



Full wwPDB EM Validation 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 Full wwPDB EM Validation 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

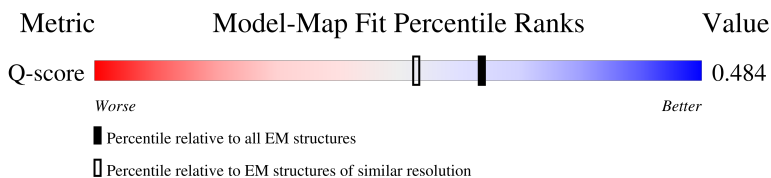
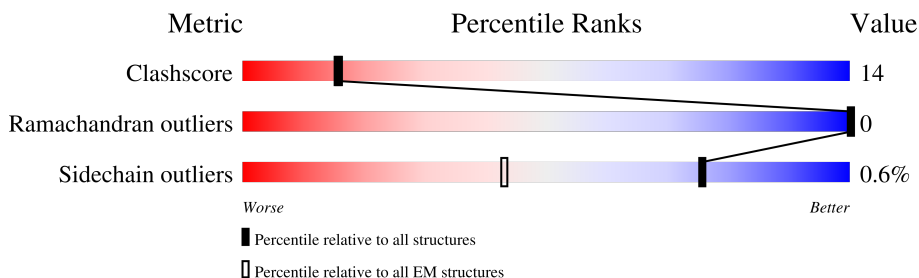
1 Overall quality at a glance

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](#)

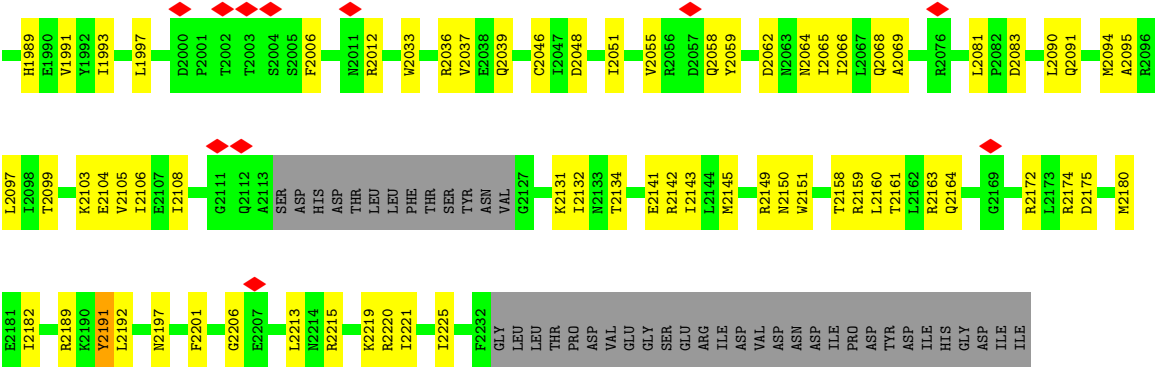
There is only 1 type of molecule in this entry. The entry contains 5588 atoms, of which 0 are hydrogens and 0 are deuteriums.

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		

C1911	A1809	L1736	E1657	G1538	I1443	VAL	ASP	PHE	THR	ILE	GLN	LYS	ASP	MET	ARG
A1912	H1810	L1740	TYR	T1542	P1444	HIS	THR	LEU	CYS	ARG	GLN	HIS	PRO	THR	VAL
L1913	L1811	F1741	VAL	T1543	L1449	ILE	GLU	GLY	ILE	ILE	TYR	GLY	LEU	ILE	PHE
V1914	Y1812	F1742	GLU	S1544	T1450	ASN	TRP	TRP	ILE	ALA	ASP	THR	ALA	GLY	LYS
H1915	A1814	L1743	TYR	R1547	Q1453	CYS	GLN	GLN	ARG	ASP	THR	MET	ILE	CYS	GLY
V1916	E1815	M1744	ILE	R1550	M1454	VAL	ASP	ASP	LEU	VAL	THR	GLU	ALA	TYR	ARG
G1920	A1819	L1745	Q1663	R1558	V1455	ASN	GLN	GLN	ARG	ASP	THR	GLU	VAL	TYR	ILE
VAL	S1820	LEU	E1665	R1562	T1458	PRO	LEU	LEU	PRO	ASP	ASP	ASP	VAL	ASP	THR
PRO	M1821	ASP	I1669	S1563	T1459	ILE	ALA	ALA	LYS	PRO	PRO	ASN	ARG	PRO	ALA
SER	S1822	ALA	R1670	S1564	GLY	LEU	LEU	LEU	LEU	ASP	ASP	THR	THR	GLN	PRO
ASN	L1823	SER	R1671	H1565	LEU	LEU	LEU	LEU	LEU	ASP	ASP	THR	THR	GLN	LYS
SER	T1826	SER	M1672	H1571	ASP	GLP	VAL	VAL	LEU	VAL	VAL	VAL	VAL	LEU	ASN
MET	F1827	GLU	I1673	T1572	ALA	THR	ALA	ALA	ASP	THR	THR	GLY	GLY	GLY	GLY
E1929	L1828	LYS	I1674	K1573	THR	LEU	LEU	LEU	ILE	ASP	LEU	VAL	VAL	VAL	GLY
E1930	TYR	TYR	I1678	K1574	SER	ILE	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY
R1931	T1833	SER	T1679	L1578	ILE	ASN	THR	THR	VAL	ILE	ASN	GLY	GLY	GLY	GLY
A1932	W1834	LEU	L1685	A1578	VAL	VAL	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
Q1933	P1845	PRO	TYR	I1598	ASP	ALA	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
H1934	P1846	SER	PHE	P1601	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
V1935	Q1847	LEU	L1688	S1604	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
A1936	R1848	LEU	S1688	R1690	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
L1937	N1849	MET	R1690	T1604	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
L1938	THR	THR	L1696	GLN	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
I1939	P1854	ALA	K1691	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
T1940	T1855	GLU	L1692	LEU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
V1941	Q1856	ASN	L1693	THR	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
V1942	F1857	MET	L1696	GLN	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
V1943	E1858	ASP	I1696	LEU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
L1944	I1859	ASN	E1700	LEU	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
K1945	S1860	ASN	W1711	LEU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
L1949	W1861	PHE	S1772	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
L1950	P1862	GLU	Q1773	D1610	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
I1951	Y1863	THR	P1774	R1611	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L1952	Y1866	GLY	P1775	N1614	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
E1957	I1866	GLY	L1776	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
H1960	I1870	TYR	H1777	R1618	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
R1961	N1874	LEU	H1778	K1619	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
F1962	G1875	GLU	V1779	L1620	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
S1963	I1876	PRO	R1781	S1621	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
F1964	V1877	ILE	L1785	L1622	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
L1965	Q1878	LEU	L1785	L1623	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
L1966	Q1878	MET	L1785	A1624	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
T1967	L1883	SER	W1790	I1625	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
V1968	L1883	LYS	I1794	P1633	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L1969	D1889	ILE	S1795	V1636	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
W1970	L1893	PHE	V1796	P1641	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q1971	L1893	ASN	L1797	P1644	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
F1972	V1899	LEU	T1800	K1644	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
F1973	V1899	SER	T1800	A1647	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
L1979	I1902	SER	M1803	T1650	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
R1980	V1906	GLU	K1804	H1651	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
P1986		ALA	I1805		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
		SER													



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.

