



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2026 – 12:52 AM JST

PDB ID : 9WFQ / pdb_00009wfq
EMDB ID : EMD-65935
Title : Structure of the wild-type ABCC2 dimer in Arabidopsis thaliana in the apo state
Authors : Sun, L.; Liu, X.; Qiu, X.; Yang, Z.; Gao, Y.
Deposited on : 2025-08-21
Resolution : 4.20 Å(reported)
Based on initial model : 9LI5

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.dev133
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) : 2.50

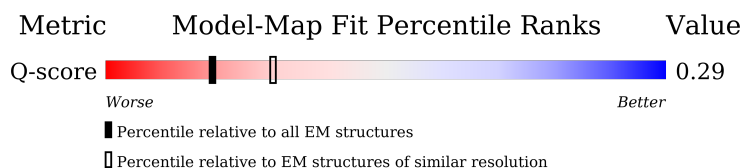
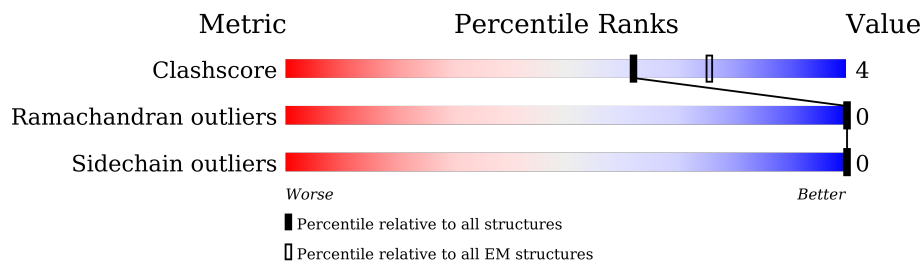
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	1623	25% 77% 11% 12%
1	B	1623	25% 77% 11% 12%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22474 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.

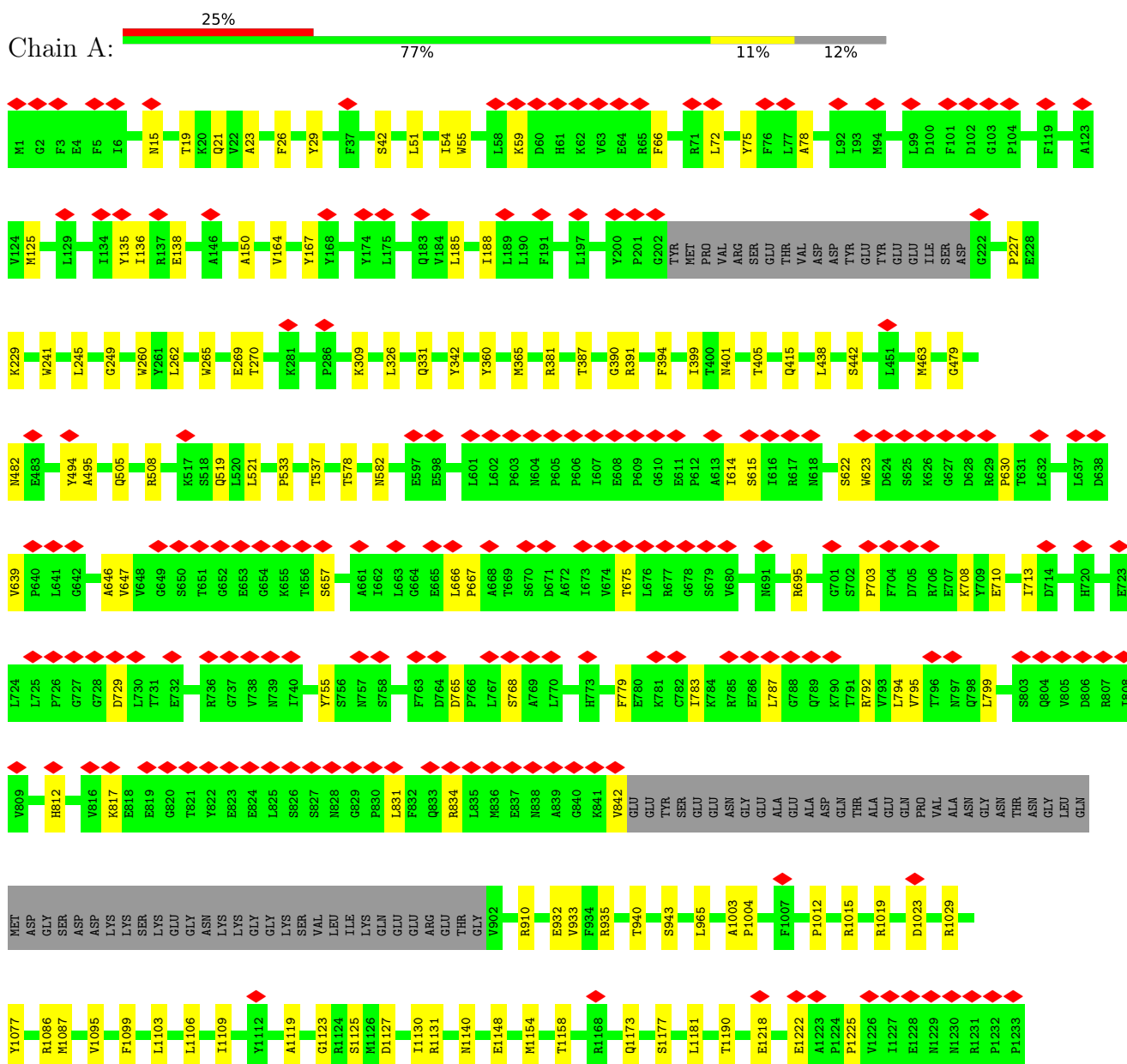
- Molecule 1 is a protein called ABC transporter C family member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1422	Total	C	N	O	S	0	0
			11237	7263	1899	2021	54		
1	B	1422	Total	C	N	O	S	0	0
			11237	7263	1899	2021	54		

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: ABC transporter C family member 2





