



Full wwPDB EM Validation Report ⓘ

Sep 23, 2025 – 03:10 PM JST

PDB ID : 9LGA / pdb_00009lga
EMDB ID : EMD-63059
Title : bovine ABCC1 bound to verapamil and GSH
Authors : Sun, P.P.; Liu, K.X.; Gao, P.
Deposited on : 2025-01-10
Resolution : 3.36 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.dev129
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

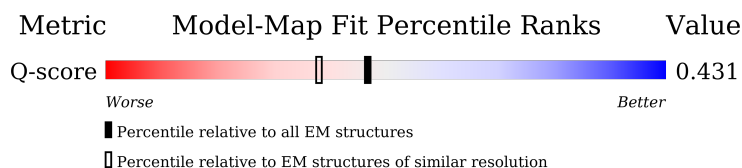
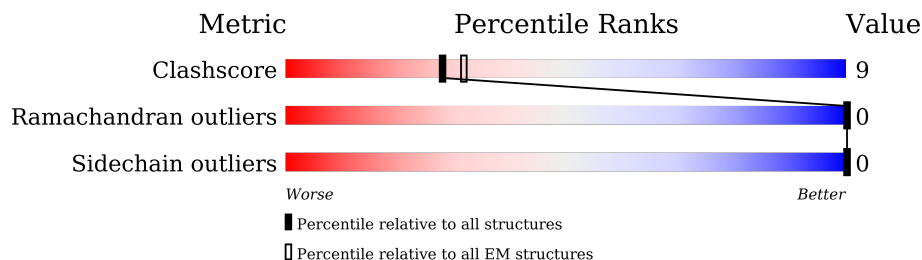
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.36 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	14332 (2.86 - 3.86)

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	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10638 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	1333	Total	C	N	O	S	0	0
			10585	6889	1756	1884	56		

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

- [illegible]

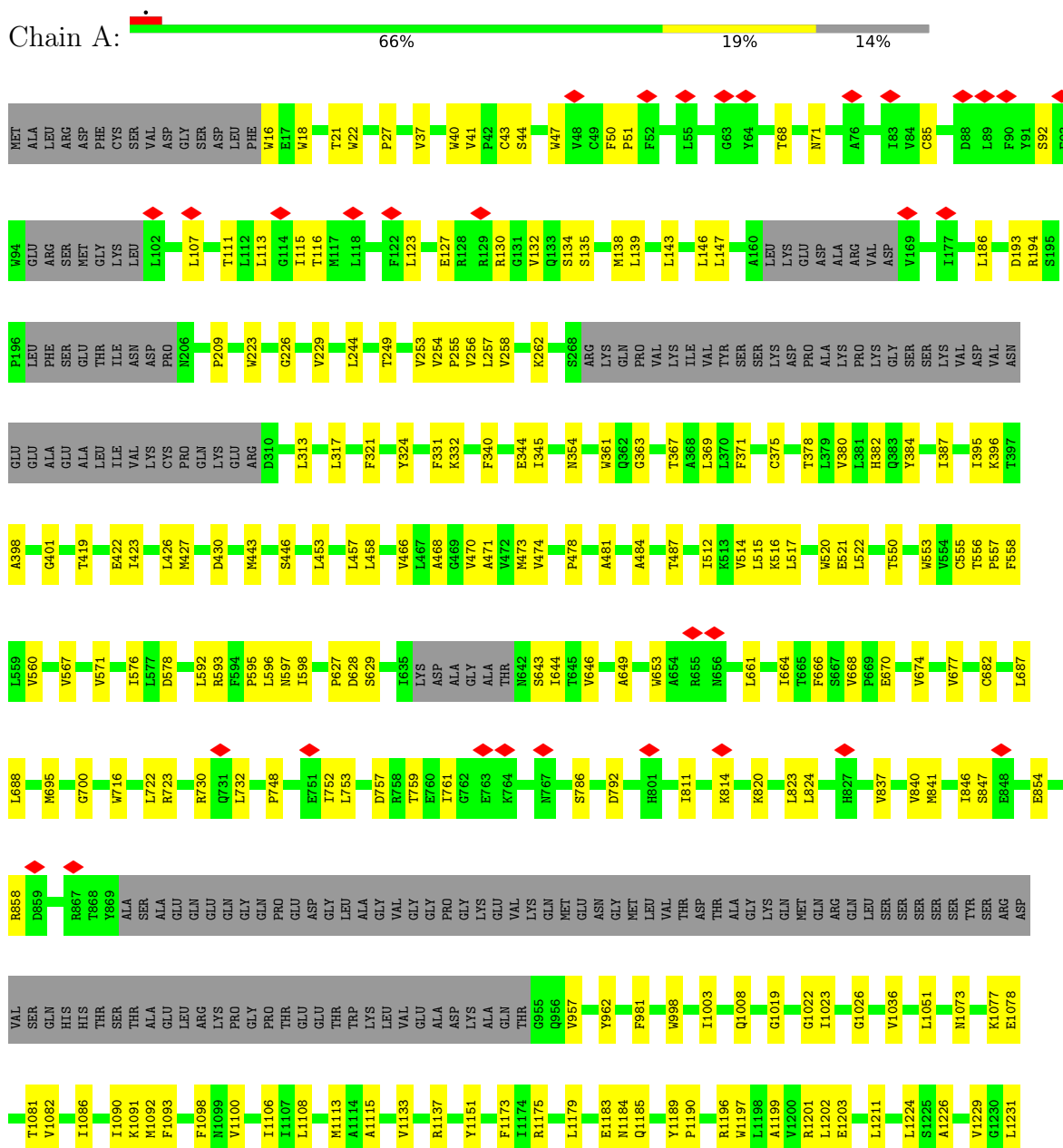
GSH

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
3	A	1	20	10	3	6	1	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: Multidrug resistance-associated protein 1



GLN	GLN	F1410	G1323	Y1235	Y1236	Y1239	M1244	M1245	M1249	M1253	E1254	T1255	M1256	I1257	L1263	E1270	Q1276	D1279	P1282	F1283	K1284	D1285	M1286	P1287	Q1288	V1289	F1294	Y1297	G1298	L1299	R1300	Y1301	ARG	GLU	ASP	LEU	D1306	L1307	V1308	L1309	K1310	H1311	I1312	N1313	V1314	D1317	G1318	G1319	E1320	K1321	V1322
ARG	GLY	S1412	R1327	R1327	S1236	T1328	G1329	A1330	S1334	L1337	R1341	I1342	K1343	A1346	E1347	I1351	D1353	D1354	I1355	N1356	I1357	T1360	G1361	L1362	H1363	D1364	L1365	T1370	I1371	Q1374	V1377	L1378	F1379	S1382	L1383	R1384	N1385	M1386	L1387	D1388	P1389	D1395	L1402	E1403	L1404	L1407	K1408	G1409			
PHE	TYR	L1414	P1415	D1416	K1417	L1418	N1419	H1420	E1421	E1424	G1425	G1426	E1427	N1428	Q1433	R1434	A1441	A1442	L1443	L1444	R1445	I1449	L1450	A1455	THR	ALA	ALA	VAL	ASP	LEU	E1462	L1481	H1485	R1486	L1487	N1488	T1489	I1490	R1495	V1496	I1497	K1501	Q1505	E1506	W1507	L1514					
GLN	GLN	V1411	A1413	L1414	P1415	D1416	K1417	L1418	N1419	H1420	E1421	E1424	G1425	G1426	E1427	N1428	Q1433	R1434	A1441	A1442	L1443	L1444	R1445	I1449	L1450	A1455	THR	ALA	ALA	VAL	ASP	LEU	E1462	L1481	H1485	R1486	L1487	N1488	T1489	I1490	R1495	V1496	I1497	K1501	Q1505	E1506	W1507	L1514			
GLN	GLN	ARG	GLY	LEU	PHE	TYR	SER	MET	ALA	LYS	ASP	SER	GLY	LEU	VAL	LYS	LEU	GLY	SER	GLU	ASN	LEU	TYR	PHE	GLN	GLY	SER	GLY	SER	GLY	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	150502	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)	200	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	4.046	Depositor
Minimum map value	-2.432	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.42	Depositor
Map size (Å)	320.0, 320.0, 320.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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: 4YH, GSH

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	0.39	0/10821	0.55	2/14690 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1289	VAL	N-CA-C	-6.37	107.66	113.71
1	A	627	PRO	N-CA-C	-5.12	106.74	113.65