All (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
1:A:1502:LEU:HB3	1:A:1622:LEU:HD11	1.69	0.73
1:A:1558:ILE:HD12	1:A:1574:LEU:HD22	1.70	0.73
1:A:2105:VAL:HG13	1:A:2132:ILE:HD12	1.70	0.72
1:A:1810:HIS:HB2	1:A:1833:ILE:HD13	1.74	0.68
1:A:1902:ILE:O	1:A:1906:VAL:HG22	1.96	0.66
1:A:1811:LEU:HB3	1:A:1914:VAL:HG22	1.77	0.66
1:A:2158:THR:HA	1:A:2161:THR:HG22	1.79	0.65
1:A:2104:GLU:O	1:A:2108:ILE:HG12	1.99	0.63
1:A:1550:ARG:HH22	1:A:1858:ILE:HD12	1.64	0.62
1:A:1866:ILE:HD11	1:A:1878:GLN:HB2	1.81	0.62
1:A:1520:ILE:HD11	1:A:1625:ILE:HG22	1.80	0.62
1:A:1777:HIS:HD2	1:A:1781:ARG:HH21	1.48	0.62
1:A:1785:LEU:H	1:A:1785:LEU:HD23	1.64	0.62
1:A:1790:TRP:HB2	1:A:1823:LEU:HD13	1.83	0.61
1:A:1531:ILE:HD11	1:A:1536:ILE:HD12	1.83	0.61
1:A:2172:ARG:HD2	1:A:2174:ARG:HH22	1.66	0.61
1:A:1813:LEU:HD23	1:A:1916:VAL:HG22	1.83	0.60
1:A:1858:ILE:HA	1:A:1863:TYR:HD2	1.66	0.60
1:A:1481:TRP:H	1:A:1542:THR:HG22	1.66	0.60
1:A:2048:ASP:HA	1:A:2163:ARG:HH12	1.67	0.59
1:A:1870:ILE:H	1:A:1870:ILE:HD12	1.67	0.58
1:A:2180:MET:N	1:A:2180:MET:SD	2.74	0.58
1:A:1790:TRP:O	1:A:1794:ILE:HG12	2.03	0.58
1:A:1558:ILE:HD11	1:A:1578:ALA:HB2	1.85	0.57
1:A:2095:ALA:HA	1:A:2182:ILE:HD13	1.86	0.57
1:A:1663:GLN:HG2	1:A:1664:ILE:HG23	1.86	0.57
1:A:1790:TRP:CD1	1:A:2066:ILE:HD12	2.39	0.57
1:A:2142:ARG:HA	1:A:2145:MET:HE2	1.86	0.57
1:A:1670:ARG:O	1:A:1674:ILE:HG12	2.05	0.57
1:A:2160:LEU:O	1:A:2164:GLN:HG2	2.05	0.57
1:A:1936:ALA:O	1:A:1940:THR:HG23	2.05	0.56
1:A:1439:LEU:HA	1:A:1442:LYS:HD2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2051:ILE:HG21	1:A:2163:ARG:HD2	1.88	0.56
1:A:1822:SER:O	1:A:1826:THR:HG23	2.06	0.56
1:A:1915:HIS:HA	1:A:1951:ILE:HG23	1.87	0.56
1:A:1484:GLU:HG3	1:A:1693:LEU:HD22	1.87	0.56
1:A:1571:TYR:HA	1:A:1574:LEU:HB2	1.88	0.56
1:A:2090:LEU:HD11	1:A:2094:MET:CE	2.36	0.55
1:A:1598:ILE:HD11	1:A:1619:LYS:HD2	1.88	0.55
1:A:1937:LEU:HD22	1:A:1969:LEU:HD21	1.87	0.55
1:A:1486:CYS:SG	1:A:1547:ARG:NH2	2.79	0.55
1:A:2215:ARG:HD3	1:A:2219:LYS:HZ2	1.72	0.55
1:A:2215:ARG:O	1:A:2219:LYS:HG3	2.08	0.54
1:A:2083:ASP:OD1	1:A:2083:ASP:N	2.36	0.54
1:A:1826:THR:HG21	1:A:2069:ALA:HA	1.89	0.54
1:A:1664:ILE:HG13	1:A:1665:GLU:HG3	1.90	0.54
1:A:1775:PRO:HB2	1:A:1778:HIS:HD2	1.72	0.53
1:A:1620:LEU:HD22	1:A:1644:LYS:HE2	1.89	0.53
1:A:1685:LEU:O	1:A:1690:ARG:NH1	2.42	0.53
1:A:1516:GLY:O	1:A:1520:ILE:HD12	2.08	0.52
1:A:1815:GLU:OE2	1:A:1820:SER:HB2	2.09	0.52
1:A:1854:PRO:HG2	1:A:1857:PHE:HB3	1.91	0.52
1:A:1913:LEU:HD13	1:A:1949:LEU:HD23	1.92	0.52
1:A:1796:VAL:HG11	1:A:1951:ILE:HD12	1.91	0.52
1:A:1678:LEU:HD13	1:A:1679:THR:N	2.24	0.52
1:A:1790:TRP:CE3	1:A:1819:ALA:HB1	2.45	0.52
1:A:2094:MET:HG2	1:A:2143:ILE:HD12	1.92	0.52
1:A:1952:LEU:HB3	1:A:1993:ILE:HB	1.91	0.51
1:A:2090:LEU:HD11	1:A:2094:MET:HE3	1.91	0.51
1:A:2141:GLU:O	1:A:2145:MET:HG3	2.10	0.51
1:A:1455:VAL:HG21	1:A:1500:ALA:HB3	1.93	0.51
1:A:2090:LEU:CD1	1:A:2094:MET:HE3	2.41	0.51
1:A:2099:THR:HG22	1:A:2192:LEU:CD1	2.41	0.51
1:A:1678:LEU:HD13	1:A:1679:THR:H	1.76	0.50
1:A:1823:LEU:HD11	1:A:2065:ILE:HG22	1.93	0.50
1:A:1609:SER:OG	1:A:1610:ASP:N	2.42	0.49
1:A:1742:ILE:HG22	1:A:1979:LEU:HB2	1.93	0.49
1:A:1809:ALA:HB3	1:A:1911:CYS:HB3	1.93	0.49
1:A:2213:LEU:HD13	1:A:2221:ILE:HD12	1.95	0.48
1:A:1563:SER:OG	1:A:1565:HIS:O	2.31	0.48
1:A:1805:ILE:HD11	1:A:1828:LEU:HB3	1.96	0.47
1:A:1449:LEU:HD12	1:A:1685:LEU:HB3	1.96	0.47
1:A:1834:TRP:CG	1:A:1906:VAL:HG12	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1800:ILE:HA	1:A:1803:MET:HE3	1.96	0.46
1:A:2192:LEU:H	1:A:2197:ASN:ND2	2.12	0.46
1:A:1536:ILE:HG21	1:A:1572:THR:HG23	1.97	0.46
1:A:1538:GLY:O	1:A:1542:THR:HG23	2.15	0.46
1:A:2151:TRP:CD2	1:A:2225:ILE:HD12	2.51	0.46
