



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 11:06 PM UTC

PDB ID : 7KVE / pdb_00007kve
EMDB ID : EMD-23048
Title : Cryo-EM structure of human Factor V at 3.3 Angstrom resolution
Authors : Ruben, E.A.; Di Cera, E.
Deposited on : 2020-11-27
Resolution : 3.30 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

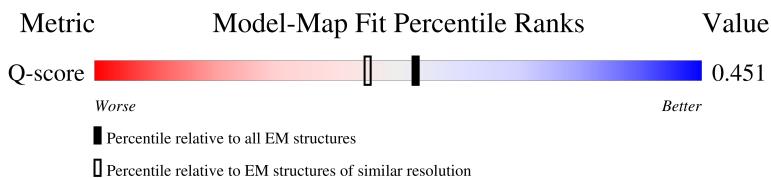
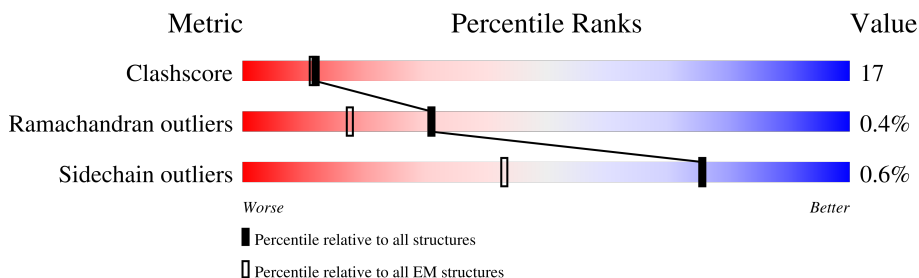
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	B	2196	40% 22% . 37%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 11142 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.

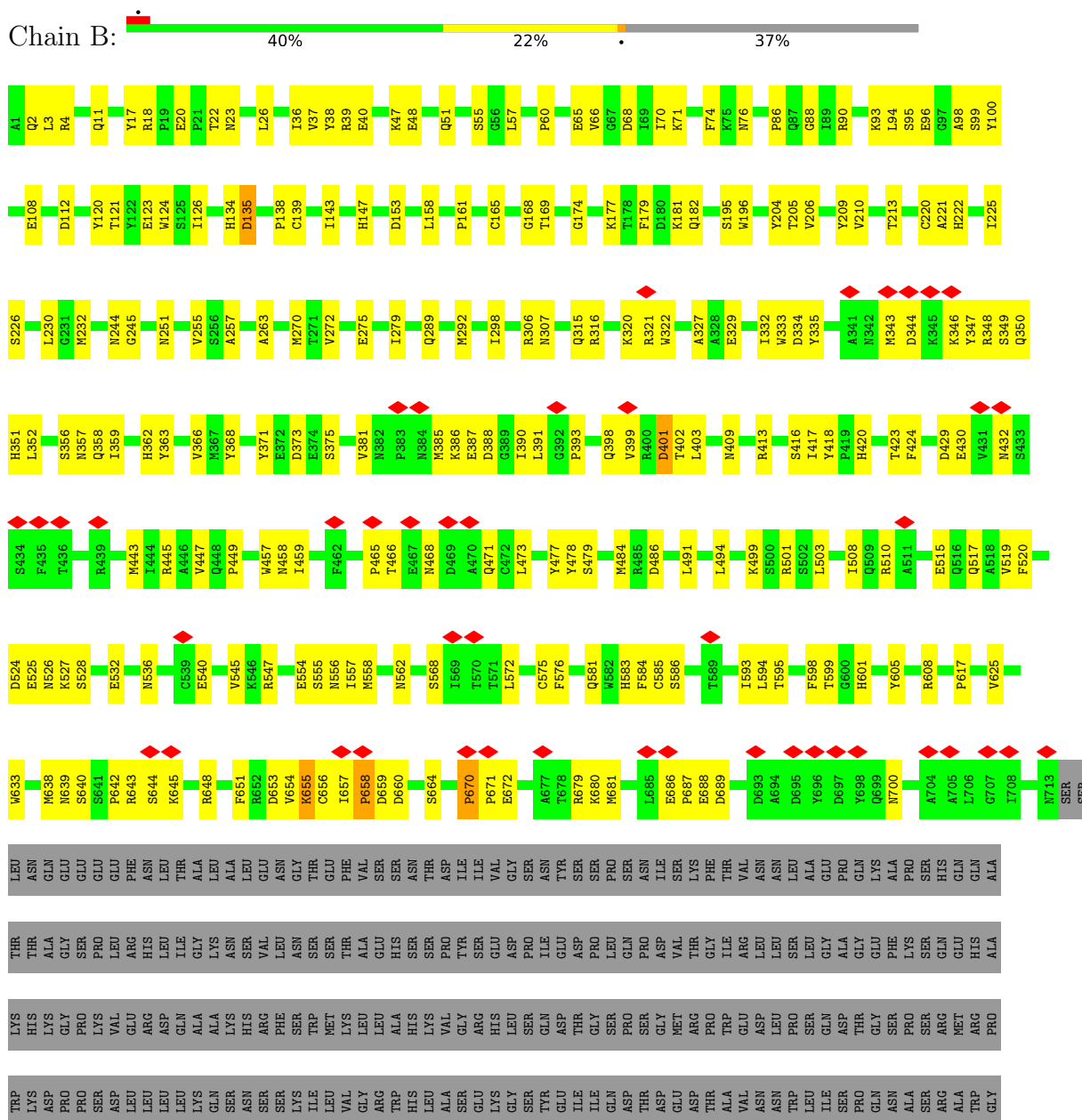
- Molecule 1 is a protein called Coagulation factor V.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1374	Total	C	N	O	S	0	0
			11142	7074	1905	2108	55		

