



Full wwPDB EM Validation Report ⓘ

Jun 29, 2026 – 10:10 AM EDT

PDB ID : 36CG / pdb_000036cg
EMDB ID : EMD-31583
Title : Apo form of human bile salts export pump ABCB11
Authors : Wang, L.; How, W.T.
Deposited on : 2026-06-01
Resolution : 3.50 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:

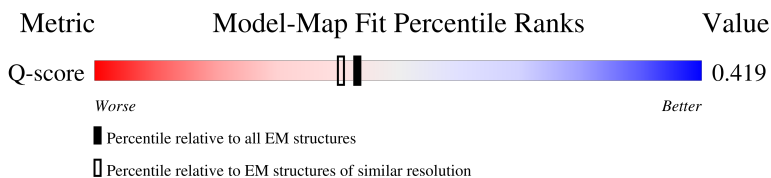
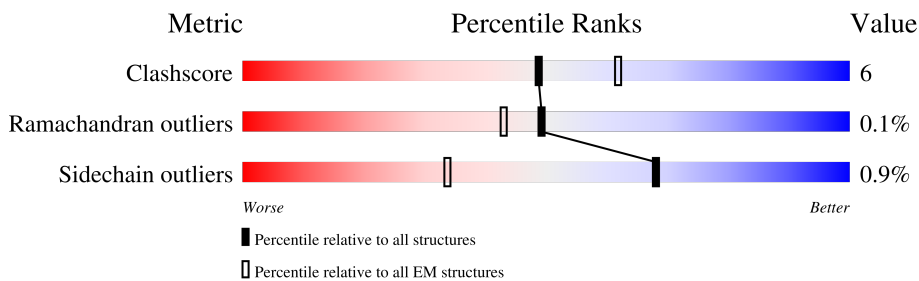
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	U	1321	<p>Bar chart showing the quality of chain for Mol 1, Chain U. The bar is divided into segments: 16% red (outliers ≥ 3), 77% green (outliers ≤ 1), 16% yellow (outliers = 2), and 7% grey (not modelled).</p>

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 9576 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.

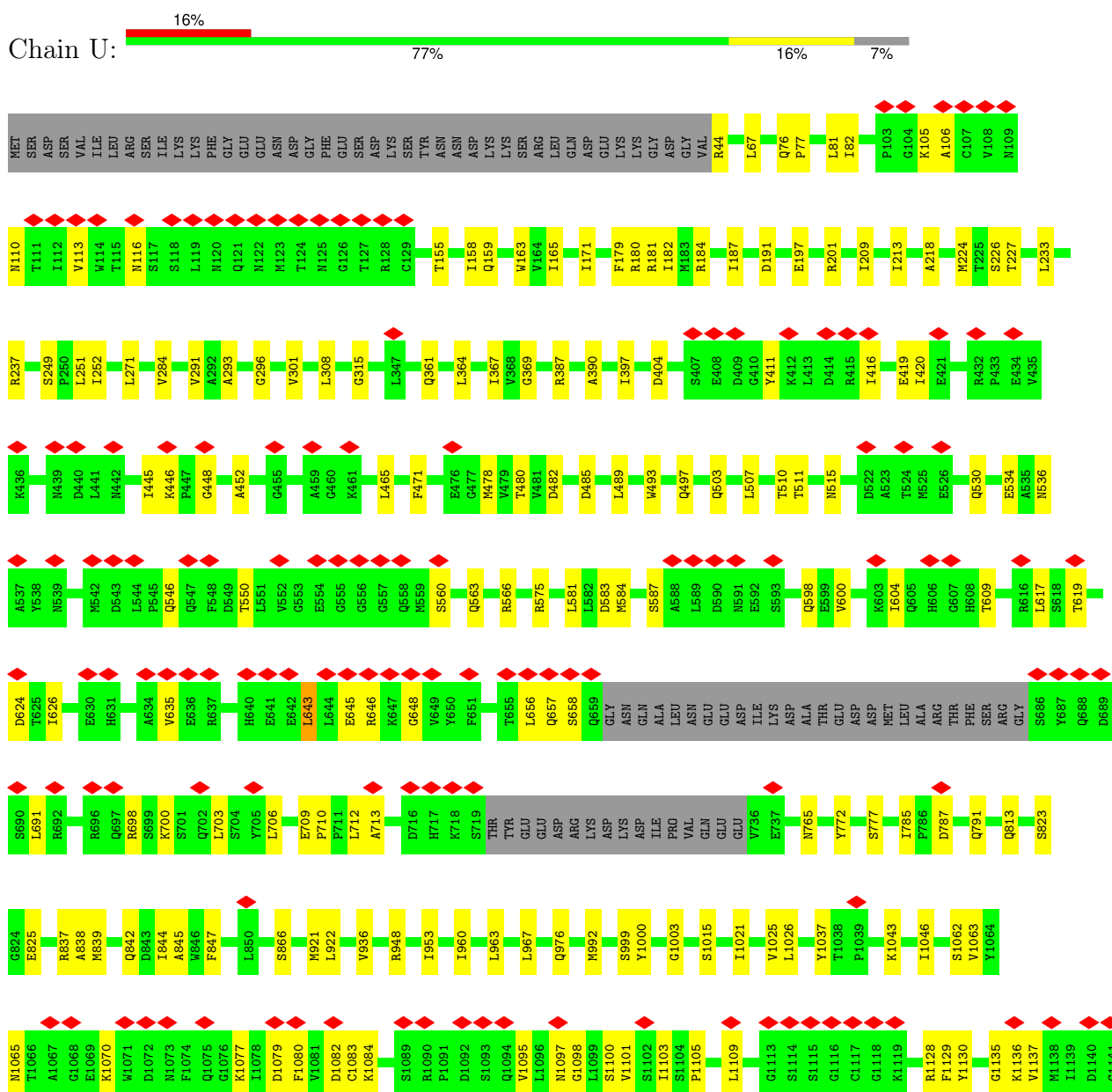
- Molecule 1 is a protein called Bile salt export pump.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	U	1230	9576	6129	1627	1766	54	0	0

