wwPDB EM Validation Summary Report (i)

Aug 10, 2026 – 12:52 PM JST

PDB ID	:	9U56 / pdb_00009u56
EMDB ID	:	EMD-63864
Title	:	Cryo-EM structure of AtABCC2 in apo form
Authors	:	Dong, J.Q.; Yang, T.-L.; Yang, G.-F.
Deposited on	:	2025-03-20
Resolution	:	2.91 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 (i) 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 (1)) were used in the production of this report:

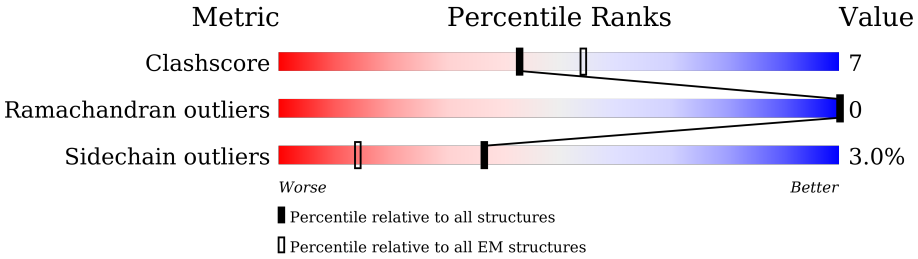
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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

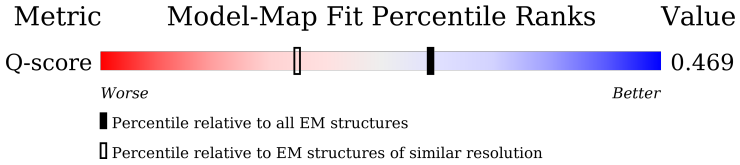
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.91 Å.

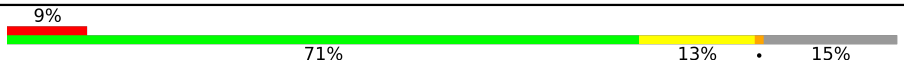
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





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	12972 (2.41 - 3.41)

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 <=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	

2 Entry composition (i)

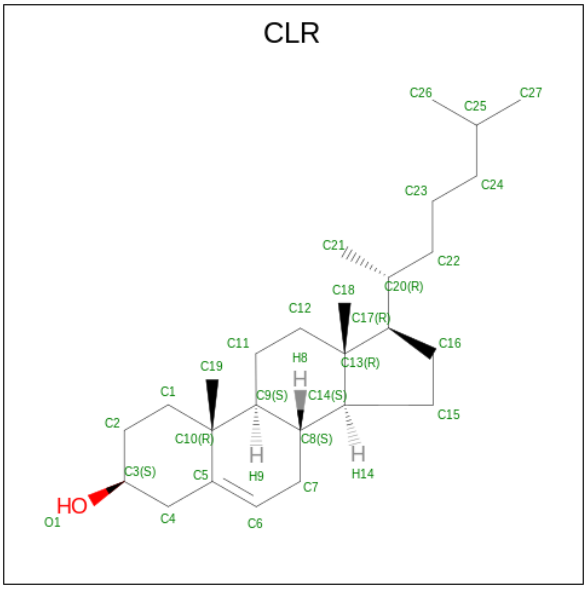
There are 2 unique types of molecules in this entry. The entry contains 11139 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S		
1	A	1379	10915	7068	1839	1956	52	0	0

- Molecule 2 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	A	1	28	27	1	0
2	A	1	28	27	1	0
2	A	1	28	27	1	0
2	A	1	28	27	1	0
2	A	1	28	27	1	0

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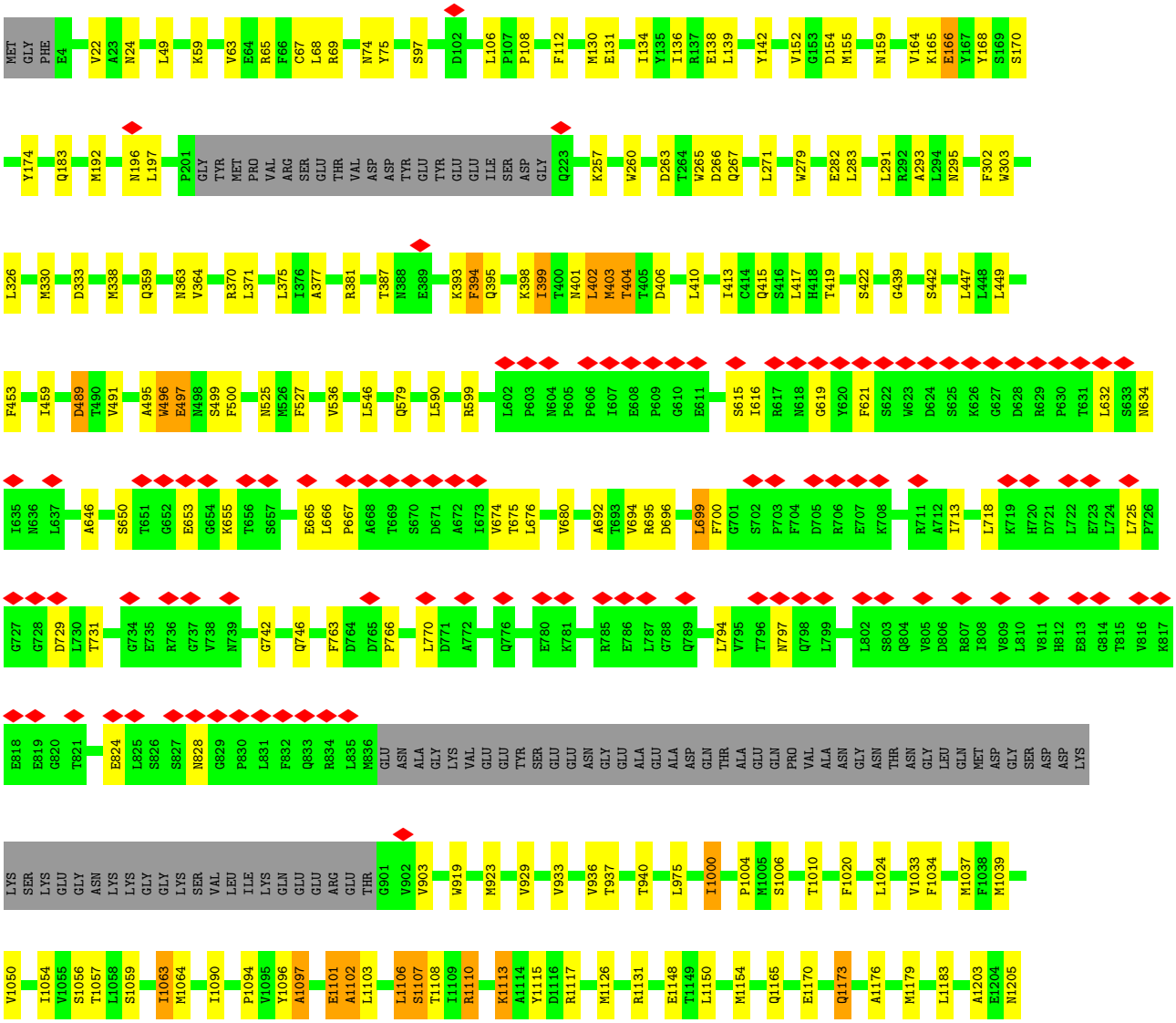
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	A	1	28	27	1	0
			Total	C	O	
2	A	1	28	27	1	0
			Total	C	O	
2	A	1	28	27	1	0

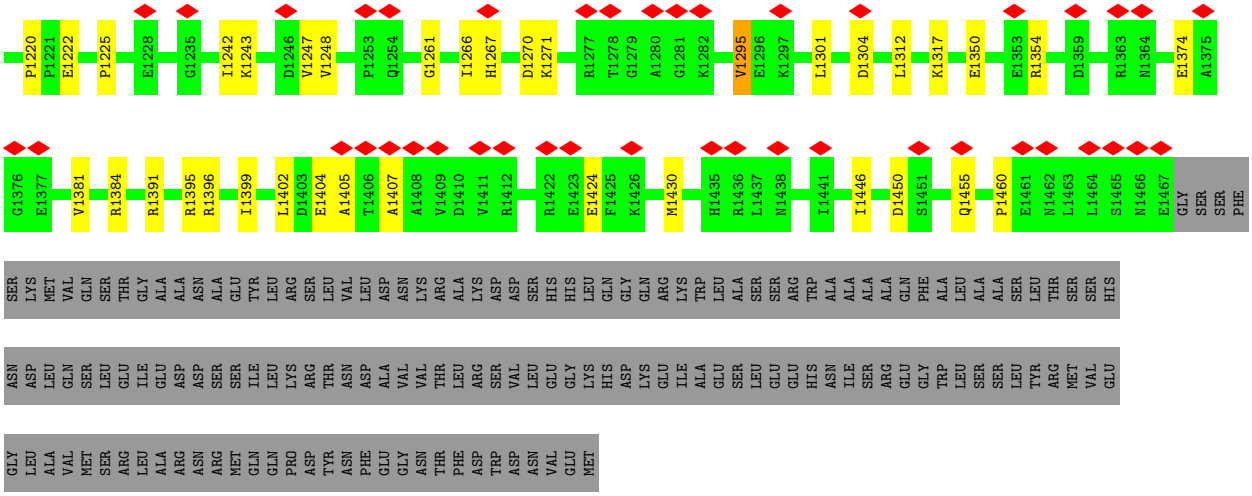
3 Residue-property plots (i)

