



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:40 PM UTC

PDB ID : 8Y1O / pdb_00008y1o
EMDB ID : EMD-38841
Title : Cryo-EM structure of human ABCA7 in the apo state
Authors : Fang, S.C.
Deposited on : 2024-01-25
Resolution : 3.92 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

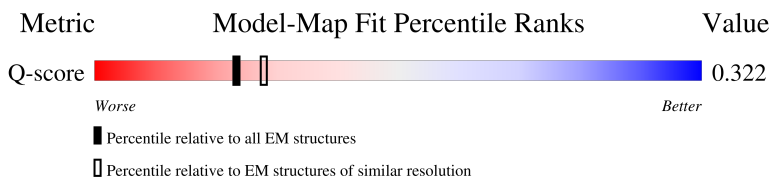
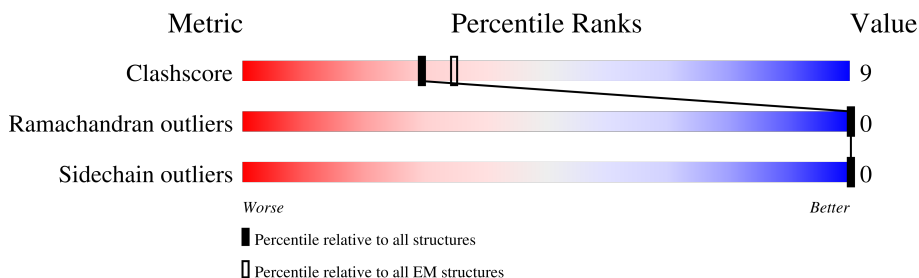
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.92 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	7862 (3.42 - 4.42)

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	2146	29% 67% 19% 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14226 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 Phospholipid-transporting ATPase ABCA7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1844	Total	C	N	O	S	0	0
			14226	9155	2511	2496	64		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	965	GLN	GLU	conflict	UNP Q8IZY2
A	1951	GLN	GLU	conflict	UNP Q8IZY2

G969	ASP	THR	ARG	GLN	GLY	LYS	ASN	PRO	GLY	SER	GLN	GLY	SER	ARG	V1073	G1074	T1075	P1076	Q1077	L1078	L1079	A1080	L1081	V1082	Q1083	H1084	W1085	V1086	P1087	G1088	A1089	R1090	L1091	V1092	E1093	E1094	L1095	H1097	E1098	L1099	V1100	L1101	V1102	L1103	P1104	V1105	T1106	G1107	A1108	H1109	D1110	G1111	S1112	A1114	T1115	L1116	F1117	
R1118	E1119	L1120	D1121	T1122	R1123	L1124	A1125	E1126	L1127	L1128	L1129	T1130	G1131	Y1132	G1133	T1134	S1135	D1136	S1138	F1143	E1148	E1149	C1150	ALA	ALA	ASP	THR	ASP	ASP	ASP	ASP	GLY	GLY	CYS	GLN	HIS	LEU	CYS	THR	THR	ILE	ALA	GLY	LEU	ASP	VAL	THR	LEU	ARG	LEU	LYS	PRO	PRO	GLN				
GLU	THR	ALA	LEU	GLU	GLY	GLU	ALA	ALA	SER	ALA	PRO	GLU	THR	ASP	GLN	SER	GLY	PRO	ALA	VAL	GLY	ARG	VAL	GLN	GLY	V1214	A1215	L1216	Q1219	A1223	K1227	R1228	F1229	L1230	L1231	R1232	R1233	R1234	S1235	A1236	R1237	G1238	L1239	F1240	A1241	Q1242	T1243	V1244	L1245	P1246	A1247	L1248						
F1249	V1250	G1251	L1252	A1253	L1254	V1255	F1256	L1258	I1259	V1260	G1264	H1265	V1280	F1283	S1284	D1290	R1293	L1301	L1306	V1311	Q1312	H1313	S1314	S1315	H1316	R1317	F1318	P1321	E1322	V1323	P1324	A1325	E1326	V1327	A1328	K1329	N1335	G1345	L1355	L1356	C1359	A1362	P1367															
A1371	V1372	T1373	V1378	L1398	W1408	R1413	Y1414	G1415	R1422	G1425	L1426	P1427	S1428	G1429	Q1430	E1431	L1432	G1433	R1434	S1435	E1436	E1437	L1438	L1439	W1440	A1441	L1442	L1443	P1447	G1448	G1449	D1452	E1459	L1465	D1466	A1467	Q1468	W1474	M1477	K1478	S1491	L1499																
A1504	R1505	H1506	A1507	L1517	M1518	L1519	T1520	Q1523	L1524	S1525	E1526	G1527	A1528	M1530	A1531	S1532	S1533	V1534	D1535	V1536	L1537	V1538	V1542	V1543	F1544	A1545	F1548	F1553	T1554	L1555	E1559	E1560	R1561	V1562	T1563	R1564	H1567	Q1569	L1570	M1571	G1572	G1573	L1574	S1575	P1576	T1577	L1578	L1581										
G1582	N1583	F1584	D1587	M1588	C1589	N1590	Y1591	L1592	V1593	C1596	I1597	V1598	V1599	L1600	T1601	F1602	L1603	A1604	F1605	Q1606	Q1607	R1608	A1609	Y1610	V1611	A1612	P1613	A1618	L1619	L1620	L1621	L1622	L1625	Y1626	G1627	W1628	S1629	T1630	T1631	P1632	L1633	M1634	Y1635	P1636	A1637	F1640	F1641	S1642	S1645	T1646	A1647	T1648	V1649					
C1653	L1656	F1657	I1658	G1659	T1660	N1661	G1662	S1663	M1664	T1666	F1667	V1668	L1669	E1670	L1671	F1672	S1673	D1674	Q1675	K1676	L1677	Q1678	E1679	V1680	S1681	R1682	T1683	L1684	K1685	Q1686	V1687	F1688	I1690	F1691	F1694	L1700	I1701	D1702	M1706	Q1707	A1708	M1709	D1710	A1711	A1712	F1713	E1714	R1715	L1716	G1717	D1718	R1719						
Q1722	R1726	V1729	V1730	G1731	M1732	M1733	L1734	L1735	I1739	Q1740	P1742	L1743	F1744	L1745	L1746	F1747	T1748	L1749	L1750	L1751	Q1752	H1753	R1754	S1755	F1756	LEU	LEU	PRO	GLN	PRO	ARG	VAL	L1689	SER	LEU	PRO	LEU	GLY	GLU	ASP	E1774	D1775	V1776	A1777	E1778	E1779	R1780	E1781	L1782	V1783	V1784	Q1785						
G1786	A1787	T1788	Q1789	D1791	V1792	L1793	V1794	L1795	R1796	N1797	T1798	L1799	K1800	V1801	R1802	R1803	G1804	Q1805	R1806	M1807	P1808	A1809	V1810	D1811	R1812	L1813	L1814	L1815	G1816	T1817	P1818	L1819	G1820	E1821	L1822	F1823	G1824	L1825	L1826	G1827	V1828	N1829	G1830	A1831	G1832	K1833	T1834	S1835	T1836	F1837	R1838	M1839	V1840	T1841	G1842	T1843	L1844	L1845
A1846	S1847	R1848	G1849	A1851	V1852	L1853	A1854	G1855	H1856	S1857	V1858	A1859	R1860	E1861	R1862	S1863	A1864	A1865	H1866	L1867	S1868	M1869	G1870	Y1871	C1872	P1873	Q1874	S1875	D1876	A1877	L1878	F1879	E1880	L1881	L1882	T1883	G1884	R1885	E1886	L1887	L1888	E1889	L1890	R1893	L1894	R1895	E1899	A1900	Q1901	V1902	A1903	Q1904	T1905	L1968	L1969	A1906	G1907	S1908
G1909	L1910	A1911	R1912	L1913	G1914	L1915	S1916	Y1917	Y1918	A1919	D1920	R1921	P1922	A1923	G1924	T1925	Y1926	S1927	G1928	G1929	R1932	K1933	L1934	A1937	L1938	A1939	L1940	V1941	G1942	A1945	V1946	V1947	F1948	D1949	D1950	Q1951	P1952	T1953	G1954	T1955	M1956	D1957	P1958	S1959	L1960	R1961	R1962	F1963	L1964	V1965	M1966	S1967	L1968	L1969	A1970	V1971		

