



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:12 PM UTC

PDB ID : 8GHA / pdb_00008gha
EMDB ID : EMD-40029
Title : Hir3 Arm/Tail, Hir2 WD40, C-terminal Hpc2
Authors : Kim, H.J.; Murakami, K.
Deposited on : 2023-03-09
Resolution : 6.80 Å(reported)
Based on initial model : .

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
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) : 2.49

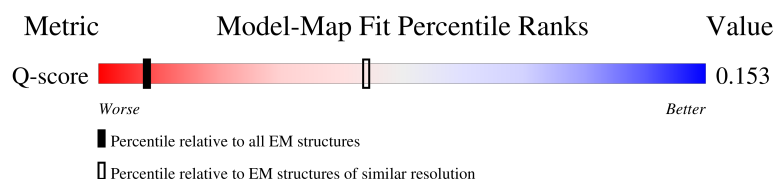
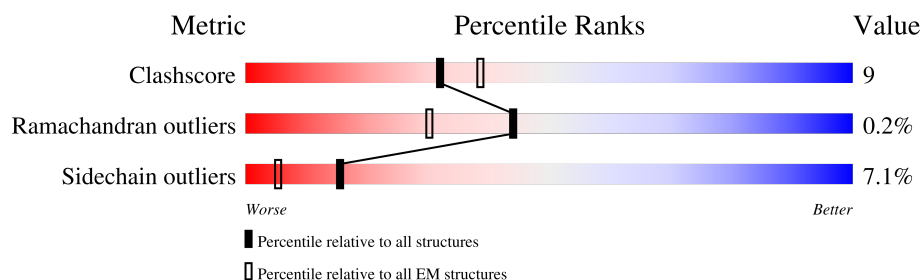
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.80 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	503 (6.30 - 7.30)

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	E	625	
2	D	1648	
3	B	875	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9783 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 Histone promoter control protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	126	Total	C	N	O	S	0	0
			1012	651	162	198	1		

- Molecule 2 is a protein called Histone transcription regulator 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	705	Total	C	N	O	S	0	0
			5762	3724	946	1068	24		

- Molecule 3 is a protein called Protein HIR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	381	Total	C	N	O	S	0	0
			3009	1921	505	570	13		



