



Full wwPDB EM Validation 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 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

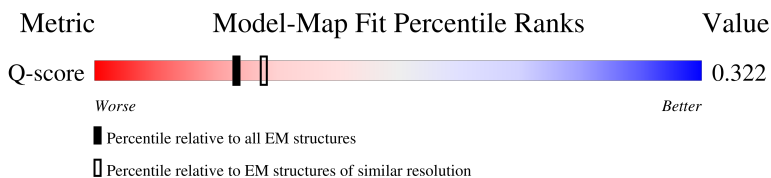
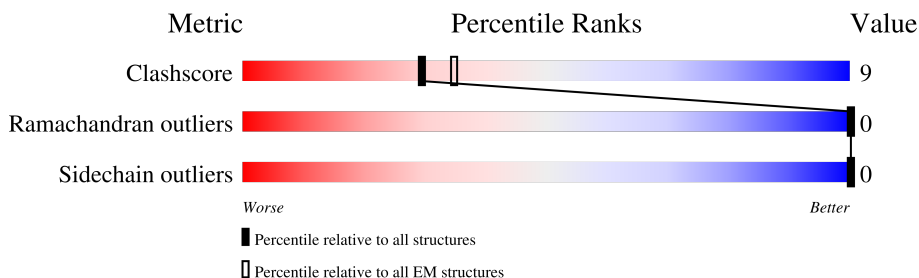
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.92 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.

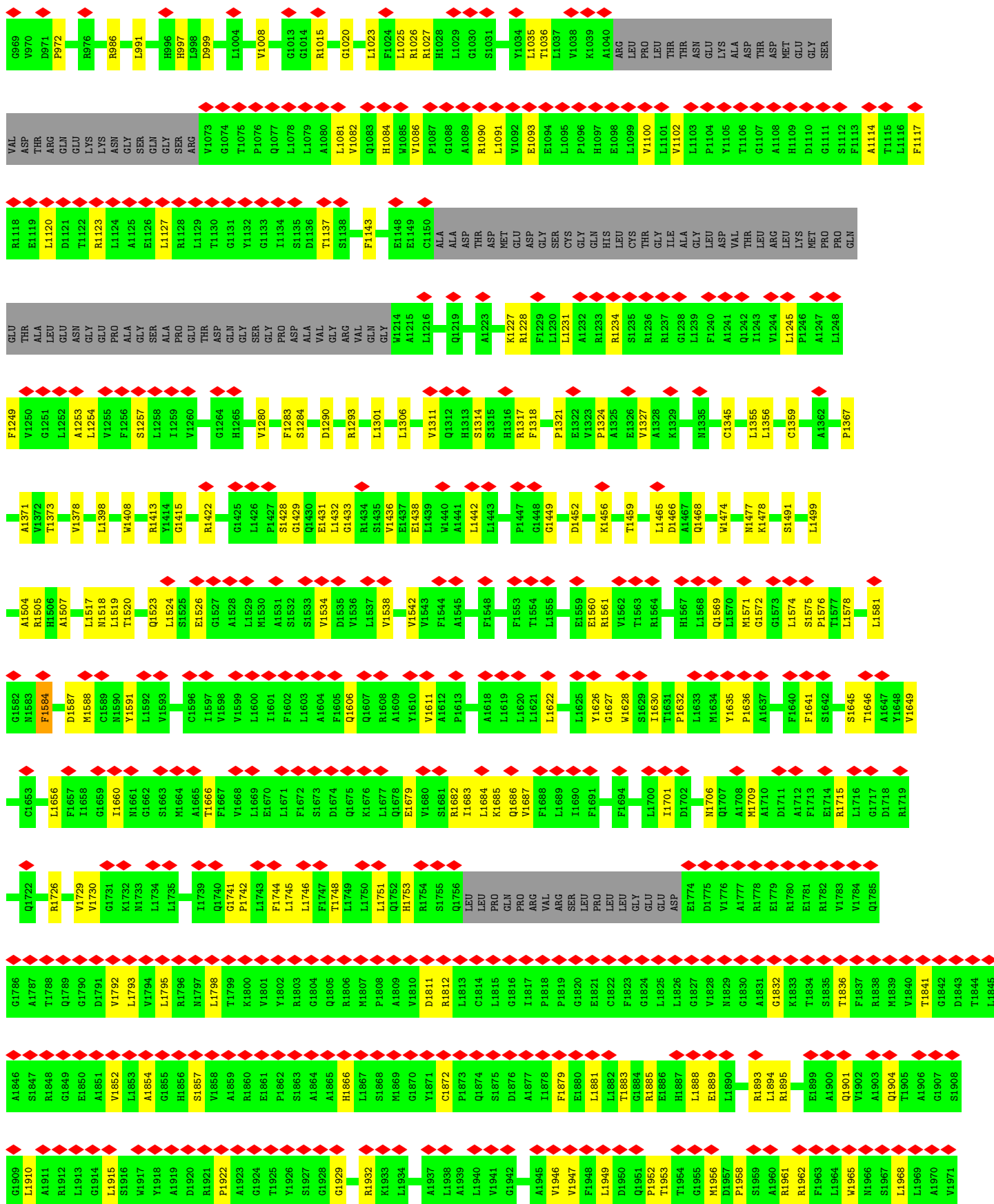
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- 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



E2094	Q2032	V1972
E2095	P2033	R1973
V2096	A2036	E1974
P2097	P2037	G1975
L2098	V2038	R1976
Y2099	A2039	S1977
F2100	A2040	V1978
K2101	E2041	M1979
K2102	P2042	L1980
D2103	P2043	T1981
GLN	G2044	H1983
GLY	A2045	S1984
GLN	E2046	M1985
LYS	L2047	E1986
ASP	R2048	E1987
THR	E2049	C1988
GLU	A2050	E1989
GLN	H2051	A1990
LYS	G2052	L1991
GLU	G2053	C1992
ALA	R2054	S1993
GLY	L2055	R1994
VAL	A2056	L1995
VAL	P2057	M1996
ASP	Q2058	L1997
PRO	L2059	M1998
PRO	P2060	V1999
LEU	P2061	H2000
GLN	G2062	G2001
HIS	P2063	R2002
PRO	R2064	F2003
LYS	A2065	R2004
ARG	C2066	C2005
VAL	A2066	L2006
SER	L2067	G2007
GLN	A2068	S2008
PHE	R2069	P2009
LEU	V2070	Q2010
ASP	F2071	H2011
ASP	G2072	L2012
PRO	E2073	K2013
SER	L2074	G2014
THR	A2075	P2015
GLU	V2076	F2016
THR	H2077	A2017
VAL	G2078	A2018
LEU	A2079	G2019
	E2080	H2020
	H2081	T2021
	G2082	L2022
	V2083	T2023
	E2084	L2024
	D2085	R2025
	F2086	V2026
		F2027
	S2089	A2028
	Q2090	A2029
	T2091	R2030
	M2092	H2031
	L2093	

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.

All (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
1	A	1584	PHE	N-CA-CB	5.32	119.22	110.39
1	A	506	LEU	CB-CA-C	5.15	118.89	110.96
1	A	330	MET	CB-CG-SD	5.03	127.77	112.70

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.