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

Chain A: 9% 71% 13% 15%




P1220
P1221
E1222
P1225
E1228
G1235
I1242
K1243
D1246
V1247
V1248
P1253
Q1254
G1261
I1266
H1267
D1270
K1271
R1277
T1278
G1279
A1280
G1281
K1282
V1295
E1296
K1297
L1301
D1304
L1312
K1317
E1350
E1353
R1354
D1359
R1363
N1364
E1374
A1375
G1376
E1377
V1381
R1384
R1391
R1395
R1396
I1399
L1402
D1403
E1404
A1405
T1406
A1407
A1408
V1409
D1410
V1411
R1412
R1422
E1423
E1424
F1425
K1426
M1430
H1435
R1436
L1437
N1438
I1441
I1446
D1450
S1451
Q1455
P1460
E1461
N1462
L1463
L1464
S1465
N1466
E1467
GLY
SER
SER
PHE
SER LYS MET VAL GLN SER THR GLY ALA ALA ASN ALA GLU TYR LEU ARG SER LEU VAL LEU ASP ASN LYS ARG ALA LYS ASP ASP SER HIS HIS LEU GLN GLY GLN ARG LYS TRP LEU ALA SER SER ARG TRP ALA ALA ALA ALA GLN PHE ALA LEU ALA ALA SER LEU THR ARG MET VAL GLU
ASN ASP LEU GLN SER LEU GLU ILE GLU ASP ASP SER SER ILE LEU LYS ARG THR ASN ASP ALA VAL VAL THR LEU ARG SER VAL LEU GLU GLY LYS HIS ASP LYS GLU ILE ALA GLU SER LEU GLU GLU HIS ASN ILE SER ARG GLU GLY TRP LEU SER SER LEU TYR ARG MET VAL GLU
GLY LEU ALA VAL MET SER ARG LEU ALA ARG ASN ARG MET GLN GLN PRO ASP TYR ASN PHE GLU GLY ASN THR PHE ASP TRP ASP ASN VAL GLU MET

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	336481	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	49.72	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.200	Depositor
Minimum map value	-2.040	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	300.0, 300.0, 300.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CLR

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	0.26	1/11160 (0.0%)	0.48	17/15159 (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	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1176	ALA	C-O	-5.72	1.17	1.24

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1102	ALA	CA-C-O	-9.14	111.12	120.90
1	A	394	PHE	CB-CA-C	-8.41	95.01	109.65
1	A	1101	GLU	N-CA-C	-7.27	103.29	111.07
1	A	496	TRP	CB-CA-C	-6.76	101.48	112.03
1	A	1101	GLU	CB-CA-C	-6.62	100.48	110.88

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1097	ALA	Mainchain

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Mol	Chain	Res	Type	Group
1	A	1110	ARG	Sidechain
1	A	393	LYS	Mainchain

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	10915	0	11098	134	0
2	A	224	0	368	34	0
All	All	11139	0	11466	150	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 7.

The worst 5 of 150 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:695:ARG:O	1:A:699:LEU:HB2	1.76	0.85
1:A:1054:ILE:HG12	2:A:1706:CLR:H72	1.61	0.80
1:A:1004:PRO:HA	1:A:1222:GLU:OE2	1.86	0.76
1:A:155:MET:HG3	2:A:1706:CLR:H112	1.68	0.75
1:A:929:VAL:HG22	2:A:1704:CLR:H262	1.68	0.75

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	1373/1623 (85%)	1333 (97%)	40 (3%)	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	1193/1399 (85%)	1157 (97%)	36 (3%)	36	68

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1115	TYR
1	A	1399	ILE
1	A	1126	MET
1	A	1173	GLN
1	A	406	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1455	GLN
1	A	1385	GLN
1	A	1173	GLN
1	A	1036	ASN
1	A	1343	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)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	CLR	A	1703	-	31,31,31	0.31	0	48,48,48	0.61	0
2	CLR	A	1706	-	31,31,31	0.30	0	48,48,48	0.51	0
2	CLR	A	1705	-	31,31,31	0.31	0	48,48,48	0.73	2 (4%)
2	CLR	A	1707	-	31,31,31	0.27	0	48,48,48	0.41	0
2	CLR	A	1704	-	31,31,31	0.32	0	48,48,48	0.64	0
2	CLR	A	1708	-	31,31,31	0.29	0	48,48,48	0.54	0
2	CLR	A	1701	-	31,31,31	0.33	0	48,48,48	0.46	0
2	CLR	A	1702	-	31,31,31	0.29	0	48,48,48	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CLR	A	1703	-	-	8/10/68/68	0/4/4/4
2	CLR	A	1706	-	-	8/10/68/68	0/4/4/4
2	CLR	A	1705	-	-	9/10/68/68	0/4/4/4
2	CLR	A	1707	-	-	7/10/68/68	0/4/4/4
2	CLR	A	1704	-	-	9/10/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CLR	A	1708	-	-	8/10/68/68	0/4/4/4
2	CLR	A	1701	-	-	7/10/68/68	0/4/4/4
2	CLR	A	1702	-	-	9/10/68/68	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1705	CLR	C14-C8-C9	-2.17	106.19	109.09
2	A	1705	CLR	C7-C8-C9	2.04	112.19	109.71

There are no chirality outliers.

5 of 65 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1703	CLR	C13-C17-C20-C22
2	A	1706	CLR	C13-C17-C20-C21
2	A	1706	CLR	C16-C17-C20-C22
2	A	1708	CLR	C13-C17-C20-C21
2	A	1708	CLR	C13-C17-C20-C22

There are no ring outliers.

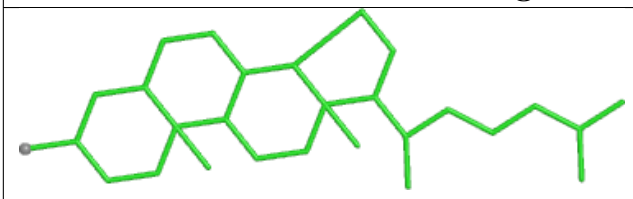
8 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1703	CLR	2	0
2	A	1706	CLR	5	0
2	A	1705	CLR	8	0
2	A	1707	CLR	2	0
2	A	1704	CLR	13	0
2	A	1708	CLR	8	0
2	A	1701	CLR	2	0
2	A	1702	CLR	1	0

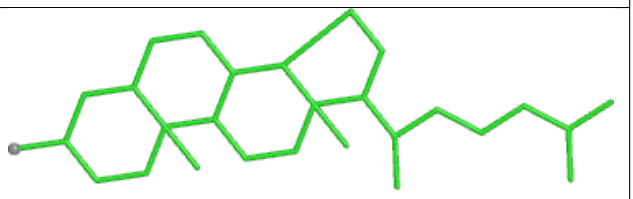
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