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: Coagulation factor V



K2061	S2062	W2063	W2064	D2065	D2066	Y2067	P2070	F2071	R2074	A2077	N2082	A2083	W2084	Q2085	A2086	Z2087	N2088	Q2093	W2094	E2096	L2099	I2102	K2103	T2110	Q2111	G2112	C2113	K2114	E2119	M2120	Y2121	V2122	N2036	K2123	G2037	C2038	S2039	M2044	K2048	N2051	T2055	A2056	S2057	S2058	F2059	K2060					
Q1949	K1958	S1959	C1960	Y1961	T1962	T1963	Q1973	K1980	G1981	N1982	S1983	T1984	R1877	D1878	N1986	N1991	G1992	S1997	K2000	E2001	N2002	I2013	R2019	R2023	P2024	T2025	L2028	E2029	L2030	C2033	E2034	V2035	N2036	G2037	C2038	S2039	M2044	K2048	N2051	T2055	A2056	S2057	S2058	F2059	K2060						
F1841	K1842	M1846	K1847	A1848	P1851	G1867	T1870	I1874	M1875	D1876	R1877	D1878	C1879	R1880	L1885	S1886	T1887	G1888	I1889	Q1894	A1897	S1898	E1899	F1900	L1901	G1902	Y1903	W1904	R1910	A1919	W1920	S1921	V1922	E1923	K1924	L1925	A1926	A1927	E1928	F1929	P1933	W1934	I1935	Q1936	V1937	D1938	M1939				
M1746	D1749	E1750	K1751	K1752	Y1756	E1757	R1761	F1777	N1781	Y1784	I1785	S1786	L1787	M1792	Y1793	E1794	Q1795	E1796	W1797	R1799	L1800	H1801	L1802	L1803	N1804	I1805	G1806	G1807	I1811	H1812	V1813	V1814	L1822	E1823	N1824	K1827	Q1828	H1829	Q1830	L1831	G1832	V1833	L1836	L1837	P1838	G1839	S1840				
K1656	P1663	E1664	W1665	F1666	K1667	E1668	D1669	N1670	P1674	S1677	Y1678	W1682	T1685	E1686	S1692	P1693	G1694	C1697	R1698	A1699	Y1703	S1704	A1705	V1706	W1707	P1708	H1713	P1719	L1720	L1721	I1722	K1725	L1728	H1729	A1730	M1733	M1734	P1735	D1737	W1738	R1739	E1740	L1743								
D1564	E1567	F1568	W1569	Q1570	R1571	E1572	T1573	D1574	I1575	E1576	D1577	S1578	D1579	P1582	E1583	D1584	T1585	T1586	V1590	D1597	F1600	T1601	Y1609	L1616	I1619	I1620	R1621	A1622	D1625	D1626	V1627	R1631	F1632	K1633	M1634	L1635	A1636	S1641	N1652	M1653	Y1654	Y1655	I1656	A1657	E1660						
GLU	ILE	ILE	PRO	LYS	GLU	GLU	VAL	GLN	SER	SER	GLU	ASP	TYR	VAL	VAL	PRO	TYR	ASP	GLY	PRO	TYR	THR	VAL	ARG	THR	SER	SER	ASP	ASP	P1536	D1537	N1538	I1539	A1540	Y1543	L1544	R1545	R1551	R1552	M1553	Y1554	Y1555	I1556	A1557	E1560						
PHE	TYR	PRO	SER	GLU	SER	GLN	GLN	SER	GLN	GLU	PHE	ASN	GLU	PHE	PRO	TYR	ASP	GLY	GLN	NET	PRO	SER	PRO	SER	PRO	THR	ASN	ASP	THR	PHE	LEU	SER	GLY	ASN	PRO	VAL	ILE	VAL	GLY	SER	PRO	LYS	ASP	GLY	THR	ASP	TYR	ILE			
PRO	ASP	LEU	ASN	GLN	MET	THR	LEU	ASP	GLY	GLU	PHE	THR	ALA	ILE	ASP	PRO	ASN	PHE	THR	THR	PRO	GLY	GLN	LEU	VAL	THR	GLN	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
THR	LEU	SER	ASP	THR	PHE	SER	PRO	GLN	ALA	GLN	THR	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
GLN	THR	ASN	LEU	GLN	SER	PRO	ALA	GLN	MET	PRO	GLY	SER	GLY	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		
LYS	SER	PHE	THR	THR	GLY	ILE	SER	GLN	MET	PRO	GLY	SER	GLY	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
SER	PRO	ARG	THR	PHE	HIS	PRO	LEU	ARG	ALA	TYR	ASN	THR	PHE	SER	GLU	VAL	ARG	PRO	ARG	VAL	LEU	VAL	LEU	GLN	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLU	SER	THR	PRO	GLN	ALA	ASN	LYS	PRO	GLN	SER	GLY	THR	HIS	GLY	SER	GLY	VAL	ARG	PRO	ARG	VAL	LEU	GLN	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

K2148
N2153
T2156
K2157
R2171
F2172
I2176
P2177
K2178
T2179
N2180
N2181
Q2182
S2183
I2184
A2185
L2186
R2187
Y2186

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	299182	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.803	Depositor
Minimum map value	-1.629	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.43	Depositor
Map size ($\text{\AA}$)	325.6, 325.6, 325.6	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	B	0.26	1/11436 (0.0%)	0.50	6/15488 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	654	VAL	C-O	-6.02	1.15	1.23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	654	VAL	N-CA-CB	-9.37	100.51	112.60
1	B	2059	PHE	N-CA-C	-7.14	103.01	112.72
1	B	1706	VAL	N-CA-C	-5.74	107.30	112.12
1	B	401	ASP	N-CA-C	-5.25	106.64	112.57
1	B	2036	ASN	CA-C-N	5.15	129.34	121.51

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	B	11142	0	10800	379	0
All	All	11142	0	10800	379	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 17.

The worst 5 of 379 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:B:656:CYS:H	1:B:660:ASP:HB2	1.16	1.10
1:B:2060:LYS:CG	1:B:2087:LYS:HA	1.84	1.08
1:B:2061:LYS:HD2	1:B:2067:TYR:HB3	1.10	1.08
1:B:2060:LYS:HG3	1:B:2087:LYS:HA	1.39	1.03
1:B:2061:LYS:CD	1:B:2067:TYR:HB3	1.91	0.99

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	B	1370/2196 (62%)	1115 (81%)	250 (18%)	5 (0%)	30 60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2060	LYS
1	B	135	ASP
1	B	700	ASN
1	B	658	PRO
1	B	670	PRO

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	B	1225/1989 (62%)	1218 (99%)	7 (1%)	78 81

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2034	GLU
1	B	2035	VAL
1	B	2061	LYS
1	B	2036	ASN
1	B	2033	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1670	ASN
1	B	2162	ASN
1	B	1781	ASN
1	B	2002	ASN
1	B	1778	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

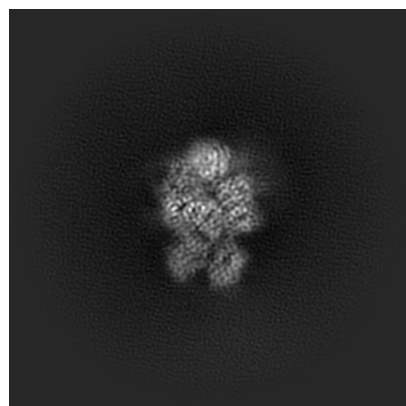
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23048. These allow visual inspection of the internal detail of the map and identification of artifacts.

