



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 12:50 AM UTC

PDB ID : 8TX1 / pdb_00008tx1
EMDB ID : EMD-41674
Title : Characterization of the Chlamydomonas Flagellar Mastigoneme Filament
Structure at 3.6Å
Authors : Yue, W.; Kai, Z.
Deposited on : 2023-08-22
Resolution : 3.62 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

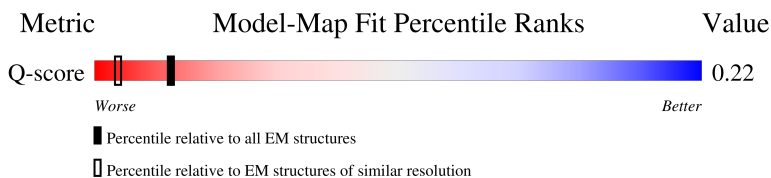
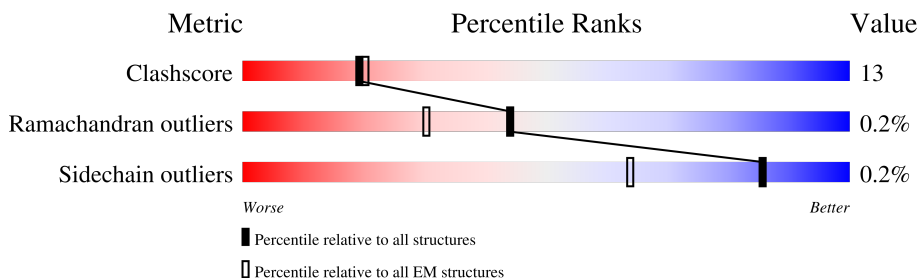
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.62 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	11773 (3.12 - 4.12)

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	1987	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13687 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 Mastigoneme-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1894	Total	C	N	O	S	0	0
			13687	8643	2234	2727	83		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	LEU	VAL	conflict	UNP Q8LRM7
A	142	LEU	THR	conflict	UNP Q8LRM7
A	143	ALA	GLY	conflict	UNP Q8LRM7
A	144	SER	LEU	conflict	UNP Q8LRM7
A	145	LYS	GLU	conflict	UNP Q8LRM7
A	146	THR	ASP	conflict	UNP Q8LRM7
A	147	VAL	GLY	conflict	UNP Q8LRM7
A	149	ILE	HIS	conflict	UNP Q8LRM7
A	150	TYR	LEU	conflict	UNP Q8LRM7
A	151	VAL	CYS	conflict	UNP Q8LRM7
A	517	ARG	LYS	conflict	UNP Q8LRM7
A	530	GLU	GLY	conflict	UNP Q8LRM7
A	619	THR	ALA	conflict	UNP Q8LRM7
A	800	SER	THR	conflict	UNP Q8LRM7
A	820	SER	PHE	conflict	UNP Q8LRM7
A	?	-	GLY	deletion	UNP Q8LRM7
A	?	-	THR	deletion	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	GLY	deletion	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	TYR	deletion	UNP Q8LRM7
A	?	-	PHE	deletion	UNP Q8LRM7
A	?	-	LEU	deletion	UNP Q8LRM7
A	1399	LYS	ARG	conflict	UNP Q8LRM7
A	?	-	PRO	deletion	UNP Q8LRM7
A	?	-	GLU	deletion	UNP Q8LRM7
A	1868	PRO	ALA	conflict	UNP Q8LRM7
A	1897	PRO	GLN	conflict	UNP Q8LRM7

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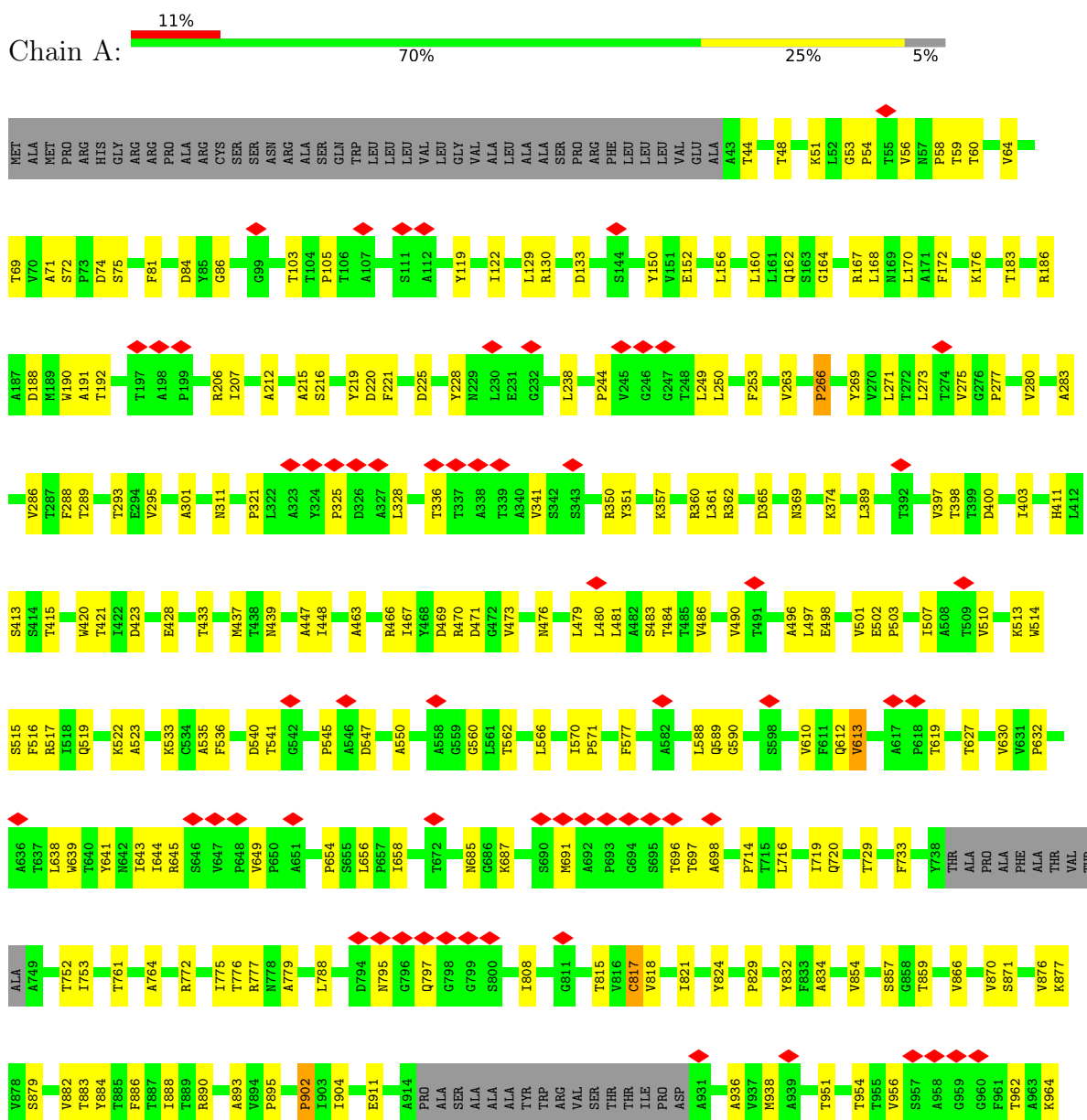
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Chain	Residue	Modelled	Actual	Comment	Reference
A	1914	PRO	ARG	conflict	UNP Q8LRM7
A	1915	PRO	ARG	conflict	UNP Q8LRM7
A	1917	PRO	HIS	conflict	UNP Q8LRM7
A	1919	SER	ALA	conflict	UNP Q8LRM7
A	1920	PRO	ARG	conflict	UNP Q8LRM7
A	1921	PRO	ARG	conflict	UNP Q8LRM7
A	1924	ASN	THR	conflict	UNP Q8LRM7
A	1925	ARG	ALA	conflict	UNP Q8LRM7
A	1926	SER	LEU	conflict	UNP Q8LRM7
A	1935	SER	PRO	conflict	UNP Q8LRM7
A	1978	ASP	-	expression tag	UNP Q8LRM7
A	1979	ALA	-	expression tag	UNP Q8LRM7
A	1980	GLU	-	expression tag	UNP Q8LRM7
A	1981	MET	-	expression tag	UNP Q8LRM7
A	1982	GLN	-	expression tag	UNP Q8LRM7
A	1983	PRO	-	expression tag	UNP Q8LRM7
A	1984	GLN	-	expression tag	UNP Q8LRM7
A	1985	ASP	-	expression tag	UNP Q8LRM7
A	1986	ASP	-	expression tag	UNP Q8LRM7
A	1987	GLU	-	expression tag	UNP Q8LRM7