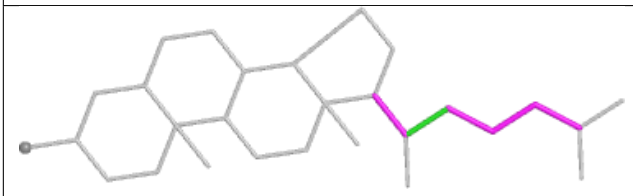
Ligand CLR A 1703



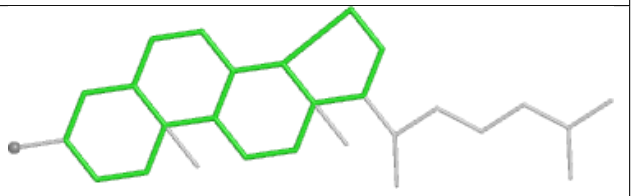
Bond lengths



Bond angles

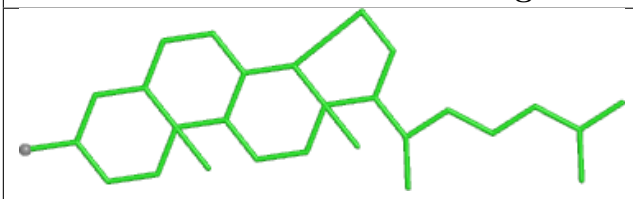


Torsions

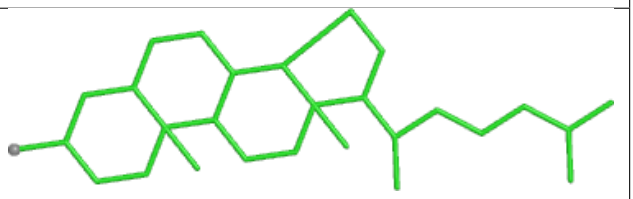


Rings

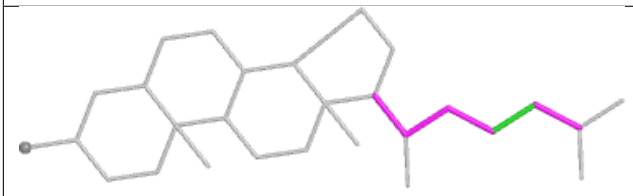
Ligand CLR A 1706



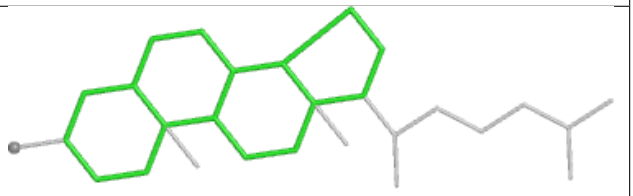
Bond lengths



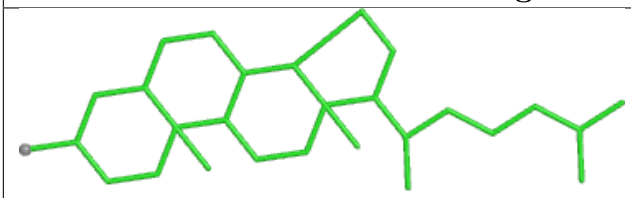
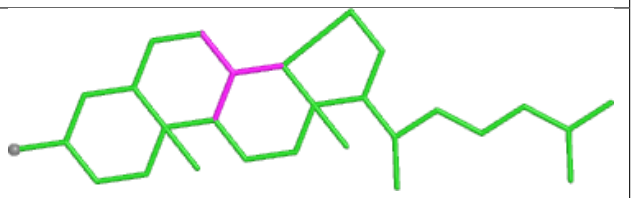
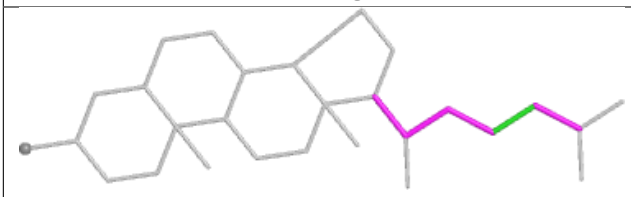
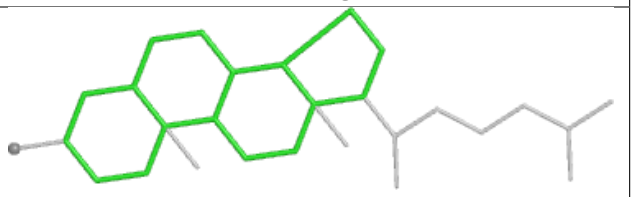
Bond angles

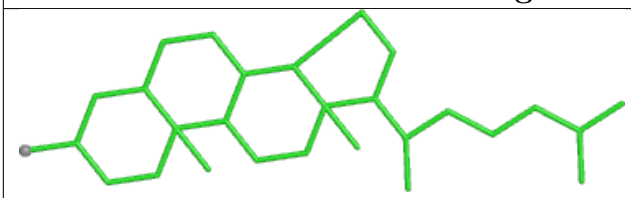
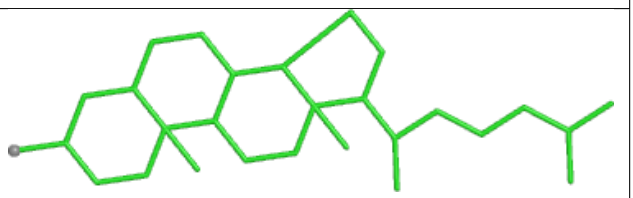
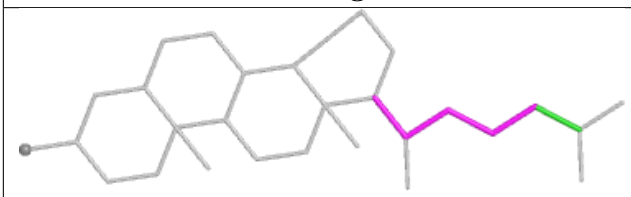
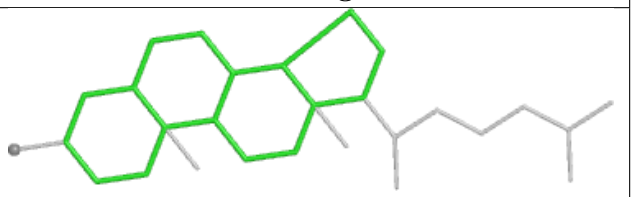


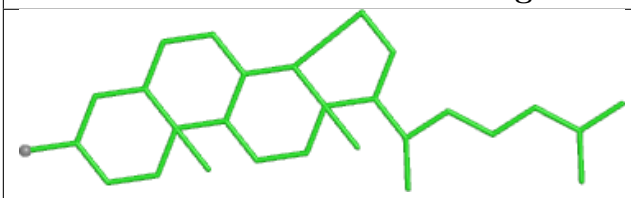
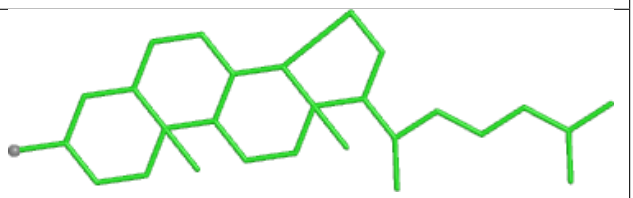
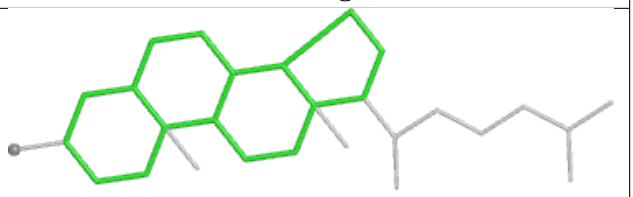
Torsions



