



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 02:57 AM UTC

PDB ID : 9LGD / pdb_00009lgd
EMDB ID : EMD-63062
Title : wild-type bovine ABCC1 under an active turnover conformation with unhydrolyzed ATP bound and hydrolyzed ADP released
Authors : Sun, P.P.; Liu, K.X.; Gao, P.
Deposited on : 2025-01-10
Resolution : 3.29 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
Mogul : 2022.3.0, CSD as543be (2022)
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) : 2.49

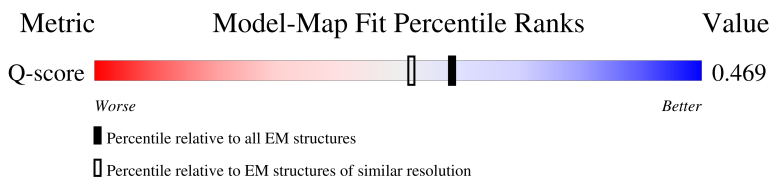
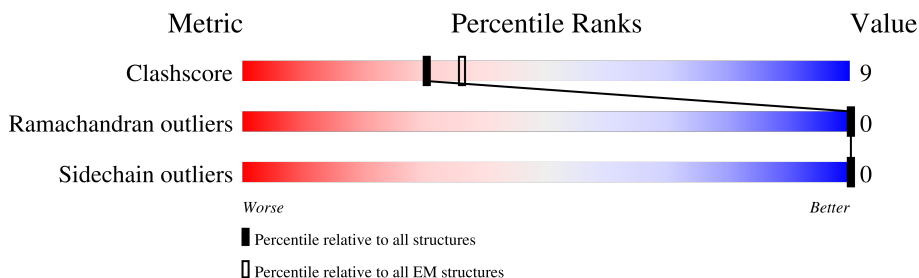
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.29 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	14466 (2.79 - 3.79)

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	1558	 68% 20% 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10856 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.

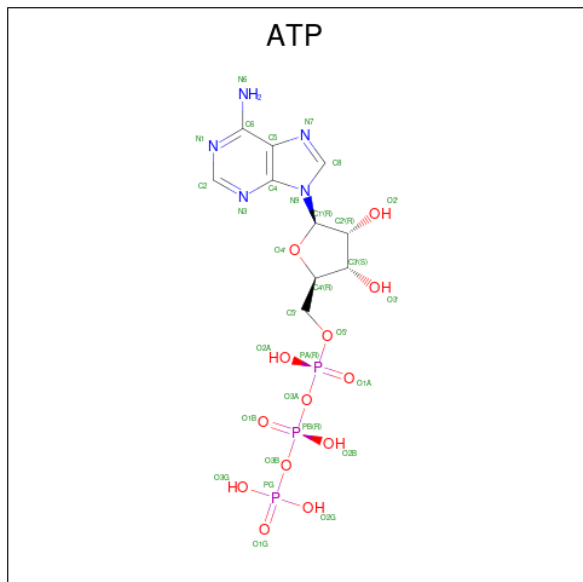
- Molecule 1 is a protein called Multidrug resistance-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1362	Total	C	N	O	S	0	0
			10824	7039	1800	1928	57		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1531	LYS	-	expression tag	UNP Q8HXQ5
A	1532	LEU	-	expression tag	UNP Q8HXQ5
A	1533	GLY	-	expression tag	UNP Q8HXQ5
A	1534	SER	-	expression tag	UNP Q8HXQ5
A	1535	GLU	-	expression tag	UNP Q8HXQ5
A	1536	ASN	-	expression tag	UNP Q8HXQ5
A	1537	LEU	-	expression tag	UNP Q8HXQ5
A	1538	TYR	-	expression tag	UNP Q8HXQ5
A	1539	PHE	-	expression tag	UNP Q8HXQ5
A	1540	GLN	-	expression tag	UNP Q8HXQ5
A	1541	GLY	-	expression tag	UNP Q8HXQ5
A	1542	GLY	-	expression tag	UNP Q8HXQ5
A	1543	SER	-	expression tag	UNP Q8HXQ5
A	1544	GLY	-	expression tag	UNP Q8HXQ5
A	1545	GLY	-	expression tag	UNP Q8HXQ5
A	1546	SER	-	expression tag	UNP Q8HXQ5
A	1547	GLY	-	expression tag	UNP Q8HXQ5
A	1548	HIS	-	expression tag	UNP Q8HXQ5
A	1549	HIS	-	expression tag	UNP Q8HXQ5
A	1550	HIS	-	expression tag	UNP Q8HXQ5
A	1551	HIS	-	expression tag	UNP Q8HXQ5
A	1552	HIS	-	expression tag	UNP Q8HXQ5
A	1553	HIS	-	expression tag	UNP Q8HXQ5
A	1554	HIS	-	expression tag	UNP Q8HXQ5
A	1555	HIS	-	expression tag	UNP Q8HXQ5
A	1556	HIS	-	expression tag	UNP Q8HXQ5
A	1557	HIS	-	expression tag	UNP Q8HXQ5
A	1558	HIS	-	expression tag	UNP Q8HXQ5

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

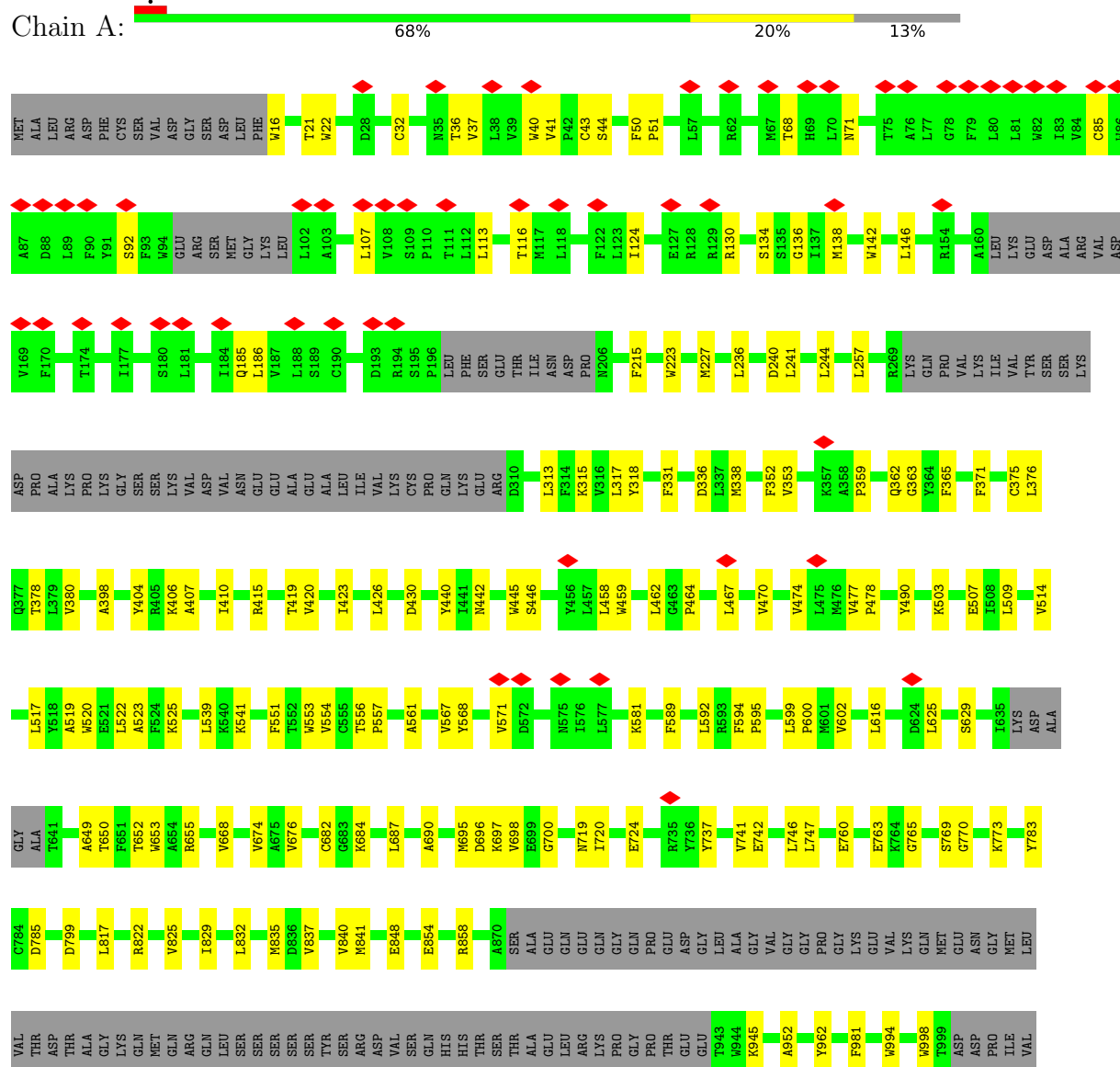
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Mg	0
			1	1	

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: Multidrug resistance-associated protein 1