3 Residue-property plots

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: Bile salt export pump



H1142	D1143	S1144	K1145	K1146	V1147	M1148	V1149	S1154	N1155	I1156	G1157	I1158	Q1161	E1162	A1167	I1170	M1171	D1172	K1175	D1178	M1179	T1180	K1181	E1182	I1183	F1184	M1185	I1189	M1190	K1193	Q1194	A1195	Q1196	D1199	M1202	S1203	L1204	P1205	E1206	K1207	M1211	V1212	G1213	S1214	Q1215	G1216	S1217	Q1218				
L1219	S1220	R1226	R1235	D1236	L1241	L1242	D1243	E1244	A1245	T1246	L1249	D1250	T1251	E1252	S1253	E1254	K1255	T1256	V1257	L1261	D1262	K1263	E1266	I1271	V1272	I1273	A1274	H1275	R1276	L1277	S1278	T1279	I1280	Q1281	N1282	A1283	D1284	I1285	I1286	A1287	V1288	M1289	A1290	Q1291	G1292	V1293	V1294	I1295	E1296	K1297	G1298	T1299
H1300	E1301	E1302	L1303	M1304	A1305	Q1306	K1307	G1308	A1309	Y1310	Y1311	K1312	L1313	V1314	T1315	THR	GLY	SER	PRO	ILE	SER																															

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	385065	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.592	Depositor
Minimum map value	-2.834	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	228.95999, 228.95999, 228.95999	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	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	U	0.46	1/9761 (0.0%)	0.79	3/13199 (0.0%)

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	U	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	U	76	GLN	C-N	5.80	1.38	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	1170	ILE	N-CA-C	-8.22	104.69	112.83
1	U	213	ILE	N-CA-C	-6.73	107.32	113.71
1	U	67	LEU	N-CA-C	-6.05	105.94	113.38

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	U	1037	TYR	Peptide
1	U	1271	ILE	Peptide
1	U	510	THR	Peptide
1	U	635	VAL	Peptide
1	U	712	LEU	Peptide
1	U	976	GLN	Peptide

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	U	9576	0	9645	112	0
All	All	9576	0	9645	112	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 6.