All (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
1:A:1438:GLU:O	1:A:1442:LEU:HB2	1.90	0.70
1:A:1965:TRP:HA	1:A:1968:LEU:HG	1.77	0.67
1:A:1093:GLU:HB3	1:A:1100:VAL:HB	1.78	0.66
1:A:897:THR:O	1:A:938:ARG:NH2	2.31	0.64
1:A:561:SER:HB3	1:A:603:PHE:HE1	1.63	0.63
1:A:2013:LYS:HE2	1:A:2093:LEU:HD22	1.80	0.63
1:A:1290:ASP:OD1	1:A:1293:ARG:NH1	2.32	0.62
1:A:1449:GLY:HA2	1:A:1452:ASP:HB2	1.80	0.62
1:A:1628:TRP:HZ3	1:A:1741:GLY:HA3	1.66	0.61
1:A:1968:LEU:HD11	1:A:1991:LEU:HD22	1.82	0.61
1:A:2020:HIS:HB3	1:A:2090:GLN:HB2	1.82	0.61
1:A:293:GLY:HA3	1:A:435:TRP:HB2	1.84	0.60
1:A:319:THR:HB	1:A:407:LEU:HD11	1.82	0.60
1:A:322:ARG:O	1:A:325:ARG:HB3	2.01	0.60
1:A:1932:ARG:HH21	1:A:1956:MET:HG3	1.66	0.60
1:A:1571:MET:HE1	1:A:1841:THR:HG23	1.84	0.60
1:A:475:ARG:HE	1:A:477:ASN:HD21	1.47	0.60
1:A:2092:MET:N	1:A:2092:MET:SD	2.75	0.59
1:A:1314:SER:HA	1:A:1317:ARG:HB2	1.84	0.59
1:A:836:ILE:HD11	1:A:986:ARG:HB2	1.84	0.59
1:A:58:ASN:OD1	1:A:530:GLN:NE2	2.37	0.58
1:A:321:LEU:HD21	1:A:404:THR:HG21	1.84	0.58
1:A:2013:LYS:HA	1:A:2017:ALA:HB3	1.86	0.57
1:A:2096:VAL:O	1:A:2099:TYR:HB3	2.05	0.57
1:A:1793:LEU:HD21	1:A:1946:VAL:HG11	1.86	0.57
1:A:2021:THR:OG1	1:A:2089:SER:O	2.21	0.57
1:A:1253:ALA:O	1:A:1257:SER:HB3	2.04	0.57
1:A:1682:ARG:O	1:A:1686:GLN:HG2	2.05	0.57
1:A:2005:CYS:SG	1:A:2006:LEU:N	2.76	0.57
1:A:888:GLN:O	1:A:946:ARG:NH1	2.38	0.57
1:A:308:MET:HB3	1:A:412:LEU:HD21	1.85	0.56
1:A:485:ASP:O	1:A:1478:LYS:NZ	2.38	0.56
1:A:1949:LEU:H	1:A:1979:MET:HE3	1.68	0.56
1:A:1036:THR:HG22	1:A:1100:VAL:HG22	1.88	0.56
1:A:319:THR:O	1:A:322:ARG:HB2	2.06	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:863:GLY:O	1:A:873:ARG:NH2	2.38	0.56
1:A:1355:LEU:HD23	1:A:1356:LEU:HG	1.86	0.56
1:A:1234:ARG:HB3	1:A:1881:LEU:HB3	1.86	0.56
1:A:1504:ALA:HA	1:A:1507:ALA:HB3	1.88	0.56
1:A:474:THR:HG23	1:A:497:ARG:HB2	1.87	0.56
1:A:825:ARG:HH11	1:A:1015:ARG:HG3	1.71	0.56
1:A:490:ALA:HB2	1:A:531:GLN:HE22	1.70	0.55
1:A:807:VAL:HG12	1:A:867:ILE:HD12	1.88	0.55
1:A:1560:GLU:OE2	1:A:1569:GLN:NE2	2.38	0.55
1:A:496:LEU:O	1:A:500:TRP:NE1	2.38	0.55
1:A:206:LEU:HA	1:A:209:ARG:HD3	1.88	0.55
1:A:1228:ARG:HA	1:A:1231:LEU:HD12	1.87	0.55
1:A:1574:LEU:HD11	1:A:1894:LEU:HD22	1.87	0.55
1:A:1632:PRO:HG2	1:A:1744:PHE:HB2	1.88	0.55
1:A:308:MET:HA	1:A:311:VAL:HG12	1.88	0.54
1:A:1227:LYS:O	1:A:1231:LEU:HG	2.08	0.54
1:A:2021:THR:OG1	1:A:2095:GLU:OE2	2.25	0.54
1:A:492:PRO:HA	1:A:496:LEU:HB2	1.89	0.54
1:A:32:PRO:HB3	1:A:557:ALA:HB1	1.90	0.54
1:A:504:VAL:HA	1:A:507:GLN:HB3	1.89	0.54
1:A:921:ASP:N	1:A:921:ASP:OD1	2.40	0.54
1:A:1321:PRO:HG2	1:A:1367:PRO:HB2	1.90	0.54
1:A:1729:VAL:HG12	1:A:1730:VAL:HG13	1.89	0.54
1:A:1901:GLN:NE2	1:A:1904:GLN:OE1	2.41	0.53
1:A:109:ALA:O	1:A:113:LEU:HB2	2.09	0.53
1:A:1293:ARG:NH2	1:A:1468:GLN:O	2.41	0.53
1:A:1314:SER:OG	1:A:1317:ARG:NH2	2.41	0.53
1:A:1345:CYS:HA	1:A:1359:CYS:HB3	1.91	0.53
1:A:2048:ARG:HB3	1:A:2056:ARG:HE	1.73	0.53
1:A:1587:ASP:OD2	1:A:1635:TYR:OH	2.26	0.53
1:A:512:ARG:NH2	1:A:523:PRO:O	2.31	0.53
1:A:809:VAL:HG23	1:A:865:ALA:HA	1.90	0.53
1:A:815:ARG:NH1	1:A:821:GLN:O	2.41	0.53
1:A:872:VAL:HG13	1:A:876:MET:SD	2.49	0.53
1:A:1231:LEU:HD21	1:A:1879:PHE:CD2	2.44	0.53
1:A:1885:ARG:HA	1:A:1888:LEU:HD12	1.91	0.53
1:A:1398:LEU:HD11	1:A:1413:ARG:HH21	1.73	0.53
1:A:815:ARG:NH2	1:A:816:PHE:O	2.42	0.52
1:A:2103:ASP:N	1:A:2103:ASP:OD1	2.42	0.52
1:A:12:TRP:HH2	1:A:900:GLU:HG3	1.74	0.52
1:A:797:GLU:HB3	1:A:1026:ARG:HH12	1.75	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:900:GLU:HA	1:A:903:TRP:HB3	1.90	0.52
1:A:2085:ASP:OD1	1:A:2086:PHE:N	2.42	0.52
1:A:333:PRO:O	1:A:336:PHE:HB3	2.10	0.52
1:A:1520:THR:N	1:A:1523:GLN:OE1	2.43	0.52
1:A:489:ALA:O	1:A:1477:ASN:ND2	2.39	0.51
1:A:911:LEU:HG	1:A:915:VAL:HG23	1.93	0.51
1:A:2013:LYS:HB3	1:A:2018:ALA:HB2	1.93	0.51
1:A:1811:ASP:OD1	1:A:1812:ARG:NH1	2.44	0.51
1:A:495:ASP:OD1	1:A:495:ASP:N	2.44	0.51
1:A:963:LEU:HD23	1:A:966:PRO:HG3	1.92	0.51
1:A:1090:ARG:NH1	1:A:1091:LEU:O	2.44	0.51
1:A:1606:GLN:HA	1:A:1611:VAL:HG21	1.91	0.50
1:A:307:LEU:HG	1:A:440:PHE:CZ	2.46	0.50
1:A:838:ALA:HB3	1:A:1008:VAL:HG22	1.93	0.50
1:A:1082:VAL:O	1:A:1086:VAL:N	2.44	0.50
1:A:1949:LEU:N	1:A:1979:MET:HE3	2.26	0.50
1:A:565:THR:OG1	1:A:599:CYS:SG	2.60	0.50
1:A:1306:LEU:HB2	1:A:1373:THR:HG22	1.93	0.50
1:A:1984:SER:OG	1:A:1986:GLU:OE1	2.24	0.50
1:A:469:ASP:HB3	1:A:472:VAL:HG23	1.94	0.50
1:A:1591:TYR:CE2	1:A:1627:GLY:HA3	2.47	0.50
1:A:379:PRO:HD3	1:A:386:TRP:HE1	1.76	0.50
1:A:1254:LEU:HD13	1:A:1538:VAL:HG11	1.94	0.50
1:A:560:TYR:CZ	1:A:564:LEU:HD21	2.47	0.50
1:A:897:THR:C	1:A:938:ARG:NH2	2.70	0.50
1:A:1561:ARG:NH2	1:A:1641:PHE:O	2.45	0.50
1:A:1872:CYS:HB3	1:A:1949:LEU:HA	1.93	0.49
1:A:61:LEU:HD13	1:A:62:PRO:HD2	1.94	0.49
1:A:1020:GLY:HA3	1:A:1026:ARG:HH11	1.77	0.49
1:A:1035:LEU:O	1:A:1100:VAL:HA	2.13	0.49
1:A:494:THR:OG1	1:A:495:ASP:N	2.44	0.49
1:A:1311:VAL:HA	1:A:1314:SER:HB3	1.95	0.49
1:A:1519:LEU:HD13	1:A:1524:LEU:HA	1.95	0.49
1:A:615:LYS:HG3	1:A:625:PRO:HG3	1.94	0.49
1:A:658:ALA:HB1	1:A:1649:VAL:HG11	1.94	0.49
1:A:924:LEU:HD13	1:A:933:GLN:HG2	1.95	0.49
1:A:1852:VAL:HG12	1:A:1857:SER:HA	1.94	0.49
1:A:2022:LEU:O	1:A:2056:ARG:HA	2.13	0.49
1:A:1090:ARG:O	1:A:1102:VAL:N	2.40	0.49
1:A:2021:THR:HA	1:A:2057:PHE:O	2.13	0.49
1:A:898:VAL:O	1:A:902:VAL:HG12	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1684:LEU:HA	1:A:1687:VAL:HG12	1.95	0.48
1:A:97:PHE:O	1:A:103:SER:OG	2.28	0.48
1:A:498:TYR:HB3	1:A:504:VAL:HG13	1.96	0.48
1:A:1027:ARG:NH1	1:A:1137:THR:O	2.41	0.48
1:A:410:ASP:N	1:A:410:ASP:OD1	2.46	0.48
1:A:487:GLY:O	1:A:1478:LYS:NZ	2.32	0.48
1:A:815:ARG:NH2	1:A:819:SER:O	2.43	0.48
1:A:611:VAL:HG23	1:A:632:LEU:HD12	1.96	0.48
1:A:1023:LEU:HD12	1:A:2025:ARG:HD2	1.95	0.48
1:A:1889:GLU:O	1:A:1893:ARG:HG3	2.14	0.48
1:A:1114:ALA:HB2	1:A:2071:PHE:HB2	1.96	0.48
1:A:43:ARG:HH12	1:A:48:PRO:HD3	1.79	0.47
1:A:200:LEU:HA	1:A:203:LEU:HG	1.96	0.47
1:A:893:PHE:HB2	1:A:896:LEU:HB2	1.96	0.47
1:A:1081:LEU:HA	1:A:1084:HIS:HD1	1.79	0.47
1:A:582:ARG:HH21	1:A:857:LEU:HA	1.78	0.47
1:A:1523:GLN:HA	1:A:1526:GLU:HB3	1.96	0.47