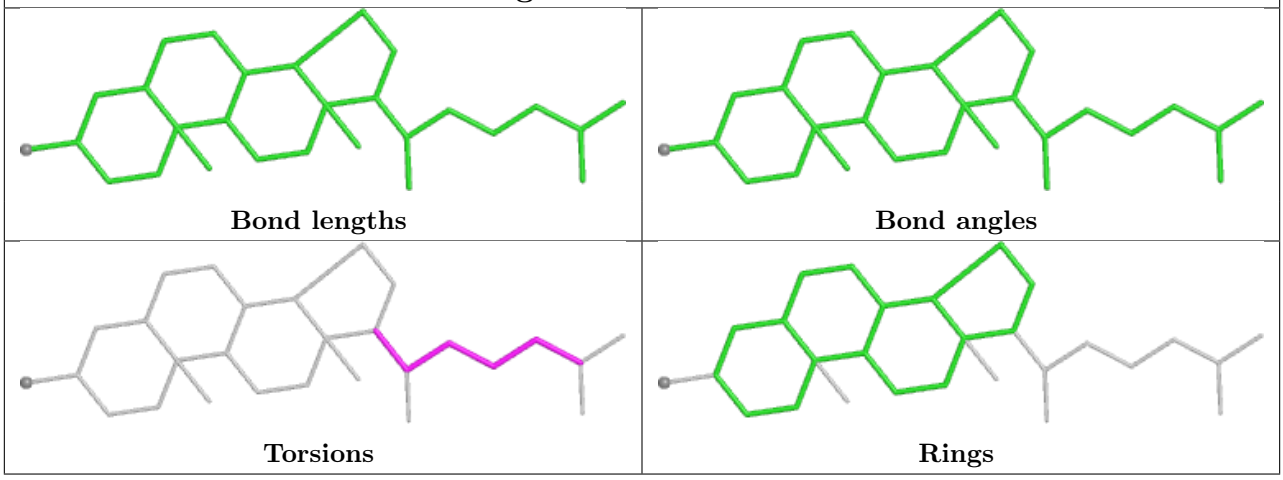
Rings

Ligand CLR A 1705	
 Bond lengths	 Bond angles
 Torsions	 Rings

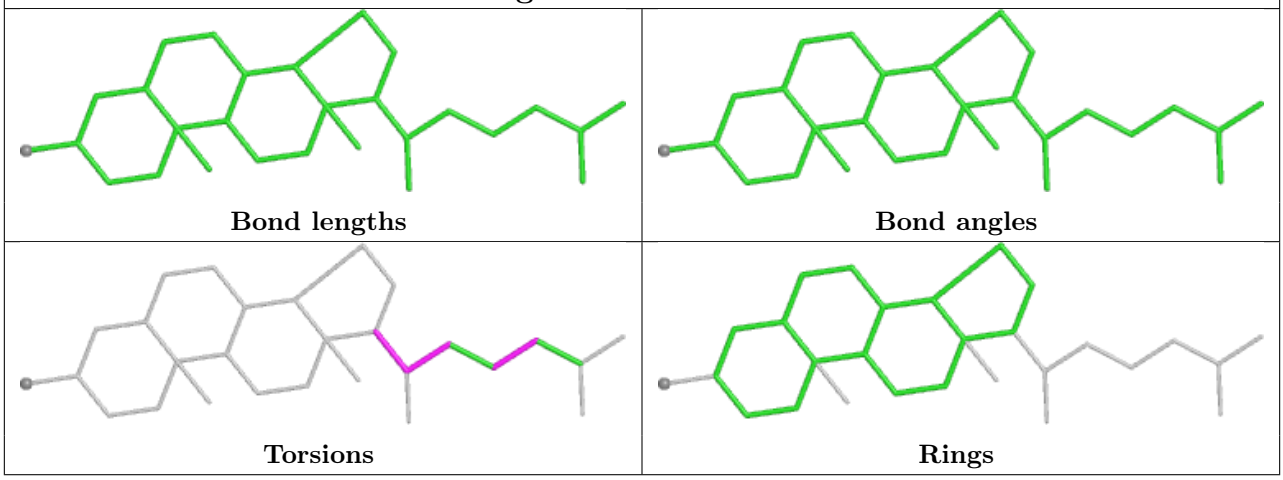
Ligand CLR A 1707	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLR A 1704	
 Bond lengths	 Bond angles
Torsions	 Rings

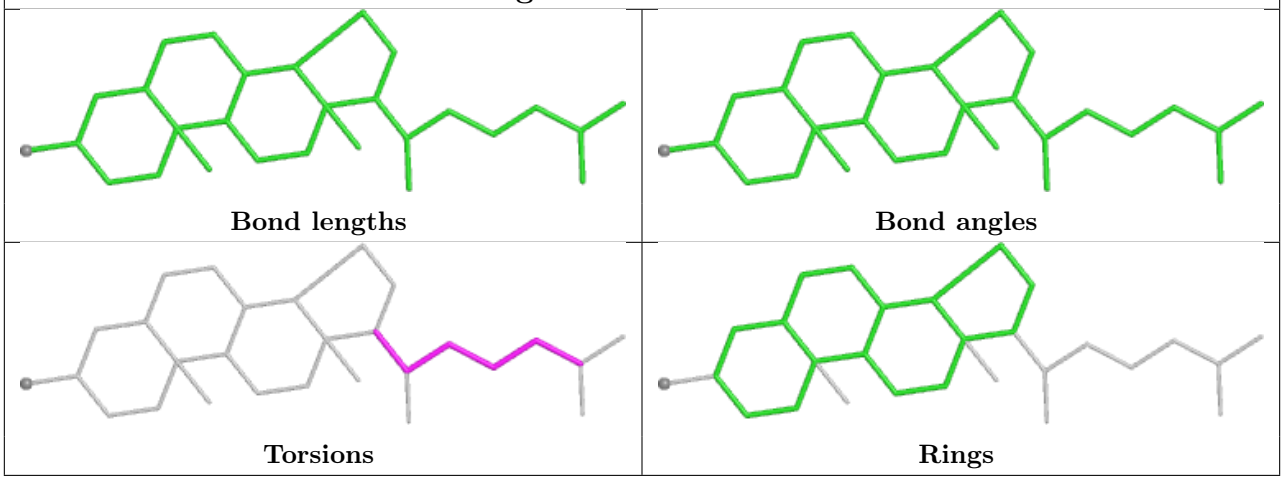
Ligand CLR A 1708



Ligand CLR A 1701



Ligand CLR A 1702



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.

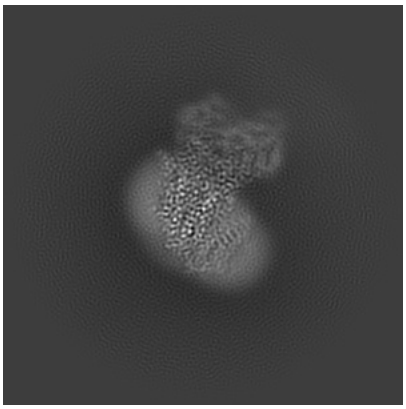
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-63864. These allow visual inspection of the internal detail of the map and identification of artifacts.

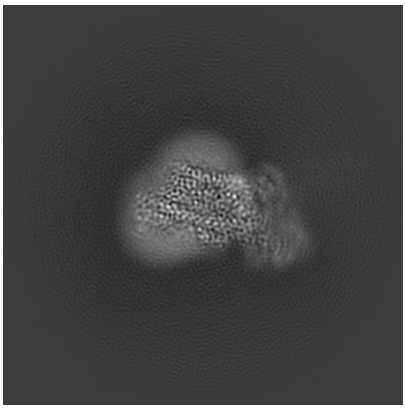
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

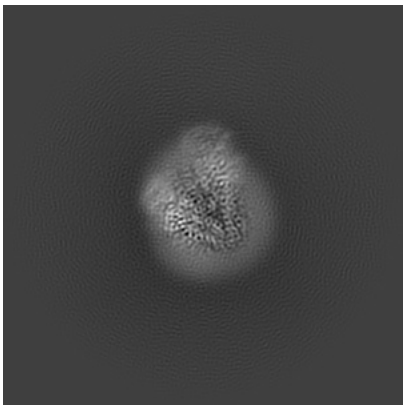
6.1.1 Primary map



X

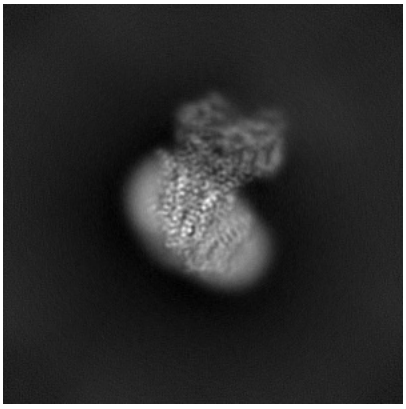


Y

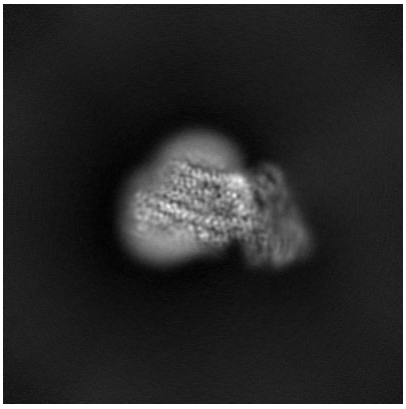


Z

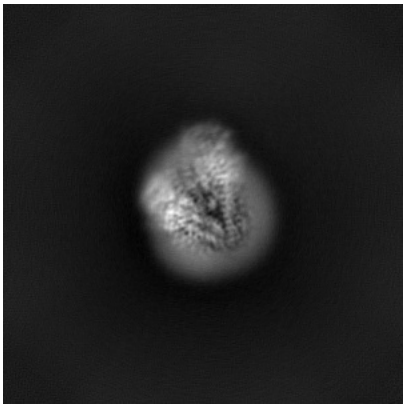
6.1.2 Raw map



X



Y

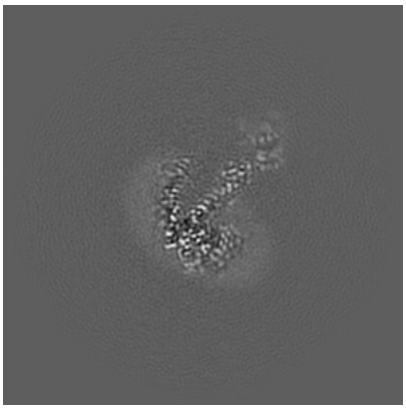


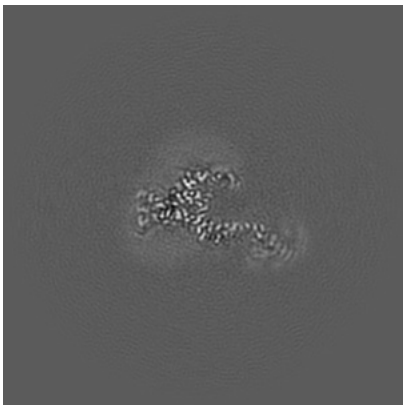
Z

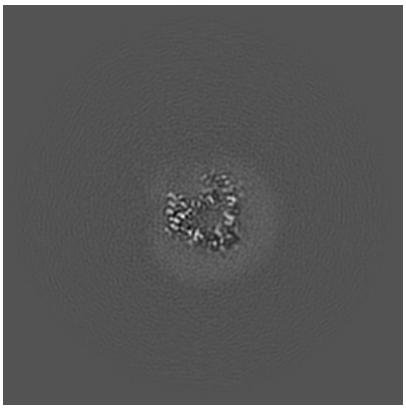
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

