



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 09:25 AM UTC

PDB ID : 8YXL / pdb_00008yxl
EMDB ID : EMD-37958
Title : Structure of C-terminal domain of L protein from Mumps virus
Authors : Li, T.H.; Shen, Q.T.
Deposited on : 2024-04-02
Resolution : 3.13 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
MolProbity : 4-5-2 with Phenix2.0
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

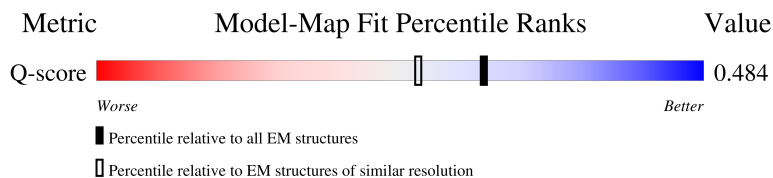
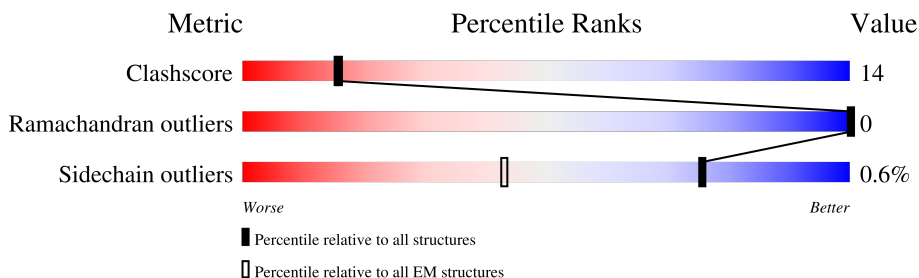
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.13 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	14478 (2.63 - 3.63)

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	2261	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 5588 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.

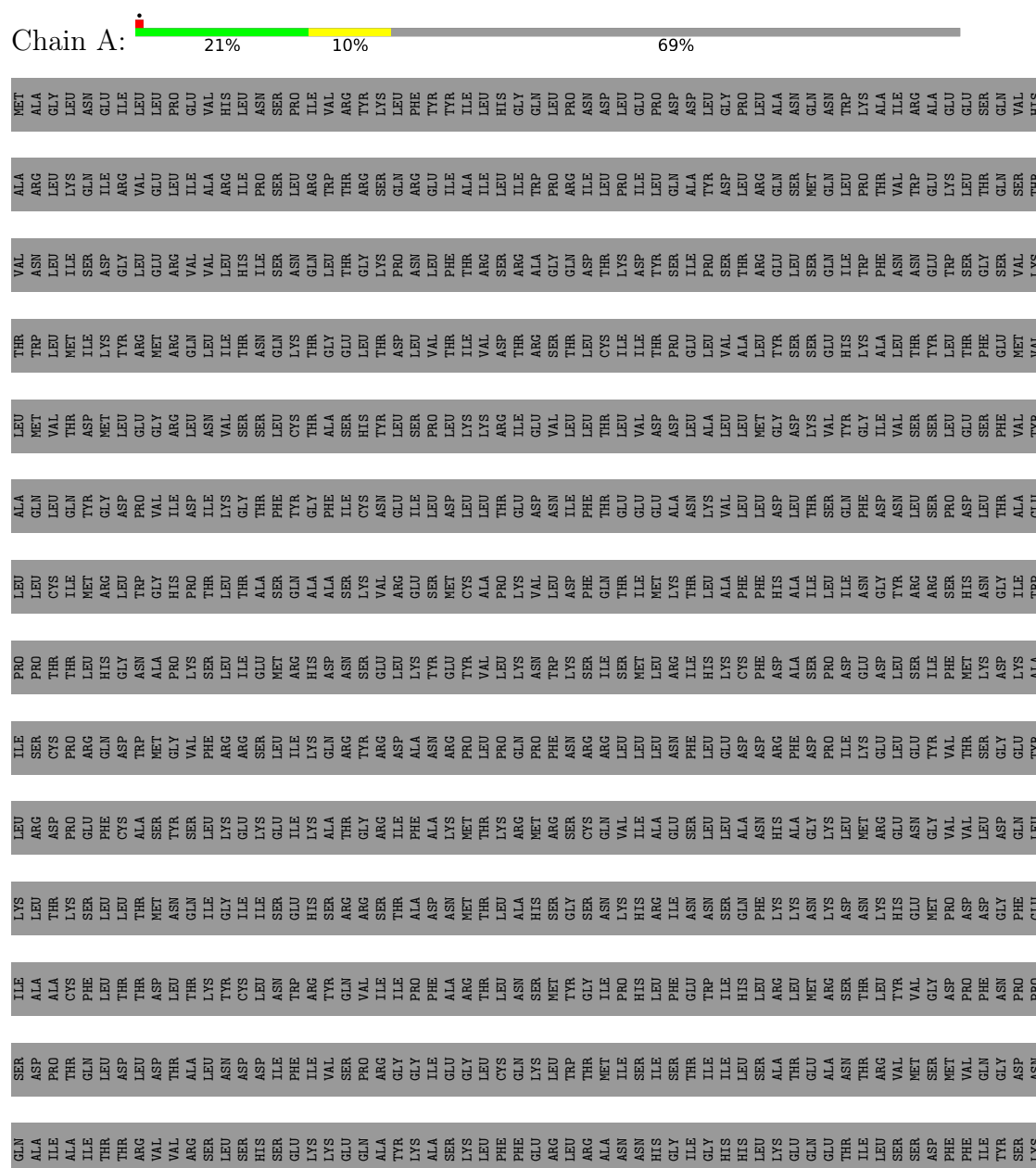
- Molecule 1 is a protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	699	Total	C	N	O	S	0	0
			5588	3601	941	1023	23		

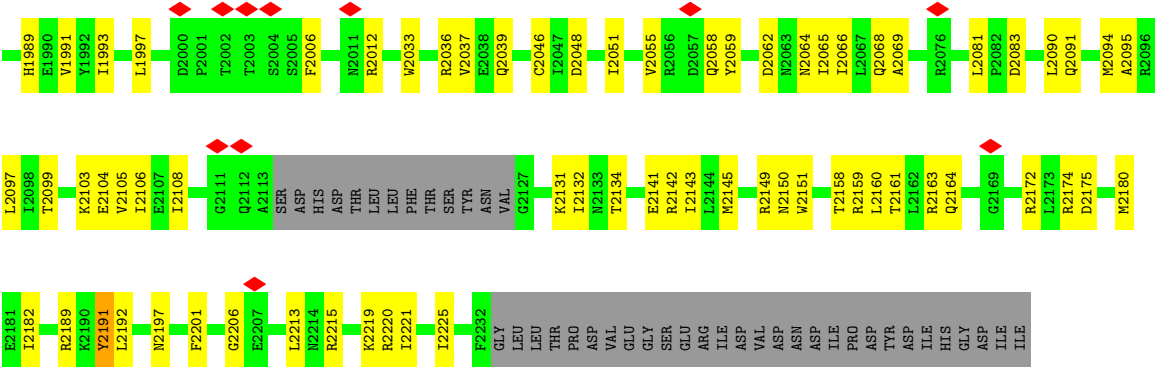
3 Residue-property plots

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: RNA-directed RNA polymerase L



