



wwPDB EM Validation Summary Report ⓘ

Apr 28, 2025 – 10:37 AM JST

PDB ID : 9JW1 / pdb_00009jw1
EMDB ID : EMD-61848
Title : Cryo-EM structure of Human RNF213
Authors : Zhang, H.
Deposited on : 2024-10-09
Resolution : 3.46 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.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.43.1

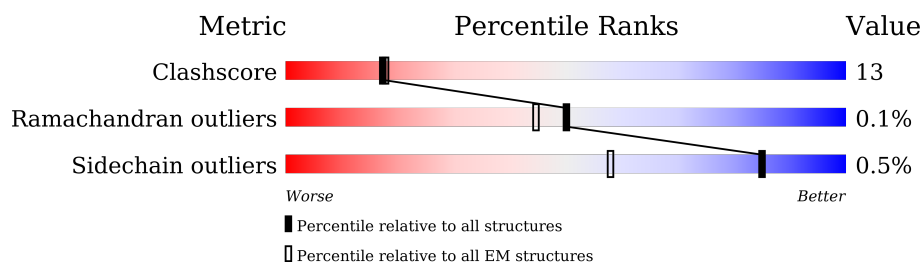
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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	4841	 64% 28% 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 35937 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.

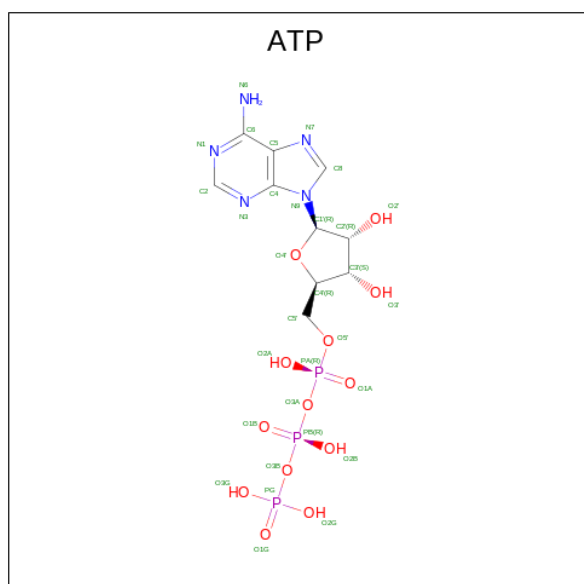
- Molecule 1 is a protein called Ring finger protein 213.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	4471	35905	22894	6203	6590	218	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	GLY	-	expression tag	UNP A0A0A0MTC1
A	368	PRO	-	expression tag	UNP A0A0A0MTC1
A	369	GLY	-	expression tag	UNP A0A0A0MTC1
A	370	THR	-	expression tag	UNP A0A0A0MTC1
A	2927	VAL	ARG	conflict	UNP A0A0A0MTC1
A	2928	ALA	VAL	conflict	UNP A0A0A0MTC1

- 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).



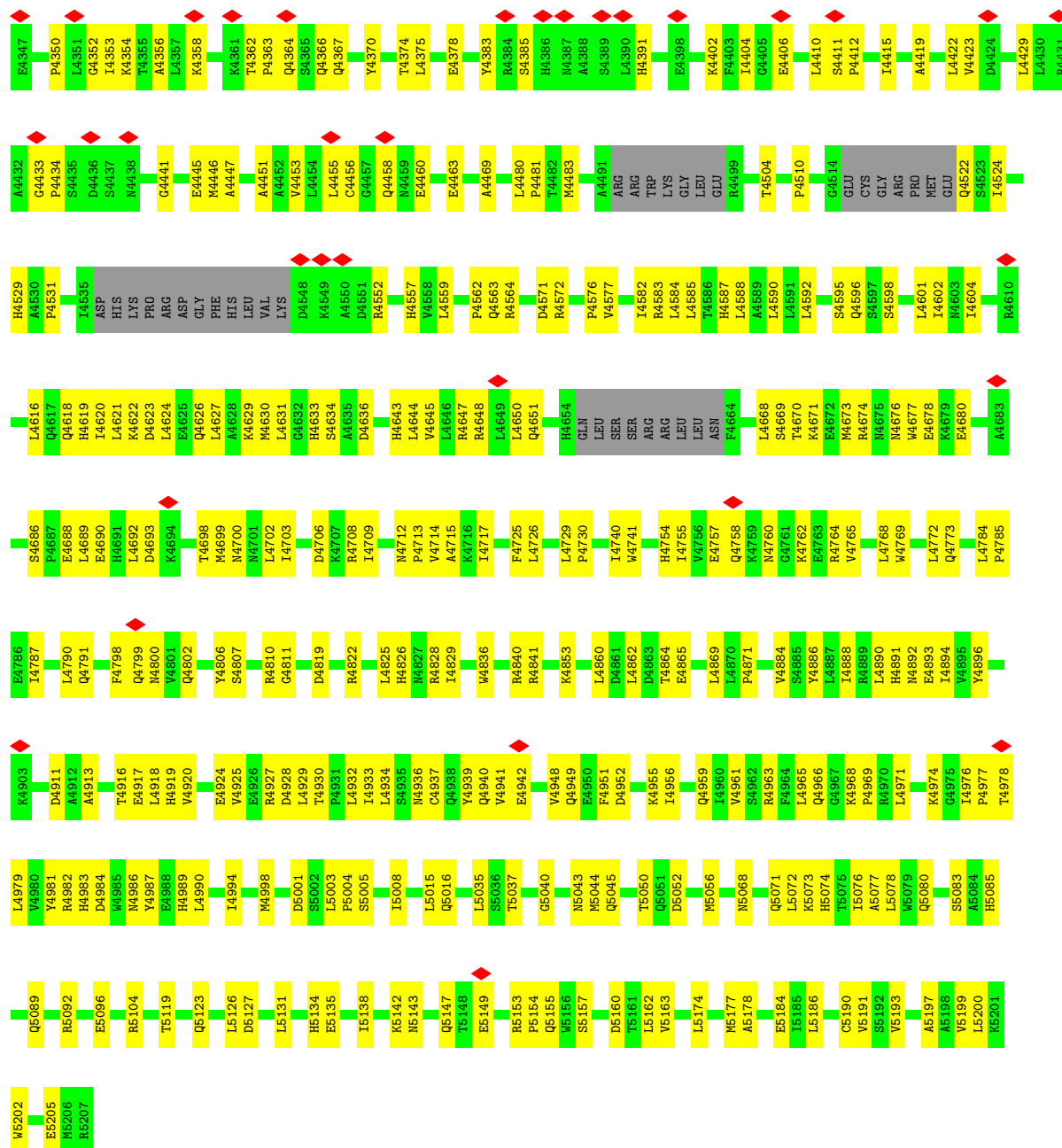
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

