



wwPDB EM Validation Summary Report ⓘ

Jul 26, 2026 – 04:11 AM JST

PDB ID : 9XE9 / pdb_00009xe9
EMDB ID : EMD-66785
Title : Crimean-Congo hemorrhagic fever virus RNA polymerase containing a 15-bp RNA product
Authors : Xue, L.; Gui, J.; Pan, H.; Chang, T.; Xiong, X.
Deposited on : 2025-10-27
Resolution : 2.81 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.50

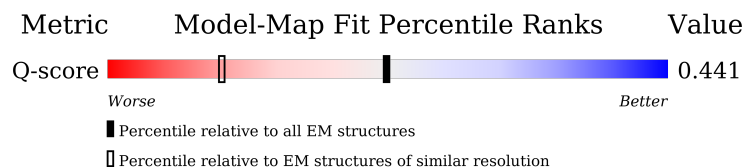
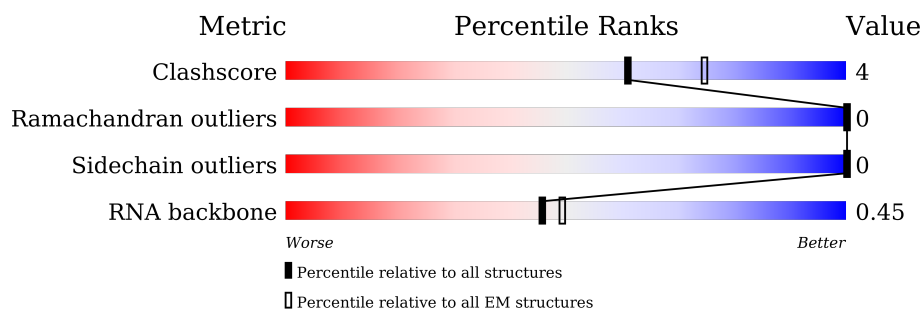
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.81 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.



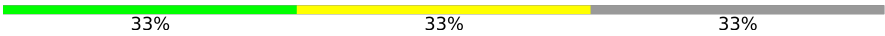
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11740 (2.31 - 3.31)

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	3945	
2	B	19	
3	C	19	

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Mol	Chain	Length	Quality of chain
3	E	19	 26% 16% 58%
4	D	15	 33% 33% 33%
5	F	3	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 25605 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3074	Total	C	N	O	S	0	0
			24614	15636	4199	4621	158		

- Molecule 2 is a RNA chain called RNA (5'-R(*UP*UP*CP*CP*AP*AP*AP*AP*AP*AP*UP*CP*GP*UP*UP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	11	Total	C	N	O	P	0	0
			231	106	45	70	10		

- Molecule 3 is a RNA chain called RNA (5'-R(P*GP*GP*GP*AP*UP*UP*GP*GP*UP*GP*UP*CP*UP*UP*UP*GP*AP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	13	Total	C	N	O	P	0	0
			280	124	48	95	13		
3	E	8	Total	C	N	O	P	0	0
			170	76	29	57	8		

- Molecule 4 is a RNA chain called RNA (5'-R(*UP*CP*UP*CP*AP*AP*AP*GP*AP*CP*AP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	10	Total	C	N	O	P	0	0
			215	97	44	64	10		

- Molecule 5 is a RNA chain called RNA (5'-R(P*UP*CP*U)-3').

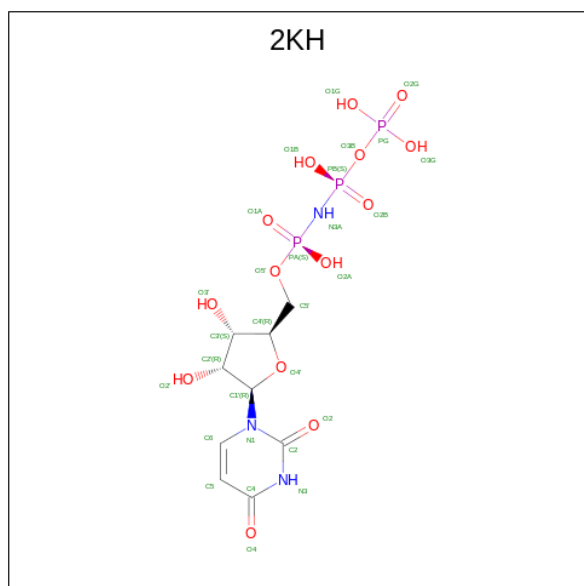
Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	3	Total	C	N	O	P	0	0
			61	27	7	24	3		

- Molecule 6 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of

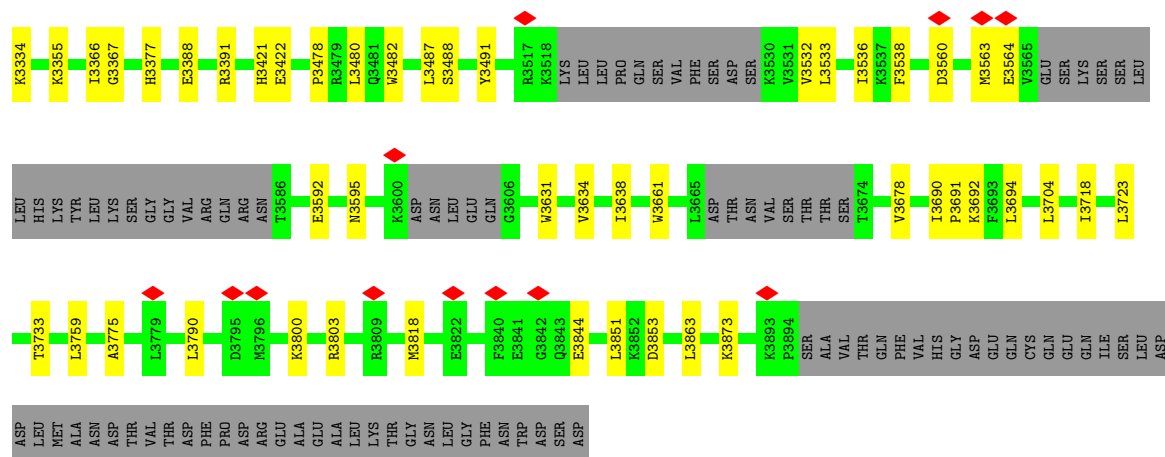
Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	A	4	Total	Mn	0
			4	4	

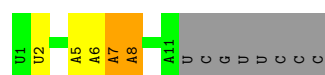
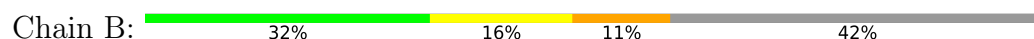
- Molecule 7 is 5'-O-[(S)-hydroxy{[(S)-hydroxy(phosphonooxy)phosphoryl]amino}phosphoryl]uridine (CCD ID: 2KH) (formula: C₉H₁₆N₃O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