C1911	A1809	L1736	E1657	G1538	I1443	VAL	ASP	PHE	THR	ILE	GLN	LYS	ASP	MET	ARG
A1912	H1810	L1740	TYR	T1542	P1444	HIS	THR	THR	CYS	ARG	GLN	HIS	PRO	THR	VAL
L1913	L1811	F1741	VAL	T1543	L1449	ILE	GLU	GLY	ILE	ILE	TYR	ALA	LEU	ILE	PHE
V1914	Y1812	F1742	GLU	S1544	T1450	ASN	ASP	TRP	ILE	ASP	THR	LEU	ALA	GLY	LYS
H1915	A1814	L1743	TYR	R1547	Q1453	CYS	GLN	GLN	ARG	SER	ASP	LEU	ILE	CYS	GLY
V1916	E1815	M1744	ILE	R1550	M1454	VAL	ASP	ASP	ARG	THR	ALA	MET	ALA	TYR	ARG
G1920	A1819	L1745	Q1663	R1558	V1455	VAL	GLN	GLN	LEU	THR	VAL	GLU	ARG	TYR	ILE
VAL	S1820	GLU	E1665	R1562	I1458	ASN	PRO	ASP	ASP	ARG	VAL	GLU	VAL	ASP	LEU
PRO	M1821	LEU	I1667	S1563	T1459	PRO	LEU	ALA	PRO	ILE	ASN	ASN	ARG	PRO	ALA
SER	S1822	ASP	I1669	S1564	GLY	ASP	LEU	ALA	LYS	ILE	PRO	PRO	VAL	PHE	ALA
MET	L1823	ALA	R1671	H1565	LEU	ASP	THR	SER	TRP	THR	GLN	MET	LEU	GLN	LYS
ASN	L1826	SER	M1672	H1571	ASP	VAL	VAL	THR	ASN	LEU	ALA	LEU	VAL	ASN	ASN
SER	F1827	LEU	I1674	Y1571	ALA	THR	ASP	ASN	ILE	ARG	GLY	GLY	GLY	SER	SER
MET	L1828	GLU	I1678	T1572	VAL	PRO	LEU	SER	ILE	LEU	VAL	ARG	VAL	GLN	GLN
E1930	T1833	LYS	T1679	K1573	ILE	ASN	THR	THR	ASN	ASN	GLN	VAL	ASP	ASP	CYS
R1931	W1834	TYR	L1685	L1574	VAL	VAL	ILE	THR	ILE	PRO	TYR	VAL	ILE	ASP	LEU
A1932	PRO	LEU	PHE	A1578	ASP	ASN	GLN	GLN	GLY	ILE	ARG	GLY	THR	THR	THR
Q1933	SER	SER	I1688	I1598	VAL	GLN	GLN	GLN	GLY	ILE	GLY	ALA	VAL	ALA	ALA
V1934	P1845	LEU	T1688	P1601	VAL	VAL	VAL	VAL	LYS	GLY	GLY	ALA	TYR	ALA	ILE
H1935	Q1846	LEU	R1690	G1604	GLN	GLN	GLN	GLN	THR	GLY	GLY	GLY	ASN	TYR	LEU
A1936	Q1847	LEU	K1691	S1604	ALA	ALA	ALA	ALA	PHE	THR	LEU	GLU	ASN	ASN	GLY
L1937	R1848	LEU	L1692	GLN	ASP	ASP	ASP	ASP	THR	THR	PRO	GLU	GLY	HIS	CYS
L1938	N1849	MET	L1693	THR	TYR	TYR	PRO	PRO	ASP	PRO	GLY	LEU	LEU	ASN	ASN
I1939	GLU	THR	I1696	LEU	T1478	ALA	THR	THR	VAL	VAL	ARG	ARG	ASP	PRO	GLN
I1940	P1854	ALA	E1700	LEU	W1481	LEU	PRO	PRO	ALA	ILE	ASN	ALA	GLY	ILE	LEU
V1941	T1855	ASN	W1711	D1610	E1484	GLU	ASN	ASN	SER	GLY	LEU	LEU	GLY	SER	CYS
T1942	Q1856	MET	SER	R1611	C1485	THR	LEU	LEU	MET	ILE	LEU	LEU	GLY	ARG	VAL
V1943	F1857	ASP	PHE	N1614	C1486	TRP	VAL	VAL	ALA	GLY	THR	LEU	LEU	LEU	ASN
L1944	I1858	ASN	I1696	GLU	Y1487	ASN	HIS	HIS	ILE	GLY	THR	ASP	ASP	CYS	LEU
K1945	E1859	PRO	E1700	THR	T1488	ASN	ARG	LYS	LYS	THR	THR	GLY	THR	LEU	ALA
L1949	S1860	PHE	W1711	LEU	W1481	PRO	GLU	GLU	ALA	ILE	ASN	ALA	VAL	PRO	THR
L1950	V1861	F1772	SER	D1610	E1484	PRO	LEU	LEU	SER	GLY	LEU	VAL	VAL	LEU	THR
I1951	P1862	Q1773	PHE	R1611	C1485	ILE	LEU	LEU	GLY	ILE	LEU	VAL	VAL	GLY	THR
L1952	Y1863	P1774	GLY	N1614	C1486	GLU	GLU	GLU	GLY	GLY	THR	ASP	ASP	GLY	ALA
E1957	I1866	L1776	TYR	R1618	Y1487	MET	THR	THR	ILE	GLY	THR	ASP	PRO	GLY	LEU
H1960	I1870	H1777	TYR	R1618	T1488	GLU	GLU	THR	GLY	GLY	THR	THR	ASP	GLY	ALA
R1961	N1874	H1778	LEU	K1619	A1500	LYS	GLU	LEU	LEU	ALA	LEU	VAL	VAL	LEU	THR
F1962	G1875	V1779	GLU	L1620	L1501	ILE	ILE	ASP	ASP	ILE	LEU	ALA	ALA	GLN	VAL
S1963	I1876	R1781	PRO	S1621	L1502	GLU	ASP	GLY	GLY	ASP	VAL	PRO	PRO	GLY	ARG
F1964	V1877	L1785	ILE	L1622	Y1510	ASP	ILE	THR	THR	ILE	ILE	VAL	VAL	ILE	LEU
L1965	Q1878	L1785	MET	L1623	R1513	SER	ALA	TYR	GLY	GLN	ALA	ASN	ASN	LEU	GLY
L1966	L1883	W1790	SER	I1625	G1516	THR	THR	THR	THR	THR	THR	VAL	ASP	ASP	GLY
T1967	L1883	I1794	LYS	P1633	G1516	ARG	ARG	ARG	ARG	ARG	ARG	VAL	ASP	ASP	GLY
V1968	D1889	I1796	ILE	V1636	I1520	ILE	THR	THR	THR	THR	THR	ALA	ALA	CYS	GLY
W1970	L1893	V1796	PHE	P1641	I1527	GLY	PRO	PRO	PRO	PRO	PRO	GLN	GLN	LEU	LYS
Q1971	L1893	L1797	ASN	P1641	T1527	GLY	ASP	SER	SER	SER	SER	ALA	ALA	SER	ASP
F1972	V1899	I1800	LEU	K1644	L1528	HIS	LEU	SER	VAL	ASP	GLY	SER	PHE	ARG	LEU
F1973	V1899	I1800	SER	K1644	R1529	THR	THR	SER	THR	THR	THR	VAL	THR	THR	THR
L1979	I1902	M1803	SER	A1647	H1530	GLY	TYR	THR	TYR	ASP	ASN	CYS	GLY	ASN	PHE
R1980	V1906	K1804	GLU	A1647	I1531	SER	ALA	ALA	ILE	LYS	LYS	ARG	ARG	ARG	LEU
P1986		I1805	ALA	T1650	I1536	CYS	SER	SER	TRP	ILE	ALA	ARG	ASN	ASN	ALA
			SER	H1651	T1537	CYS	THR	THR	PHE	ASP	VAL	GLN	LYS	GLY	PHE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	438014	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.732	Depositor
Minimum map value	-0.453	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0858	Depositor
Map size (Å)	233.19998, 233.19998, 233.19998	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.53, 0.53, 0.53	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.30	3/5705 (0.1%)	0.48	5/7754 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1932	ALA	C-N	-7.67	1.23	1.33
1	A	1845	PRO	C-O	-7.39	1.16	1.24
1	A	1933	GLN	C-N	5.49	1.40	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1636	VAL	N-CA-C	-5.88	107.55	113.20
1	A	2191	TYR	O-C-N	5.61	129.74	122.89
1	A	1932	ALA	O-C-N	-5.22	116.59	122.12
1	A	1678	LEU	CA-C-N	5.20	129.73	121.72
1	A	1678	LEU	C-N-CA	5.20	129.73	121.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5588	0	5695	163	0
All	All	5588	0	5695	163	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 14.