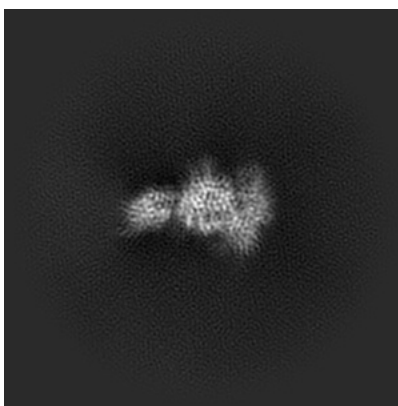
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

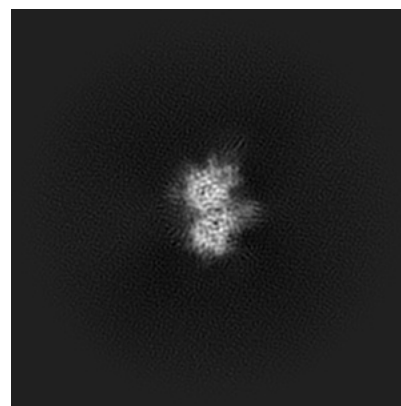
6.1.1 Primary map



X

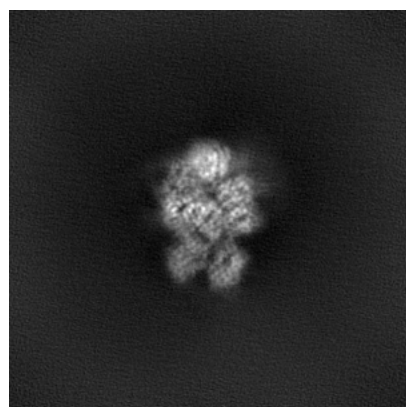


Y

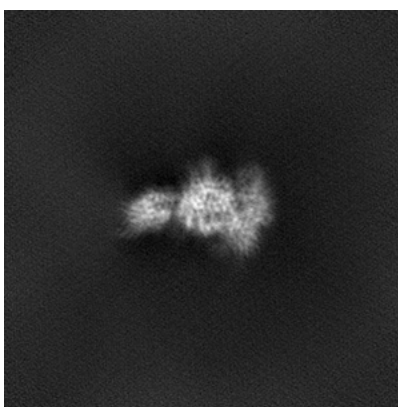


Z

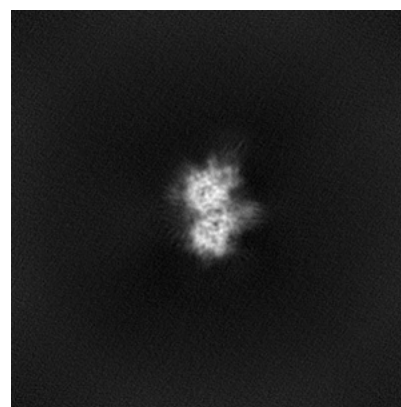
6.1.2 Raw map



X



Y

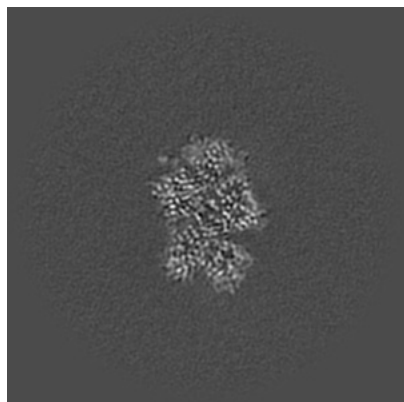


Z

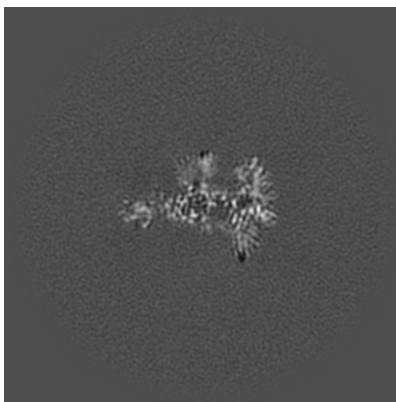
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

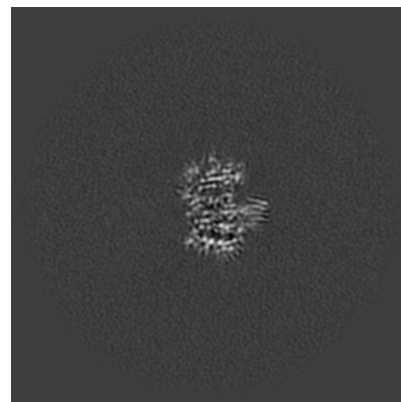
6.2.1 Primary map



X Index: 148

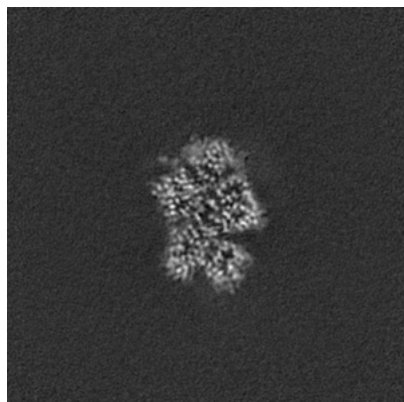


Y Index: 148

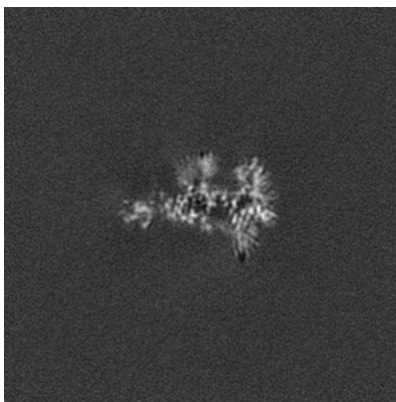


Z Index: 148

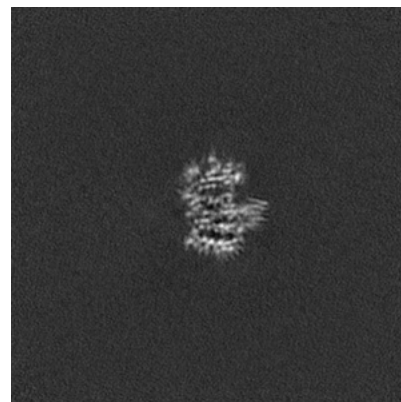
6.2.2 Raw map



X Index: 148



Y Index: 148

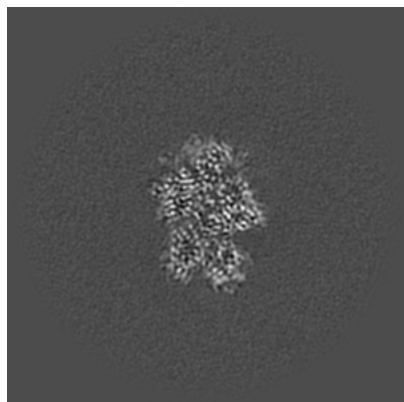


Z Index: 148

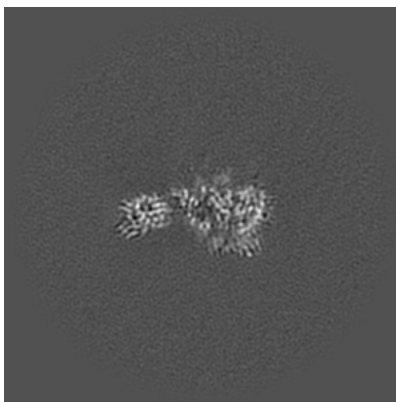
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