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	10585	0	10808	200	0
2	A	33	0	38	8	0
3	A	20	0	15	3	0
All	All	10638	0	10861	202	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 (202) 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:674:VAL:HG22	1:A:837:VAL:HB	1.70	0.72
1:A:558:PHE:CZ	1:A:1022:GLY:HA3	2.26	0.71
1:A:811:ILE:HG21	1:A:824:LEU:HD12	1.77	0.67
1:A:1289:VAL:HG22	1:A:1318:GLY:HA3	1.79	0.64
1:A:47:TRP:HZ2	1:A:115:ILE:HG22	1.63	0.62
1:A:209:PRO:HB2	1:A:223:TRP:HB2	1.83	0.61
1:A:1202:LEU:HD12	1:A:1244:ASN:HA	1.82	0.61
1:A:1341:ARG:NH1	1:A:1357:ILE:O	2.34	0.60
1:A:1286:TRP:HE1	1:A:1355:ILE:HB	1.67	0.60
1:A:668:VAL:HG21	1:A:823:LEU:HD11	1.85	0.59
1:A:1337:LEU:HD22	1:A:1342:ILE:HG13	1.84	0.59
1:A:331:PHE:HD1	1:A:380:VAL:HG13	1.67	0.59
1:A:517:LEU:HB3	1:A:1371:ILE:HG21	1.83	0.58
1:A:1090:ILE:HA	1:A:1253:MET:HE1	1.86	0.58
1:A:1051:LEU:HD22	1:A:1263:LEU:HD22	1.84	0.58
1:A:324:TYR:HD2	1:A:387:ILE:HG23	1.69	0.58
1:A:522:LEU:HG	1:A:1363:HIS:HE1	1.68	0.58
1:A:957:VAL:HG22	1:A:1254:GLU:HG2	1.85	0.58
1:A:1300:ARG:HB2	1:A:1346:ALA:HB2	1.85	0.57
1:A:520:TRP:CH2	1:A:1386:ASN:O	2.58	0.57
1:A:520:TRP:CD2	1:A:1389:PRO:HG2	2.38	0.57
1:A:1086:ILE:HG12	1:A:1256:ASN:HB3	1.85	0.57
1:A:1352:ILE:HD13	1:A:1449:ILE:HD12	1.87	0.56
1:A:962:TYR:CE1	1:A:1257:ILE:HG13	2.41	0.56
1:A:649:ALA:HA	1:A:700:GLY:HA3	1.86	0.56
1:A:1402:LEU:HD13	1:A:1411:VAL:HG21	1.87	0.56
1:A:1301:TYR:C	1:A:1343:LYS:HE3	2.31	0.55
1:A:244:LEU:HD11	1:A:1185:GLN:HB2	1.89	0.55
1:A:473:MET:HE3	1:A:596:LEU:HD21	1.89	0.55
1:A:664:ILE:HG13	1:A:846:ILE:HG12	1.89	0.55
1:A:396:LYS:NZ	1:A:1184:ASN:OD1	2.37	0.54
1:A:643:SER:HB2	1:A:670:GLU:HG2	1.89	0.54
1:A:1286:TRP:HB3	1:A:1287:PRO:HD3	1.90	0.54
1:A:998:TRP:HE1	1:A:1008:GLN:HE22	1.55	0.54
1:A:345:ILE:HD12	1:A:369:LEU:HD23	1.91	0.53
1:A:558:PHE:CE2	1:A:1022:GLY:HA3	2.43	0.53
1:A:1298:GLY:N	1:A:1347:GLU:O	2.42	0.53
1:A:682:CYS:SG	1:A:841:MET:HG3	2.48	0.53
1:A:1445:ARG:HH11	1:A:1445:ARG:HG3	1.73	0.53
1:A:123:LEU:HD23	1:A:138:MET:SD	2.49	0.53
1:A:1407:LEU:HD21	1:A:1433:GLN:OE1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:PRO:O	1:A:481:ALA:HB3	2.09	0.52
1:A:345:ILE:CD1	1:A:369:LEU:HD23	2.40	0.52
1:A:443:MET:HA	1:A:446:SER:HB3	1.91	0.52
1:A:443:MET:HE2	1:A:598:ILE:HG21	1.90	0.52
1:A:1245:TRP:CZ3	3:A:1602:GSH:HB22	2.44	0.52
1:A:1317:ASP:HB2	1:A:1320:GLU:HG3	1.92	0.52
1:A:1294:PHE:O	1:A:1313:ASN:HA	2.10	0.52
1:A:1382:SER:HB2	1:A:1419:ASN:HA	1.92	0.51
1:A:628:ASP:O	1:A:629:SER:C	2.53	0.51
1:A:1323:GLY:HA3	1:A:1490:ILE:HD11	1.93	0.51
1:A:556:THR:N	1:A:557:PRO:HD2	2.26	0.51
1:A:674:VAL:HA	1:A:837:VAL:O	2.10	0.51
1:A:453:LEU:O	1:A:457:LEU:HG	2.11	0.51
1:A:419:THR:HG23	1:A:422:GLU:H	1.76	0.50
1:A:520:TRP:CE2	1:A:1389:PRO:HG2	2.46	0.50
1:A:646:VAL:HG11	1:A:664:ILE:HG22	1.92	0.50
1:A:1093:PHE:HB2	1:A:1249:MET:HB3	1.94	0.50
1:A:1286:TRP:CD1	1:A:1355:ILE:HD12	2.45	0.50
1:A:653:TRP:CE2	1:A:695:MET:HE3	2.47	0.50
1:A:1378:LEU:HD22	1:A:1434:ARG:HG2	1.93	0.50
1:A:1073:ASN:OD1	1:A:1077:LYS:HE3	2.12	0.50
1:A:1106:ILE:HD12	1:A:1231:LEU:HD21	1.92	0.50
1:A:132:VAL:HG12	1:A:134:SER:O	2.11	0.50
1:A:135:SER:O	1:A:139:LEU:HB2	2.12	0.50
1:A:723:ARG:HD2	1:A:757:ASP:OD2	2.12	0.50
1:A:840:VAL:HG13	1:A:847:SER:O	2.12	0.49
1:A:1236:SER:O	1:A:1239:VAL:HG12	2.13	0.49
1:A:723:ARG:HH22	1:A:732:LEU:HD13	1.76	0.49
1:A:1384:ARG:HH12	1:A:1395:ASP:HA	1.77	0.49
1:A:111:THR:O	1:A:115:ILE:HG12	2.13	0.49
1:A:427:MET:HG2	1:A:1151:TYR:HD1	1.77	0.49
1:A:981:PHE:CZ	1:A:1098:PHE:HB2	2.48	0.49
1:A:1404:LEU:HB3	1:A:1443:LEU:HD21	1.94	0.49
1:A:515:LEU:HD21	1:A:1379:PHE:CZ	2.47	0.48
1:A:653:TRP:CD2	1:A:695:MET:HE3	2.48	0.48
1:A:1108:LEU:HD11	1:A:1115:ALA:HB2	1.93	0.48
1:A:427:MET:HG2	1:A:1151:TYR:CD1	2.49	0.48
1:A:556:THR:O	1:A:560:VAL:HG23	2.14	0.48
1:A:258:VAL:O	1:A:262:LYS:HG2	2.14	0.48
1:A:1245:TRP:CD1	2:A:1601:4YH:H8	2.49	0.48
1:A:1383:LEU:HD13	1:A:1420:HIS:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:GLY:O	1:A:367:THR:HG23	2.14	0.48
1:A:1224:LEU:HD23	1:A:1229:VAL:HG22	1.95	0.48
1:A:43:CYS:SG	1:A:116:THR:HG21	2.54	0.48
1:A:423:ILE:HA	1:A:426:LEU:HD12	1.96	0.48
1:A:753:LEU:HD13	1:A:759:THR:HG21	1.95	0.47
1:A:1282:PRO:HD3	1:A:1360:ILE:HD12	1.96	0.47
1:A:1370:THR:HG23	1:A:1450:LEU:HD13	1.96	0.47
1:A:748:PRO:O	1:A:752:ILE:HG22	2.14	0.47
1:A:1310:LYS:HG2	1:A:1311:HIS:ND1	2.29	0.47
1:A:1362:LEU:O	1:A:1365:LEU:HG	2.14	0.47
1:A:257:LEU:HD22	1:A:398:ALA:HB1	1.97	0.47
1:A:786:SER:O	1:A:820:LYS:HD2	2.14	0.47
1:A:1245:TRP:CE3	3:A:1602:GSH:HB22	2.49	0.47
1:A:474:VAL:O	1:A:478:PRO:HD3	2.15	0.47
1:A:1189:TYR:HB3	1:A:1190:PRO:HD3	1.97	0.47
1:A:716:TRP:HH2	1:A:1173:PHE:CZ	2.33	0.47
1:A:1307:LEU:HB2	1:A:1310:LYS:HE2	1.97	0.47
1:A:371:PHE:HB2	1:A:1211:LEU:HB2	1.96	0.46
1:A:578:ASP:OD1	1:A:578:ASP:N	2.42	0.46