The worst 5 of 163 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:2090:LEU:HD13	1:A:2150:ASN:HD22	1.20	1.03
1:A:2090:LEU:HD13	1:A:2150:ASN:ND2	1.96	0.80
1:A:1914:VAL:HG11	1:A:1940:THR:HG22	1.66	0.77
1:A:1529:ARG:HH11	1:A:1573:LYS:HZ1	1.32	0.77
1:A:1624:ALA:HB2	1:A:1651:HIS:NE2	2.01	0.74

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	681/2261 (30%)	668 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	629/2037 (31%)	625 (99%)	4 (1%)	78	80

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1669	ILE
1	A	1678	LEU
1	A	1685	LEU
1	A	1855	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2198	GLN
1	A	2150	ASN
1	A	2039	GLN
1	A	2011	ASN
1	A	2091	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](#)

There are no ligands in this entry.

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.

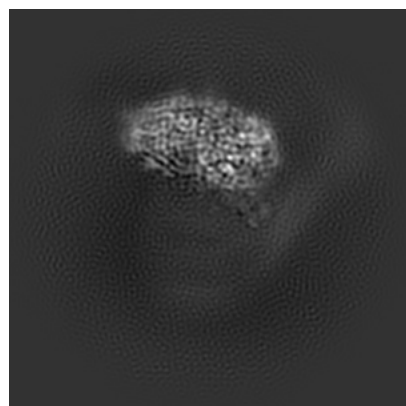
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37958. These allow visual inspection of the internal detail of the map and identification of artifacts.

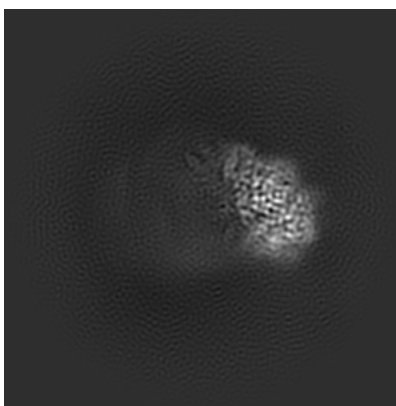
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

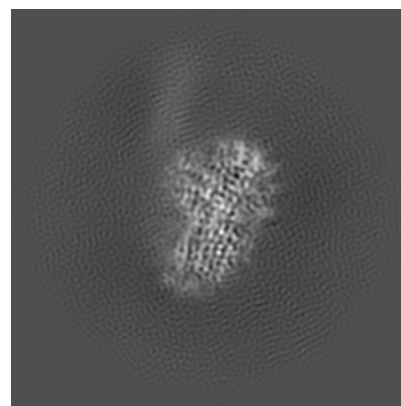
6.1.1 Primary map



X

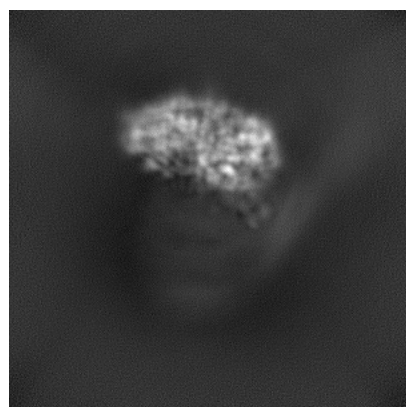


Y

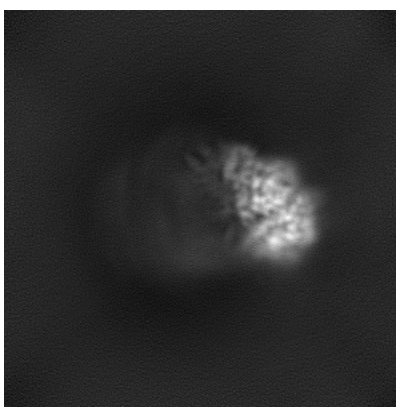


Z

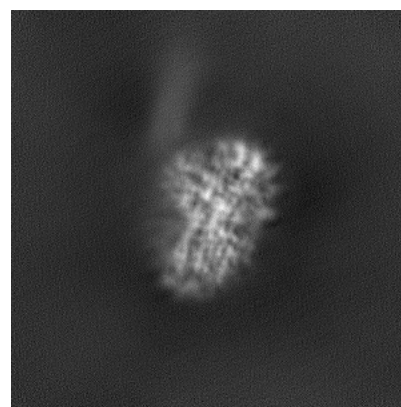
6.1.2 Raw map



X



Y

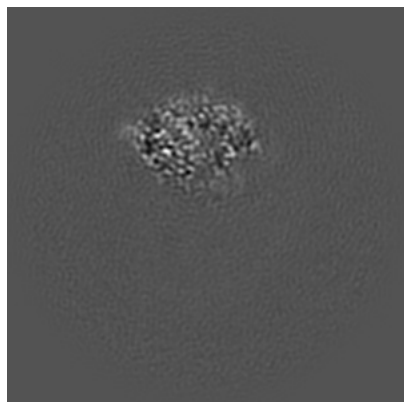


Z

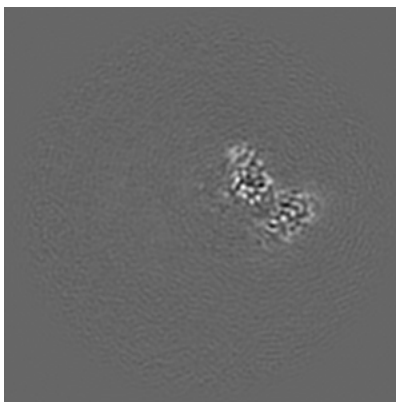
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