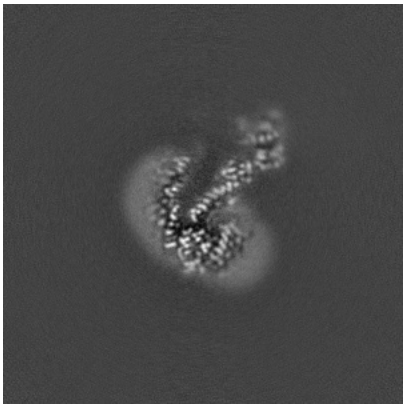
6.2.1 Primary map

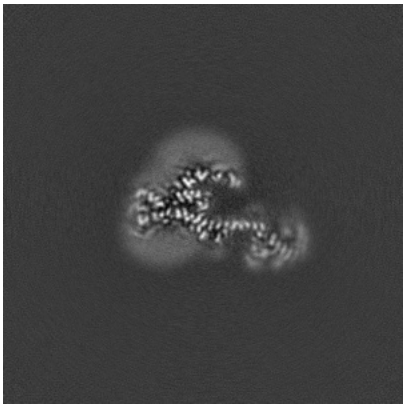

X Index: 200

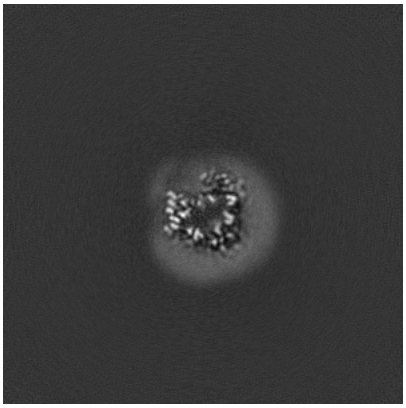

Y Index: 200


Z Index: 200

6.2.2 Raw map


X Index: 200

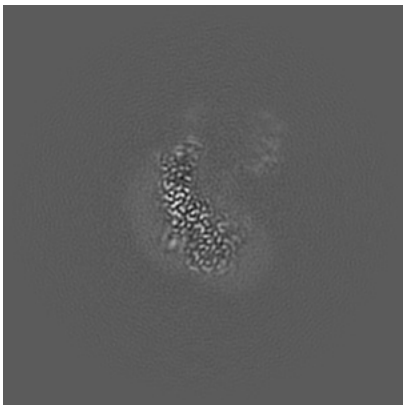

Y Index: 200

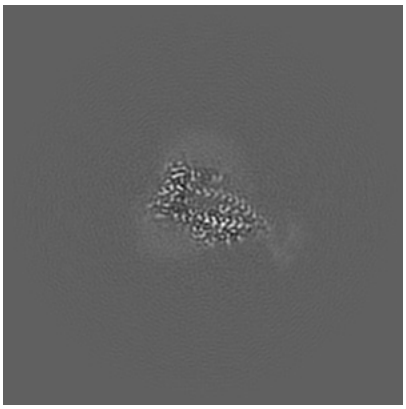

Z Index: 200

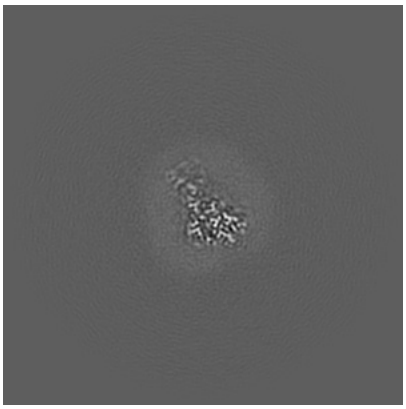
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

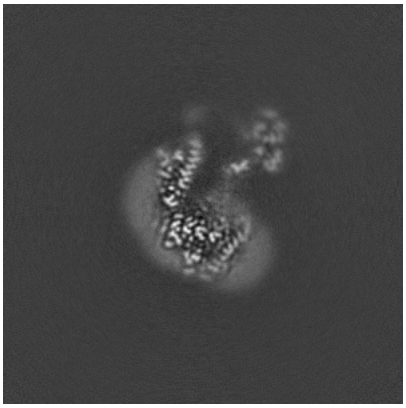
6.3.1 Primary map

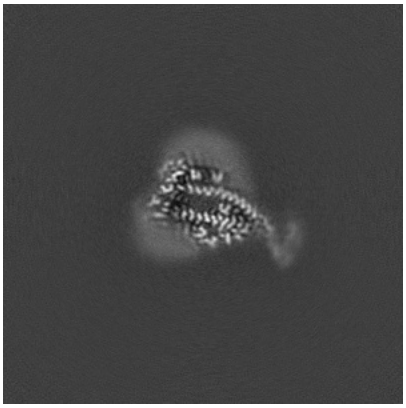

X Index: 187

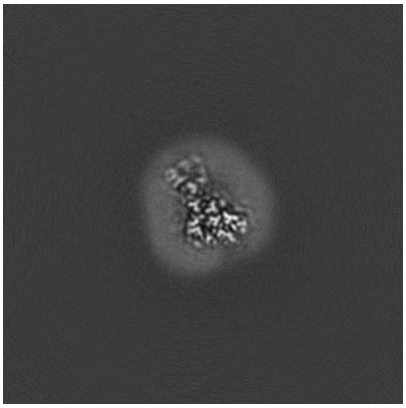

Y Index: 178


Z Index: 174

6.3.2 Raw map


X Index: 193

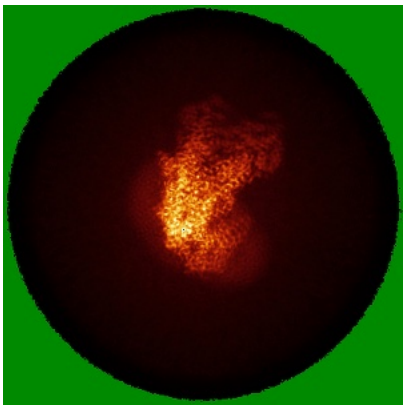

Y Index: 177

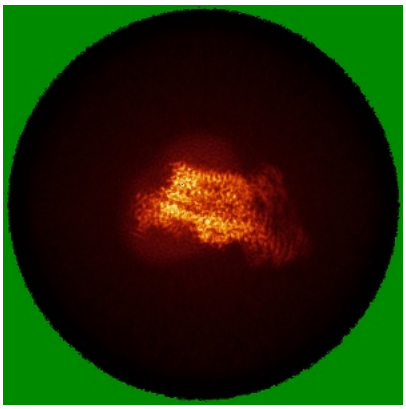

Z Index: 174

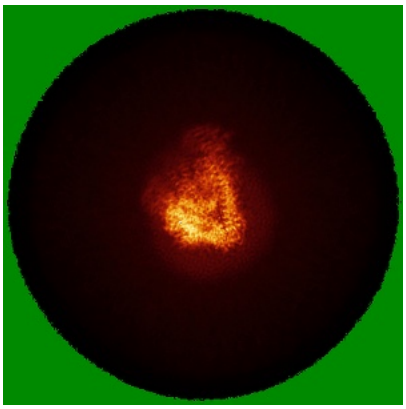
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

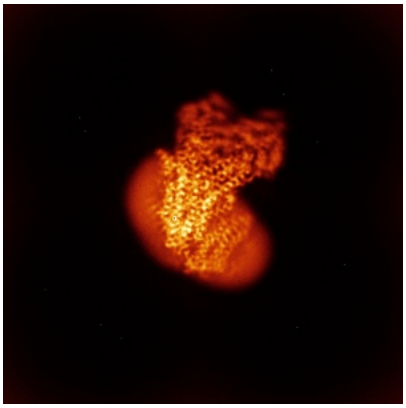
6.4.1 Primary map

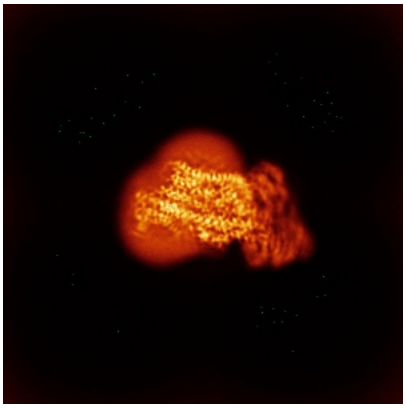

X

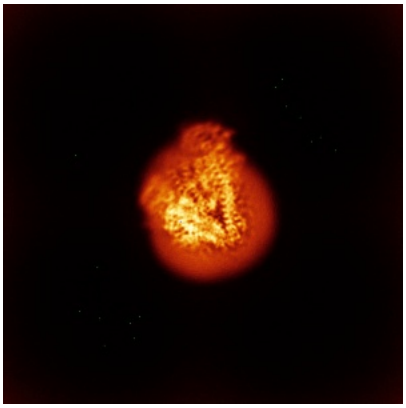

Y


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.