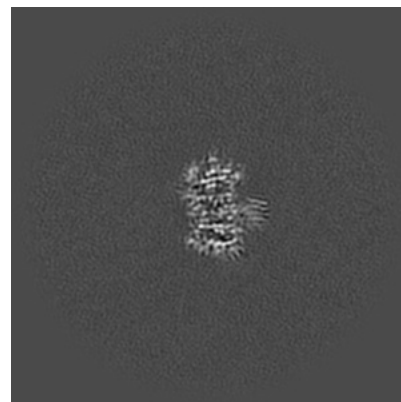
6.3.1 Primary map



X Index: 149

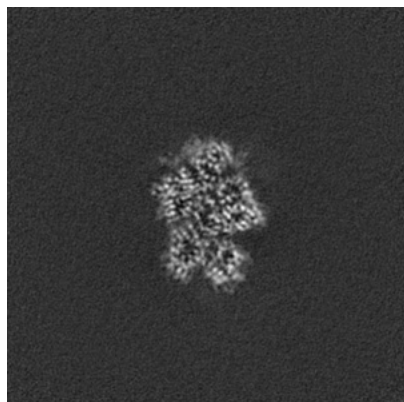


Y Index: 157

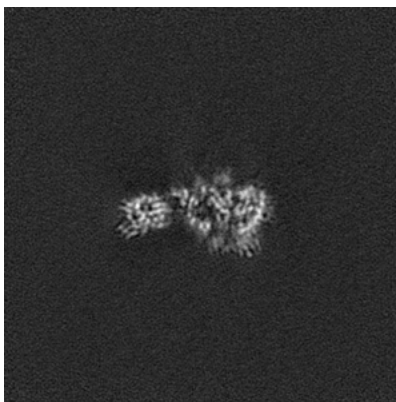


Z Index: 147

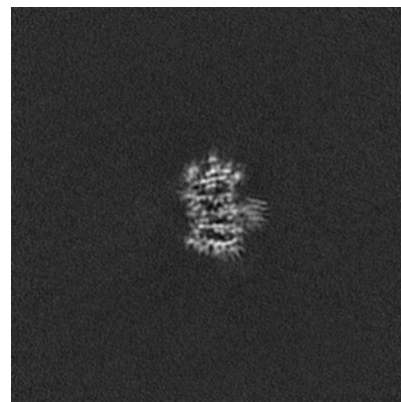
6.3.2 Raw map



X Index: 149



Y Index: 157

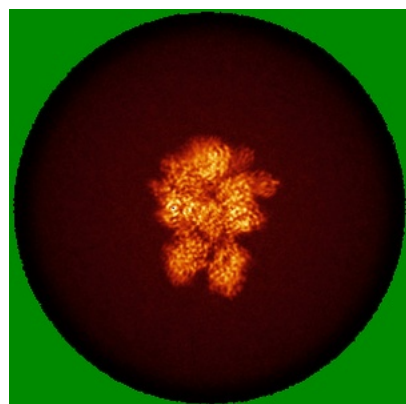


Z Index: 147

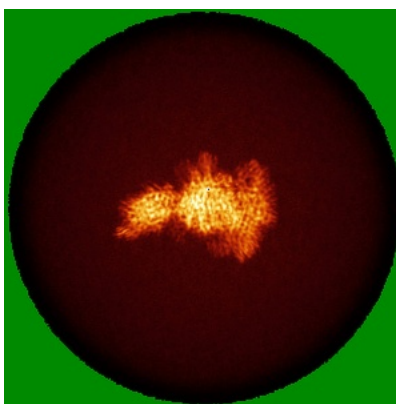
The images above show the largest variance slices of the map in three orthogonal directions.

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

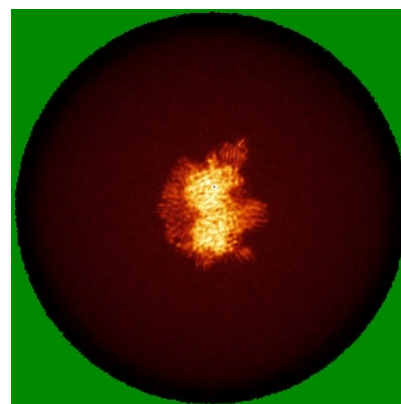
6.4.1 Primary map



X

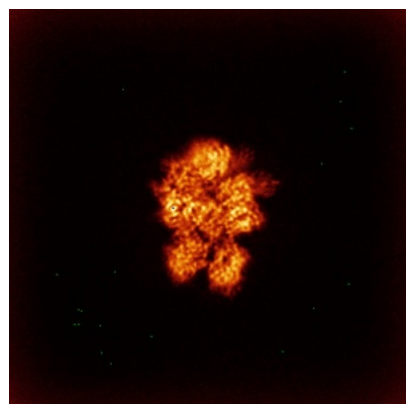


Y

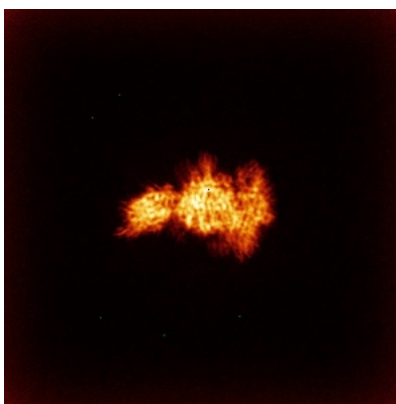


Z

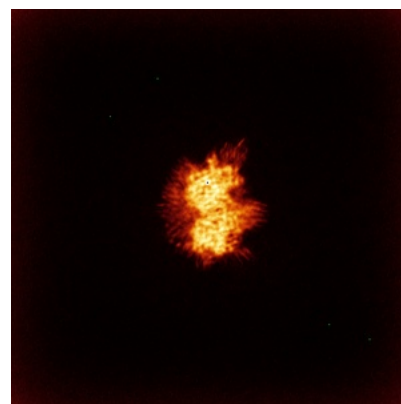
6.4.2 Raw map



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.