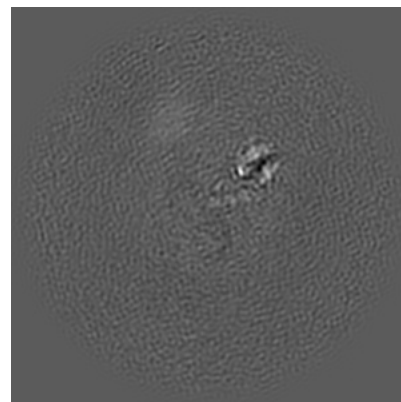
6.2.1 Primary map



X Index: 220

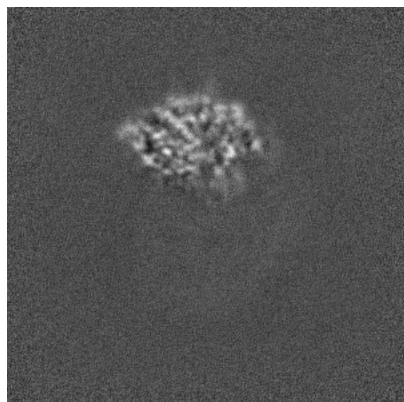


Y Index: 220

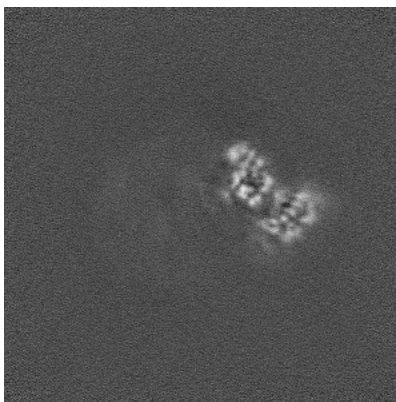


Z Index: 220

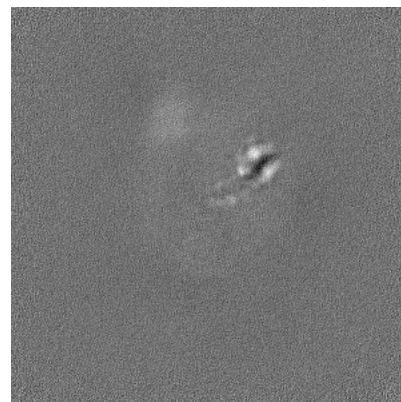
6.2.2 Raw map



X Index: 220



Y Index: 220

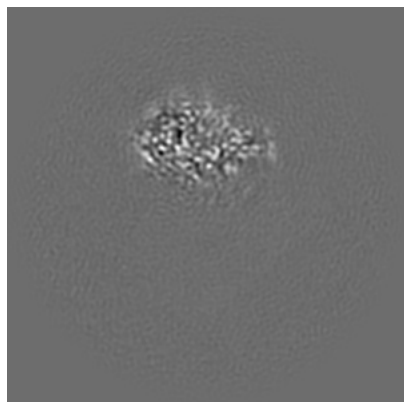


Z Index: 220

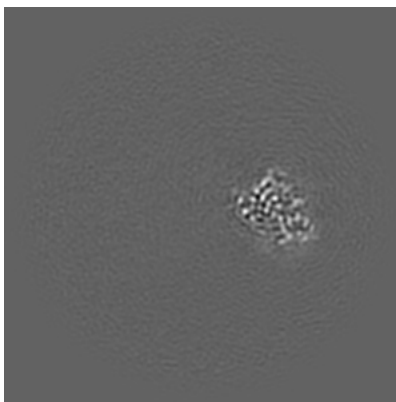
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

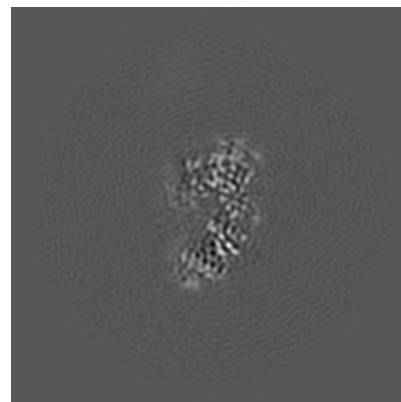
6.3.1 Primary map



X Index: 231

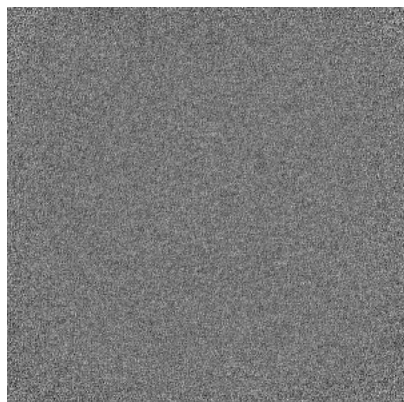


Y Index: 170

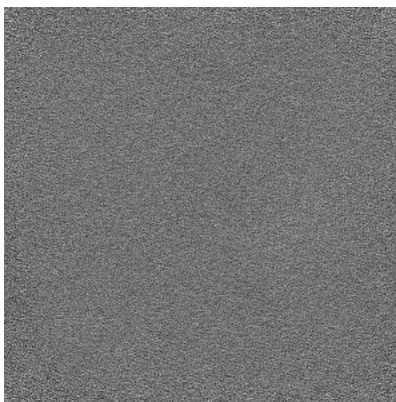


Z Index: 285

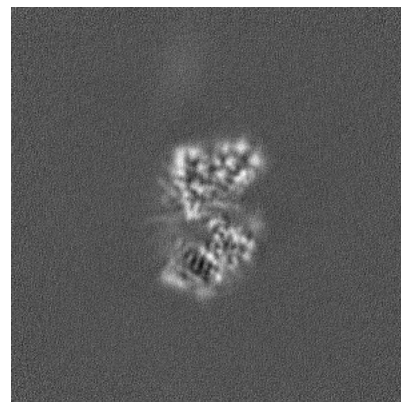
6.3.2 Raw map



X Index: 0



Y Index: 0

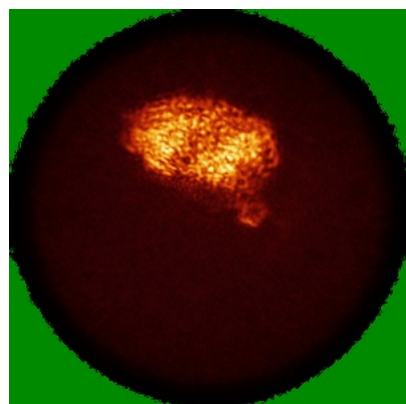


Z Index: 297

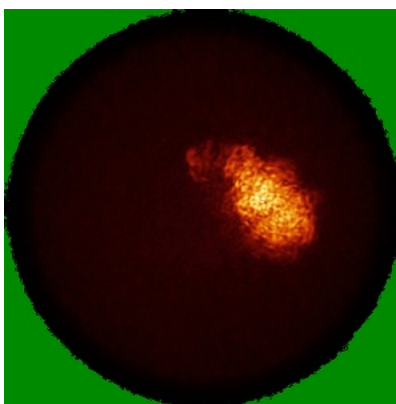
The images above show the largest variance slices of the map in three orthogonal directions.