1:A:290:LEU:O	1:A:411:LYS:NZ	2.35	0.47
1:A:809:VAL:HG22	1:A:812:LEU:HD21	1.96	0.47
1:A:324:VAL:O	1:A:327:VAL:HB	2.15	0.47
1:A:1456:LYS:O	1:A:1459:THR:OG1	2.25	0.47
1:A:1622:LEU:O	1:A:1626:TYR:HB3	2.15	0.47
1:A:654:ASN:OD1	1:A:1646:THR:OG1	2.31	0.46
1:A:807:VAL:HG12	1:A:867:ILE:HG23	1.97	0.46
1:A:436:ALA:HB2	1:A:468:MET:HE3	1.97	0.46
1:A:646:LEU:HD21	1:A:663:ALA:HB3	1.96	0.46
1:A:1284:SER:O	1:A:1284:SER:OG	2.34	0.46
1:A:1538:VAL:O	1:A:1542:VAL:HG13	2.16	0.46
1:A:377:LEU:O	1:A:385:SER:OG	2.27	0.46
1:A:1666:THR:HG23	1:A:1685:LYS:HE2	1.98	0.46
1:A:1832:GLY:O	1:A:1836:THR:OG1	2.31	0.46
1:A:1962:ARG:HD3	1:A:1965:TRP:CZ3	2.50	0.46
1:A:1422:ARG:NE	1:A:1466:ASP:OD1	2.45	0.46
1:A:334:ARG:O	1:A:337:THR:OG1	2.25	0.46
1:A:53:GLU:OE2	1:A:55:HIS:NE2	2.45	0.46
1:A:586:LEU:HD21	1:A:908:LEU:HD11	1.97	0.46
1:A:547:SER:O	1:A:671:TYR:OH	2.30	0.45
1:A:1994:ARG:HH22	1:A:2006:LEU:HG	1.80	0.45
1:A:1571:MET:HA	1:A:1866:HIS:HB3	1.99	0.45
1:A:511:GLU:OE1	1:A:1491:SER:OG	2.25	0.45
1:A:1576:PRO:HB2	1:A:1753:HIS:CE1	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:PRO:HB2	1:A:435:TRP:HD1	1.81	0.45
1:A:1961:ARG:HH12	1:A:1987:GLU:HB3	1.80	0.45
1:A:1949:LEU:HB3	1:A:1952:PRO:HG3	1.98	0.45
1:A:344:ASN:OD1	1:A:344:ASN:N	2.48	0.45
1:A:972:PRO:HD3	1:A:1983:HIS:HB2	1.98	0.45
1:A:1081:LEU:HA	1:A:1084:HIS:ND1	2.31	0.45
1:A:1518:ASN:OD1	1:A:1715:ARG:NH1	2.49	0.45
1:A:610:LEU:O	1:A:614:LEU:HG	2.17	0.45
1:A:1117:PHE:HA	1:A:1120:LEU:HB2	1.99	0.45
1:A:1253:ALA:O	1:A:1257:SER:CB	2.65	0.45
1:A:2031:SER:HB2	1:A:2055:LEU:HD22	1.97	0.45
1:A:512:ARG:HA	1:A:515:VAL:HG12	1.98	0.45
1:A:1499:LEU:HD23	1:A:1505:ARG:HA	1.99	0.45
1:A:1742:PRO:O	1:A:1746:LEU:HG	2.16	0.45
1:A:112:VAL:HG11	1:A:197:LEU:HD11	1.99	0.44
1:A:1433:GLY:HA2	1:A:1436:VAL:HG12	1.99	0.44
1:A:2059:LEU:HG	1:A:2060:PRO:HD2	1.99	0.44
1:A:819:SER:OG	1:A:821:GLN:O	2.33	0.44
1:A:2077:HIS:O	1:A:2080:GLU:HB2	2.18	0.44
1:A:876:MET:HA	1:A:879:ILE:HD11	1.99	0.44
1:A:1656:LEU:O	1:A:1660:ILE:HG22	2.17	0.44
1:A:26:LEU:HD23	1:A:26:LEU:HA	1.83	0.44
1:A:467:ARG:HH11	1:A:1517:LEU:HA	1.83	0.44
1:A:1428:SER:OG	1:A:1431:GLU:OE2	2.34	0.44
1:A:2038:VAL:HG12	1:A:2057:PHE:HE2	1.82	0.44
1:A:2059:LEU:HD23	1:A:2060:PRO:N	2.33	0.44
1:A:867:ILE:N	1:A:870:HIS:O	2.49	0.44
1:A:1123:ARG:HG3	1:A:1127:LEU:HG	2.00	0.44
1:A:1306:LEU:HD11	1:A:1317:ARG:HD3	2.00	0.44
1:A:600:LEU:HD12	1:A:600:LEU:HA	1.87	0.44
1:A:1883:THR:HG22	1:A:1922:PRO:HA	1.99	0.44
1:A:2025:ARG:O	1:A:2084:GLU:N	2.49	0.44
1:A:2070:VAL:O	1:A:2074:LEU:N	2.39	0.44
1:A:1301:LEU:HD12	1:A:1306:LEU:HD13	1.98	0.44
1:A:1575:SER:HB3	1:A:1578:LEU:HD23	2.00	0.44
1:A:2066:ALA:O	1:A:2069:ARG:NH1	2.44	0.44
1:A:488:PRO:HB3	1:A:534:TYR:HB2	1.99	0.43
1:A:961:VAL:HB	1:A:991:LEU:HD13	2.00	0.43
1:A:1956:MET:SD	1:A:1956:MET:N	2.91	0.43
1:A:2094:GLU:HA	1:A:2097:PHE:CE2	2.53	0.43
1:A:2097:PHE:O	1:A:2101:SER:N	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:PRO:HB2	1:A:435:TRP:CD1	2.53	0.43
1:A:1748:THR:HA	1:A:1751:LEU:HG	1.99	0.43
1:A:2038:VAL:HG12	1:A:2057:PHE:CE2	2.53	0.43
1:A:1581:LEU:HA	1:A:1584:PHE:CZ	2.53	0.43
1:A:1795:LEU:HB3	1:A:1798:LEU:HD13	2.00	0.43
1:A:654:ASN:OD1	1:A:1645:SER:OG	2.36	0.43
1:A:619:ILE:HG22	1:A:620:LEU:HD23	2.00	0.43
1:A:120:ARG:HH22	1:A:1438:GLU:HB3	1.84	0.43
1:A:1318:PHE:HA	1:A:1371:ALA:HB2	2.01	0.43
1:A:1792:VAL:O	1:A:1854:ALA:N	2.49	0.43
1:A:1953:THR:HA	1:A:1956:MET:HE1	2.01	0.43
1:A:402:ARG:HA	1:A:402:ARG:HD2	1.72	0.43
1:A:2042:PHE:HE1	1:A:2069:ARG:HG3	1.84	0.43
1:A:844:GLY:H	1:A:847:LYS:HG2	1.84	0.42
1:A:1961:ARG:NH2	1:A:1986:GLU:OE2	2.52	0.42
1:A:1534:VAL:O	1:A:1538:VAL:HG22	2.20	0.42
1:A:2060:PRO:HA	1:A:2061:PRO:HD3	1.87	0.42
1:A:2072:GLY:O	1:A:2075:ALA:HB3	2.19	0.42
1:A:9:LEU:HD11	1:A:904:PHE:HD1	1.85	0.42
1:A:997:HIS:NE2	1:A:1984:SER:OG	2.53	0.42
1:A:1947:VAL:O	1:A:1979:MET:N	2.39	0.42
1:A:1572:GLY:HA3	1:A:1895:ARG:NH2	2.34	0.42
1:A:307:LEU:O	1:A:311:VAL:HG12	2.20	0.42
1:A:1025:LEU:O	1:A:1026:ARG:NE	2.53	0.42
1:A:78:ASN:HB3	1:A:80:THR:HG23	2.02	0.42
1:A:1428:SER:OG	1:A:1428:SER:O	2.37	0.42
1:A:1465:LEU:HD12	1:A:1465:LEU:HA	1.94	0.42
1:A:1415:GLY:HA2	1:A:1474:TRP:O	2.20	0.42
1:A:308:MET:HA	1:A:311:VAL:CG1	2.49	0.41
1:A:388:ASP:OD1	1:A:388:ASP:N	2.51	0.41
1:A:482:ARG:HG3	1:A:1408:TRP:HE1	1.84	0.41
1:A:1628:TRP:CZ3	1:A:1741:GLY:HA3	2.51	0.41
1:A:1726:ARG:HD3	1:A:1726:ARG:HA	1.84	0.41
1:A:1588:MET:SD	1:A:1588:MET:N	2.93	0.41
1:A:2005:CYS:HA	1:A:2015:ARG:HH22	1.84	0.41
1:A:636:ALA:HA	1:A:639:THR:HG22	2.02	0.41
1:A:476:THR:O	1:A:476:THR:OG1	2.34	0.41
1:A:2024:LEU:HD21	1:A:2055:LEU:HD23	2.03	0.41
1:A:825:ARG:HD3	1:A:1015:ARG:HG3	2.03	0.41
1:A:509:LEU:HD23	1:A:509:LEU:HA	1.90	0.41
1:A:991:LEU:HD13	1:A:991:LEU:HA	1.96	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:999:ASP:OD1	1:A:999:ASP:N	2.45	0.41
1:A:1143:PHE:CE2	1:A:1958:PRO:HB2	2.56	0.41
1:A:56:PHE:HA	1:A:57:PRO:HD3	1.94	0.41
1:A:347:MET:SD	1:A:351:LEU:HB2	2.61	0.41
1:A:879:ILE:H	1:A:879:ILE:HG12	1.68	0.41
1:A:1679:GLU:HA	1:A:1682:ARG:HG2	2.03	0.41
1:A:1429:GLY:HA2	1:A:1432:LEU:HB2	2.03	0.40
1:A:1701:ILE:HD13	1:A:1701:ILE:HA	1.87	0.40
1:A:1742:PRO:HA	1:A:1745:LEU:HB2	2.03	0.40
1:A:1910:LEU:HA	1:A:1915:LEU:HD12	2.03	0.40
1:A:1929:GLY:HA2	1:A:1956:MET:HG2	2.02	0.40
1:A:1994:ARG:HA	1:A:2009:PRO:HD3	2.04	0.40
1:A:1626:TYR:CZ	1:A:1630:ILE:HD13	2.56	0.40
1:A:1706:ASN:HA	1:A:1709:MET:HG3	2.04	0.40
1:A:667:LEU:HB3	1:A:692:LEU:HD23	2.03	0.40
1:A:1283:PHE:CE2	1:A:1301:LEU:HD21	2.56	0.40
1:A:1683:ILE:HD13	1:A:1683:ILE:HA	1.94	0.40
1:A:339:MET:HE2	1:A:339:MET:HB3	2.01	0.40
1:A:1324:PRO:HG2	1:A:1327:VAL:HB	2.04	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	1826/2146 (85%)	1722 (94%)	104 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	387	GLN
1	A	432	HIS
1	A	522	ASN
1	A	531	GLN
1	A	718	ASN
1	A	1279	GLN
1	A	1316	HIS
1	A	1488	ASN
1	A	1607	GLN
1	A	1661	ASN
1	A	1740	GLN
1	A	1785	GLN
1	A	1805	GLN
1	A	1901	GLN
1	A	1983	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 [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.