C1478	G1348	G1230	L1121	P1120	ASN
A1484	I1351	L1231	I1124	Q1008	GLY
H1485	N1356	S1232	V1128	E1009	
R1486	I1357	S1233			
L1487	A1358	S1234	Q1138	Q1012	
N1488	K1359	Y1235	L1139	V1013	
T1489	I1360	Q1238	K1140	R1014	
I1490	L1365	V1239	R1141	V1017	
R1495	R1366	Y1242	L1142	V1018	
V1496	F1367	M1249	S1148	G1019	
I1497	K1368	M1253	P1149	A1020	
K1501	I1369	E1254	F1154	L1021	
G1502	T1370	T1255	L1158	G1022	
E1503	I1371	M1256	E1169	I1023	
I1504		I1257			
P1510	P1376	V1258		I1027	
S1511	V1377			T1028	
D1512	S1380	L1263	R1172	V1029	
L1529	R1384	K1264	L1179	Y1032	
V1530	D1388	E1265	K1180	V1036	
LYS	P1389	K1271	V1181	S1044	
LEU	F1390		E1183	L1051	
GLY	Y1393	D1279	N1184	P1059	
SER	L1402	P1282	Q1185	P1067	
GLU	V1411	P1283	K1186		
ASN	E1424	K1284	A1187		
LEU	R1434	D1285		L1071	
TYR	V1437	W1286	P1190	R1074	
PHE			S1191	L1079	
GLN	SER	E1293	I1192	D1083	
GLY	GLY	F1294	V1193	V1089	
GLY	GLY	R1295	A1194	I1090	
SER	GLY	D1296	N1195	K1091	
GLY	HIS	Y1297	L1202	M1094	
HIS	HIS	G1298	L1211	F1098	
HIS	HIS	R1441	S1214	N1099	
HIS	HIS	R1445	L1215	V1100	
HIS	HIS	K1446	F1216	A1103	
HIS	HIS	T1447	A1217	C1104	
HIS	HIS	D1460	V1218	I1105	
HIS	HIS	L1461	I1219	I1106	
HIS	HIS	E1462	S1220	I1107	
HIS	HIS	T1463	R1221		
HIS	HIS	D1464	H1222		
			S1223		
		I1467	LEU		
		Q1468	SER		
		F1475	ALA		
		D1476	GLY		
		D1477	LEU		
				P1119	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	127454	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	4.362	Depositor
Minimum map value	-2.520	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.071	Depositor
Recommended contour level	0.44	Depositor
Map size ($\text{\AA}$)	332.8, 332.8, 332.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	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: MG, ATP

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	0.41	0/11063	0.58	1/15015 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1009	GLU	N-CA-C	-5.29	105.56	112.23