3 Residue-property plots [i](#)

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: Mastigoneme-like protein



L965	M966	V967	F968	G969	E970	T973	ALA	ALA	PRO	LEU	LEU	THR	SER	SER	VAL	T984	F985	L988	L989	V1001	A1002	V1006	A1007	V1008	T1012	T1013	S1014	P1015	N1016	Y1017	N1018	P1019	T1020	T1021	P1022	Y1023	T1024	N1025	T1028	T1031	F1032	T1033	L1034	L1035	R1036	P1041	G1047	V1048	Q1049										
	C1052	A1053	L1054	Y1055	T1056	G1057	Q1058	P1062	A1063	S1064	A1065	P1066	T1070	D1071	A1072	T1073	Y1074	C1075	T1076	F1077	T1078	D1079	V1080	T1081	T1082	A1083	D1093	R1097	T1100	M1101	A1102	T1105	V1108	F1112	P1113	T1114	F1122	S1123	P1124	K1125	F1126	F1127	A1132	S1133	S1134	T1135	V1136	V1143											
A1144	D1145	T1146	V1147	T1148	T1154	A1158	Q1170	R1171	V1172	M1192	D1193	N1194	Y1195	T1196	N1197	A1202	V1203	D1204	A1205	Y1206	K1215	G1216	P1217	G1218	G1219	T1220	M1223	I1229	P1230	S1237	N1238	E1239	G1240	A1241	R1242	E1243	C1244	C1247	P1248	A1256	A1257	L1258	T1259	R1261	A1262	K1263	Y1264												
S1265	I1266	T1270	Y1271	Y1274	L1277	E1282	K1285	K1286	C1287	P1288	K1289	G1290	Y1291	F1292	Q1293	C1301	L1302	P1303	C1304	P1305	S1306	G1307	F1308	Y1309	S1310	T1311	S1312	G1313	G1316	C1317	S1321	T1324	Y1325	H1326	T1327	D1328	G1329	G1336	E1337	A1338	D1342	T1346	F1347	T1350	Y1351														
T1357	C1358	R1359	Q1360	L1367	G1371	Q1372	A1373	A1374	P1388	D1394	W1397	S1398	K1399	A1400	C1405	Q1406	K1407	C1408	P1409	T1412	Y1413	R1414	N1415	Q1421	L1422	G1423	S1424	I1427	T1428	A1429	D1430	G1431	V1432	P1433	V1434	A1435	T1436	T1437	C1445	S1446	Q1447	T1456	F1457	G1458	N1459	S1460	P1466												
T1469	Q1481	P1484	G1485	G1491	D1492	R1493	T1494	Q1495	Q1496	M1497	A1498	L1499	V1500	N1503	A1504	A1505	N1506	D1507	F1508	P1509	Y1514	T1515	I1516	V1520	A1521	G1522	P1523	A1524	Y1525	A1526	K1527	P1528	T1531	M1539	K1542	P1551	G1552	Y1553	Y1554	T1555	D1556	Q1563	L1564	P1565	C1566	K1567	P1568												
G1569	T1570	T1576	N1580	L1581	L1582	D1583	L1586	T1587	V1588	D1589	G1590	T1591	T1595	C1596	Q1597	N1602	D1603	E1604	Q1607	P1608	V1609	S1620	L1624	P1625	I1629	P1632	G1633	T1634	A1639	A1640	A1641	A1642	N1643	A1644	N1647	T1648	A1649	T1650	L1651	I1652	P1653	T1654	G1655	L1656	Q1661	A1662													
M1668	Q1672	A1675	T1687	Y1688	A1695	P1699	R1704	M1707	S1708	I1709	G1710	Q1711	R1712	K1715	P1716	M1719	R1724	G1736	T1737	K1741	S1744	S1745	T1748	P1749	C1750	A1751	A1752	Y1755	A1756	N1757	A1758	P1759	D1760	S1761	A1762	T1763	S1764	C1765	R1766	A1767	C1768	P1769	R1770																
G1771	Y1772	Y1773	G1774	P1775	Y1776	S1777	G1778	A1779	Y1780	A1781	D1782	N1783	L1784	G1785	D1786	E1787	F1788	E1789	G1790	P1791	R1792	G1793	C1794	Y1795	K1796	C1797	P1798	Y1799	D1800	F1801	F1802	A1803	D1804	R1805	P1806	G1807	V1808	R1809	Q1810	C1811	T1812	A1813	C1814	P1815	P1816	L1817	D1818	L1819	G1820	G1821	G1822	N1823	L1824	V1825	E1826	Q1827	C1828	T1829	E1830
D1831	L1832	G1833	S1834	Q1835	R1836	C1837	K1838	P1839	C1840	S1841	L1842	L1843	S1844	K1845	P1846	K1847	T1848	A1849	R1850	T1851	E1852	Q1853	S1854	P1855	P1856	P1920	P1921	P1931	P1939	ASN	GLY	ASP	PRO	VAL	GLY	HIS	ARG	ARG	ALA	T1956	A1968	E1971	E1980	M1981	Q1982	PRO	GLN	ASP	ASP	GLU									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98875	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 ($e^-/\text{\AA}^2$)	39.2	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	3.145	Depositor
Minimum map value	-1.930	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.321	Depositor
Map size ($\text{\AA}$)	494.7598, 494.7598, 494.7598	wwPDB
Map dimensions	372, 372, 372	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3299994, 1.3299994, 1.3299994	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	0.20	2/14067 (0.0%)	0.49	12/19393 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	902	PRO	CB-CG	-10.02	0.99	1.49
1	A	902	PRO	CG-CD	-6.67	1.28	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	902	PRO	N-CD-CG	-19.37	74.15	103.20
1	A	902	PRO	CA-CB-CG	-17.33	71.58	104.50
1	A	902	PRO	CB-CG-CD	16.30	158.28	106.10
1	A	902	PRO	CA-N-CD	-13.22	93.50	112.00
1	A	266	PRO	CA-N-CD	-6.63	102.72	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1282	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	13687	0	13237	342	0
All	All	13687	0	13237	342	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 342 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:1055:TYR:O	1:A:1124:PRO:HA	1.40	1.17
1:A:238:LEU:HB3	1:A:253:PHE:HB3	1.61	0.82
1:A:1223:MET:SD	1:A:1242:ARG:NH1	2.53	0.80
1:A:1336:GLY:H	1:A:1357:THR:HG22	1.45	0.80
1:A:1220:THR:HG22	1:A:1230:PRO:HB3	1.62	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1884/1987 (95%)	1756 (93%)	124 (7%)	4 (0%)	43 71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	490	VAL
1	A	1143	VAL
1	A	613	VAL
1	A	1939	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	A	1488/1571 (95%)	1485 (100%)	3 (0%)	87 84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	817	CYS
1	A	1394	ASP
1	A	1437	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1827	GLN
1	A	1647	ASN
1	A	1192	ASN
1	A	1506	ASN
1	A	1089	ASN