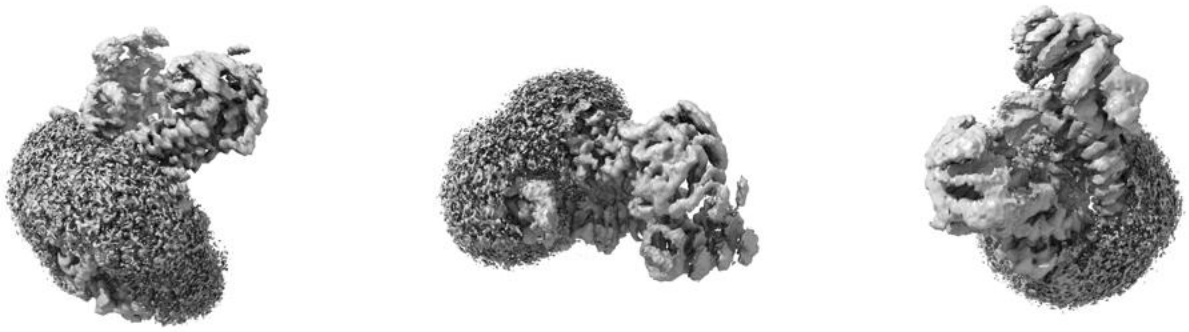
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. 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



X Y Z

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.

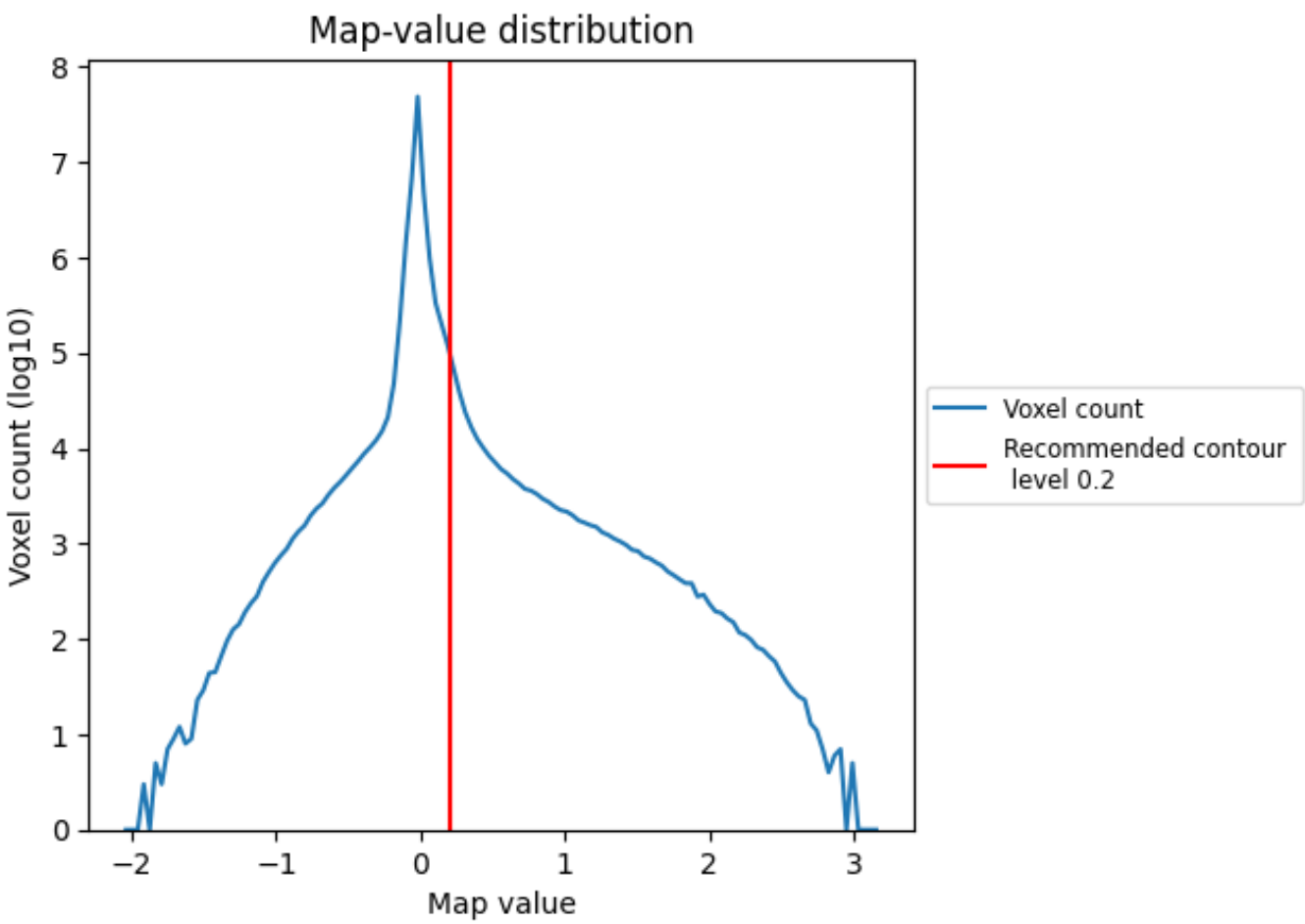
6.6 Mask visualisation (i)

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

7 Map analysis (i)

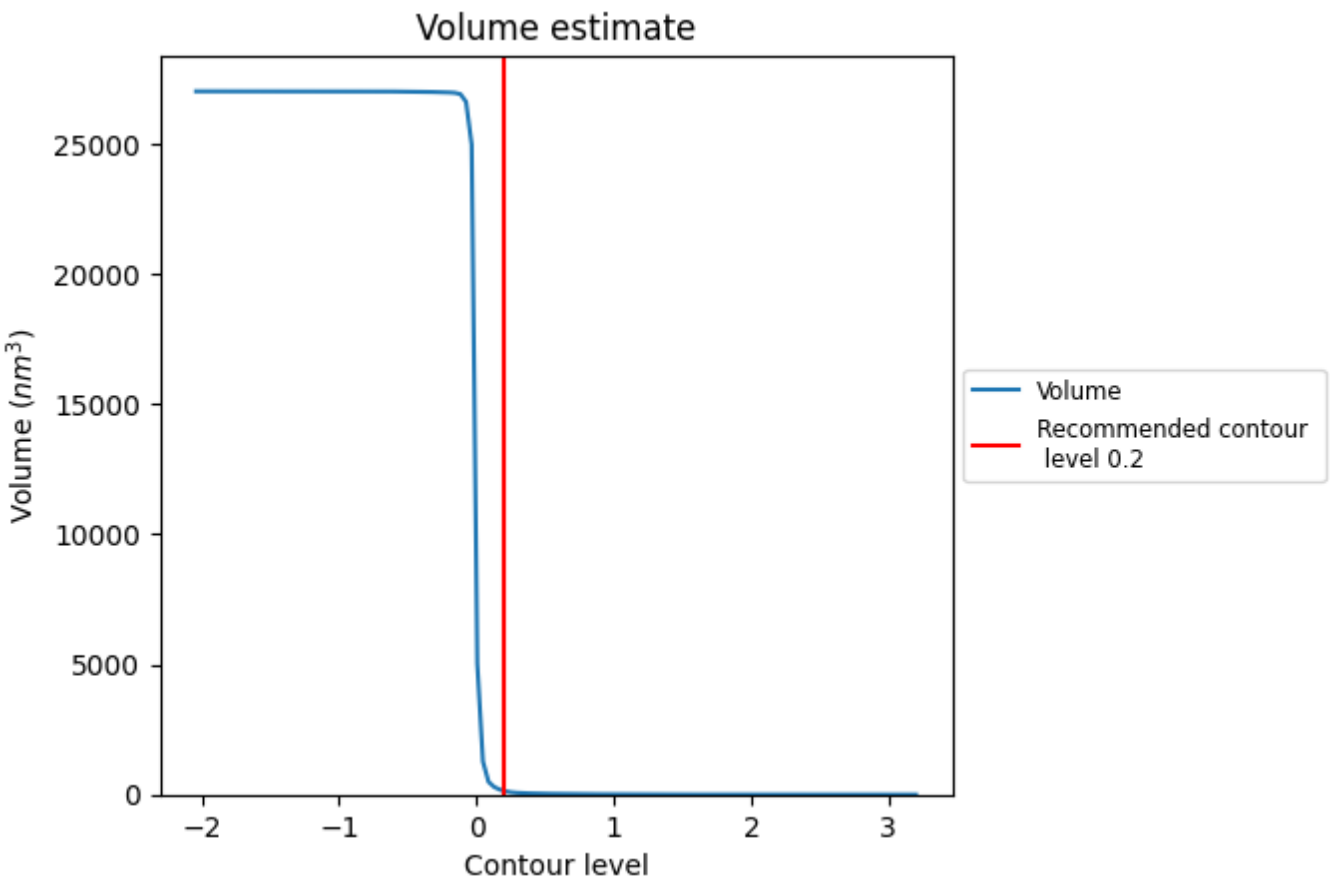
This section contains the results of statistical analysis of the map.