E2094	E2095	V2096	F2097	L2098	Y2099	F2100	S2101	K2102	D2103	GLN	GLY	LYS	ASP	GLU	ASP	THR	GLU	GLU	GLN	LYS	GLU	ALA	GLY	VAL	GLY	VAL	ASP	PRO	ALA	PRO	GLY	LEU	GLN	HIS	PRO	LYS	ARG	VAL	SER	SER	GLN	PHE	LEU	ASP	ASP	PRO	SER	THR	ALA	GLU	THR	VAL	LEU						
Q2032	P2033	A2036	F2037	V2038	A2039	A2040	E2041	F2042	P2043	G2044	A2045	E2046	L2047	R2048	E2049	A2050	H2051	G2052	G2053	R2054	L2055	R2056	F2057	Q2058	L2059	P2060	P2061	G2062	G2063	R2064	C2065	A2066	L2067	A2068	R2069	V2070	F2071	G2072	E2073	L2074	A2075	V2076	H2077	G2078	A2079	E2080	H2081	G2082	V2083	E2084	D2085	F2086	S2089	Q2090	T2091	M2092	L2093		
V1972	R1973	E1974	G1975	R1976	S1977	V1978	M1979	L1980	T1981	S1982	H1983	S1984	M1985	E1986	E1987	C1988	E1989	A1990	L1991	C1992	S1993	R1994	L1995	A1996	I1997	M1998	V1999	N2000	G2001	R2002	F2003	R2004	C2005	L2006	G2007	S2008	P2009	Q2010	H2011	L2012	K2013	G2014	R2015	F2016	A2017	A2018	G2019	H2020	T2021	L2022	T2023	L2024	R2025	V2026	F2027	A2028	A2029	R2030	S2031

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44853	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.165	Depositor
Minimum map value	-0.655	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.162	Depositor
Map size (Å)	299.6, 299.6, 299.6	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.25	0/14567	0.57	8/19812 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1979	MET	CB-CG-SD	9.48	141.16	112.70
1	A	898	VAL	N-CA-C	8.51	120.27	111.00
1	A	506	LEU	N-CA-C	-6.68	103.69	110.97
1	A	897	THR	CB-CA-C	6.08	122.52	110.42
1	A	70	LEU	N-CA-C	-5.96	104.47	110.97

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	14226	0	14439	264	0
All	All	14226	0	14439	264	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 9.

The worst 5 of 264 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:1245:LEU:O	1:A:1249:PHE:HB2	1.65	0.95
1:A:1280:VAL:HG12	1:A:1378:VAL:HB	1.69	0.73
1:A:897:THR:O	1:A:901:HIS:HB2	1.88	0.72
1:A:815:ARG:HD2	1:A:822:PRO:HA	1.72	0.72
1:A:1636:PRO:HB3	1:A:1751:LEU:HD21	1.72	0.71

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	1826/2146 (85%)	1722 (94%)	104 (6%)	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	1505/1764 (85%)	1505 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
1	A	1901	GLN
1	A	1805	GLN
1	A	1488	ASN
1	A	1785	GLN
1	A	1316	HIS

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.

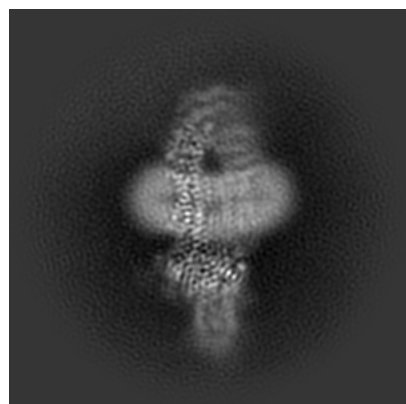
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38841. These allow visual inspection of the internal detail of the map and identification of artifacts.