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	10824	0	11048	197	0
2	A	31	0	12	0	0
3	A	1	0	0	0	0
All	All	10856	0	11060	197	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 (197) 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:1496:VAL:HG21	1:A:1510:PRO:HB3	1.68	0.74
1:A:1464:ASP:O	1:A:1468:GLN:HG2	1.97	0.65
1:A:1497:ILE:HD11	1:A:1504:ILE:HD11	1.79	0.64
1:A:1214:SER:HA	1:A:1233:VAL:HG22	1.80	0.63
1:A:462:LEU:HD12	1:A:581:LYS:HE2	1.79	0.62
1:A:998:TRP:HB3	1:A:1014:ARG:NH2	2.15	0.62
1:A:687:LEU:HD22	1:A:841:MET:HE1	1.82	0.61
1:A:1029:VAL:HA	1:A:1032:TYR:CE1	2.35	0.61
1:A:1051:LEU:HD22	1:A:1263:LEU:HD22	1.83	0.61
1:A:136:GLY:HA2	1:A:215:PHE:CE1	2.36	0.60
1:A:1036:VAL:HG11	1:A:1091:LYS:HB2	1.83	0.60
1:A:1357:ILE:HD12	1:A:1365:LEU:HD13	1.83	0.60
1:A:1074:ARG:NH2	1:A:1265:GLU:OE1	2.35	0.59
1:A:994:TRP:C	1:A:994:TRP:CD1	2.79	0.59
1:A:134:SER:OG	1:A:215:PHE:HB2	2.02	0.59
1:A:1217:ALA:O	1:A:1221:ARG:HB3	2.03	0.59
1:A:503:LYS:O	1:A:507:GLU:HG2	2.02	0.59
1:A:1238:GLN:HG2	1:A:1242:TYR:CE1	2.38	0.58
1:A:138:MET:HE3	1:A:142:TRP:NE1	2.19	0.58
1:A:676:VAL:HG12	1:A:684:LYS:HG2	1.86	0.58
1:A:682:CYS:SG	1:A:684:LYS:HG3	2.43	0.58
1:A:1297:TYR:HA	1:A:1348:GLY:HA3	1.84	0.58
1:A:994:TRP:HE1	1:A:1014:ARG:HE	1.54	0.56
1:A:244:LEU:HB2	1:A:1186:LYS:HG3	1.88	0.56
1:A:650:THR:HG23	1:A:698:VAL:HB	1.88	0.56
1:A:1295:ARG:HH12	1:A:1351:ILE:HD12	1.70	0.55
1:A:1464:ASP:OD1	1:A:1486:ARG:NH1	2.36	0.55
1:A:1215:LEU:O	1:A:1219:ILE:HG22	2.06	0.55
1:A:1192:ILE:HA	1:A:1195:ASN:HD22	1.71	0.54
1:A:352:PHE:HE2	1:A:1218:VAL:HG13	1.69	0.54
1:A:1249:MET:HE3	1:A:1249:MET:HA	1.89	0.54
1:A:1286:TRP:HE3	1:A:1368:LYS:HD3	1.73	0.54
1:A:16:TRP:CZ3	1:A:21:THR:HG21	2.43	0.54
1:A:567:VAL:O	1:A:571:VAL:N	2.39	0.54
1:A:962:TYR:CE1	1:A:1257:ILE:HG13	2.43	0.54
1:A:994:TRP:CZ2	1:A:1017:VAL:HG11	2.43	0.53
1:A:1181:VAL:O	1:A:1185:GLN:HG2	2.09	0.53
1:A:142:TRP:CZ2	1:A:185:GLN:HG2	2.43	0.53
1:A:1232:SER:HA	1:A:1235:TYR:HB2	1.91	0.52
1:A:553:TRP:HD1	1:A:600:PRO:HG3	1.75	0.52
1:A:520:TRP:HH2	1:A:1441:ARG:HD3	1.74	0.52
1:A:1463:THR:O	1:A:1467:ILE:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:PHE:O	1:A:353:VAL:C	2.51	0.52
1:A:832:LEU:HA	1:A:835:MET:HG2	1.92	0.51
1:A:331:PHE:HD1	1:A:380:VAL:HG23	1.76	0.51
1:A:43:CYS:SG	1:A:116:THR:HG21	2.51	0.51
1:A:1402:LEU:HD13	1:A:1411:VAL:HG21	1.93	0.50
1:A:1169:GLU:O	1:A:1169:GLU:HG3	2.11	0.50
1:A:561:ALA:HB2	1:A:589:PHE:HD1	1.77	0.50
1:A:514:VAL:HG11	1:A:1377:VAL:HG21	1.93	0.50
1:A:138:MET:HE3	1:A:142:TRP:HE1	1.75	0.50
1:A:1029:VAL:HA	1:A:1032:TYR:CD1	2.46	0.50
1:A:440:TYR:HB3	1:A:602:VAL:HG22	1.94	0.49
1:A:467:LEU:O	1:A:470:VAL:HB	2.11	0.49
1:A:1351:ILE:HG12	1:A:1356:ASN:HA	1.94	0.49
1:A:1384:ARG:NH2	1:A:1393:TYR:O	2.46	0.49
1:A:1169:GLU:OE1	1:A:1172:ARG:HD3	2.13	0.49
1:A:652:THR:HG23	1:A:696:ASP:HB3	1.95	0.49
1:A:799:ASP:OD1	1:A:799:ASP:N	2.42	0.49
1:A:829:ILE:HB	1:A:832:LEU:HG	1.95	0.49
1:A:1304:ASP:N	1:A:1304:ASP:OD1	2.42	0.48
1:A:817:LEU:HB3	1:A:822:ARG:HD3	1.95	0.48
1:A:1282:PRO:HG3	1:A:1360:ILE:HD11	1.96	0.48
1:A:1179:LEU:O	1:A:1183:GLU:HG2	2.12	0.48
1:A:458:LEU:HG	1:A:589:PHE:HE2	1.77	0.48
1:A:426:LEU:O	1:A:430:ASP:HB2	2.13	0.48
1:A:352:PHE:CE2	1:A:363:GLY:HA3	2.49	0.48
1:A:442:ASN:OD1	1:A:445:TRP:NE1	2.45	0.48
1:A:1090:ILE:O	1:A:1094:MET:HG2	2.14	0.48
1:A:1376:PRO:HB2	1:A:1434:ARG:HB3	1.94	0.47
1:A:50:PHE:HB3	1:A:51:PRO:HD3	1.96	0.47
1:A:407:ALA:HB1	1:A:1158:LEU:HD21	1.96	0.47
1:A:676:VAL:HB	1:A:825:VAL:HG22	1.96	0.47
1:A:1139:LEU:HD11	1:A:1190:PRO:HB2	1.97	0.47
1:A:1293:GLU:HG2	1:A:1315:THR:HA	1.97	0.47
1:A:241:LEU:HD13	1:A:1187:ALA:HA	1.97	0.47
1:A:1370:THR:OG1	1:A:1447:THR:HB	2.15	0.47
1:A:124:ILE:CG2	1:A:138:MET:HE2	2.45	0.47
1:A:1100:VAL:HG23	1:A:1242:TYR:HB3	1.97	0.47
1:A:1148:SER:HB2	1:A:1149:PRO:HD3	1.96	0.47
1:A:415:ARG:HH21	1:A:420:VAL:HB	1.80	0.46
1:A:40:TRP:O	1:A:44:SER:CB	2.64	0.46
1:A:551:PHE:CE1	1:A:1027:ILE:HD12	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1477:ASP:OD1	1:A:1477:ASP:N	2.47	0.46
1:A:509:LEU:HD22	1:A:1071:LEU:HD13	1.97	0.46
1:A:1089:VAL:HG21	1:A:1256:ASN:ND2	2.31	0.46
1:A:1138:GLN:O	1:A:1142:LEU:HG	2.16	0.46
1:A:146:LEU:HD22	1:A:186:LEU:HD22	1.98	0.46
1:A:85:CYS:SG	1:A:113:LEU:HD22	2.56	0.45
1:A:649:ALA:HA	1:A:700:GLY:HA3	1.98	0.45
1:A:1079:LEU:HD23	1:A:1079:LEU:HA	1.82	0.45
1:A:1496:VAL:O	1:A:1496:VAL:HG12	2.17	0.45
1:A:317:LEU:HD23	1:A:317:LEU:HA	1.72	0.45
1:A:470:VAL:O	1:A:474:VAL:HG23	2.17	0.45
1:A:1100:VAL:CG2	1:A:1242:TYR:HB3	2.46	0.45
1:A:223:TRP:CH2	1:A:1193:VAL:HG11	2.51	0.45
1:A:1326:GLY:N	1:A:1332:LYS:HD3	2.32	0.45
1:A:1488:ASN:N	1:A:1529:LEU:HD11	2.31	0.45
1:A:227:MET:HG3	1:A:236:LEU:HD21	1.98	0.45
1:A:359:PRO:HD2	1:A:362:GLN:NE2	2.31	0.45
1:A:655:ARG:NH1	1:A:696:ASP:OD2	2.50	0.44
1:A:315:LYS:HA	1:A:318:TYR:CE1	2.52	0.44
1:A:514:VAL:HG11	1:A:1377:VAL:CG2	2.47	0.44
1:A:490:TYR:CE1	1:A:541:LYS:HE3	2.52	0.44
1:A:769:SER:O	1:A:773:LYS:HG3	2.18	0.44
1:A:1437:VAL:O	1:A:1441:ARG:HG3	2.18	0.44
1:A:1441:ARG:O	1:A:1445:ARG:HG3	2.17	0.44
1:A:840:VAL:HB	1:A:848:GLU:HB2	2.00	0.44
1:A:1255:THR:O	1:A:1258:VAL:HB	2.17	0.44
1:A:43:CYS:CB	1:A:116:THR:HG21	2.48	0.44
1:A:423:ILE:HA	1:A:426:LEU:HD12	2.00	0.44
1:A:854:GLU:O	1:A:858:ARG:NH1	2.51	0.44
1:A:1107:ILE:HD12	1:A:1239:VAL:HG21	1.99	0.44
1:A:522:LEU:HA	1:A:525:LYS:HB3	2.00	0.44
1:A:1044:SER:OG	1:A:1083:ASP:OD1	2.32	0.44
1:A:477:VAL:HB	1:A:478:PRO:HD3	2.00	0.44
1:A:556:THR:N	1:A:557:PRO:HD2	2.33	0.44
1:A:371:PHE:HB2	1:A:1211:LEU:HD13	2.00	0.43
1:A:674:VAL:HG22	1:A:837:VAL:HB	2.00	0.43
1:A:952:ALA:HB1	1:A:1141:ARG:HB3	2.00	0.43
1:A:539:LEU:HD12	1:A:539:LEU:HA	1.85	0.43
1:A:1120:PRO:O	1:A:1124:ILE:HG22	2.18	0.43
1:A:785:ASP:N	1:A:785:ASP:OD1	2.50	0.43
1:A:1299:LEU:O	1:A:1308:VAL:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1357:ILE:HD13	1:A:1357:ILE:HA	1.84	0.43
1:A:517:LEU:HD13	1:A:1371:ILE:HD13	2.00	0.43
1:A:68:THR:CG2	1:A:71:ASN:H	2.31	0.43
1:A:981:PHE:HB3	1:A:1098:PHE:CD2	2.52	0.43
1:A:1238:GLN:HG2	1:A:1242:TYR:HE1	1.83	0.43
1:A:1320:GLU:OE2	1:A:1495:ARG:NE	2.52	0.43
1:A:1488:ASN:N	1:A:1488:ASN:OD1	2.52	0.43
1:A:1359:LYS:HA	1:A:1359:LYS:HD3	1.91	0.43
1:A:22:TRP:HH2	1:A:365:PHE:CE2	2.37	0.43
1:A:37:VAL:O	1:A:41:VAL:HG23	2.18	0.43
1:A:592:LEU:O	1:A:595:PRO:HD2	2.19	0.43
1:A:690:ALA:HB2	1:A:695:MET:HE2	2.01	0.43
1:A:404:TYR:HB2	1:A:1154:PHE:CZ	2.54	0.42
1:A:1310:LYS:HB2	1:A:1503:GLU:HG3	2.00	0.42
1:A:1475:PHE:HB3	1:A:1478:CYS:SG	2.59	0.42
1:A:769:SER:OG	1:A:770:GLY:N	2.52	0.42
1:A:1253:MET:HE2	1:A:1253:MET:HB3	1.89	0.42
1:A:426:LEU:HD23	1:A:430:ASP:OD2	2.19	0.42
1:A:1105:ILE:HD13	1:A:1105:ILE:HA	1.91	0.42
1:A:257:LEU:HD22	1:A:398:ALA:HB1	2.02	0.42
1:A:419:THR:HA	1:A:1424:GLU:OE2	2.19	0.42
1:A:765:GLY:O	1:A:773:LYS:HE2	2.19	0.42
1:A:1083:ASP:OD1	1:A:1083:ASP:N	2.53	0.42
1:A:1128:VAL:HG11	1:A:1202:LEU:HD21	2.02	0.42
1:A:375:CYS:O	1:A:378:THR:HG22	2.19	0.42
1:A:553:TRP:CZ2	1:A:599:LEU:HD23	2.54	0.42
1:A:994:TRP:CH2	1:A:1017:VAL:HG11	2.54	0.42
1:A:40:TRP:O	1:A:44:SER:HB2	2.20	0.42
1:A:313:LEU:HD21	1:A:616:LEU:HD23	2.02	0.42
1:A:568:TYR:O	1:A:571:VAL:HG12	2.18	0.42
1:A:338:MET:HE3	1:A:376:LEU:HB2	2.02	0.42
1:A:459:TRP:HE1	1:A:464:PRO:HA	1.84	0.41
1:A:629:SER:HB2	1:A:697:LYS:HE3	2.01	0.41
1:A:719:ASN:HB2	1:A:763:GLU:HA	2.01	0.41
1:A:336:ASP:OD2	1:A:446:SER:OG	2.31	0.41
1:A:553:TRP:CE2	1:A:599:LEU:HD23	2.55	0.41
1:A:1476:ASP:OD1	1:A:1476:ASP:N	2.54	0.41
1:A:130:ARG:HH11	1:A:130:ARG:HG3	1.86	0.41
1:A:519:ALA:HB2	1:A:1366:ARG:CB	2.49	0.41
1:A:1300:ARG:HB2	1:A:1307:LEU:HD23	2.01	0.41
1:A:668:VAL:HG22	1:A:674:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:ILE:HB	1:A:1119:PRO:HD3	2.03	0.41
1:A:240:ASP:O	1:A:241:LEU:C	2.63	0.41
1:A:507:GLU:HG3	1:A:1380:SER:OG	2.19	0.41
1:A:520:TRP:CH2	1:A:1441:ARG:HD3	2.55	0.41
1:A:1019:GLY:O	1:A:1023:ILE:HG12	2.20	0.41
1:A:551:PHE:O	1:A:554:VAL:HG12	2.19	0.41
1:A:625:LEU:HD23	1:A:625:LEU:HA	1.89	0.41
1:A:406:LYS:O	1:A:410:ILE:N	2.54	0.41
1:A:737:TYR:HB2	1:A:783:TYR:HE2	1.85	0.41
1:A:92:SER:OG	1:A:107:LEU:HD13	2.21	0.41
1:A:653:TRP:CE3	1:A:695:MET:HG3	2.56	0.41
1:A:742:GLU:HA	1:A:747:LEU:HD23	2.02	0.41
1:A:1103:ALA:HA	1:A:1106:ILE:HG22	2.03	0.41
1:A:1229:VAL:C	1:A:1231:LEU:N	2.78	0.41
1:A:1484:ALA:HB3	1:A:1490:ILE:HD11	2.02	0.41
1:A:1501:LYS:HD2	1:A:1501:LYS:HA	1.96	0.41
1:A:1221:ARG:HG3	1:A:1222:HIS:N	2.36	0.41
1:A:1388:ASP:N	1:A:1388:ASP:OD1	2.54	0.41
1:A:720:ILE:HD12	1:A:724:GLU:HB2	2.02	0.40
1:A:746:LEU:HD23	1:A:746:LEU:HA	1.87	0.40
1:A:760:GLU:OE1	1:A:945:LYS:HD2	2.21	0.40
1:A:594:PHE:HB2	1:A:595:PRO:HD3	2.03	0.40
1:A:741:VAL:HG12	1:A:747:LEU:HD22	2.03	0.40
1:A:1460:ASP:OD1	1:A:1462:GLU:HG2	2.21	0.40
1:A:1059:PRO:HD3	1:A:1271:LYS:HA	2.04	0.40
1:A:32:CYS:O	1:A:36:THR:HG23	2.22	0.40
1:A:458:LEU:HG	1:A:589:PHE:CE2	2.56	0.40
1:A:523:ALA:HB2	1:A:1390:PHE:CZ	2.57	0.40
1:A:763:GLU:HG3	1:A:1067:PRO:HA	2.03	0.40
1:A:1021:LEU:HD23	1:A:1021:LEU:HA	1.96	0.40
1:A:1121:LEU:HD23	1:A:1121:LEU:HA	1.89	0.40
1:A:1306:ASP:OD1	1:A:1306:ASP:N	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1344/1558 (86%)	1290 (96%)	54 (4%)	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	1194/1358 (88%)	1194 (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 (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	HIS
1	A	60	HIS
1	A	66	GLN
1	A	230	GLN
1	A	260	ASN
1	A	386	HIS
1	A	533	GLN
1	A	575	ASN
1	A	642	ASN
1	A	1155	ASN
1	A	1176	GLN
1	A	1222	HIS
1	A	1244	ASN
1	A	1363	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	ATP	A	1601	3	32,33,33	0.55	0	48,52,52	0.55	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	ATP	A	1601	3	-	0/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