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.

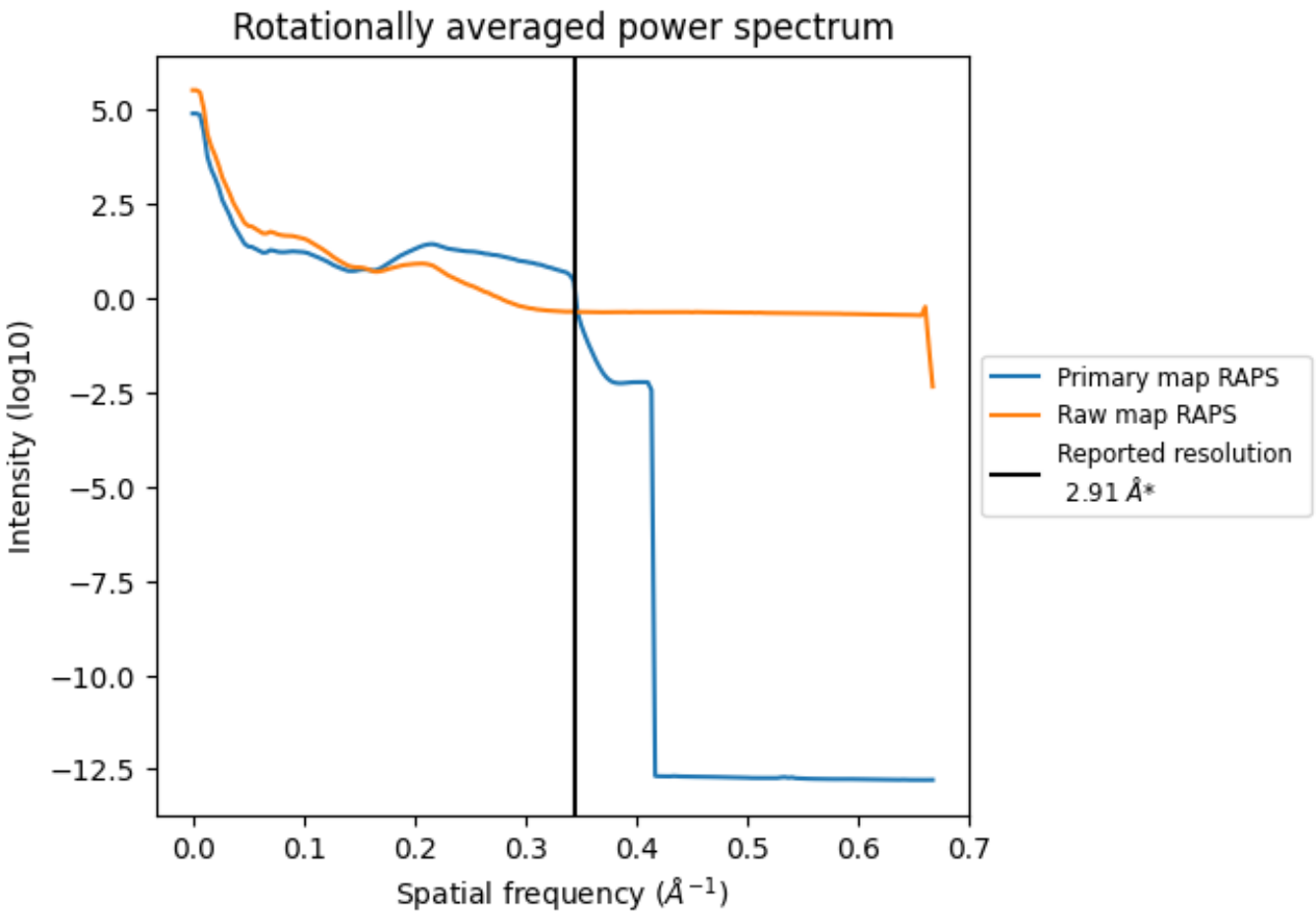
7.2 Volume estimate (i)



The volume at the recommended contour level is 143 nm^3; this corresponds to an approximate mass of 130 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 (i)

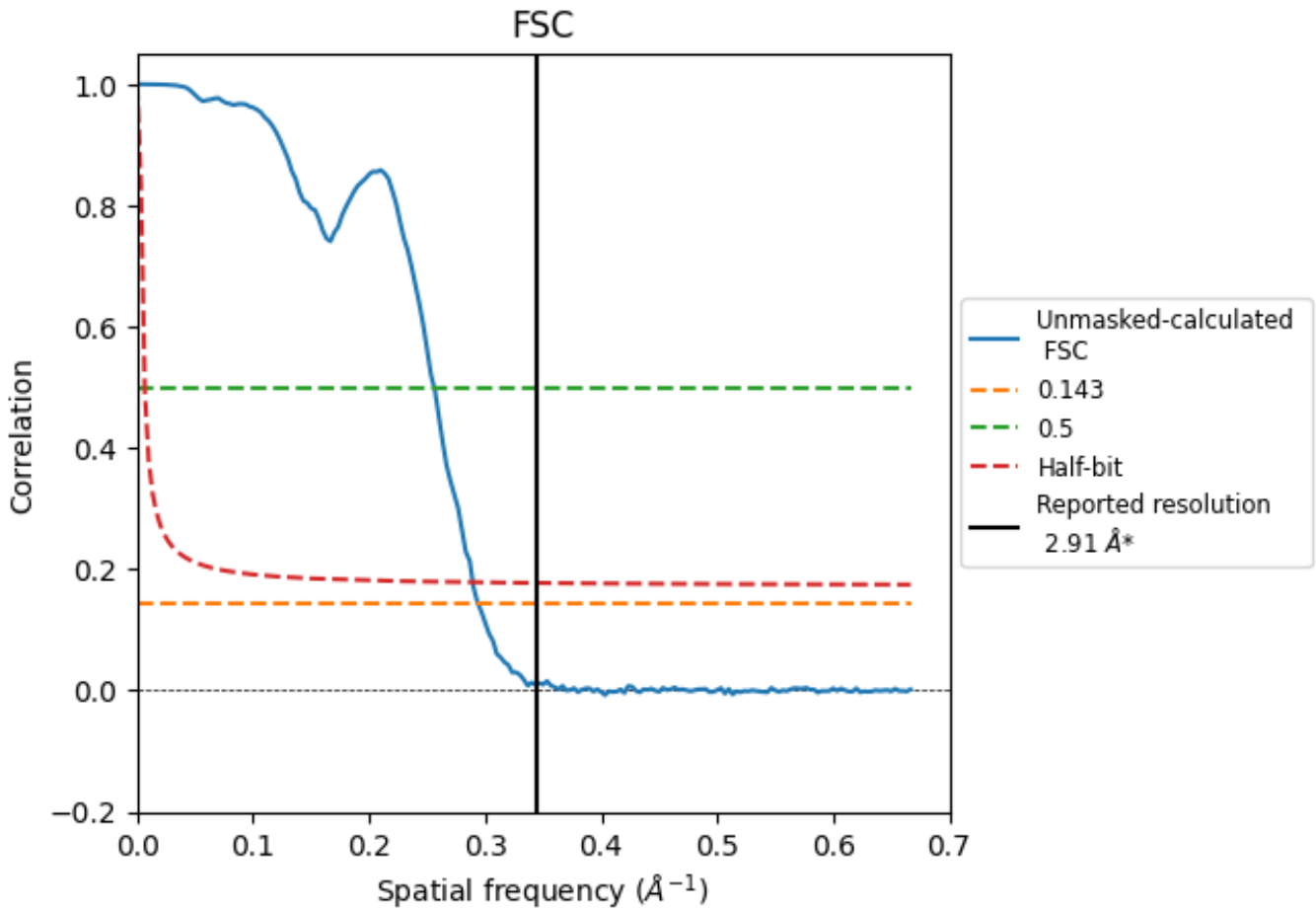


*Reported resolution corresponds to spatial frequency of 0.344 Å^{-1}

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 0.344 Å^{-1}

8.2 Resolution estimates (i)

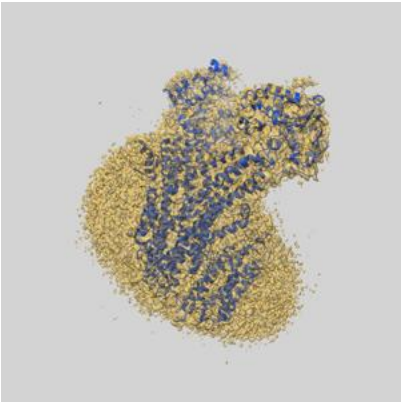
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.40	3.90	3.46

*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 3.40 differs from the reported value 2.91 by more than 10 %

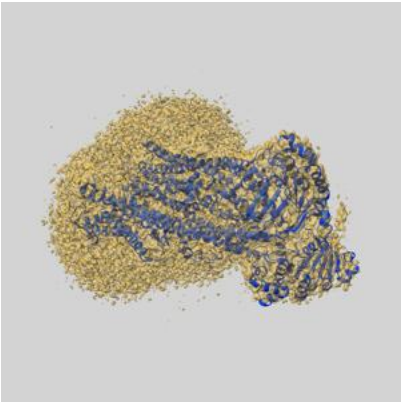
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-63864 and PDB model 9U56. Per-residue inclusion information can be found in section 3 on page 5.