1:A:1299:LEU:CB	1:A:1309:LEU:HB2	2.45	0.46
1:A:1299:LEU:HD23	1:A:1334:SER:HB3	1.97	0.46
1:A:1317:ASP:HB2	1:A:1320:GLU:CG	2.44	0.46
1:A:1197:TRP:O	1:A:1201:ARG:HG2	2.15	0.46
1:A:27:PRO:HB3	1:A:361:TRP:CE2	2.50	0.46
1:A:85:CYS:SG	1:A:113:LEU:HD22	2.56	0.46
1:A:1299:LEU:HB3	1:A:1309:LEU:HB2	1.98	0.46
1:A:854:GLU:O	1:A:858:ARG:HG3	2.16	0.46
1:A:50:PHE:HB3	1:A:51:PRO:HD3	1.96	0.46
1:A:1092:MET:SD	2:A:1601:4YH:H28	2.55	0.46
1:A:1351:ILE:HG12	1:A:1356:ASN:HA	1.97	0.46
1:A:1351:ILE:HG23	1:A:1355:ILE:C	2.41	0.46
1:A:40:TRP:O	1:A:44:SER:CB	2.64	0.46
1:A:722:LEU:HD12	1:A:761:ILE:HG21	1.97	0.46
1:A:146:LEU:HD22	1:A:186:LEU:HD22	1.98	0.46
1:A:512:ILE:HD11	1:A:516:LYS:HZ3	1.81	0.46
1:A:595:PRO:HA	1:A:598:ILE:HG22	1.98	0.45
1:A:1082:VAL:HA	1:A:1086:ILE:HD12	1.97	0.45
1:A:520:TRP:HH2	1:A:1386:ASN:O	1.97	0.45
1:A:981:PHE:HZ	1:A:1098:PHE:HB2	1.81	0.45
1:A:1090:ILE:HG12	1:A:1253:MET:HE1	1.99	0.45
1:A:1387:LEU:HA	1:A:1441:ARG:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:VAL:HG21	1:A:401:GLY:HA3	1.97	0.45
1:A:517:LEU:HD22	1:A:1371:ILE:HD13	1.98	0.45
1:A:576:ILE:HG12	1:A:1003:ILE:HG12	1.98	0.45
1:A:1351:ILE:HG23	1:A:1355:ILE:O	2.17	0.45
1:A:1403:GLU:HA	1:A:1408:LYS:HB2	1.98	0.45
1:A:593:ARG:O	1:A:597:ASN:ND2	2.49	0.45
1:A:1196:ARG:NH2	3:A:1602:GSH:O32	2.43	0.45
1:A:1294:PHE:HB2	1:A:1314:VAL:HG12	1.99	0.44
1:A:331:PHE:HB3	1:A:384:TYR:HB2	2.00	0.44
1:A:661:LEU:HB3	1:A:664:ILE:HD13	1.98	0.44
1:A:37:VAL:O	1:A:41:VAL:HG23	2.18	0.44
1:A:127:GLU:HG2	1:A:132:VAL:HG21	1.99	0.44
1:A:354:ASN:HB3	1:A:1226:ALA:HB2	1.98	0.44
1:A:313:LEU:HG	1:A:317:LEU:HD23	2.00	0.44
1:A:644:ILE:HD12	1:A:823:LEU:HD13	2.00	0.44
1:A:1100:VAL:HA	1:A:1239:VAL:HG23	2.00	0.44
1:A:226:GLY:O	1:A:229:VAL:HG22	2.17	0.43
1:A:193:ASP:OD1	1:A:194:ARG:N	2.47	0.43
1:A:332:LYS:HE3	1:A:446:SER:OG	2.18	0.43
1:A:1137:ARG:HD3	1:A:1254:GLU:HB3	2.00	0.43
1:A:1497:ILE:HG12	1:A:1507:TRP:CE3	2.54	0.43
1:A:68:THR:CG2	1:A:71:ASN:H	2.31	0.43
1:A:688:LEU:HD12	1:A:792:ASP:HB2	2.00	0.43
1:A:553:TRP:CE3	2:A:1601:4YH:H2	2.52	0.43
1:A:668:VAL:HG22	1:A:674:VAL:HG21	2.01	0.43
1:A:253:VAL:O	1:A:256:VAL:HG12	2.19	0.43
1:A:998:TRP:NE1	1:A:1008:GLN:HE22	2.16	0.43
1:A:1199:ALA:O	1:A:1203:GLU:HG3	2.18	0.43
1:A:553:TRP:CZ3	2:A:1601:4YH:H2	2.54	0.43
1:A:1019:GLY:O	1:A:1023:ILE:HG12	2.19	0.43
1:A:1245:TRP:NE1	2:A:1601:4YH:H8	2.34	0.43
1:A:555:CYS:SG	1:A:1026:GLY:HA2	2.58	0.42
1:A:473:MET:SD	1:A:592:LEU:HD21	2.58	0.42
1:A:340:PHE:O	1:A:344:GLU:HG2	2.18	0.42
1:A:430:ASP:N	1:A:430:ASP:OD1	2.52	0.42
1:A:1092:MET:HE3	1:A:1245:TRP:HE1	1.84	0.42
1:A:516:LYS:HZ2	1:A:521:GLU:CD	2.27	0.42
1:A:382:HIS:NE2	1:A:1199:ALA:HB1	2.35	0.42
1:A:1414:LEU:HG	1:A:1420:HIS:CG	2.54	0.42
1:A:458:LEU:C	1:A:466:VAL:HG21	2.45	0.42
1:A:677:VAL:HG12	1:A:840:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:730:ARG:HH11	1:A:730:ARG:HB2	1.85	0.42
1:A:567:VAL:O	1:A:571:VAL:HG22	2.20	0.42
1:A:1175:ARG:CZ	1:A:1175:ARG:HB2	2.49	0.42
1:A:375:CYS:O	1:A:378:THR:HG22	2.20	0.42
1:A:1495:ARG:HD3	1:A:1507:TRP:CH2	2.55	0.41
1:A:43:CYS:CB	1:A:116:THR:HG21	2.51	0.41
1:A:666:PHE:HE1	1:A:687:LEU:HD11	1.85	0.41
1:A:814:LYS:HE2	1:A:814:LYS:HB2	1.83	0.41
1:A:514:VAL:HG21	1:A:1377:VAL:CG2	2.50	0.41
1:A:1113:MET:HA	1:A:1113:MET:HE2	2.02	0.41
1:A:18:TRP:HE3	1:A:22:TRP:HB2	1.84	0.41
1:A:466:VAL:O	1:A:470:VAL:HG23	2.21	0.41
1:A:27:PRO:HB3	1:A:361:TRP:CZ2	2.56	0.41
1:A:40:TRP:O	1:A:44:SER:HB2	2.20	0.41
1:A:130:ARG:HH11	1:A:130:ARG:HG3	1.86	0.41
1:A:143:LEU:O	1:A:147:LEU:HG	2.21	0.41
1:A:1179:LEU:O	1:A:1183:GLU:HG2	2.21	0.41
1:A:1322:VAL:O	1:A:1481:LEU:HA	2.20	0.41
1:A:254:VAL:HB	1:A:255:PRO:HD3	2.02	0.41
1:A:550:THR:HG23	2:A:1601:4YH:H38	2.03	0.41
1:A:1078:GLU:HB2	1:A:1263:LEU:HD21	2.03	0.41
1:A:1081:THR:O	1:A:1086:ILE:HG13	2.21	0.41
2:A:1601:4YH:H29	2:A:1601:4YH:H21	1.79	0.41
1:A:1106:ILE:HG21	1:A:1235:TYR:HD2	1.86	0.40
1:A:92:SER:OG	1:A:107:LEU:HD13	2.21	0.40
1:A:468:ALA:O	1:A:471:ALA:HB3	2.21	0.40
2:A:1601:4YH:H18	2:A:1601:4YH:H16	1.78	0.40
1:A:16:TRP:CH2	1:A:21:THR:HG21	2.56	0.40
1:A:16:TRP:CZ3	1:A:21:THR:HG21	2.56	0.40
1:A:321:PHE:CD2	1:A:395:ILE:HG12	2.56	0.40
1:A:1036:VAL:HG11	1:A:1091:LYS:HG3	2.03	0.40
1:A:1092:MET:CE	1:A:1245:TRP:HE1	2.35	0.40
1:A:249:THR:O	1:A:253:VAL:HG22	2.20	0.40
1:A:427:MET:HE3	1:A:427:MET:HB2	1.99	0.40
1:A:484:ALA:O	1:A:487:THR:OG1	2.30	0.40
1:A:516:LYS:NZ	1:A:521:GLU:CD	2.80	0.40
1:A:1133:VAL:O	1:A:1137:ARG:HG3	2.21	0.40
1:A:1297:TYR:HB3	1:A:1312:ILE:HB	2.03	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	1315/1558 (84%)	1273 (97%)	42 (3%)	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	1171/1358 (86%)	1171 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	HIS
1	A	66	GLN
1	A	245	ASN
1	A	260	ASN
1	A	335	HIS
1	A	362	GLN
1	A	642	ASN
1	A	701	HIS
1	A	718	GLN
1	A	774	GLN
1	A	992	ASN