- 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	



K4264	R4191	F4097	A4026	V3941	T3857	P3747	W3685	R3537	ASP	L3375	R3147	Q3027
V4270	E4194	V4098	S4027	P3942	L3858	L3748	D3671	S3538	LEU	G3276	L3146	K3028
E4271	L4205	Q4099	E4028	E3943	D3859	G3749	D3672	E3939	PRO	F3277	I3149	
R4272	R4203	L4206	R4029	L3944	A3860	R3750	M3673	V3540	GLU	F3278		
R4273	R4204	ARG	R4030	G3945	F3861	A3753	L3674	A3543	GLY	A3279	K3159	R3040
E4201	E4201	ARG	R4031	G3946	M3864	H3756	L3675	M3546	LEU	A3280	H3160	L3052
R4276	R4202	ASP	L4031	V3948	C3865	H3766	L3676	L3000	LEU	L3300	F3161	L3055
R4277	L4035	L3949		V3948	A3866	L3764	L3677	E3310	GLU	E3310	P3162	L3056
R4281	L4036	E3950		V3948	C3866	C3765	P3678	Q3550	ARG	E3310	P3164	L3057
S4285	L4037	H3951		V3948	M3869	C3766	N3682	R3556	ALA	T3316	I3167	T3058
Q4286	L4038	F3952		V3948	N3873	Y3767		N3557	GLU	ASP	F3059	F3060
R4287	L4039	L3953		V3948	K3876	L3773		R3560	GLY	ASP	R3168	
Q4287	L4040	D3956		V3948	W3882	M3776		L3324	HIS	HIS	L3169	D3063
V4282	L4041	K3957		V3948	L3883	F3786		L3565	GLU	GLU	K3171	Q3064
L4295	E4042	C3958		V3948	Q3884	F3786		D3571	ALA	ALA	V3179	Q3065
S4296	F4043	L3959		V3948	L3885	S3793		S3577	THR	THR	I3187	P3066
R4297	S4044	R3960		V3948	V3886	K3797		V3581	ALA	ALA	E3190	F3067
F4298	P4045	E3961		V3948	K3887	E3806		R3585	THR	THR	V3195	R3085
R4299	A4046	N3962		V3948	L3888	E3807		F3589	SER	SER	I3199	I3087
R4300	V4047	K3966		V3948	S3890	E3807		N3707	GLY	GLY	N3200	N3088
P4301	Q4048	F3971		V3948	M3891	S3810		K3592	VAL	VAL	V3201	V3090
R4302	A4050	E3972		V3948	P3892	L3811		L3601	GLU	GLU	K3211	I3092
P4301	L4051	A3973		V3948	L3893	P3812		A3605	VAL	VAL	V3217	E3095
V4305	R4052	V3974		V3948	E3894	S3810		N3610	GLU	GLU	I3218	K3099
K4308	E4053	M3975		V3948	L3895	L3825		A3613	ALA	ALA	G3220	V3100
K4312	A4056	R3976		V3948	L3896	Q3826		L3614	GLU	GLU	Y3221	L3101
Q4313	R4057	L3977		V3948	E3900	N3827		T3623	THR	THR	H3222	L3102
L4316	H4058	C3978		V3948	M3901	F3828		L3624	GLU	GLU	C3226	L3103
D4319	F4061	L3978		V3948	H3902	R3829		A3629	SER	SER	I3257	V3104
R4320	R4062	C3979		V3948	Q3903	R3830		V3628	GLU	GLU	L3257	L3105
P4321	M4066	E3980		V3948	L3913	L3831		Q3629	LYS	LYS	E3235	Q3106
Q4322	S4067	C3981		V3948	V3916	T3832		R3422	VAL	VAL	Q3248	L3108
Q4323	F4068	K3982		V3948	W3916	F3833		R3425	GLY	GLY	E3253	L3112
M4324	V4070	E3983		V3948	V3916	Y3835		G3431	THR	THR	I3257	A3115
D4325	D4071	L3989		V3948	W3920	R3839		C3435	SER	SER	L3258	L3123
R4326	L4072	C3993		V3948	R3922	H3840		N3648	GLU	GLU	N3260	V3128
V4327	L4073	A4004		V3948	F3924	S3841		E3650	LEU	LEU	D3265	V3129
F4327	V4074	P4007		V3948	L3928	L3842		L3651	GLY	GLY	R3269	D3130
G4248	T4075	H4014		V3948	F3929	R3846		L3652	ASP	ASP	I3270	V3138
G4249	I4076	C4017		V3948	V3930	W3847		R3662	GLU	GLU	S3271	K3139
P4250	I4076	L4018		V3948	E3931	H3848		L3466	THR	THR	A3272	C3140
E4251	D4080	R4019		V3948	H3932	S3841		R3663	GLY	GLY	Y3273	R3141
M4252	N4081	R4020		V3948	V3933	W3847		L3664	ASP	ASP	S3274	
A4253	P4083	C4020		V3948	L3934	N3848						
K4256	P4084	L4021		V3948	L3935	H3849						
Q4257	V4088	R4022		V3948	G3936	S3849						
G4258	I4089	A4023		V3948	T3937	H3849						
Y4259	L4089	A4023		V3948	E3938	H3849						
Q4262	L4092	L4093		V3948	S3939	E3855						
V4263	L4093	S4094		V3948	R3940	M3856						
	L4095	L4095		V3948								
	L4096			V3948								



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	179169	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 ($e^-/\text{\AA}^2$)	49.41	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.518	Depositor
Minimum map value	-1.526	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	527.5, 527.5, 527.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.055, 1.055, 1.055	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.21	5/36657 (0.0%)	0.46	16/49608 (0.0%)

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	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2134	PRO	CA-C	-12.01	1.41	1.52
1	A	1920	HIS	CA-C	-5.93	1.45	1.52
1	A	2002	VAL	CA-CB	-5.34	1.47	1.54
1	A	2000	LEU	CA-C	-5.18	1.46	1.52
1	A	1998	LYS	C-O	-5.01	1.17	1.24

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4969	PRO	O-C-N	16.86	145.41	122.64
1	A	2000	LEU	N-CA-C	-13.46	96.17	112.59
1	A	4969	PRO	CA-C-O	-13.22	96.53	120.60
1	A	1921	ARG	N-CA-C	-9.25	94.42	109.96
1	A	2785	ALA	N-CA-C	7.94	120.01	111.36

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1719	GLN	Peptide
1	A	3058	THR	Peptide
1	A	895	GLY	Peptide

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	35905	0	36077	966	0
2	A	31	0	12	1	0
3	A	1	0	0	0	0
All	All	35937	0	36089	966	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 13.

The worst 5 of 966 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:4084:PRO:HB2	1:A:4088:VAL:HG21	1.55	0.87
1:A:3832:LEU:HG	1:A:3838:VAL:HG11	1.58	0.84
1:A:731:ARG:HE	1:A:765:LEU:HG	1.43	0.83
1:A:3934:LEU:O	1:A:3938:GLU:HB2	1.80	0.80
1:A:3199:ILE:HB	1:A:3217:VAL:HG21	1.63	0.80

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	4439/4841 (92%)	4117 (93%)	316 (7%)	6 (0%)	48 79

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	896	ASN
1	A	2787	GLN
1	A	2922	ILE
1	A	541	LEU
1	A	2790	ALA

5.3.2 Protein sidechains ⓘ

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	3999/4329 (92%)	3978 (100%)	21 (0%)	86 92

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3059	PHE
1	A	3316	THR
1	A	3951	HIS
1	A	3379	THR
1	A	3258	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4619	HIS
1	A	4653	GLN
1	A	4837	ASN
1	A	2652	HIS
1	A	2623	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ATP	A	5301	3	26,33,33	1.02	0	31,52,52	1.86	8 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	A	5301	3	-	1/18/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5301	ATP	PA-O3A-PB	-4.58	117.11	132.83
2	A	5301	ATP	PB-O3B-PG	-4.50	117.38	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5301	ATP	N3-C2-N1	-3.04	123.92	128.68
2	A	5301	ATP	O5'-C5'-C4'	-2.82	99.30	108.99
2	A	5301	ATP	C3'-C2'-C1'	2.73	105.08	100.98

There are no chirality outliers.

