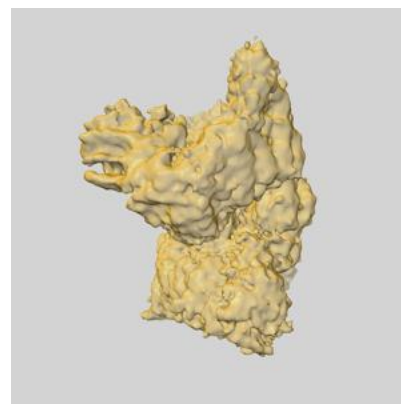
6.6.1 emd_12932_msk_2.map [i](#)



X

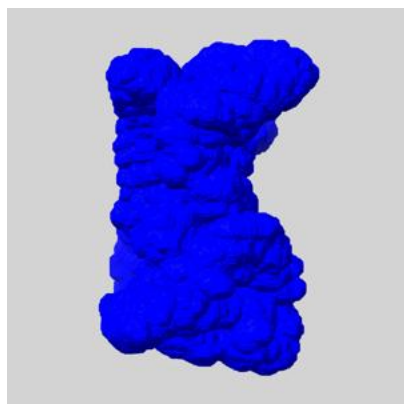


Y

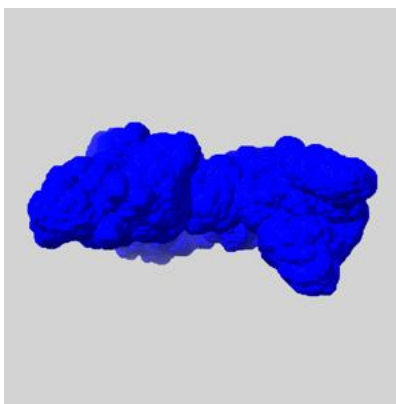


Z

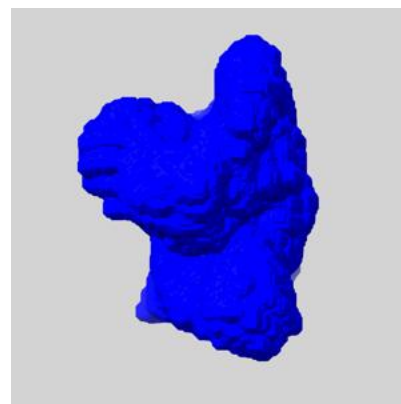
6.6.2 emd_12932_msk_1.map [i](#)