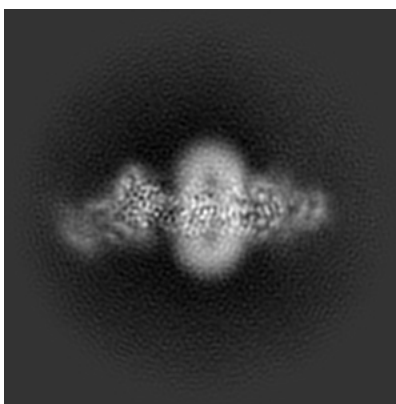
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

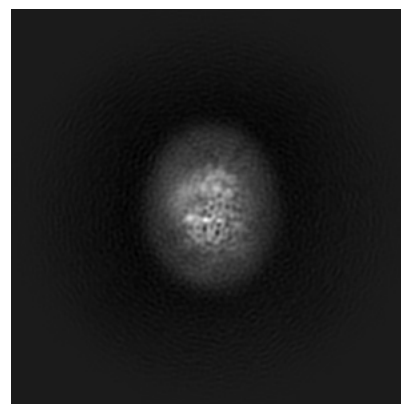
6.1.1 Primary map



X

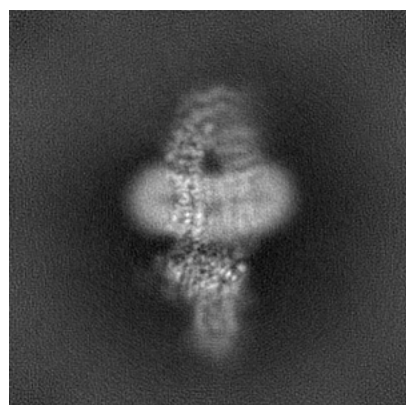


Y

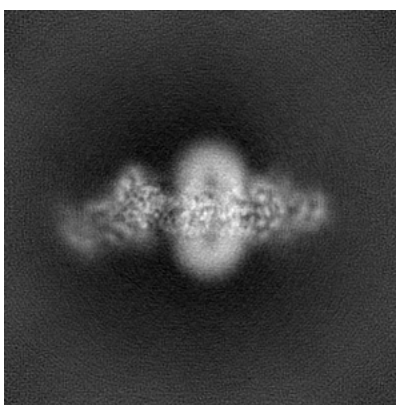


Z

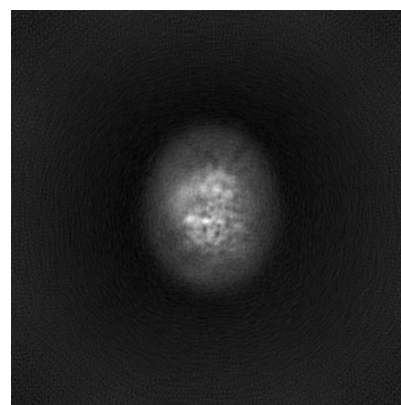
6.1.2 Raw map



X



Y

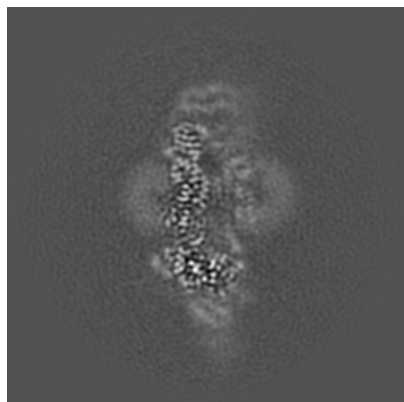


Z

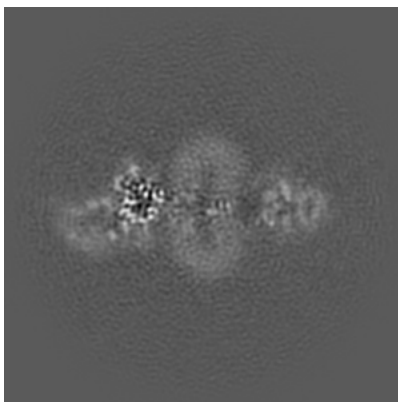
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

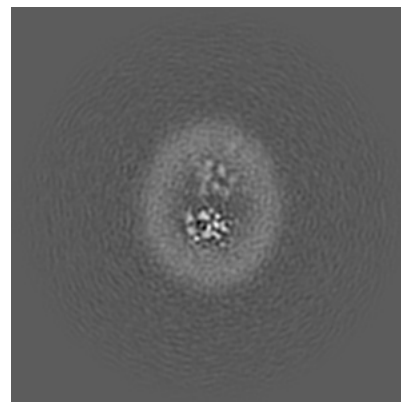
6.2.1 Primary map



X Index: 140

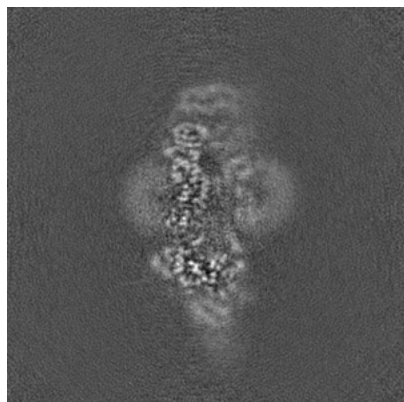


Y Index: 140

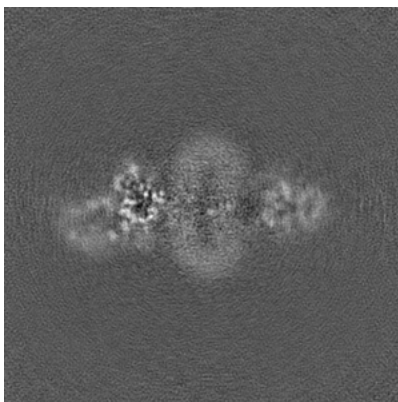


Z Index: 140

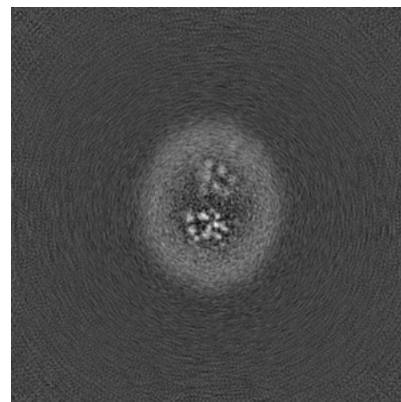
6.2.2 Raw map



X Index: 140



Y Index: 140

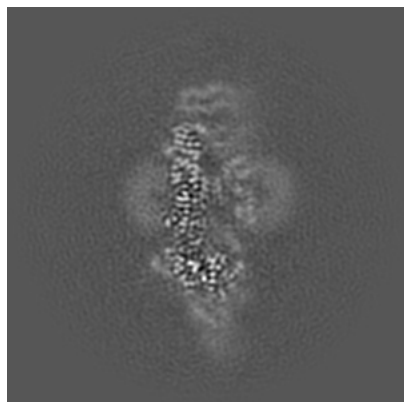


Z Index: 140

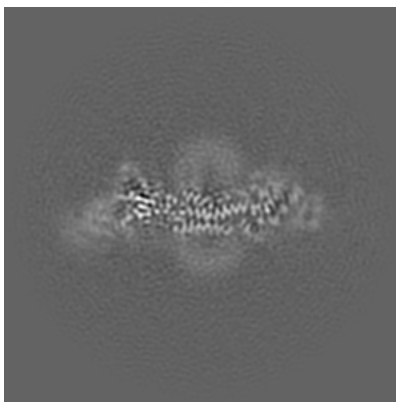
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