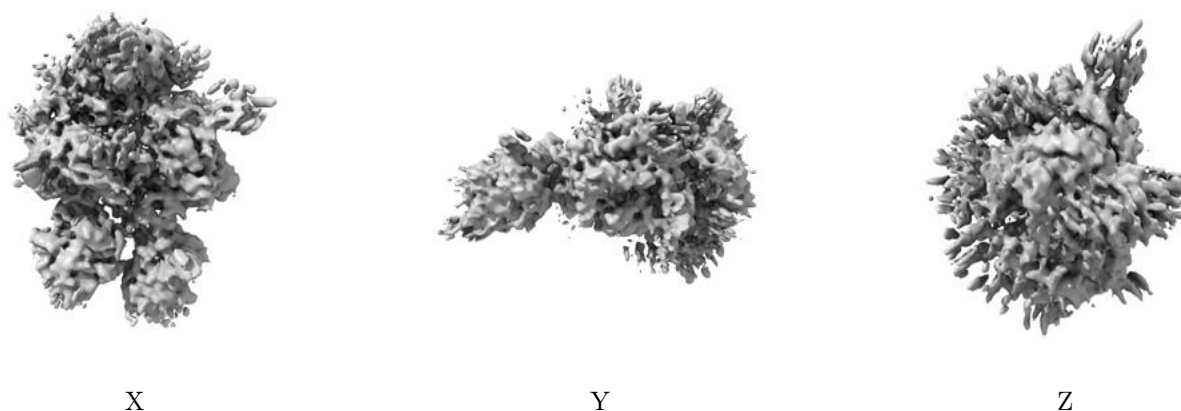
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.43. 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.

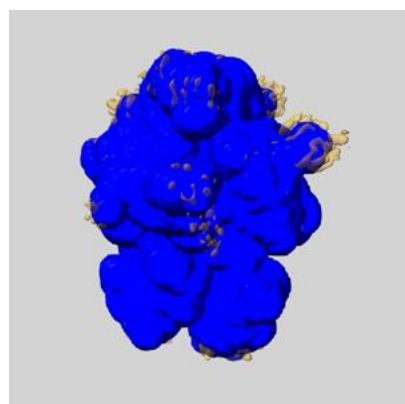
6.6 Mask visualisation [i](#)

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

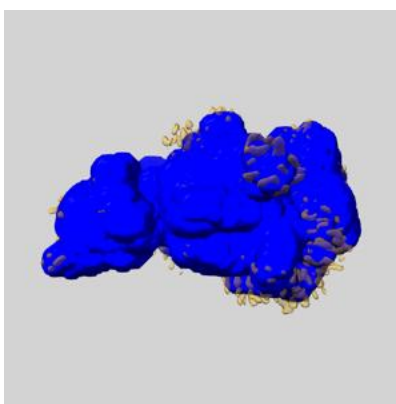
A mask typically either:

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

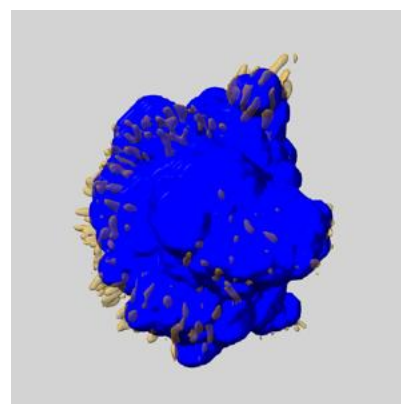
6.6.1 emd_23048_msk_1.map [i](#)