X



Y

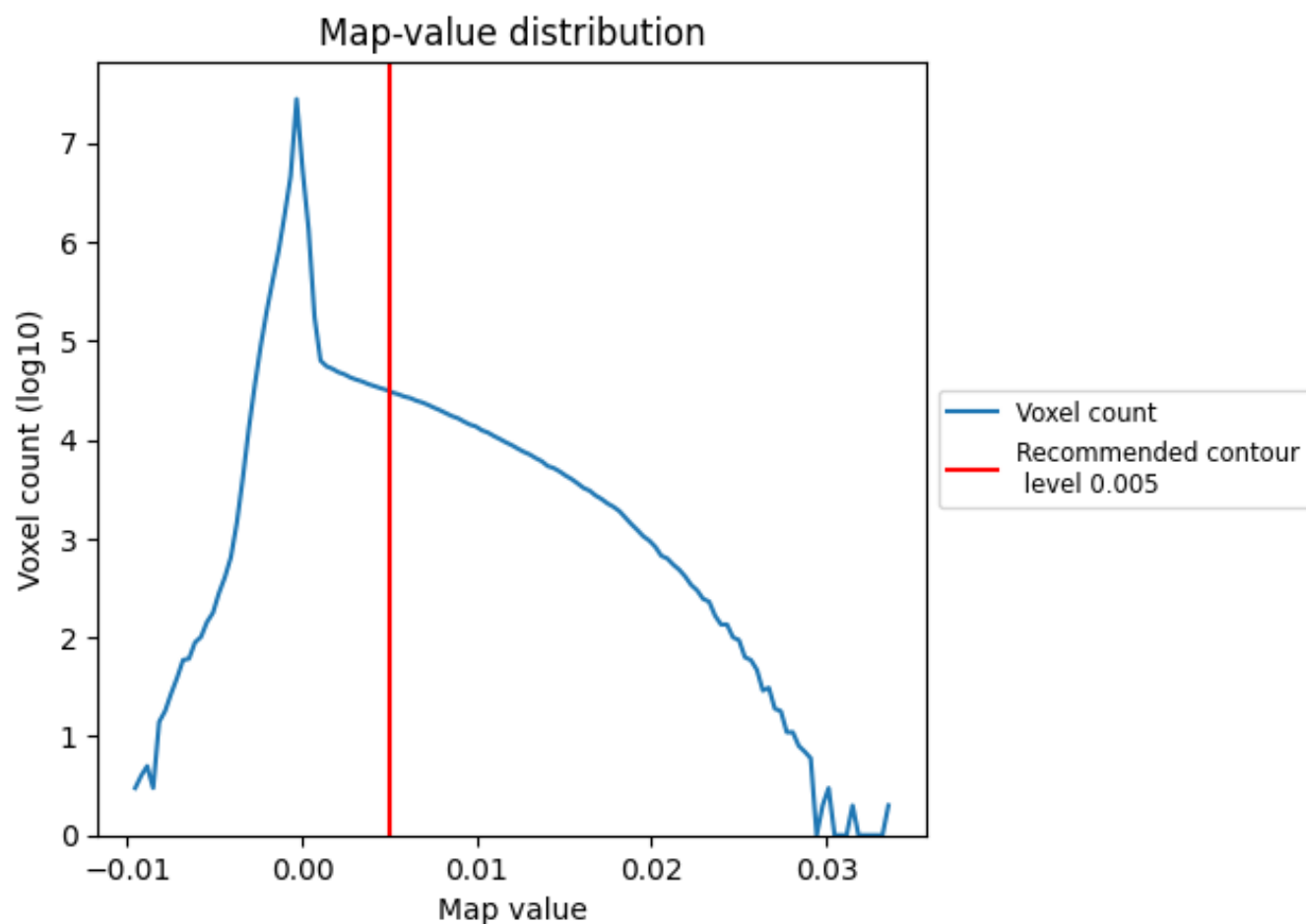


Z

7 Map analysis [i](#)

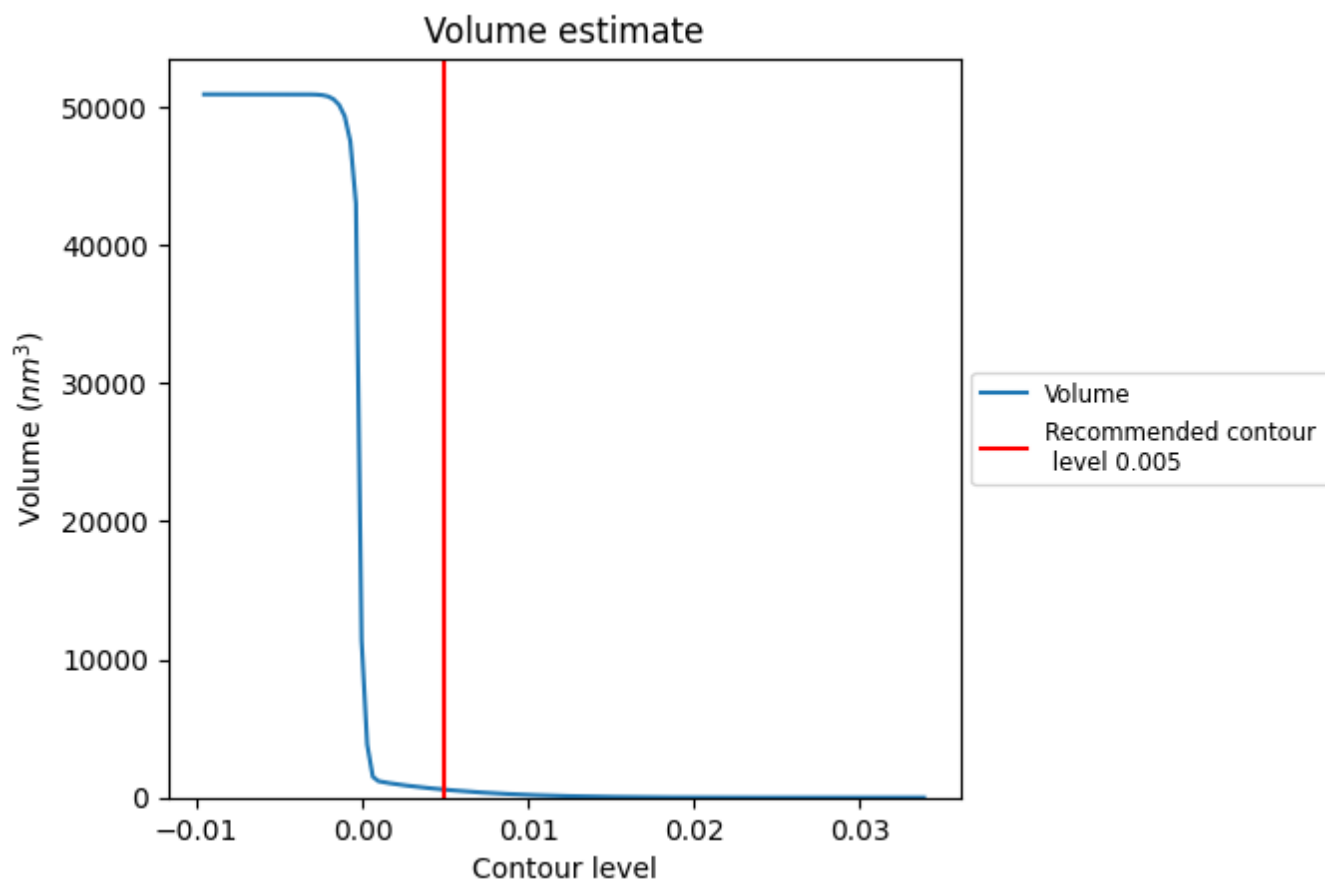
This section contains the results of statistical analysis of the map.

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.