All (1) torsion outliers are listed below:

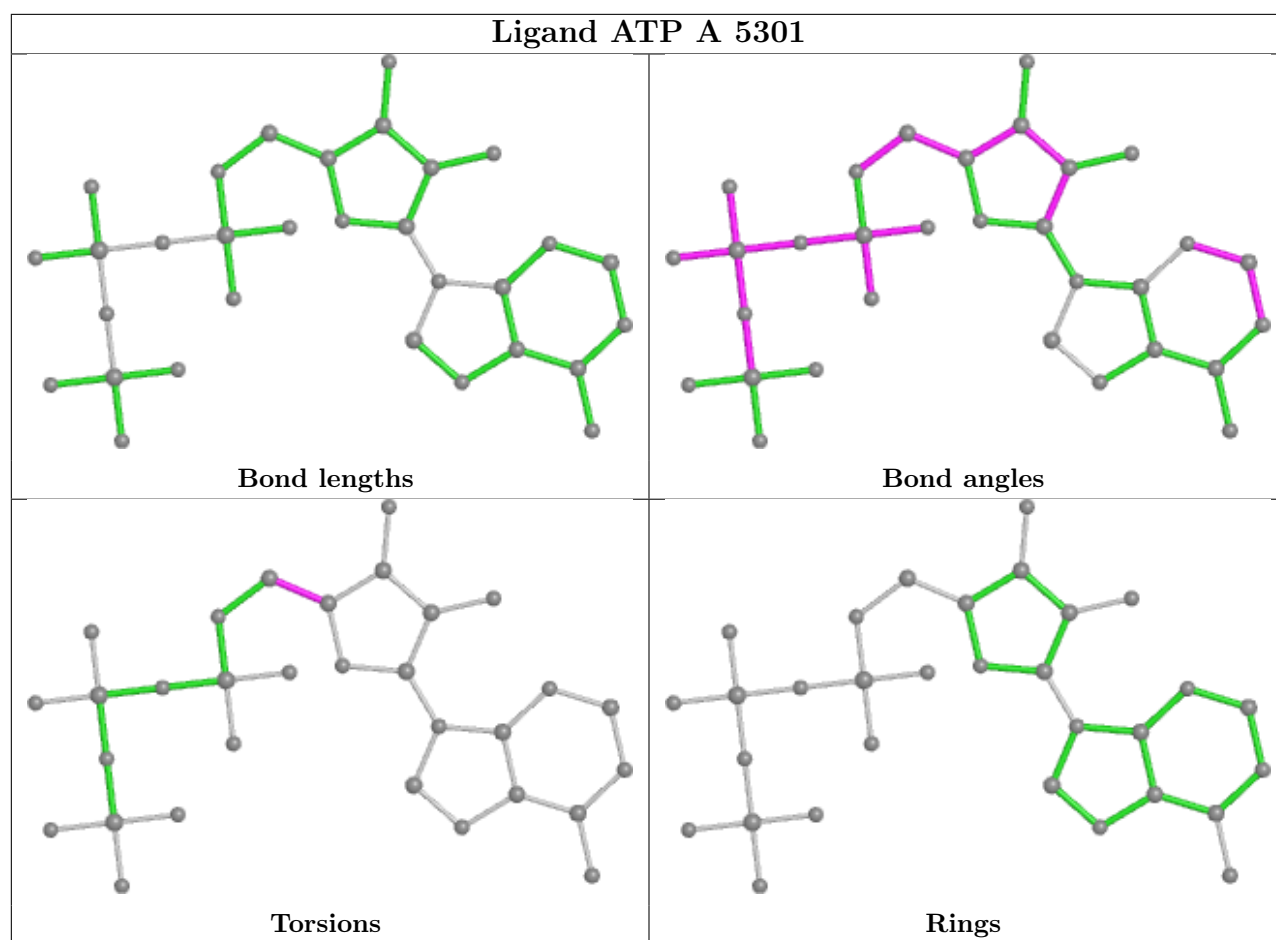
Mol	Chain	Res	Type	Atoms
2	A	5301	ATP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5301	ATP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

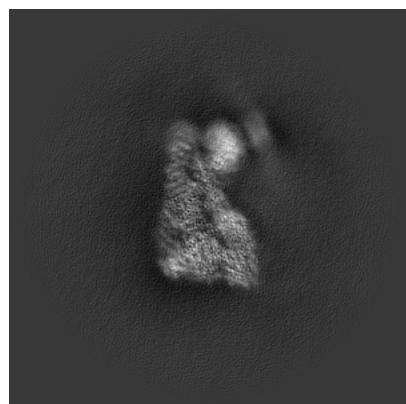
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61848. These allow visual inspection of the internal detail of the map and identification of artifacts.

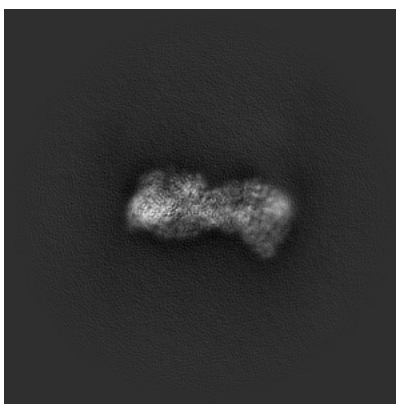
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