GLU	ALA	D1492	I1432	N1364	G1298	G1235	M1087	R807
GLY	VAL	N1493	I1433	P1365	R1299	W1236		I808
ASN	VAL	K1494	A1434	L1366	I1300	P1237	V1095	V809
THR	THR	L1495	H1435	G1367	L1301	S1238	F1099	
PHE	LEU	R1496	R1436	L1368	I1302	S1239	L1103	H812
ASP	ARG		L1437	D1369	D1303	S1240		
TRP	VAL	K1497	N1438	A1370	D1304	I1241	L1106	V816
ASP	VAL		T1439	E1371	C1305	I1242	L1109	K817
ASN	GLU	D1498	I1440	V1372	D1306	K1243		E818
GLU	GLY	S1500	I1441	S1373	V1307	F1244	Y1112	E919
MEI	LYS	HIS	D1442	E1374	G1308	D1245		G820
	ASP	LEU	C1443	A1375	G1309	D1246	A1119	T821
	LYS	GLN	K1444	G1376	F1310	V1247		Y822
	GLU	GLY	D1444	E1377	G1311	W1248	G1123	E823
	ILE	GLY	K1445	E1378	L1312	R1124	R1125	E924
	ALA	ARG	I1446	N1378	M1313	R1250	S1125	L825
	GLU	SER	L1447	F1379	D1314	Y1251	I1130	S826
	LEU	TRP	V1448	Q1383	L1315	R1252	R1131	S827
	GLU	ALA	L1449	R1384	K1317	Q1254	N1140	N828
	GLU	SER	D1450		V1318	L1255	E1148	G829
	HIS	ASN	S1451		L1387	P1256	M1154	P830
	ASN	ARG	G1452		S1390	P1257		L831
	ILE	TRP	R1453		R1391	V1258		F832
	ARG	ALA	V1454		L1392	L1259	T1158	R834
	GLU	ALA	E1455		L1393	H1260	A1162	L835
	GLY	ALA	E1456		L1394	G1261		M836
	TRP	GLN	F1457		R1395	V1262		E837
	LEU	PHE	S1458		R1396	S1263		N838
	SER	ALA	S1459		S1397	F1264		A839
	LEU	ALA	S1460		K1398	F1265		G840
	TYR	ARG	E1461		L1399	I1266		K841
	MET	SER	N1462		L1400	H1267		V842
	VAL	LEU	L1463					GLU
	GLU	THR	L1464					GLU
	GLY	SER						ASN
	ALA	SER	S1465		D1403	T1268	T1190	GLU
	VAL	ASN	N1466		E1404	T1269		GLU
	MET	ASP	E1467		A1405	D1270	Y1216	THR
	SER	LEU	G1468		T1406	K1271	I1217	SER
	GLN	SER	S1469		A1407	V1272	E1218	GLU
	LEU	GLU	S1470		A1408	G1273	E1222	ASN
	ALA	LEU	F1471		V1409	I1274	A1223	GLY
	ILE	LEU			D1410	V1275	P1224	GLU
	GLU	ASP	S1472		D1411	G1276	P1225	ALA
	ASP	GLU	K1473		H1343	R1277	V1226	ALA
	ASP	ASP	M1474		V1411	T1278	I1227	ASP
	GLN	SER	V1475		D1345	G1279	E1228	GLN
	GLN	SER	T1413		A1346	A1280	N1229	THR
	PRO	ILE	Q1476		D1347	I1281	N1230	ALA
	ASP	LEU	S1477		L1348	G1282	R1231	GLU
	ASN	LYS	T1478		L1416	K1282	P1232	GLN
	ARG	ARG	G1479		I1417	S1283		PRO
	THR	THR						VAL
	ASN	ASN	A1480		R1422			ALA
	ASP	ASP	A1481		E1423	A1288	P1233	ALA
	GLN	SER	N1482		E1424	L1289		GLY
	GLN	SER	A1483		F1425	F1290		ASN
	THR	THR	E1484		K1426	R1291		THR
	ASP	THR	Y1485		S1427	I1292		ASN
	ASN	ASN	L1486		C1428	V1293		GLY
	PHE	PHE	R1487		T1429	E1294		THR
			S1488		M1430	V1295		ASN
			L1489		L1431	E1296		GLY
			V1490			K1297		
			L1491					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52445	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.799	Depositor
Minimum map value	-1.165	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.36	Depositor
Map size ($\text{\AA}$)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	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

5.1 Standard geometry

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	0.22	0/11485	0.44	0/15591
1	B	0.22	0/11485	0.44	0/15591
All	All	0.22	0/22970	0.44	0/31182

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	11237	0	11422	99	0
1	B	11237	0	11422	100	0
All	All	22474	0	22844	195	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 4.

The worst 5 of 195 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:26:PHE:HB3	1:B:29:TYR:HB2	1.83	0.61
1:A:26:PHE:HB3	1:A:29:TYR:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:787:LEU:O	1:B:792:ARG:NH1	2.34	0.60
1:A:787:LEU:O	1:A:792:ARG:NH1	2.34	0.60
1:B:1291:ARG:NH1	1:B:1307:VAL:O	2.35	0.59

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	1416/1623 (87%)	1346 (95%)	70 (5%)	0	100	100
1	B	1416/1623 (87%)	1346 (95%)	70 (5%)	0	100	100
All	All	2832/3246 (87%)	2692 (95%)	140 (5%)	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	1227/1399 (88%)	1227 (100%)	0	100	100
1	B	1227/1399 (88%)	1227 (100%)	0	100	100
All	All	2454/2798 (88%)	2454 (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 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	193	HIS
1	B	437	GLN
1	B	415	GLN
1	B	482	ASN
1	A	482	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.

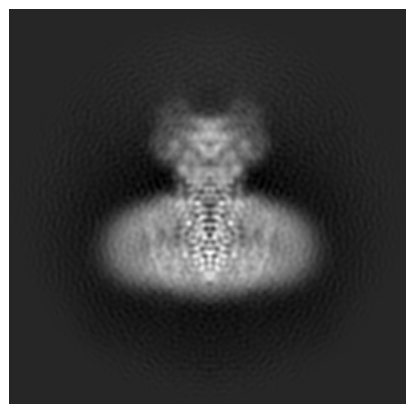
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65935. These allow visual inspection of the internal detail of the map and identification of artifacts.