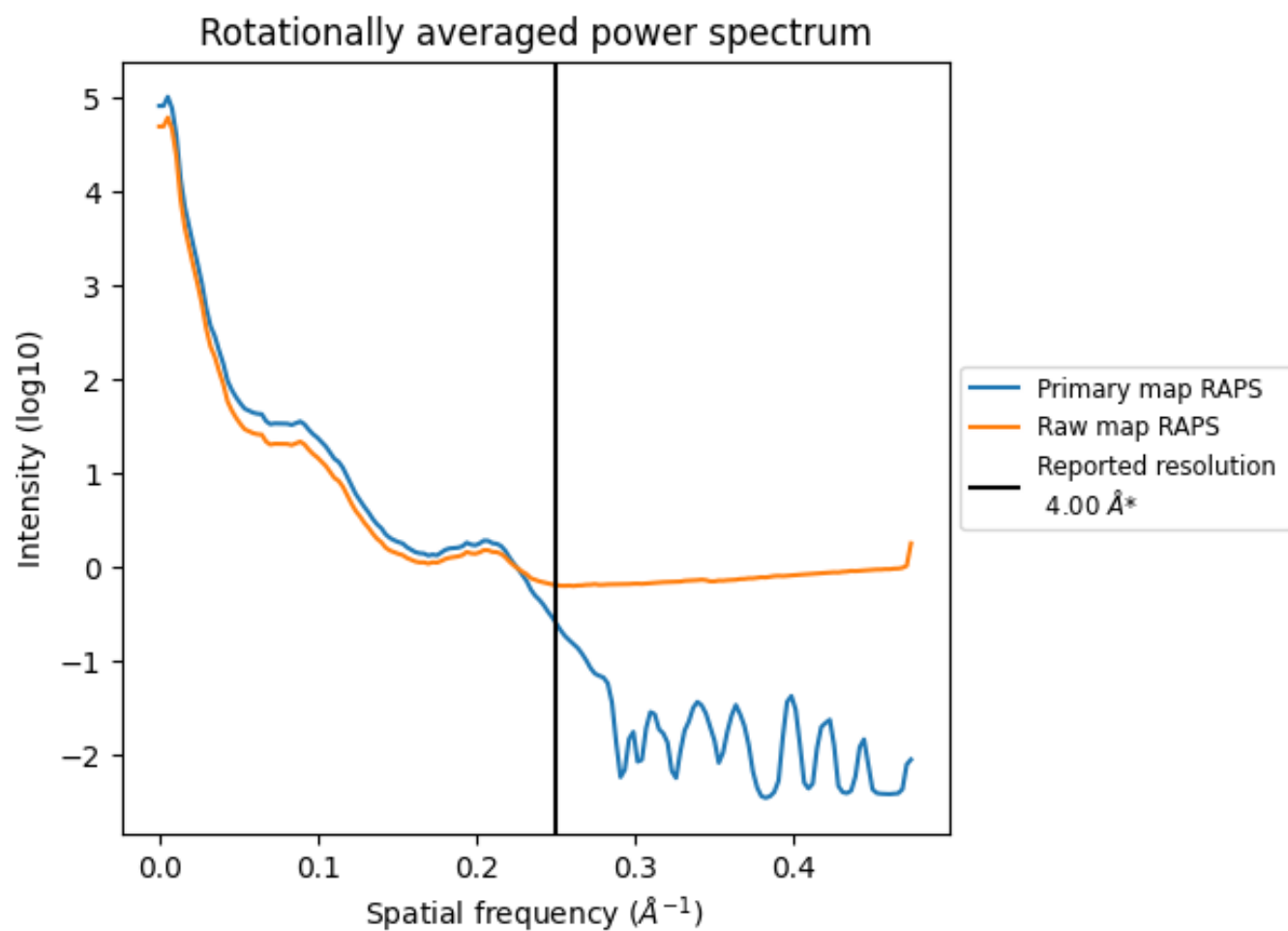
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 572 nm³; this corresponds to an approximate mass of 517 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 ⓘ