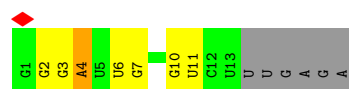
L2944	R3104	L2437	M2206	SER	F2076	K1973	K1911	Q1768	ASP	V1689	V1321
P2947	P3105	T2438	L2207	S2137	A2077	K1974	N1912	I1769	ARG	P1592	E1335
I2961	L3112	L2441	A2208	S2138	A2078	L1975	E1915	P1774	ARG	I1611	I1342
V2962	L3121	S2443	R2209	L2139	L2079	L1976	V1916	H1776	TYR	H1615	I1303
L2966	K3122	G2446	R2211	L2141	S2080	L1977	L1917	L1783	SER	M1621	I1368
F3128	K3123	M2471	F2212	L2149	A2081	ASN	L1918	I1784	SER	L1632	K1373
D3134	P3129	A2487	R2213	T2150	P2082	GLN	T1919	I1787	LYS	R1638	L1374
K3137	L3149	Y2498	L2216	S2154	W2083	GLN	E1920	K1808	ILE	M1647	K1378
L3152	L3152	V2508	R2217	N2155	C2084	ASP	D1921	K1846	ARG	N1648	L1383
P3166	F3195	H2509	L2219	G2156	L2085	GLN	G1922	M1850	PHE	S1649	L1386
L3202	K3202	V2524	L2227	E2157	H2086	GLU	H1923	G1853	GLY	C1651	Q1395
K3218	R3221	V2525	L2232	P2158	Y2087	LEU	L1924	LEU	TYR	SER	P1397
L3246	L3249	L2529	R2232	F2159	K1987	K1988	I1925	L1876	ASN	D1657	I1414
G3250	C3251	L2533	V2269	S2160	D1989	D1989	F1926	L1871	LYS	T1660	T1417
K3259	L3262	S2515	K2273	L2161	L1990	L1991	W1928	L1663	GLN	L1663	Q1424
L3263	L3276	V2552	L2282	L2163	I1992	I1993	K1930	G1868	ARG	R1671	I1458
T3277	C3280	T2552	M2298	N2164	S1994	W1995	T1931	K1869	GLY	LYS	V1502
L3289	E3286	L2599	K2305	ASP	W1996	I1996	I1932	R1870	ASN	GLU	L1506
S3304	K3310	Q2618	G2311	THR	I1999	K2003	S1935	L1876	ASP	LEU	R1526
L3318	L3318	M2621	T2360	THR	K2004	D2004	V1936	D1884	PRO	GLY	F1527
		Y2622	K2361	THR	F2005	A2006	K1937	K1887	PHE	LYS	G1532
		V2625	W2362	THR	L2012	K2010	L1940	P1897	ASP	TYR	R1535
		L2419	G2363	THR	Q2013	K2014	K1941	SER	ASN	GLN	L1536
		T2631	M2374	THR	Q2014	Y2017	F1946	L1876	ASP	LEU	V1537
		L2636	L2374	THR	L2114	H2018	N1947	D1884	ASP	LEU	G1538
			S2387	THR	D2115	L2019	N1949	K1887	ASP	LEU	P1539
			K2395	THR	V2118	S2020	H1950	LEU	THR	THR	N1540
			C2398	THR	S2119	E2021	S1951	LEU	ASP	ASP	I1553
			P2404	THR	K2120	D2025	F1952	PHE	ASP	ASP	I1557
			R2418	THR	L2121	V2043	L1953	LEU	ASP	ASP	C1568
			L2419	THR	V2123	R2054	M1955	LEU	ASP	ASP	V1573
			E2430	THR	C2124	K2057	F1956	LEU	ASP	ASP	V1577
			L2433	THR	Y2126	Q2062	N1958	LEU	ASP	ASP	W1580
			R2435	THR	Q2127	H2063	C1959	LEU	ASP	ASP	
			L2436	THR	K2128	E2066	L1960	LEU	ASP	ASP	
				THR	ASP	E2069	F1961	LEU	ASP	ASP	
				THR	ASP	L2073	S1962	LEU	ASP	ASP	
				THR	ASP		E1964	LEU	ASP	ASP	
				THR	ASP		E1965	LEU	ASP	ASP	
				THR	ASP		F1966	LEU	ASP	ASP	
				THR	ASP		N1967	LEU	ASP	ASP	
				THR	ASP		E1968	LEU	ASP	ASP	
				THR	ASP		L1969	LEU	ASP	ASP	
				THR	ASP		I1970	LEU	ASP	ASP	
				THR	ASP		K1971	LEU	ASP	ASP	
				THR	ASP		L1972	LEU	ASP	ASP	



- Molecule 2: RNA (5'-R(*UP*UP*CP*CP*AP*AP*AP*AP*AP*AP*UP*CP*GP*UP*UP*CP*CP*C)-3')



- Molecule 3: RNA (5'-R(P*GP*GP*GP*AP*UP*UP*GP*GP*UP*GP*UP*CP*UP*UP*UP*G P*AP*GP*A)-3')



- Molecule 3: RNA (5'-R(P*GP*GP*GP*AP*UP*UP*GP*GP*UP*GP*UP*CP*UP*UP*UP*G P*AP*GP*A)-3')



- Molecule 4: RNA (5'-R(*UP*CP*UP*CP*AP*AP*AP*GP*AP*CP*AP*CP*CP*AP*A)-3')



- Molecule 5: RNA (5'-R(P*UP*CP*U)-3')

Chain F:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51896	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.417	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	262.44, 262.44, 262.44	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8748, 0.8748, 0.8748	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: 2KH, MN, ZN

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	0.15	0/25034	0.32	0/33767
2	B	0.13	0/259	0.27	0/401
3	C	0.15	0/312	0.25	0/485
3	E	0.16	0/189	0.36	0/292
4	D	0.15	0/241	0.19	0/373
5	F	0.18	0/66	0.49	0/98
All	All	0.15	0/26101	0.32	0/35416

There are no bond length outliers.

There are no bond angle outliers.

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	24614	0	25007	217	0
2	B	231	0	121	1	0
3	C	280	0	139	4	0
3	E	170	0	86	0	0
4	D	215	0	111	4	0
5	F	61	0	32	0	0
6	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	29	0	13	0	0
8	A	1	0	0	0	0
All	All	25605	0	25509	224	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 4.

The worst 5 of 224 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:1535:ARG:HD3	1:A:1577:VAL:HG11	1.71	0.72
1:A:542:GLY:HA3	1:A:900:THR:HG21	1.74	0.69
1:A:3113:LEU:HD21	1:A:3152:LEU:HD13	1.75	0.69
1:A:586:PRO:HD2	1:A:589:ILE:HD13	1.75	0.69
1:A:1638:ARG:HH21	1:A:2361:LYS:HG3	1.58	0.68

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	3028/3945 (77%)	2926 (97%)	102 (3%)	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	2828/3601 (78%)	2828 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3098	GLN
1	A	3595	ASN
1	A	1369	ASN
1	A	1381	ASN
1	A	1401	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	10/19 (52%)	5 (50%)	0
3	C	12/19 (63%)	3 (25%)	0
3	E	7/19 (36%)	3 (42%)	0
4	D	9/15 (60%)	1 (11%)	0
5	F	2/3 (66%)	0	0
All	All	40/75 (53%)	12 (30%)	0

5 of 12 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	U
2	B	5	A
2	B	6	A
2	B	7	A
2	B	8	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 5 are 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	$\# Z > 2$
7	2KH	A	4005	6	29,30,30	3.95	21 (72%)	42,47,47	1.59	6 (14%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	2KH	A	4005	6	-	6/19/38/38	0/2/2/2

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	4005	2KH	C3'-C2'	-8.82	1.29	1.53
7	A	4005	2KH	C2-N3	6.98	1.50	1.38
7	A	4005	2KH	C2-N1	6.46	1.48	1.38
7	A	4005	2KH	C6-C5	6.16	1.49	1.35
7	A	4005	2KH	PB-O3B	6.04	1.66	1.59

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	4005	2KH	C4-N3-C2	-4.93	120.08	126.58
7	A	4005	2KH	N3-C2-N1	3.94	120.13	114.89
7	A	4005	2KH	C5-C4-N3	3.33	119.83	114.84
7	A	4005	2KH	PB-O3B-PG	-2.99	122.08	132.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	4005	2KH	O4-C4-C5	-2.65	120.50	125.16

There are no chirality outliers.