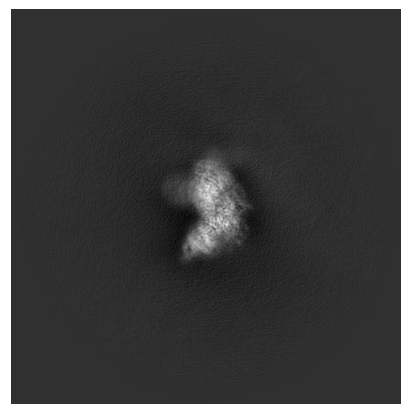
6.1.1 Primary map



X

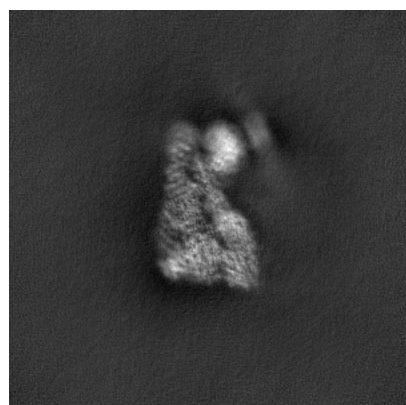


Y

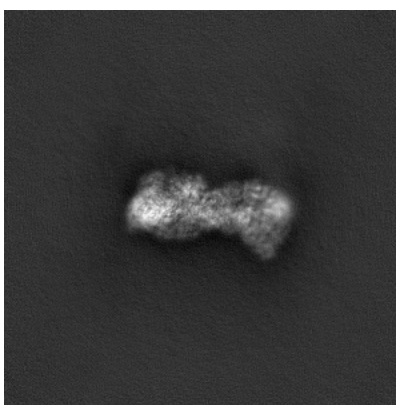


Z

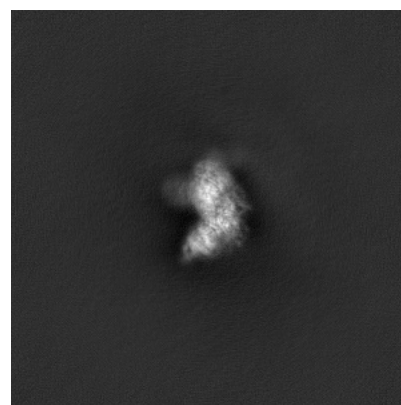
6.1.2 Raw map



X



Y

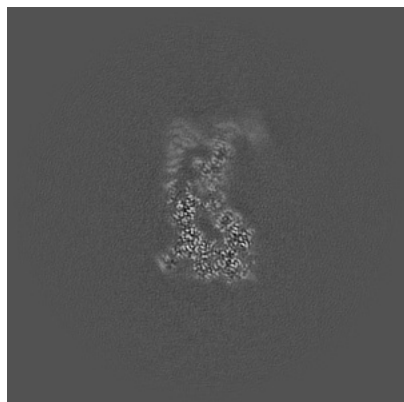


Z

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

6.2 Central slices [i](#)

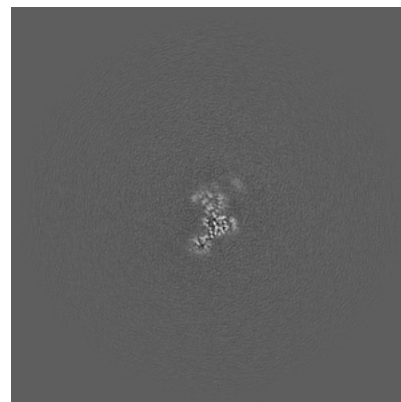
6.2.1 Primary map



X Index: 250

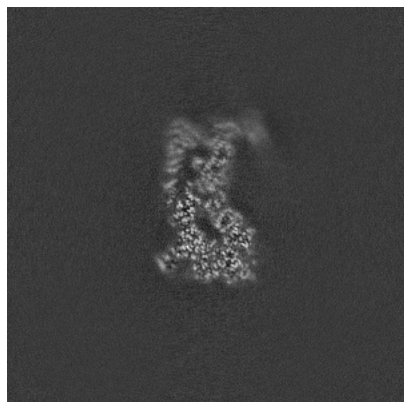


Y Index: 250



Z Index: 250

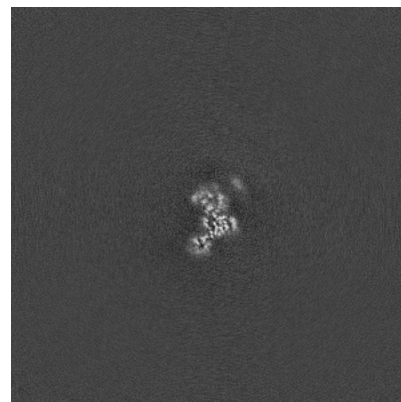
6.2.2 Raw map



X Index: 250



Y Index: 250

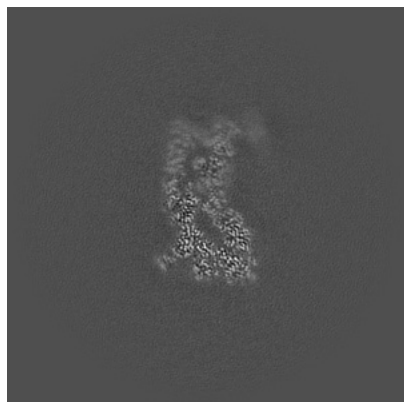


Z Index: 250

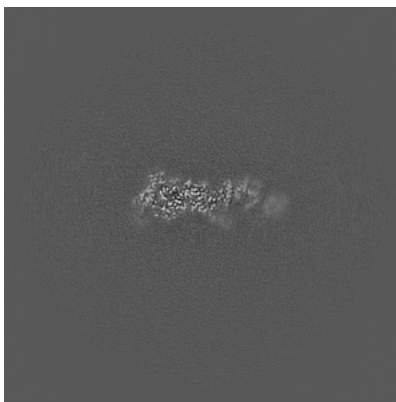
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

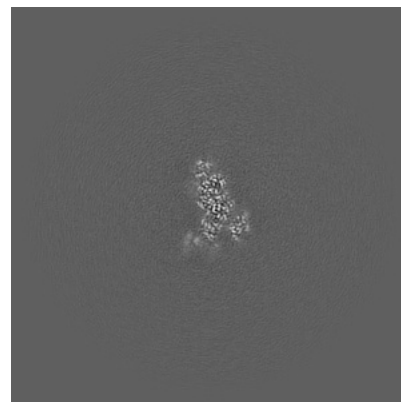
6.3.1 Primary map



X Index: 248

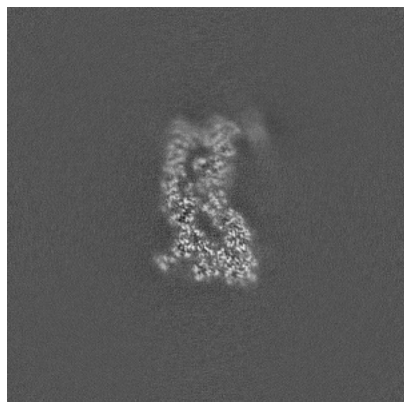


Y Index: 232



Z Index: 191

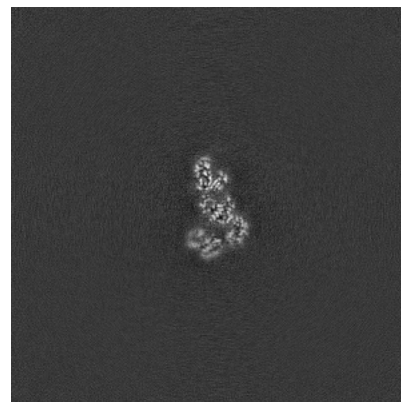
6.3.2 Raw map



X Index: 247



Y Index: 235

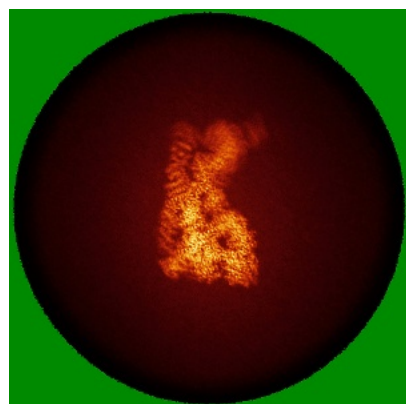


Z Index: 184

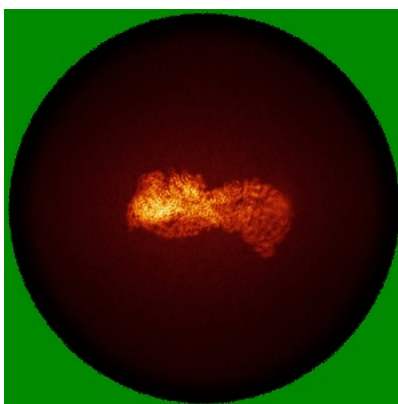
The images above show the largest variance slices of the map in three orthogonal directions.