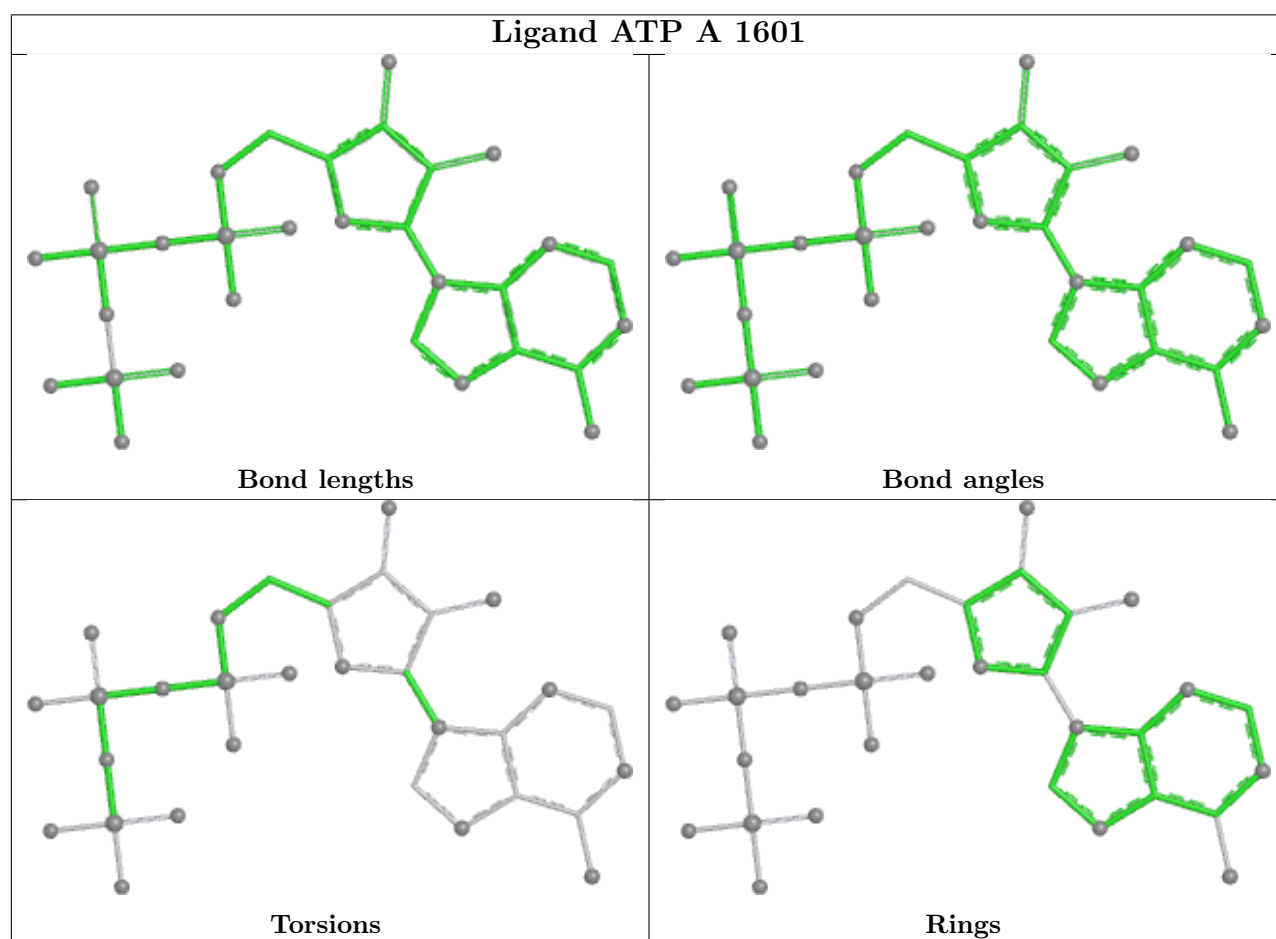
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

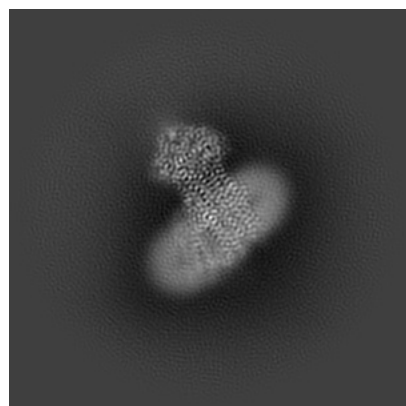
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63062. These allow visual inspection of the internal detail of the map and identification of artifacts.

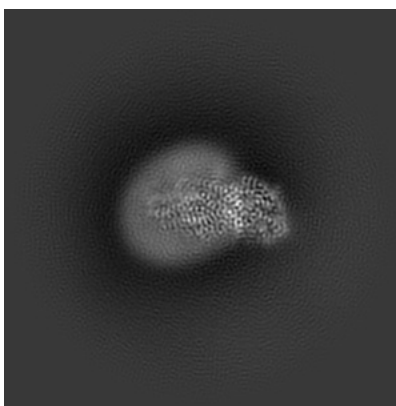
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

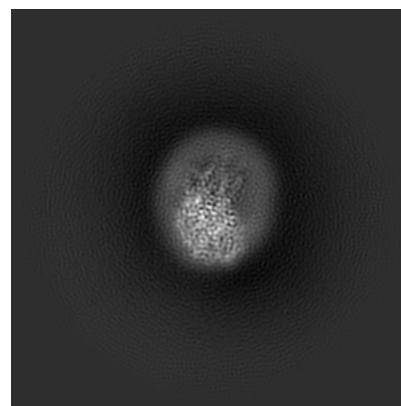
6.1.1 Primary map



X

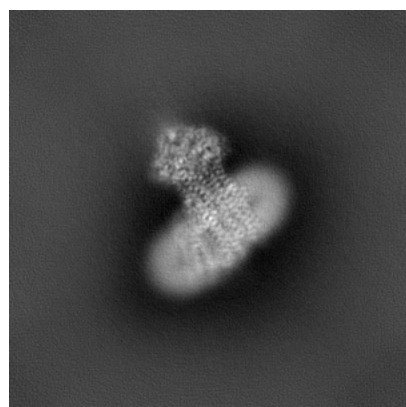


Y

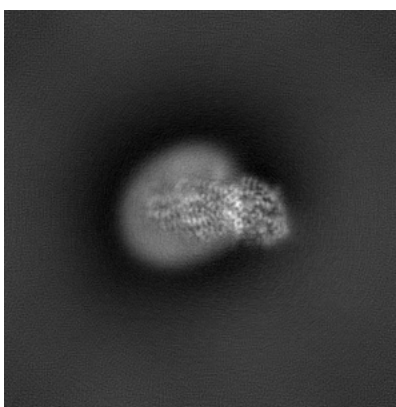


Z

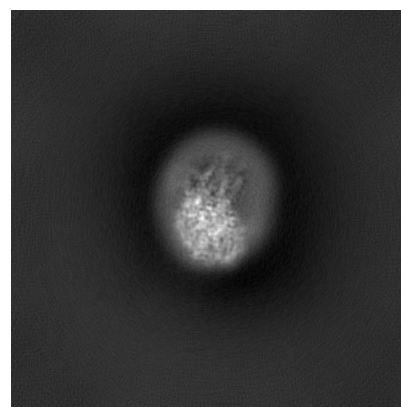
6.1.2 Raw map



X



Y

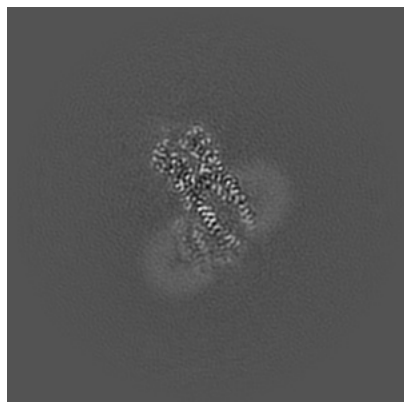


Z

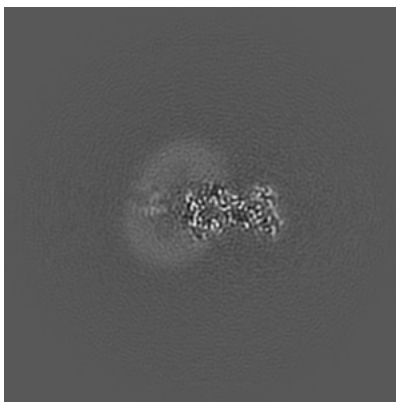
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