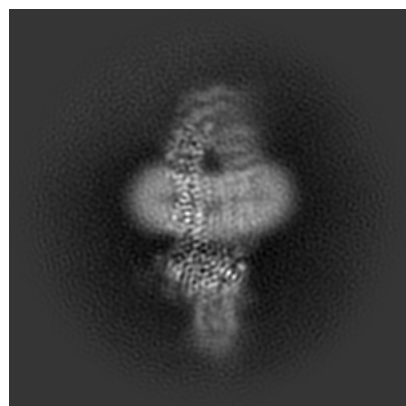
6 Map visualisation [i](#)

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.

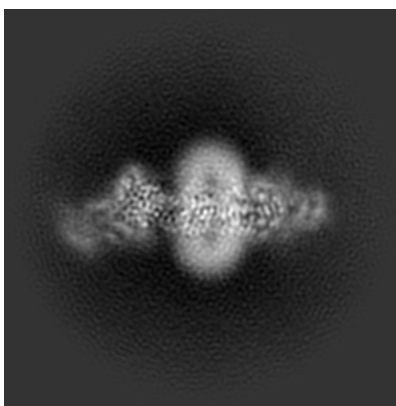
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

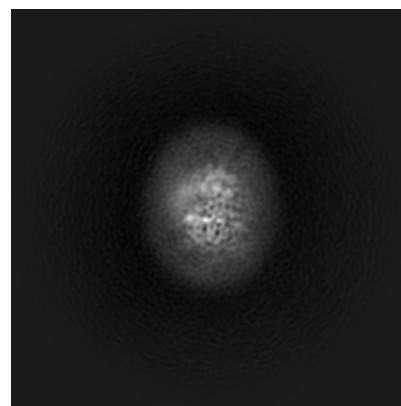
6.1.1 Primary map



X

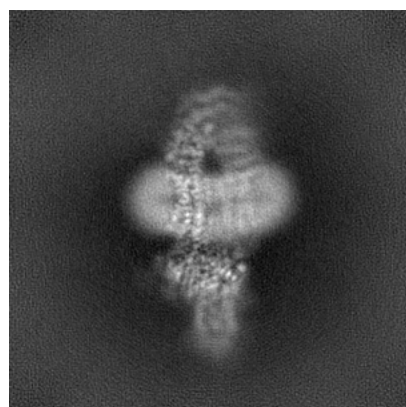


Y

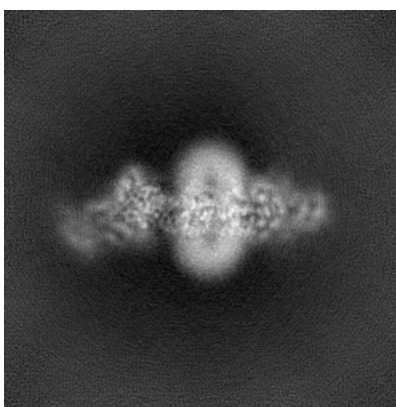


Z

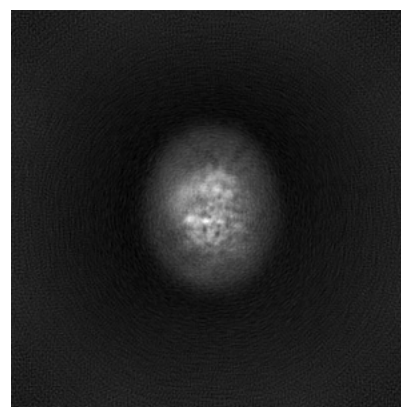
6.1.2 Raw map



X



Y

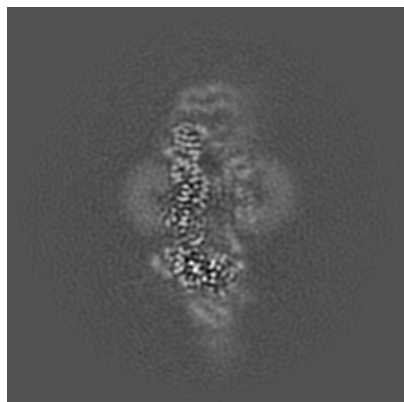


Z

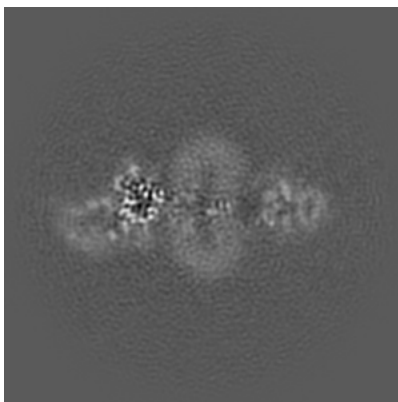
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