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.

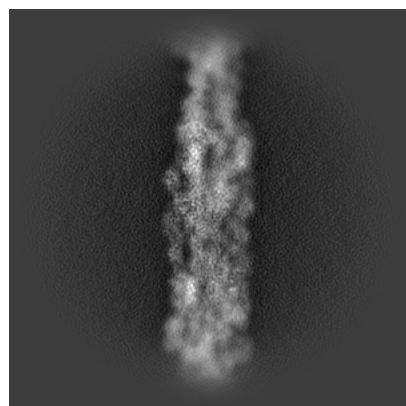
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41674. These allow visual inspection of the internal detail of the map and identification of artifacts.

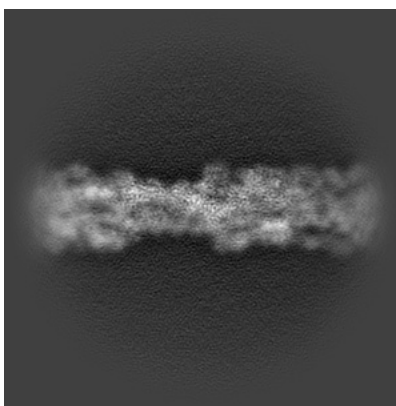
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

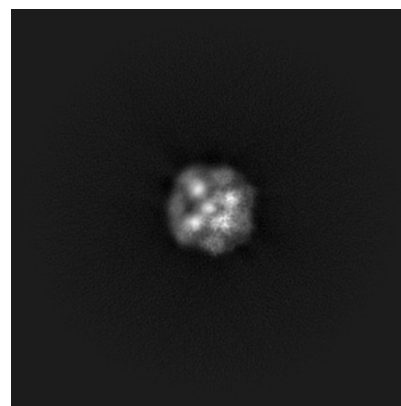
6.1.1 Primary map



X

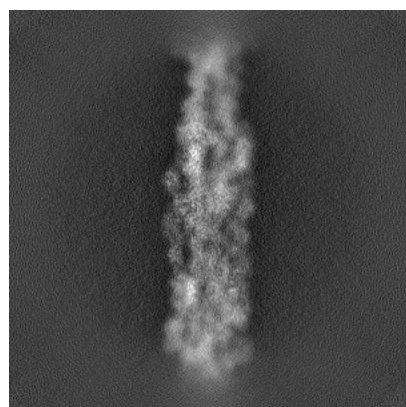


Y

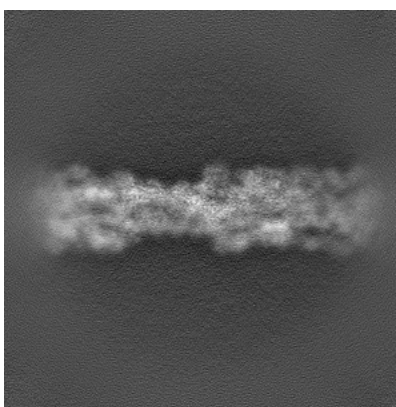


Z

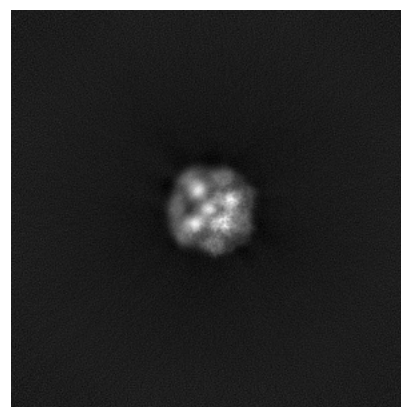
6.1.2 Raw map



X



Y

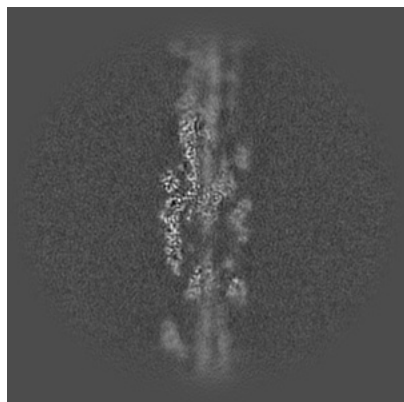


Z

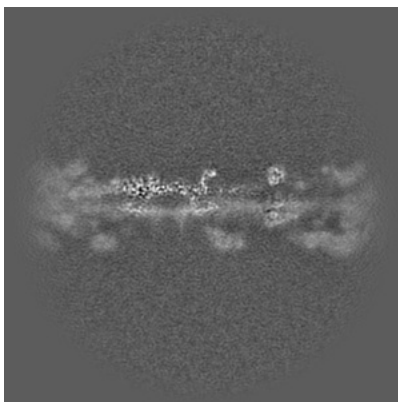
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