1:A:1647:ALA:HA	1:A:1650:THR:HG22	1.97	0.46
1:A:1899:VAL:HG21	1:A:1935:HIS:CD2	2.51	0.46
1:A:1692:LEU:O	1:A:1696:ILE:HG13	2.16	0.45
1:A:2055:VAL:HB	1:A:2058:GLN:HE21	1.81	0.45
1:A:1744:ASN:N	1:A:1744:ASN:OD1	2.49	0.45
1:A:1779:VAL:HG21	1:A:2051:ILE:HD11	1.98	0.45
1:A:1513:ARG:HH21	1:A:1633:PRO:HG2	1.82	0.45
1:A:1962:PHE:HZ	1:A:1991:VAL:HG11	1.81	0.45
1:A:1449:LEU:O	1:A:1453:GLN:HG3	2.17	0.45
1:A:2033:TRP:O	1:A:2037:VAL:HG22	2.17	0.45
1:A:2192:LEU:H	1:A:2197:ASN:HD22	1.64	0.45
1:A:2097:LEU:HD12	1:A:2143:ILE:HD11	1.98	0.45
1:A:1544:SER:HB2	1:A:1848:ARG:HH11	1.82	0.45
1:A:1847:GLN:O	1:A:1848:ARG:NE	2.49	0.45
1:A:2172:ARG:HB2	1:A:2175:ASP:OD2	2.17	0.45
1:A:1797:LEU:HD13	1:A:1800:ILE:HD11	1.98	0.45
1:A:2174:ARG:HD3	1:A:2206:GLY:HA2	1.97	0.45
1:A:1856:GLN:O	1:A:1860:SER:OG	2.34	0.44
1:A:1937:LEU:O	1:A:1941:VAL:HG23	2.17	0.44
1:A:2189:ARG:HG3	1:A:2191:TYR:O	2.17	0.44
1:A:1935:HIS:HA	1:A:1938:LEU:CD2	2.47	0.44
1:A:1690:ARG:HD3	1:A:1690:ARG:H	1.82	0.44
1:A:1601:PRO:O	1:A:1611:ARG:NH2	2.48	0.44
1:A:1558:ILE:HG23	1:A:1574:LEU:HD22	2.00	0.44
1:A:2182:ILE:HG21	1:A:2201:PHE:HZ	1.83	0.44
1:A:2046:CYS:HG	1:A:2059:TYR:HH	1.60	0.44
1:A:1964:PHE:O	1:A:1968:VAL:HG12	2.18	0.43
1:A:2182:ILE:HG21	1:A:2201:PHE:CZ	2.53	0.43
1:A:2191:TYR:O	1:A:2192:LEU:HB2	2.17	0.43
1:A:1960:ASN:N	1:A:1960:ASN:OD1	2.51	0.43
1:A:1945:LYS:HB2	1:A:1945:LYS:HE2	1.68	0.43
1:A:2062:ASP:O	1:A:2066:ILE:HG12	2.18	0.43
1:A:1443:ILE:HG23	1:A:1488:THR:HA	2.01	0.43
1:A:1774:PRO:HA	1:A:1775:PRO:HD3	1.88	0.43
1:A:1614:ASN:O	1:A:1618:ARG:HG3	2.19	0.43
1:A:1562:ASN:HD21	1:A:2220:ARG:HG2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1529:ARG:NH1	1:A:1573:LYS:HZ1	2.07	0.42
1:A:2064:ASN:O	1:A:2068:GLN:HG3	2.18	0.42
1:A:2090:LEU:O	1:A:2091:GLN:C	2.61	0.42
1:A:1857:PHE:HE1	1:A:1862:PRO:HB2	1.84	0.42
1:A:1931:ARG:HD3	1:A:1935:HIS:HE1	1.84	0.42
1:A:1972:PHE:HD1	1:A:1973:PHE:CD1	2.37	0.42
1:A:2103:LYS:HE3	1:A:2103:LYS:HB2	1.81	0.42
1:A:2221:ILE:O	1:A:2225:ILE:HG12	2.18	0.42
1:A:1502:LEU:HD23	1:A:1502:LEU:HA	1.87	0.42
1:A:1669:ILE:O	1:A:1672:MET:HG2	2.19	0.42
1:A:1796:VAL:O	1:A:1800:ILE:HG12	2.20	0.42
1:A:1598:ILE:HB	1:A:1678:LEU:HD22	2.02	0.42
1:A:1670:ARG:HA	1:A:1673:ILE:HD12	2.00	0.42
1:A:1931:ARG:O	1:A:1935:HIS:ND1	2.53	0.42
1:A:1458:ILE:HG13	1:A:1459:THR:N	2.34	0.42
1:A:1641:PRO:O	1:A:1644:LYS:HG2	2.19	0.42
1:A:1933:GLN:HE21	1:A:1965:LEU:HD11	1.84	0.42
1:A:1939:ILE:O	1:A:1943:VAL:HG22	2.19	0.42
1:A:1485:CYS:HA	1:A:1488:THR:HG22	2.02	0.42
1:A:2081:LEU:HB2	1:A:2149:ARG:HG2	2.02	0.42
1:A:1450:THR:O	1:A:1454:MET:HG3	2.20	0.42
1:A:1933:GLN:O	1:A:1937:LEU:HG	2.19	0.42
1:A:1934:VAL:HG23	1:A:2006:PHE:HE2	1.84	0.41
1:A:2106:ILE:HG13	1:A:2191:TYR:CE1	2.55	0.41
1:A:2131:LYS:HA	1:A:2134:THR:HG22	2.02	0.41
1:A:1443:ILE:HB	1:A:1444:PRO:HD3	2.02	0.41
1:A:1966:LEU:HD23	1:A:1966:LEU:HA	1.84	0.41
1:A:1443:ILE:HG12	1:A:1696:ILE:HD13	2.01	0.41
1:A:1434:LEU:N	1:A:1436:GLN:OE1	2.53	0.41
1:A:1527:THR:O	1:A:1531:ILE:HG23	2.20	0.41
1:A:1573:LYS:HA	1:A:1573:LYS:HD3	1.93	0.41
1:A:1944:LEU:HB2	1:A:1997:LEU:HD22	2.03	0.41
1:A:1574:LEU:HA	1:A:1574:LEU:HD23	1.79	0.40
1:A:1971:GLN:OE1	1:A:2012:ARG:HD3	2.21	0.40
1:A:1980:ARG:HG3	1:A:2039:GLN:HE22	1.87	0.40
1:A:2132:ILE:HD13	1:A:2132:ILE:HA	1.92	0.40
1:A:1883:LEU:HD13	1:A:1902:ILE:HG12	2.03	0.40
1:A:1986:PRO:C	1:A:2036:ARG:HH22	2.29	0.40
1:A:2151:TRP:CZ2	1:A:2159:ARG:HG3	2.56	0.40
1:A:1510:TYR:CA	1:A:1625:ILE:HD11	2.51	0.40
1:A:1529:ARG:HD3	1:A:1573:LYS:NZ	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1813:LEU:HD12	1:A:1893:LEU:HD21	2.03	0.40
1:A:2090:LEU:HG	1:A:2094:MET:HE3	2.04	0.40
1:A:1989:HIS:H	1:A:2036:ARG:HH21	1.69	0.40