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	639629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.051	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	217.6, 217.6, 217.6	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	E	0.22	0/1032	0.48	0/1397
2	D	0.22	0/5887	0.51	1/7948 (0.0%)
3	B	0.21	0/3070	0.48	0/4168
All	All	0.22	0/9989	0.50	1/13513 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1517	ASP	N-CA-C	5.04	116.78	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1012	0	1019	15	0
2	D	5762	0	5786	94	0
3	B	3009	0	3053	69	0
All	All	9783	0	9858	169	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 (169) 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)
3:B:215:HIS:H	3:B:268:ARG:HH21	1.38	0.70
2:D:1452:LYS:O	2:D:1456:TYR:HB2	1.97	0.64
3:B:71:ILE:HA	3:B:85:SER:HA	1.80	0.63
2:D:1182:LYS:NZ	2:D:1189:ASP:OD2	2.31	0.62
2:D:956:GLN:NE2	2:D:960:CYS:SG	2.71	0.61
2:D:1189:ASP:N	2:D:1189:ASP:OD1	2.31	0.61
2:D:1281:SER:O	2:D:1285:ASN:ND2	2.33	0.61
2:D:1539:GLN:O	2:D:1543:VAL:HB	2.01	0.60
3:B:95:TRP:HA	3:B:109:MET:HG2	1.83	0.60
3:B:267:CYS:HA	3:B:297:GLY:HA2	1.84	0.60
2:D:1362:GLN:OE1	2:D:1387:ARG:NH2	2.35	0.59
2:D:952:LEU:HA	2:D:955:LYS:HE2	1.85	0.59
3:B:65:GLN:NE2	3:B:69:GLY:O	2.35	0.59
2:D:1270:LYS:HD2	2:D:1278:LEU:HD21	1.85	0.58
3:B:271:VAL:HG23	3:B:294:ALA:HB3	1.86	0.58
1:E:499:LYS:NZ	1:E:573:ASP:O	2.37	0.58
2:D:1304:LYS:HG2	2:D:1308:GLN:HE22	1.69	0.58
2:D:940:LYS:O	2:D:944:GLN:NE2	2.37	0.57
3:B:187:SER:HA	3:B:206:THR:HA	1.85	0.57
3:B:217:ARG:HB3	3:B:269:VAL:HG13	1.84	0.57
3:B:280:PRO:HA	3:B:287:SER:HA	1.85	0.57
2:D:1430:ILE:HG12	2:D:1440:VAL:HG22	1.85	0.57
2:D:1356:ASN:HA	2:D:1359:PHE:HB2	1.86	0.57
3:B:192:GLN:NE2	3:B:376:PRO:O	2.33	0.57
3:B:44:ASP:HB3	3:B:49:ARG:HB2	1.87	0.56
1:E:473:VAL:HB	3:B:315:PHE:HB2	1.88	0.56
2:D:1110:ASP:N	2:D:1110:ASP:OD1	2.39	0.55
3:B:2:ARG:HB2	3:B:350:ALA:HB3	1.87	0.55
2:D:949:ASP:N	2:D:949:ASP:OD1	2.39	0.55
2:D:1114:ARG:HA	2:D:1117:LYS:HD2	1.89	0.55
2:D:928:ASP:OD1	2:D:928:ASP:N	2.40	0.55
2:D:1180:TYR:O	2:D:1185:ARG:NH2	2.39	0.55
1:E:578:ASP:OD1	1:E:578:ASP:N	2.40	0.54
3:B:225:ASP:N	3:B:225:ASP:OD1	2.39	0.54
3:B:247:LEU:HD13	3:B:253:TYR:HB3	1.88	0.54
2:D:1059:THR:HA	2:D:1177:SER:HB2	1.89	0.54
2:D:1520:TYR:HA	2:D:1524:ILE:HD12	1.90	0.54
2:D:1188:ASP:N	2:D:1188:ASP:OD1	2.39	0.54
1:E:471:GLY:O	3:B:310:ARG:NH2	2.36	0.53
2:D:955:LYS:HA	2:D:966:ILE:HD12	1.90	0.53
3:B:183:THR:HG1	3:B:187:SER:HG	1.54	0.53
1:E:500:ARG:NH1	2:D:1252:GLU:OE1	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:439:ILE:HA	1:E:454:ILE:HG12	1.92	0.52
3:B:45:THR:HG21	3:B:55:LEU:HD22	1.91	0.52
2:D:1269:ILE:O	2:D:1273:ASP:N	2.43	0.52
2:D:969:ASP:N	2:D:969:ASP:OD1	2.43	0.51
3:B:5:LYS:HE3	3:B:345:THR:HG21	1.93	0.51
3:B:328:MET:HA	3:B:339:ALA:HA	1.91	0.51