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

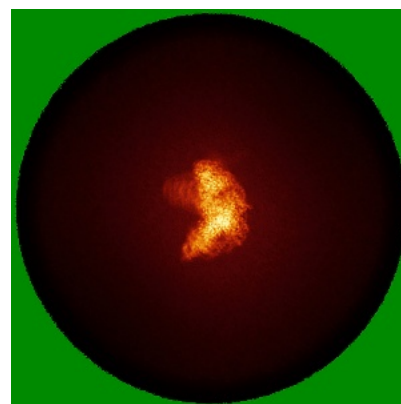
6.4.1 Primary map



X

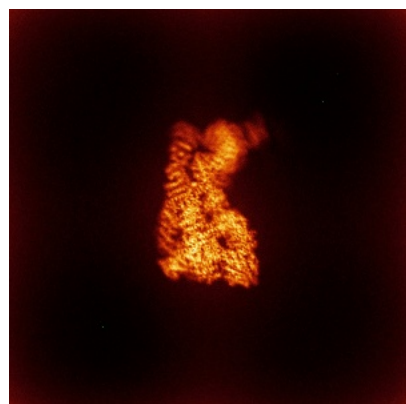


Y

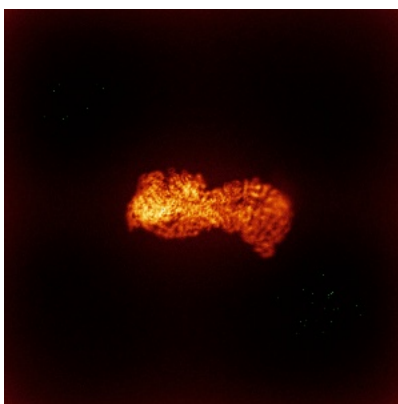


Z

6.4.2 Raw map



X



Y

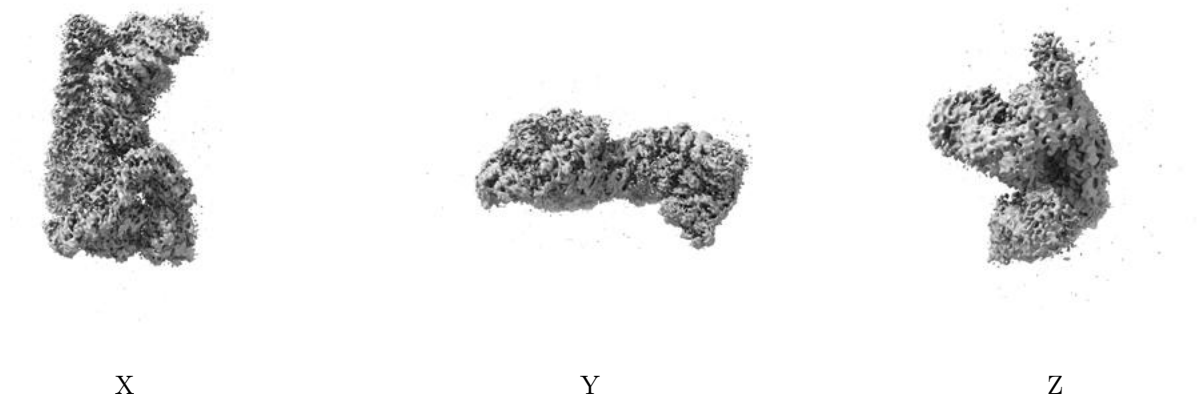


Z

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.

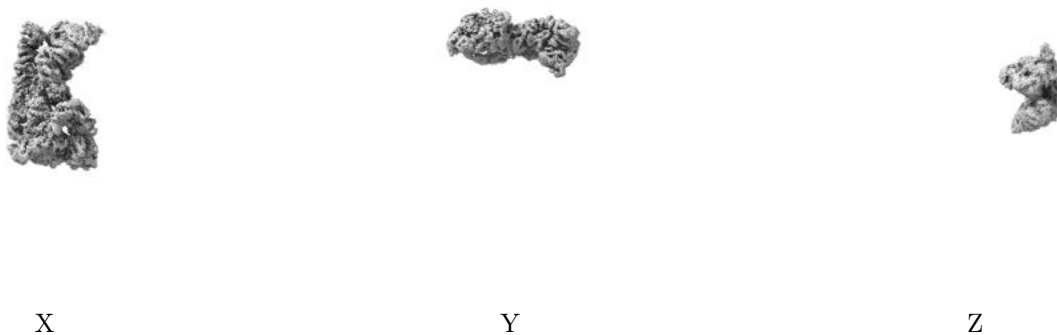
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

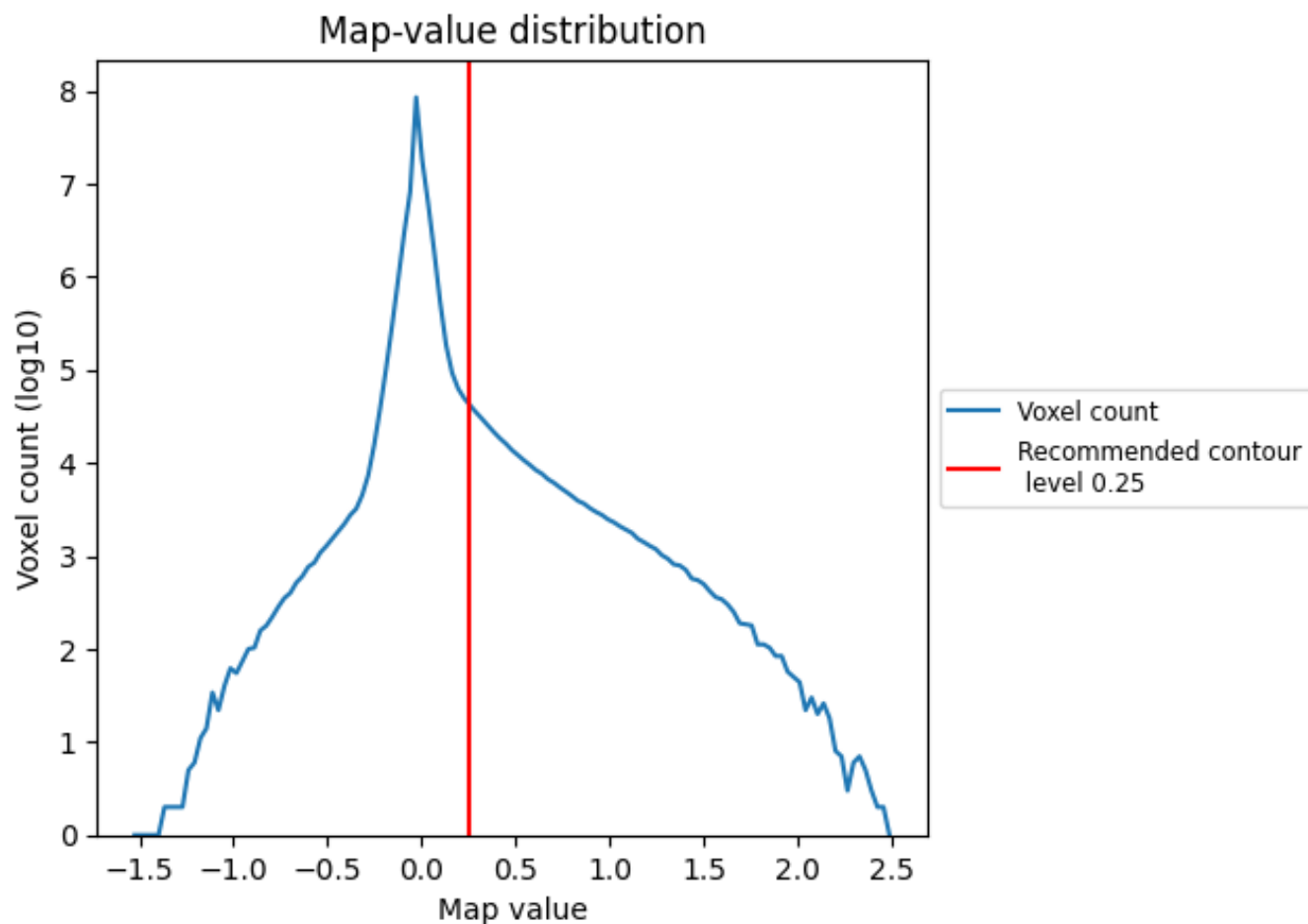
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