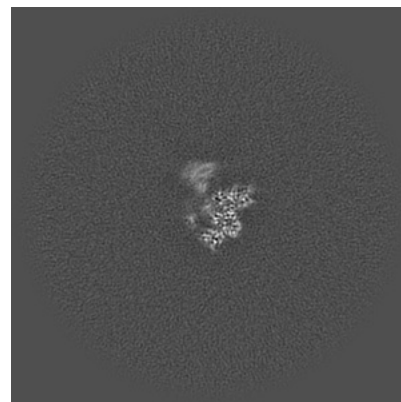
6.2.1 Primary map



X Index: 186

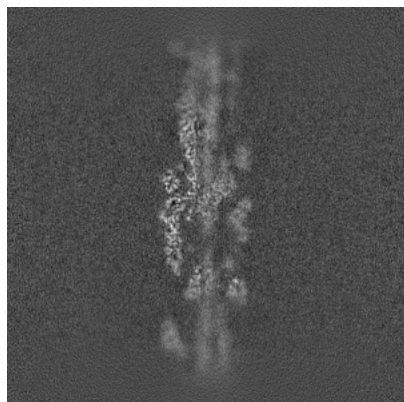


Y Index: 186

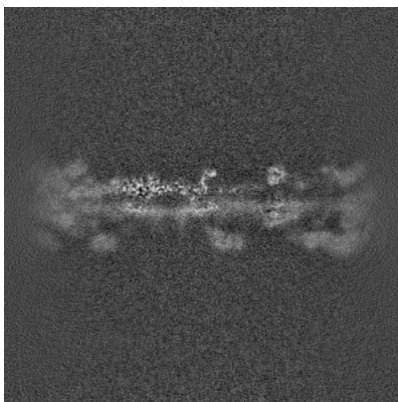


Z Index: 186

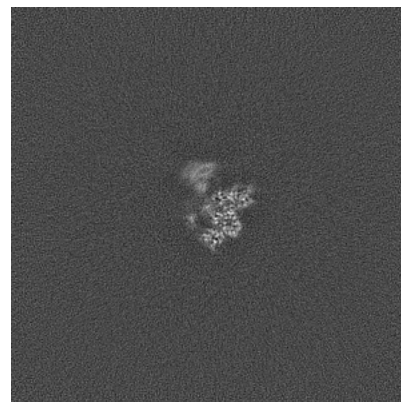
6.2.2 Raw map



X Index: 186



Y Index: 186

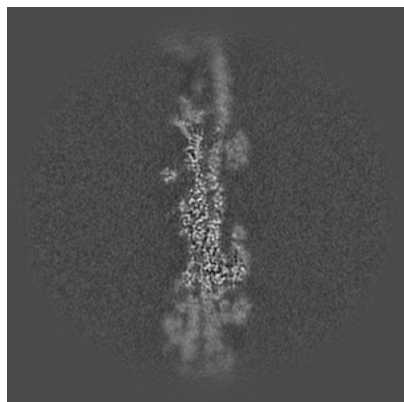


Z Index: 186

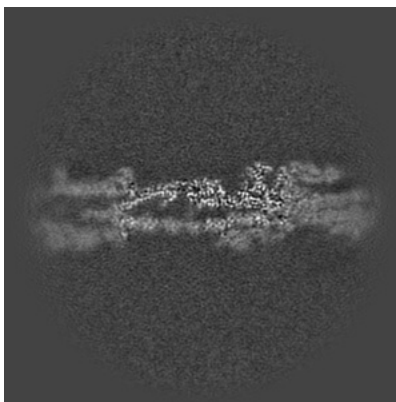
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