All (112) 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:U:1063:VAL:HA	1:U:1149:VAL:HG11	1.72	0.71
1:U:187:ILE:HG21	1:U:471:PHE:HB3	1.77	0.66
1:U:411:TYR:H	1:U:489:LEU:HA	1.61	0.65
1:U:1196:GLN:O	1:U:1226:ARG:NH2	2.32	0.63
1:U:1136:LYS:HE3	1:U:1143:ASP:HB3	1.79	0.63
1:U:645:GLU:HG3	1:U:646:ARG:HG3	1.82	0.62
1:U:1095:VAL:HG12	1:U:1097:ASN:H	1.64	0.62
1:U:656:LEU:HD12	1:U:657:GLN:HG2	1.82	0.61
1:U:1070:LYS:HD3	1:U:1148:ASN:HD21	1.66	0.61
1:U:448:GLY:H	1:U:609:THR:HG22	1.65	0.60
1:U:1175:LYS:HE2	1:U:1183:ILE:HG22	1.83	0.60
1:U:159:GLN:NE2	1:U:218:ALA:O	2.34	0.60
1:U:493:TRP:O	1:U:497:GLN:NE2	2.35	0.60
1:U:575:ARG:NH1	1:U:953:ILE:O	2.35	0.59
1:U:105:LYS:O	1:U:110:ASN:ND2	2.35	0.59
1:U:249:SER:HA	1:U:252:ILE:HG22	1.86	0.58
1:U:1178:ASP:HB3	1:U:1235:ARG:HD3	1.86	0.58
1:U:106:ALA:HB1	1:U:113:VAL:HG11	1.85	0.58
1:U:503:GLN:NE2	1:U:583:ASP:OD2	2.37	0.58
1:U:1080:PHE:HB2	1:U:1101:VAL:H	1.70	0.57
1:U:1083:CYS:HA	1:U:1135:GLY:HA3	1.87	0.57
1:U:936:VAL:HG23	1:U:963:LEU:HD11	1.88	0.56
1:U:1243:ASP:HA	1:U:1273:ILE:HD13	1.88	0.56
1:U:184:ARG:HG2	1:U:404:ASP:HB2	1.88	0.56
1:U:480:THR:HA	1:U:485:ASP:HA	1.87	0.55
1:U:507:LEU:HB3	1:U:515:ASN:HD21	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:1128:ARG:NH1	1:U:1144:SER:O	2.39	0.55
1:U:110:ASN:O	1:U:116:ASN:ND2	2.40	0.55
1:U:1277:LEU:HD22	1:U:1313:LEU:HD21	1.87	0.55
1:U:113:VAL:O	1:U:116:ASN:ND2	2.40	0.55
1:U:1097:ASN:HB3	1:U:1292:GLY:HA3	1.89	0.55
1:U:1245:ALA:HB3	1:U:1261:LEU:HD21	1.89	0.55
1:U:209:ILE:HG21	1:U:390:ALA:HB2	1.88	0.54
1:U:271:LEU:HD23	1:U:691:LEU:HD22	1.88	0.54
1:U:420:ILE:HB	1:U:445:ILE:HB	1.89	0.54
1:U:838:ALA:O	1:U:842:GLN:NE2	2.40	0.54
1:U:446:LYS:NZ	1:U:624:ASP:OD2	2.40	0.54
1:U:237:ARG:HG3	1:U:361:GLN:HE22	1.72	0.53
1:U:419:GLU:HB3	1:U:482:ASP:HB2	1.90	0.53
1:U:1154:SER:O	1:U:1235:ARG:NH1	2.42	0.52
1:U:284:VAL:HG13	1:U:291:VAL:HG21	1.92	0.52
1:U:1128:ARG:NH2	1:U:1147:VAL:O	2.43	0.52
1:U:698:ARG:NH1	1:U:866:SER:O	2.42	0.52
1:U:600:VAL:HA	1:U:604:ILE:HD12	1.90	0.52
1:U:224:MET:HA	1:U:227:THR:HG22	1.91	0.52
1:U:296:GLY:HA2	1:U:1179:ASN:HD21	1.74	0.51
1:U:1082:ASP:H	1:U:1100:SER:HB3	1.76	0.51
1:U:1308:GLY:H	1:U:1311:TYR:HB3	1.75	0.51
1:U:643:LEU:HD21	1:U:648:GLY:HA3	1.92	0.51
1:U:155:THR:HA	1:U:158:ILE:HG22	1.93	0.51
1:U:844:ILE:HA	1:U:847:PHE:HD2	1.76	0.50
1:U:546:GLN:O	1:U:550:THR:OG1	2.29	0.50
1:U:1254:GLU:OE1	1:U:1276:ARG:NH1	2.44	0.50
1:U:452:ALA:HB3	1:U:626:ILE:HA	1.93	0.50
1:U:367:ILE:HG21	1:U:710:PRO:HB3	1.94	0.49
1:U:191:ASP:OD1	1:U:948:ARG:NH2	2.45	0.49
1:U:1080:PHE:HA	1:U:1137:VAL:HG12	1.93	0.49
1:U:1246:THR:HB	1:U:1254:GLU:HG3	1.95	0.49
1:U:1109:LEU:HD13	1:U:1271:ILE:HG22	1.95	0.48
1:U:1246:THR:HG22	1:U:1257:VAL:HG13	1.95	0.48
1:U:530:GLN:NE2	1:U:534:GLU:OE2	2.45	0.46
1:U:1084:LYS:HD2	1:U:1098:GLY:HA3	1.96	0.46
1:U:1284:ASP:HA	1:U:1299:THR:HG23	1.98	0.46
1:U:465:LEU:HG	1:U:581:LEU:HD22	1.98	0.45
1:U:617:LEU:HD21	1:U:658:SER:HB2	1.99	0.45
1:U:785:ILE:HG23	1:U:791:GLN:HB3	1.98	0.45
1:U:845:ALA:HA	1:U:1130:TYR:HE1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:181:ARG:HG3	1:U:397:ILE:HA	1.99	0.45
1:U:1000:TYR:CZ	1:U:1021:ILE:HD11	2.52	0.45
1:U:81:LEU:HD21	1:U:233:LEU:HD21	1.99	0.45
1:U:77:PRO:HD3	1:U:226:SER:HB2	1.99	0.44
1:U:765:ASN:HD21	1:U:813:GLN:NE2	2.16	0.44
1:U:999:SER:HB3	1:U:1021:ILE:HG21	1.99	0.44
1:U:197:GLU:OE2	1:U:201:ARG:NH2	2.50	0.44
1:U:839:MET:HE3	1:U:839:MET:HB2	1.87	0.44
1:U:777:SER:O	1:U:1015:SER:OG	2.36	0.43
1:U:1062:SER:HB3	1:U:1065:ASN:HB2	2.00	0.43
1:U:560:SER:H	1:U:563:GLN:HE21	1.65	0.43
1:U:703:LEU:HD13	1:U:706:LEU:HD12	2.00	0.43
1:U:709:GLU:O	1:U:772:TYR:OH	2.36	0.43
1:U:478:MET:HE2	1:U:485:ASP:HB3	2.01	0.43
1:U:180:ARG:HA	1:U:960:ILE:HD11	2.01	0.43
1:U:999:SER:O	1:U:1003:GLY:N	2.42	0.43
1:U:921:MET:HE3	1:U:921:MET:HB3	1.90	0.43
1:U:179:PHE:HA	1:U:182:ILE:HG22	2.00	0.43
1:U:301:VAL:HG11	1:U:837:ARG:HB3	2.01	0.43
1:U:823:SER:O	1:U:823:SER:OG	2.37	0.43
1:U:1158:ILE:HG22	1:U:1241:LEU:HB2	2.01	0.42
1:U:227:THR:OG1	1:U:369:GLY:O	2.29	0.42
1:U:1156:ILE:H	1:U:1156:ILE:HG13	1.72	0.42
1:U:293:ALA:HB2	1:U:1129:PHE:HZ	1.85	0.42
1:U:1043:LYS:HA	1:U:1046:ILE:HG22	2.01	0.42
1:U:1077:LYS:HG2	1:U:1105:PRO:HD3	2.02	0.42
1:U:416:ILE:HD12	1:U:497:GLN:HG2	2.02	0.42
1:U:503:GLN:HG3	1:U:584:MET:HB3	2.02	0.42
1:U:992:MET:HE1	1:U:1025:VAL:HG11	2.02	0.41
1:U:209:ILE:HD13	1:U:390:ALA:HB2	2.03	0.41
1:U:700:LYS:HA	1:U:703:LEU:HD23	2.01	0.41
1:U:584:MET:HG3	1:U:587:SER:HB3	2.03	0.41
1:U:163:TRP:CD1	1:U:218:ALA:HB2	2.55	0.41
1:U:364:LEU:HD13	1:U:713:ALA:HB2	2.03	0.41
1:U:165:ILE:HD12	1:U:165:ILE:HA	1.79	0.41
1:U:404:ASP:OD1	1:U:404:ASP:N	2.51	0.41
1:U:536:ASN:O	1:U:566:ARG:NH1	2.54	0.41
1:U:1211:ASN:O	1:U:1215:GLN:NE2	2.53	0.41
1:U:1079:ASP:OD1	1:U:1103:ILE:N	2.54	0.40
1:U:1301:GLU:HG2	1:U:1302:GLU:HG2	2.02	0.40
1:U:1304:MET:N	1:U:1304:MET:SD	2.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:44:ARG:N	1:U:387:ARG:O	2.54	0.40
1:U:315:GLY:HA3	1:U:825:GLU:HG3	2.02	0.40
1:U:787:ASP:OD1	1:U:787:ASP:N	2.49	0.40
1:U:598:GLN:HE22	1:U:619:THR:HG23	1.86	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	U	1224/1321 (93%)	1088 (89%)	135 (11%)	1 (0%)	48 79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	U	511	THR

