



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:27 PM UTC

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.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

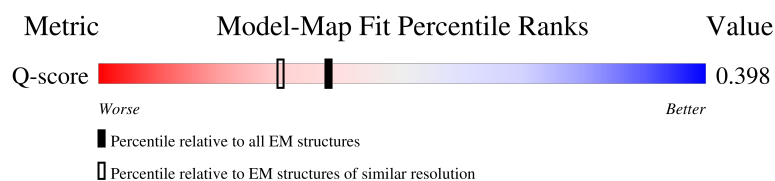
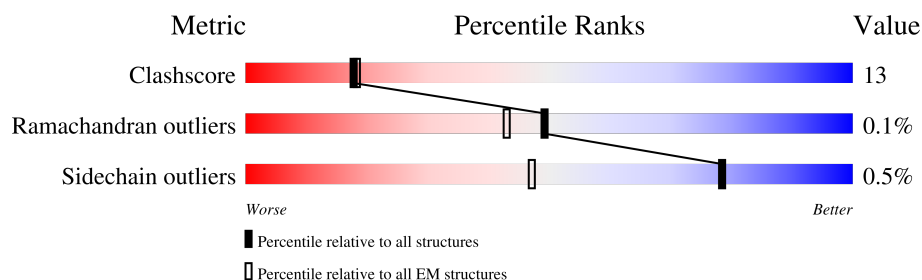
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13788 (2.96 - 3.96)

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.

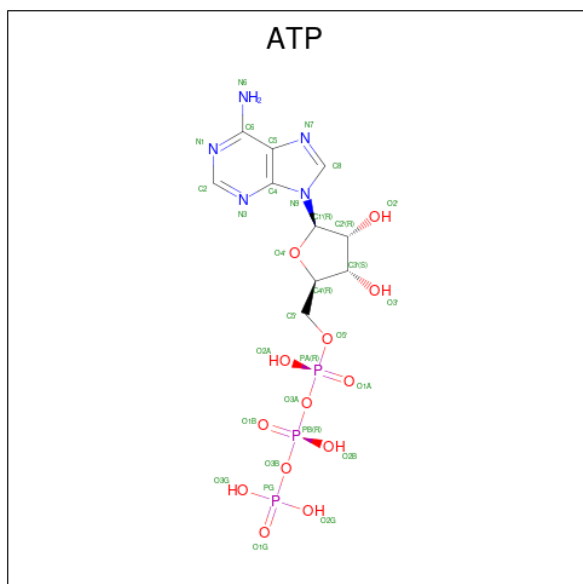
- Molecule 1 is a protein called Ring finger protein 213.

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	

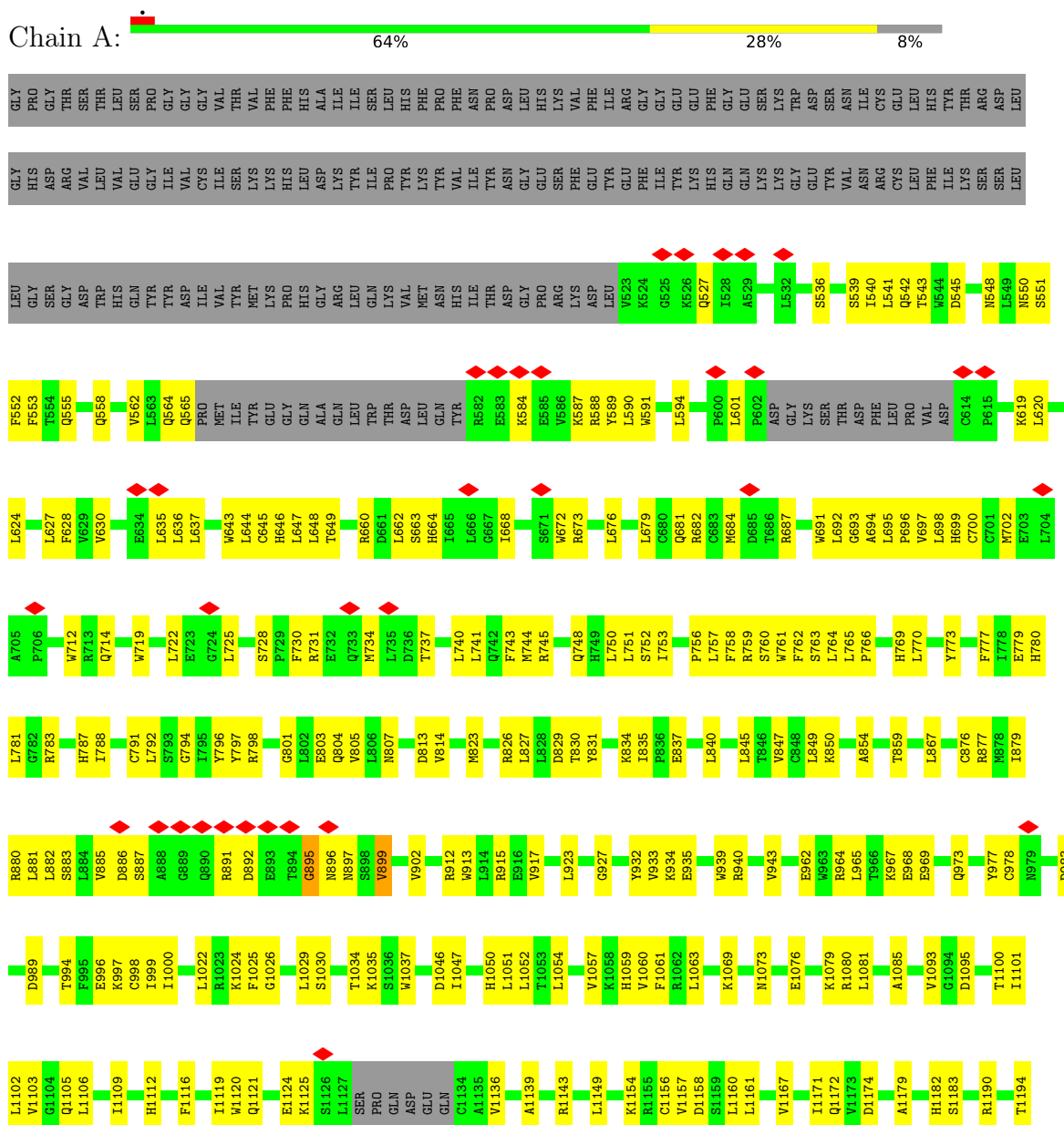
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