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

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Mol	Chain	Res	Type
1	A	1855	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1554	ASN
1	A	1778	HIS
1	A	1933	GLN
1	A	2011	ASN
1	A	2039	GLN
1	A	2091	GLN
1	A	2150	ASN
1	A	2198	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.

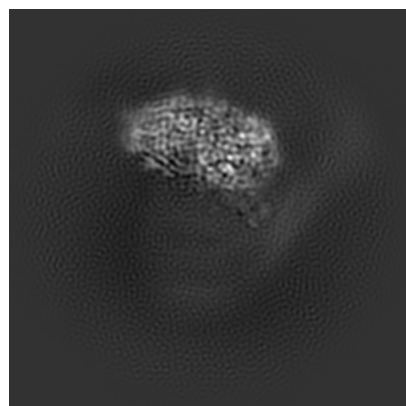
6 Map visualisation [i](#)

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.

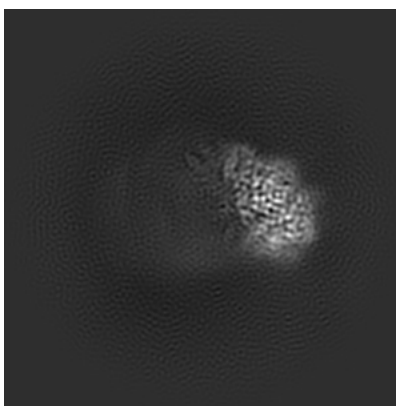
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

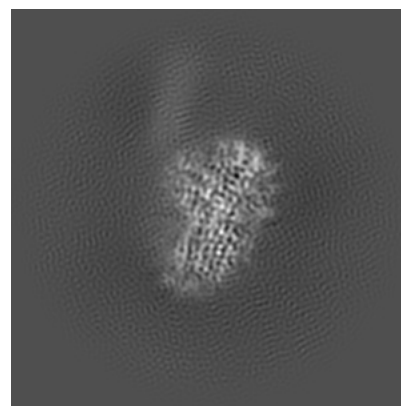
6.1.1 Primary map



X

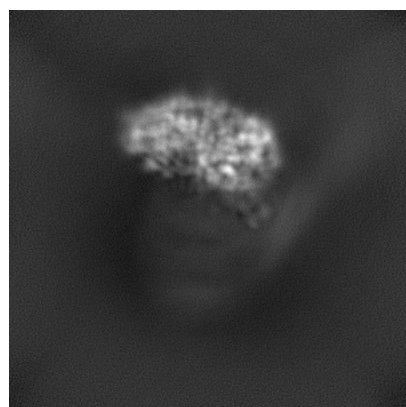


Y

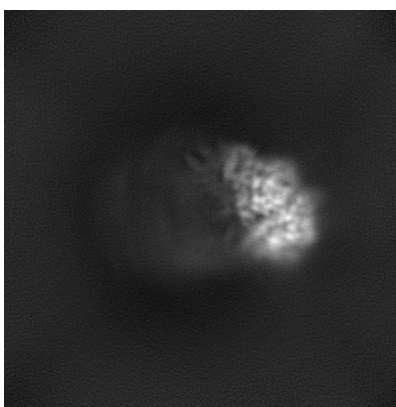


Z

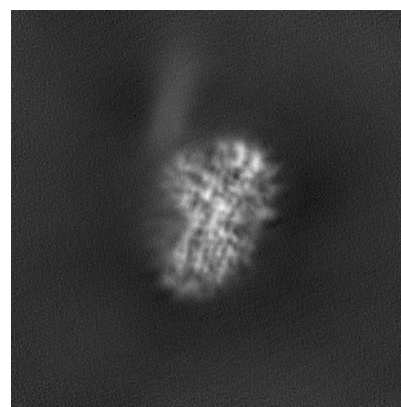
6.1.2 Raw map



X



Y

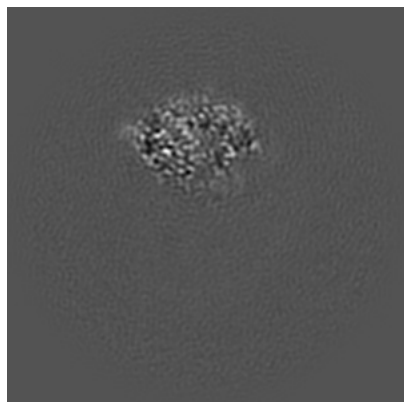


Z

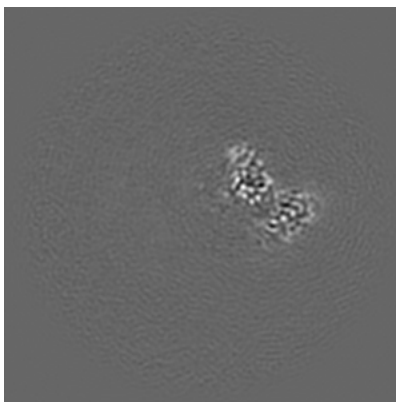
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

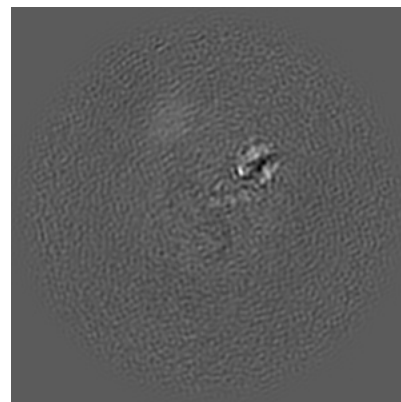
6.2.1 Primary map



X Index: 220

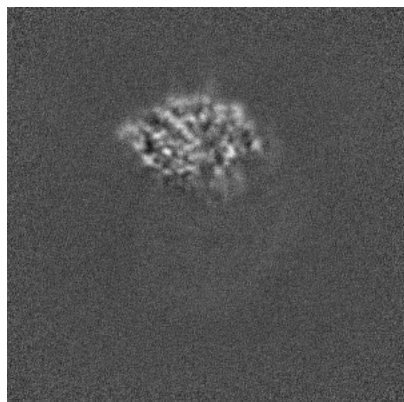


Y Index: 220

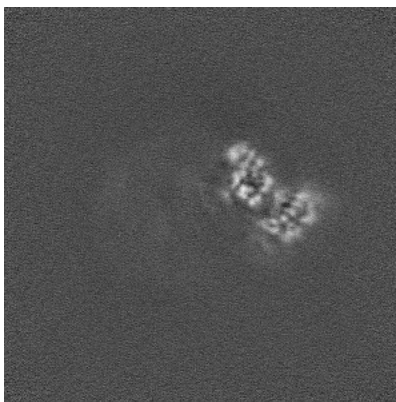


Z Index: 220

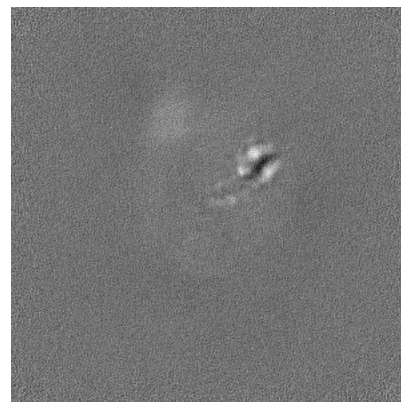
6.2.2 Raw map



X Index: 220



Y Index: 220

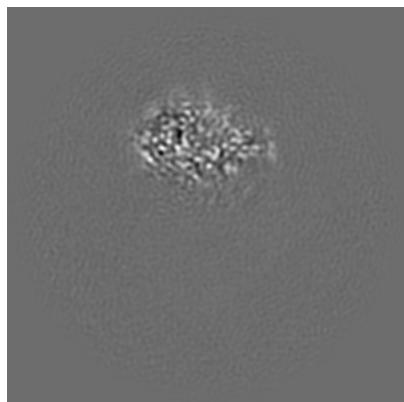


Z Index: 220

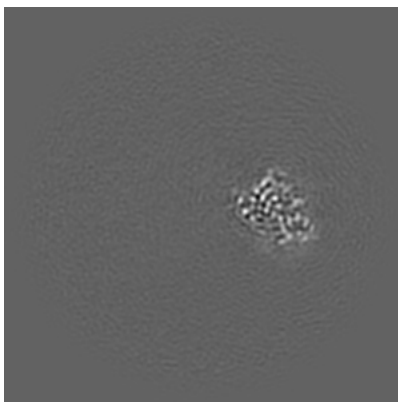
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