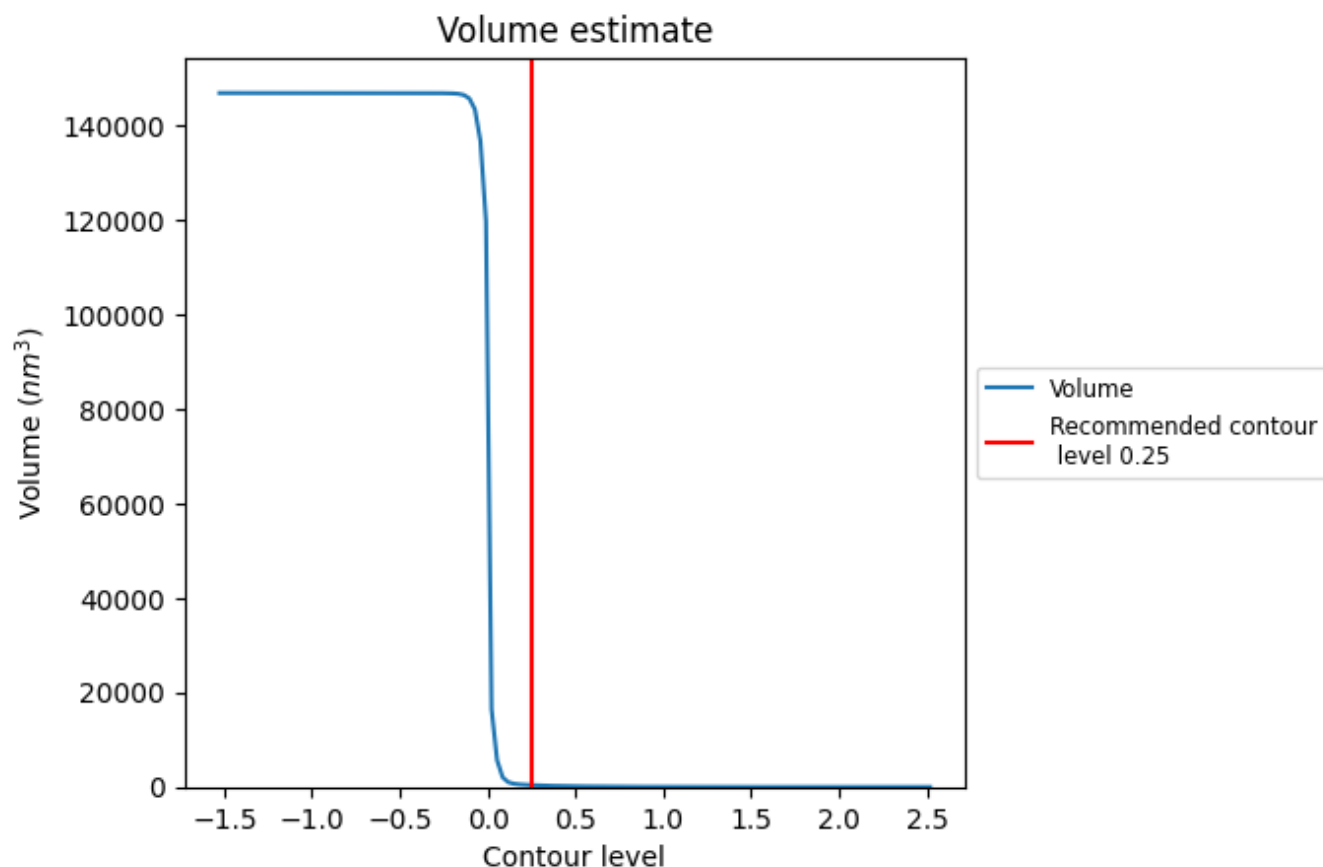
This section contains the results of statistical analysis of the map.

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.

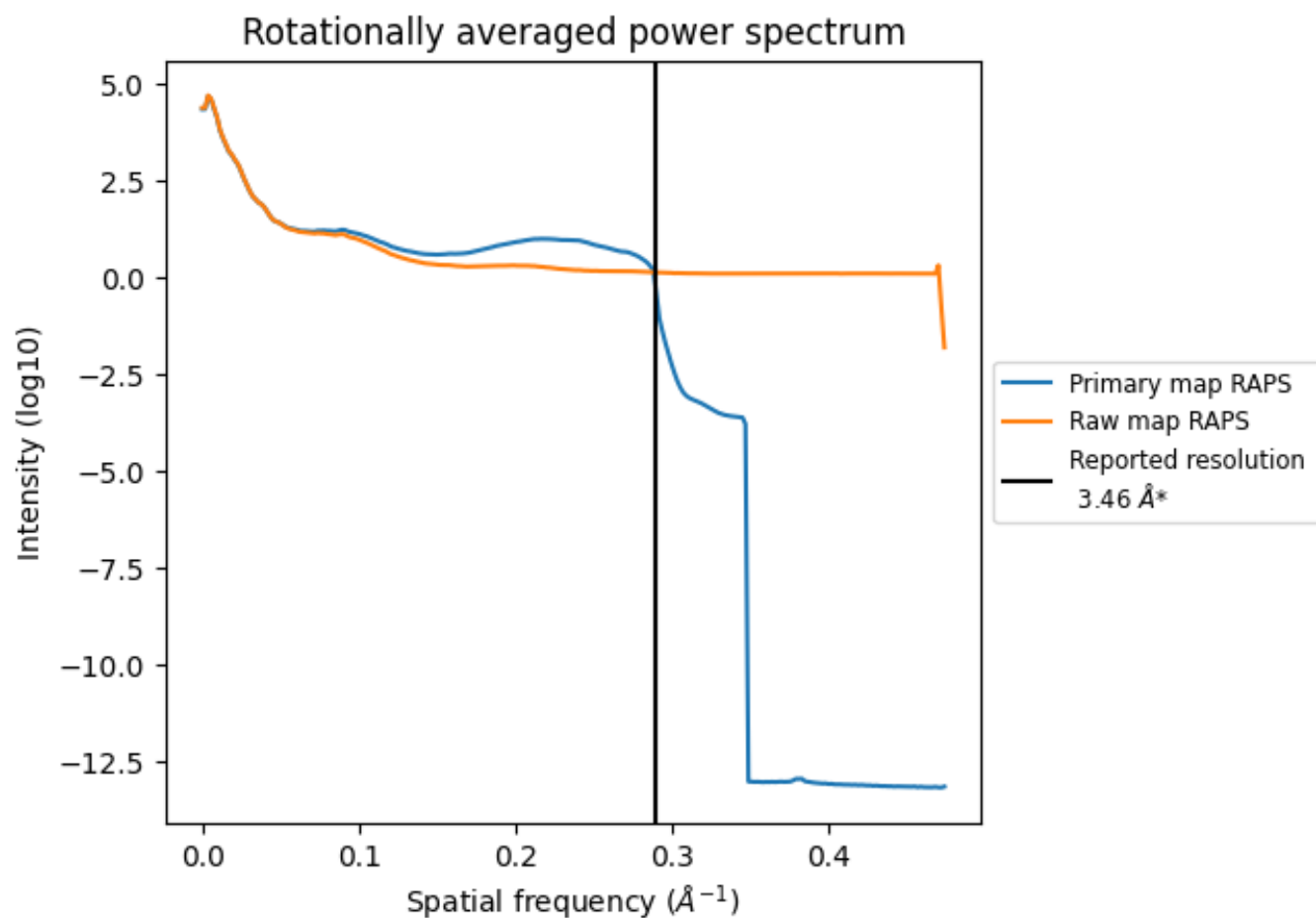
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm^3 ; this corresponds to an approximate mass of 349 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 ⓘ