3 Residue-property plots

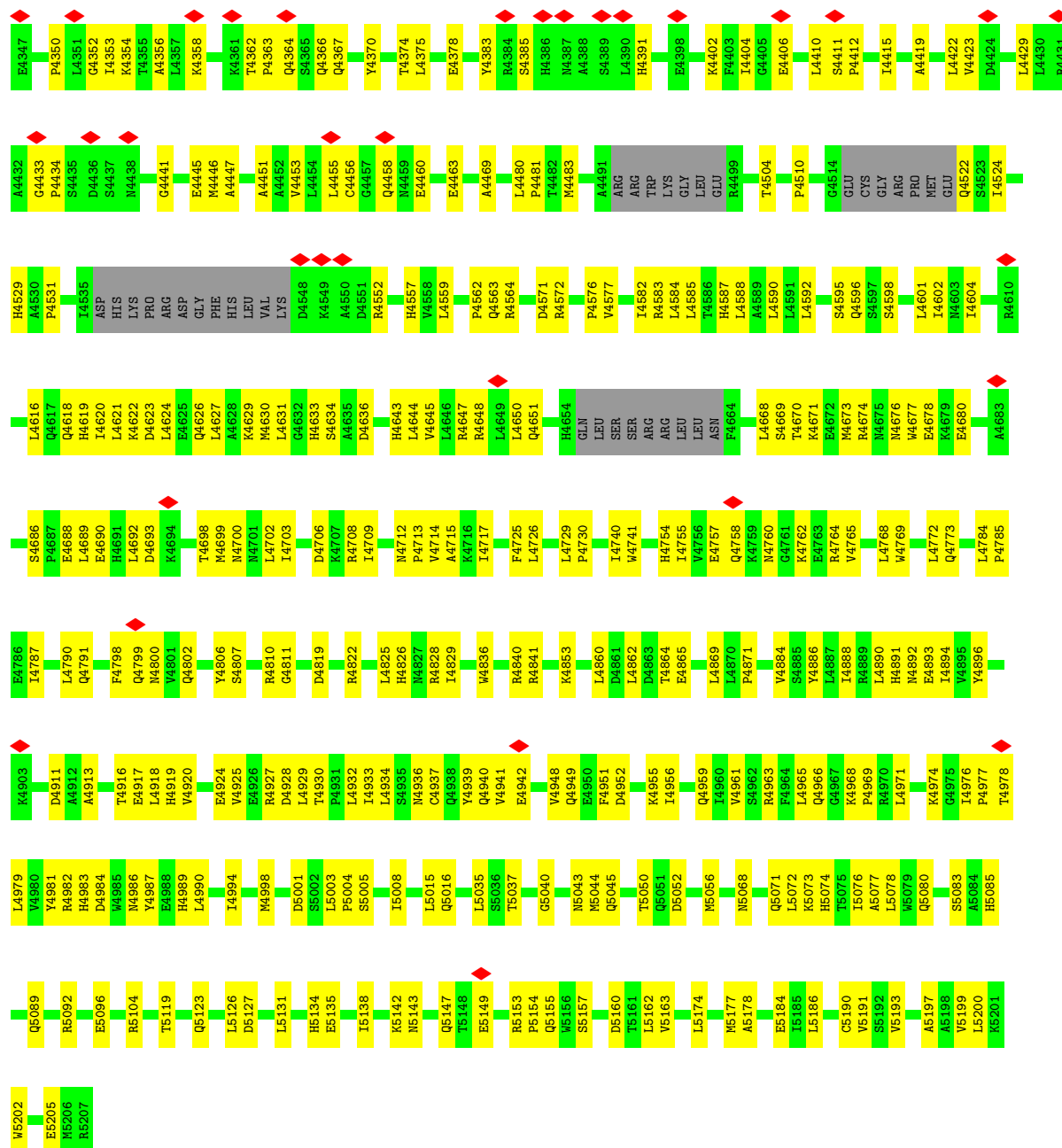
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ring finger protein 213



V2906	N2761	A2589	E2421	P2304	L2215	E2098	Q1826	V1860	F1388	R1286	S1200
E2907	M2765	E2590	R2437	V2305	R2216	I2099	V1827	T1661	R1389	L1269	THR
L2910	L2910	L2910	F2307	G1997	Q1828	K1998	Q1829	E1662	L1393	E1270	SER
L2911	L2760	L2593	L2448	F2308	L2222	S1999	L1832	L1676	I1401	E1272	SER
D2921	L2761	L2594	Y2461	N2309	Q2225	L2104	L1832	C1677	GLU	E1273	ASN
L2922	L2765	L2601	Y2464	T2314	E2230	SER	A1844	R1695	K1404	E1274	SER
L2923	L2772	L2615	R2465	M2315	F2234	VAL	M1849	R1850	K1405	Y1274	GLN
Q2925	G2772	L2615	R2465	L2322	F2234	SER	Q1850	Y1700	K1406	Y1276	R1207
Q2925	S2773	L2619	F2485	Q2323	C2235	ARG	T1851	L1701	L1407	D1276	A1208
Q2929	S2774	Q2623	N2490	P2324	Q2236	SER	Q1854	M1702	Q1408	Y1277	T1209
G2930	K2779	Q2623	N2490	N2325	P2237	SER	Q1854	Q1708	D1409	Y1278	H1210
Y2931	A2785	S2634	I2495	S2329	S2238	ALA	T1858	L1709	I1410	D1279	Y1211
F2932	M2786	V2641	I2498	H2335	F2239	ARG	D1860	Y1710	S1411	Q1281	Q1216
F2935	Q2787	V2641	I2498	L2244	F2243	THR	Y1859	Q1719	R1414	P1281	V1217
Y2939	G2788	C2644	V2501	R2245	T2243	ARG	D1860	P1720	G1415	S1282	Q1218
D2947	F2789	V2647	I2520	K2342	R2245	VAL	T1870	D1723	K1416	Y1287	E1219
F2951	A2790	V2647	I2520	T2346	K2248	PRO	E1873	D1723	Q1419	K1284	K1223
F2951	D2794	R2649	C2524	M2346	R2249	Q2120	R1879	K1733	S1422	A1301	I1224
D2955	L2795	V2650	P2526	L2354	F2250	P2134	R1880	R1743	R1423	E1302	D1225
S2958	F2796	V2650	Y2527	R2368	V2251	F2135	C1881	R1743	R1424	E1302	R1228
K2800	R2797	H2654	Y2528	V2359	M2255	K2136	L1882	A1753	L1435	D1304	I1303
M2962	K2800	M2657	M2534	F2361	F2257	S2144	L1884	R1754	L1438	D1309	S1230
V2963	S2813	M2657	M2534	F2361	M2258	Q2144	L1884	R1754	I1438	D1309	H1231
K2968	F2822	Q2661	V2547	F2365	L2267	Q2165	L1887	M1757	A1452	K1313	I1232
P2976	V2846	L2662	S2548	K2373	H2268	R2166	G1888	R1758	D1458	F1236	F1233
I2979	A2849	L2685	H2549	C2378	T2269	P2167	H1889	R1759	M1610	Y1237	F1236
L2984	M2855	M2686	E2550	L2381	SER	Q2169	K1890	P1790	S1610	M1324	Y1238
F2987	P2856	C2692	E2550	G2382	ASP	Y2170	V1891	L1764	D1467	H1329	E1239
D2992	L2857	Y2693	E2550	L2383	GLN	L2171	L1895	M1767	Y1472	Q1390	E1242
I2993	K2858	H2694	E2550	L2383	PRO	R2172	Q1919	L1778	F1477	Q1332	S1245
L3000	L2862	R2704	V2565	Q2384	GLY	F2174	H1920	L1778	F1477	R1332	GLU
A3001	L2863	L2721	Y2566	Q2385	LYS	N2175	E1921	I1781	D1625	D1334	PRO
P3004	L2863	L2721	Y2566	Q2385	HIS	Q2176	D1923	M1782	L1626	W1336	LYS
A3006	E2865	L2731	Y2566	Q2385	VAL	Q2177	Y1924	L1789	M1631	K1337	GLU
K3007	L2869	L2732	V2567	Q2385	THR	N2177	Y1924	P1790	M1632	D1338	ASP
S3013	V2882	F2737	V2567	Q2385	ASP	D2179	Y1924	L1799	L1633	R1339	GLN
F3014	S2885	L2738	V2567	Q2385	GLY	L2180	Y1924	L1799	M1637	Q1342	ALA
N3015	L2889	L2738	V2567	Q2385	VAL	D2181	Y1924	L1799	M1637	Q1342	ALA
K3019	N2895	L2742	V2567	Q2385	ARG	F2183	Y1924	L1799	M1637	Q1342	ALA
	R2896	G2583	V2567	Q2385	E2286	F2183	Y1924	L1799	M1637	Q1342	ALA
	P2905	Q2584	V2567	Q2385	L2294	F2201	Y1924	L1799	M1637	Q1342	ALA
		L2585	V2567	Q2385	W2298	C2205	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	E2299	G2206	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	L2414	V2207	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	T2418	L2094	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	E2301	Y2095	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	P2302	T2096	Y1924	L1799	M1637	Q1342	ALA
			V2567	Q2385	H2303	S2211	Y1924	L1799	M1637	Q1342	ALA