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	U	1026/1107 (93%)	1017 (99%)	9 (1%)	70 76

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	U	82	ILE
1	U	171	ILE
1	U	251	LEU
1	U	308	LEU
1	U	643	LEU
1	U	922	LEU
1	U	967	LEU
1	U	1026	LEU
1	U	1273	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	U	101	GLN
1	U	116	ASN
1	U	207	ASN
1	U	442	ASN
1	U	492	GLN
1	U	515	ASN
1	U	563	GLN
1	U	598	GLN
1	U	640	HIS
1	U	697	GLN
1	U	765	ASN
1	U	778	GLN
1	U	813	GLN
1	U	842	GLN
1	U	852	ASN
1	U	1009	ASN
1	U	1107	GLN
1	U	1211	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.

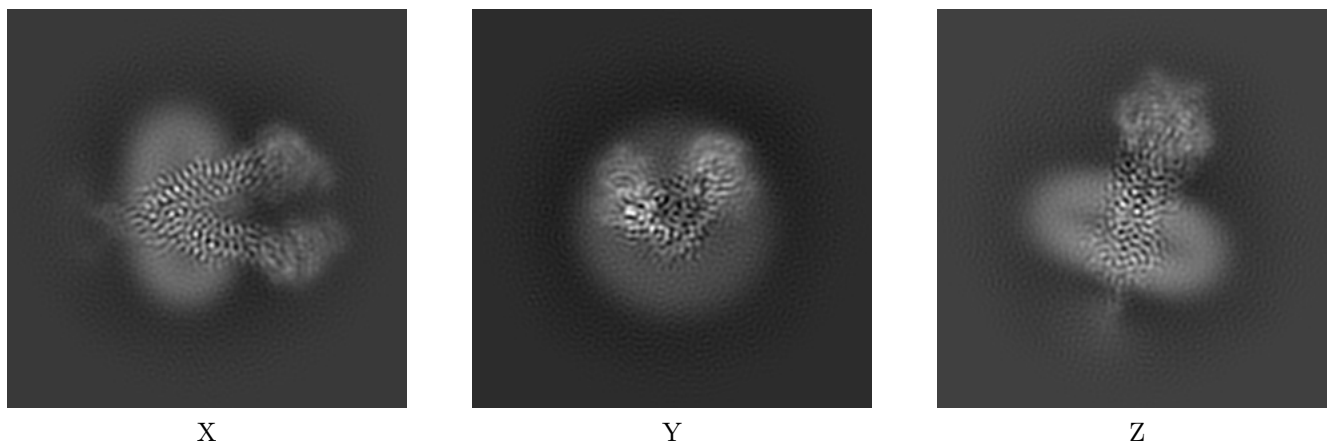
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31583. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

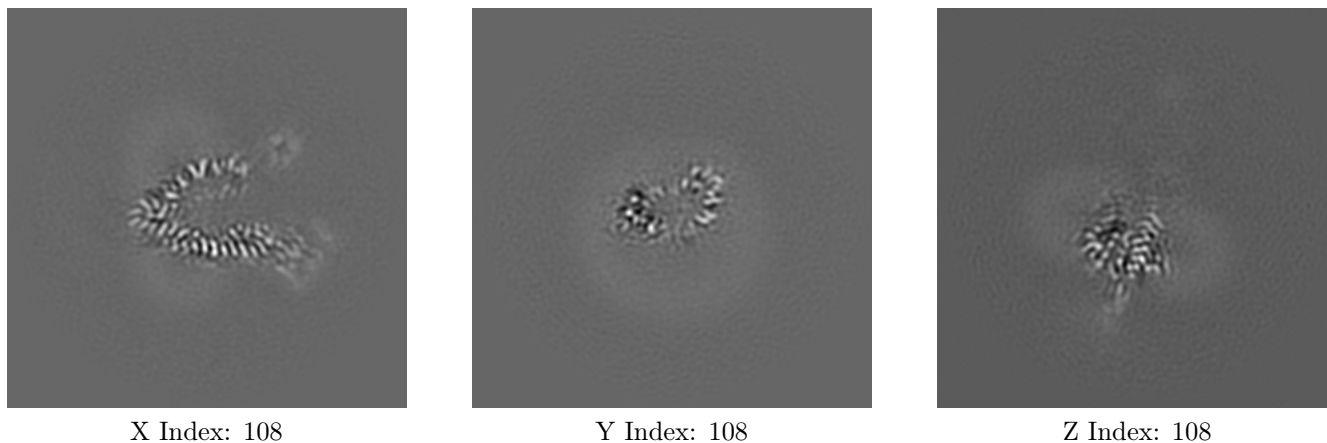
6.1.1 Primary map



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

6.2 Central slices [i](#)

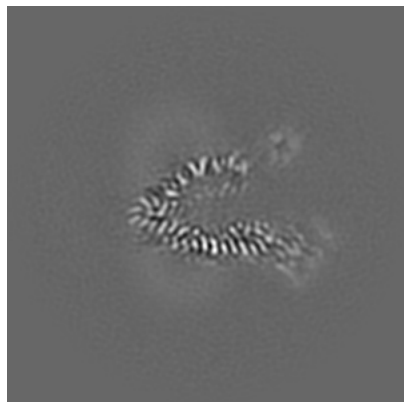
6.2.1 Primary map



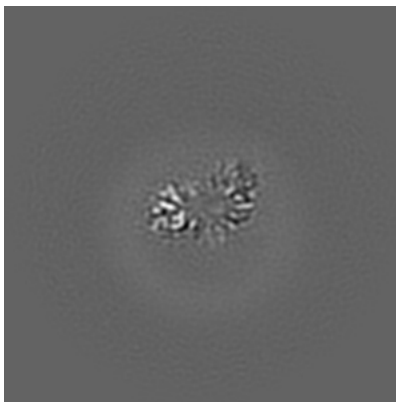
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