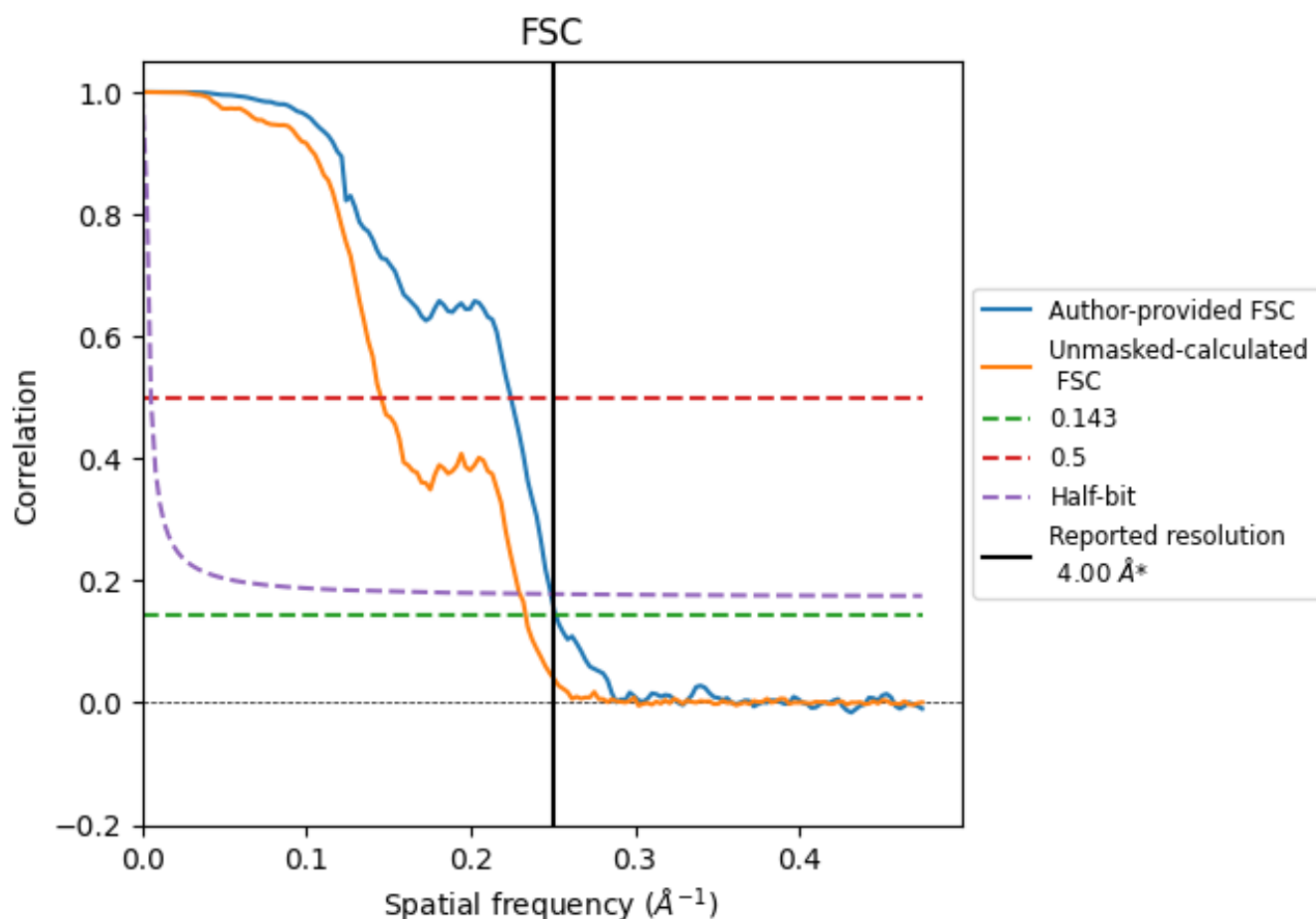


*Reported resolution corresponds to spatial frequency of 0.250 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

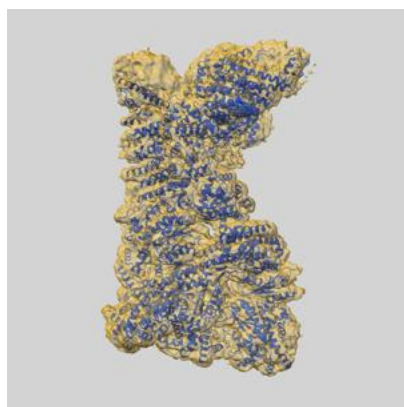
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.97	4.46	4.02
Unmasked-calculated*	4.28	6.88	4.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

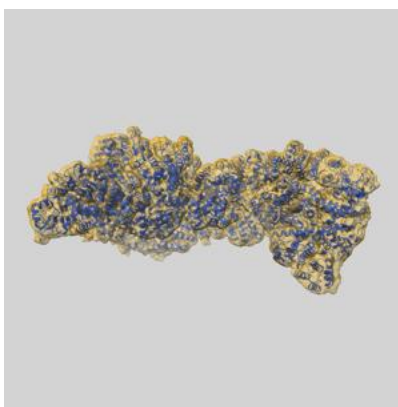
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12932 and PDB model 7OIM. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