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 ($\text{\AA}$)	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 ($\text{\AA}$)	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%)	81 81

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	32,33,33	1.45	5 (15%)	48,52,52	1.85	12 (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	-	3/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5301	ATP	C5-C4	3.61	1.45	1.39
2	A	5301	ATP	C5-N7	-2.83	1.33	1.39
2	A	5301	ATP	C4-N9	-2.75	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5301	ATP	PB-O3B	-2.42	1.56	1.59
2	A	5301	ATP	C8-N9	-2.03	1.34	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5301	ATP	C5-C4-N3	-5.33	119.38	126.72
2	A	5301	ATP	N3-C4-N9	4.82	135.37	127.17
2	A	5301	ATP	C4-N9-C8	3.74	109.67	105.74
2	A	5301	ATP	C2-N3-C4	3.46	120.28	111.83
2	A	5301	ATP	N3-C2-N1	-3.08	123.92	128.58

There are no chirality outliers.

All (3) torsion outliers are listed below:

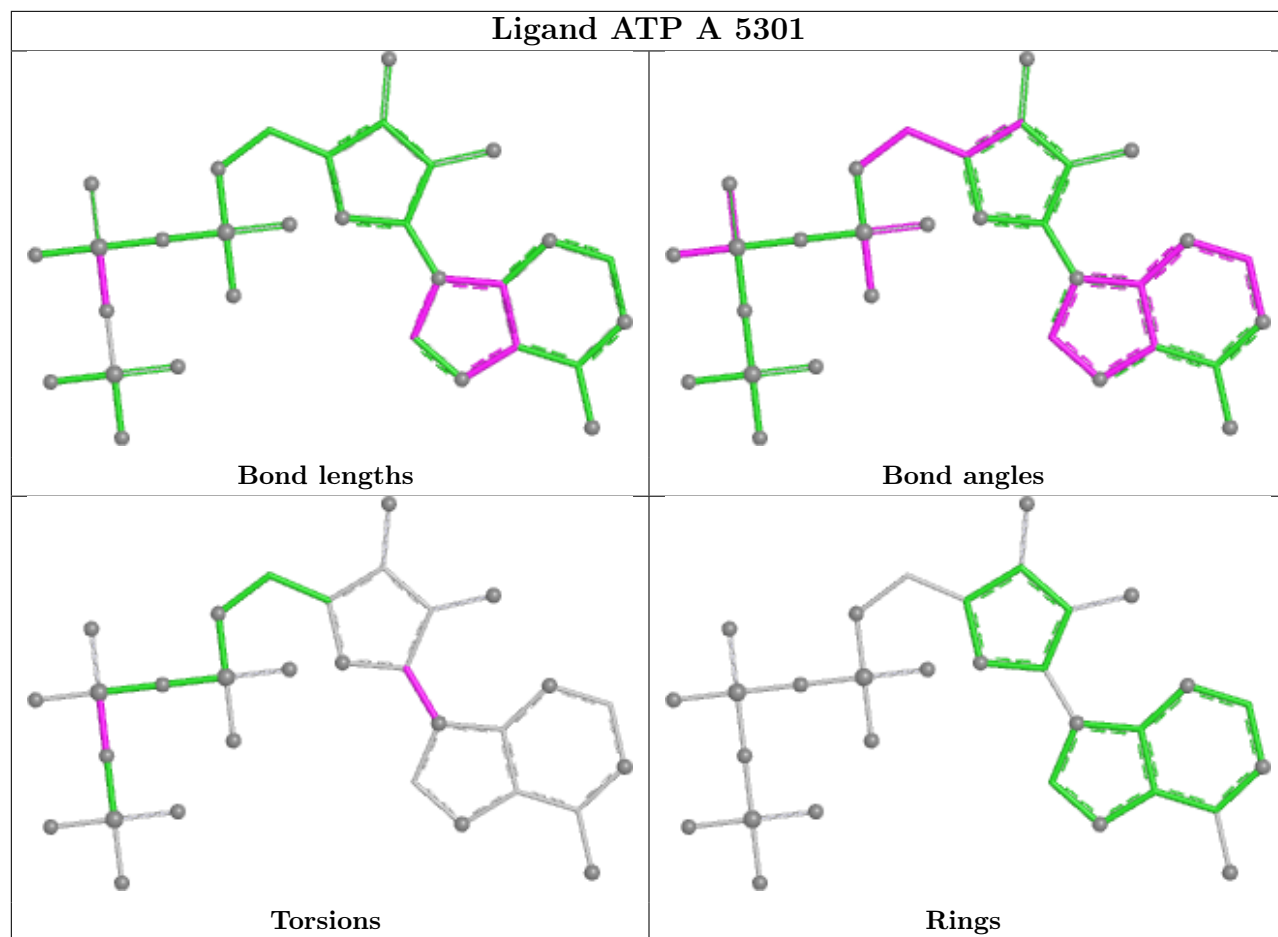
Mol	Chain	Res	Type	Atoms
2	A	5301	ATP	O4'-C1'-N9-C4
2	A	5301	ATP	O4'-C1'-N9-C8
2	A	5301	ATP	PG-O3B-PB-O2B

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.

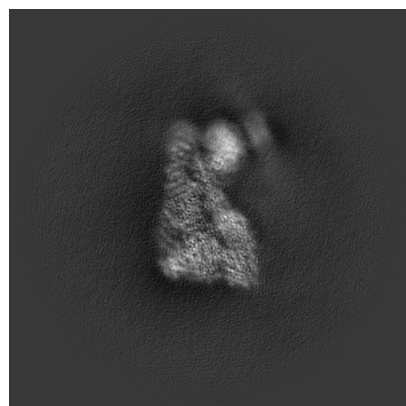
6 Map visualisation [i](#)

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.

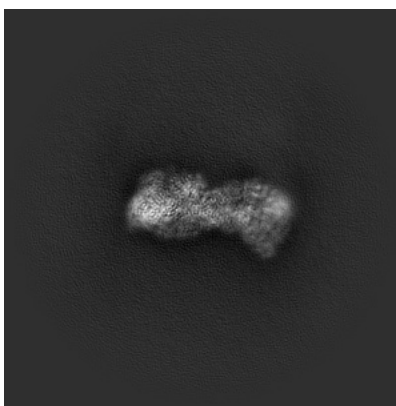
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