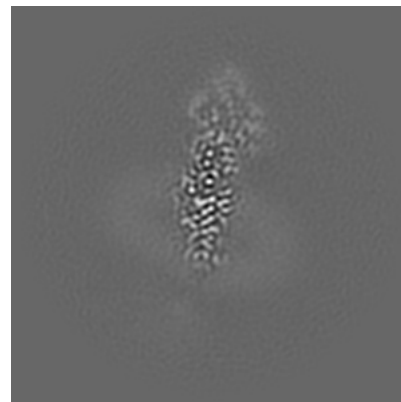
6.3.1 Primary map



X Index: 108



Y Index: 106

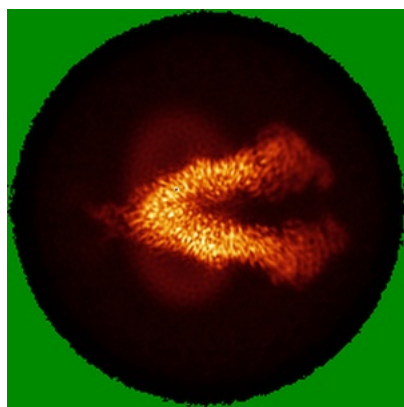


Z Index: 88

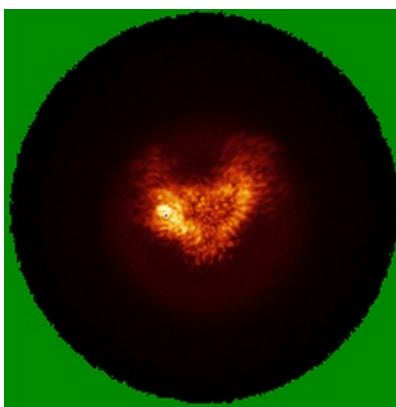
The images above show the largest variance slices of the map in three orthogonal directions.

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

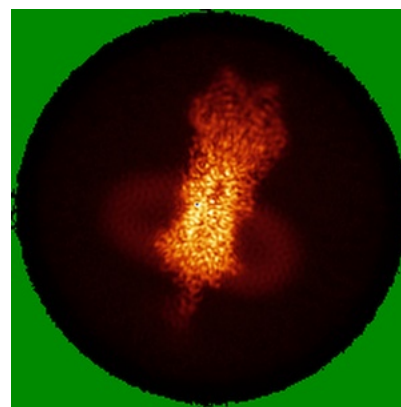
6.4.1 Primary map



X



Y

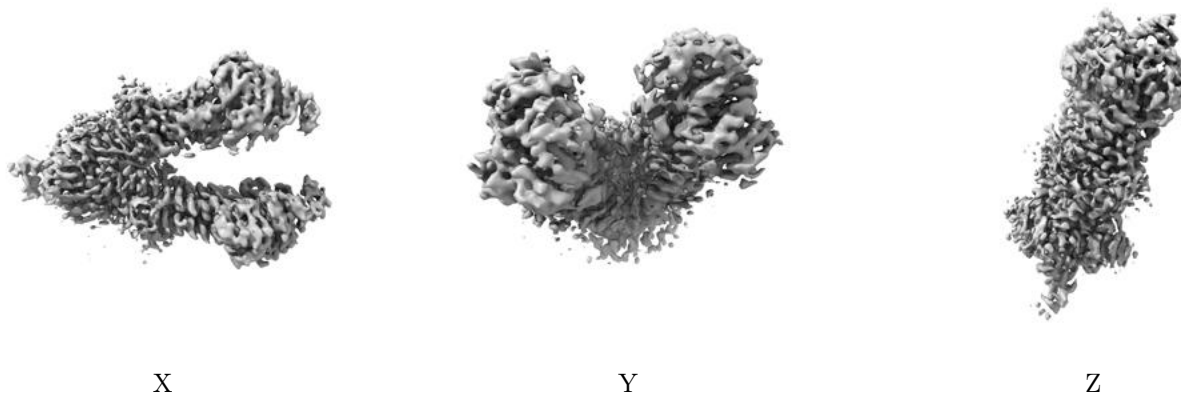


Z

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 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