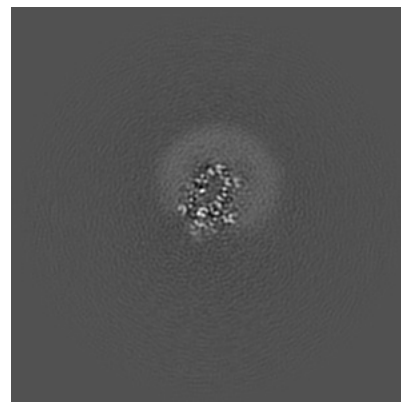
6.2.1 Primary map



X Index: 160

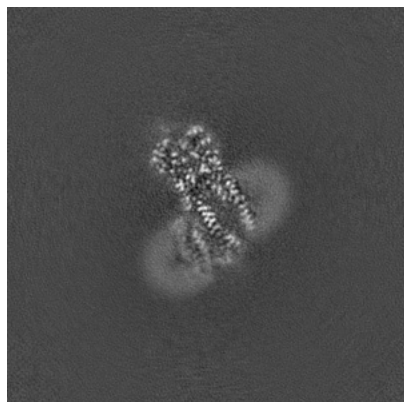


Y Index: 160

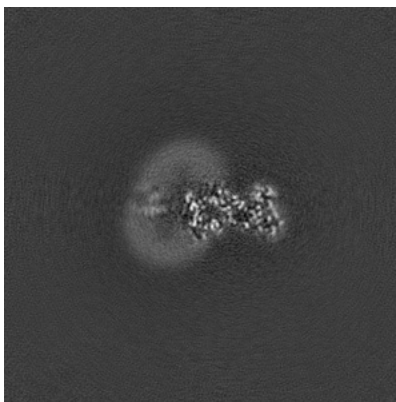


Z Index: 160

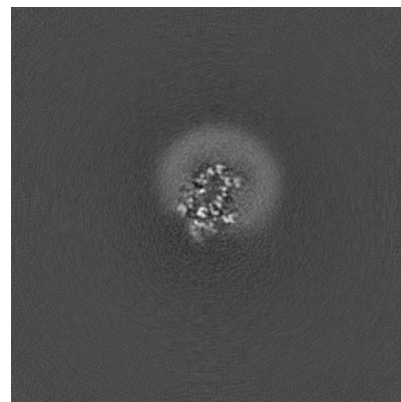
6.2.2 Raw map



X Index: 160



Y Index: 160

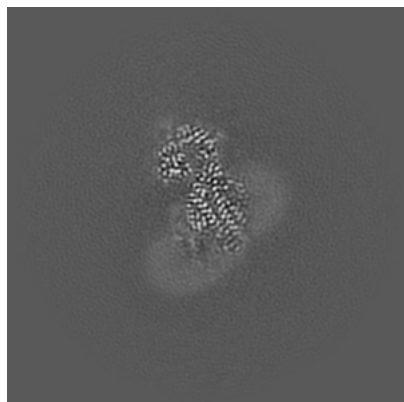


Z Index: 160

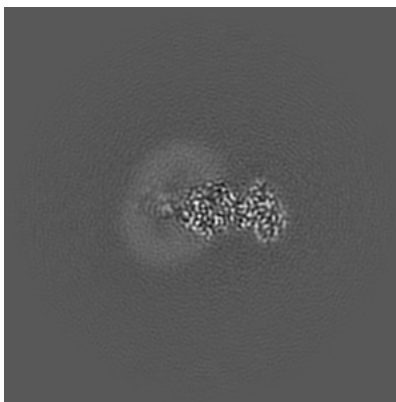
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

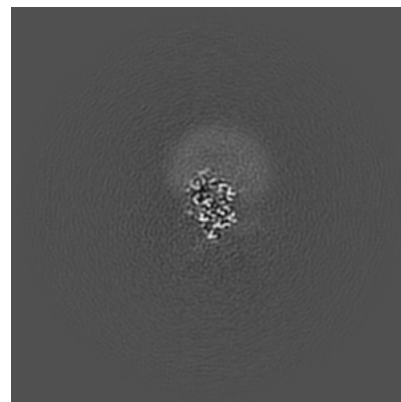
6.3.1 Primary map



X Index: 151

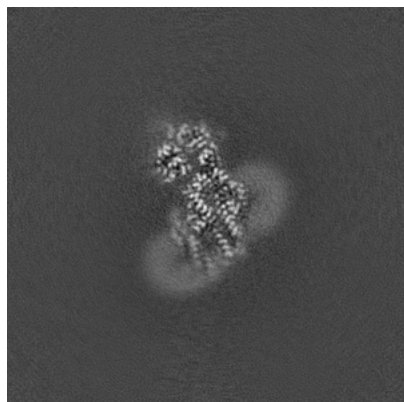


Y Index: 156

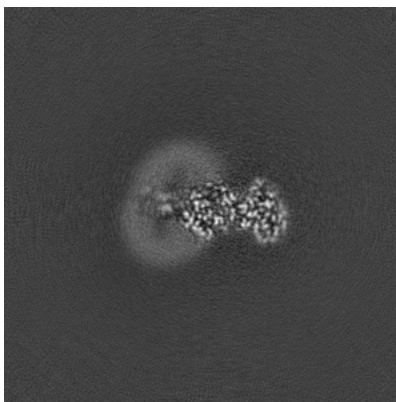


Z Index: 177

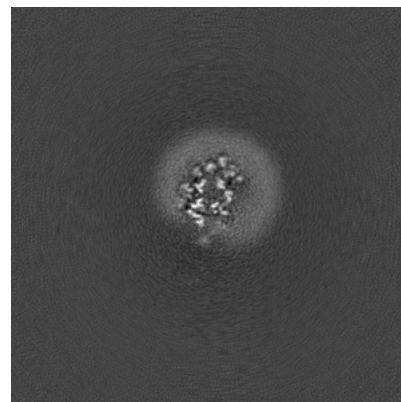
6.3.2 Raw map



X Index: 153



Y Index: 156

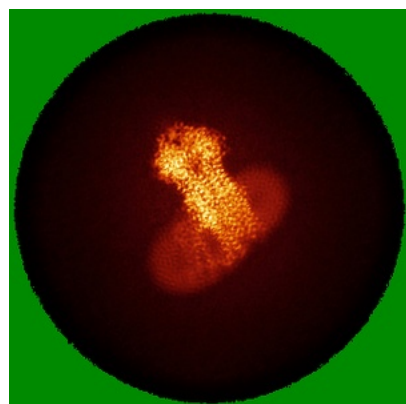


Z Index: 152

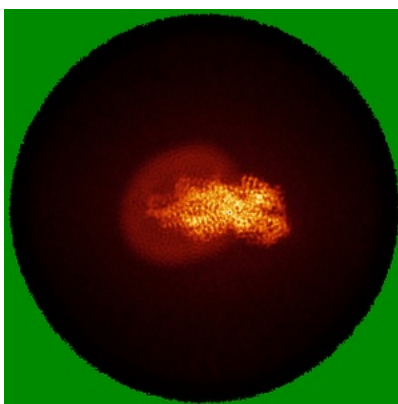
The images above show the largest variance slices of the map in three orthogonal directions.