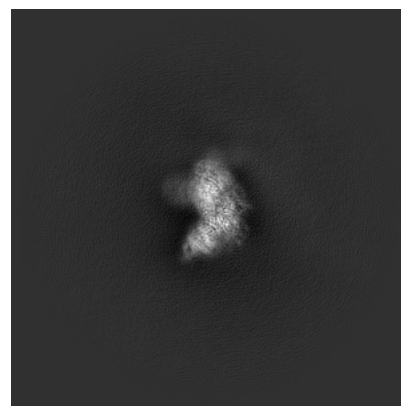
6.1.1 Primary map



X

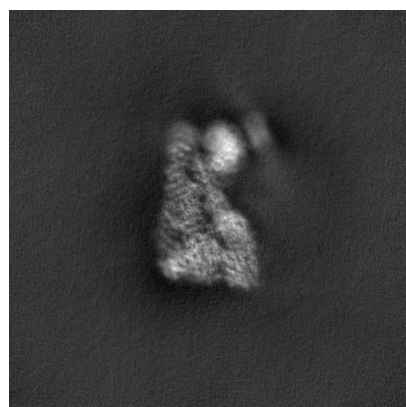


Y

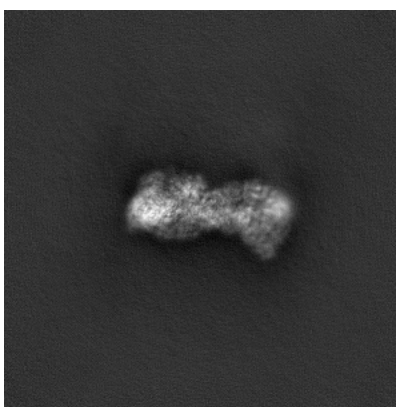


Z

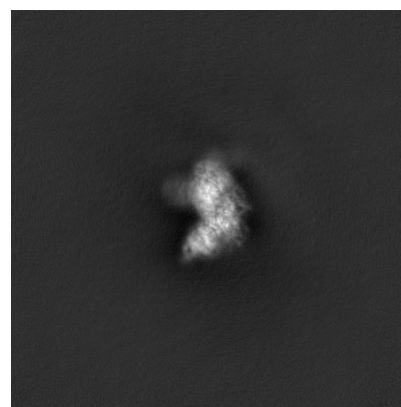
6.1.2 Raw map



X



Y

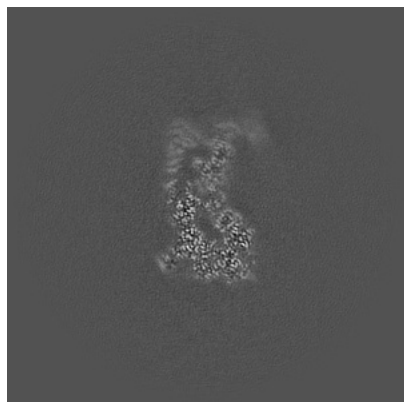


Z

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

6.2 Central slices [i](#)

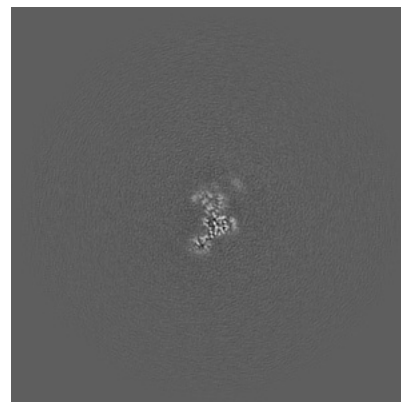
6.2.1 Primary map



X Index: 250

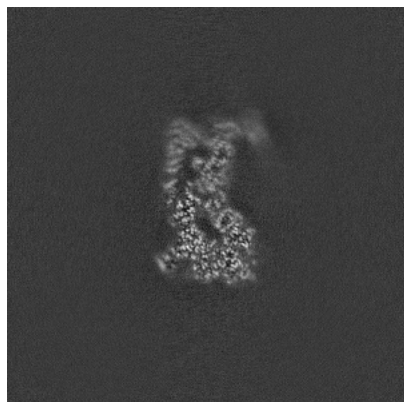


Y Index: 250



Z Index: 250

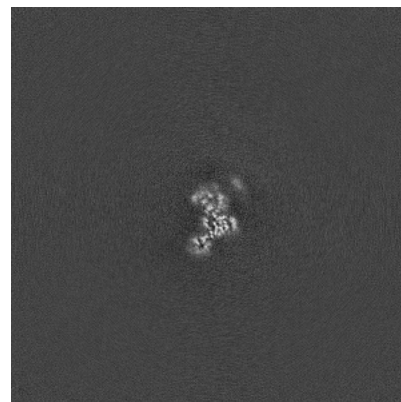
6.2.2 Raw map



X Index: 250



Y Index: 250

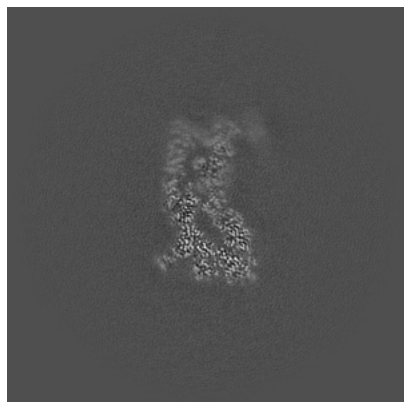


Z Index: 250

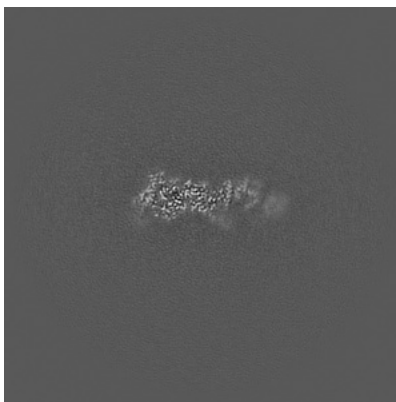
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

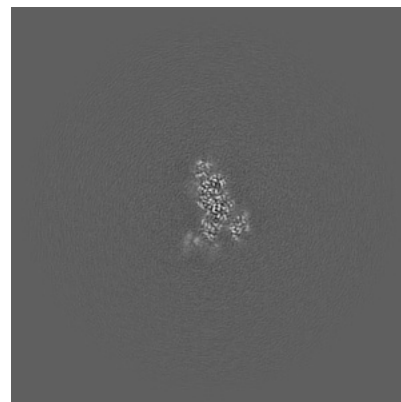
6.3.1 Primary map



X Index: 248

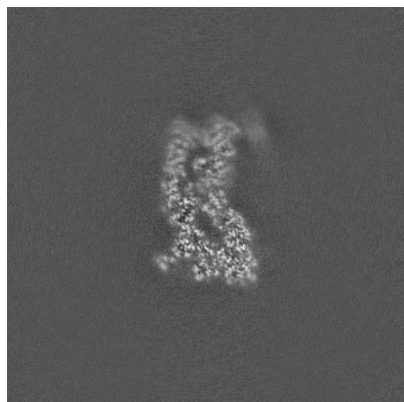


Y Index: 232



Z Index: 191

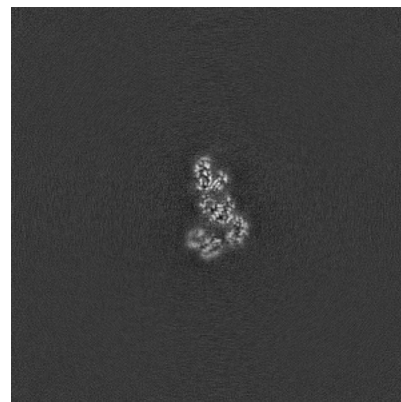
6.3.2 Raw map



X Index: 247



Y Index: 235

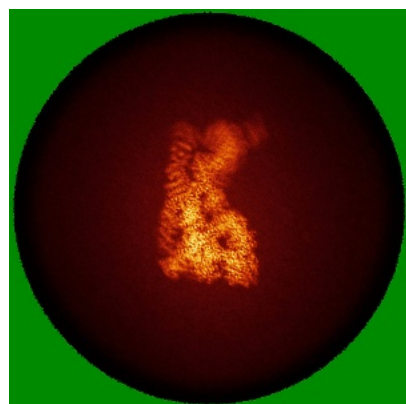


Z Index: 184

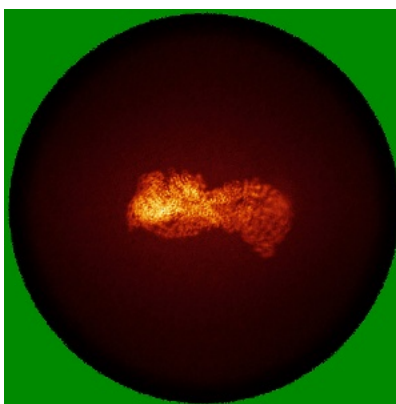
The images above show the largest variance slices of the map in three orthogonal directions.