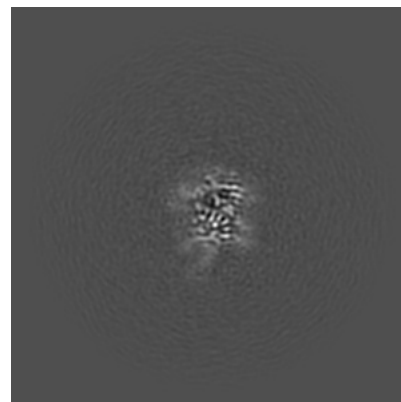
6.3.1 Primary map



X Index: 139

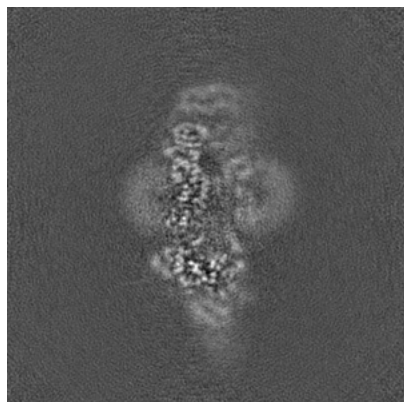


Y Index: 132

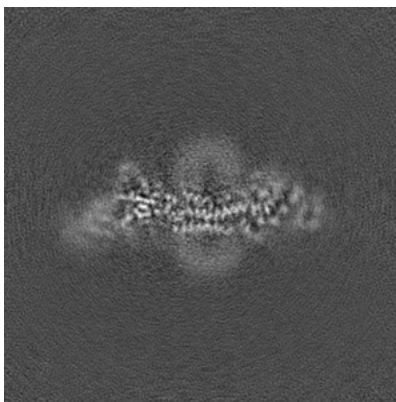


Z Index: 95

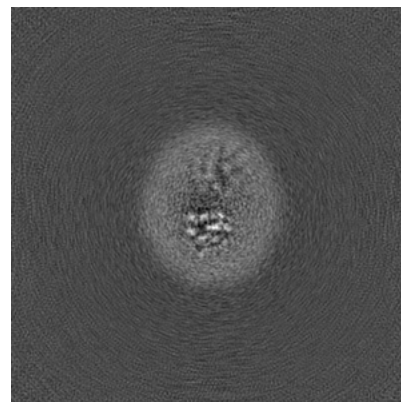
6.3.2 Raw map



X Index: 140



Y Index: 132

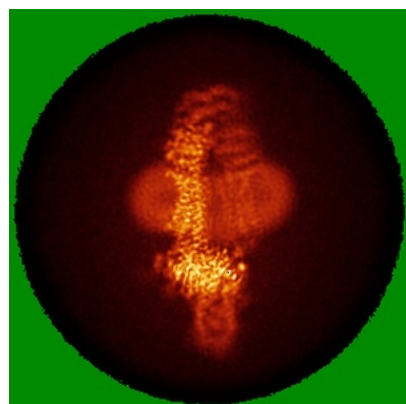


Z Index: 136

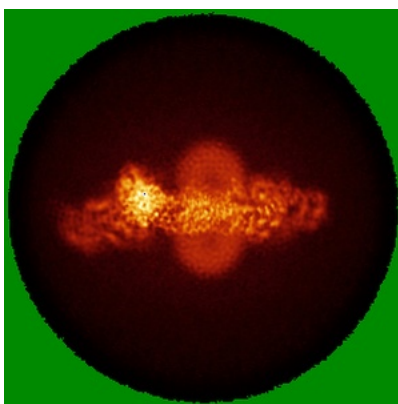
The images above show the largest variance slices of the map in three orthogonal directions.