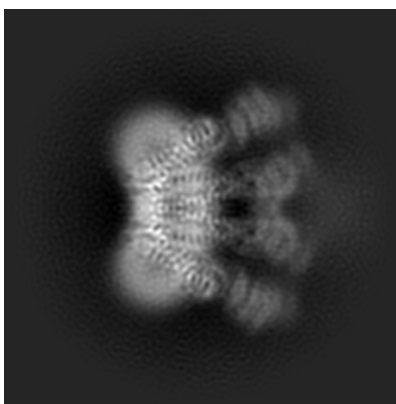
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

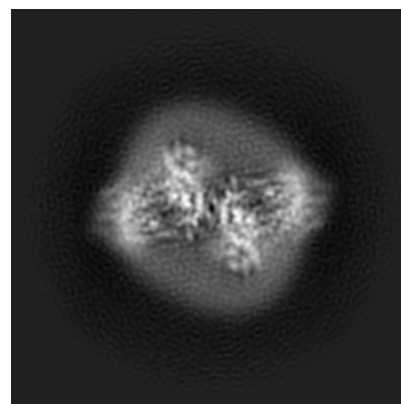
6.1.1 Primary map



X

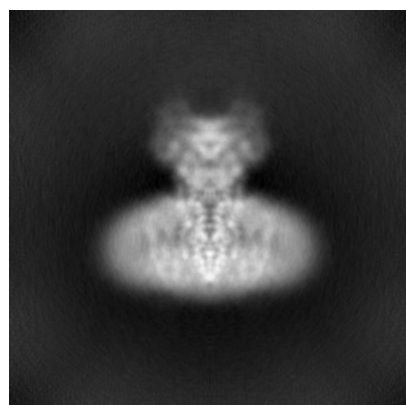


Y

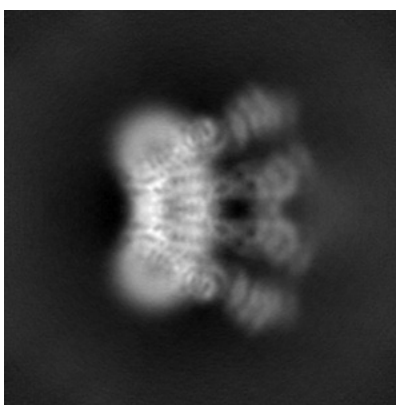


Z

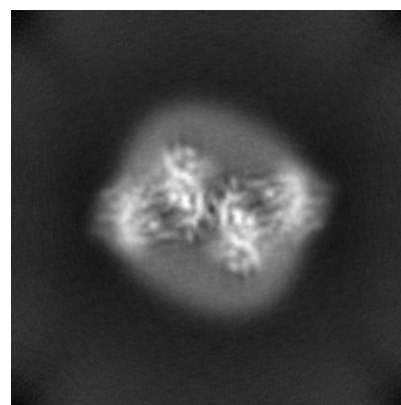
6.1.2 Raw map



X



Y

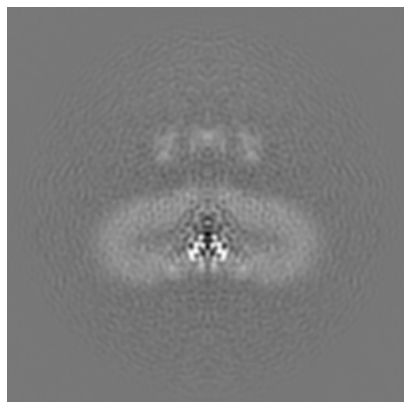


Z

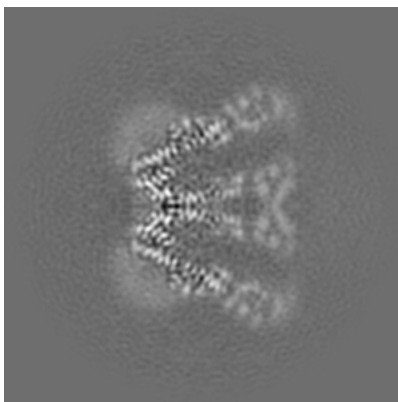
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

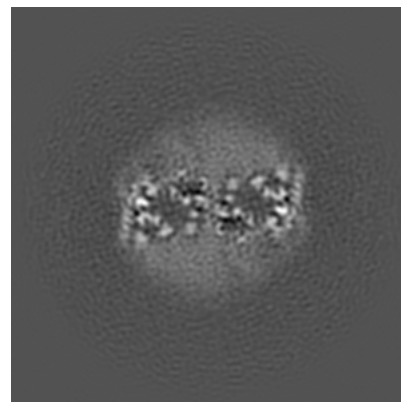
6.2.1 Primary map



X Index: 128

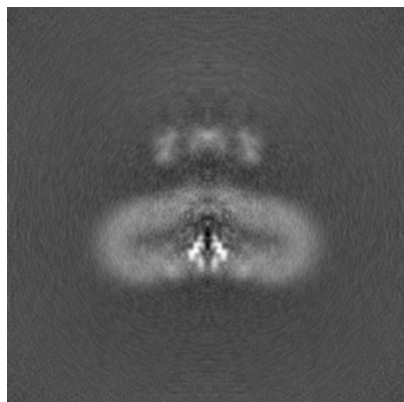


Y Index: 128

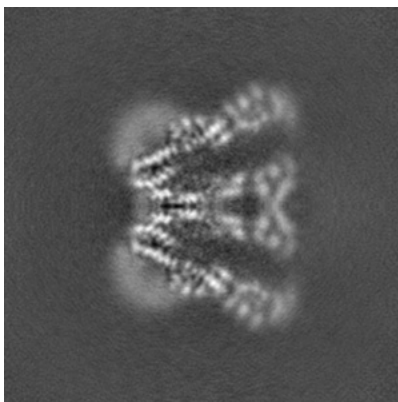


Z Index: 128

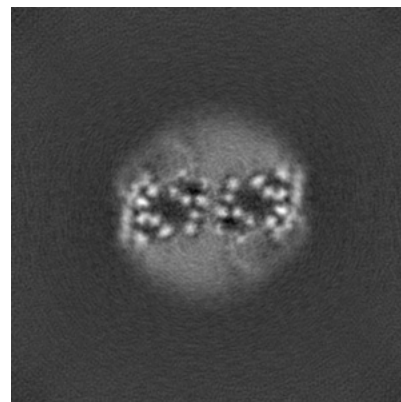
6.2.2 Raw map



X Index: 128



Y Index: 128

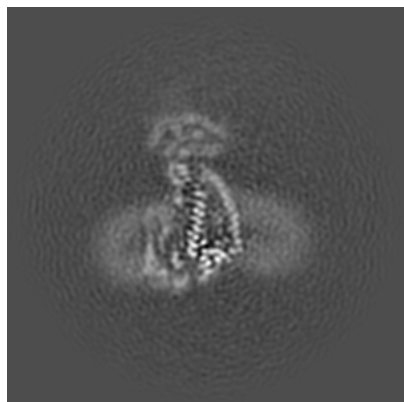


Z Index: 128

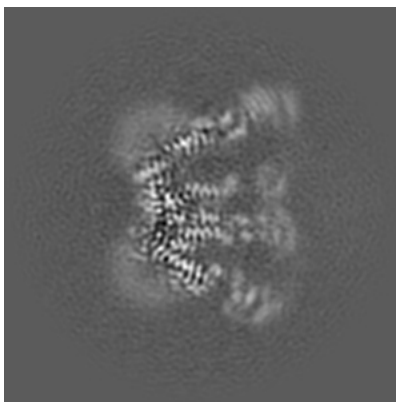
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