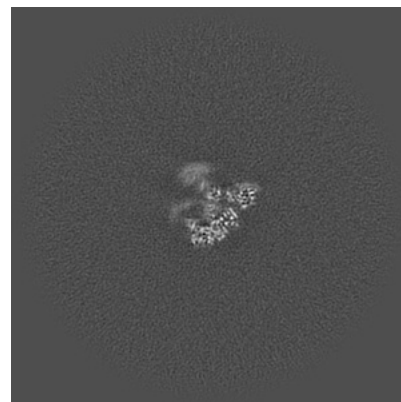
6.3.1 Primary map



X Index: 202

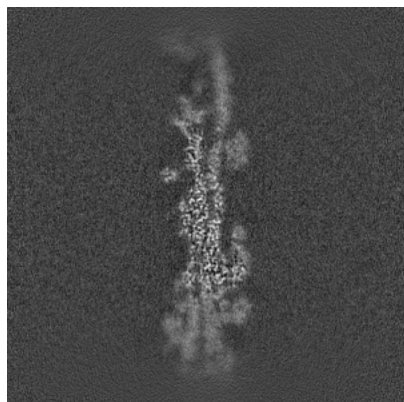


Y Index: 171

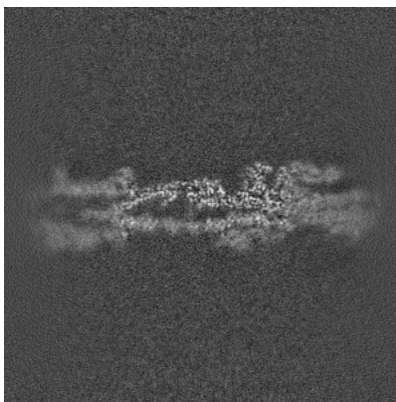


Z Index: 194

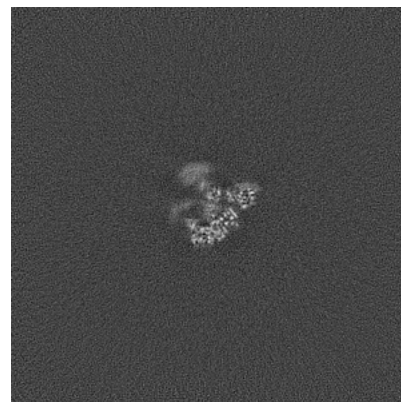
6.3.2 Raw map



X Index: 202



Y Index: 171

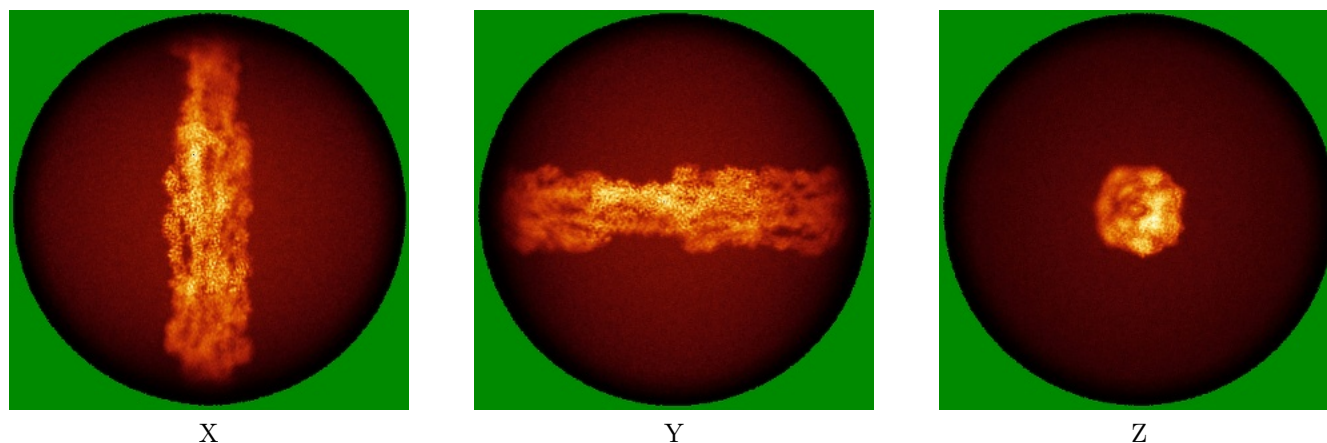


Z Index: 194

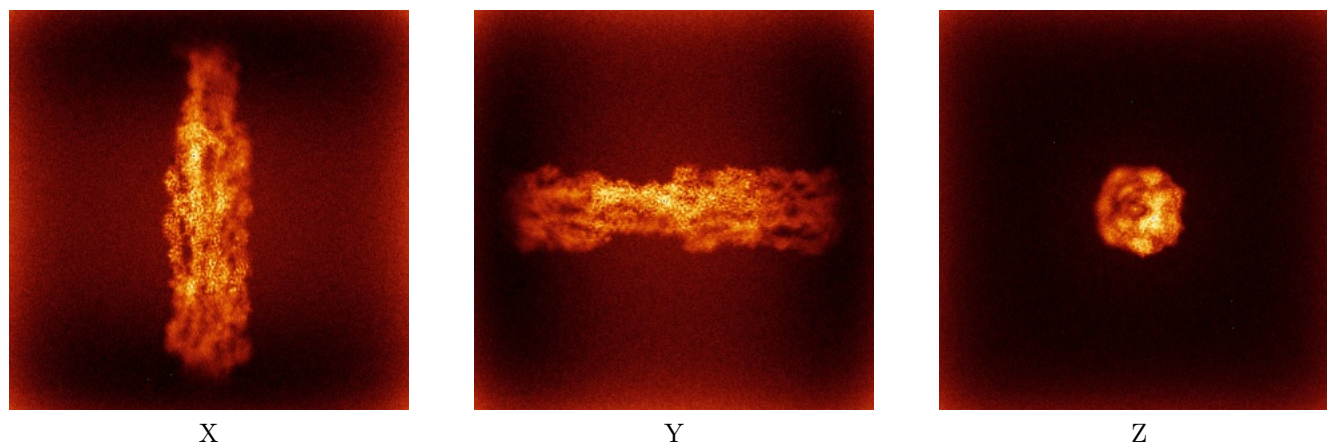
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

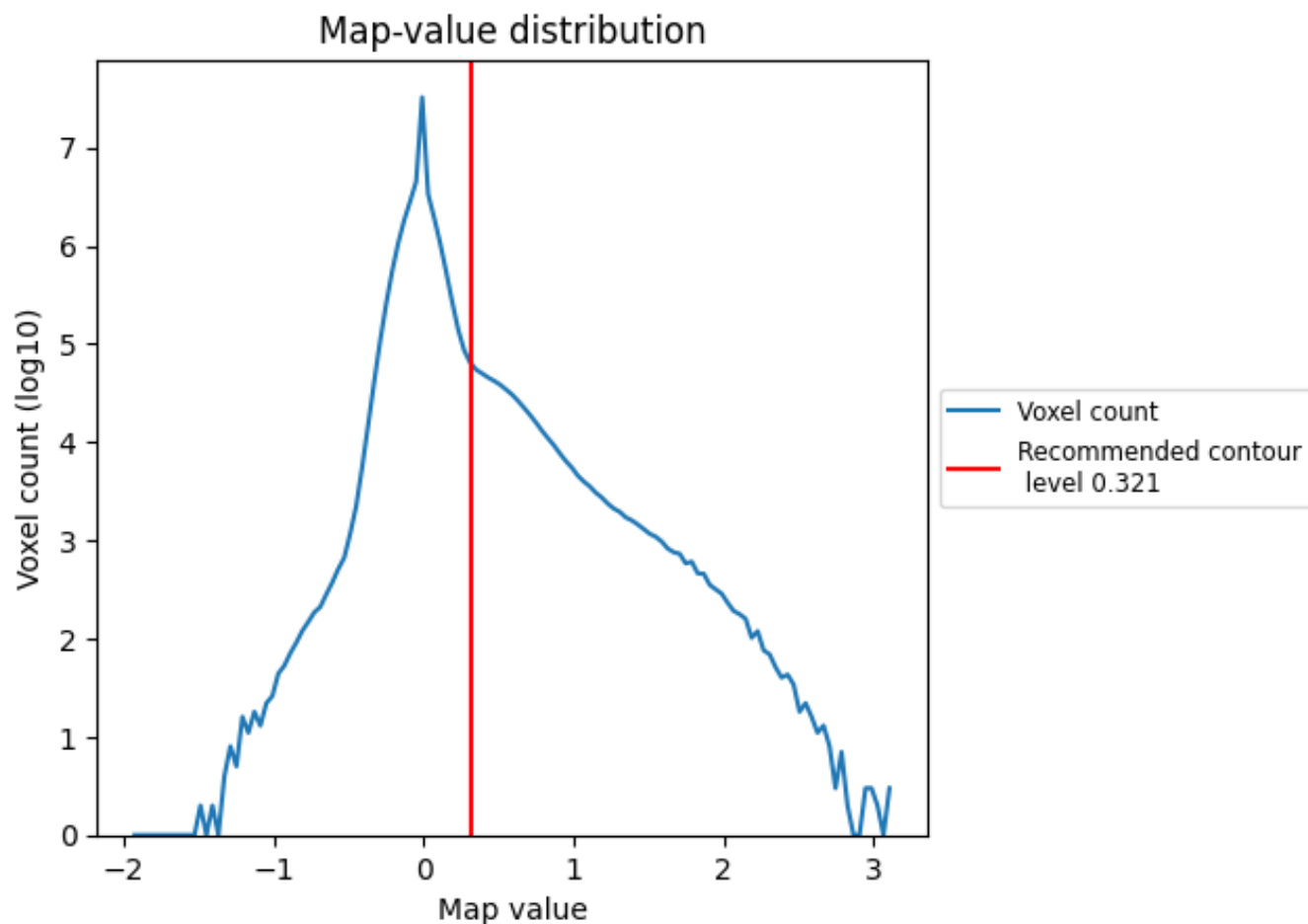
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