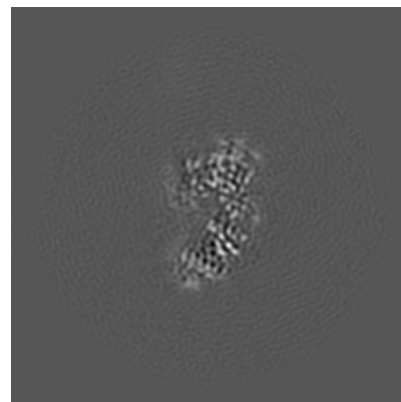
6.3.1 Primary map



X Index: 231

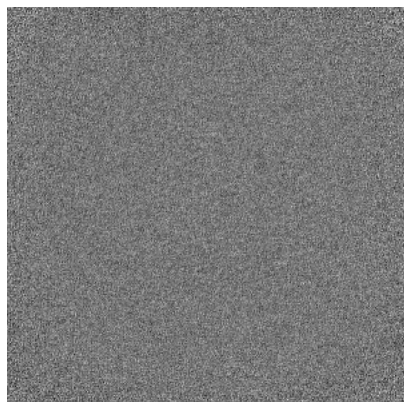


Y Index: 170

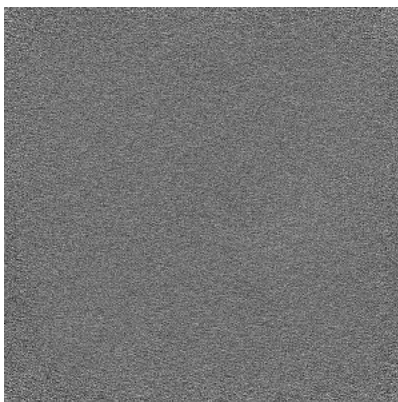


Z Index: 285

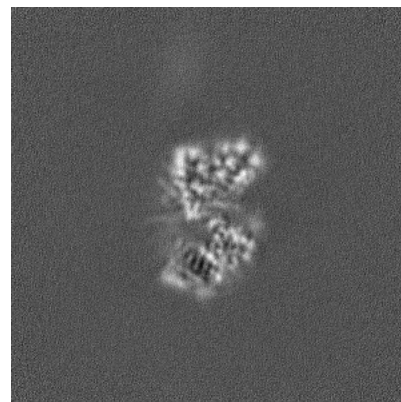
6.3.2 Raw map



X Index: 0



Y Index: 0

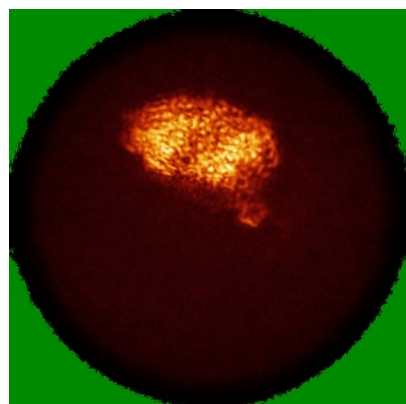


Z Index: 297

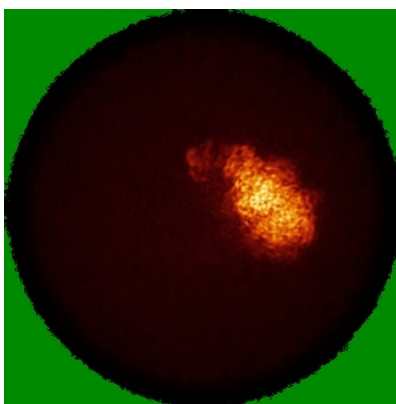
The images above show the largest variance slices of the map in three orthogonal directions.

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

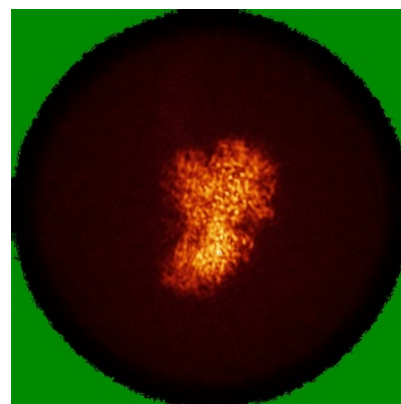
6.4.1 Primary map



X

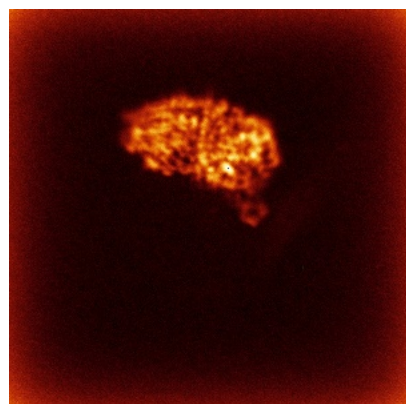


Y

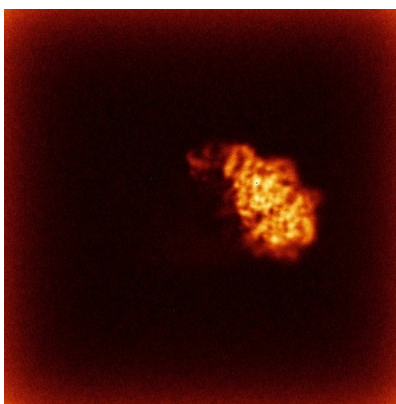


Z

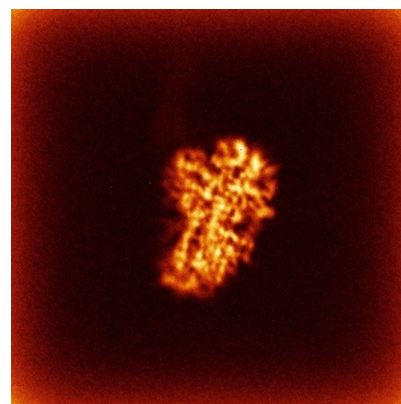
6.4.2 Raw map



X



Y

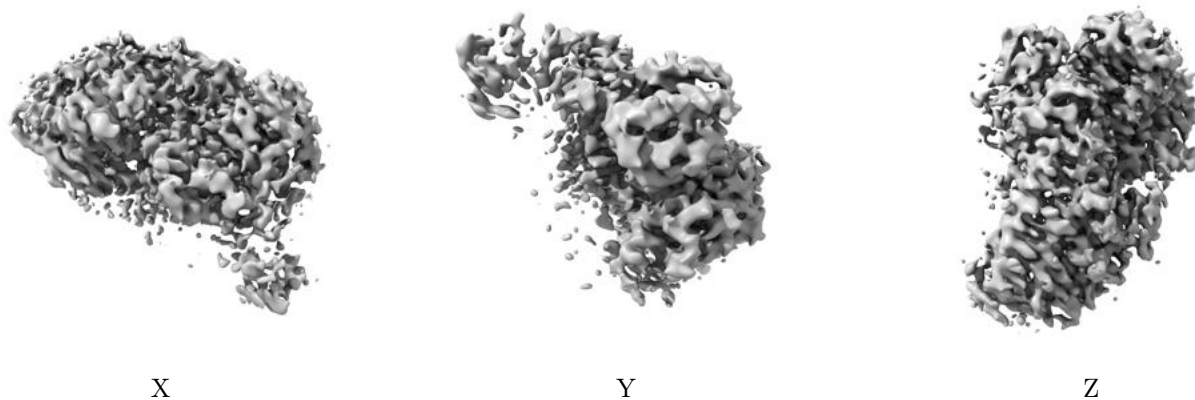


Z

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.