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

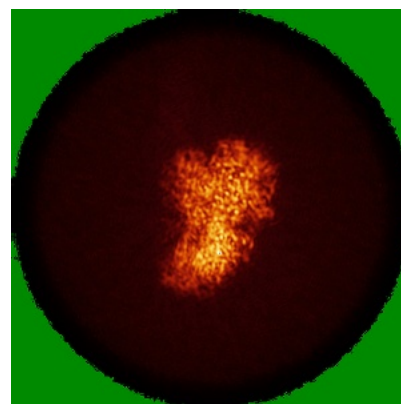
6.4.1 Primary map



X

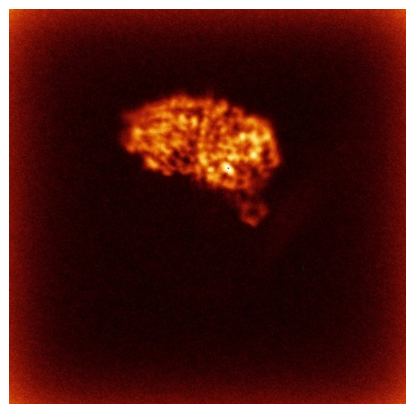


Y

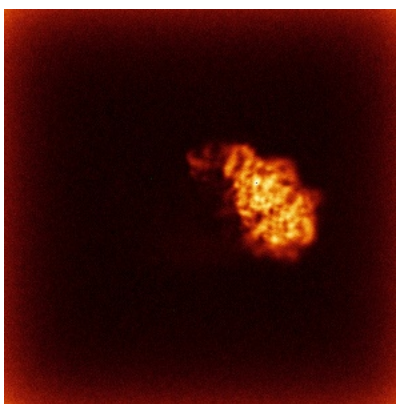


Z

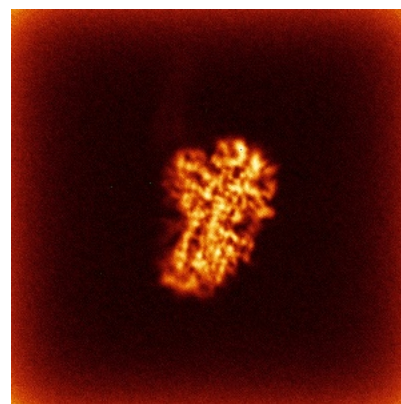
6.4.2 Raw map



X



Y

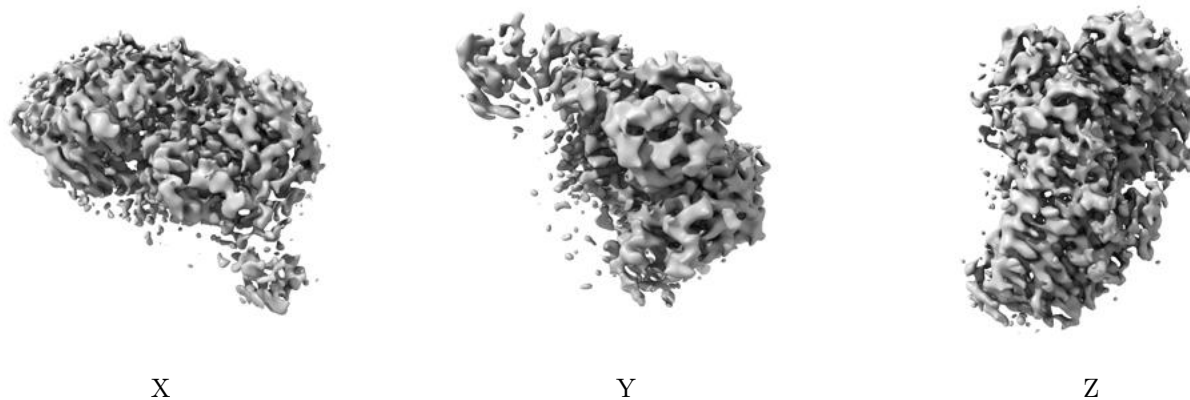


Z

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.

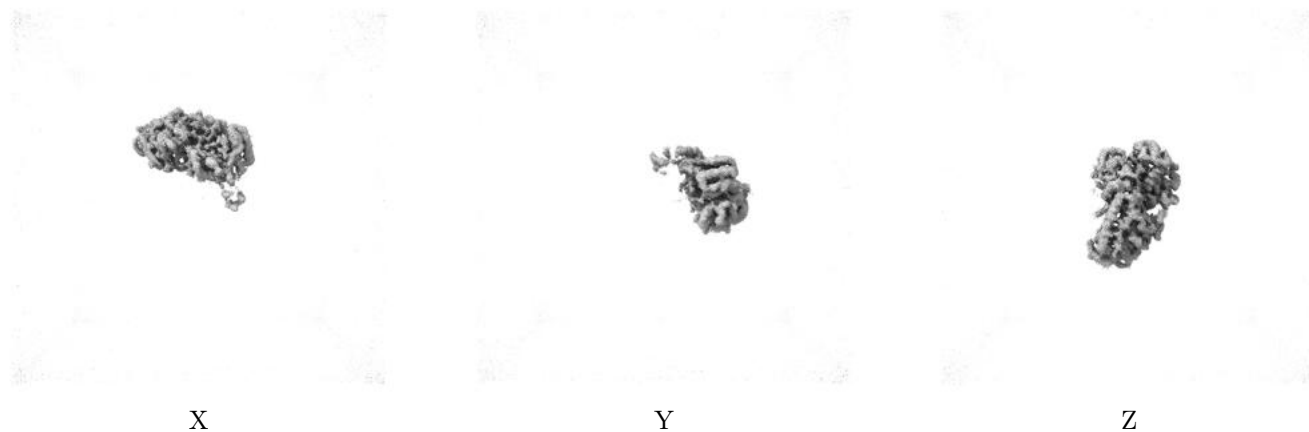
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0858. 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.