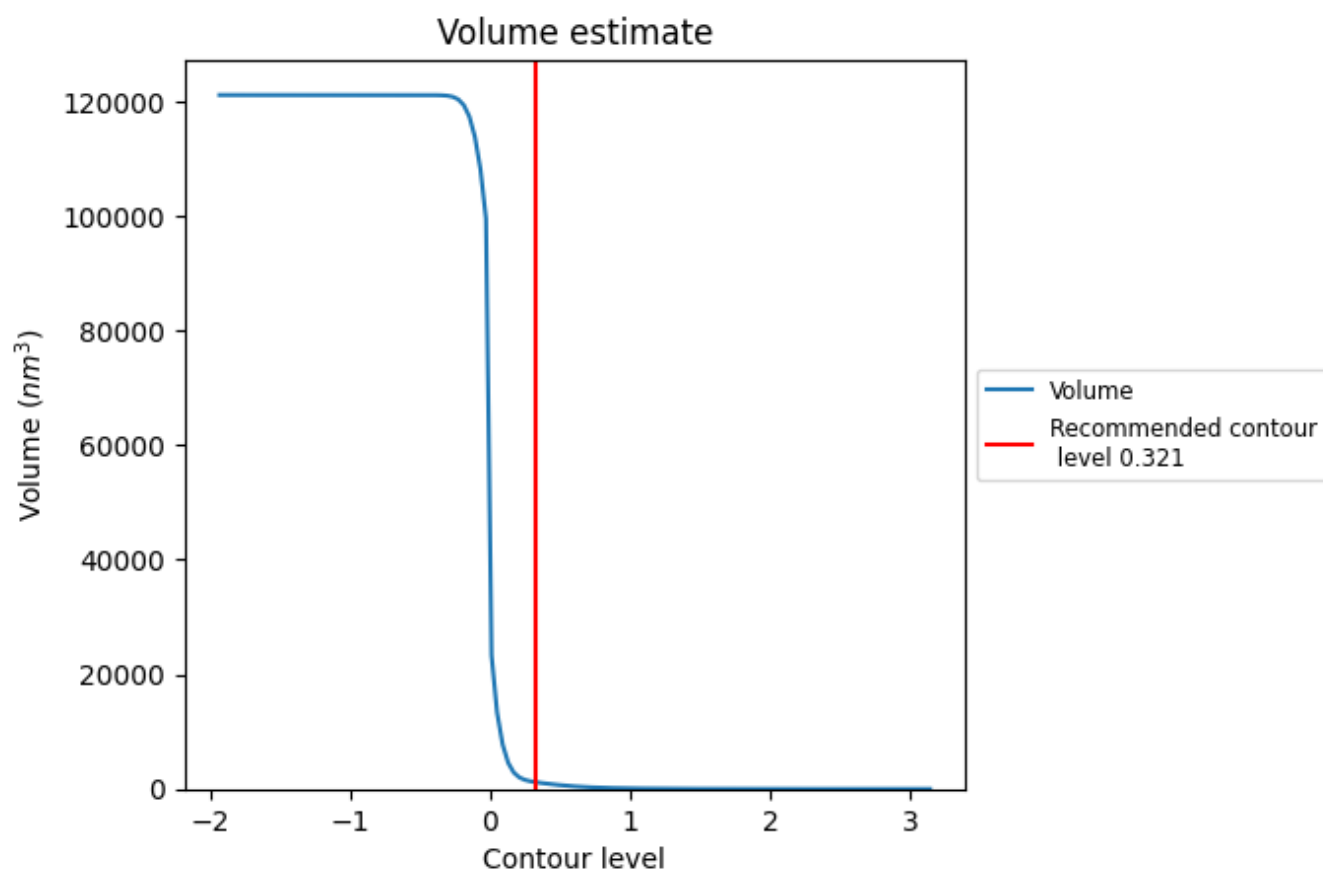
This section contains the results of statistical analysis of the map.

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.