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Mol	Chain	Res	Type
1	A	1138	GLN
1	A	1207	ASN
1	A	1363	HIS
1	A	1386	ASN
1	A	1406	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](#)

2 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	4YH	A	1601	-	32,34,34	0.29	0	36,46,46	0.51	0
3	GSH	A	1602	-	18,19,19	0.76	0	23,24,24	0.95	1 (4%)

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	4YH	A	1601	-	-	8/32/35/35	0/2/2/2
3	GSH	A	1602	-	-	15/24/24/24	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1602	GSH	CB1-CG1-CD1	-2.44	107.60	113.04

There are no chirality outliers.

All (23) torsion outliers are listed below:

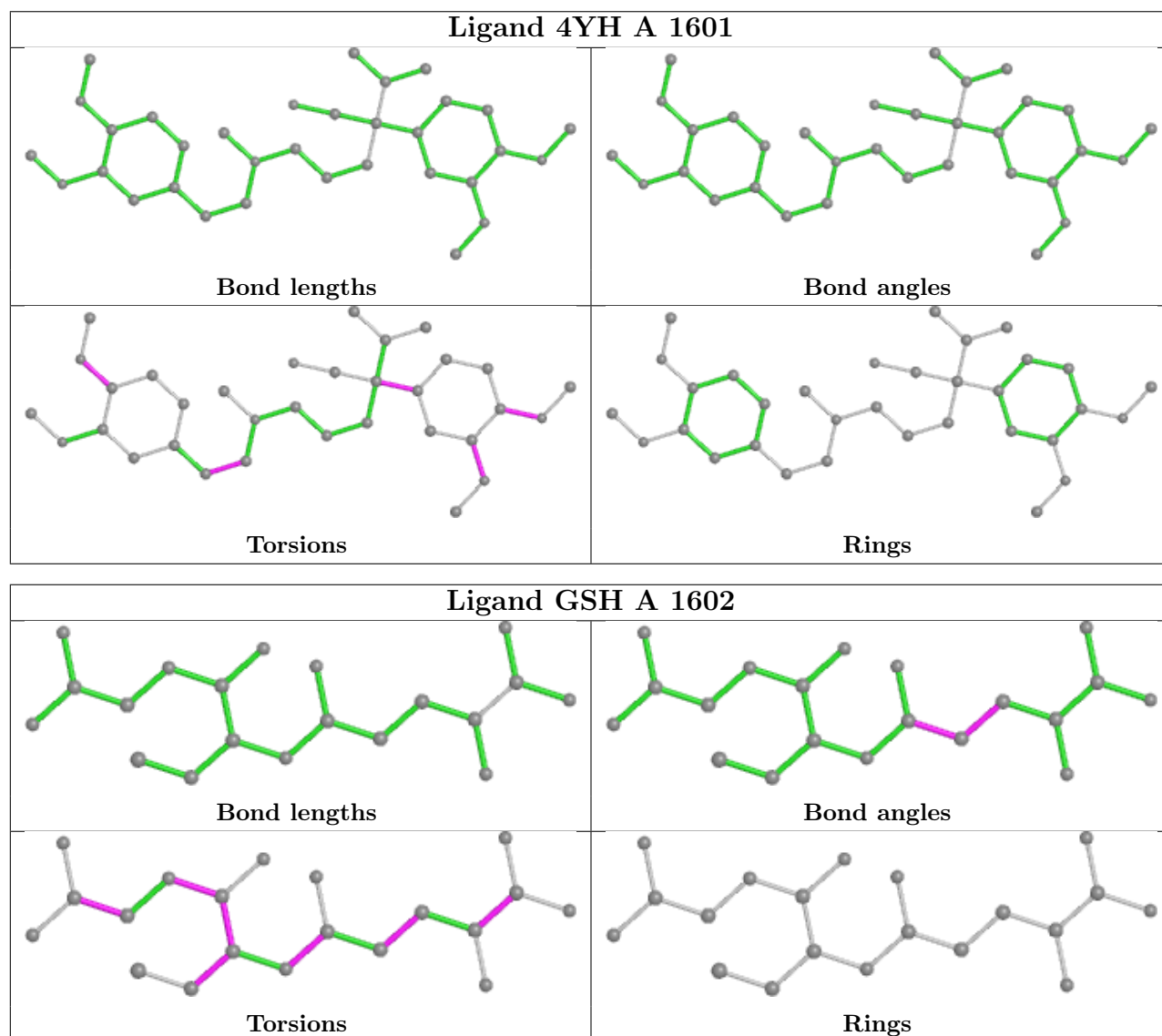
Mol	Chain	Res	Type	Atoms
3	A	1602	GSH	O11-C1-CA1-N1
3	A	1602	GSH	O2-C2-CA2-CB2
3	A	1602	GSH	N3-C2-CA2-CB2
3	A	1602	GSH	N2-CA2-CB2-SG2
3	A	1602	GSH	C2-CA2-CB2-SG2
3	A	1602	GSH	O31-C3-CA3-N3
3	A	1602	GSH	O32-C3-CA3-N3
2	A	1601	4YH	C6-C9-O23-C32
2	A	1601	4YH	C13-C9-O23-C32
2	A	1601	4YH	C5-C6-O19-C30
3	A	1602	GSH	O12-C1-CA1-N1
3	A	1602	GSH	CG1-CD1-N2-CA2
3	A	1602	GSH	OE1-CD1-N2-CA2
3	A	1602	GSH	CA2-C2-N3-CA3
2	A	1601	4YH	C9-C6-O19-C30
3	A	1602	GSH	CA1-CB1-CG1-CD1
3	A	1602	GSH	O2-C2-N3-CA3
2	A	1601	4YH	N8-C16-C21-C17
2	A	1601	4YH	C7-C10-O24-C33
2	A	1601	4YH	C15-C1-C2-C11
2	A	1601	4YH	C14-C10-O24-C33
3	A	1602	GSH	O11-C1-CA1-CB1
3	A	1602	GSH	O12-C1-CA1-CB1

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1601	4YH	8	0
3	A	1602	GSH	3	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 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

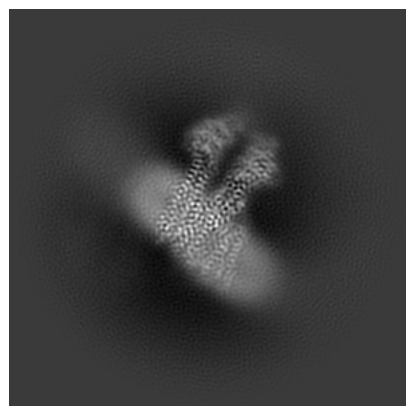
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63059. These allow visual inspection of the internal detail of the map and identification of artifacts.

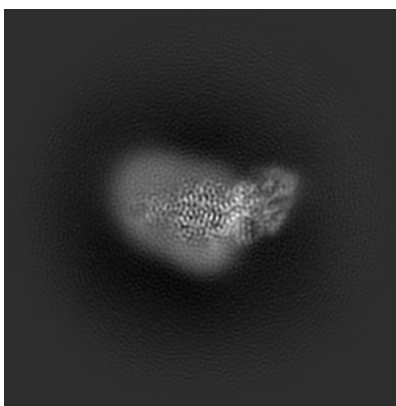
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

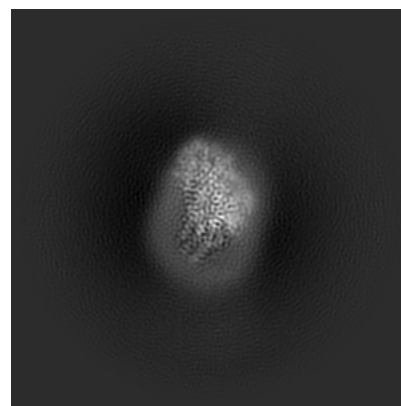
6.1.1 Primary map



X

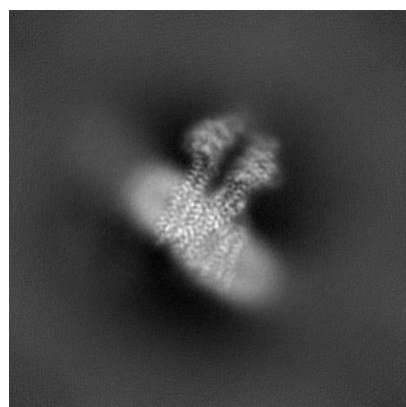


Y

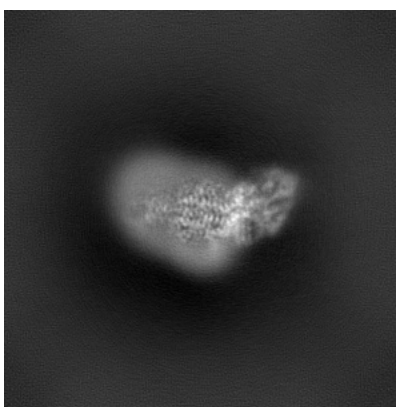


Z

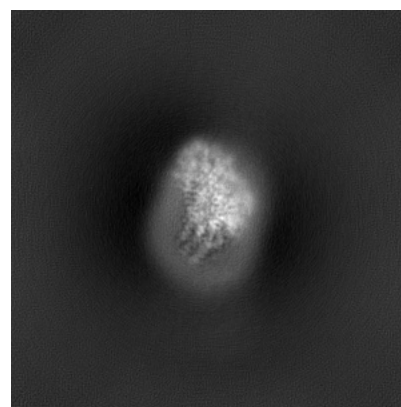
6.1.2 Raw map



X



Y

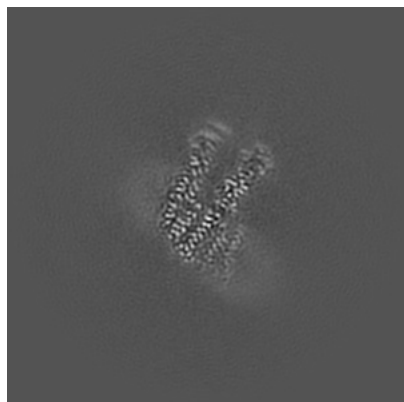


Z

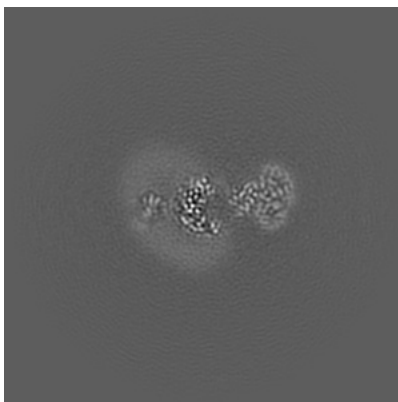
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