2:D:939:GLU:OE1	2:D:961:ARG:NH1	2.41	0.51
2:D:1128:GLU:HA	2:D:1131:ILE:HD12	1.92	0.50
3:B:192:GLN:HB2	3:B:202:ILE:HD13	1.93	0.50
3:B:229:VAL:N	3:B:245:ALA:O	2.39	0.50
2:D:1188:ASP:HA	2:D:1191:LYS:HD2	1.93	0.50
2:D:1250:ASN:O	2:D:1254:SER:OG	2.30	0.50
1:E:587:ARG:HD3	2:D:1243:ILE:HG21	1.92	0.50
2:D:1357:GLN:O	2:D:1360:GLN:NE2	2.44	0.50
2:D:912:GLU:O	2:D:916:SER:OG	2.27	0.50
3:B:219:SER:H	3:B:270:LEU:HD23	1.76	0.50
2:D:1389:LEU:HD13	2:D:1408:ILE:HG13	1.92	0.50
2:D:1058:HIS:O	2:D:1063:ALA:N	2.44	0.50
3:B:228:PRO:HG3	3:B:272:TYR:HE1	1.76	0.50
3:B:229:VAL:HB	3:B:245:ALA:HB3	1.94	0.50
3:B:295:THR:OG1	3:B:306:TRP:NE1	2.36	0.49
3:B:16:ASN:HA	3:B:326:ASN:HD22	1.77	0.49
2:D:1087:SER:O	2:D:1091:SER:OG	2.27	0.49
2:D:1304:LYS:O	2:D:1308:GLN:NE2	2.45	0.49
3:B:15:VAL:O	3:B:326:ASN:ND2	2.45	0.49
2:D:1368:ASN:ND2	2:D:1370:GLU:OE2	2.46	0.49
2:D:1187:ILE:HG22	2:D:1191:LYS:HE3	1.95	0.49
3:B:325:ILE:HD13	3:B:341:SER:HB3	1.94	0.49
3:B:137:VAL:HB	3:B:146:LEU:HB2	1.94	0.48
3:B:7:PRO:HA	3:B:345:THR:HA	1.95	0.48
3:B:81:LEU:HB3	3:B:92:TYR:HB2	1.94	0.48
2:D:1127:PHE:HA	2:D:1130:TRP:HD1	1.78	0.48
3:B:326:ASN:N	3:B:326:ASN:OD1	2.46	0.48
2:D:1473:ASP:O	2:D:1477:THR:OG1	2.32	0.48
2:D:1198:ASP:O	2:D:1202:SER:OG	2.32	0.48
2:D:963:HIS:NE2	2:D:978:THR:O	2.37	0.47
2:D:1150:ASP:OD1	2:D:1150:ASP:N	2.42	0.47
2:D:1218:SER:HA	2:D:1244:THR:HA	1.96	0.47
2:D:1260:ASN:O	2:D:1264:SER:OG	2.28	0.47
2:D:1313:ALA:O	2:D:1317:SER:OG	2.32	0.47
3:B:278:GLU:N	3:B:358:VAL:O	2.46	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1399:LYS:HA	2:D:1399:LYS:HD2	1.72	0.47
1:E:444:GLU:HA	1:E:450:PRO:HB3	1.96	0.46
3:B:149:ARG:HB2	3:B:156:LEU:HD21	1.97	0.46
2:D:968:SER:HB3	2:D:971:PHE:HB2	1.98	0.46
2:D:1444:LYS:HG3	2:D:1448:GLU:HB3	1.97	0.46
3:B:146:LEU:HD22	3:B:155:LYS:HE3	1.98	0.46
3:B:20:ALA:HA	3:B:25:ILE:HA	1.98	0.46
2:D:1517:ASP:C	2:D:1519:SER:H	2.24	0.46
3:B:271:VAL:HB	3:B:330:TRP:CD1	2.50	0.46
2:D:1040:SER:O	2:D:1044:ASN:ND2	2.49	0.45
2:D:1363:GLU:HA	2:D:1366:TRP:CD1	2.51	0.45
1:E:594:PHE:HD1	3:B:262:PRO:HG3	1.80	0.45
2:D:946:ILE:HA	2:D:994:TYR:HE2	1.81	0.45
2:D:1143:ASP:HA	2:D:1147:TRP:HD1	1.81	0.45
2:D:1397:LYS:O	2:D:1397:LYS:NZ	2.45	0.45
3:B:223:GLN:O	3:B:372:ASN:ND2	2.47	0.45
3:B:281:ASN:N	3:B:286:THR:O	2.48	0.45
3:B:310:ARG:HH21	3:B:312:LYS:HB2	1.81	0.45
2:D:1247:SER:OG	2:D:1250:ASN:ND2	2.50	0.45
3:B:22:GLY:O	3:B:39:GLN:NE2	2.49	0.45
3:B:210:GLN:HB3	3:B:231:ASN:HB3	1.99	0.45
2:D:1405:ARG:NH1	2:D:1425:GLU:O	2.42	0.45
3:B:171:ILE:N	3:B:180:THR:O	2.46	0.45
2:D:1006:TYR:HE2	2:D:1132:LEU:HD21	1.82	0.45
3:B:215:HIS:O	3:B:268:ARG:NE	2.50	0.45
2:D:925:HIS:HA	2:D:976:HIS:HA	1.99	0.44
2:D:1298:ASN:O	2:D:1302:VAL:N	2.42	0.44
1:E:437:PRO:HB3	1:E:456:VAL:HG13	1.98	0.44
2:D:1248:ASP:HA	2:D:1251:ILE:HD12	1.99	0.44
3:B:80:THR:HA	3:B:93:SER:HA	2.00	0.44