X



Y

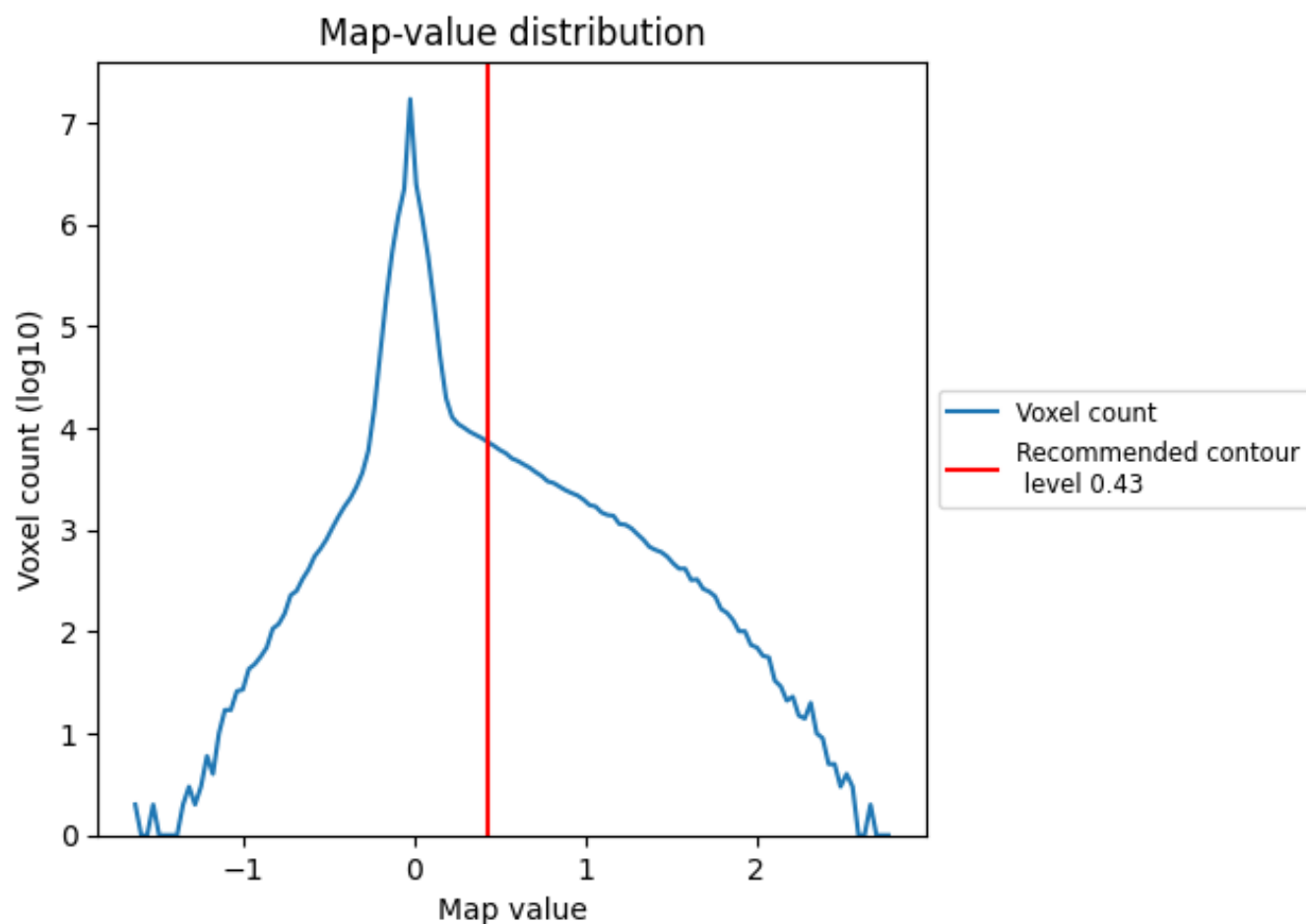


Z

7 Map analysis [i](#)

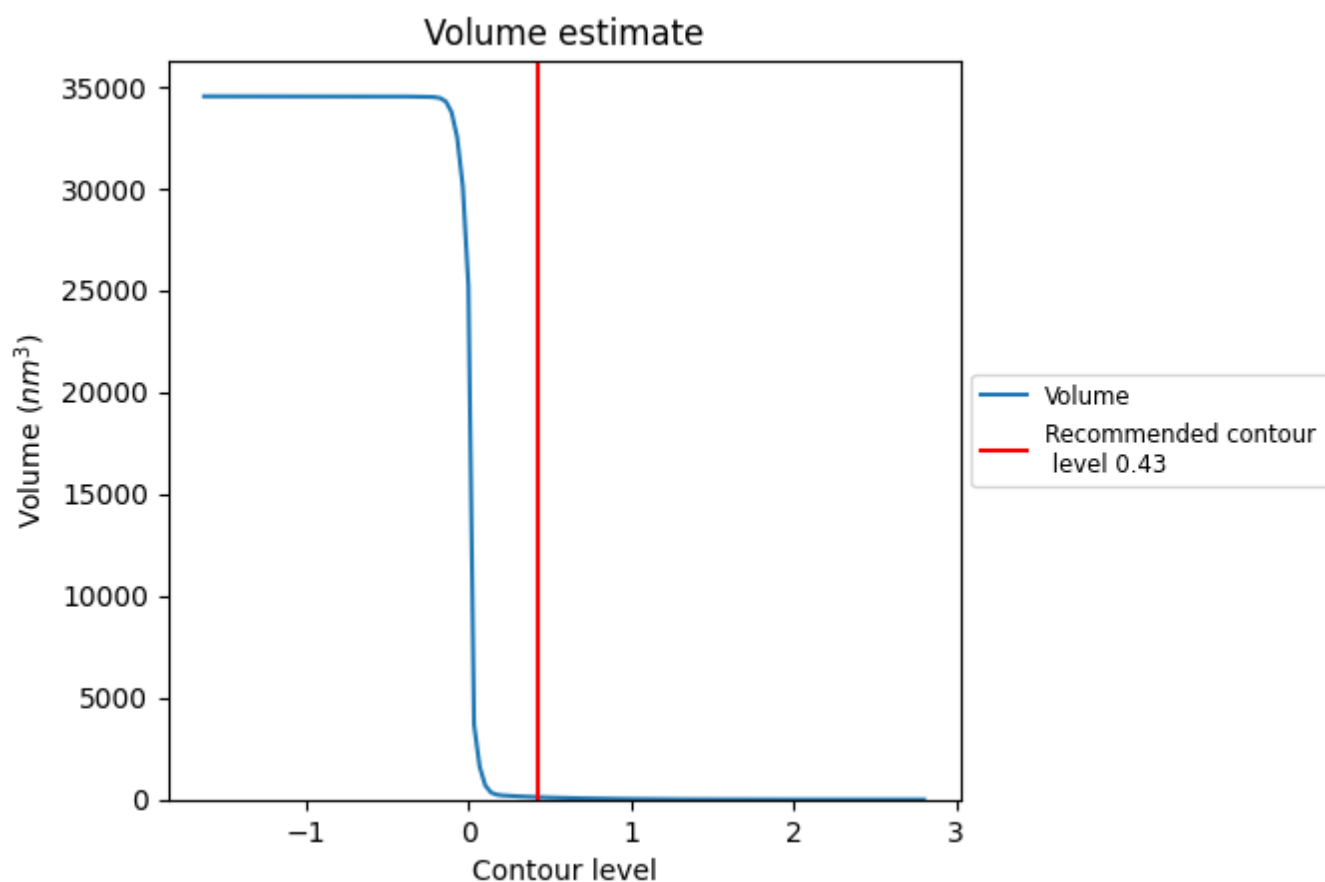
This section contains the results of statistical analysis of the map.

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.

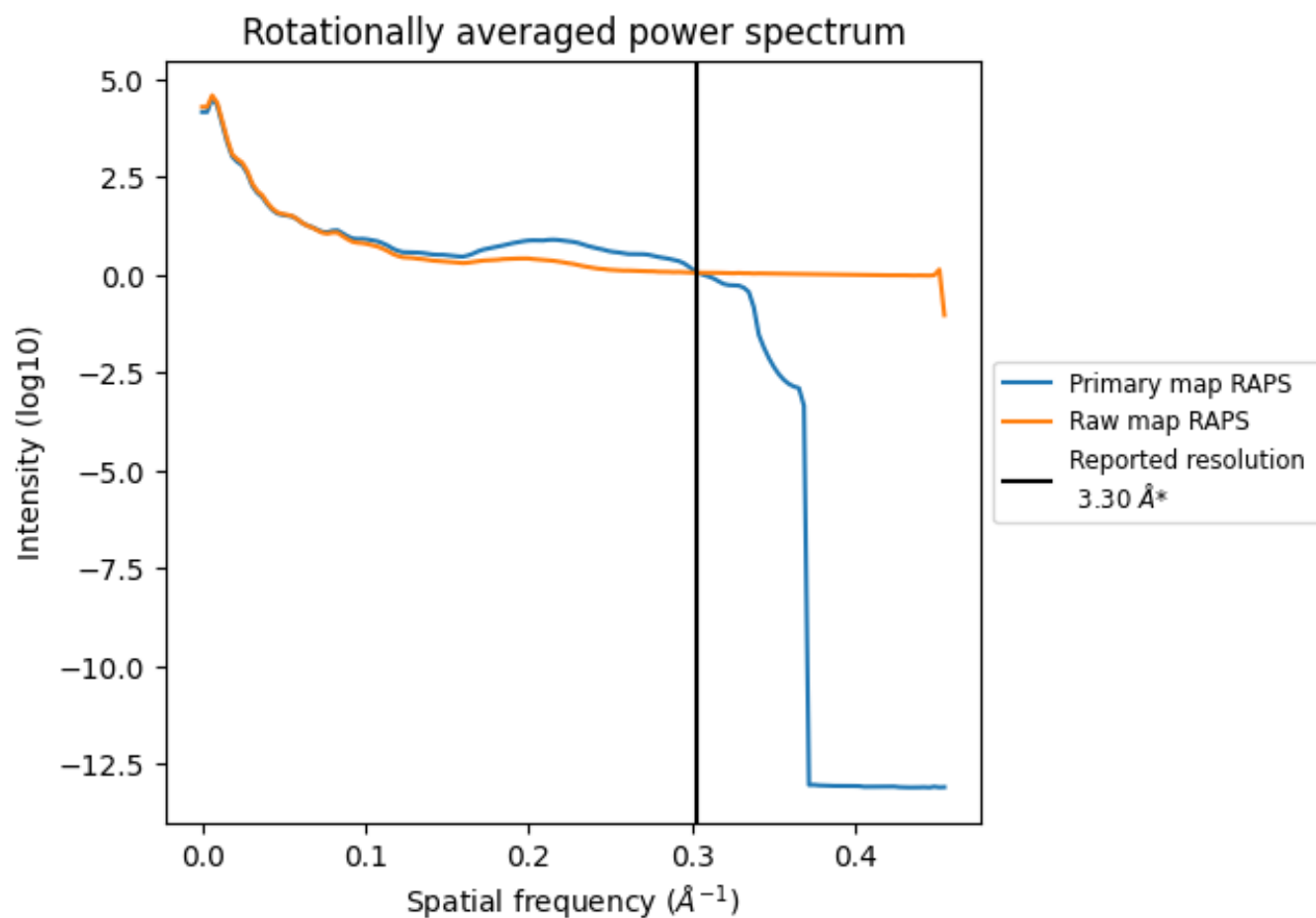
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm³; this corresponds to an approximate mass of 106 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 ⓘ