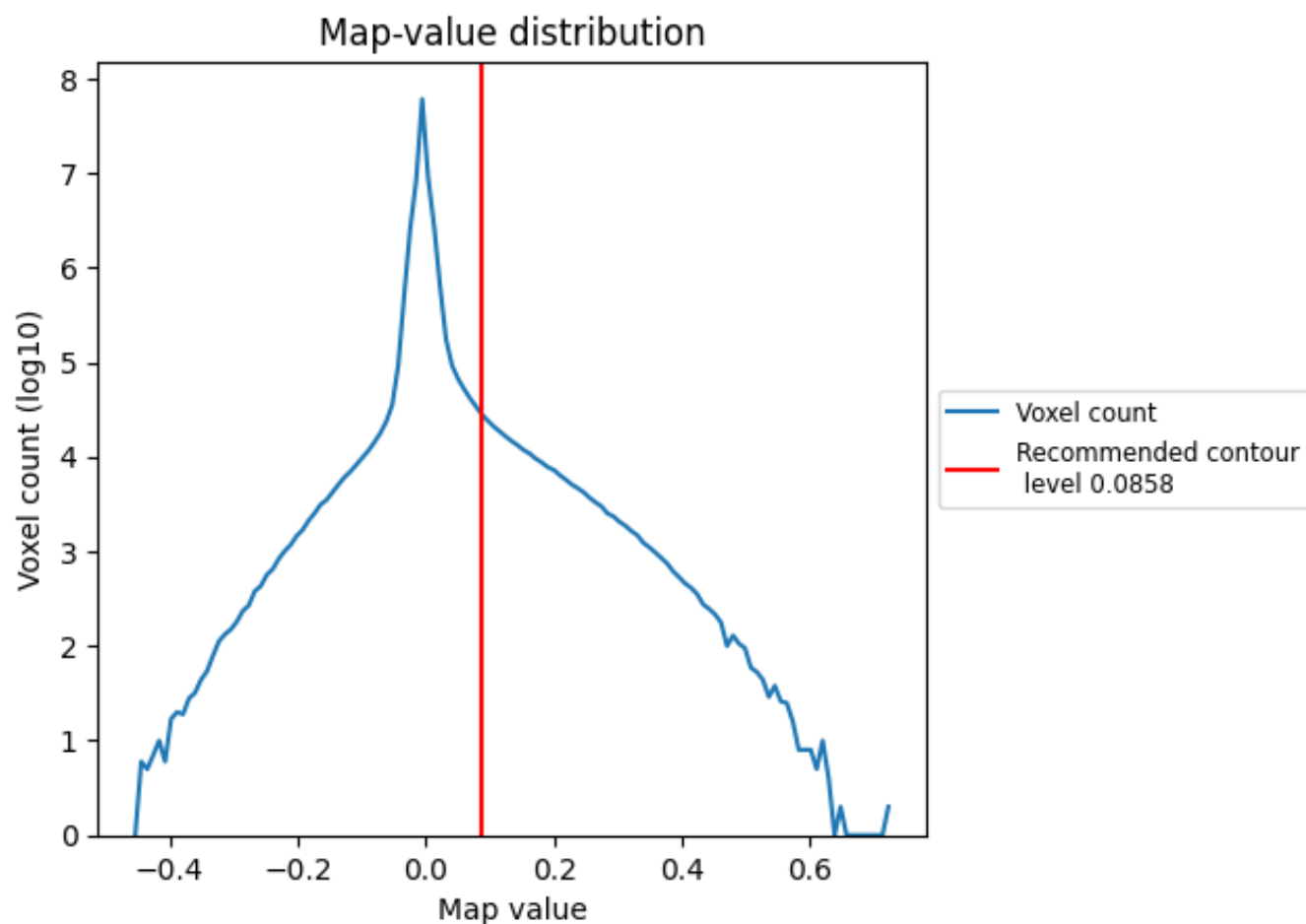
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

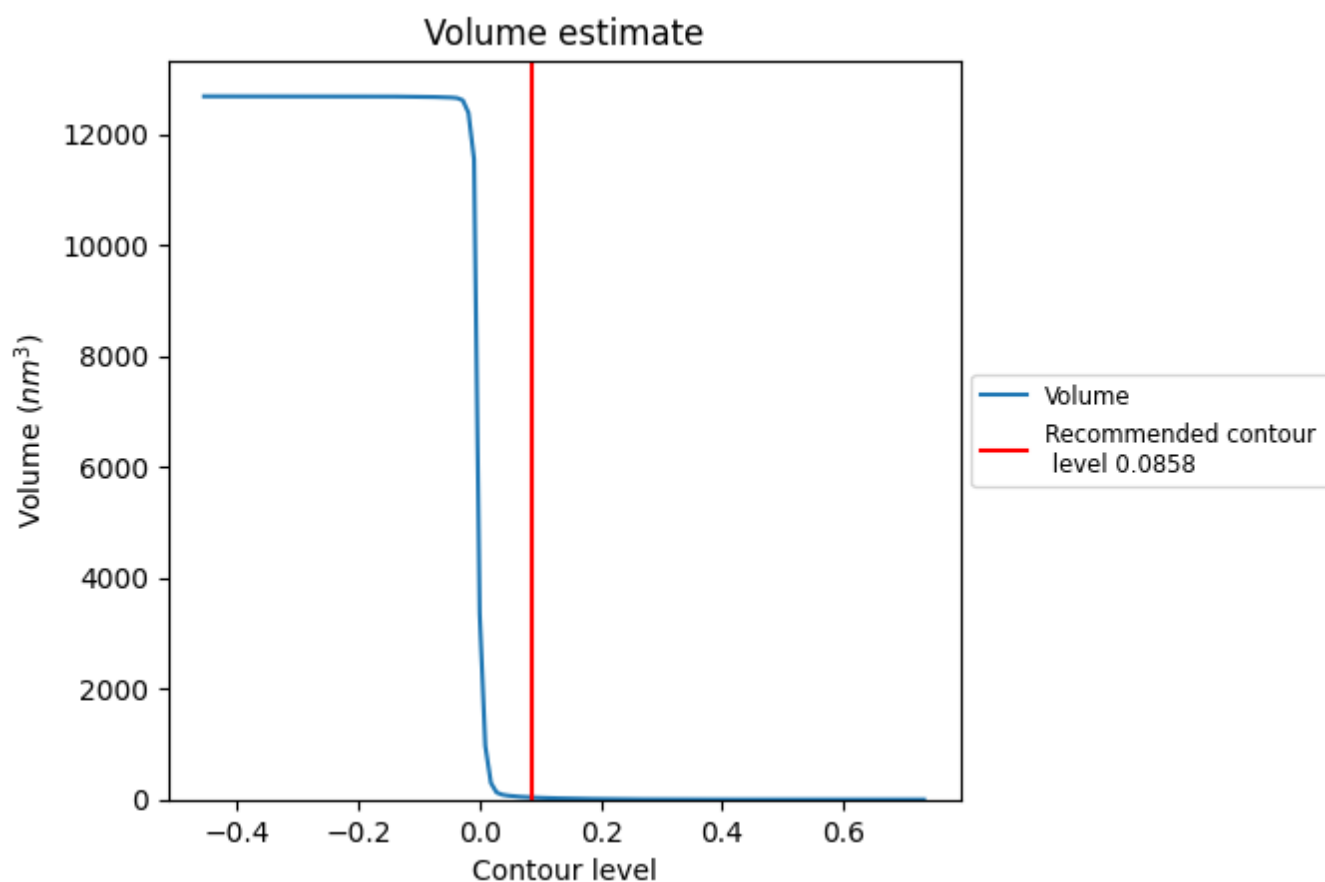
This section contains the results of statistical analysis of the map.