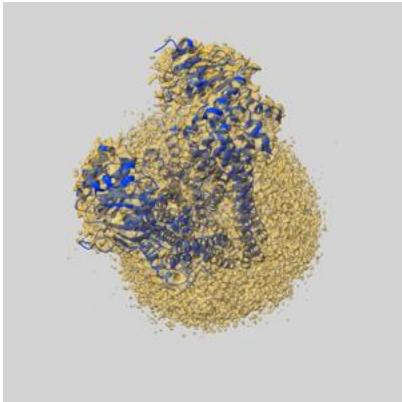
9.1 Map-model overlay (i)



X



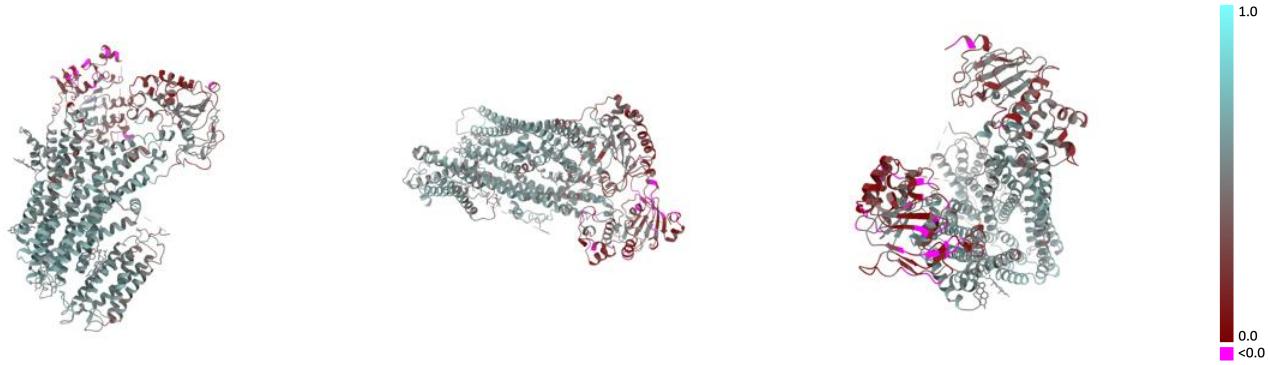
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

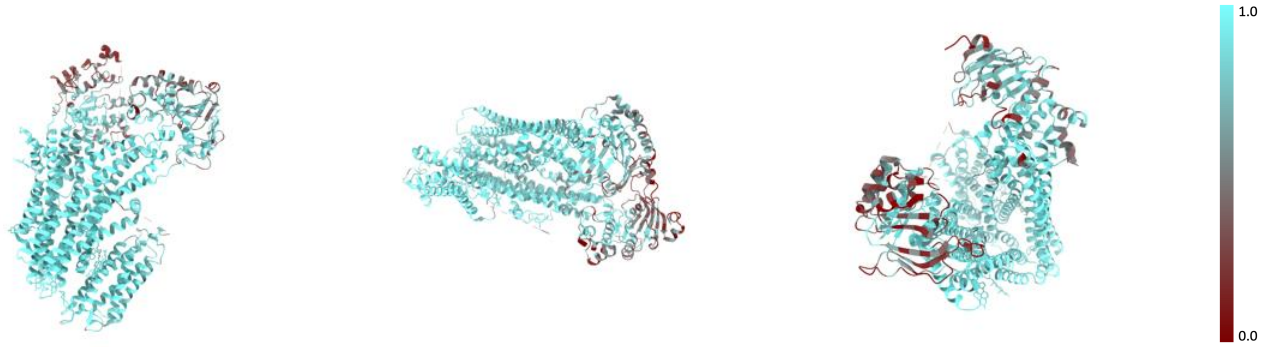
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

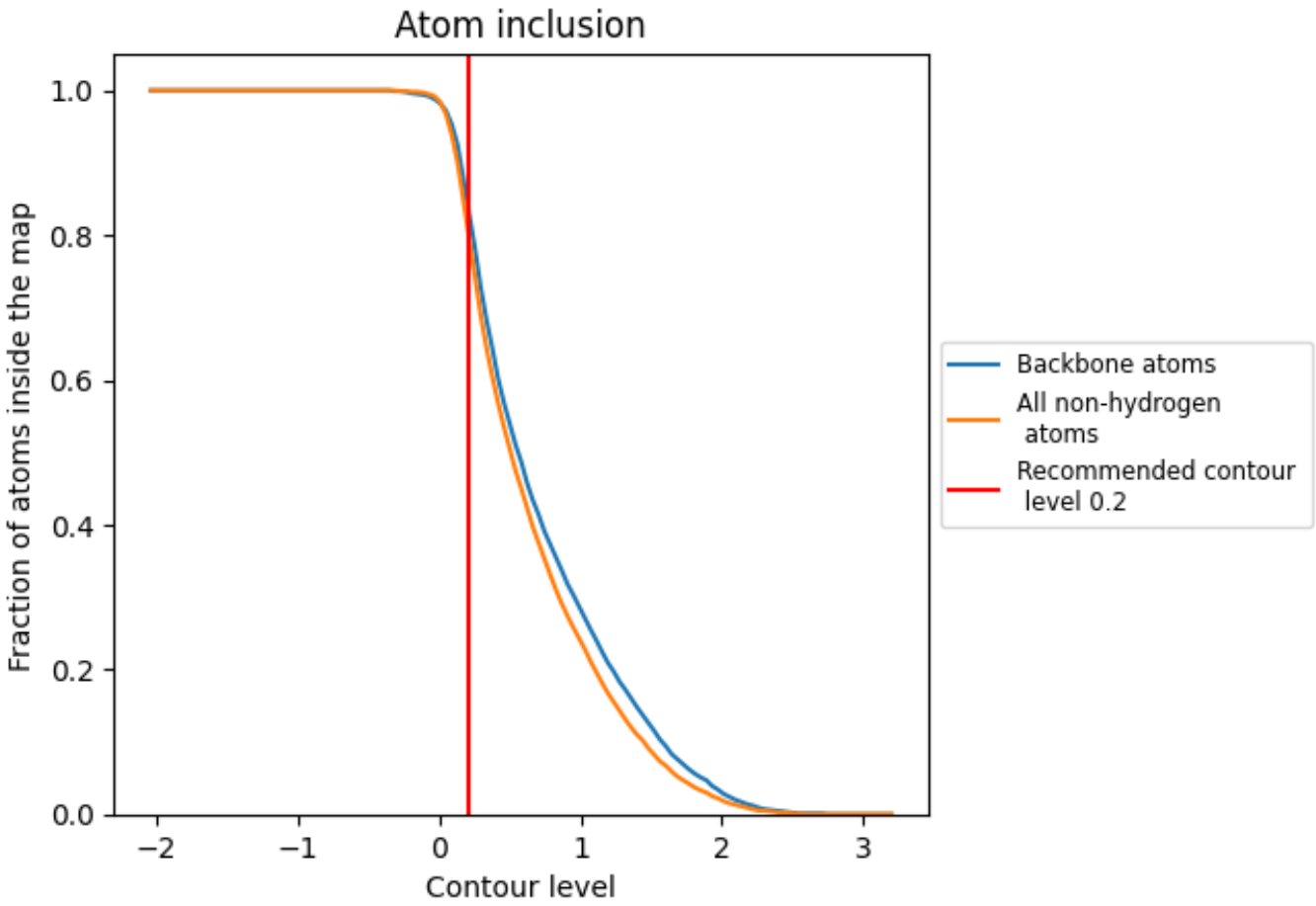
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8110	0.4690
A	0.8110	0.4690