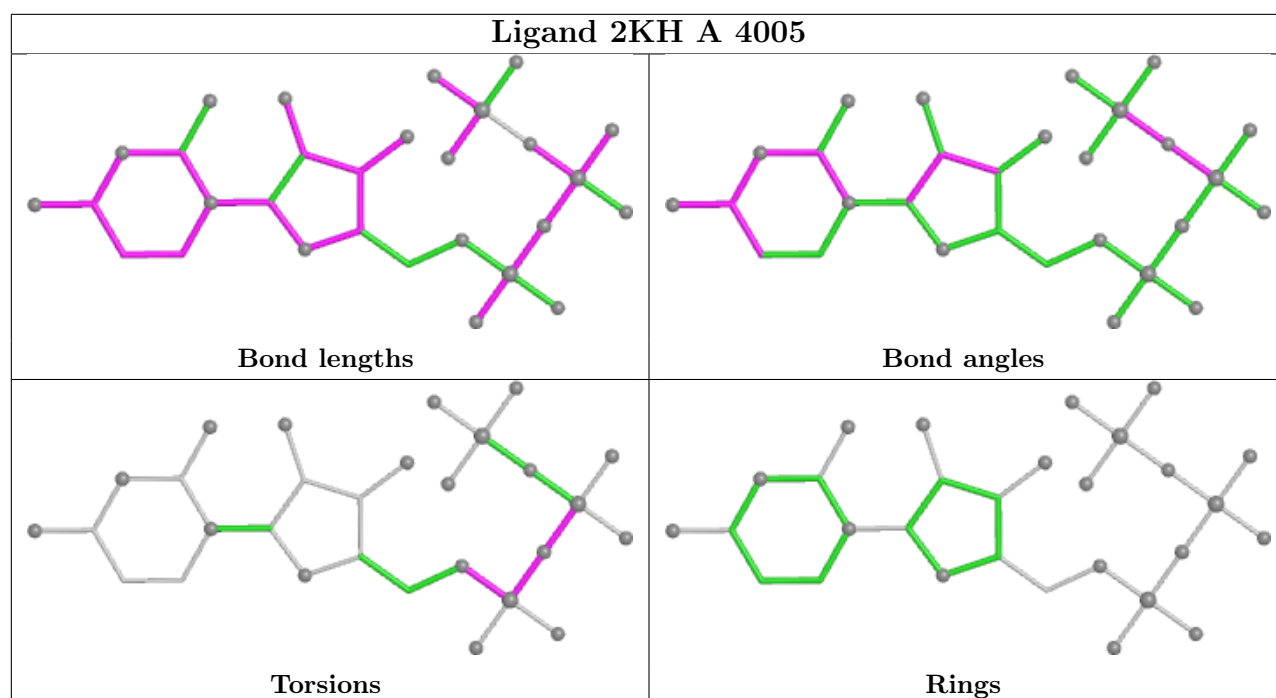
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	4005	2KH	PB-N3A-PA-O1A
7	A	4005	2KH	C5'-O5'-PA-O2A
7	A	4005	2KH	PA-N3A-PB-O2B
7	A	4005	2KH	PA-N3A-PB-O3B
7	A	4005	2KH	C5'-O5'-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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.

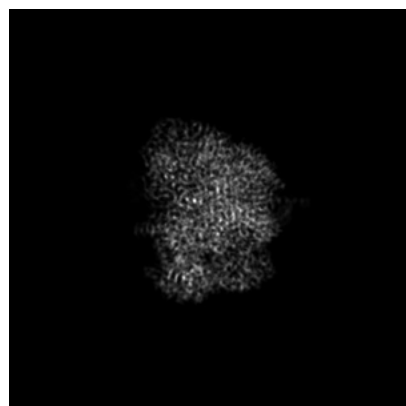
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66785. These allow visual inspection of the internal detail of the map and identification of artifacts.

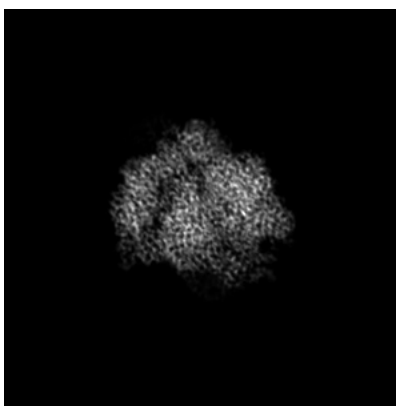
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