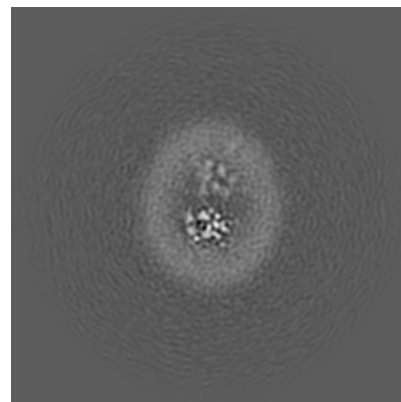
6.2.1 Primary map



X Index: 140

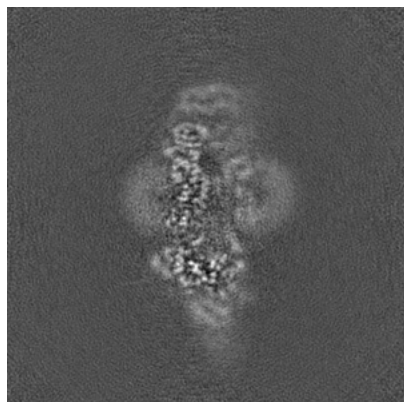


Y Index: 140

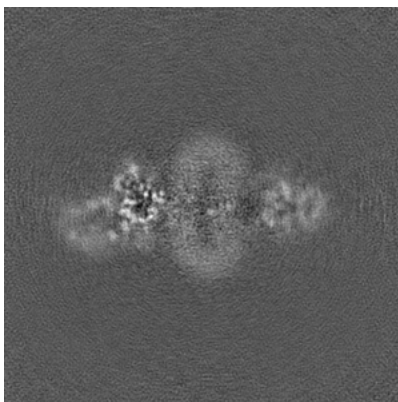


Z Index: 140

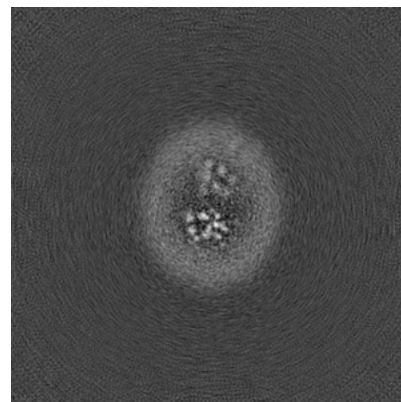
6.2.2 Raw map



X Index: 140



Y Index: 140

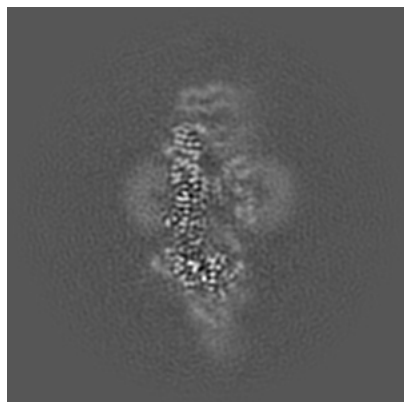


Z Index: 140

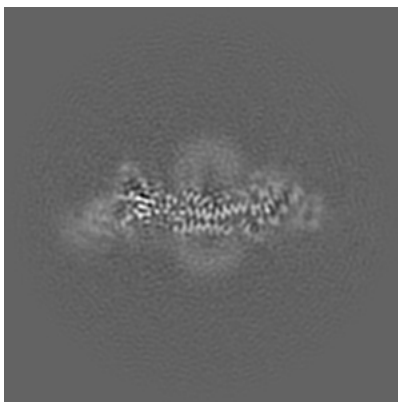
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

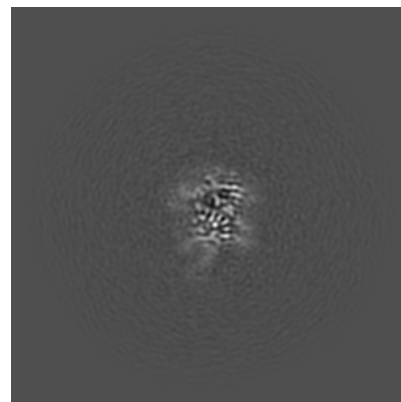
6.3.1 Primary map



X Index: 139

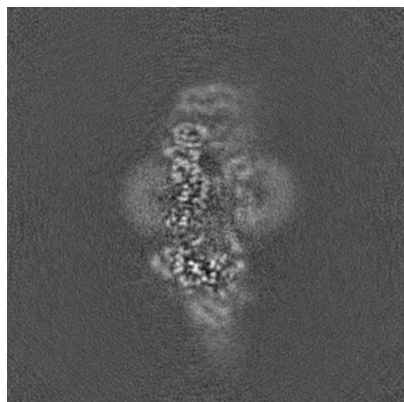


Y Index: 132

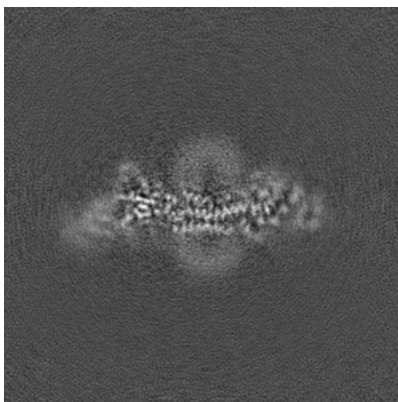


Z Index: 95

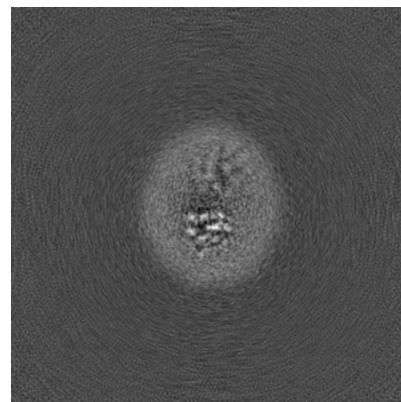
6.3.2 Raw map



X Index: 140



Y Index: 132

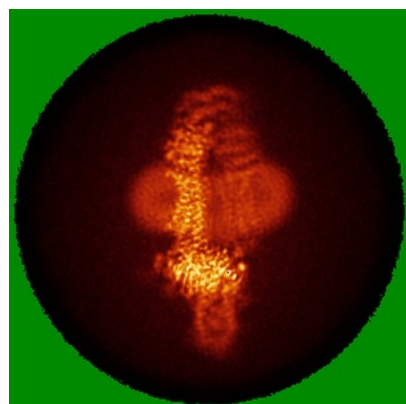


Z Index: 136

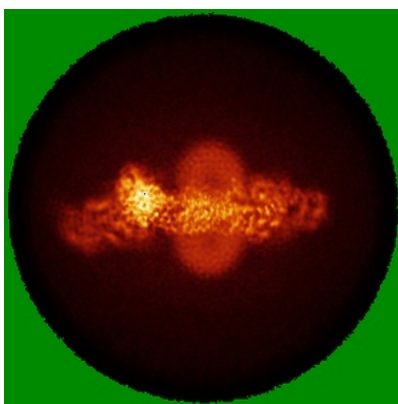
The images above show the largest variance slices of the map in three orthogonal directions.