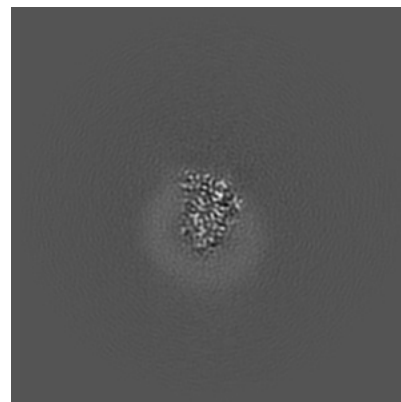
6.2.1 Primary map



X Index: 160

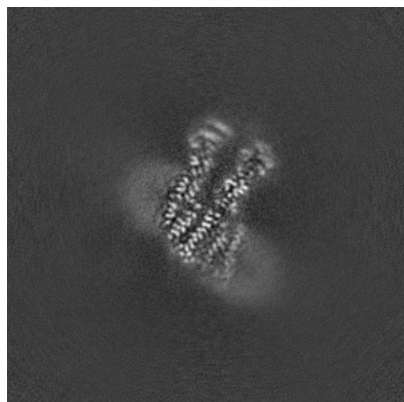


Y Index: 160

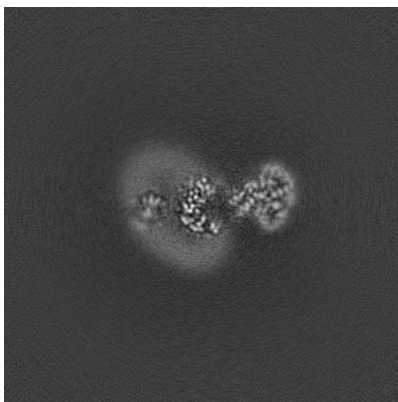


Z Index: 160

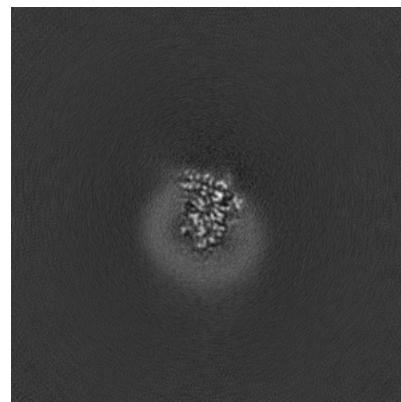
6.2.2 Raw map



X Index: 160



Y Index: 160

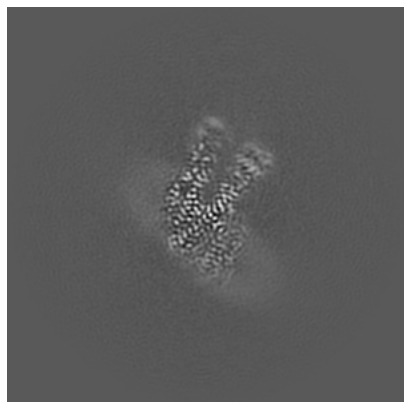


Z Index: 160

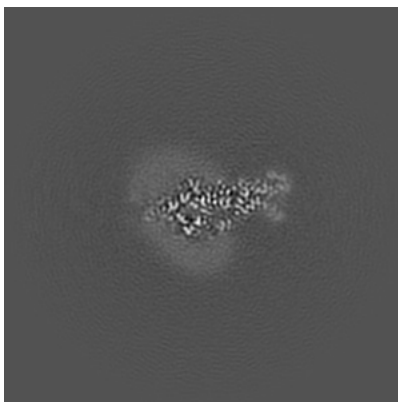
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

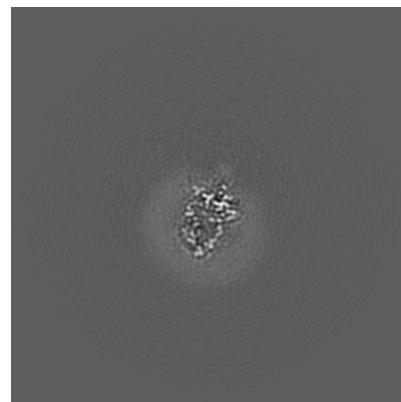
6.3.1 Primary map



X Index: 164

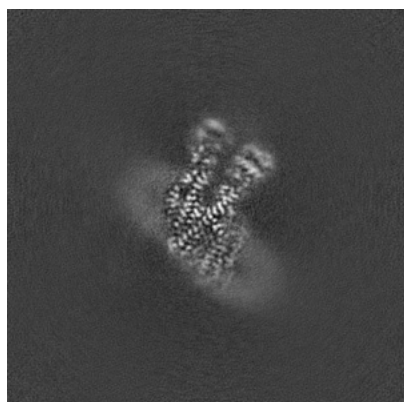


Y Index: 150

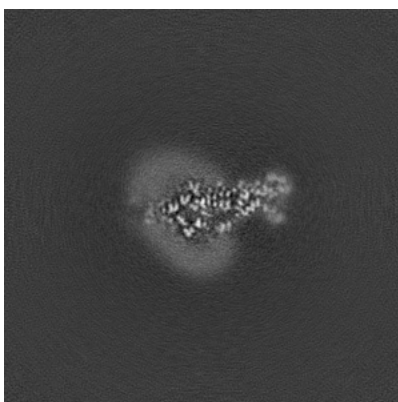


Z Index: 153

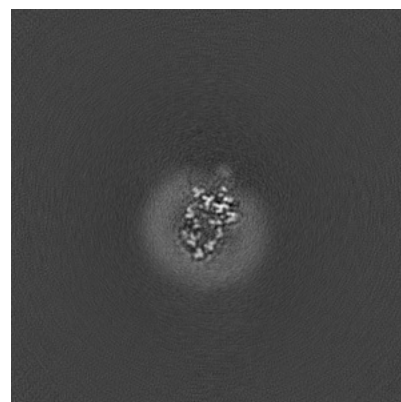
6.3.2 Raw map



X Index: 164



Y Index: 150

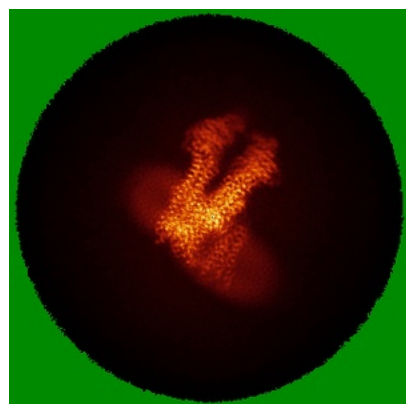


Z Index: 153

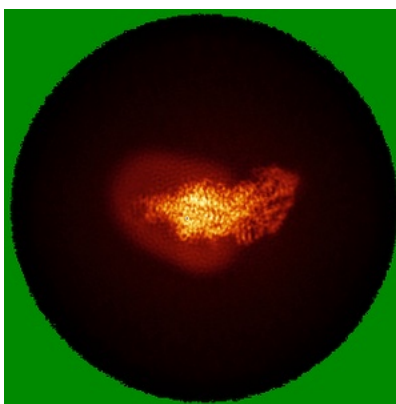
The images above show the largest variance slices of the map in three orthogonal directions.

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

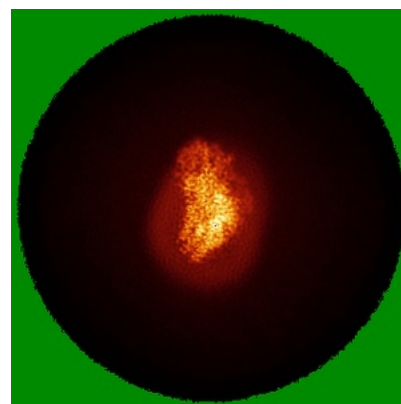
6.4.1 Primary map



X

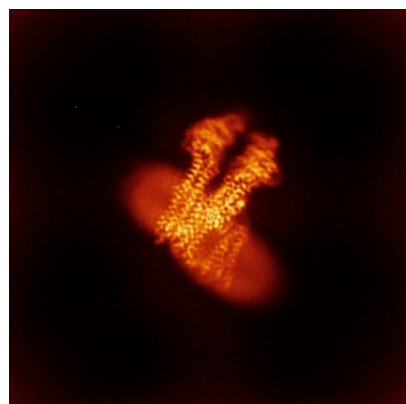


Y

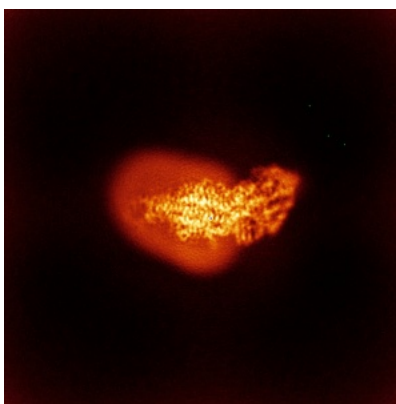


Z

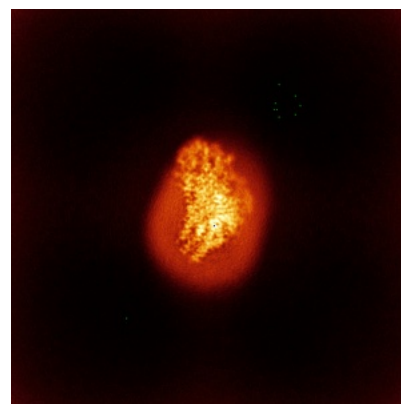
6.4.2 Raw map



X



Y

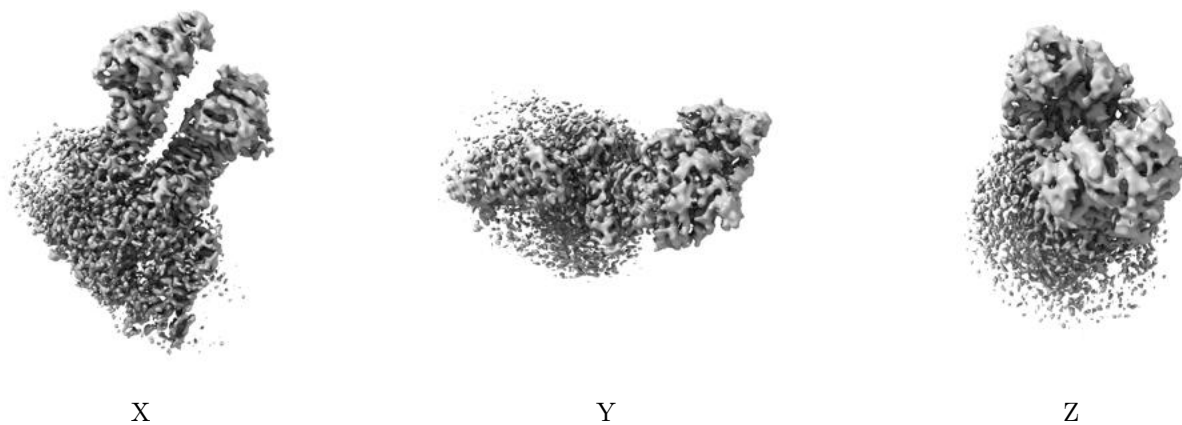


Z

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.