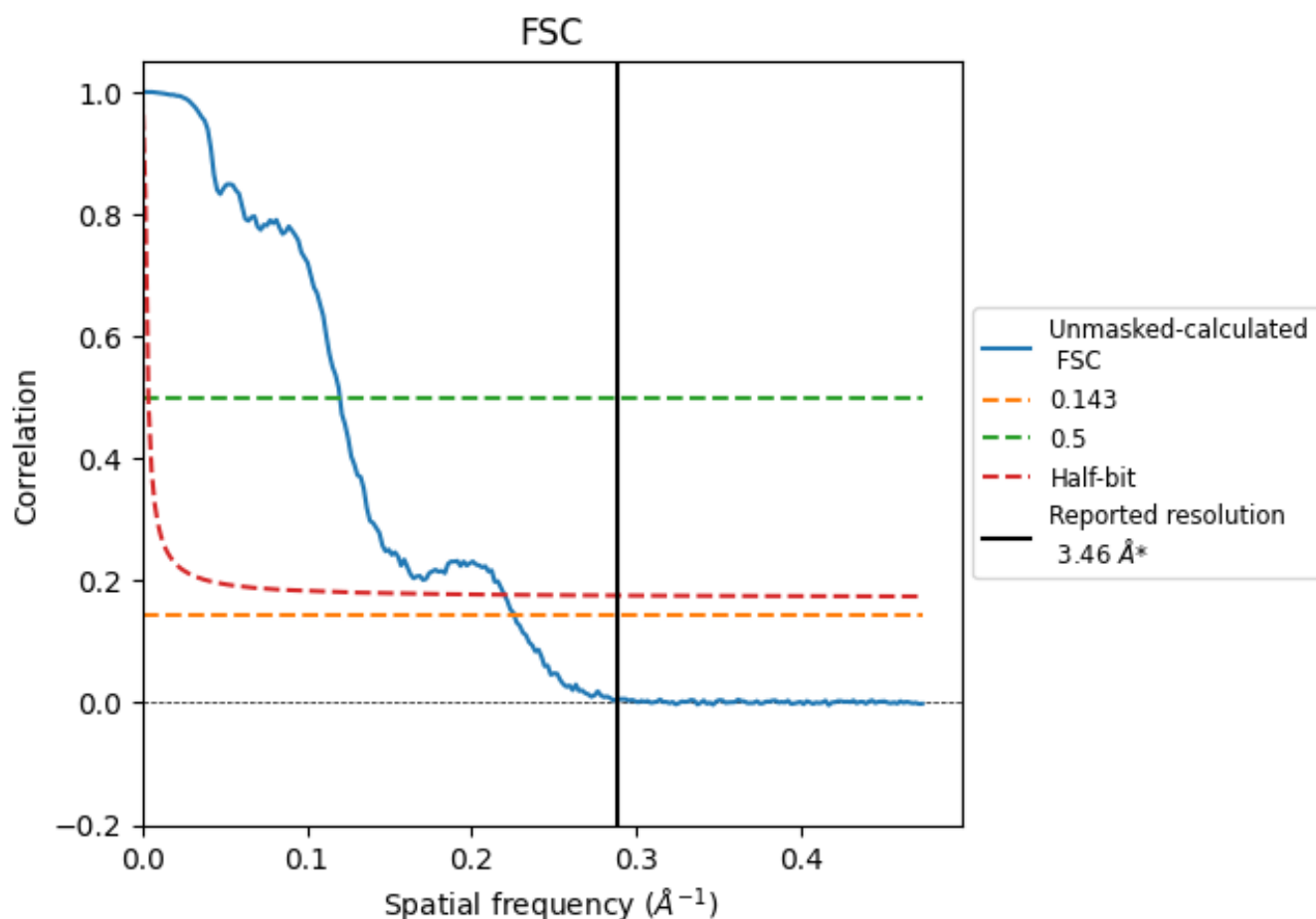


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

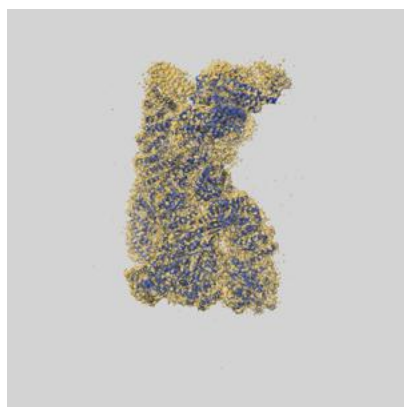
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	8.33	4.54

*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 4.42 differs from the reported value 3.46 by more than 10 %

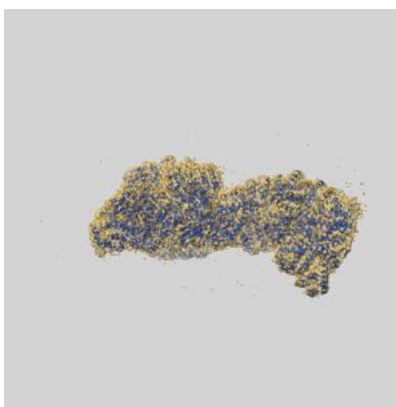
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61848 and PDB model 9JW1. Per-residue inclusion information can be found in section [3](#) on page [5](#).