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

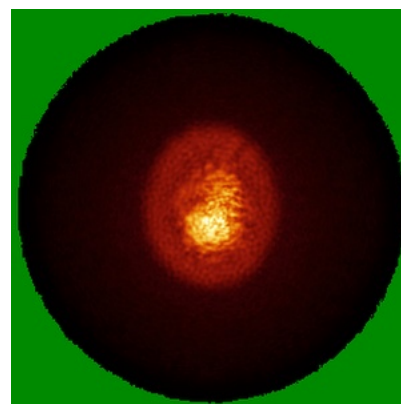
6.4.1 Primary map



X

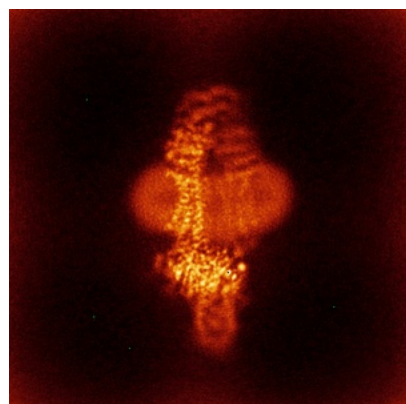


Y

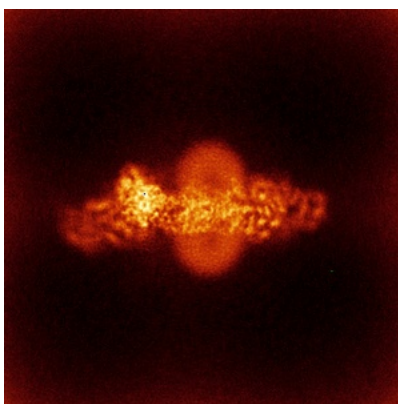


Z

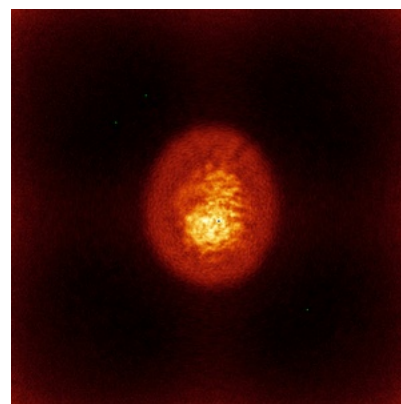
6.4.2 Raw map



X



Y

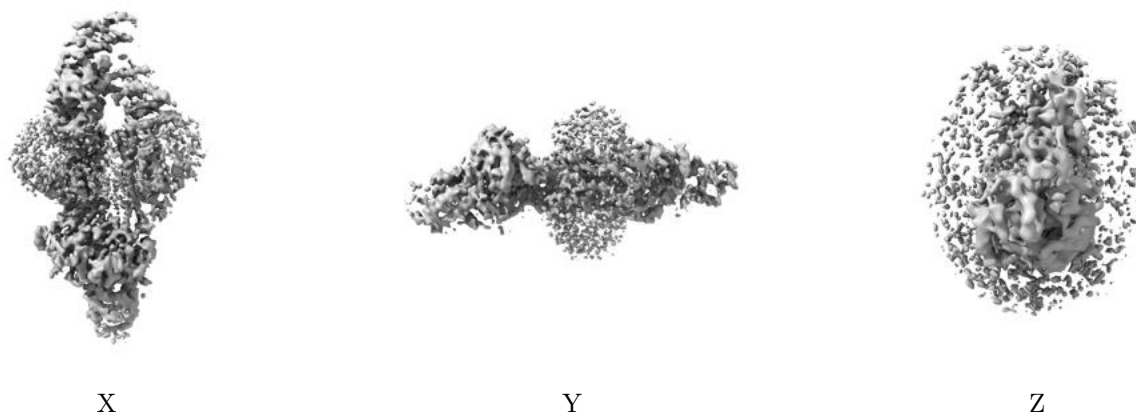


Z

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.

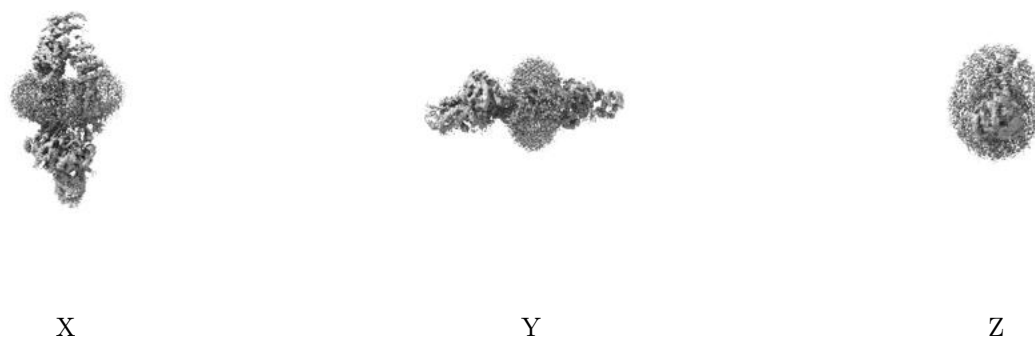
6.5 Orthogonal surface views [i](#)

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.

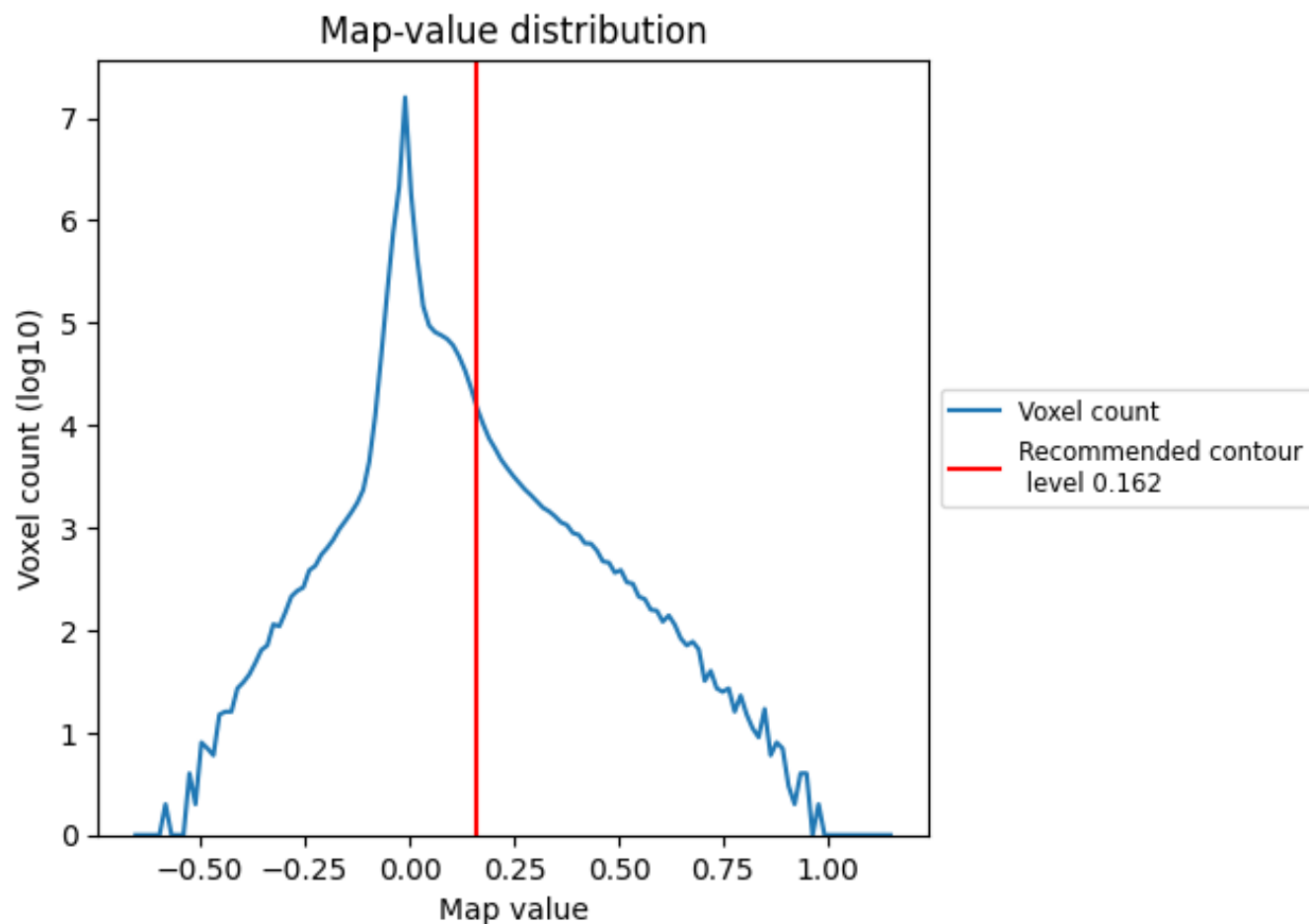
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