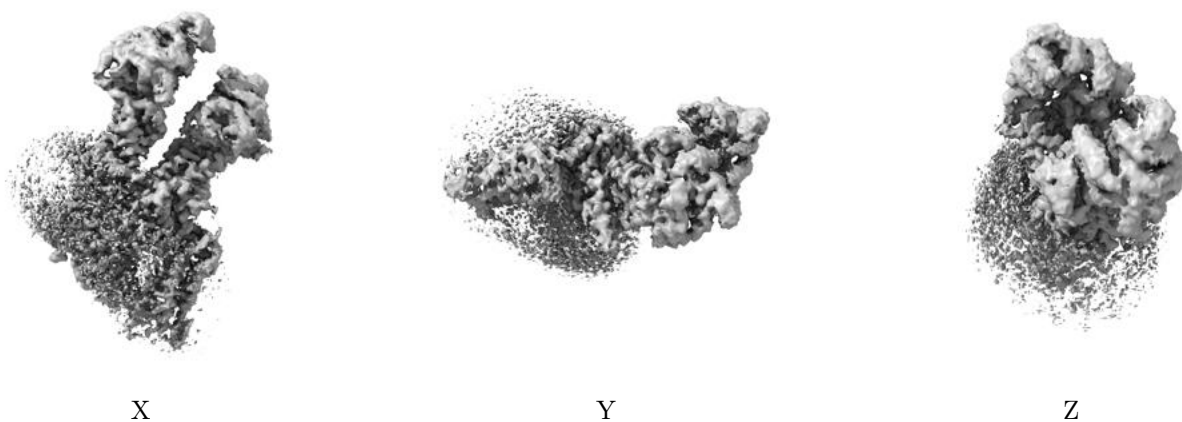
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.42. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

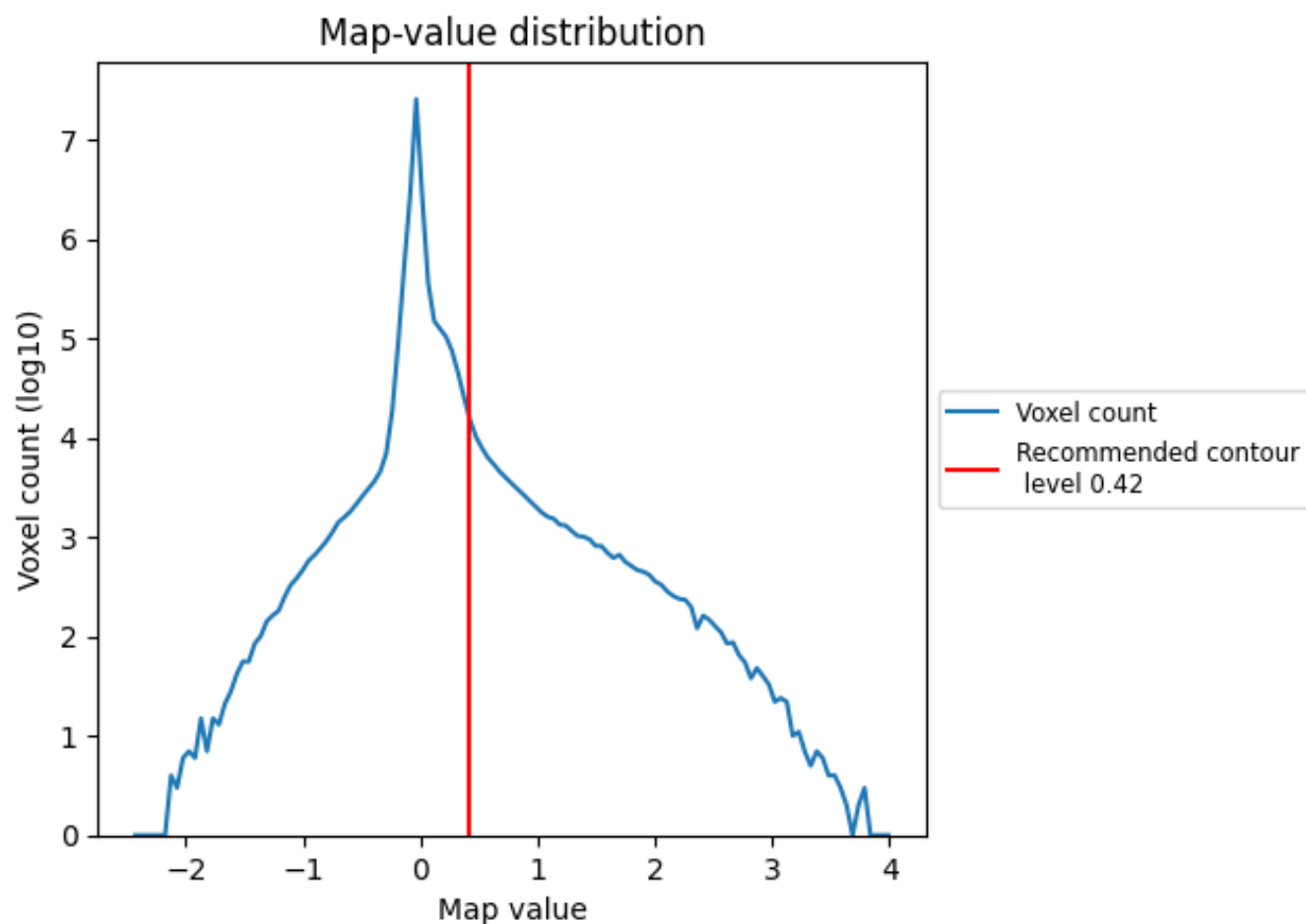
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

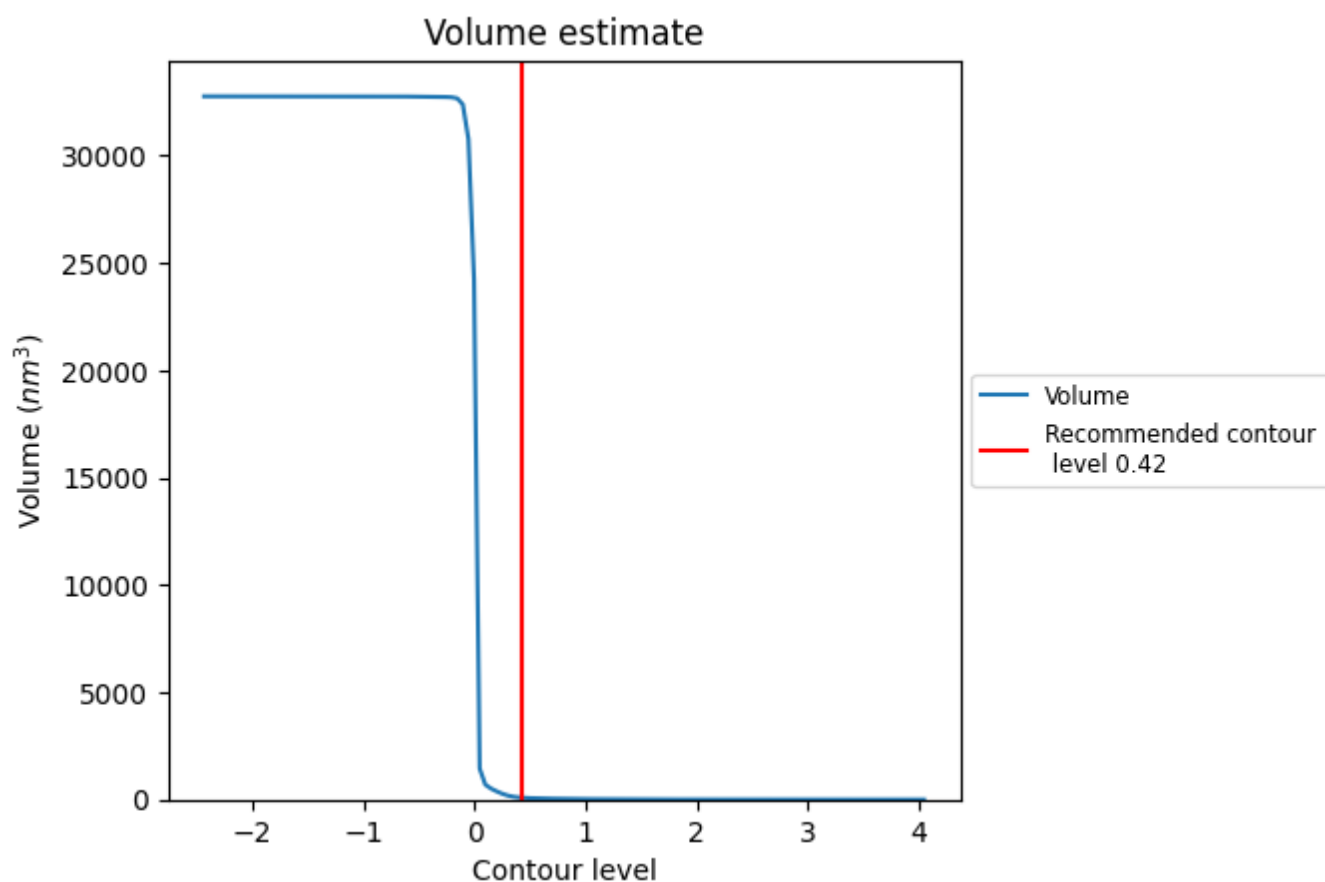
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