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

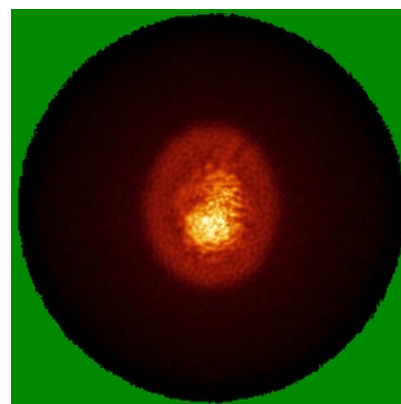
6.4.1 Primary map



X

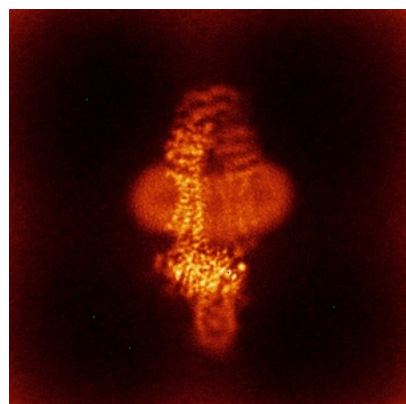


Y

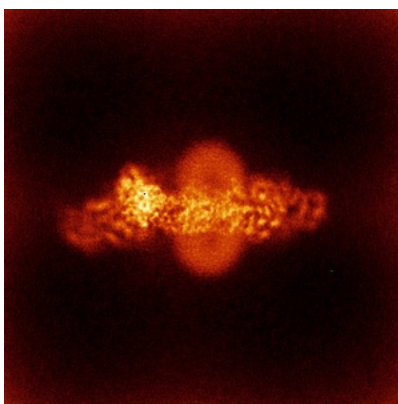


Z

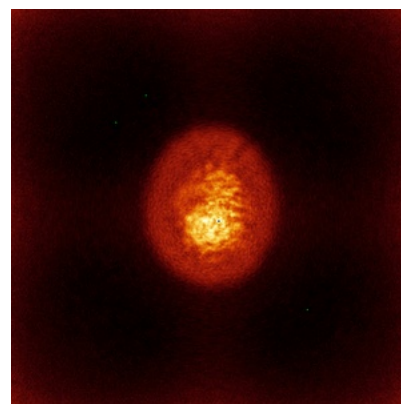
6.4.2 Raw map



X



Y

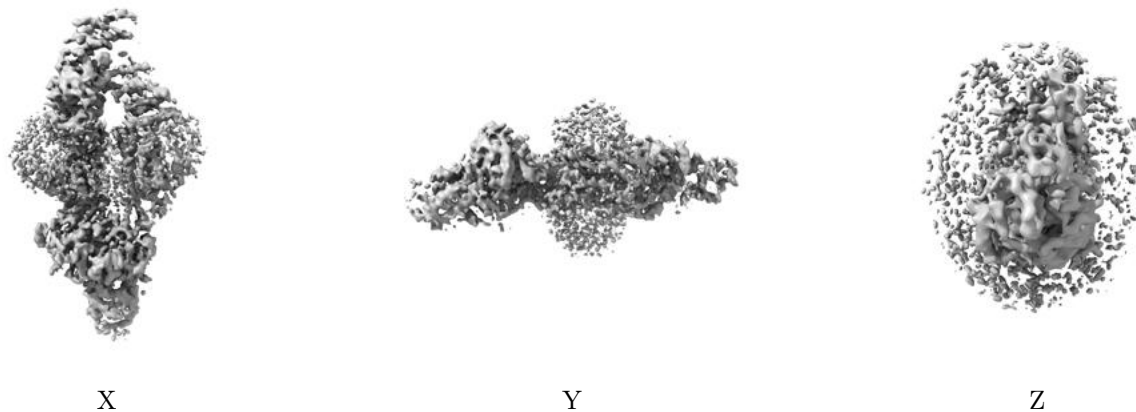


Z

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.

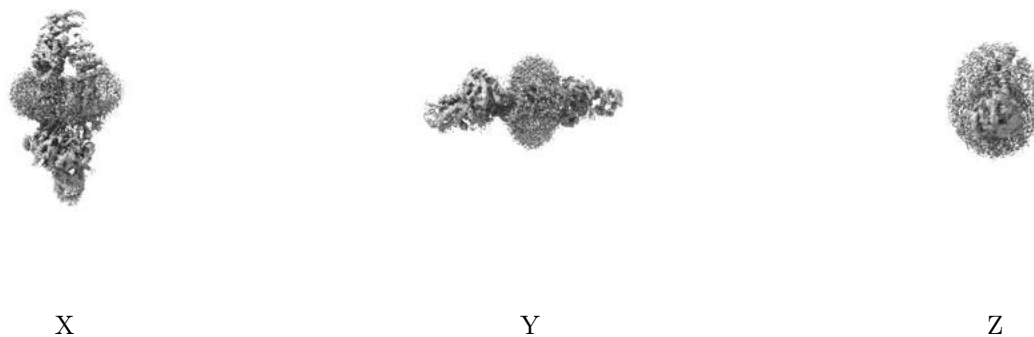
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.162. 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.

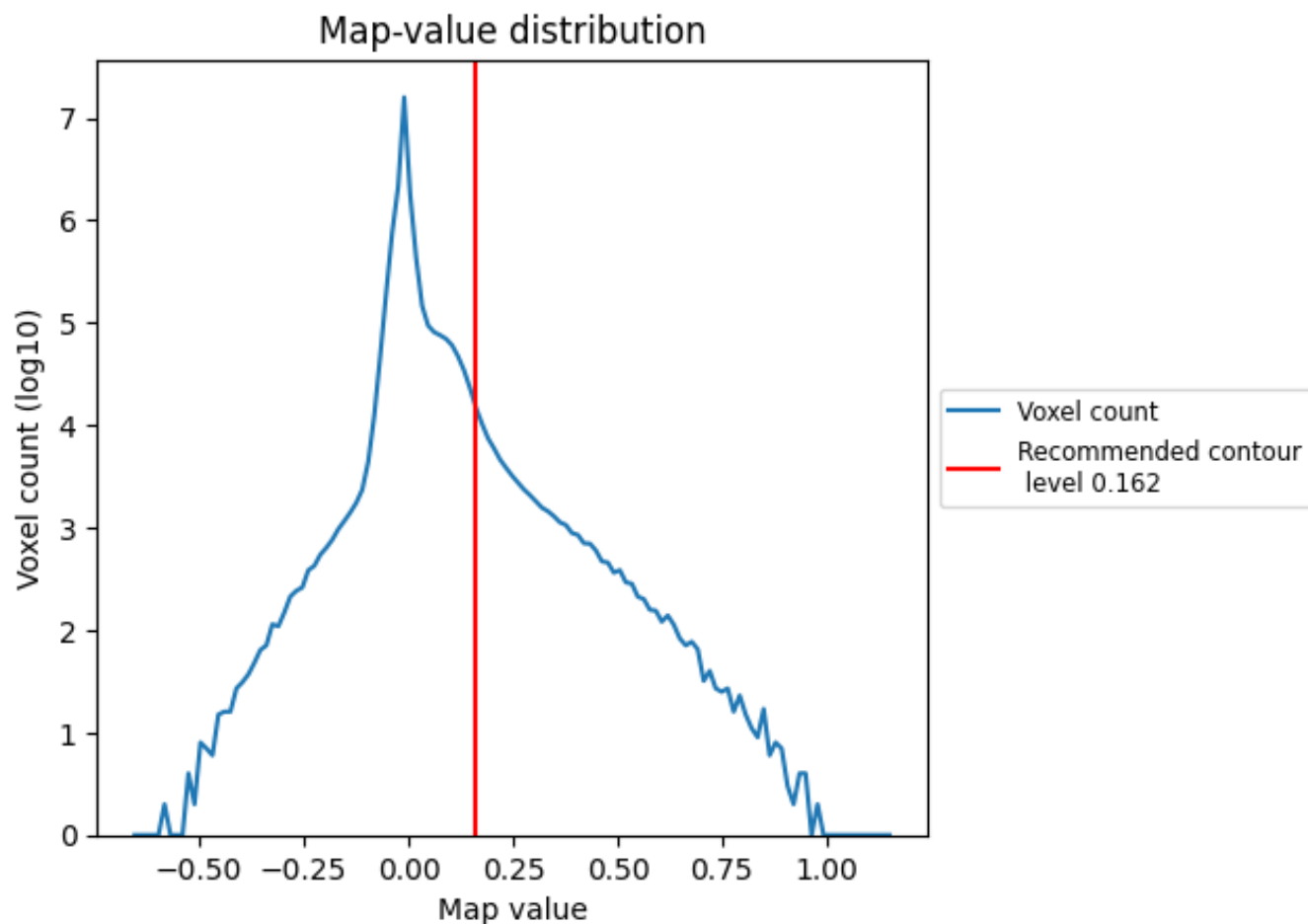
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