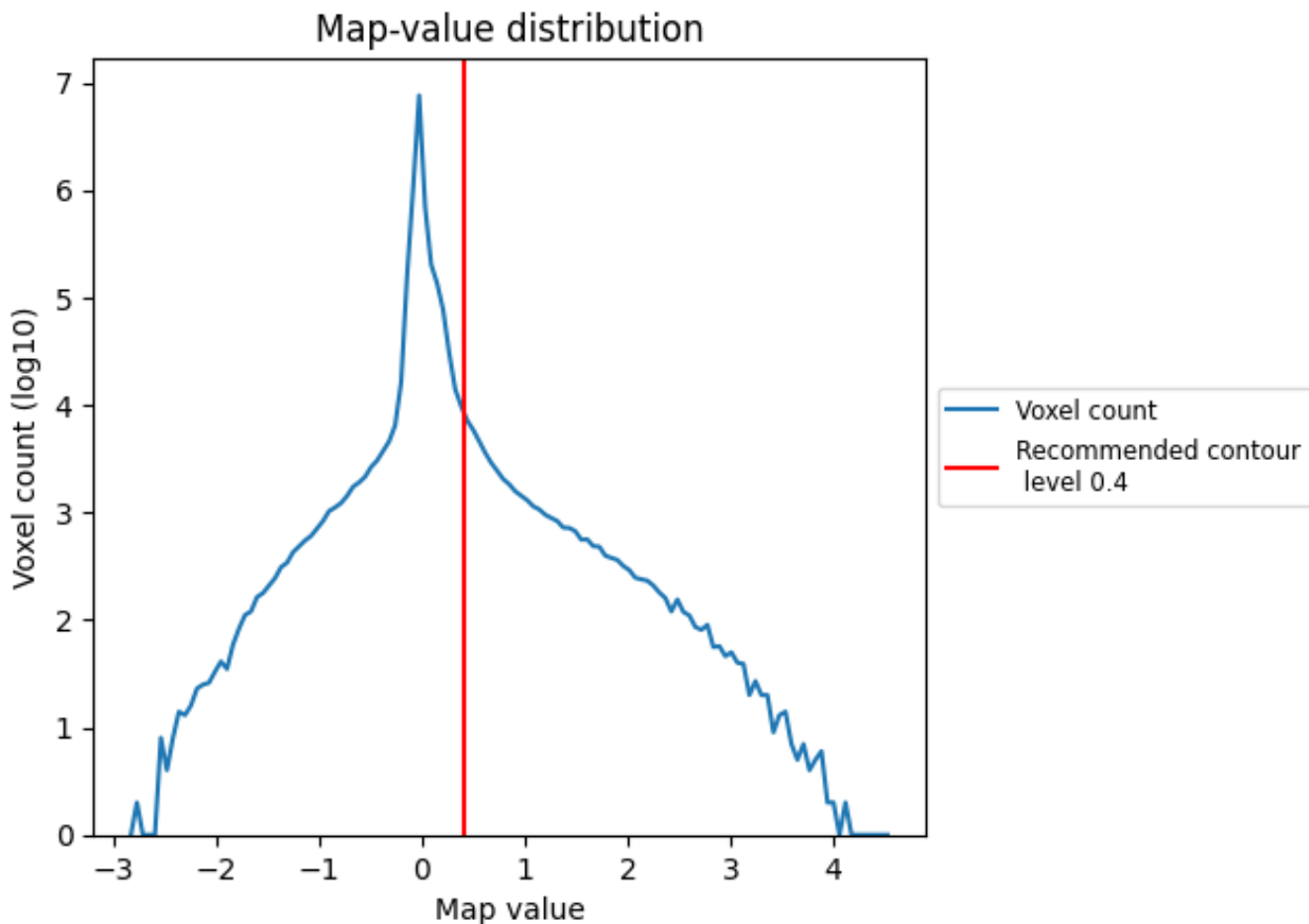
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

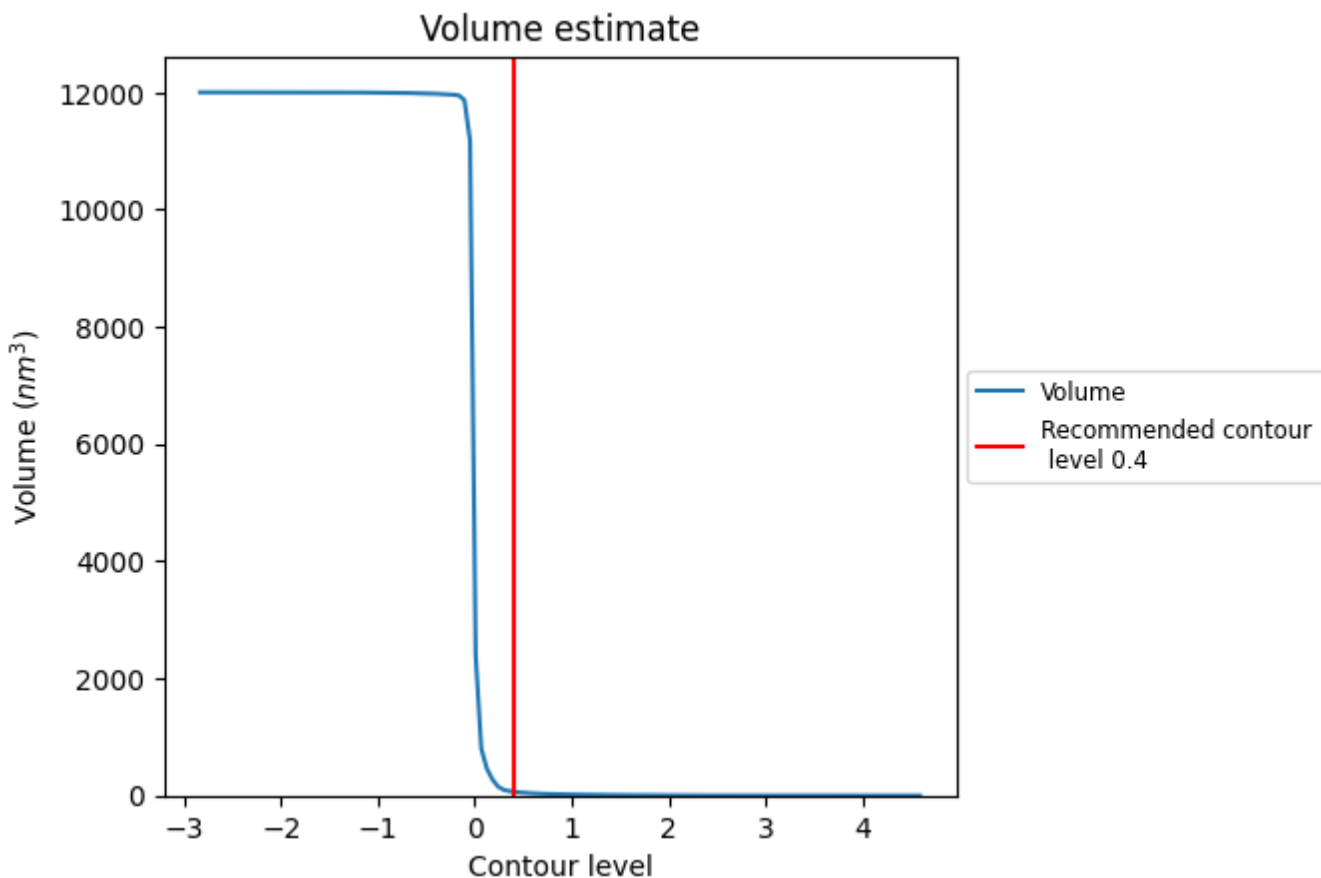
This section contains the results of statistical analysis of the map.