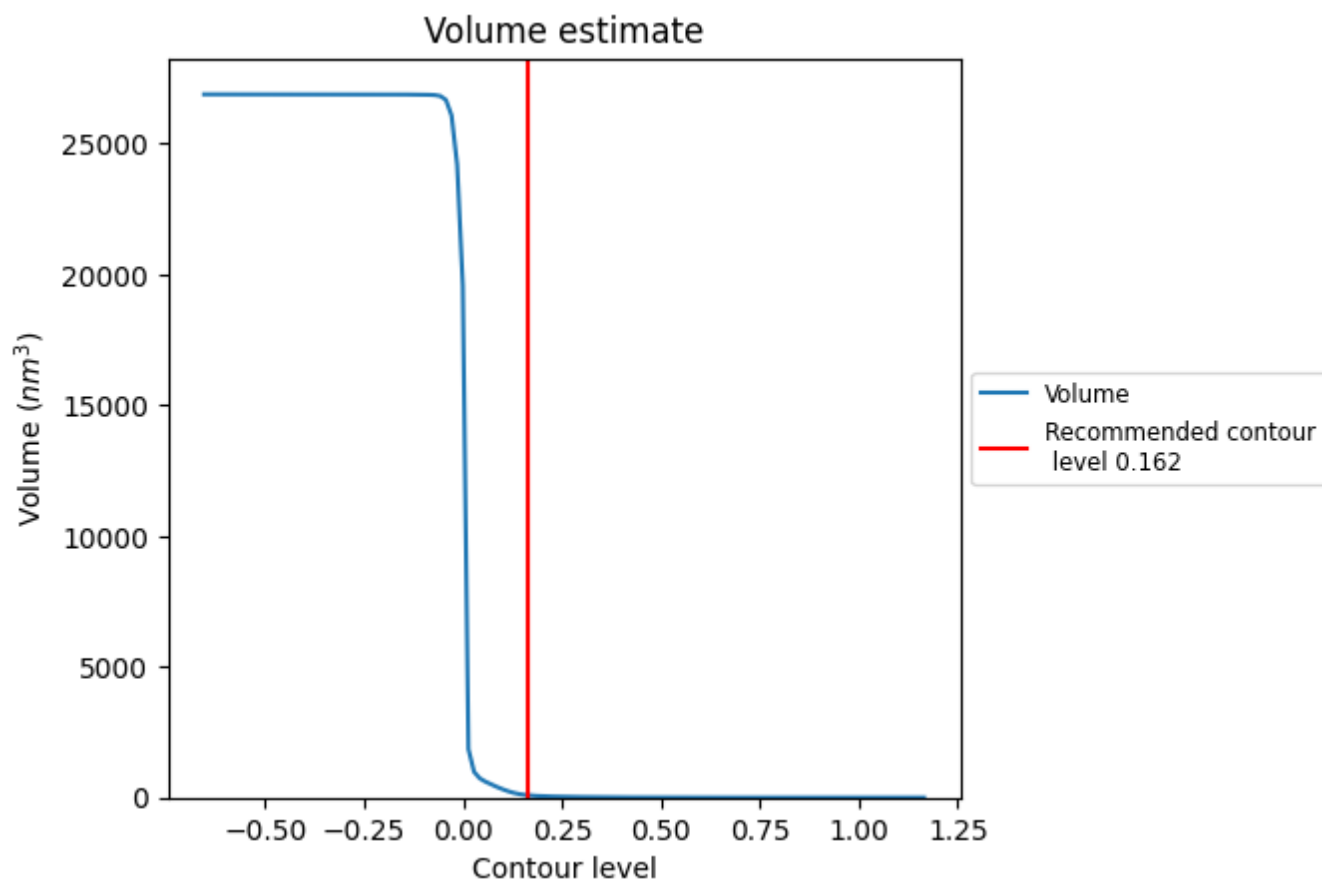
This section contains the results of statistical analysis of the map.

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.

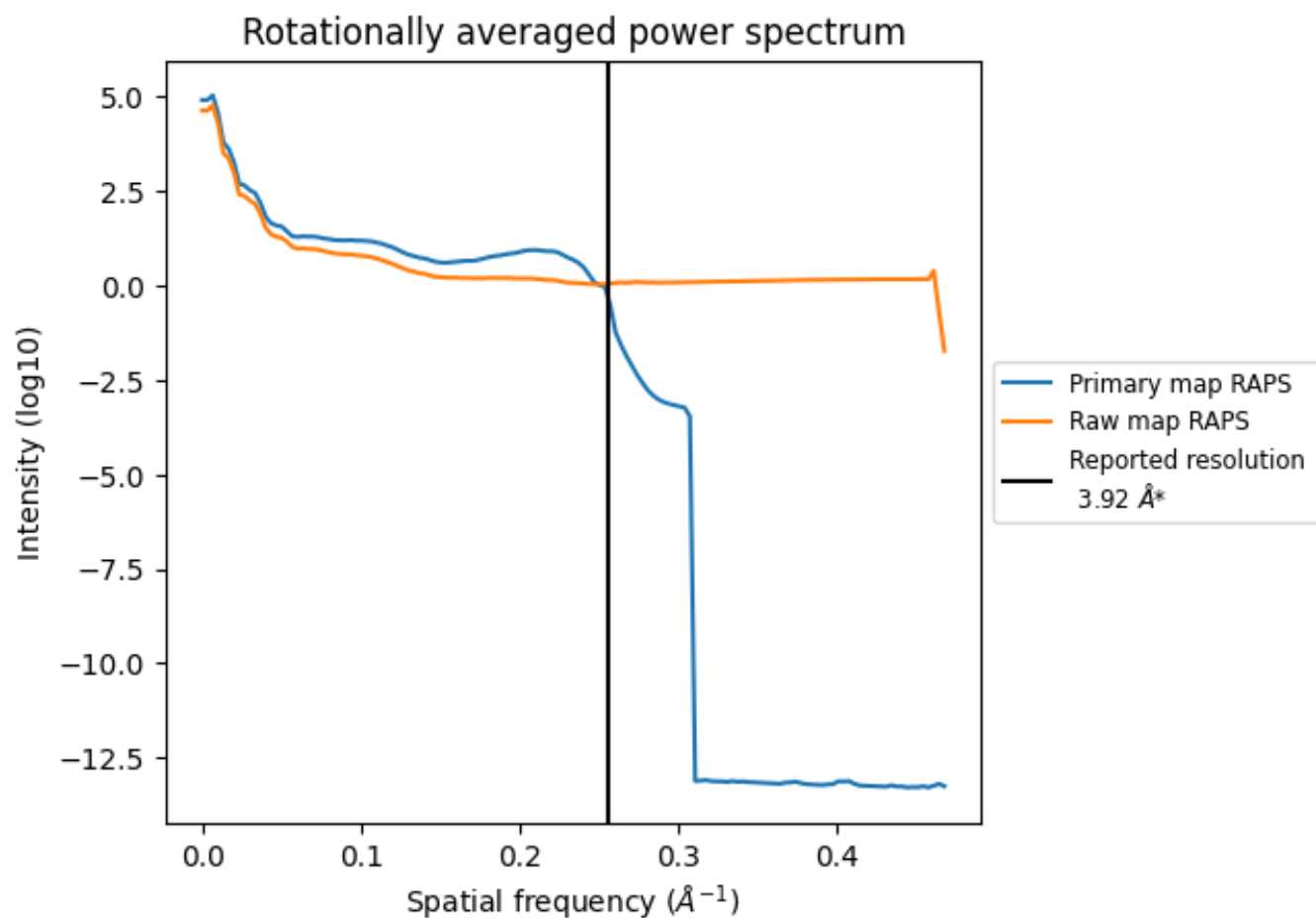
7.2 Volume estimate [i](#)