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

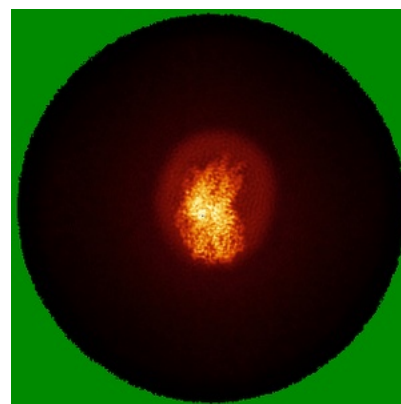
6.4.1 Primary map



X

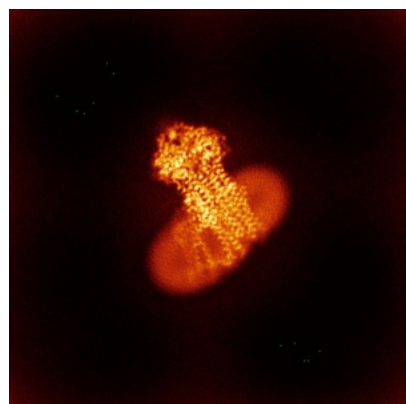


Y

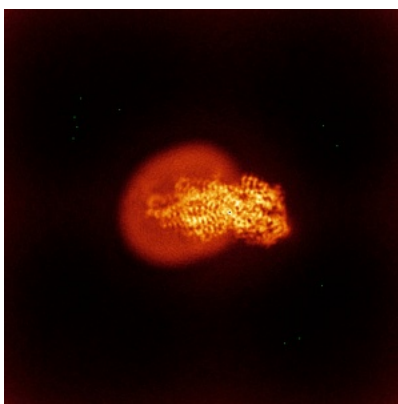


Z

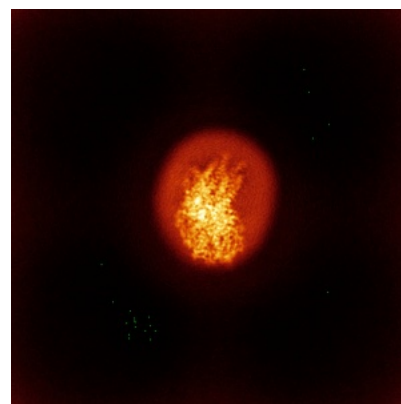
6.4.2 Raw map



X



Y

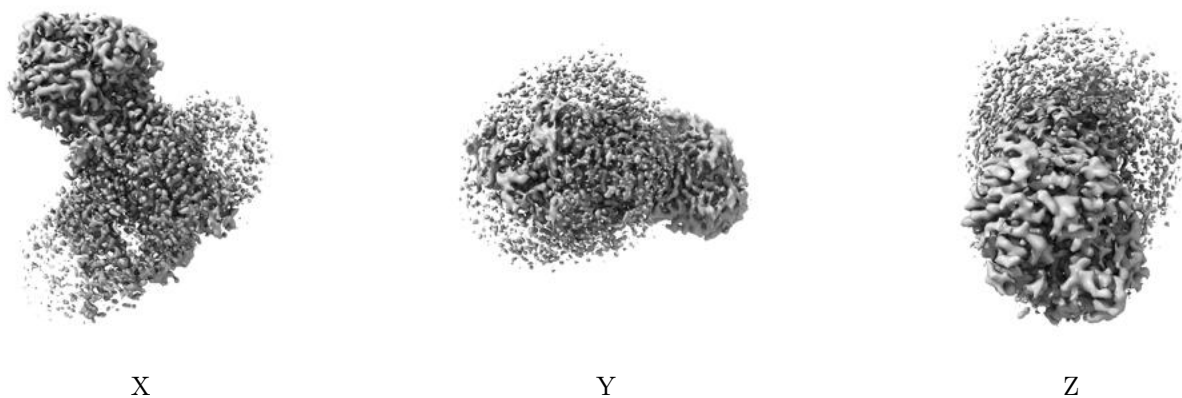


Z

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.

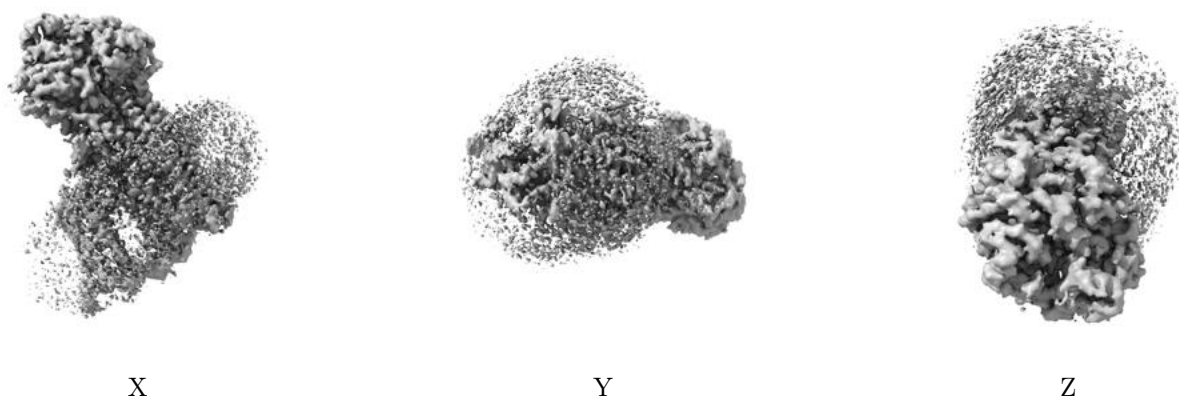
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.44. 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.

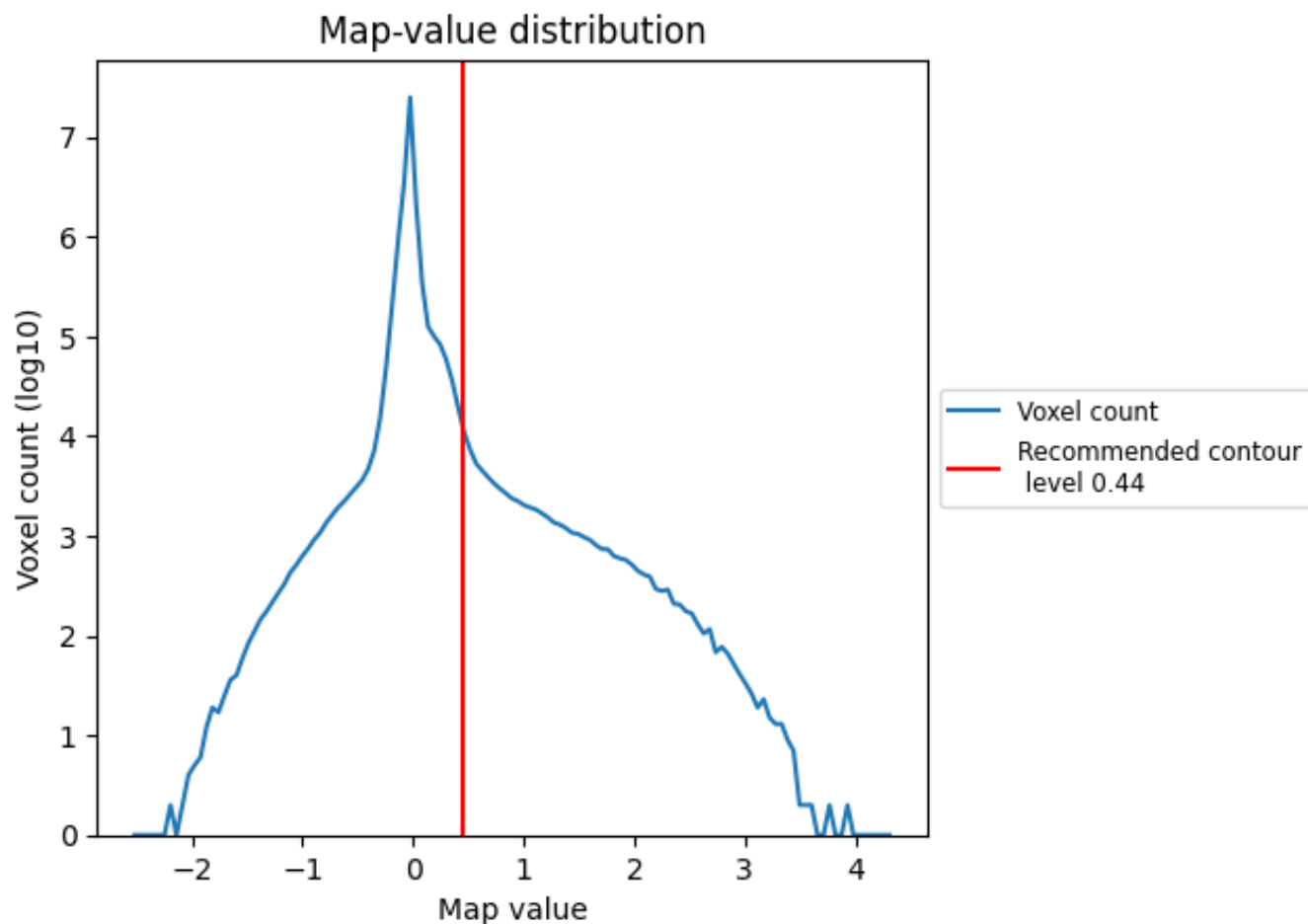
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

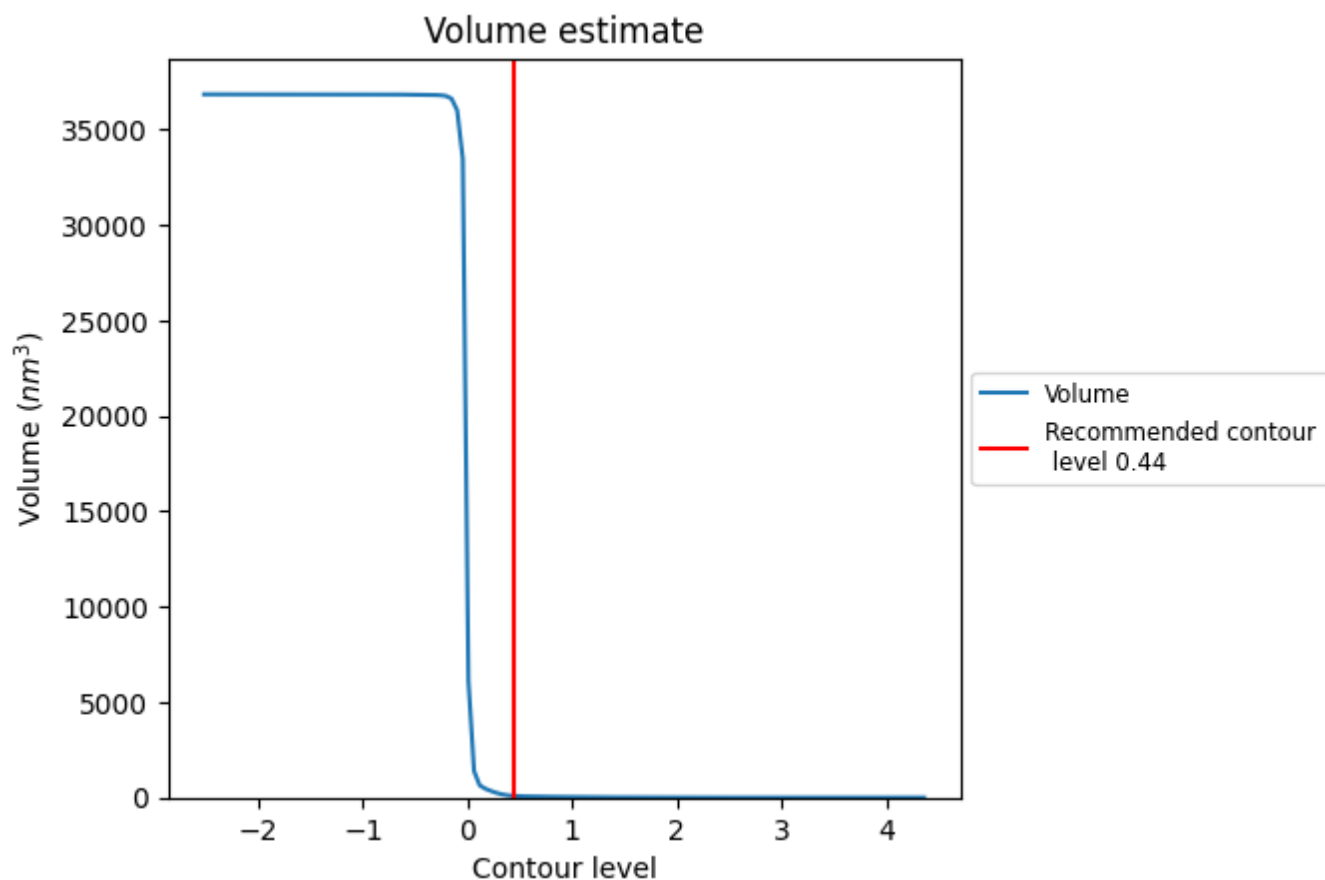
This section contains the results of statistical analysis of the map.