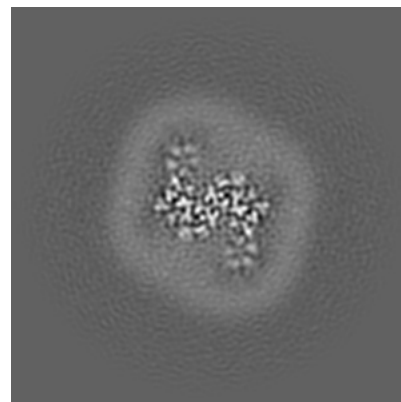
6.3.1 Primary map



X Index: 143

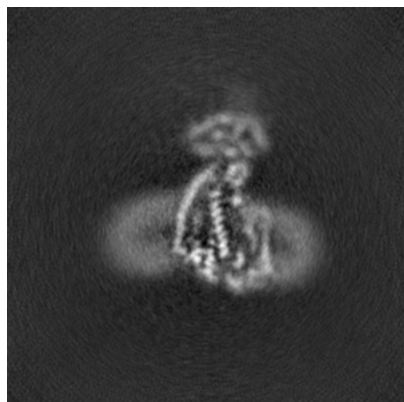


Y Index: 133

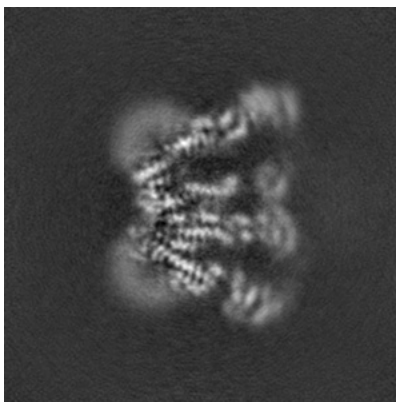


Z Index: 99

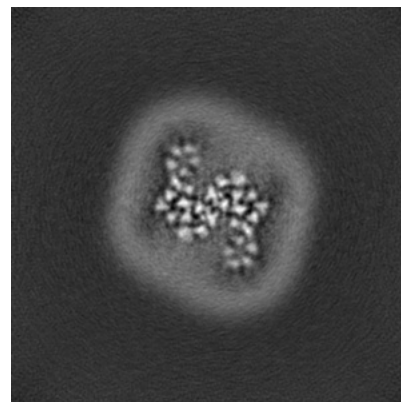
6.3.2 Raw map



X Index: 113



Y Index: 133

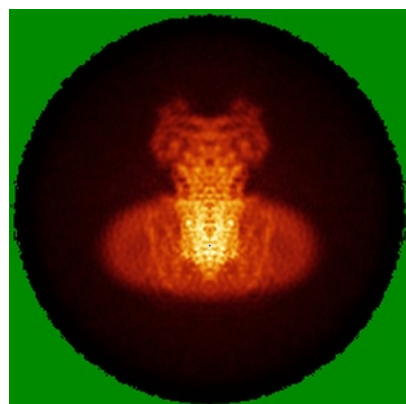


Z Index: 99

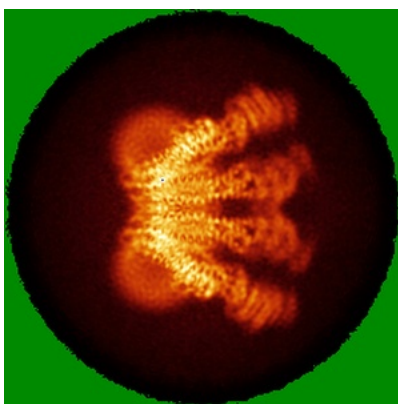
The images above show the largest variance slices of the map in three orthogonal directions.

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

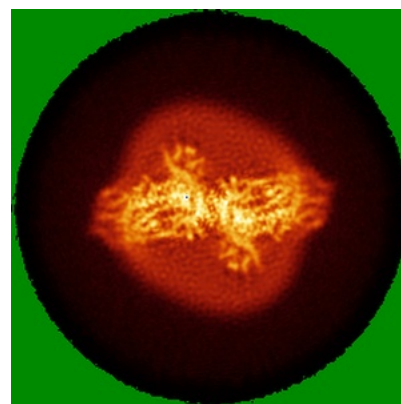
6.4.1 Primary map



X

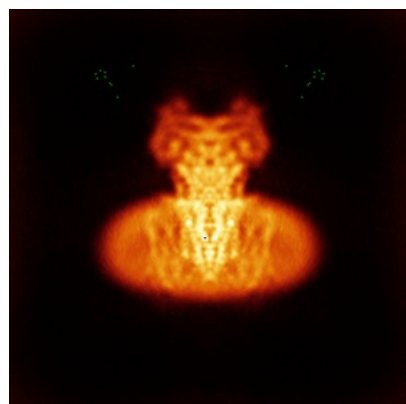


Y

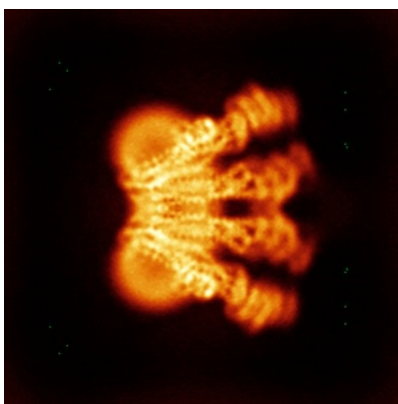


Z

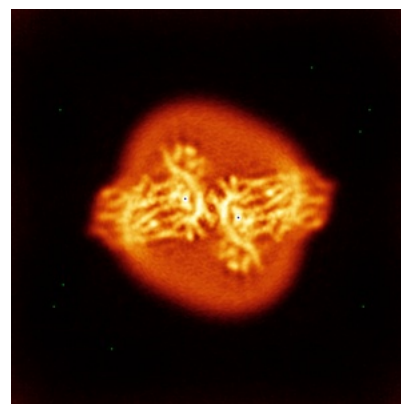
6.4.2 Raw map



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 0.36. 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.