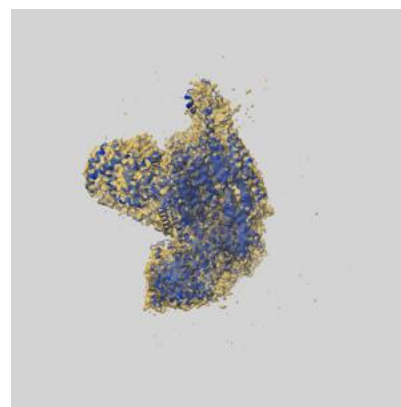
9.1 Map-model overlay [i](#)



X



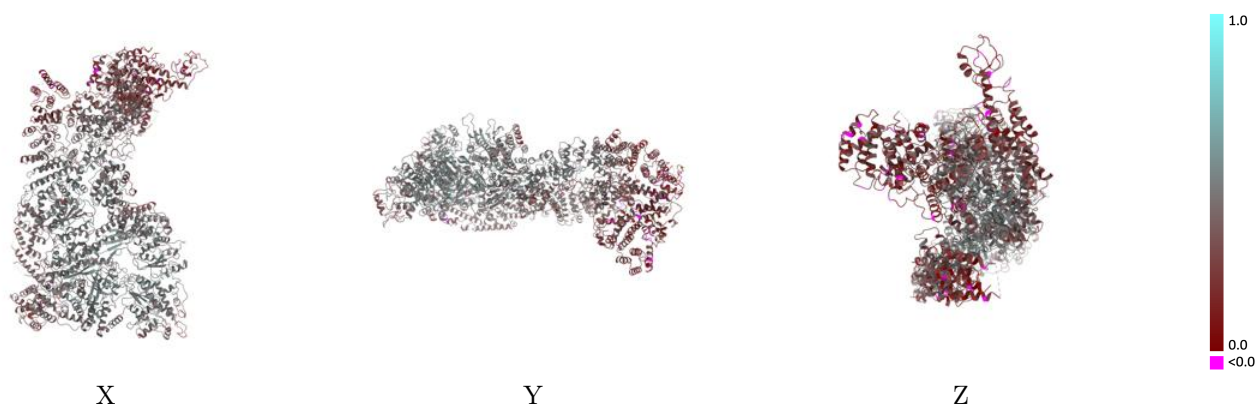
Y



Z

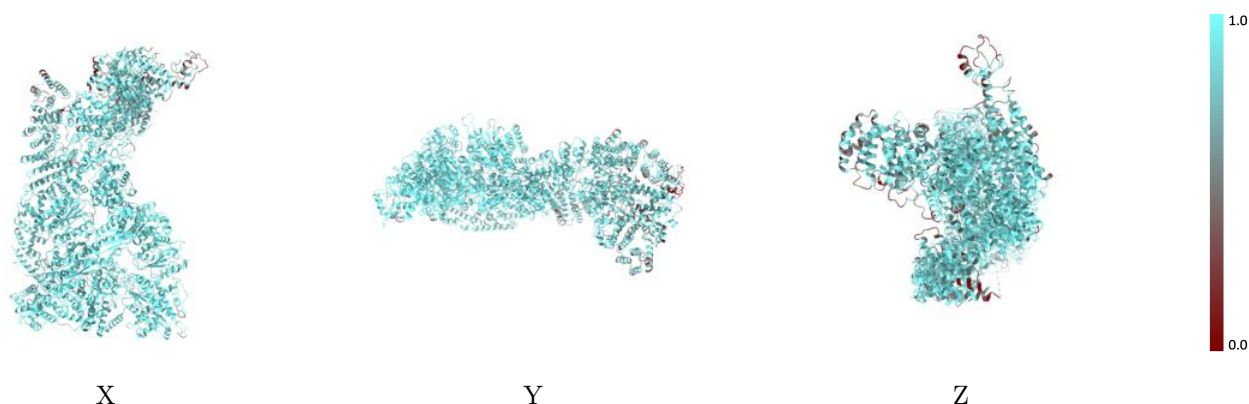
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



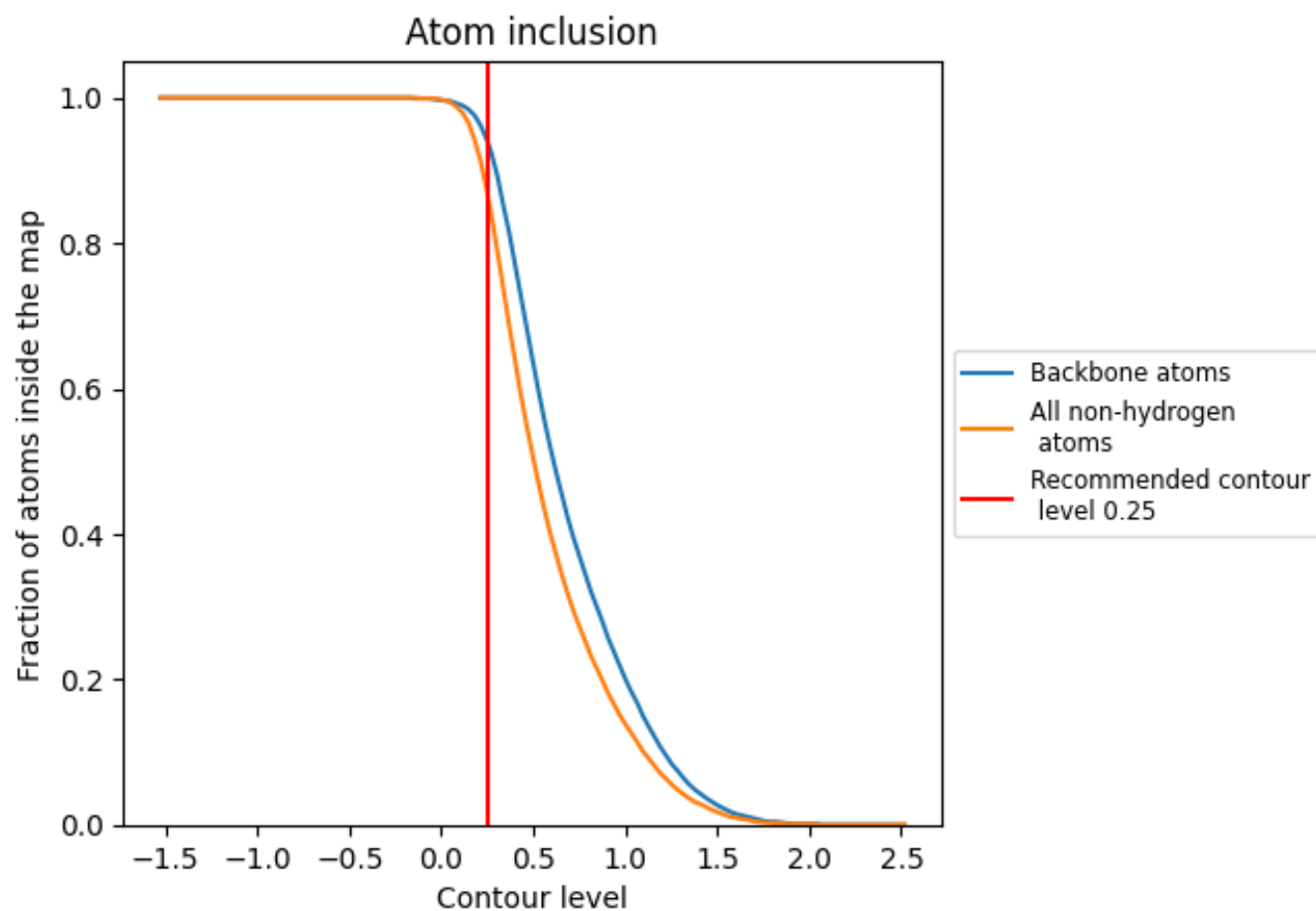
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 87% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8700	<div></div> 0.3980
A	<div></div> 0.8700	<div></div> 0.3980