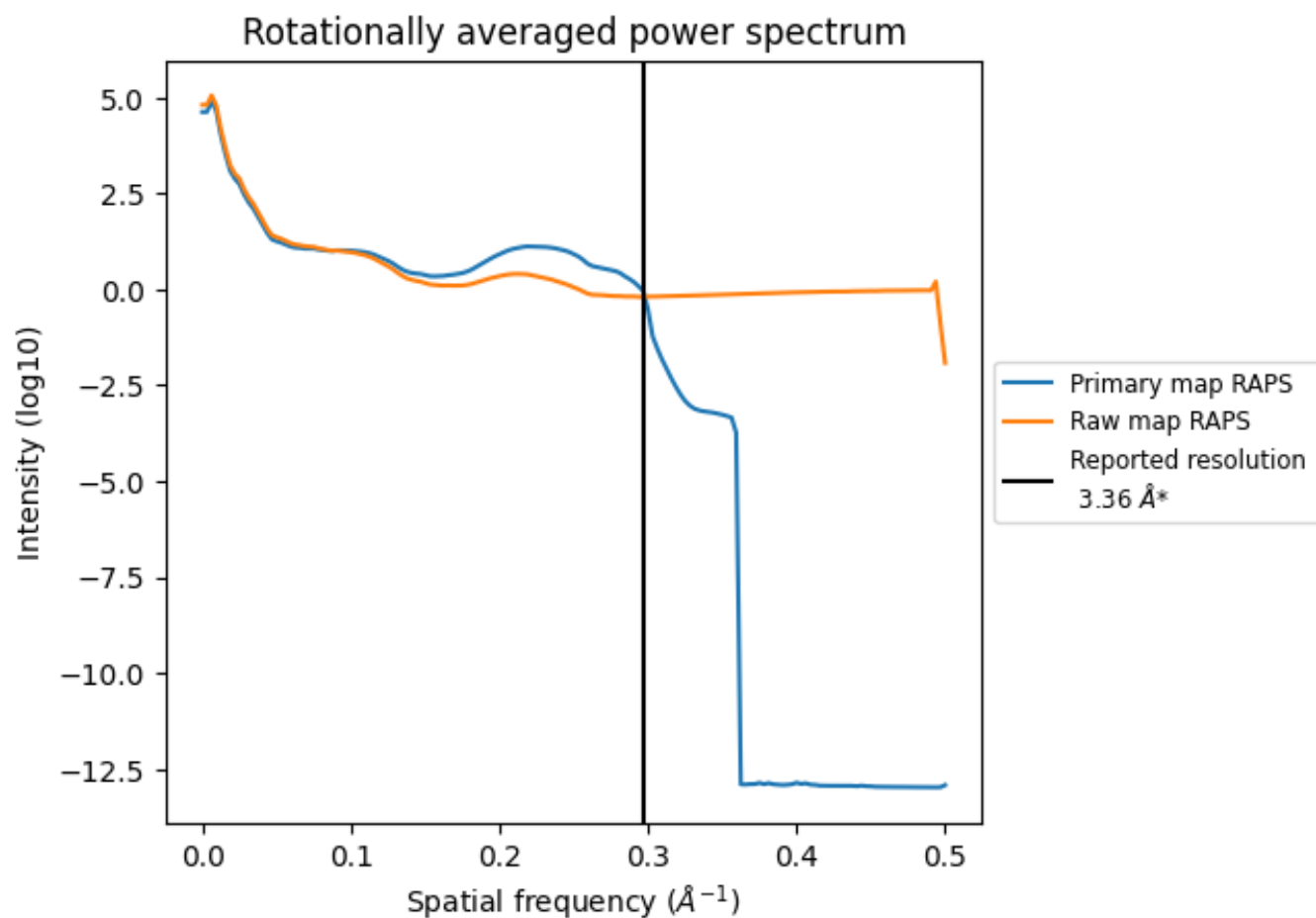
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 91 nm³; this corresponds to an approximate mass of 82 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