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.

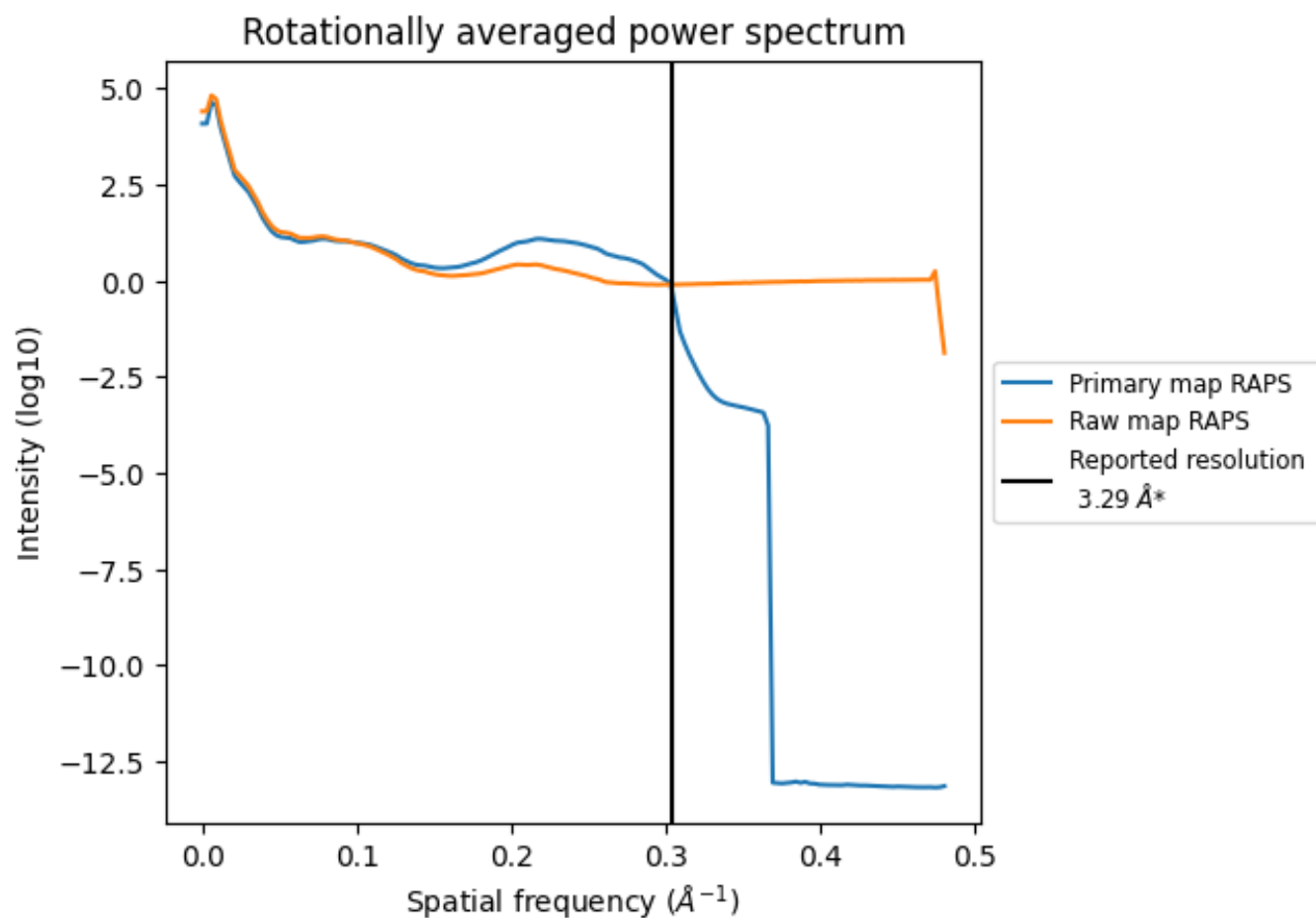
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 87 nm^3 ; this corresponds to an approximate mass of 78 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 ⓘ

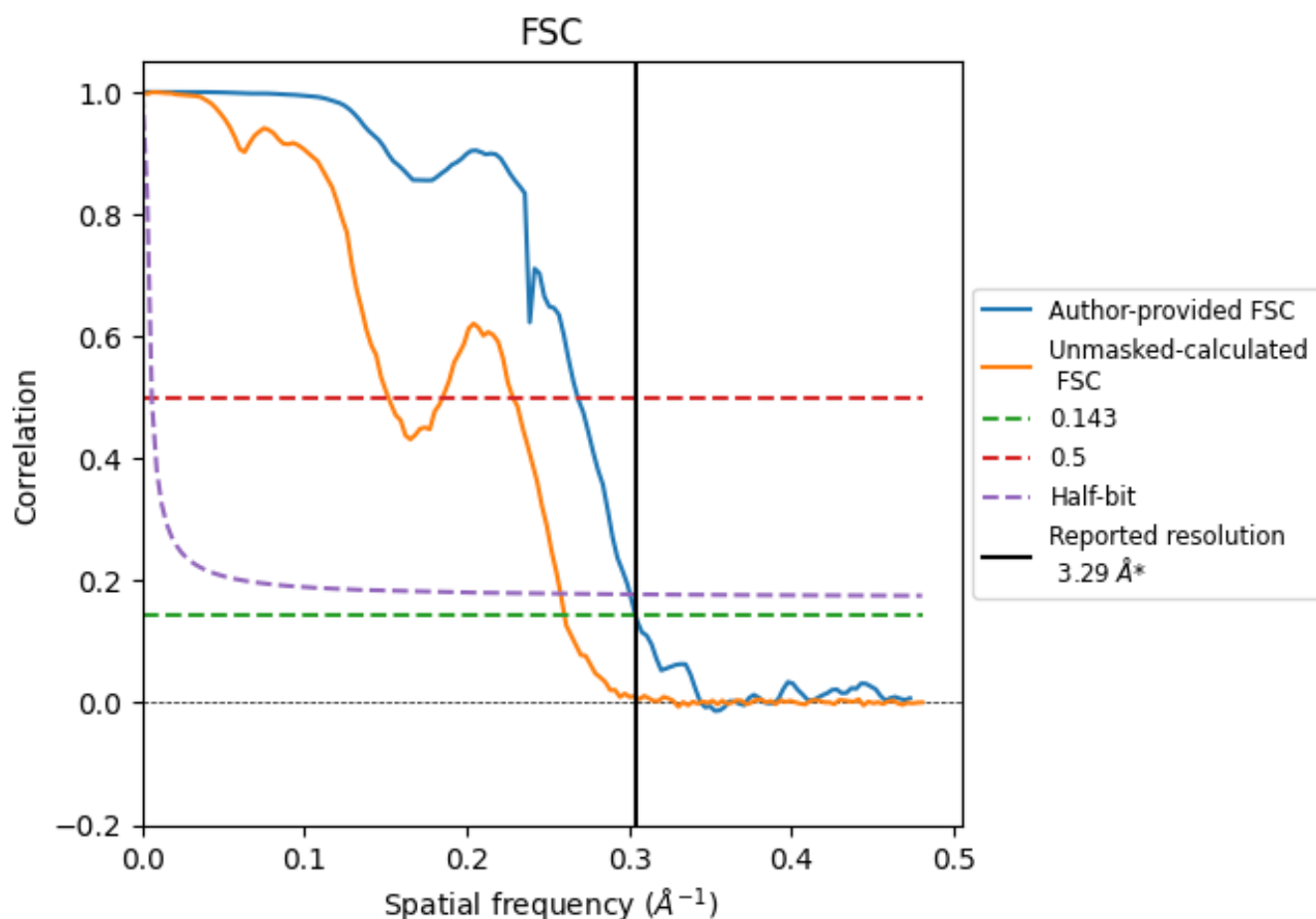


*Reported resolution corresponds to spatial frequency of 0.304 Å⁻¹

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 0.304 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