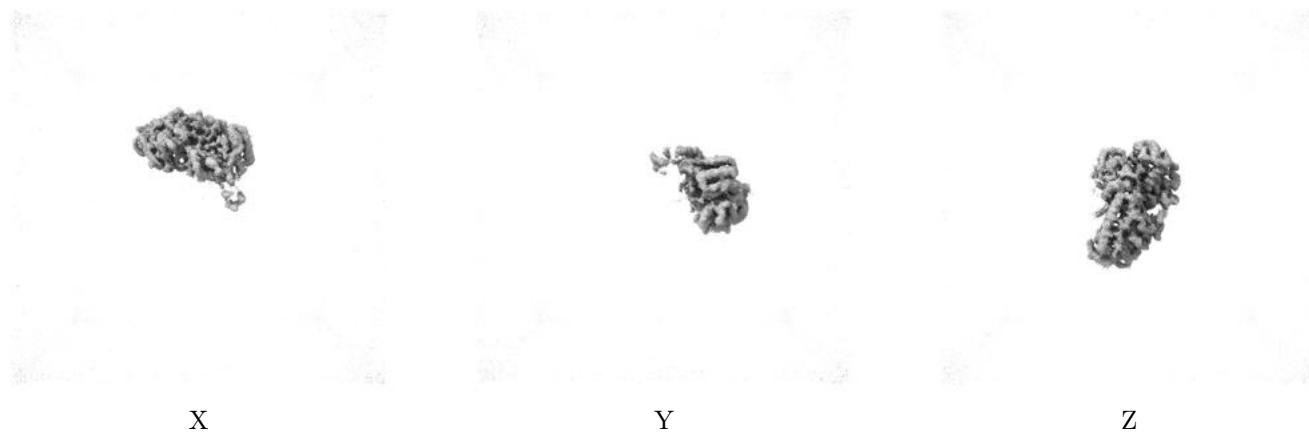
6.5 Orthogonal surface views [i](#)

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.

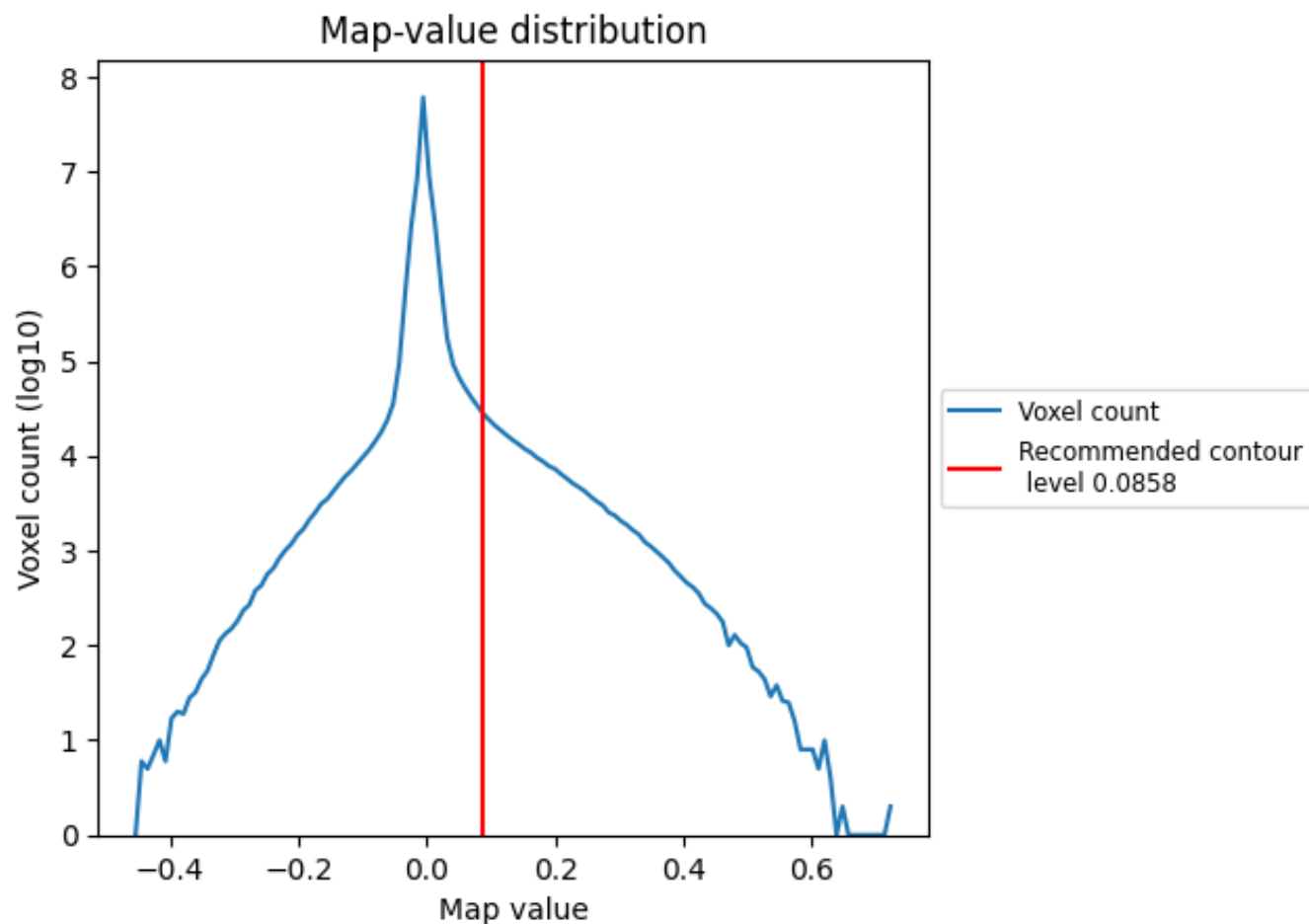
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

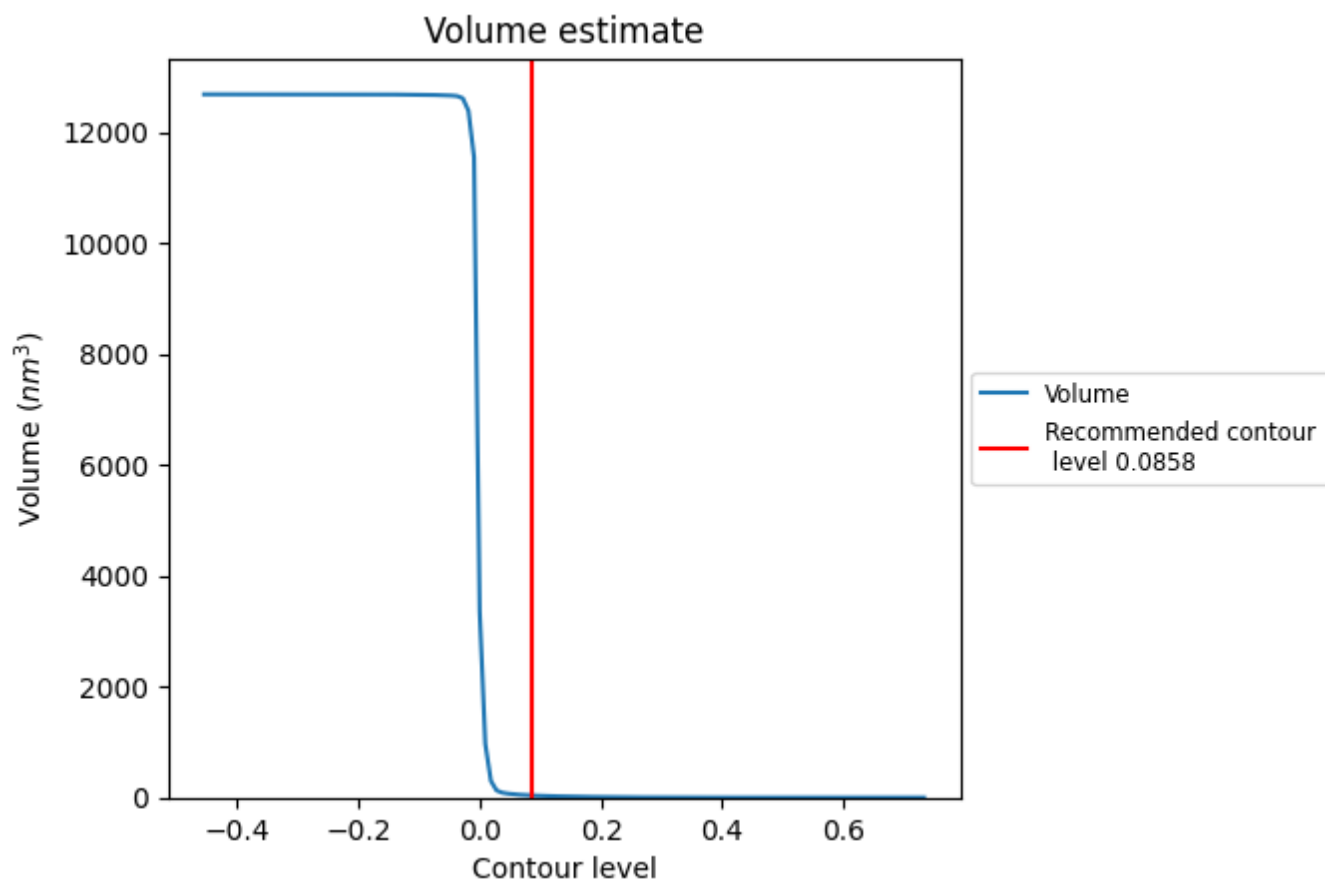
This section contains the results of statistical analysis of the map.