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 ⓘ

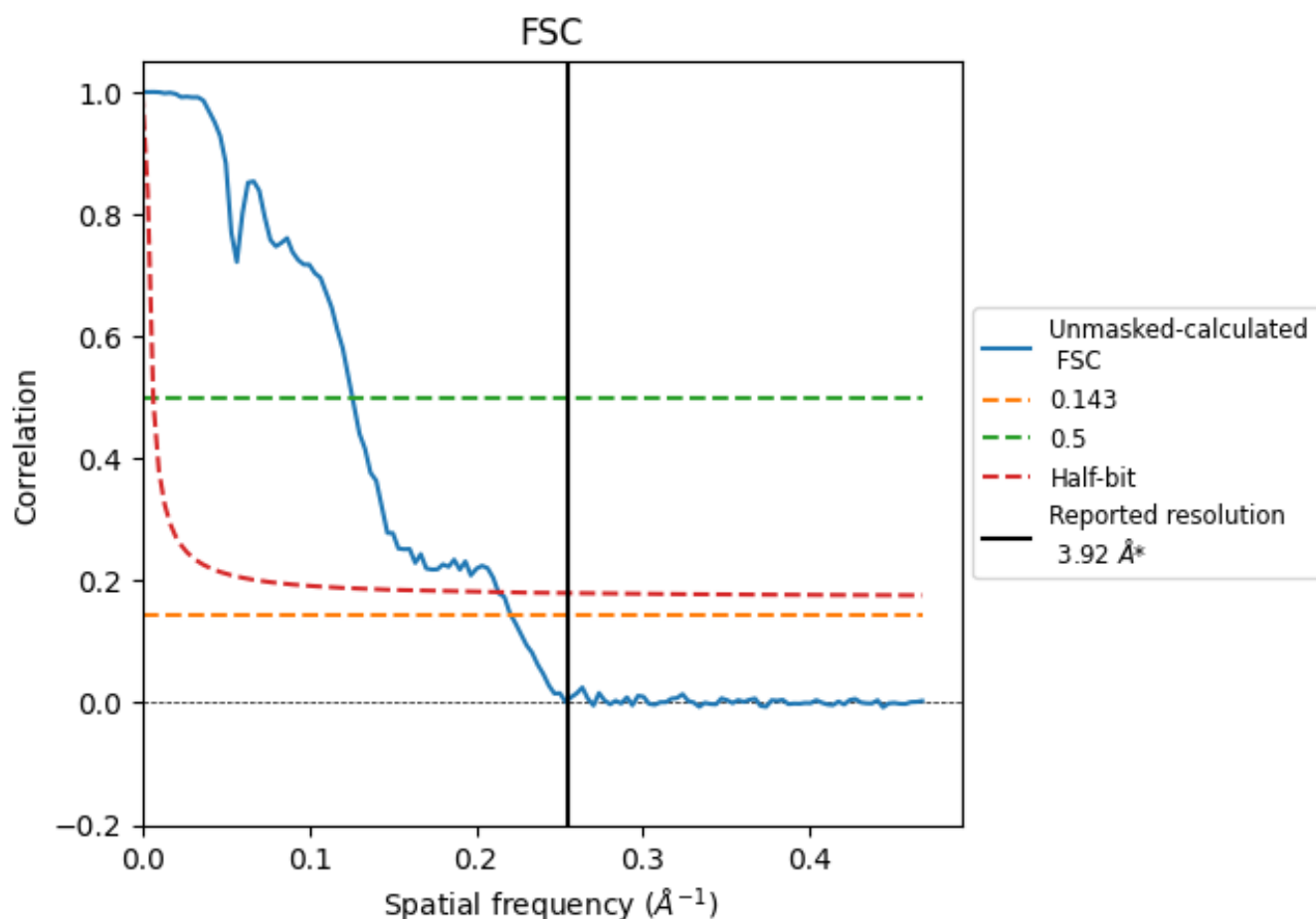


*Reported resolution corresponds to spatial frequency of 0.255 Å⁻¹

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

8.2 Resolution estimates [i](#)

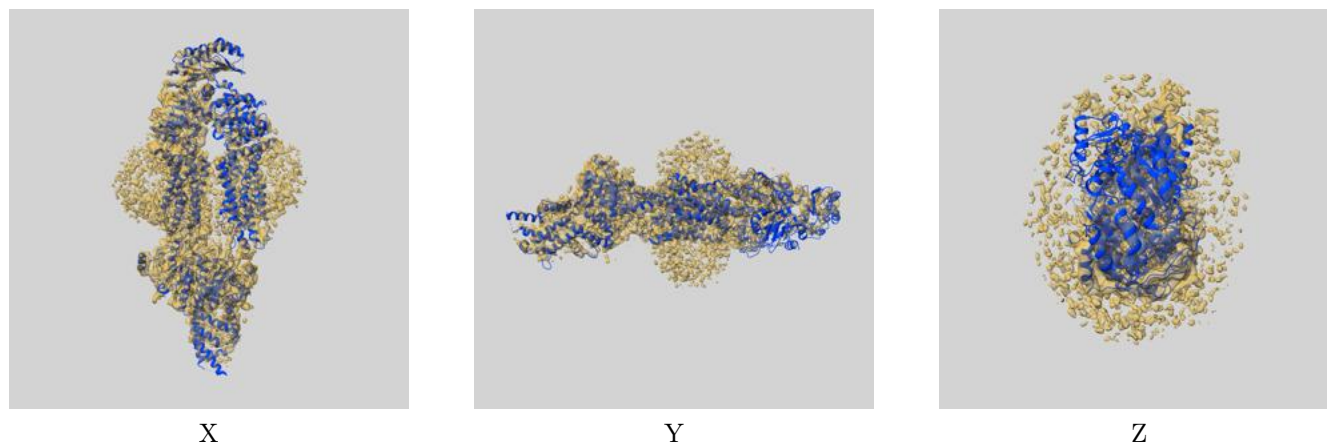
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.92	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.52	7.94	4.69

*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](#)

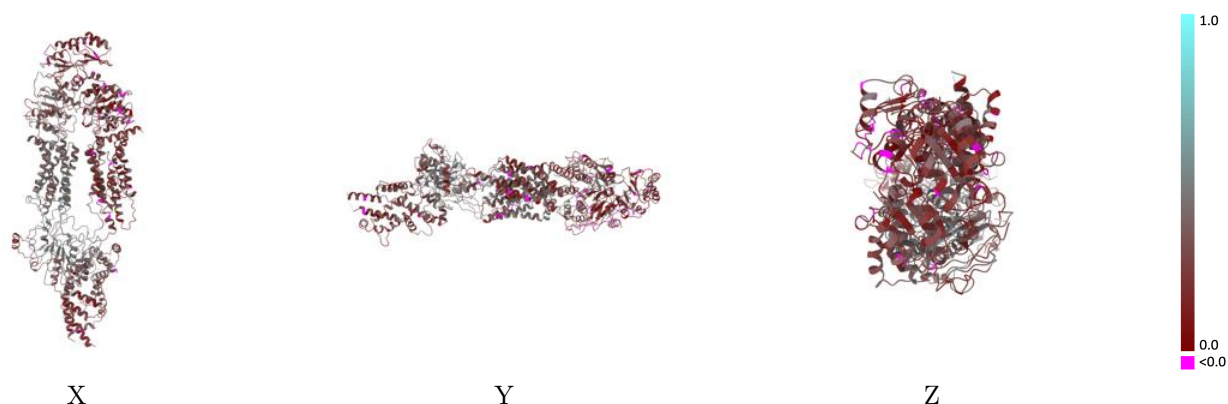
This section contains information regarding the fit between EMDB map EMD-38841 and PDB model 8Y1O. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

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](#)

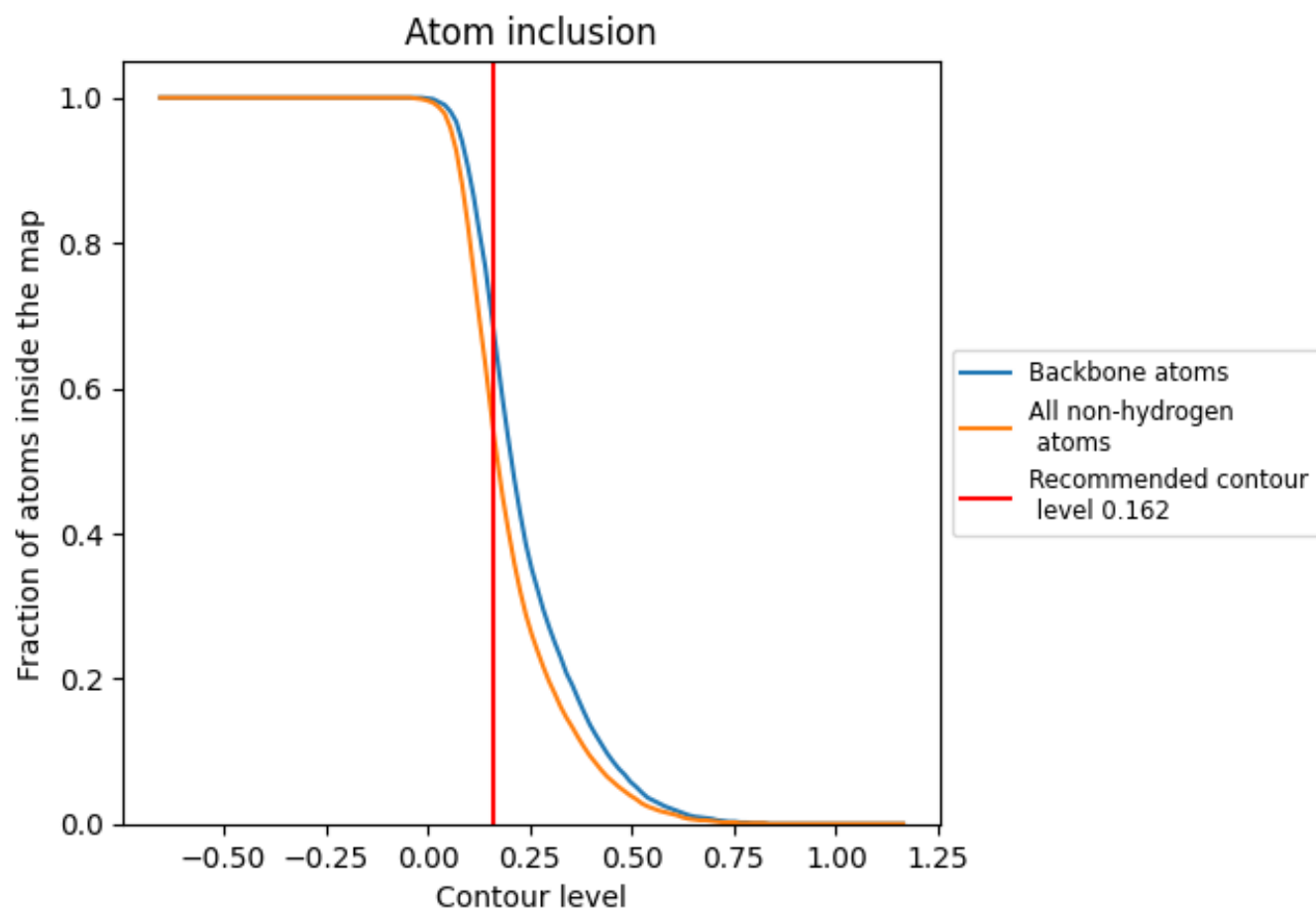


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