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.

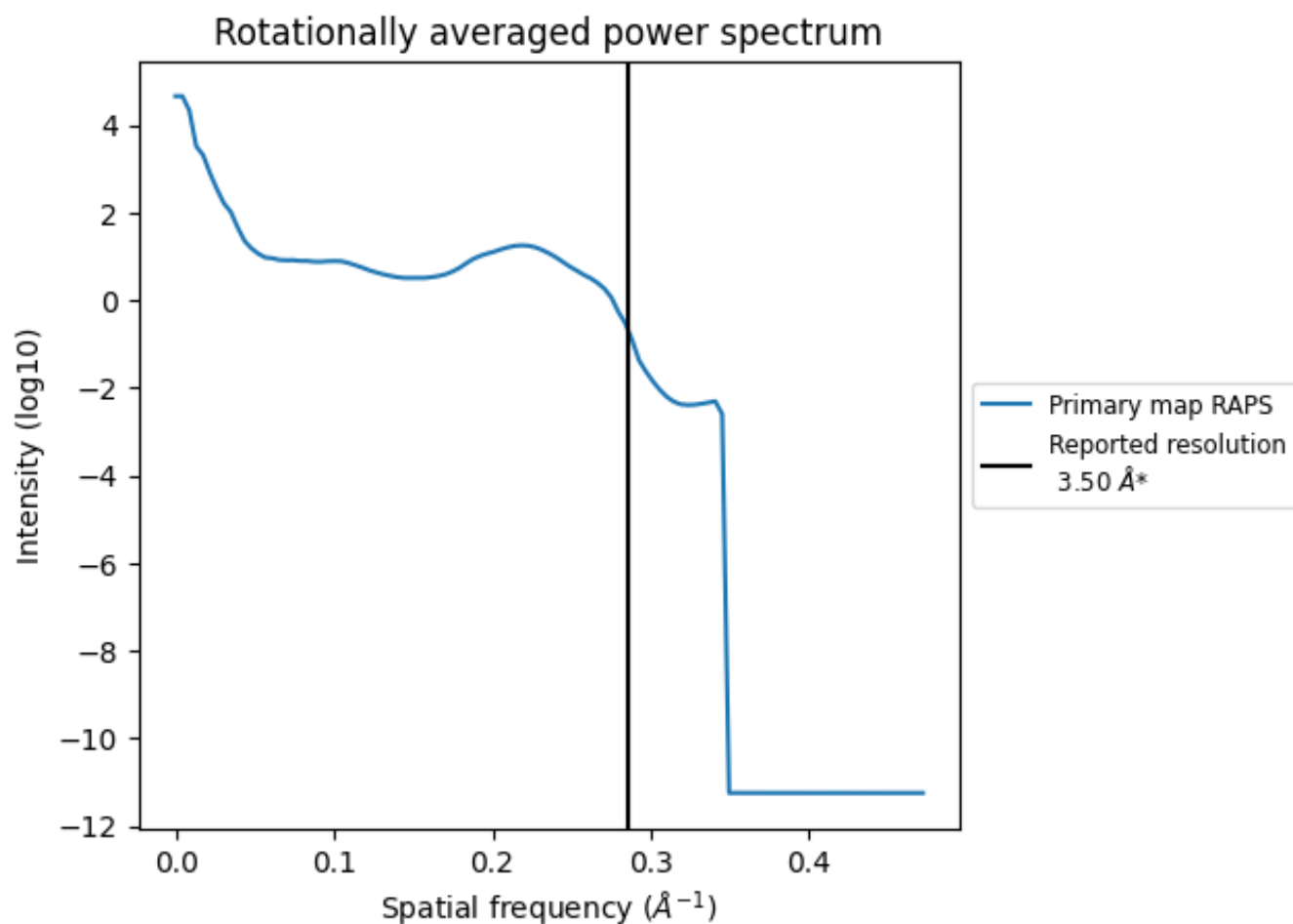
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 65 nm³; this corresponds to an approximate mass of 59 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 0.286 Å⁻¹

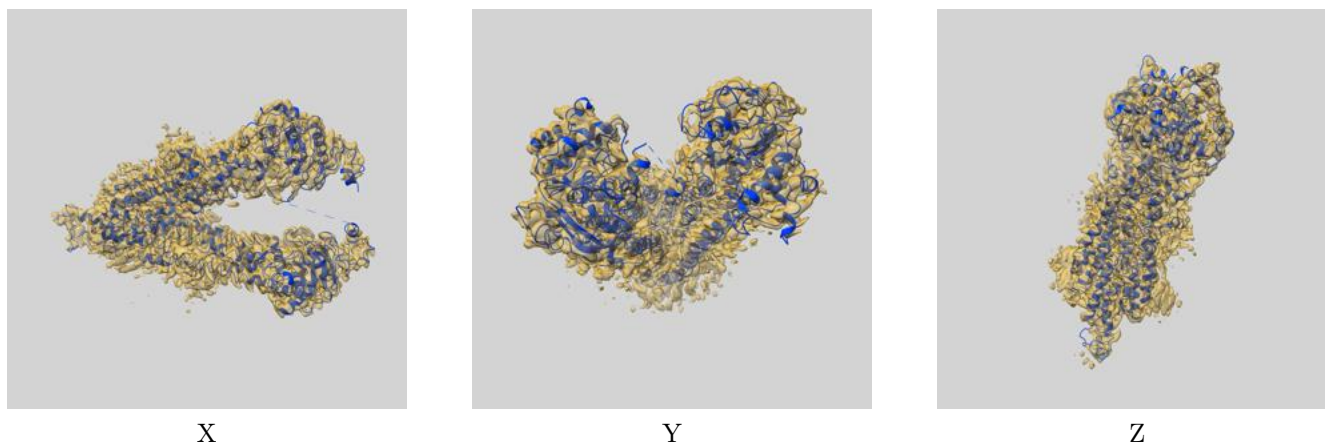
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31583 and PDB model 36CG. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