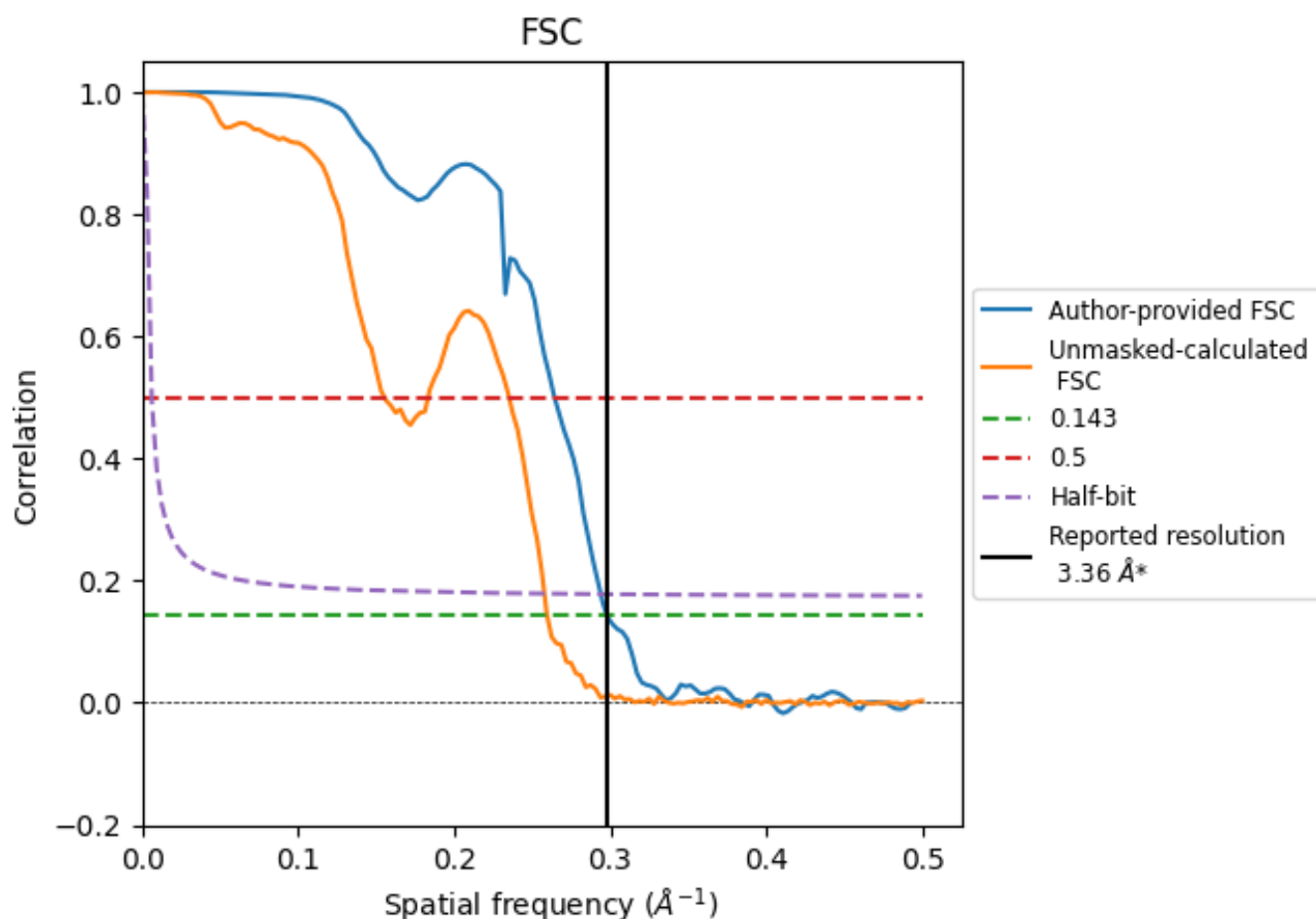


*Reported resolution corresponds to spatial frequency of 0.298 Å⁻¹

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 0.298 \AA^{-1}

8.2 Resolution estimates [i](#)

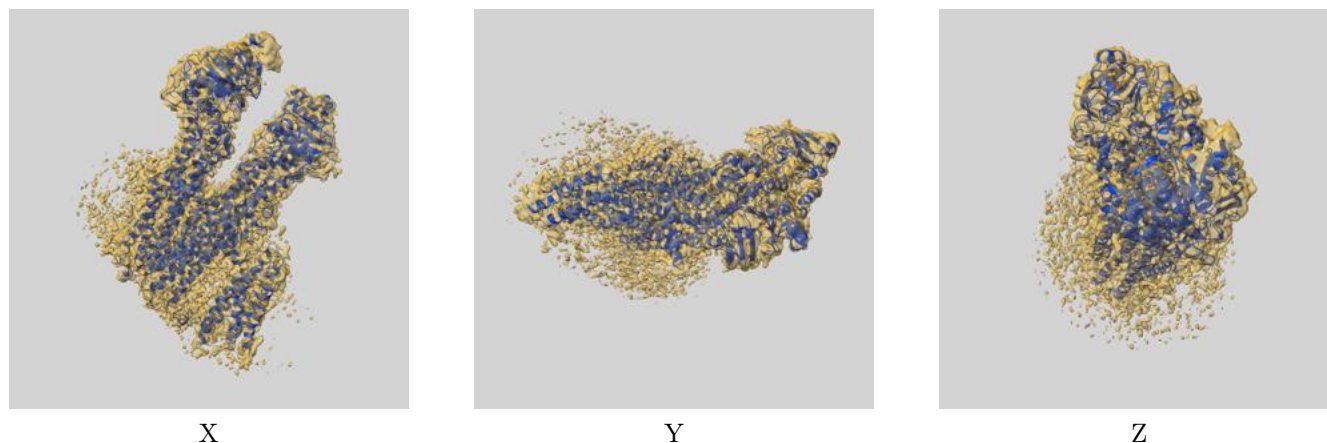
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.36	-	-
Author-provided FSC curve	3.36	3.78	3.40
Unmasked-calculated*	3.85	6.44	3.88

*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 3.85 differs from the reported value 3.36 by more than 10 %

9 Map-model fit [i](#)

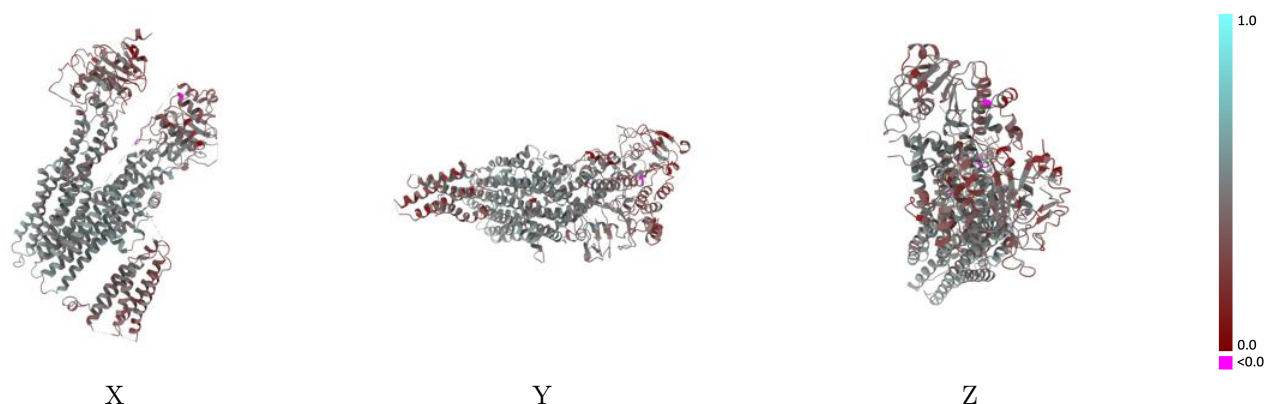
This section contains information regarding the fit between EMDB map EMD-63059 and PDB model 9LGA. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



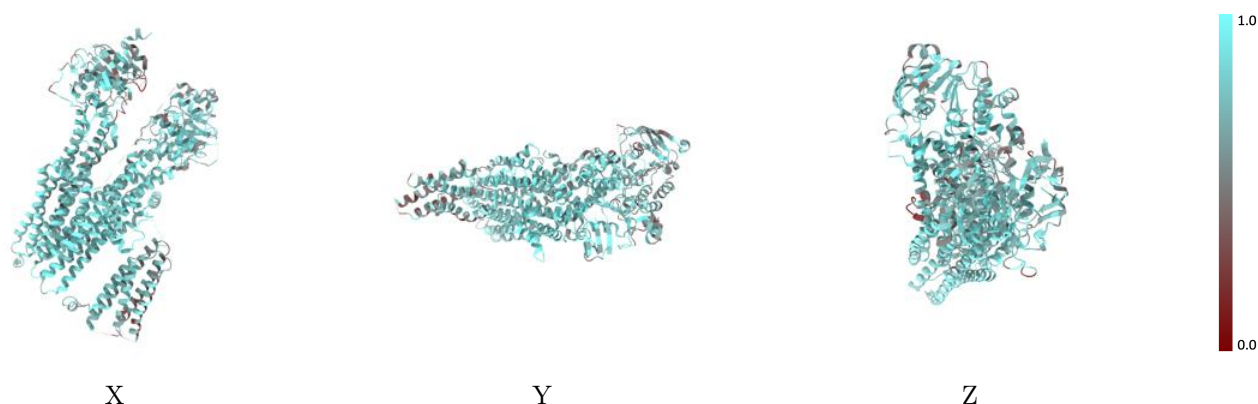
The images above show the 3D surface view of the map at the recommended contour level 0.42 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



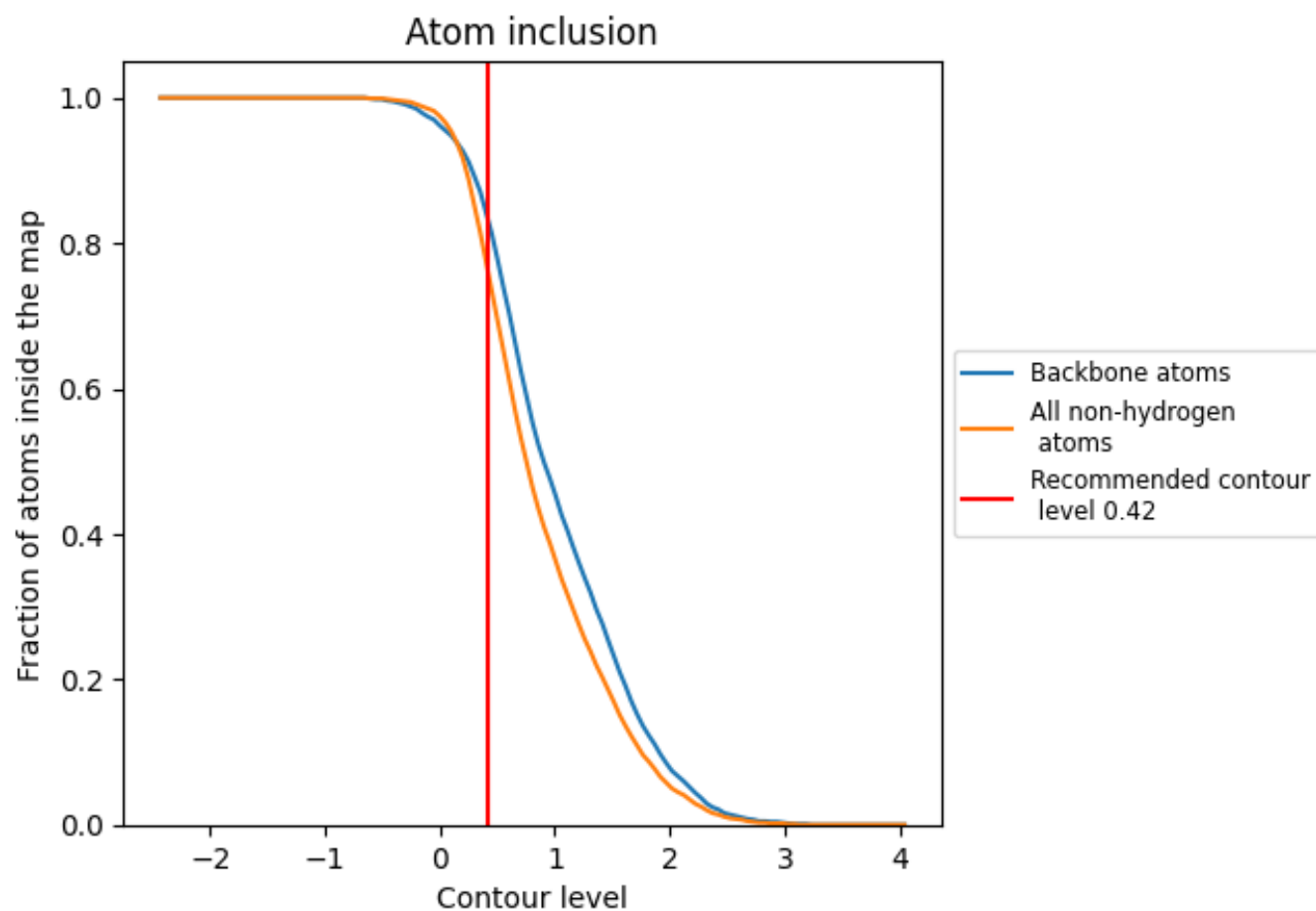
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.42).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 76% 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 (0.42) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.7610	<div><div></div></div> 0.4310
A	<div><div></div></div> 0.7610	<div><div></div></div> 0.4310