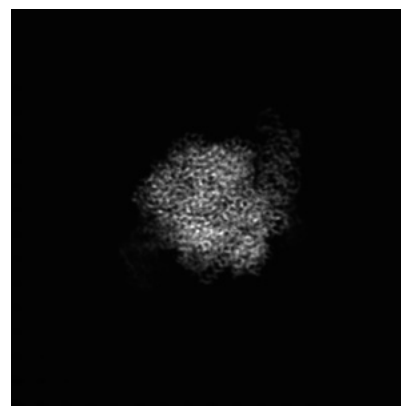
6.1.1 Primary map



X

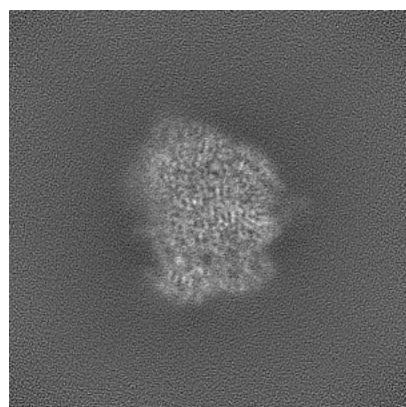


Y

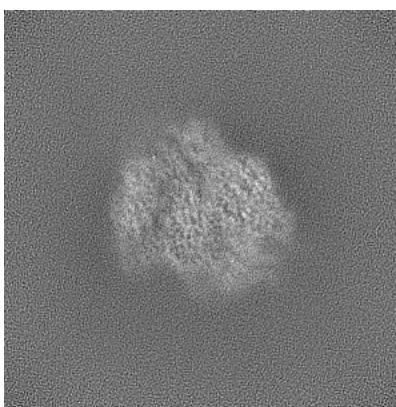


Z

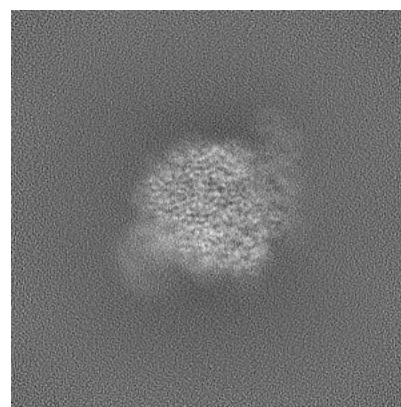
6.1.2 Raw map



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: 150

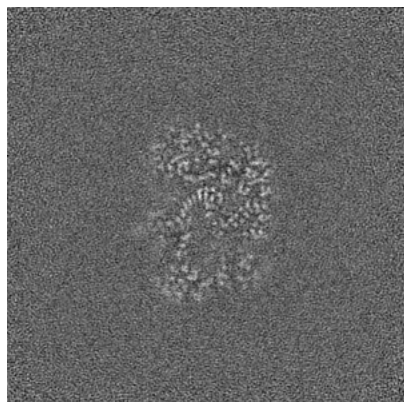


Y Index: 150

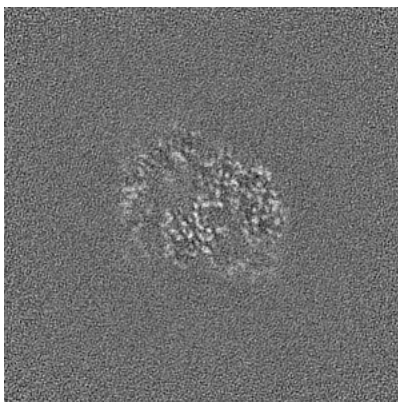


Z Index: 150

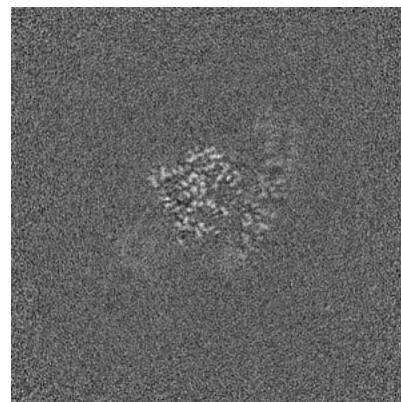
6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

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: 142

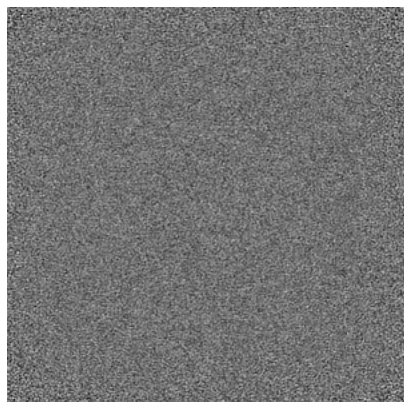


Y Index: 143

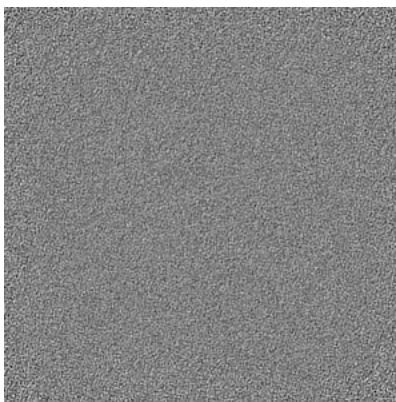


Z Index: 135

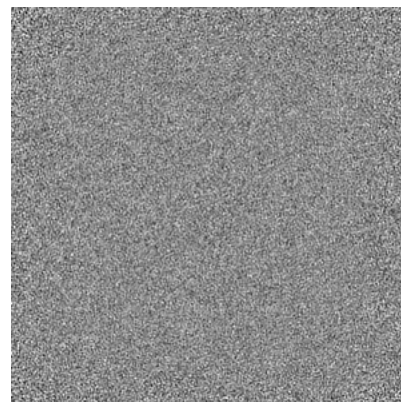
6.3.2 Raw map



X Index: 0



Y Index: 0

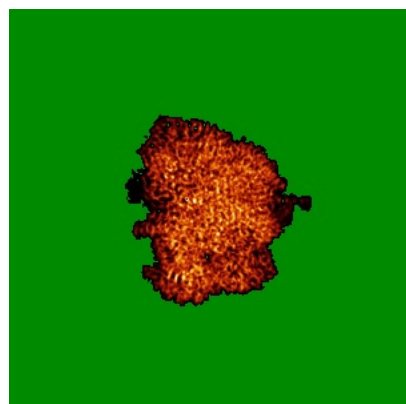


Z Index: 0

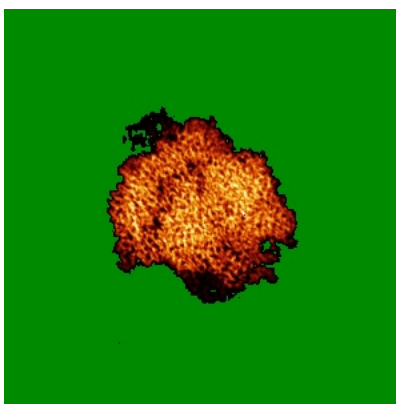
The images above show the largest variance slices of the map in three orthogonal directions.