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

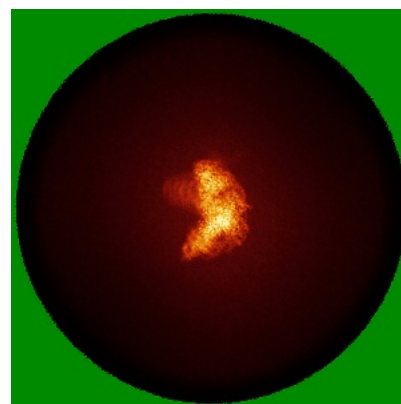
6.4.1 Primary map



X

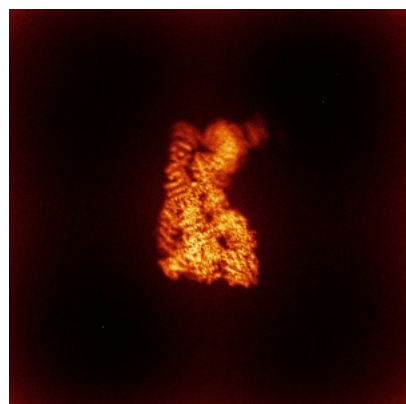


Y

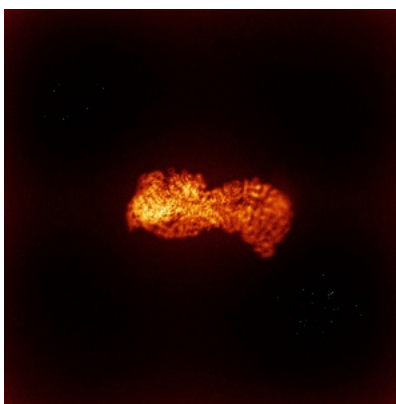


Z

6.4.2 Raw map



X



Y

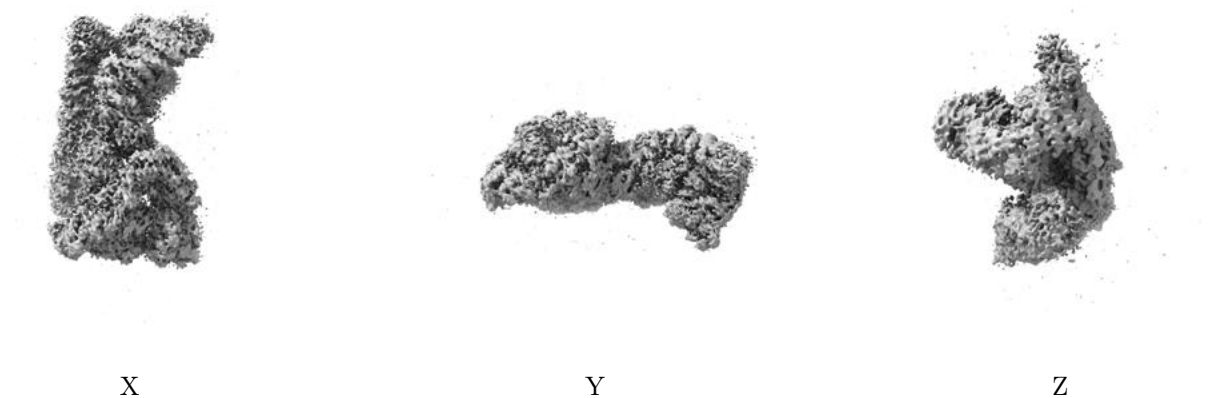


Z

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.

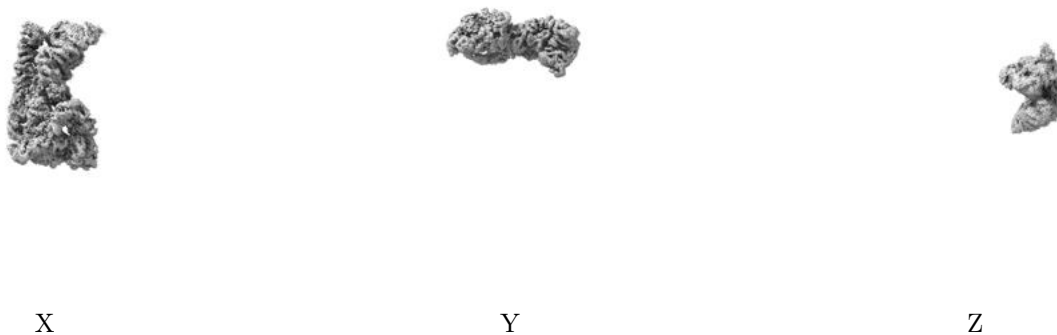
6.5 Orthogonal surface views [i](#)

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.

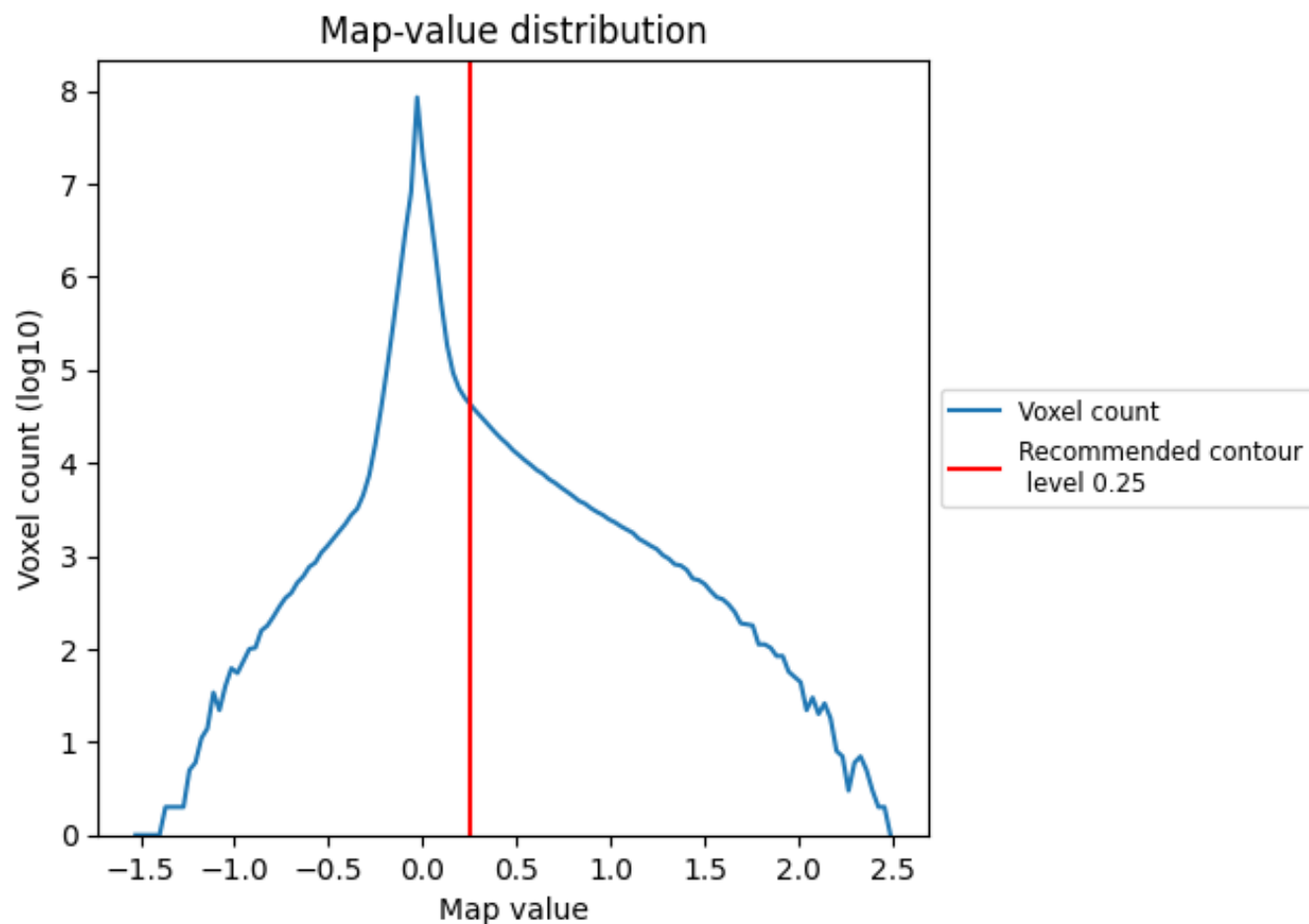
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