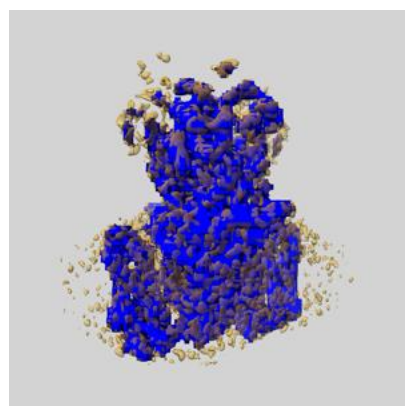
6.6 Mask visualisation [i](#)

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

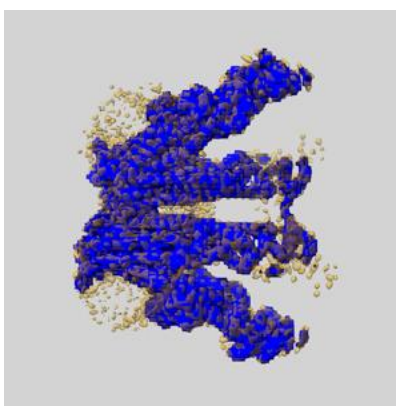
A mask typically either:

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

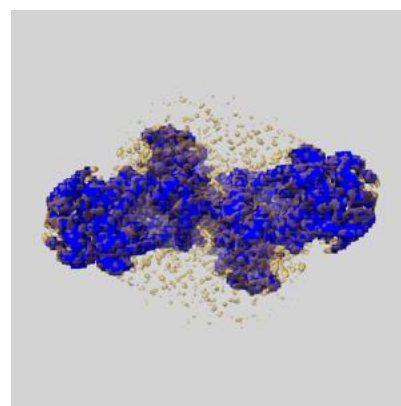
6.6.1 emd_65935_msk_1.map [i](#)