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

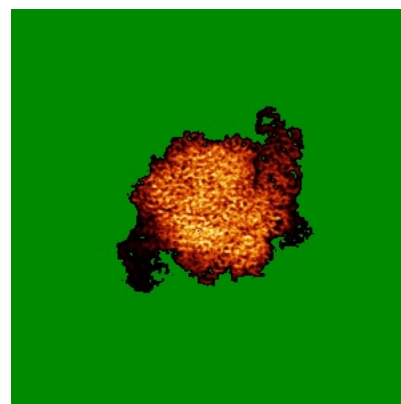
6.4.1 Primary map



X

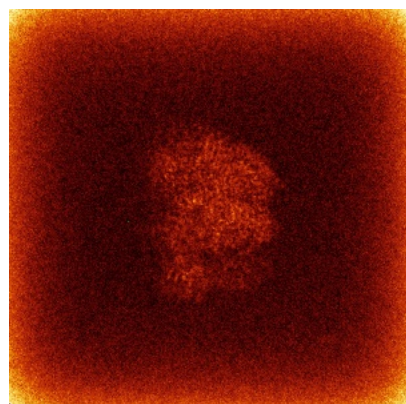


Y

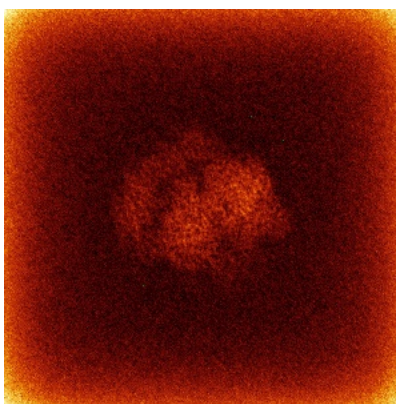


Z

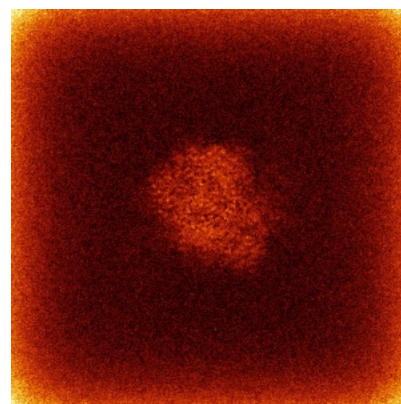
6.4.2 Raw map



X



Y

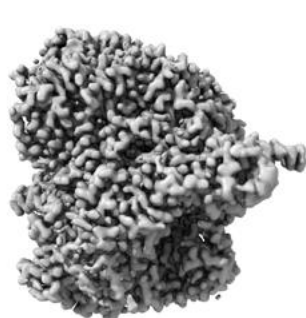


Z

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



X



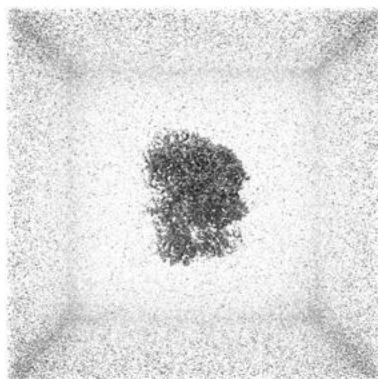
Y



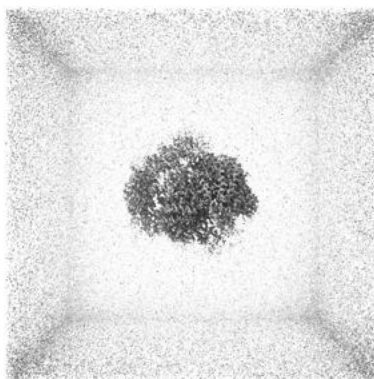
Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

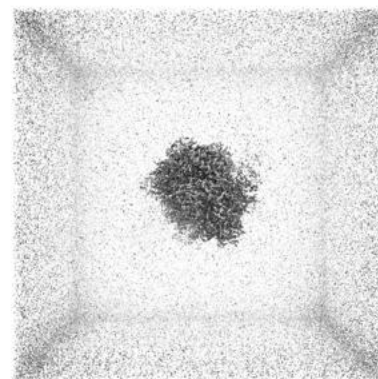
6.5.2 Raw map



X



Y



Z

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.

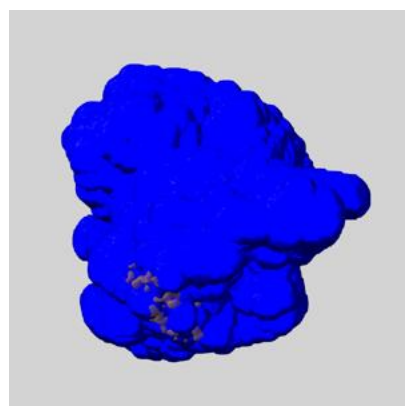
6.6 Mask visualisation [i](#)

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

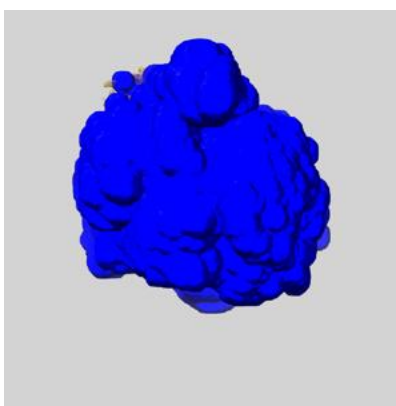
A mask typically either:

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

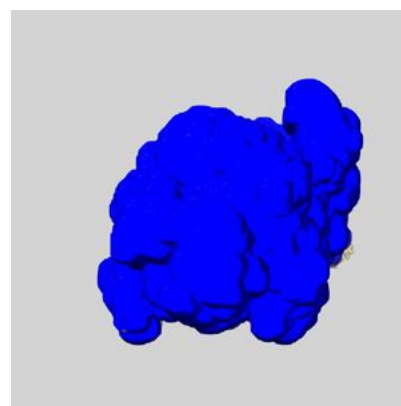
6.6.1 emd_66785_msk_1.map [i](#)