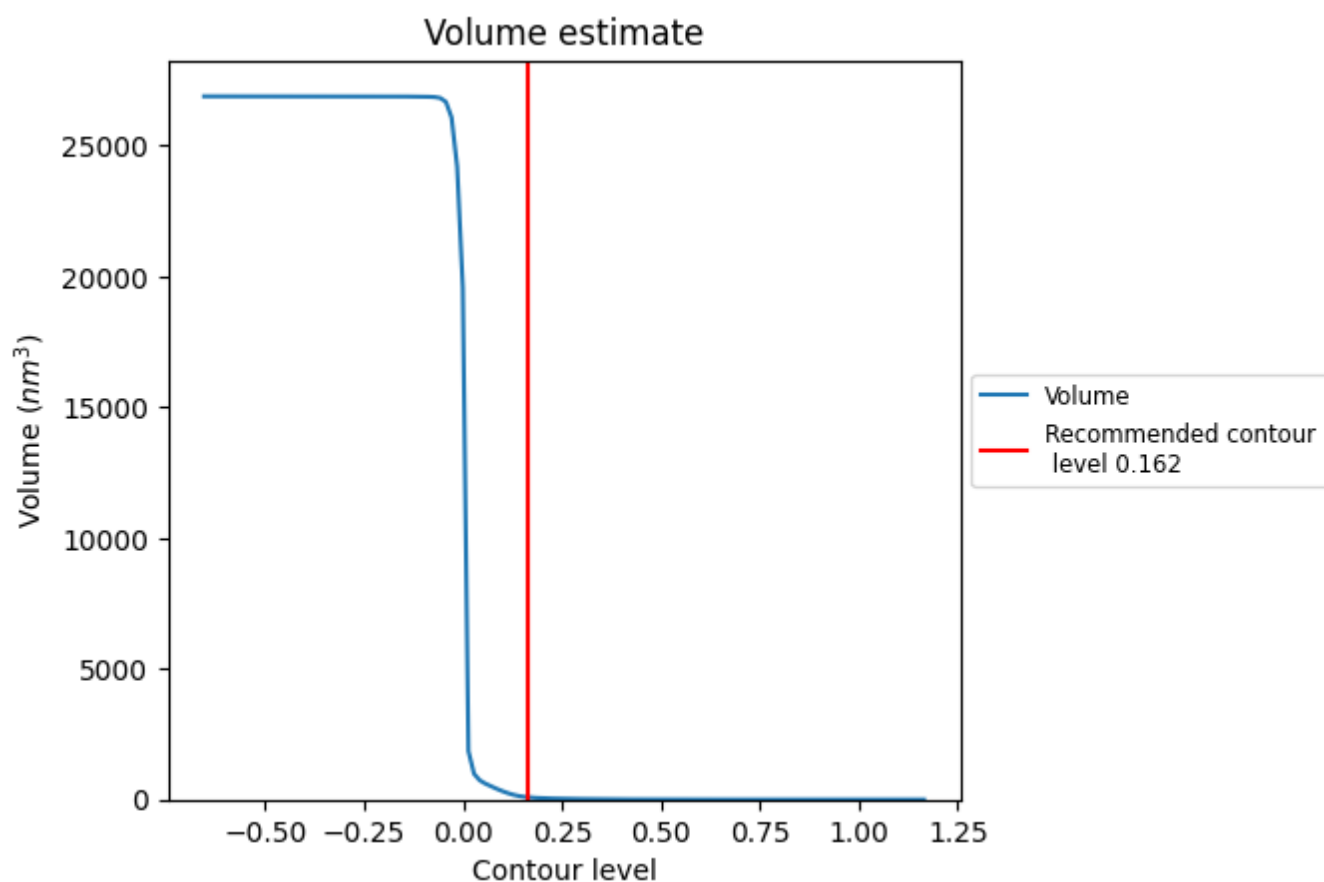
This section contains the results of statistical analysis of the map.

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.

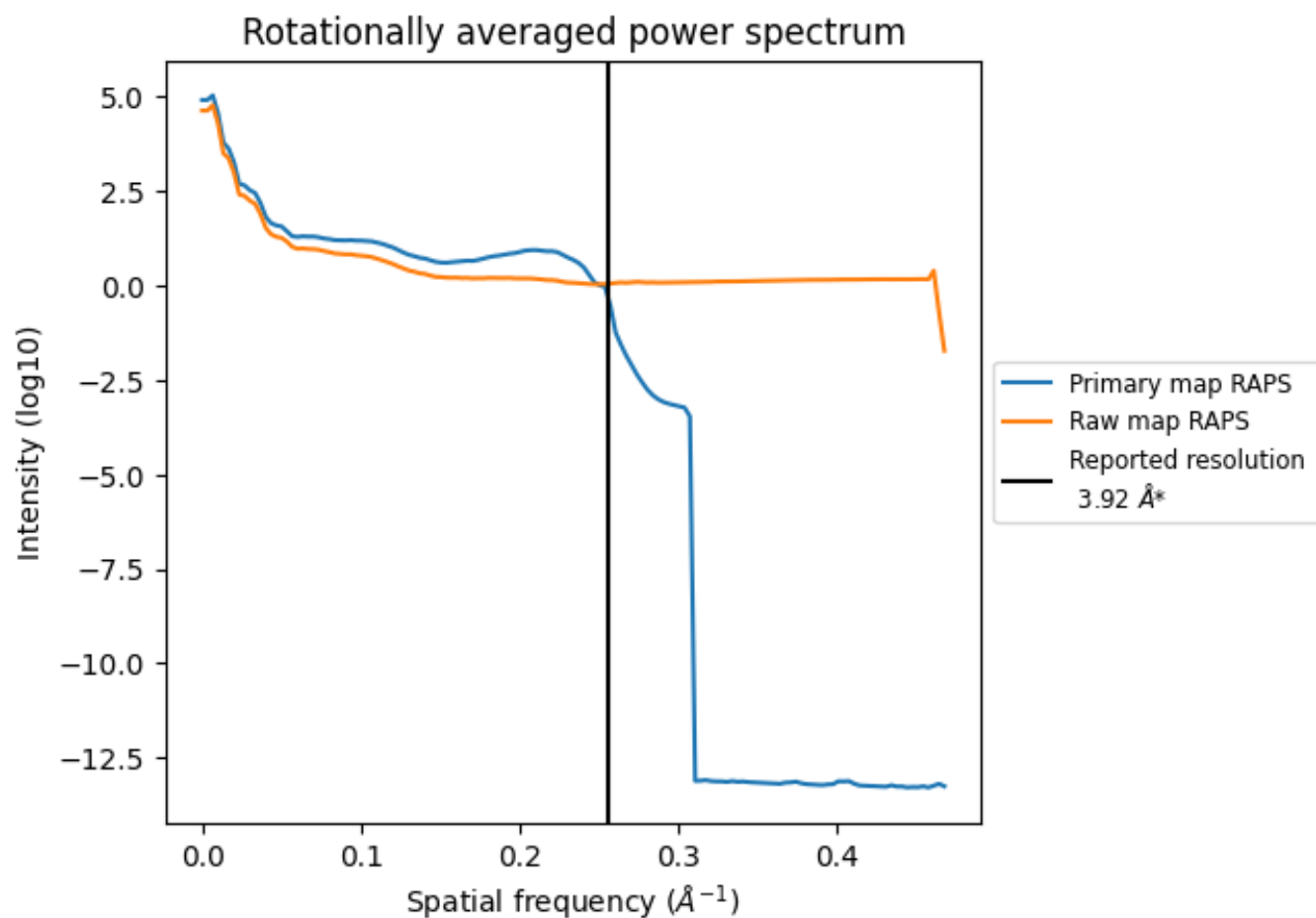
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 91 nm^3 ; this corresponds to an approximate mass of 82 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 ⓘ