X



Y

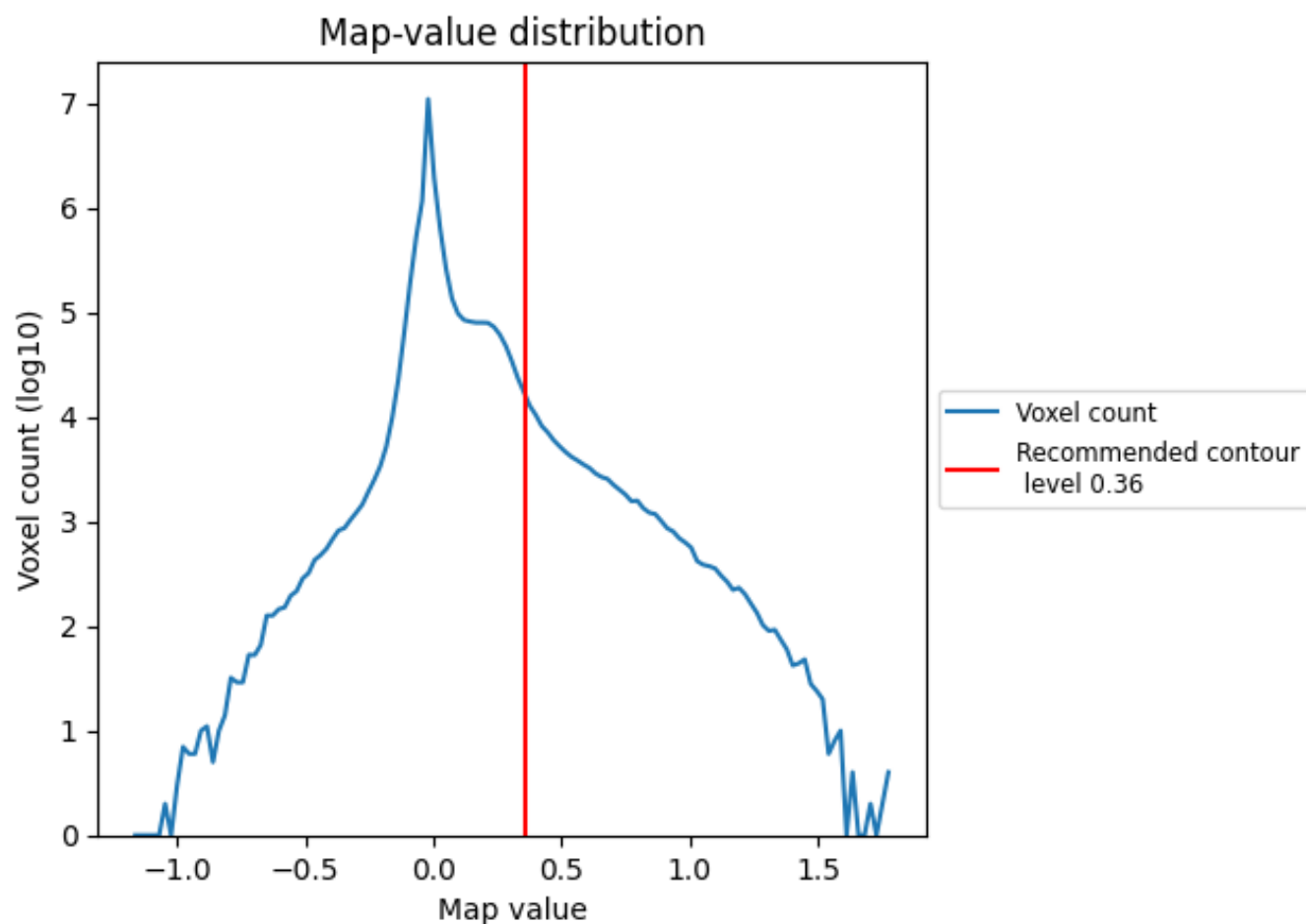


Z

7 Map analysis [i](#)

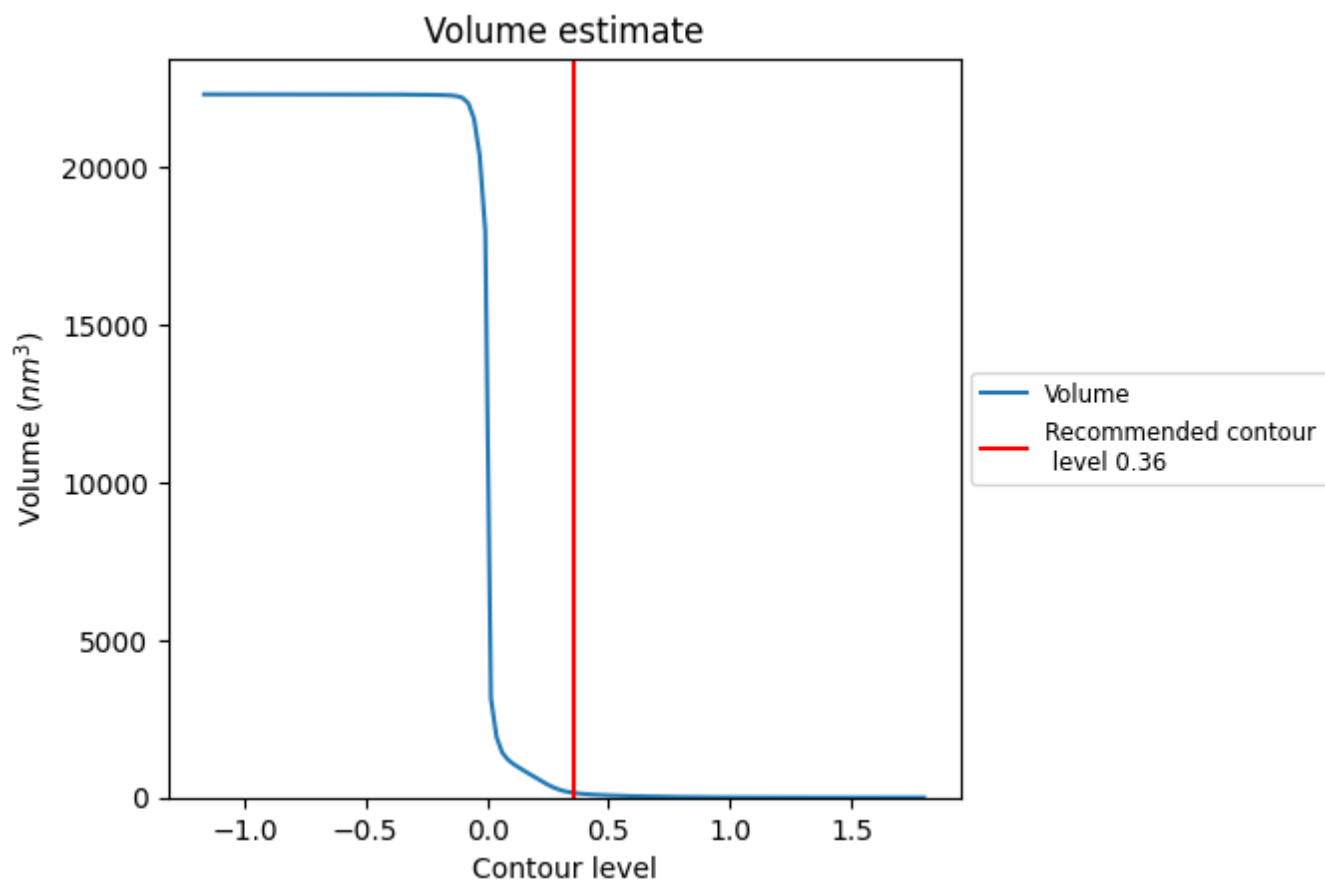
This section contains the results of statistical analysis of the map.

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.

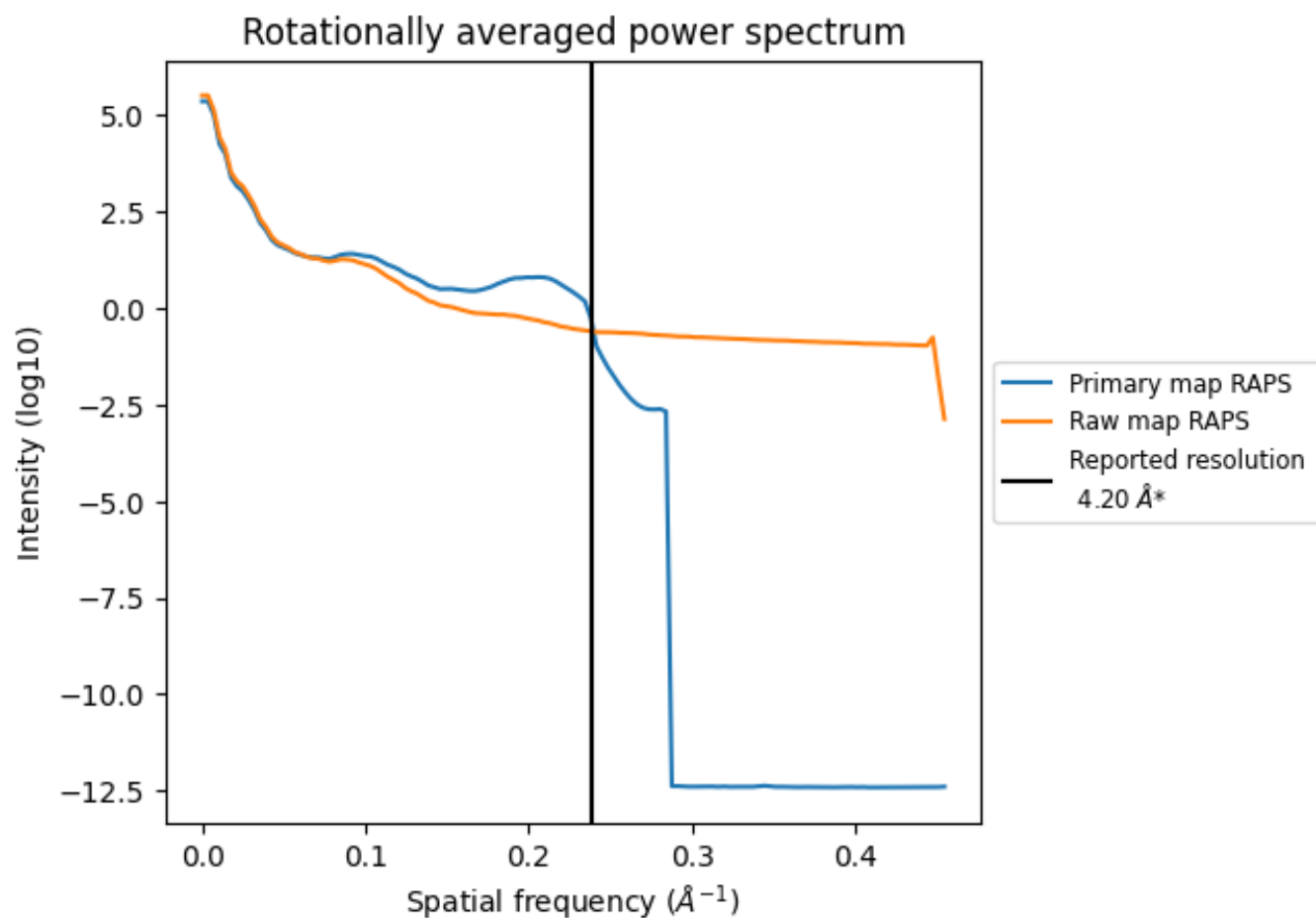
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 146 nm³; this corresponds to an approximate mass of 132 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 ⓘ