X



Y

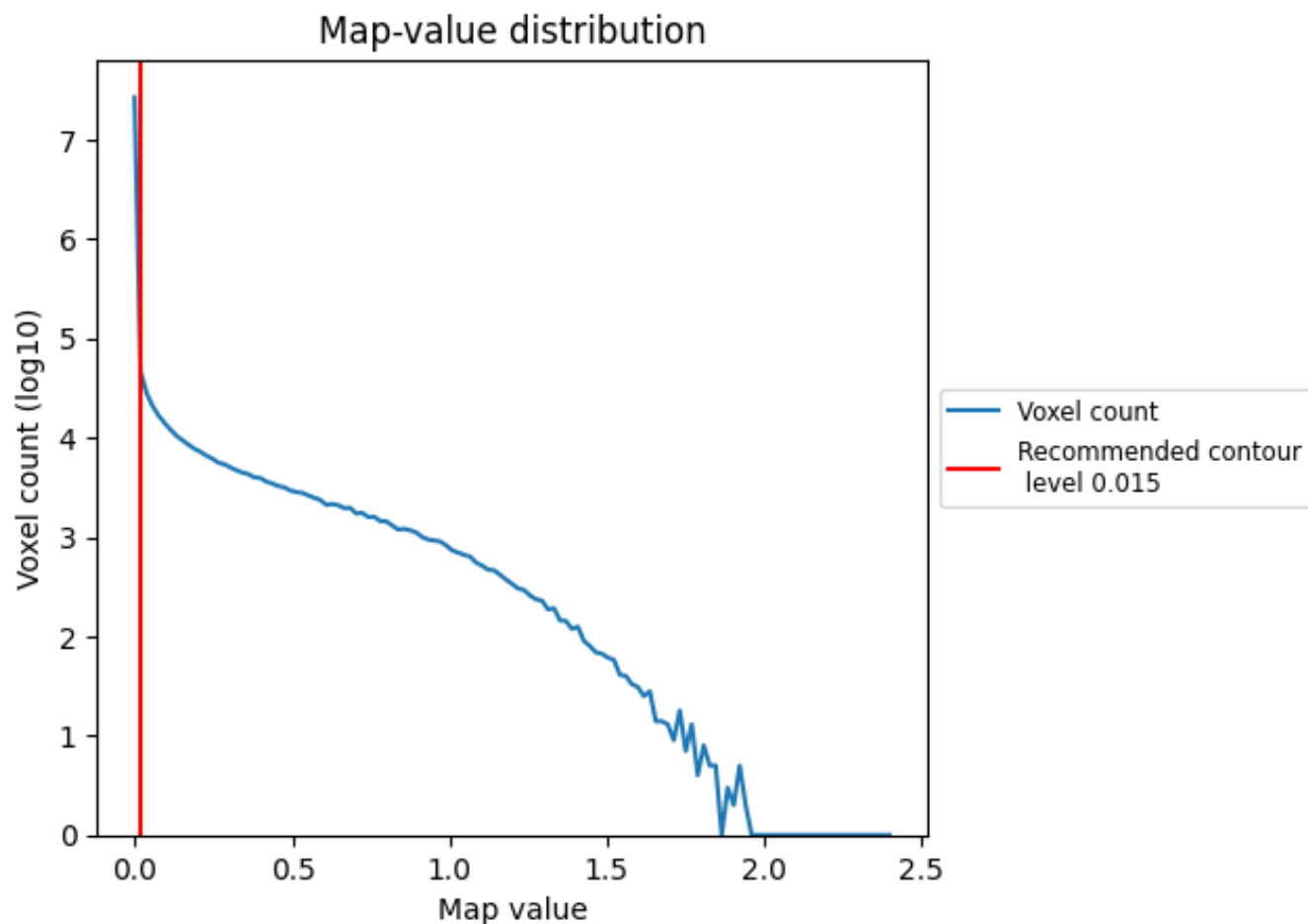


Z

7 Map analysis [i](#)

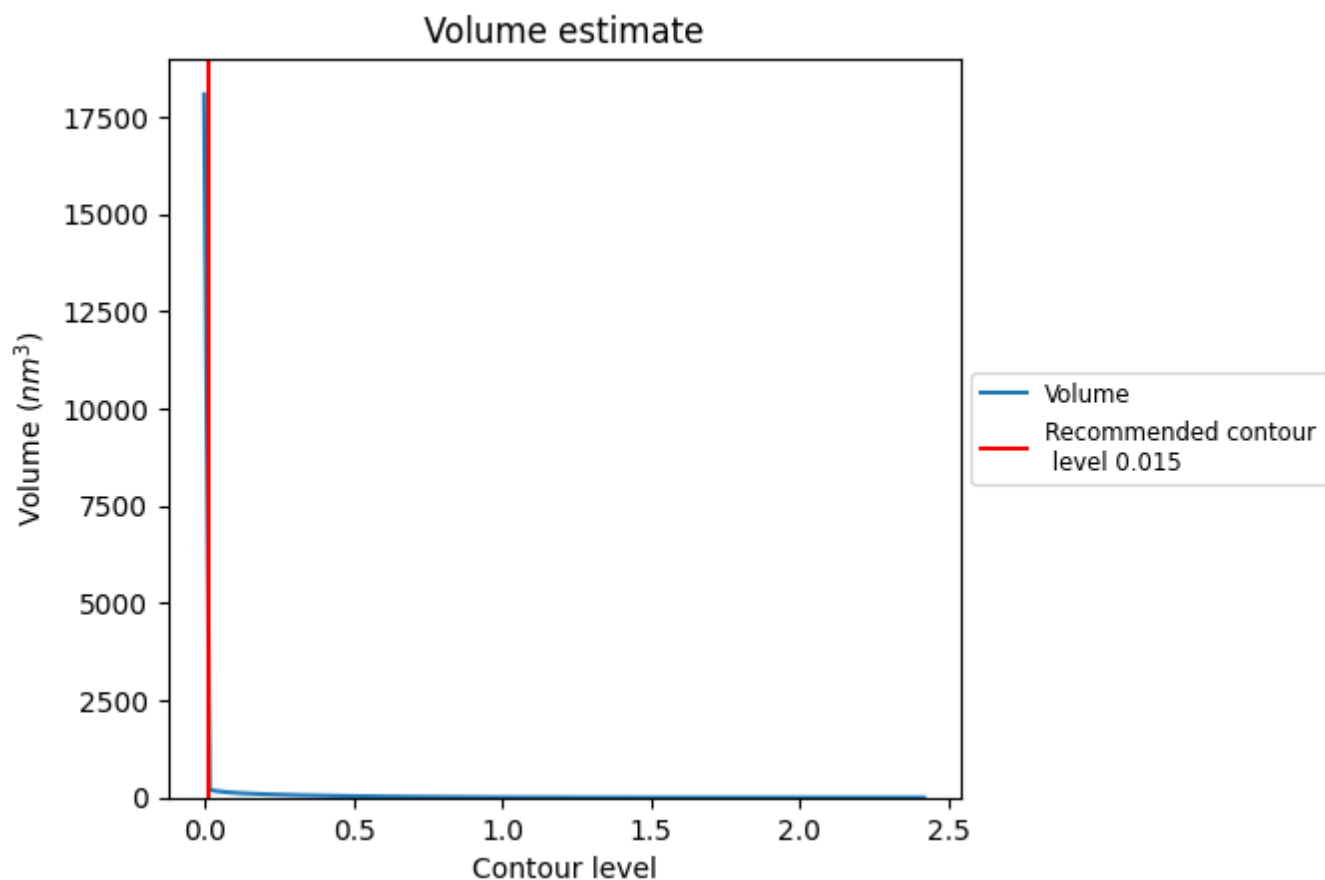
This section contains the results of statistical analysis of the map.

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.

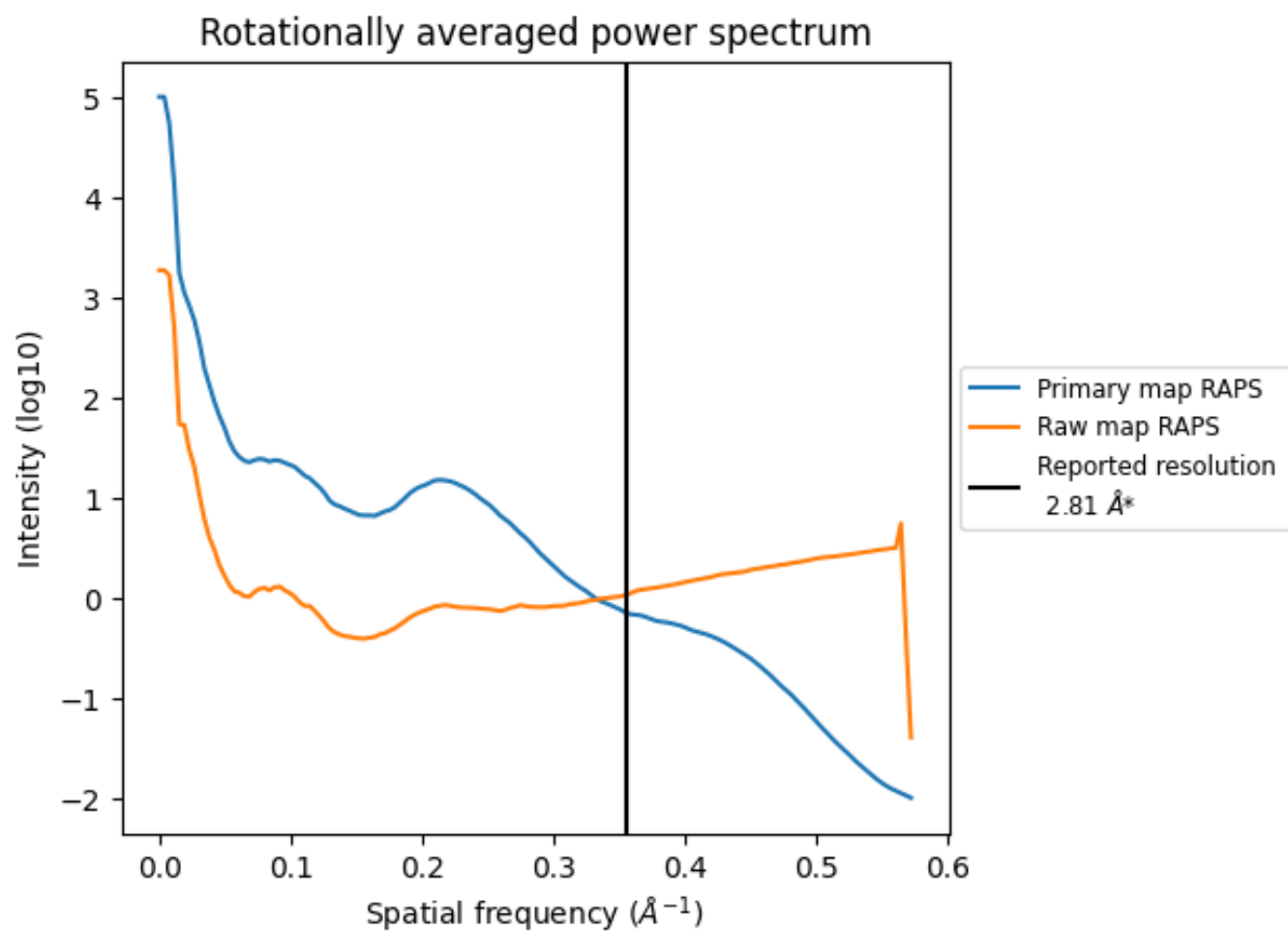
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2225 nm³; this corresponds to an approximate mass of 2010 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 ⓘ