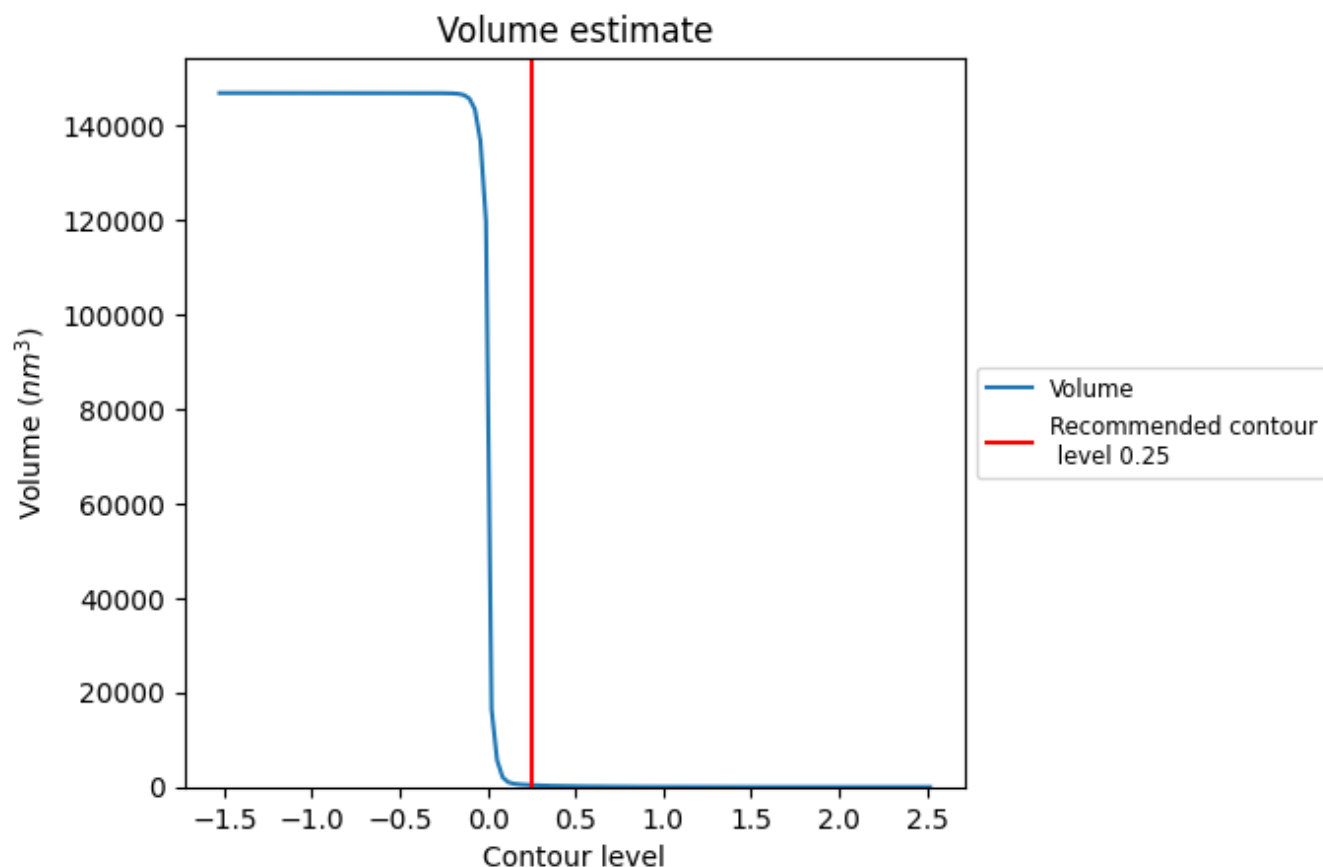
This section contains the results of statistical analysis of the map.

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.

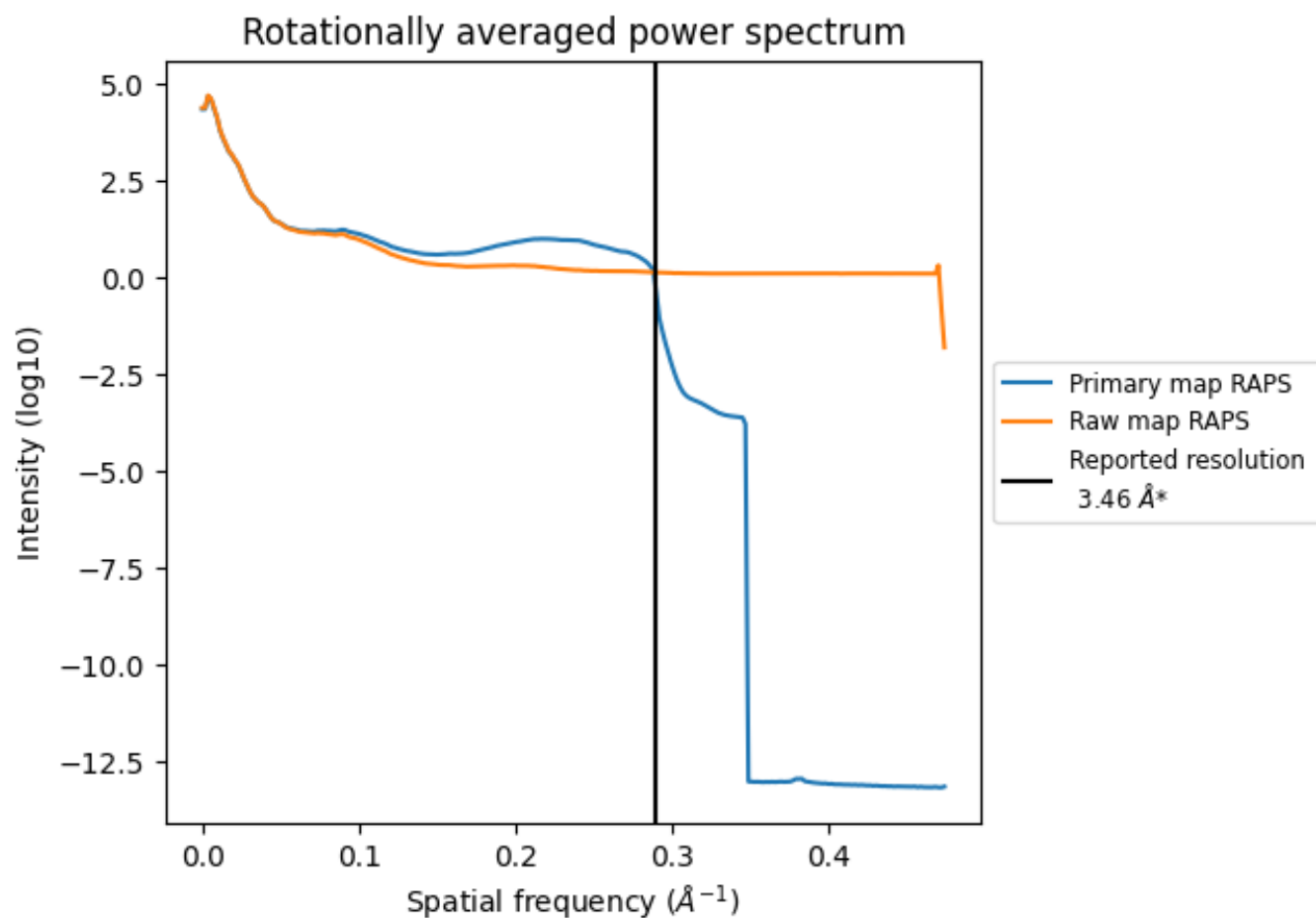
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm³; 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 ⓘ