2:D:1072:ASN:N	2:D:1076:GLN:OE1	2.51	0.44
3:B:75:THR:OG1	3:B:76:GLY:N	2.51	0.44
3:B:360:LEU:HD13	3:B:364:GLU:HG2	2.00	0.44
2:D:959:TRP:NE1	2:D:973:PRO:HB3	2.33	0.44
3:B:37:TRP:HZ3	3:B:55:LEU:HG	1.83	0.44
3:B:230:ILE:HA	3:B:244:THR:HA	2.00	0.43
1:E:580:GLU:OE2	2:D:1250:ASN:ND2	2.51	0.43
3:B:13:GLU:OE2	3:B:33:HIS:ND1	2.51	0.43
3:B:301:GLY:HA3	3:B:321:SER:H	1.83	0.43
2:D:1159:ASP:OD1	2:D:1242:LYS:NZ	2.45	0.43
2:D:1427:ASP:OD1	2:D:1464:TYR:OH	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:194:ASN:ND2	3:B:196:THR:OG1	2.48	0.43
2:D:1349:LEU:HD12	2:D:1368:ASN:HA	2.01	0.43
3:B:218:ILE:HG23	3:B:270:LEU:HD22	2.00	0.43
3:B:290:TYR:OH	3:B:356:LEU:O	2.27	0.43
2:D:1047:LEU:HA	2:D:1170:LEU:HD13	2.00	0.42
3:B:166:LYS:O	3:B:184:SER:N	2.51	0.42
1:E:466:TYR:OH	3:B:307:ASN:ND2	2.50	0.42
2:D:1074:GLU:H	2:D:1074:GLU:HG3	1.59	0.42
2:D:1028:PRO:HG2	2:D:1118:ASN:HB3	2.01	0.42
2:D:1373:ALA:HB3	2:D:1376:TYR:HD2	1.84	0.42
3:B:82:TYR:HA	3:B:91:GLY:HA2	2.01	0.42
3:B:331:SER:N	3:B:336:THR:O	2.45	0.42
2:D:1515:LEU:HD23	2:D:1515:LEU:HA	1.91	0.42
2:D:1550:PRO:HD2	2:D:1553:ILE:HD12	2.01	0.42
2:D:1299:CYS:HA	2:D:1302:VAL:HB	2.01	0.42
2:D:1517:ASP:HA	2:D:1520:TYR:CE2	2.55	0.41
2:D:948:ASN:HA	2:D:951:PHE:HB3	2.02	0.41
2:D:1035:ILE:HG23	2:D:1038:ARG:HH22	1.84	0.41
2:D:1148:THR:HG21	2:D:1151:LYS:HE3	2.01	0.41
2:D:922:GLY:N	2:D:976:HIS:HD1	2.18	0.41
2:D:1288:LYS:HA	2:D:1288:LYS:HD2	1.88	0.41
2:D:1334:CYS:O	2:D:1338:VAL:HB	2.20	0.41
3:B:188:ILE:N	3:B:205:LEU:O	2.51	0.41
2:D:947:ASN:O	2:D:950:SER:OG	2.35	0.41
2:D:989:LEU:O	2:D:993:THR:OG1	2.32	0.41
2:D:942:LEU:HD22	2:D:950:SER:HB2	2.02	0.41
2:D:1038:ARG:HB2	3:B:213:PRO:HB2	2.03	0.41
2:D:1361:GLU:OE1	2:D:1387:ARG:NE	2.49	0.41
1:E:584:GLU:HG3	1:E:587:ARG:NH2	2.34	0.41
2:D:915:TRP:O	2:D:919:THR:OG1	2.31	0.41
3:B:88:ARG:HG2	3:B:116:GLU:HG3	2.03	0.41
2:D:956:GLN:HE22	2:D:959:TRP:HD1	1.69	0.41
2:D:1350:THR:O	2:D:1353:SER:OG	2.30	0.41
2:D:1584:LEU:HD13	2:D:1643:LEU:HD13	2.03	0.41
1:E:439:ILE:HD12	1:E:484:LYS:HD2	2.03	0.40
1:E:469:GLU:HG2	3:B:310:ARG:HG2	2.03	0.40
3:B:14:GLN:H	3:B:30:SER:HB3	1.86	0.40
3:B:307:ASN:HB3	3:B:310:ARG:HB2	2.03	0.40
2:D:983:MET:HE2	2:D:983:MET:HB3	1.80	0.40
3:B:75:THR:HG23	3:B:82:TYR:HB2	2.02	0.40
2:D:1433:LYS:HA	2:D:1479:LEU:HD13	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1510:LYS:O	2:D:1514:GLN:HA	2.22	0.40
3:B:145:ILE:HD12	3:B:159:ILE:HB	2.03	0.40
3:B:246:LEU:HD12	3:B:257:LYS:HB2	2.03	0.40
2:D:1346:ASN:O	2:D:1350:THR:OG1	2.29	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	E	122/625 (20%)	118 (97%)	4 (3%)	0	100	100
2	D	701/1648 (42%)	681 (97%)	18 (3%)	2 (0%)	36	72
3	B	379/875 (43%)	365 (96%)	14 (4%)	0	100	100
All	All	1202/3148 (38%)	1164 (97%)	36 (3%)	2 (0%)	44	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	1518	LYS
2	D	1445	PRO