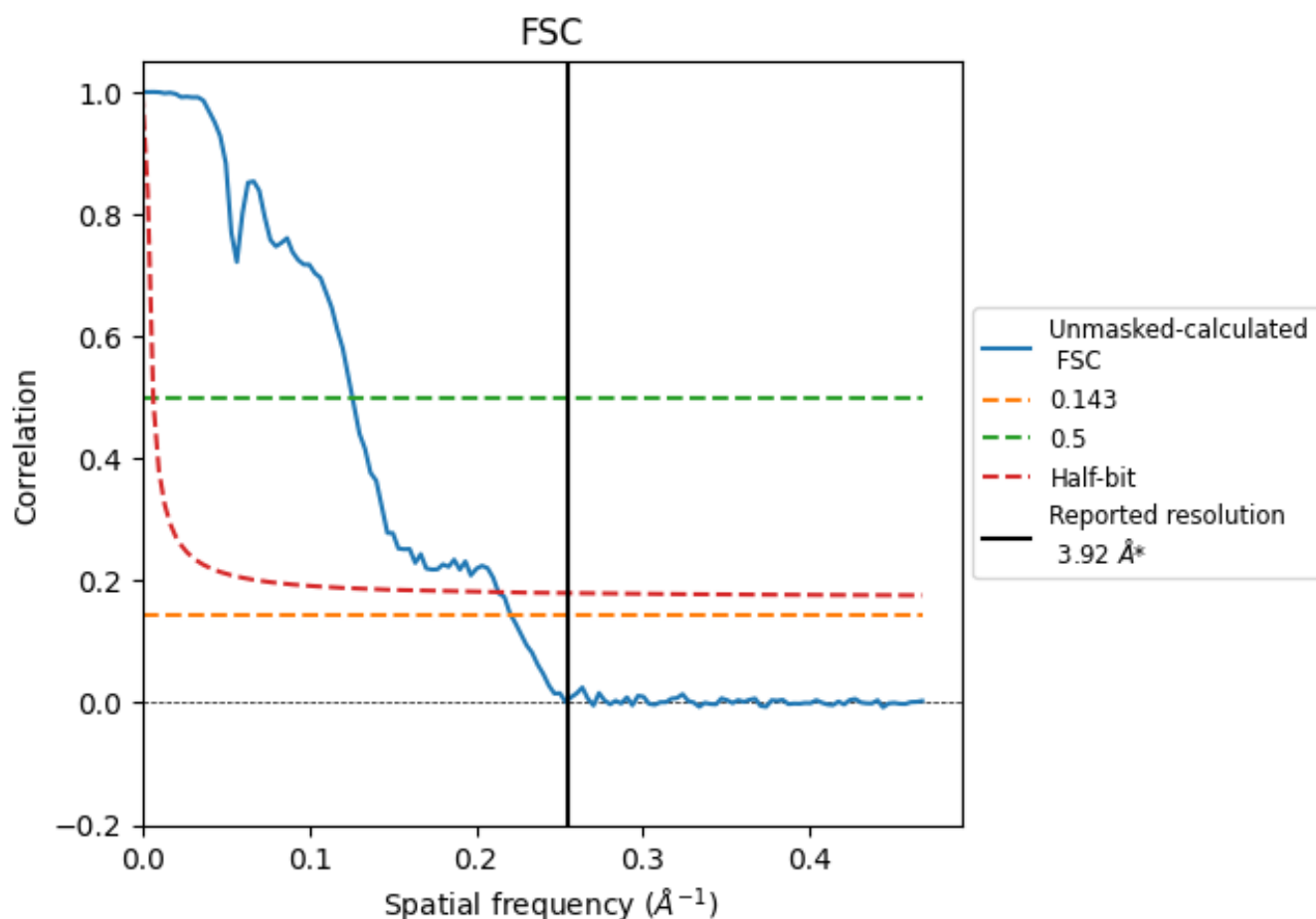


*Reported resolution corresponds to spatial frequency of 0.255 Å⁻¹

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 0.255 Å⁻¹

8.2 Resolution estimates [i](#)

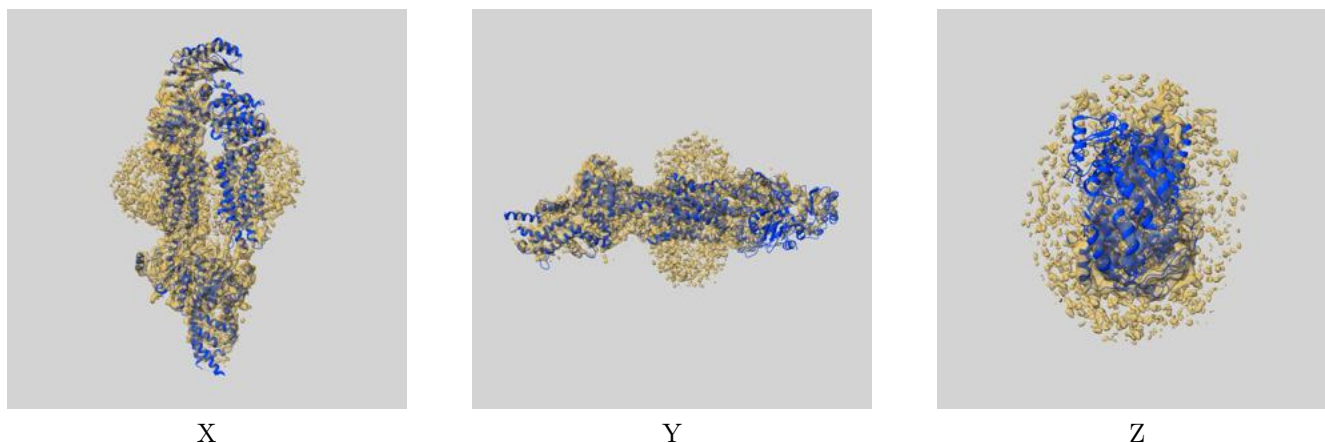
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.92	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.52	7.94	4.69