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.

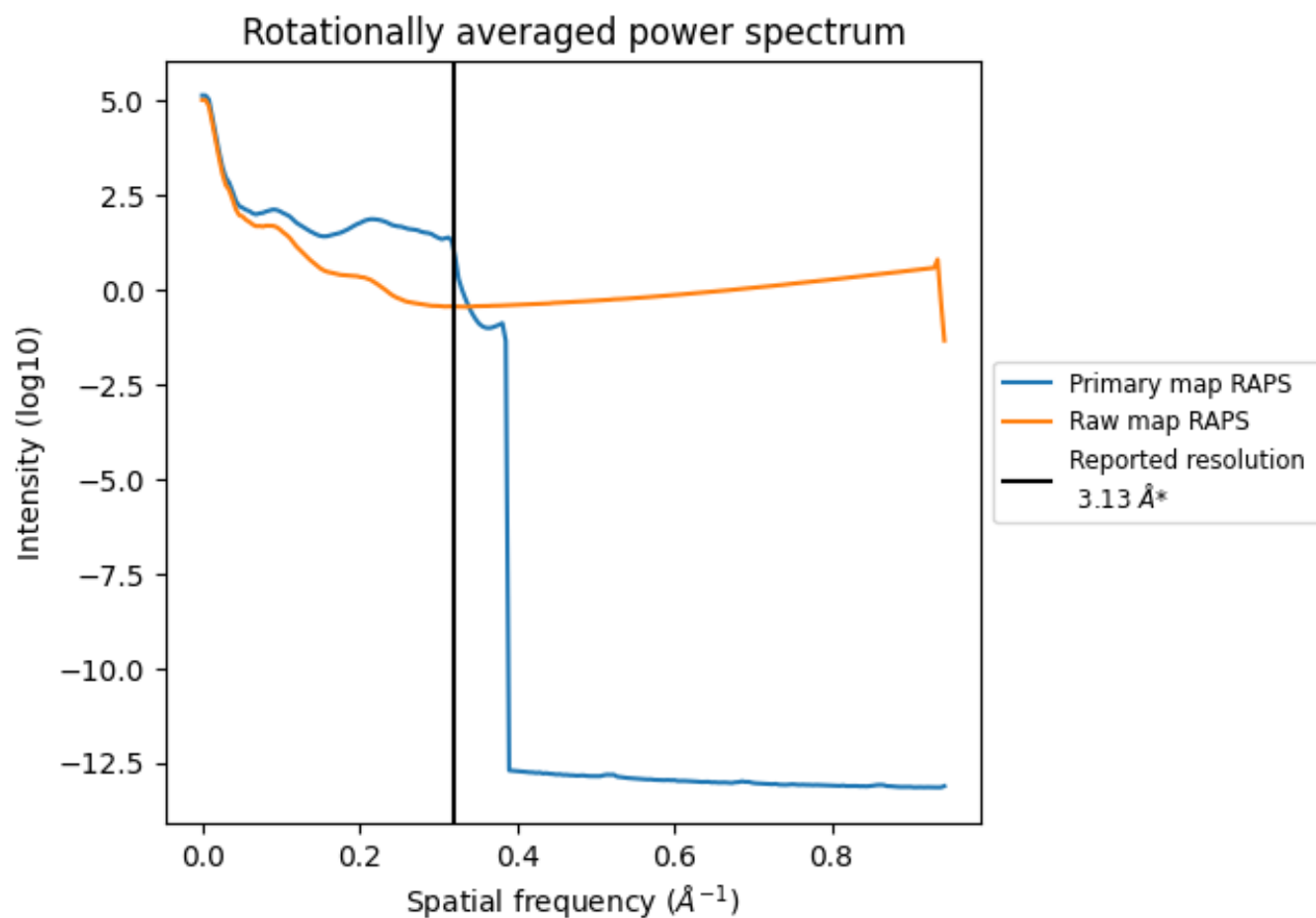
7.2 Volume estimate [i](#)