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.

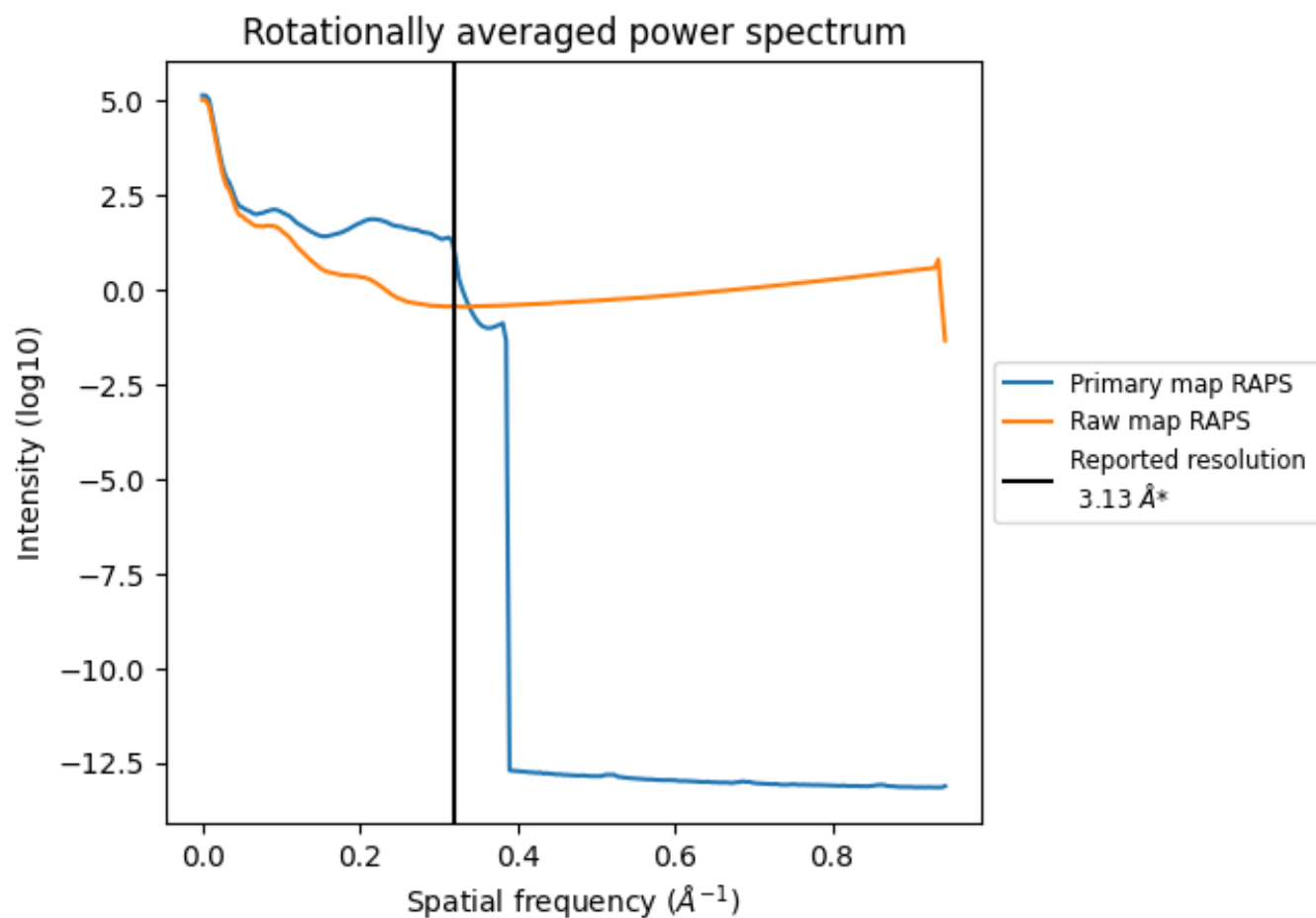
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 38 nm³; this corresponds to an approximate mass of 34 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 ⓘ