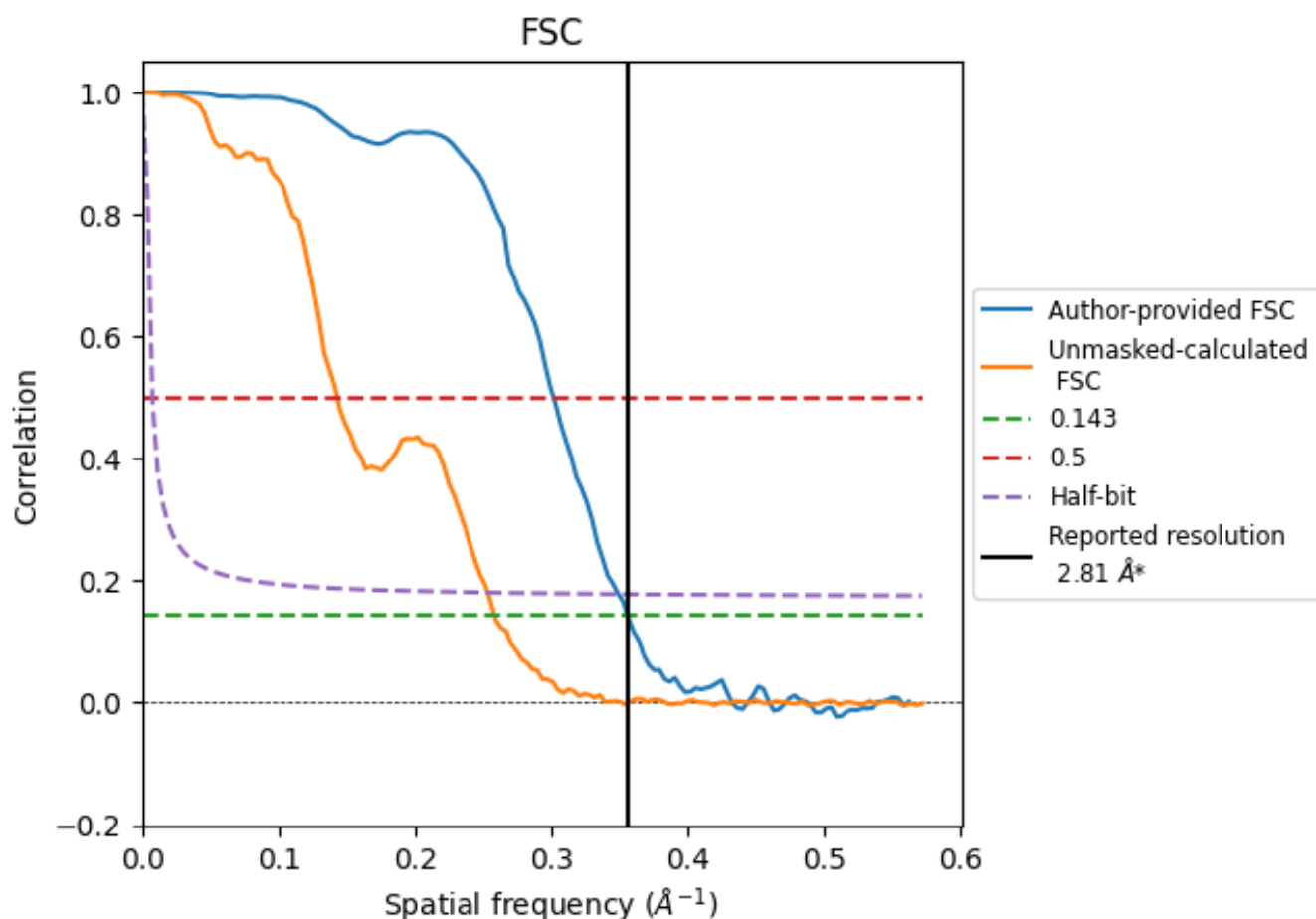


*Reported resolution corresponds to spatial frequency of 0.356 $\text{\AA}^{-1}$

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 $0.356 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

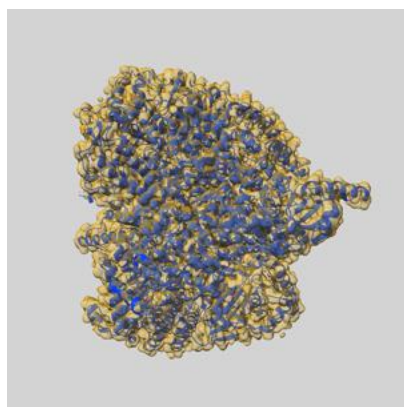
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.81	-	-
Author-provided FSC curve	2.81	3.32	2.87
Unmasked-calculated*	3.87	7.00	3.95

*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 3.87 differs from the reported value 2.81 by more than 10 %

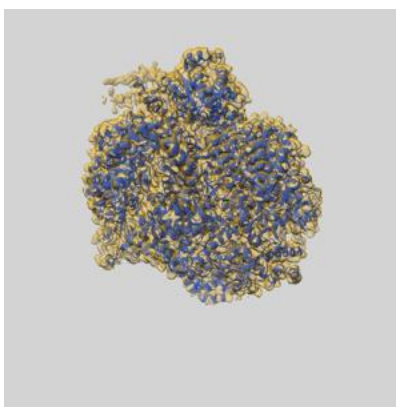
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66785 and PDB model 9XE9. Per-residue inclusion information can be found in section [3](#) on page [6](#).