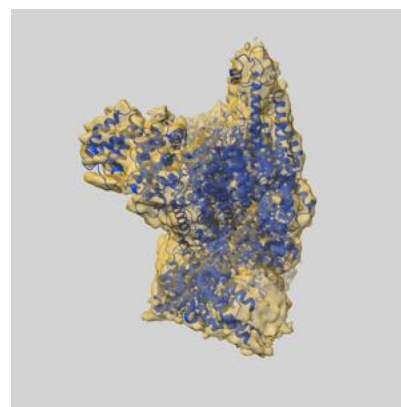
9.1 Map-model overlay [i](#)



X



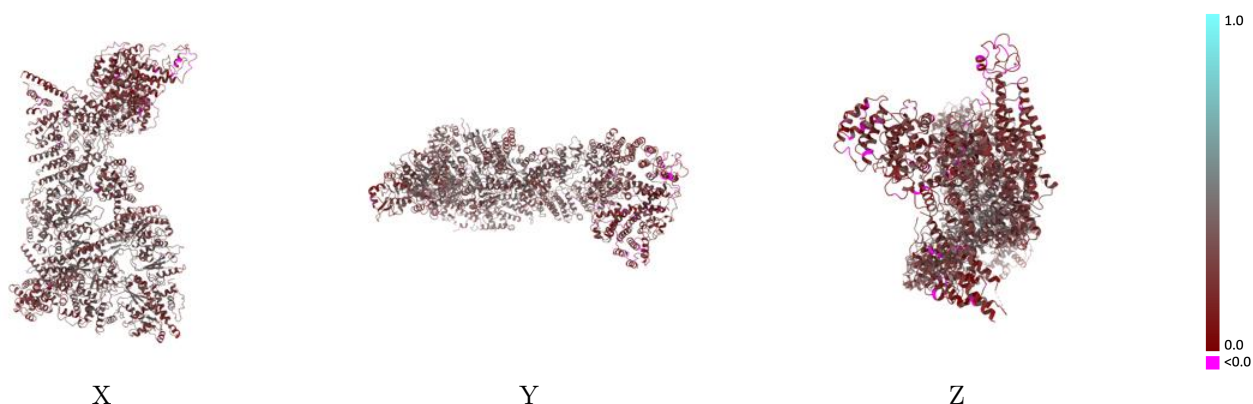
Y



Z

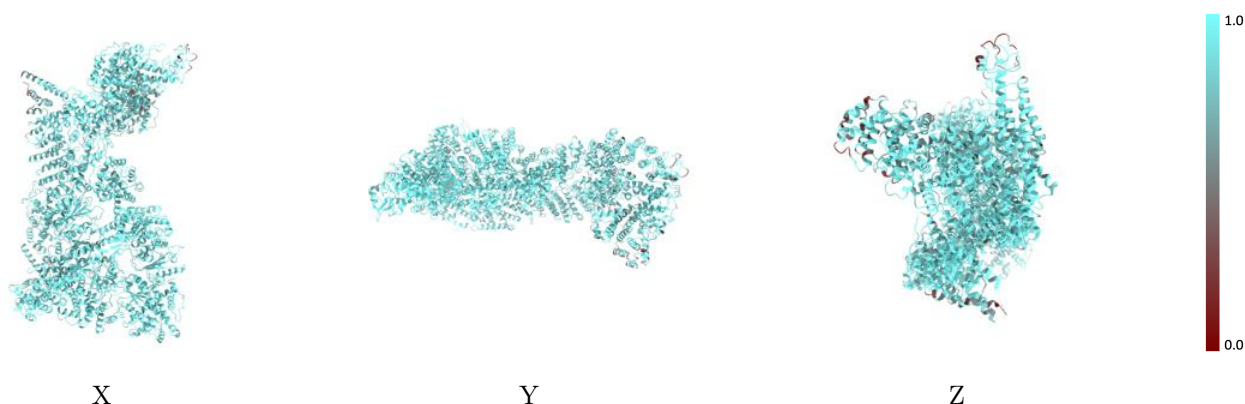
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