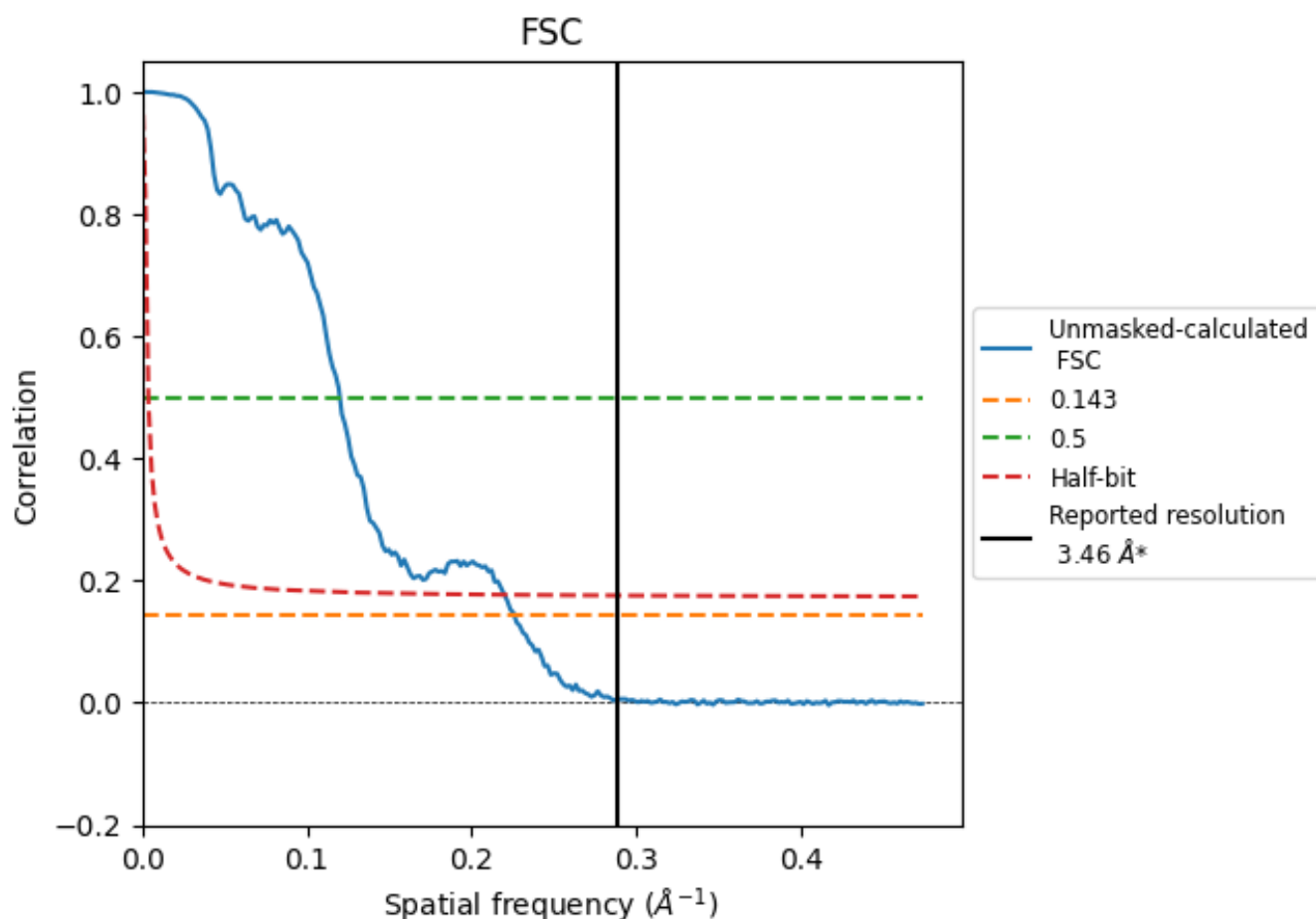


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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](#)

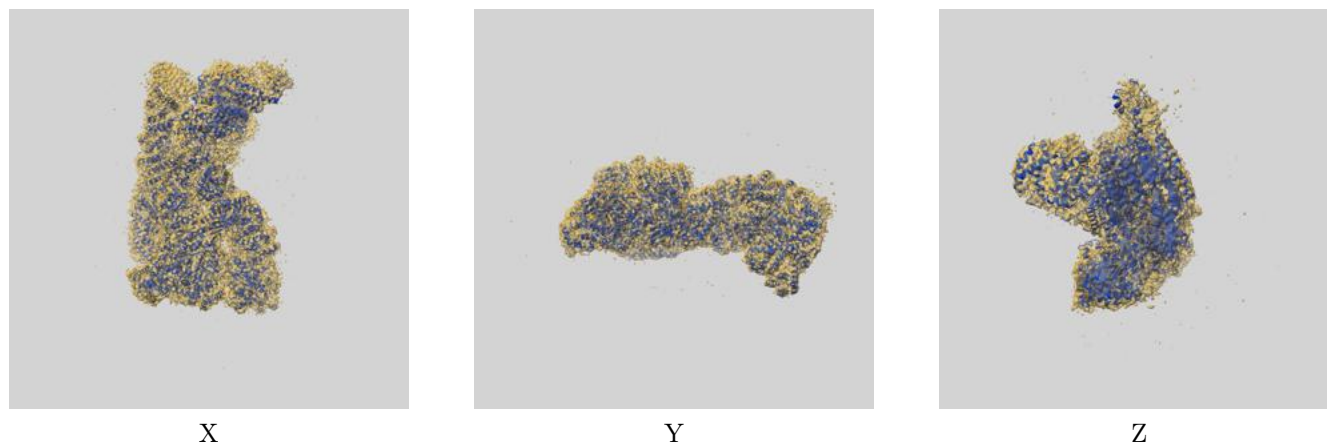
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	8.33	4.54