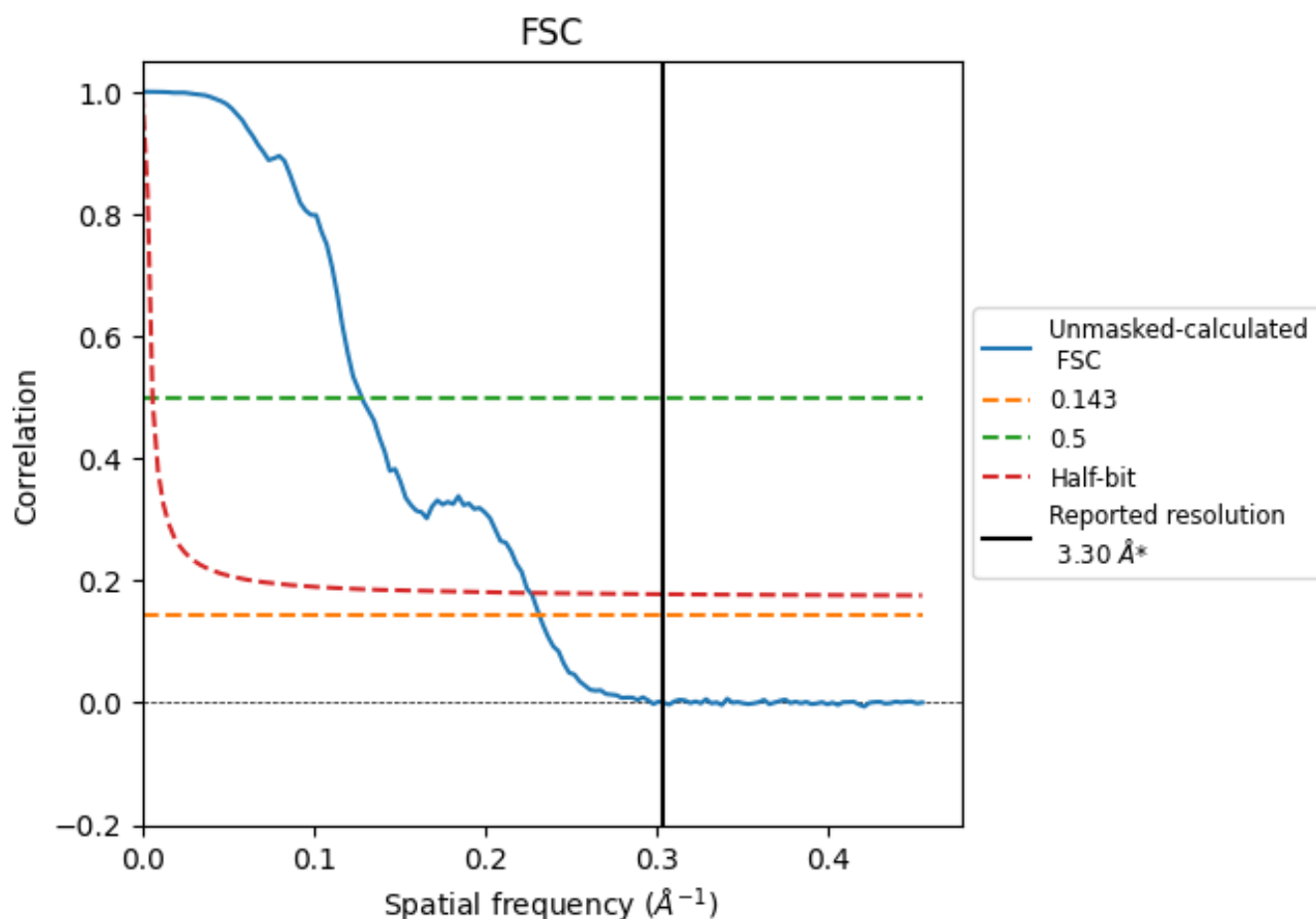


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

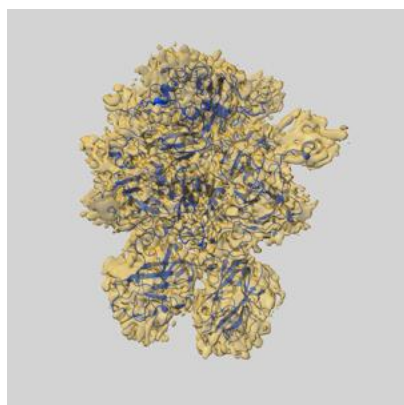
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.32	7.82	4.42

*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 4.32 differs from the reported value 3.3 by more than 10 %

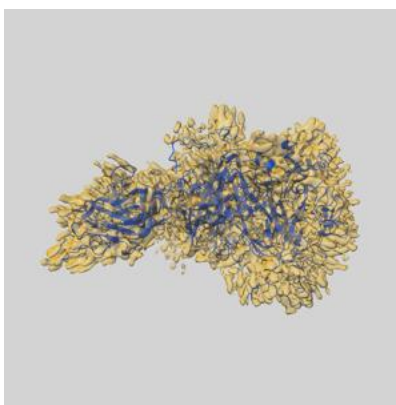
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23048 and PDB model 7KVE. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

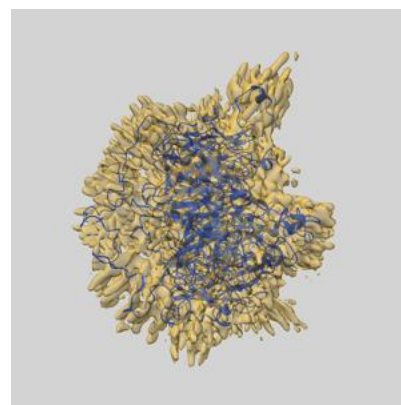
9.1 Map-model overlay [i](#)