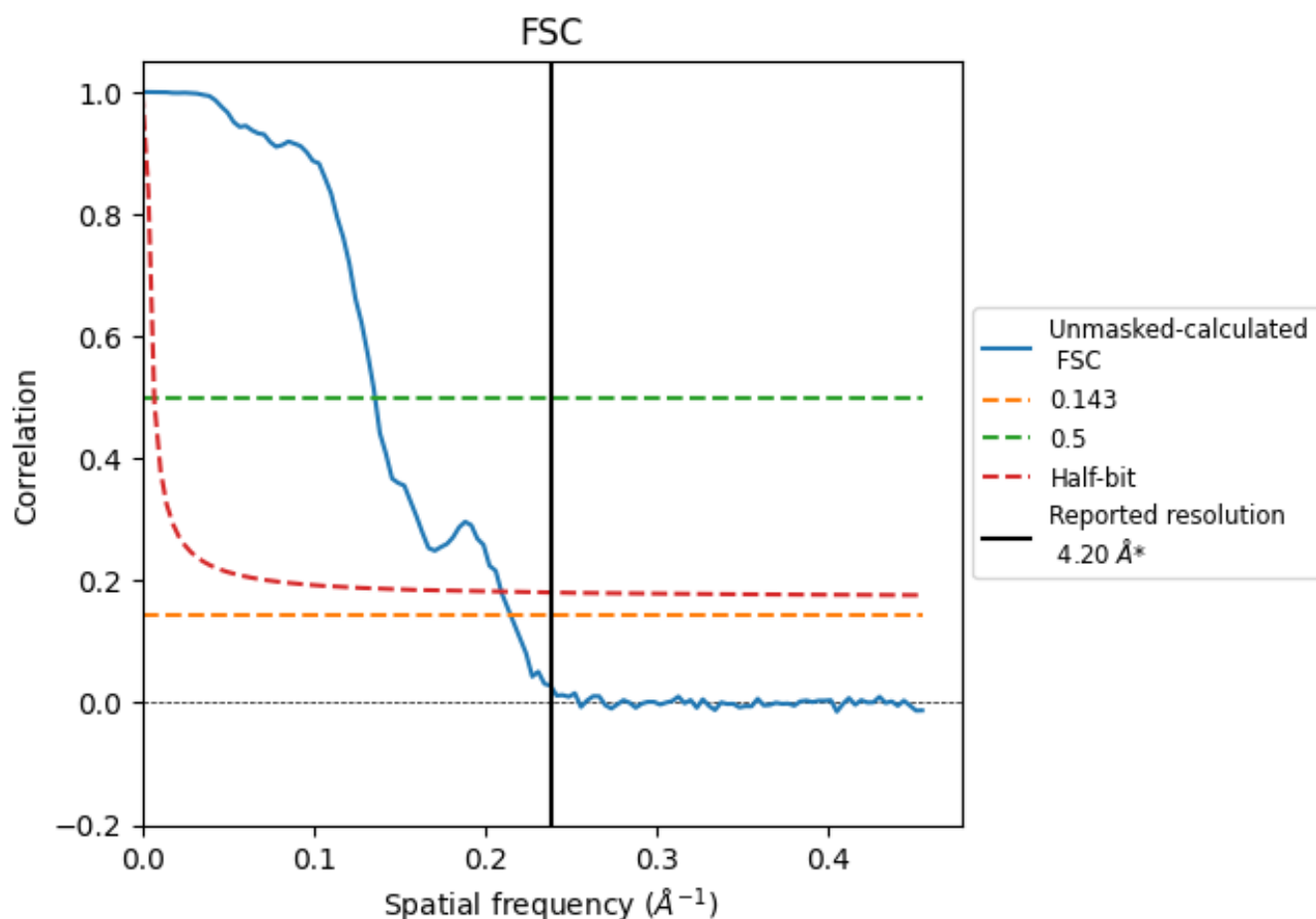


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

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 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

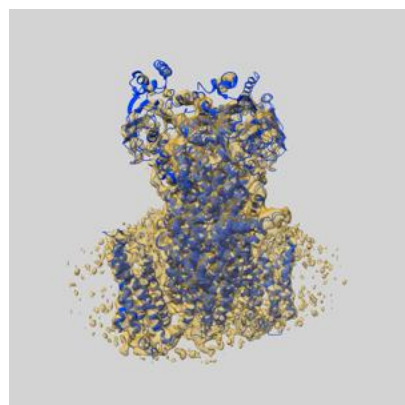
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.66	7.37	4.78

*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 4.66 differs from the reported value 4.2 by more than 10 %

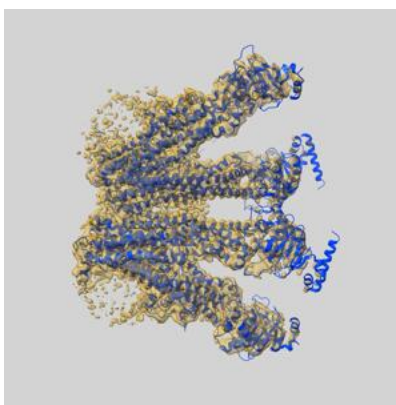
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65935 and PDB model 9WFQ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

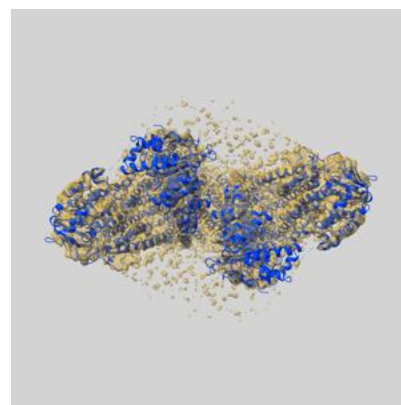
9.1 Map-model overlay [i](#)