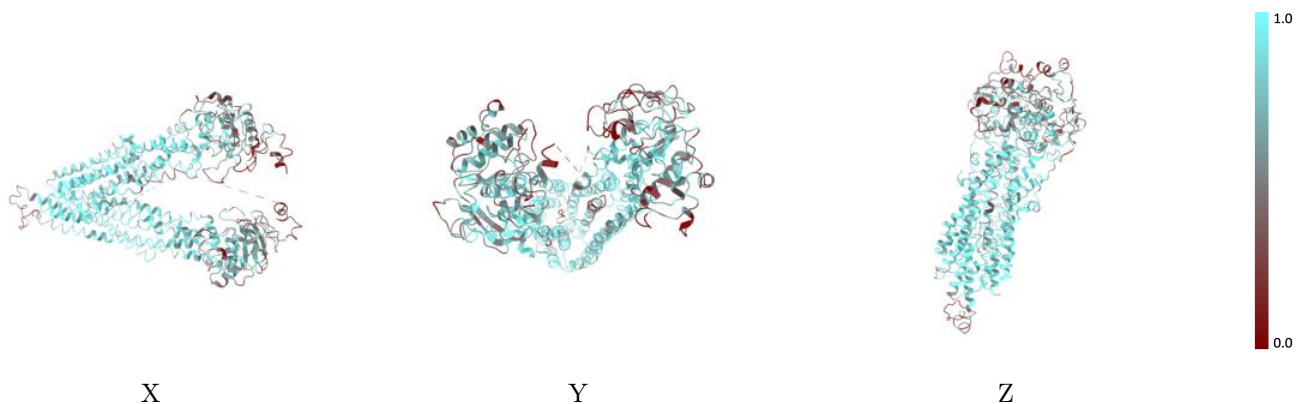
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



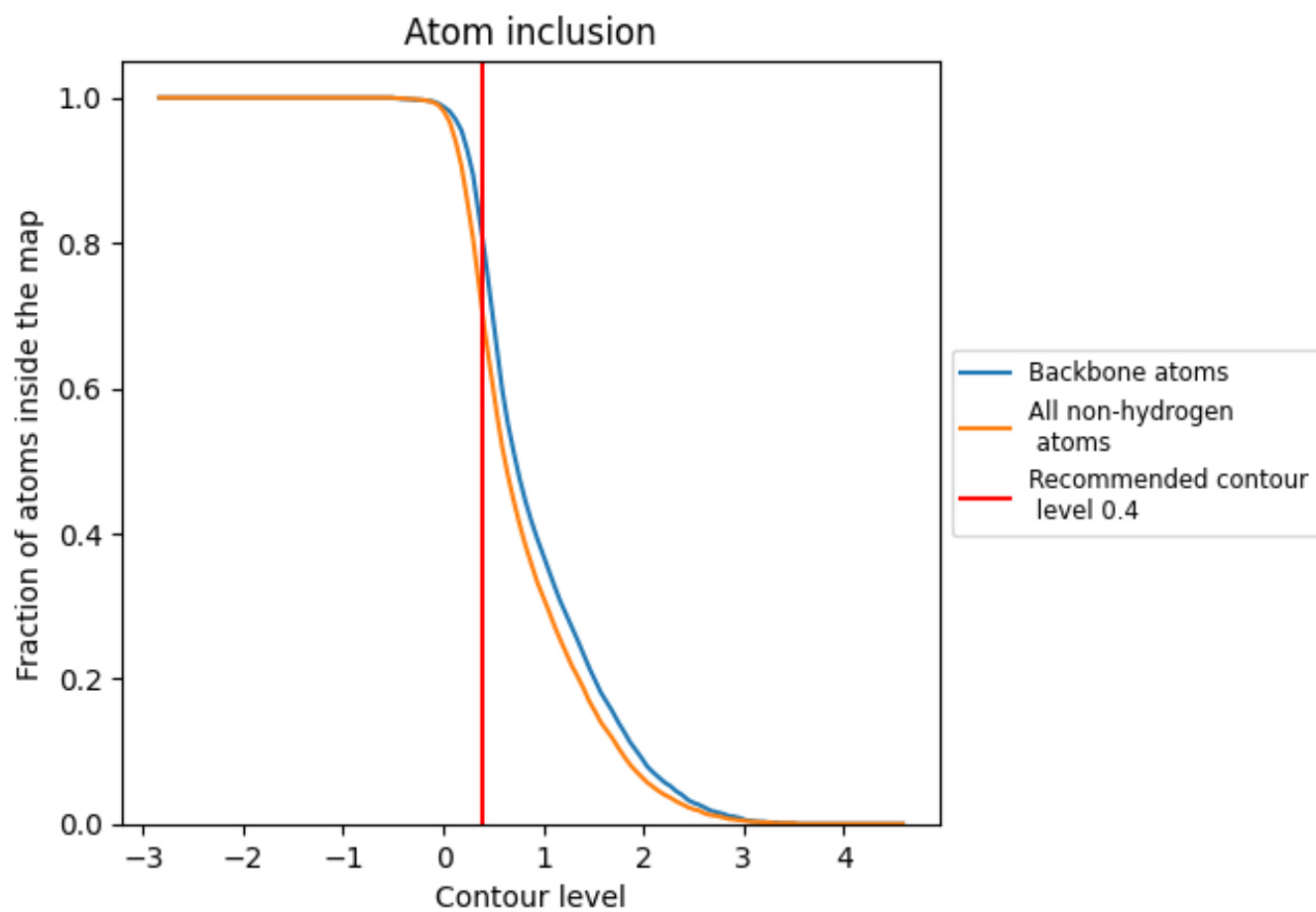
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).


9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 69% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6940	 0.4190
U	 0.6940	 0.4190