X



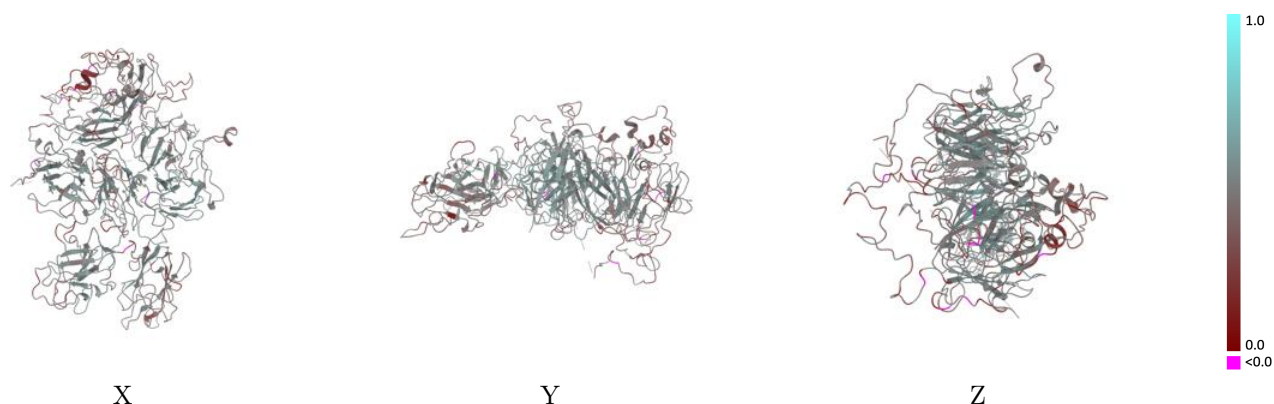
Y



Z

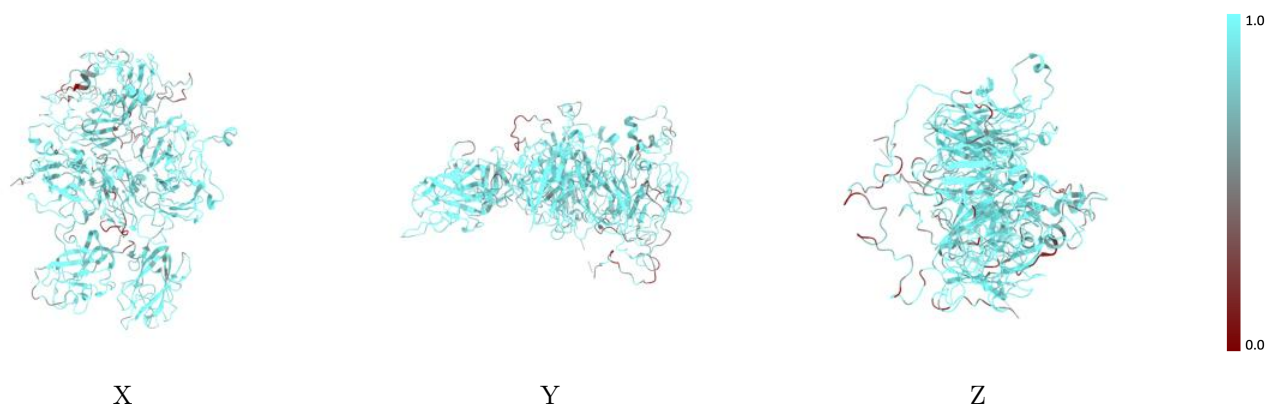
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



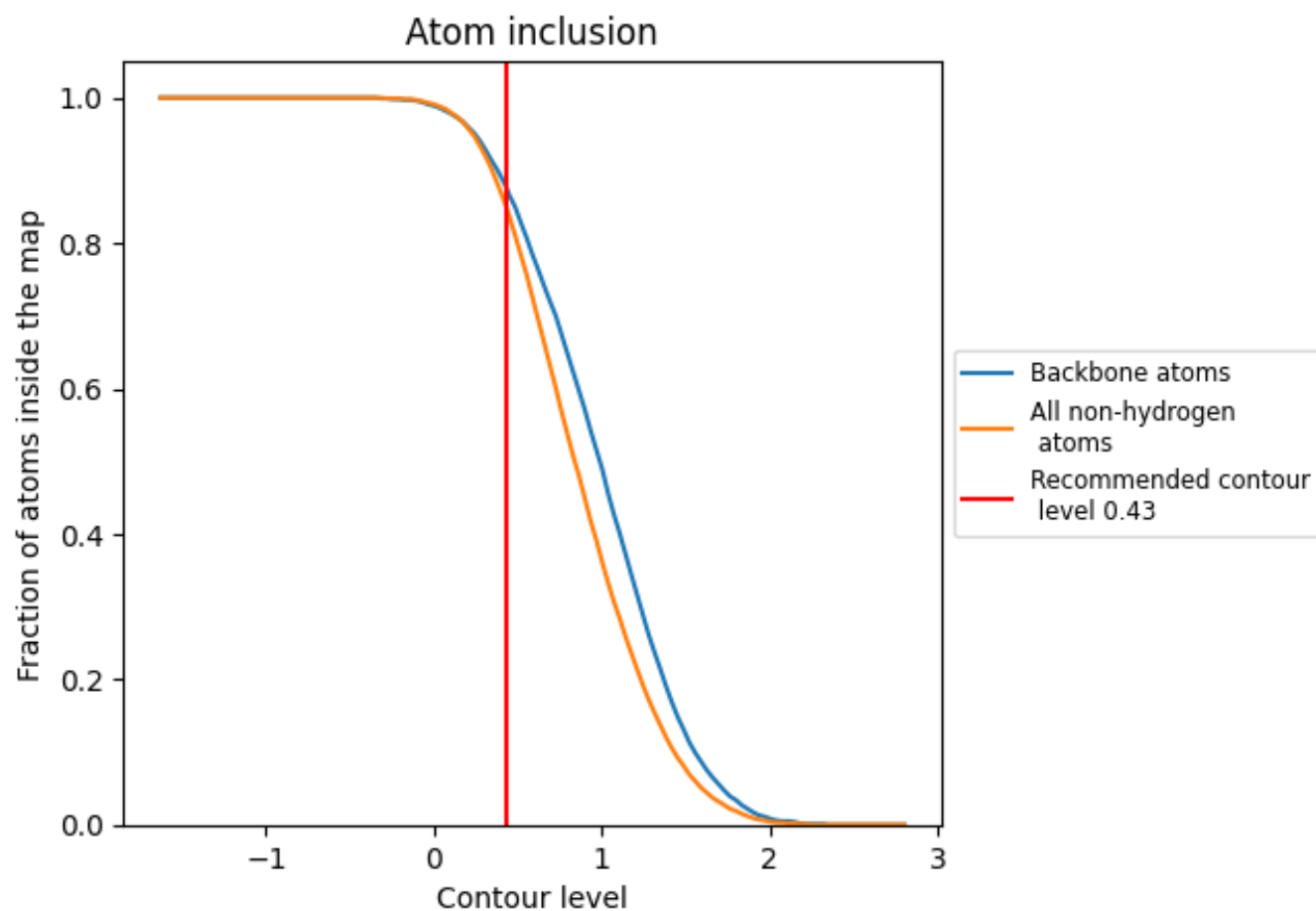
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.4510
B	0.8510	0.4510