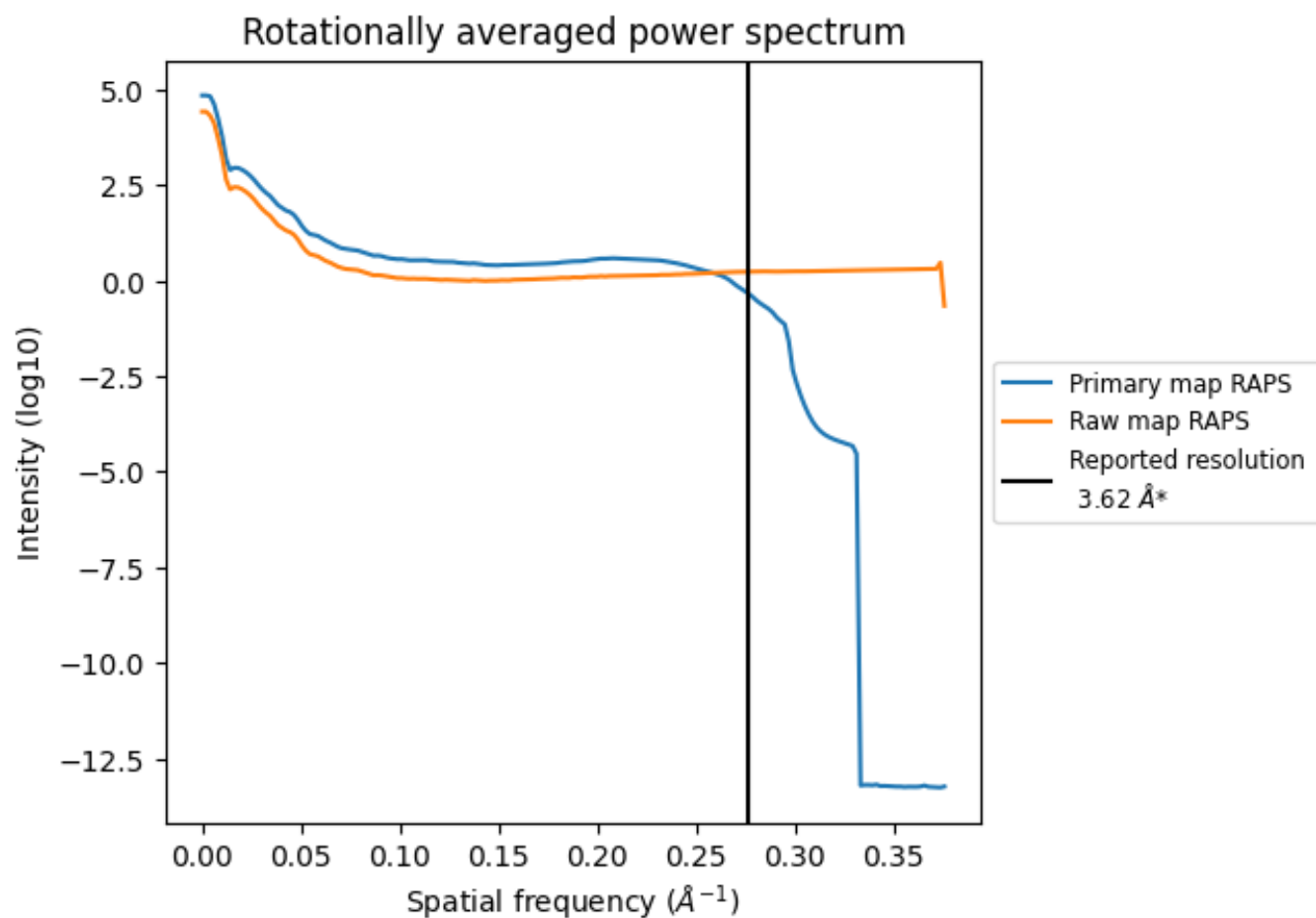
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1211 nm³; this corresponds to an approximate mass of 1094 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 ⓘ