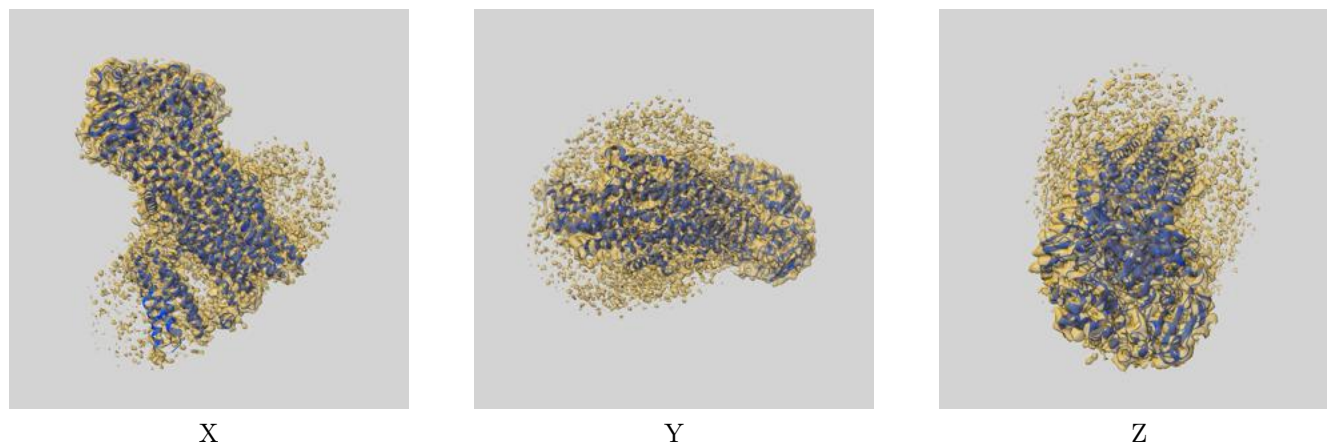
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.29	-	-
Author-provided FSC curve	3.29	3.72	3.33
Unmasked-calculated*	3.84	6.59	3.88

*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 3.84 differs from the reported value 3.29 by more than 10 %

9 Map-model fit [i](#)

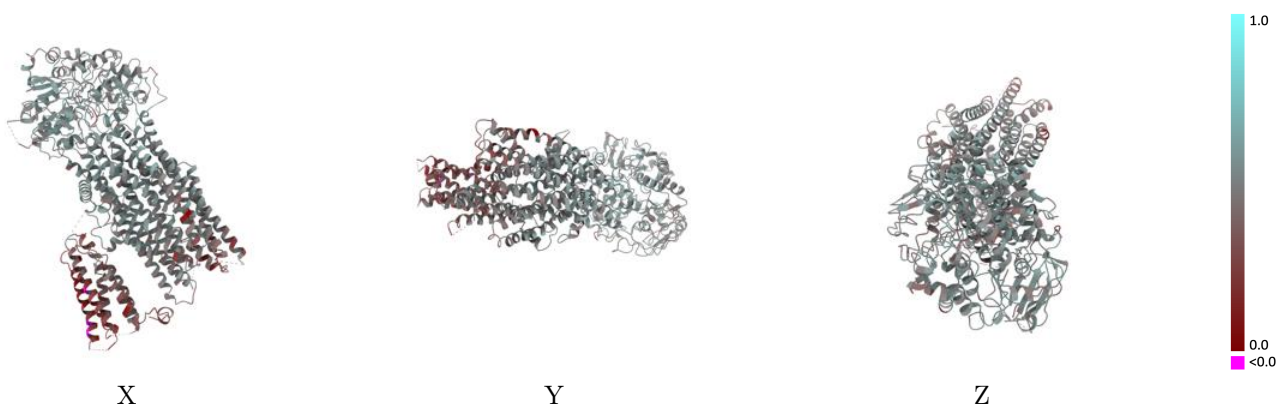
This section contains information regarding the fit between EMDB map EMD-63062 and PDB model 9LGD. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



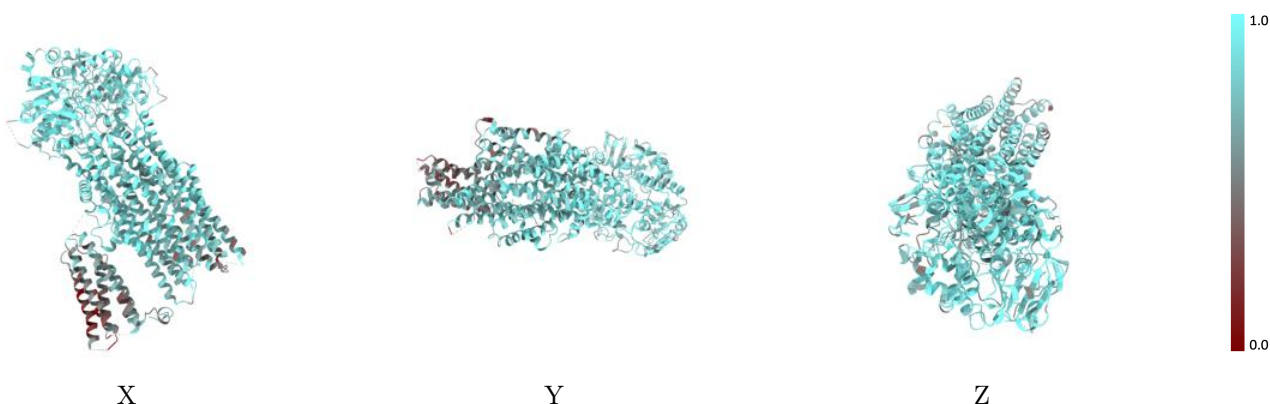
The images above show the 3D surface view of the map at the recommended contour level 0.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



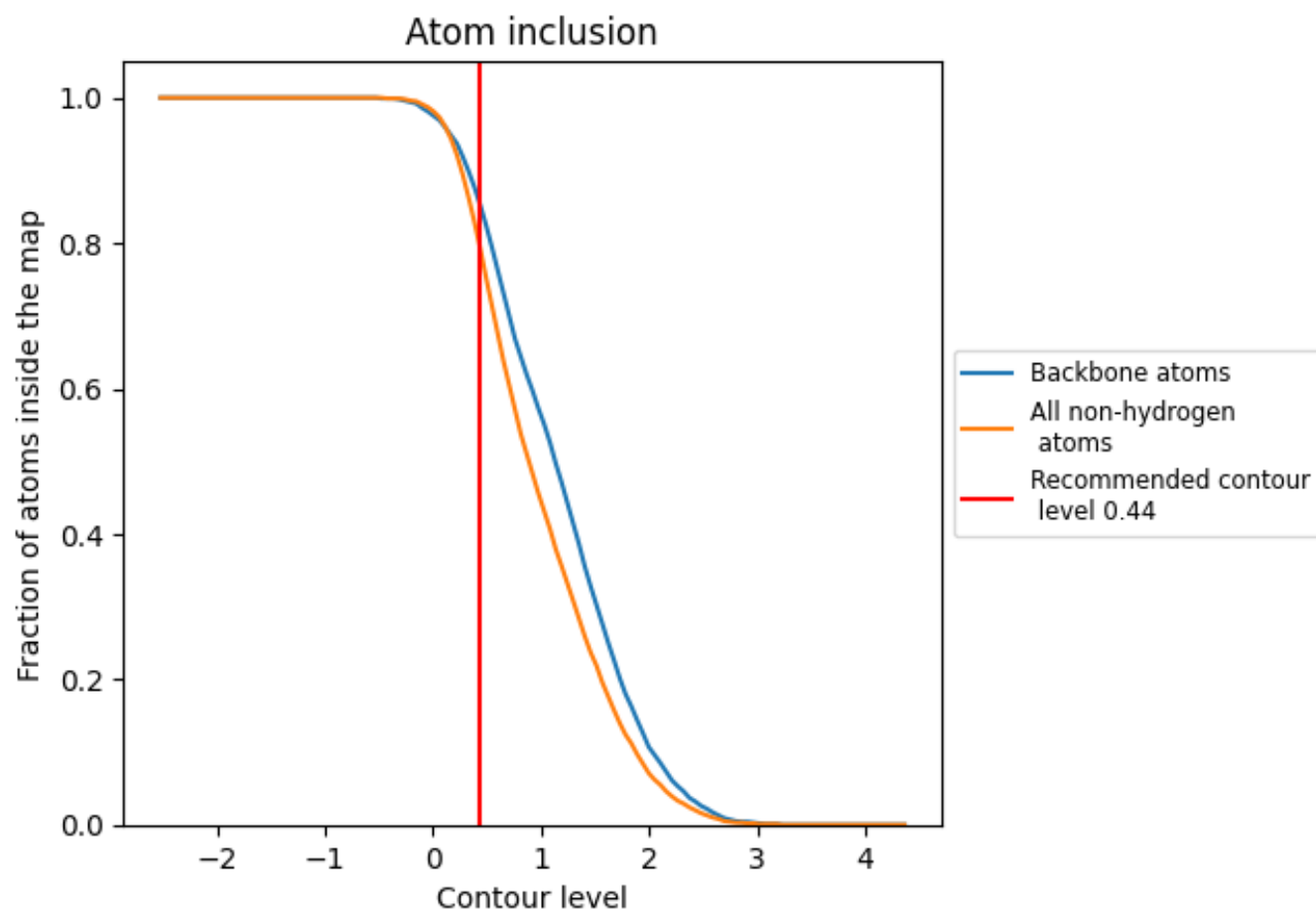
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.44).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 79% 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 (0.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7910	0.4690
A	0.7910	0.4690