*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 4.52 differs from the reported value 3.92 by more than 10 %

9 Map-model fit [i](#)

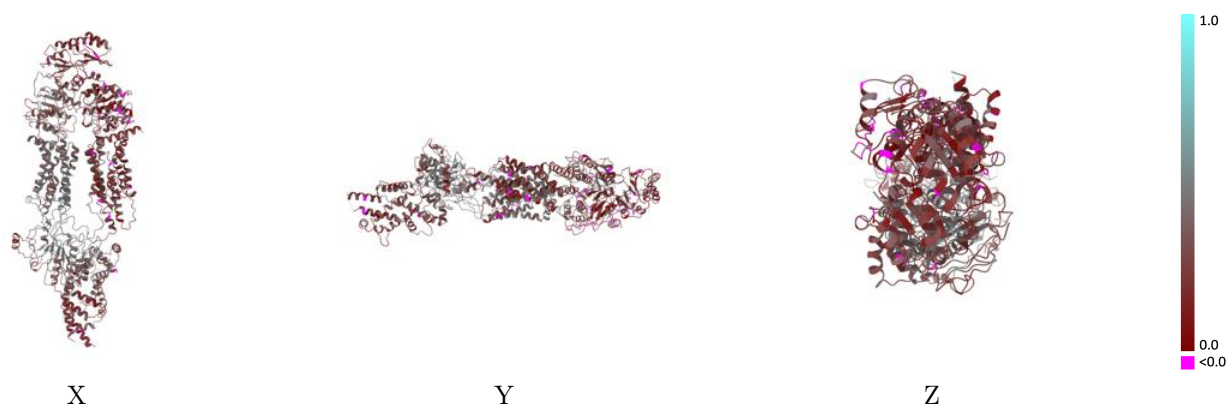
This section contains information regarding the fit between EMDB map EMD-38841 and PDB model 8Y1O. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.162 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](#)

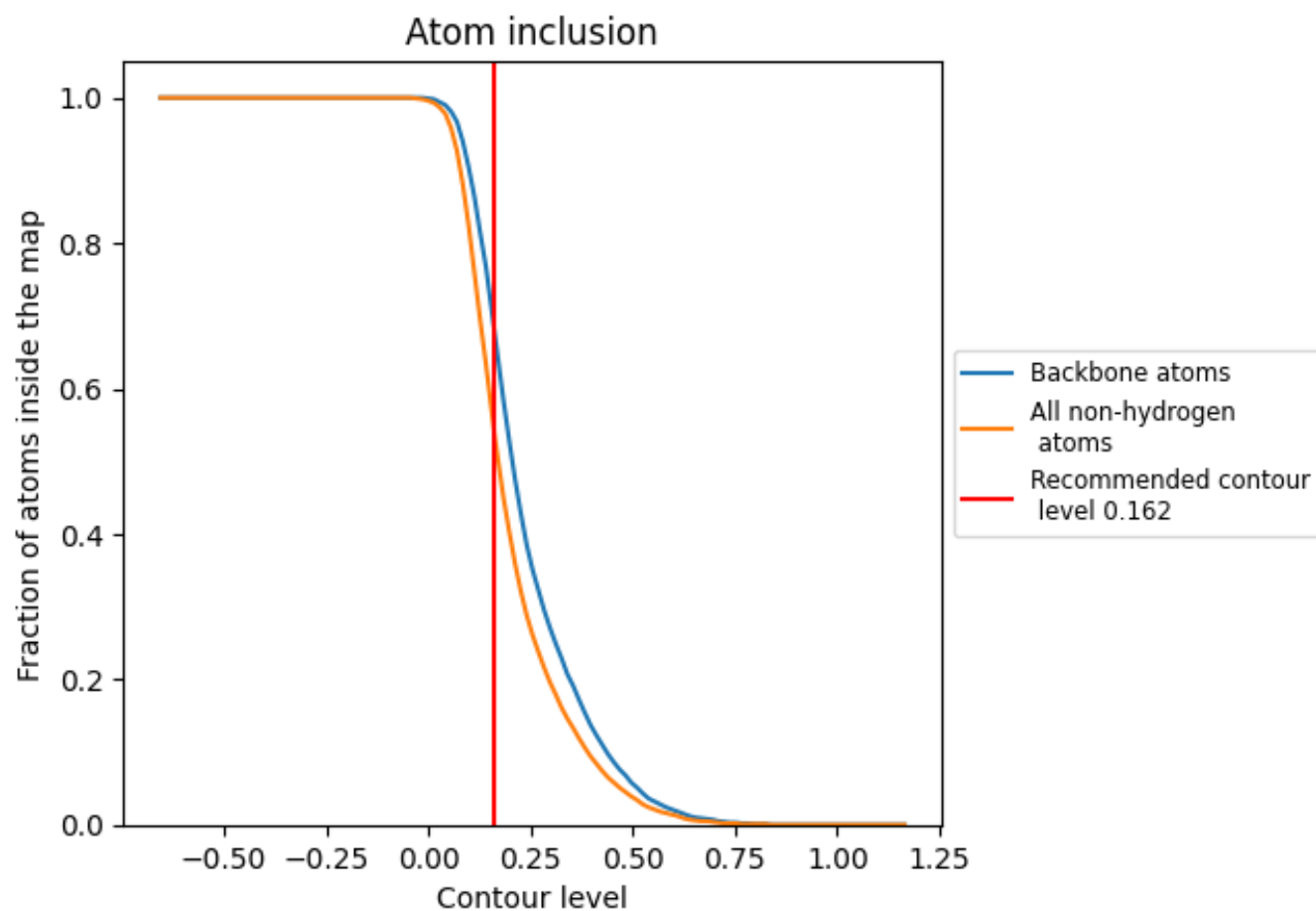


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 68% of all backbone atoms, 54% 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 (0.162) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5360	0.3220
A	0.5360	0.3220