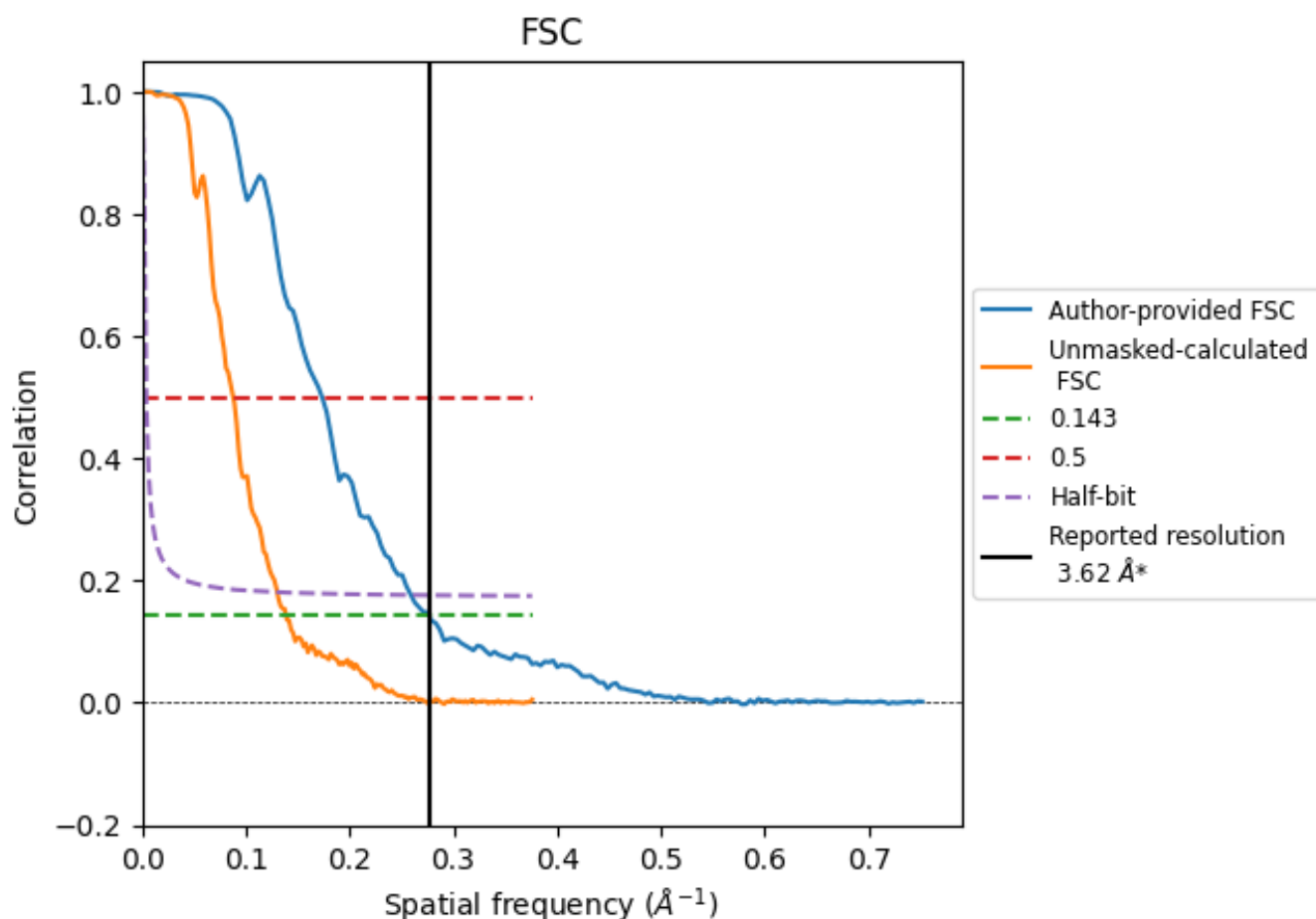


*Reported resolution corresponds to spatial frequency of 0.276 Å⁻¹

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 0.276 Å⁻¹

8.2 Resolution estimates [i](#)

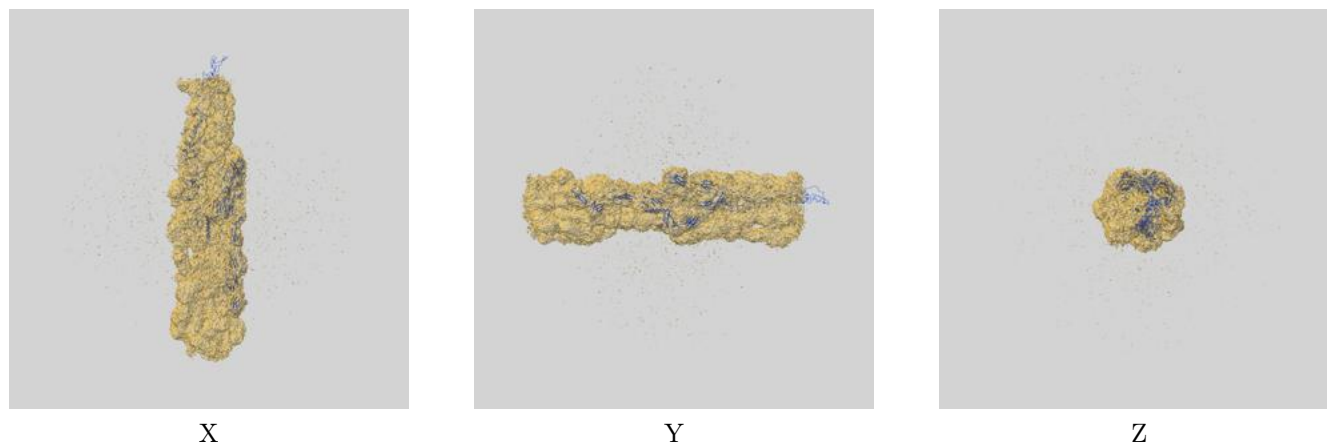
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.62	-	-
Author-provided FSC curve	3.62	5.77	3.88
Unmasked-calculated*	7.22	11.39	7.69

*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 7.22 differs from the reported value 3.62 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41674 and PDB model 8TX1. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.321 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](#)

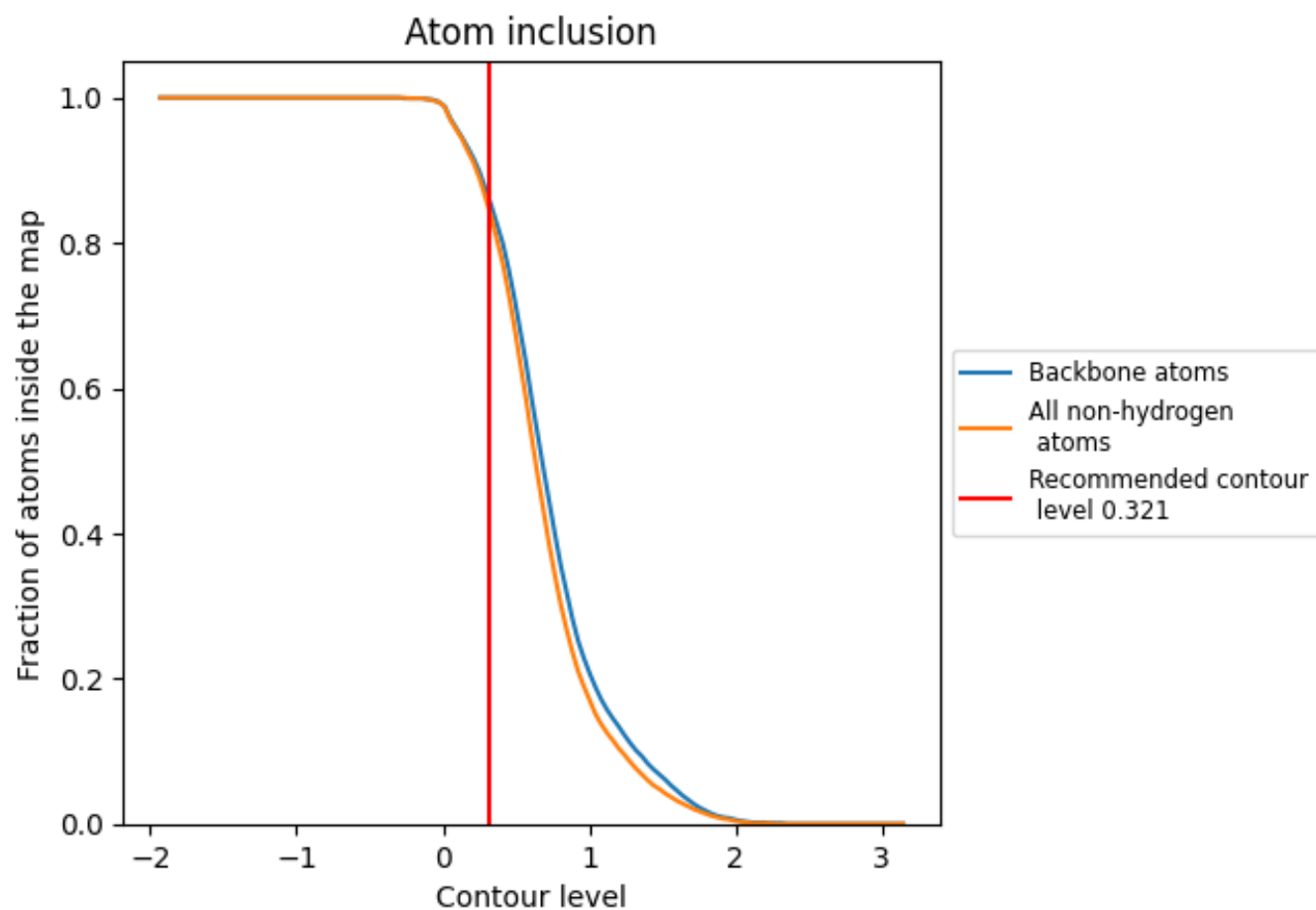


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 84% 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 (0.321) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8420	0.2200
A	0.8420	0.2200