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 ⓘ

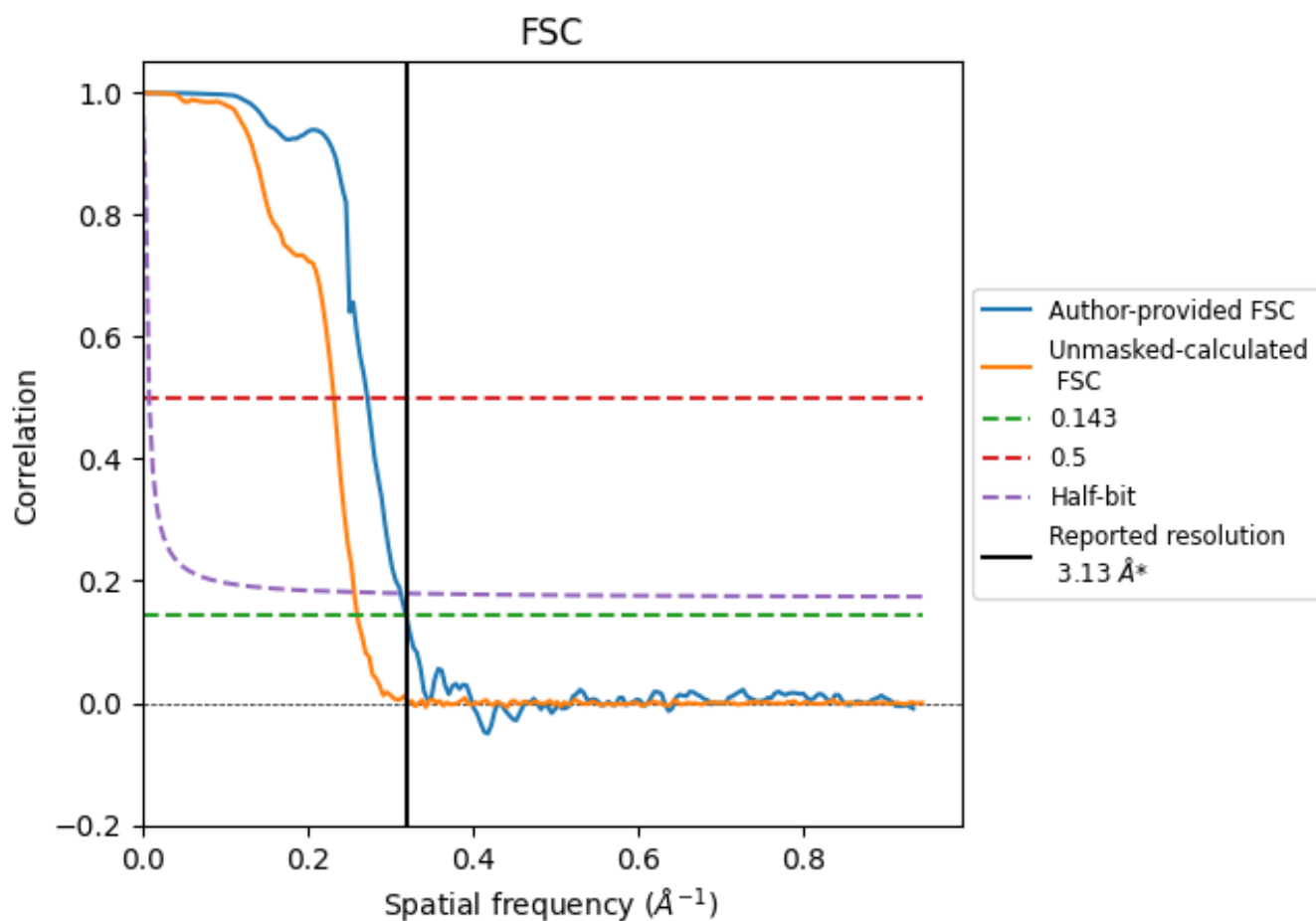


*Reported resolution corresponds to spatial frequency of 0.319 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
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 %

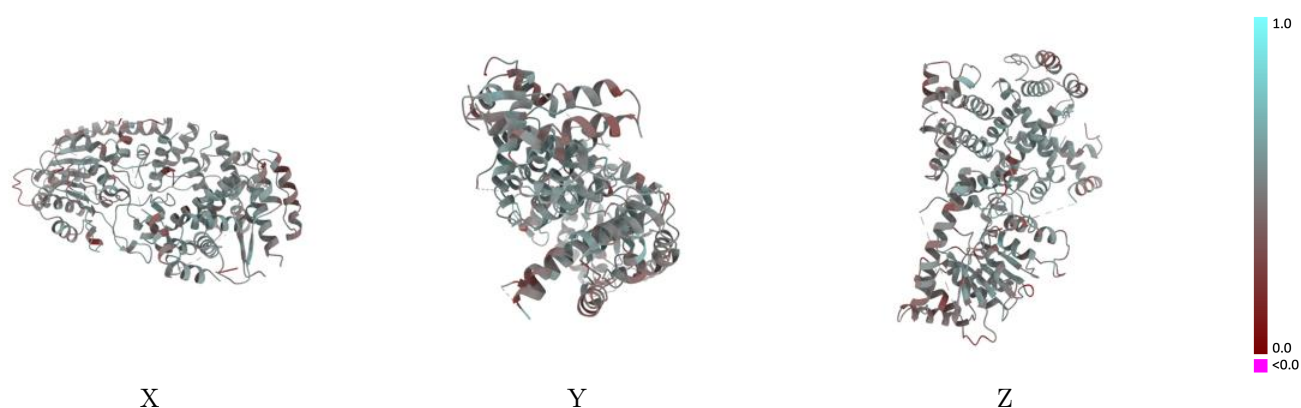
9 Map-model fit [i](#)

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](#)



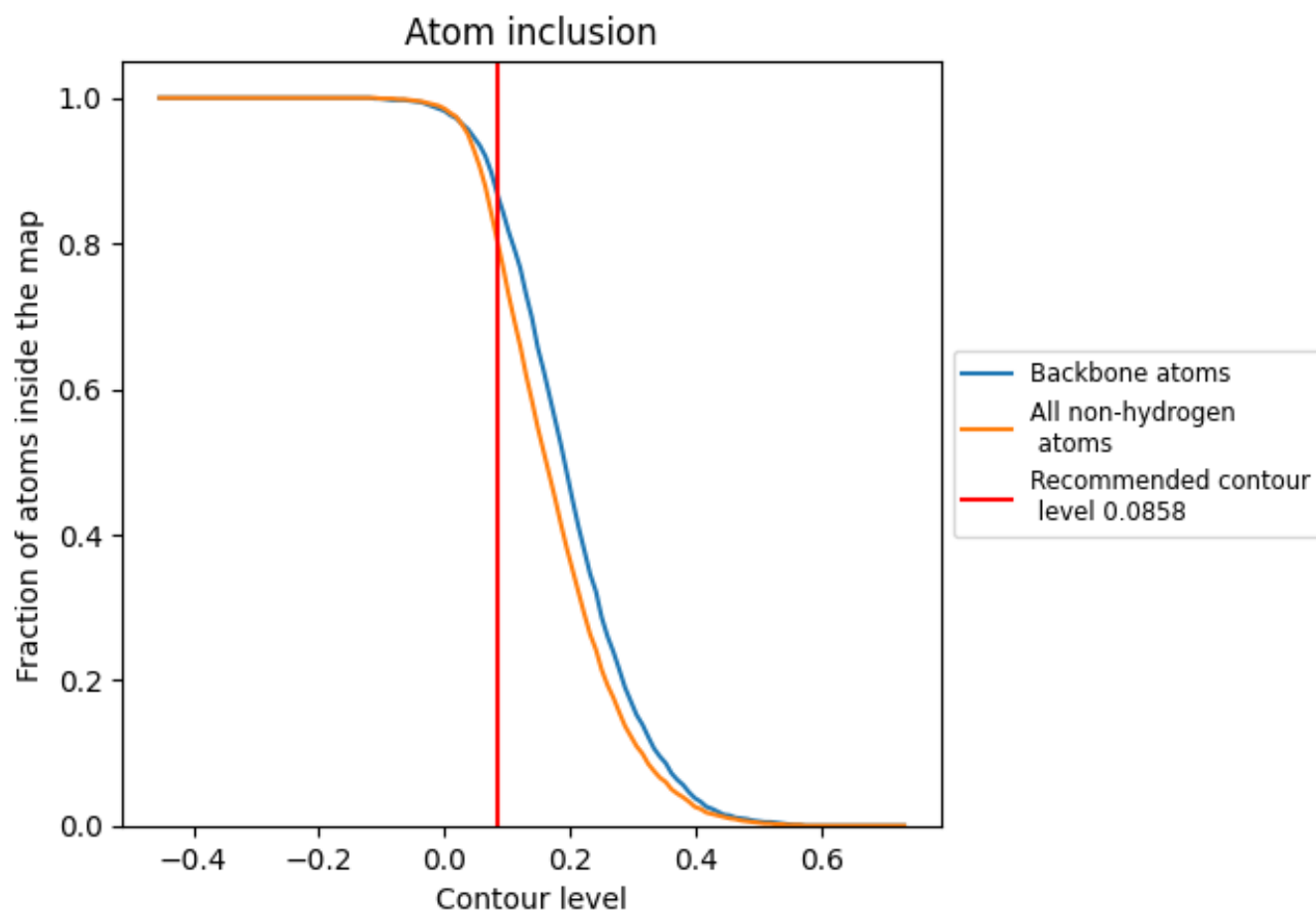
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