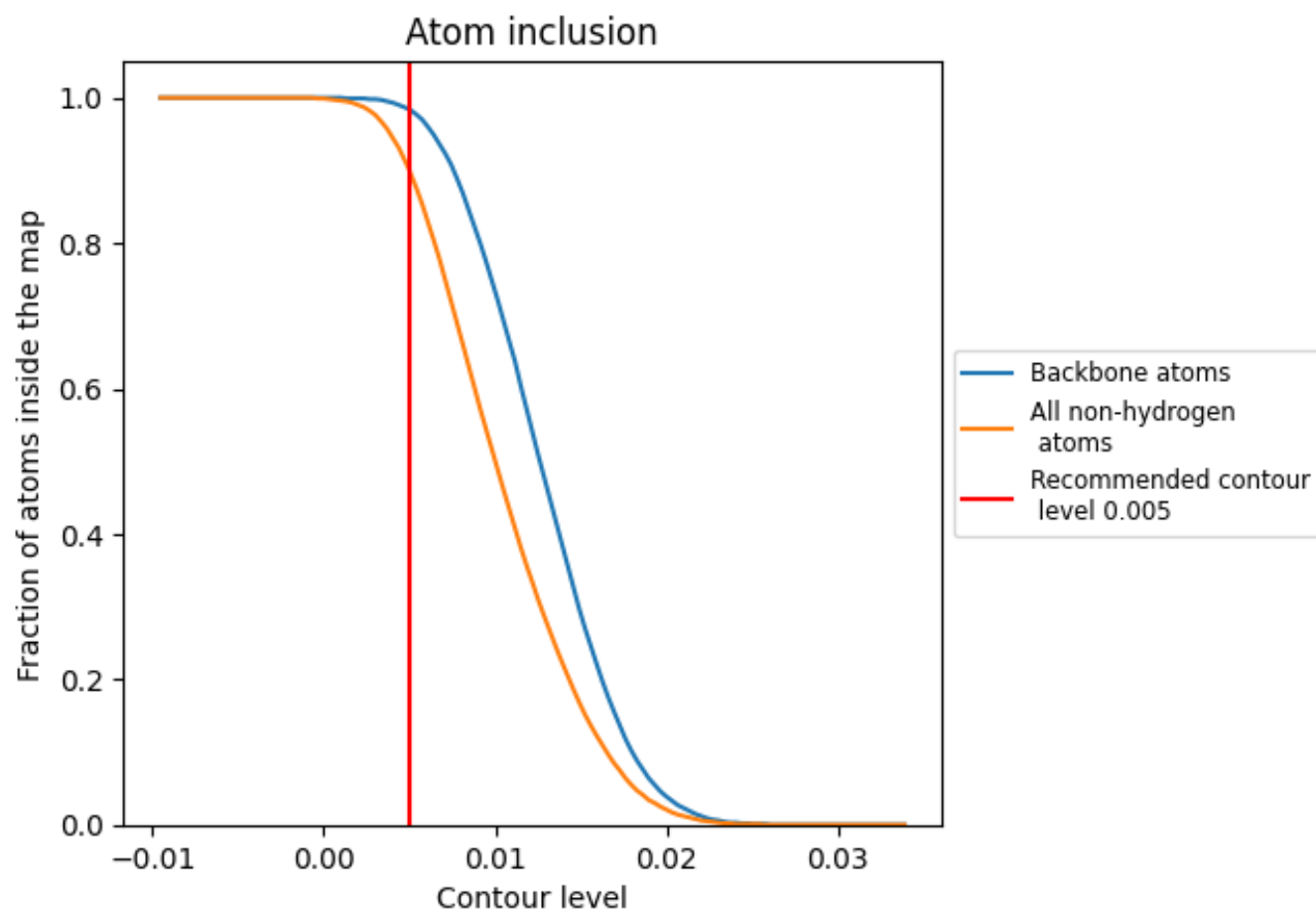
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 90% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9000	0.2870
A	0.9000	0.2870