*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](#)

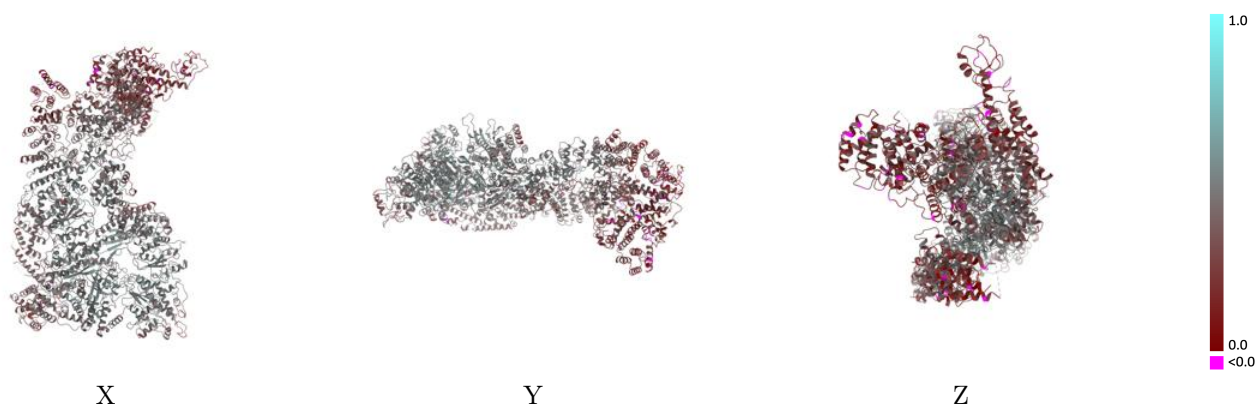
This section contains information regarding the fit between EMDB map EMD-61848 and PDB model 9JW1. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



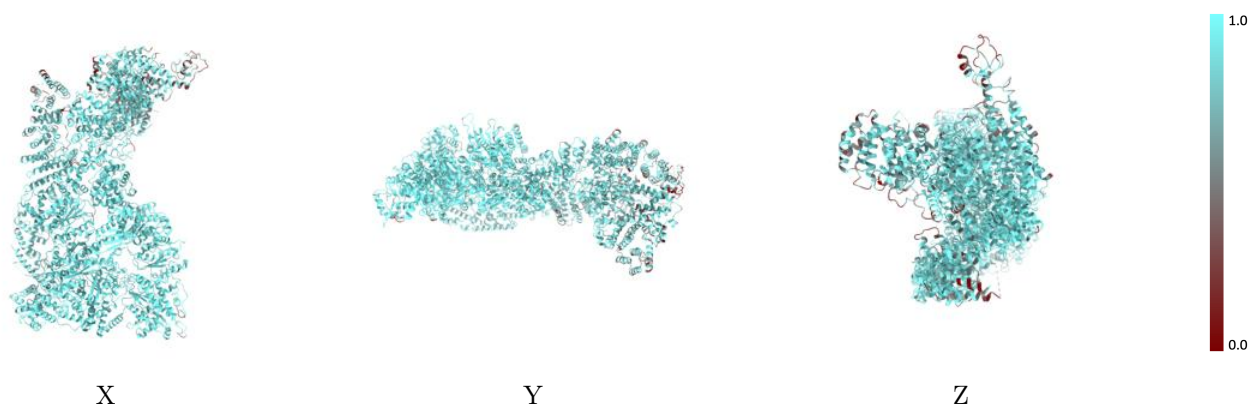
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



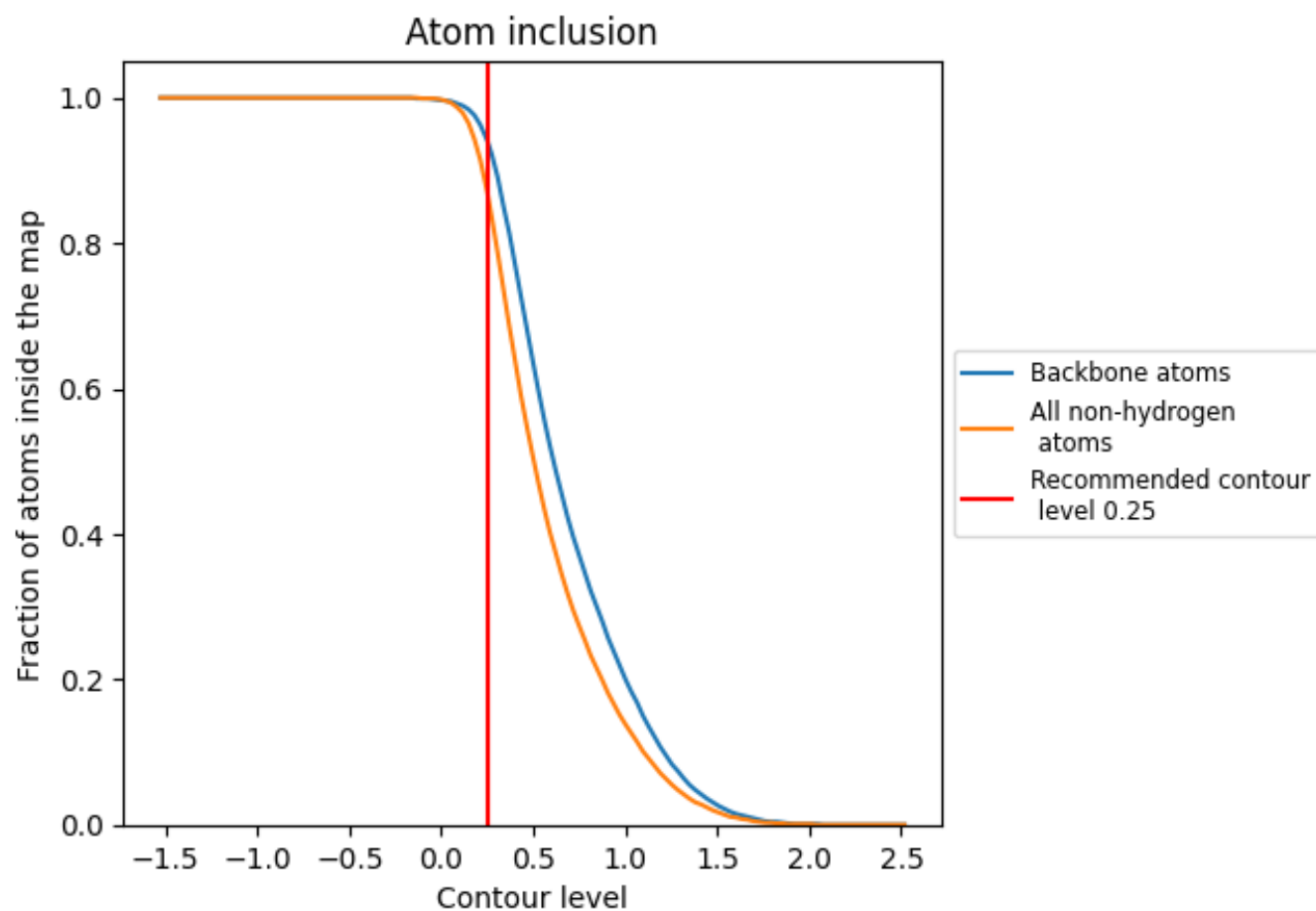
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.8700	0.3980
A	0.8700	0.3980