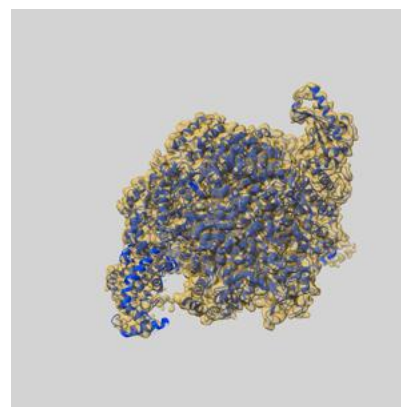
9.1 Map-model overlay [i](#)



X



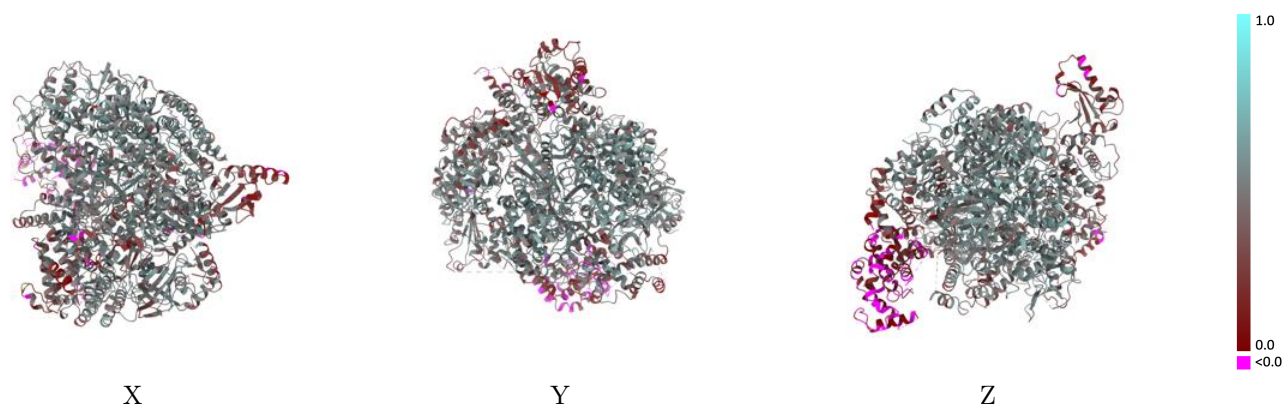
Y



Z

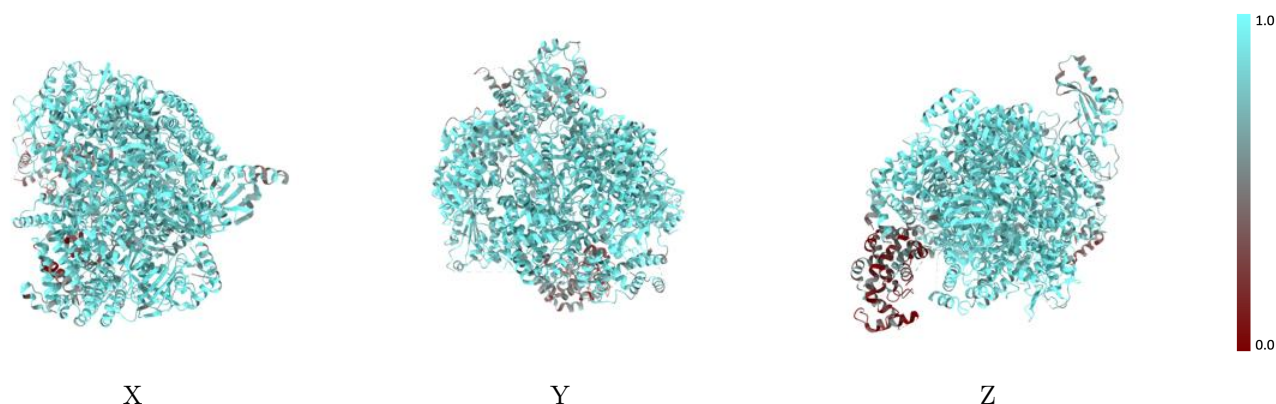
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



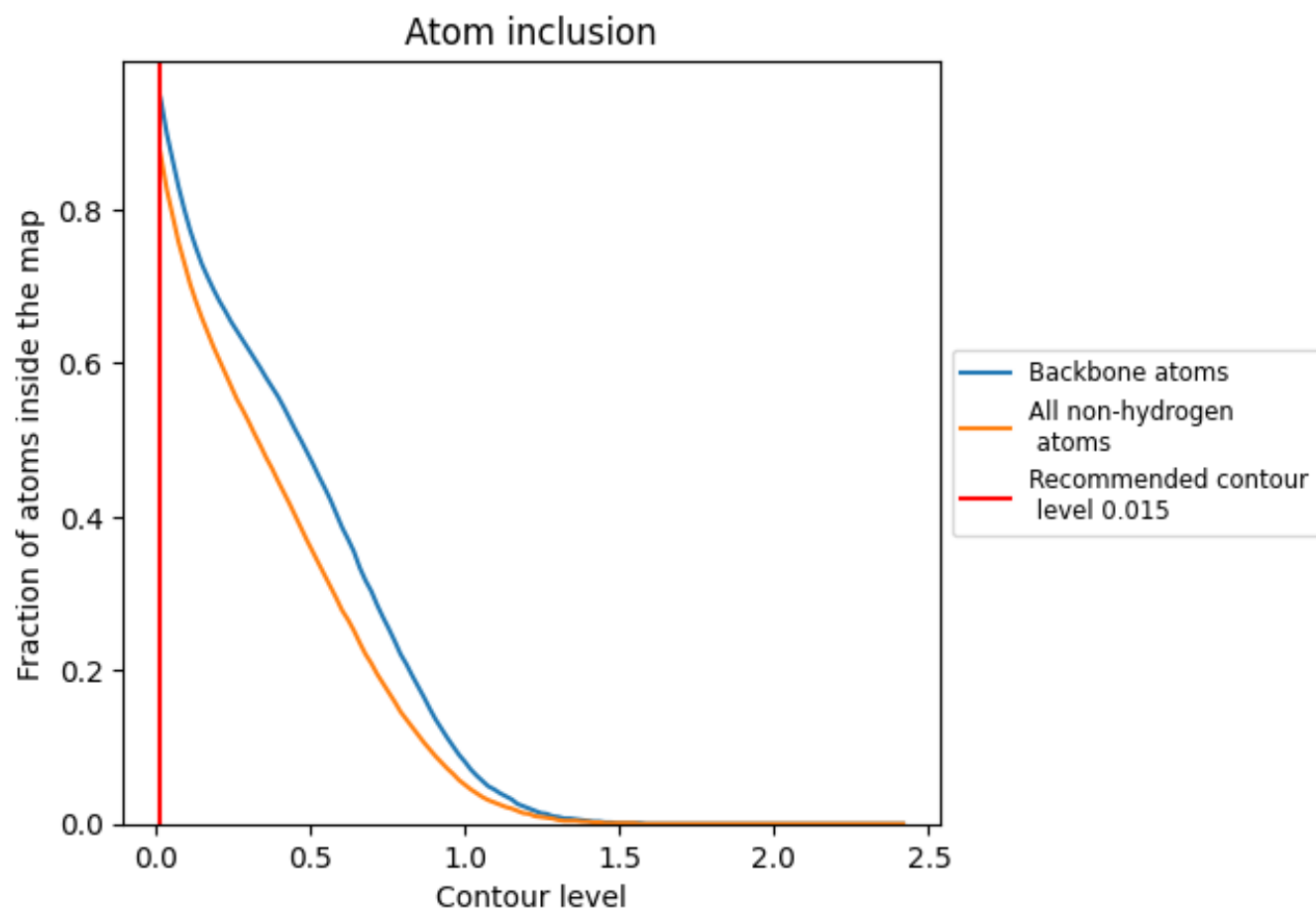
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8740	0.4410
A	0.8710	0.4390
B	0.9610	0.4840
C	0.9250	0.4650
D	0.9770	0.4940
E	0.9650	0.5140
F	1.0000	0.5510

1.0

0.0

<0.0