X



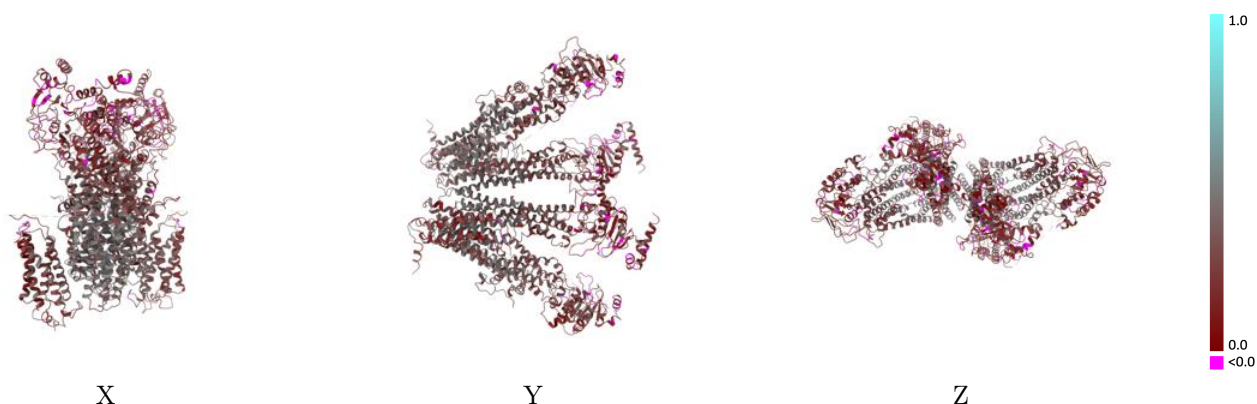
Y



Z

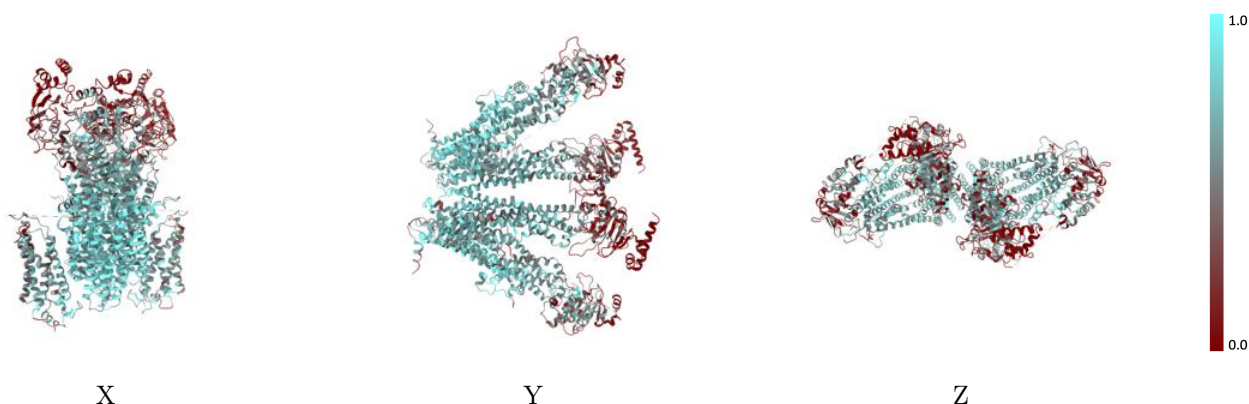
The images above show the 3D surface view of the map at the recommended contour level 0.36 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



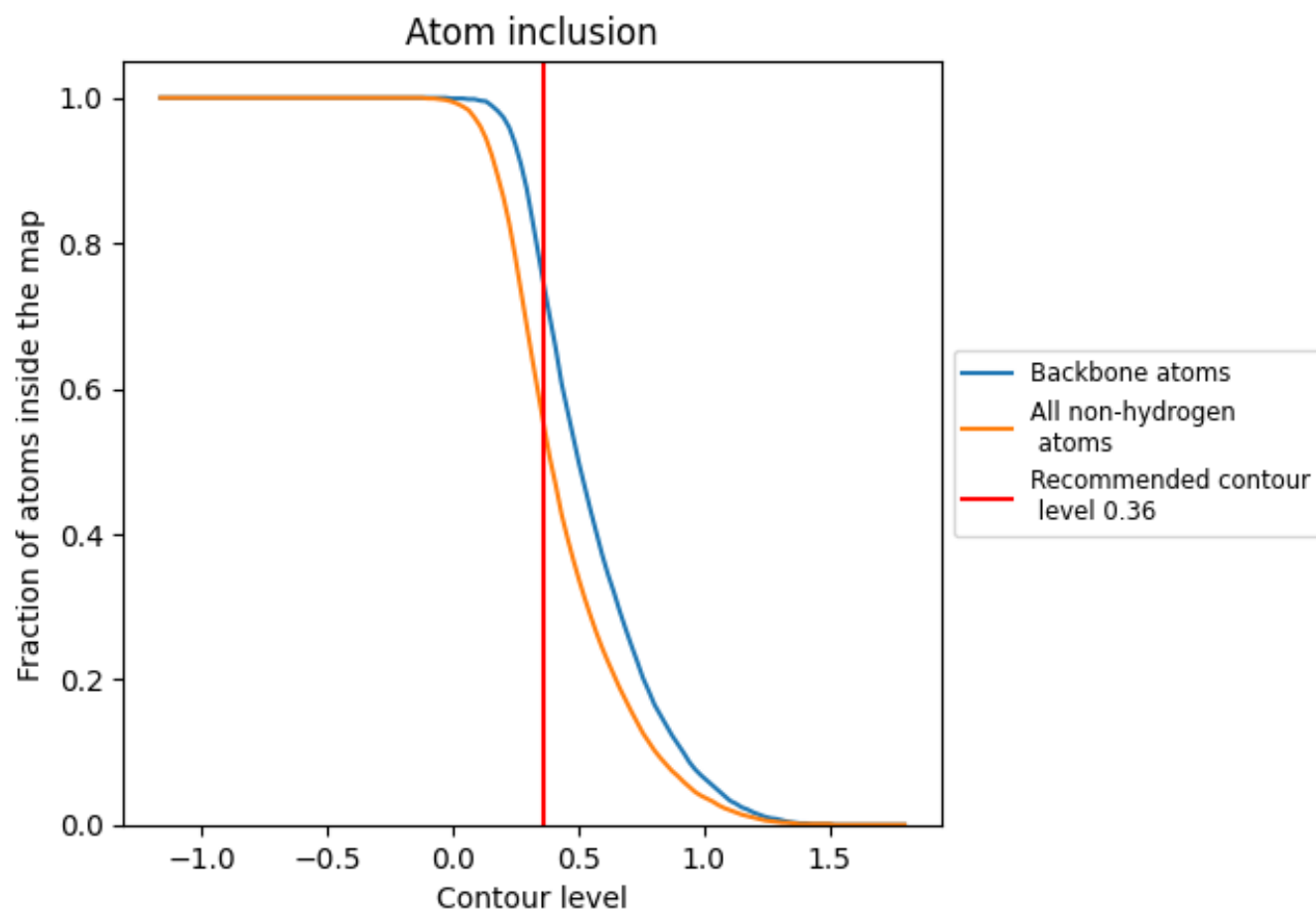
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.36).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 55% 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 (0.36) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5520	0.2900
A	0.5520	0.2900
B	0.5520	0.2900