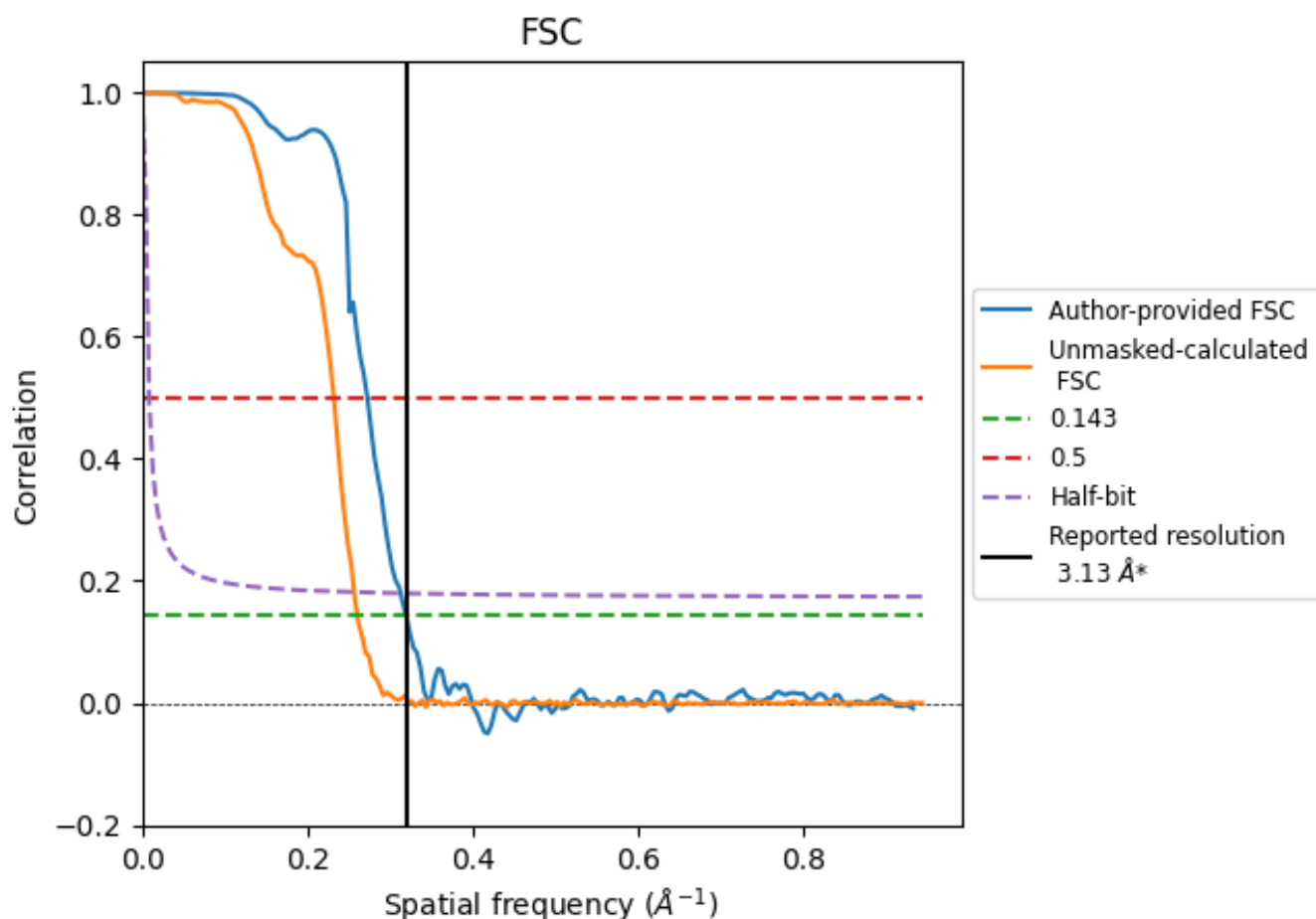


*Reported resolution corresponds to spatial frequency of 0.319 Å⁻¹

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 $0.319 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
Author-provided FSC curve	3.13	3.67	3.20
Unmasked-calculated*	3.84	4.31	3.90

*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 3.84 differs from the reported value 3.13 by more than 10 %

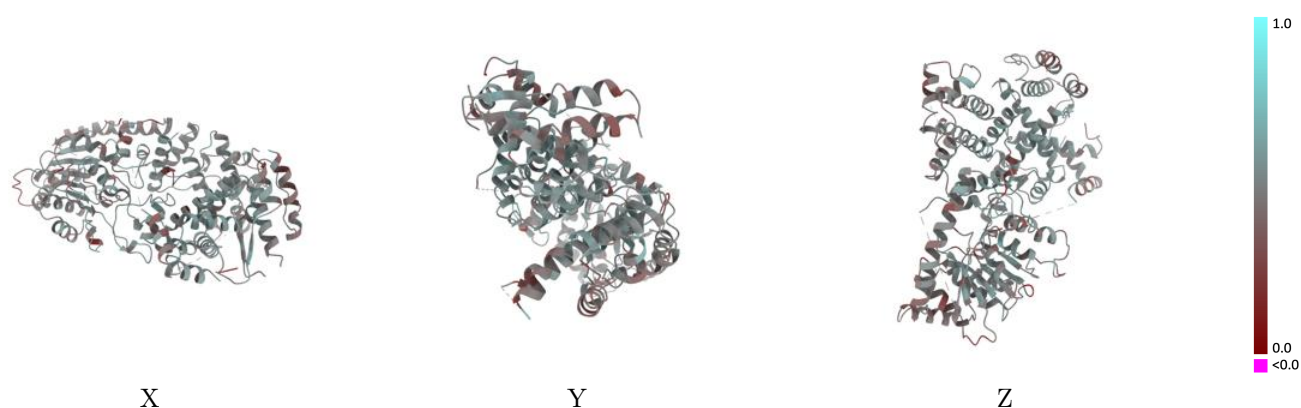
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37958 and PDB model 8YXL. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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



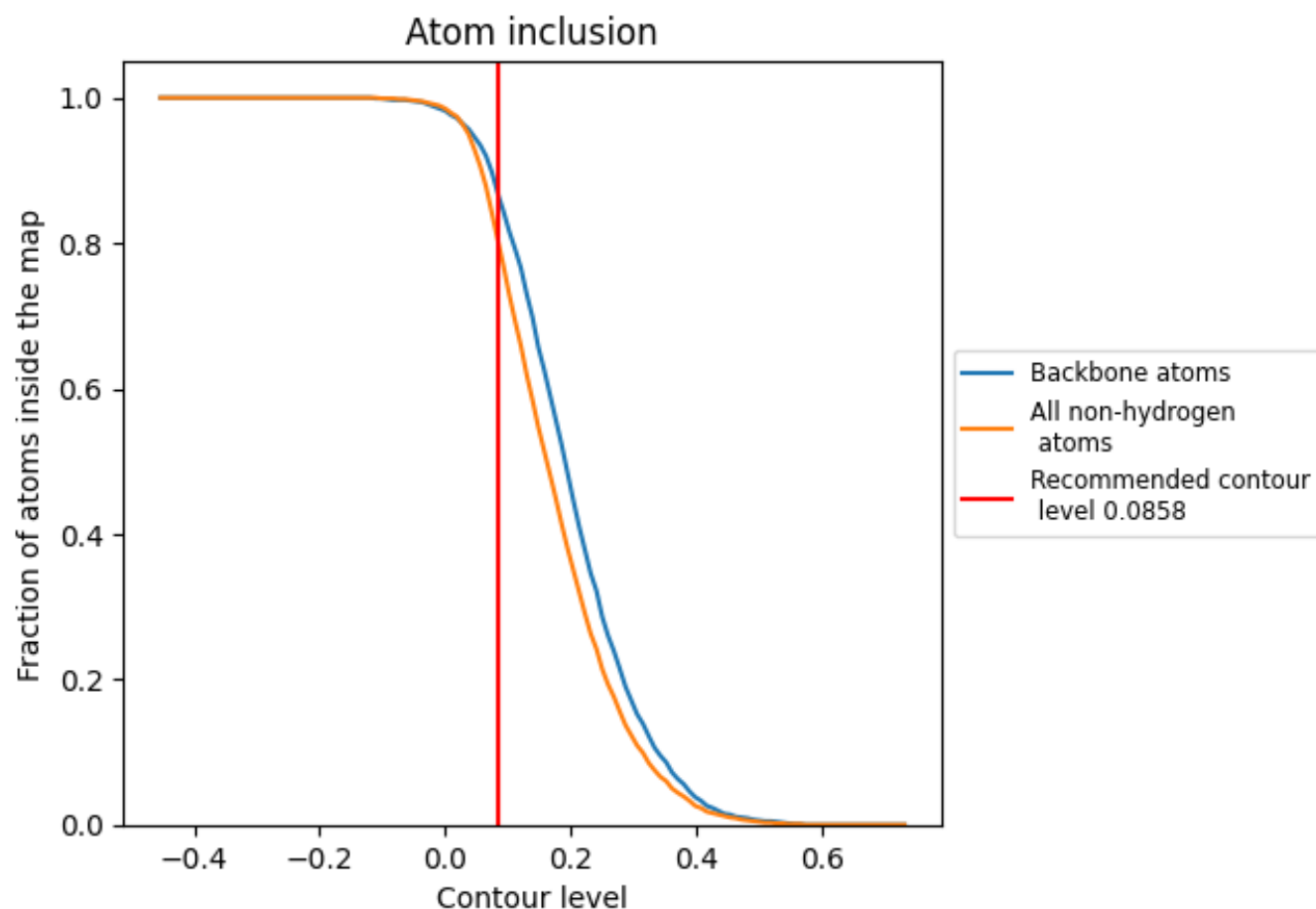
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0858).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.0858) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7970	0.4840
A	0.7970	0.4840