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	E	114/557 (20%)	112 (98%)	2 (2%)	51	68
2	D	642/1528 (42%)	583 (91%)	59 (9%)	8	27
3	B	343/790 (43%)	326 (95%)	17 (5%)	22	43
All	All	1099/2875 (38%)	1021 (93%)	78 (7%)	15	35

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	578	ASP
1	E	591	LYS
2	D	905	GLU
2	D	916	SER
2	D	918	HIS
2	D	927	CYS
2	D	936	ASP
2	D	944	GLN
2	D	949	ASP
2	D	952	LEU
2	D	969	ASP
2	D	976	HIS
2	D	981	VAL
2	D	998	LEU
2	D	1015	LYS
2	D	1016	GLN
2	D	1017	ILE
2	D	1037	SER
2	D	1052	THR
2	D	1074	GLU
2	D	1091	SER
2	D	1110	ASP
2	D	1125	ASN
2	D	1148	THR
2	D	1186	THR
2	D	1188	ASP
2	D	1189	ASP
2	D	1202	SER
2	D	1214	LYS
2	D	1229	LEU
2	D	1248	ASP
2	D	1249	PHE
2	D	1254	SER
2	D	1264	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	1275	VAL
2	D	1284	TYR
2	D	1304	LYS
2	D	1308	GLN
2	D	1332	ASN
2	D	1338	VAL
2	D	1342	VAL
2	D	1345	VAL
2	D	1362	GLN
2	D	1386	ILE
2	D	1387	ARG
2	D	1397	LYS
2	D	1398	LYS
2	D	1399	LYS
2	D	1403	ARG
2	D	1429	LEU
2	D	1442	ILE
2	D	1444	LYS
2	D	1446	ASP
2	D	1449	ARG
2	D	1471	ILE
2	D	1477	THR
2	D	1480	VAL
2	D	1492	VAL
2	D	1516	GLN
2	D	1543	VAL
2	D	1559	LEU
3	B	18	LEU
3	B	25	ILE
3	B	54	ASP
3	B	70	ASP
3	B	74	ILE
3	B	86	GLU
3	B	140	SER
3	B	161	ILE
3	B	193	ILE
3	B	202	ILE
3	B	220	MET
3	B	241	THR
3	B	271	VAL
3	B	299	THR
3	B	326	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	B	371	VAL
3	B	378	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	476	ASN
2	D	948	ASN
2	D	953	GLN
2	D	970	ASN
2	D	1044	ASN
2	D	1250	ASN
2	D	1260	ASN
2	D	1475	ASN
2	D	1516	GLN
3	B	39	GLN
3	B	65	GLN

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 ⓘ

There are no chain breaks in this entry.

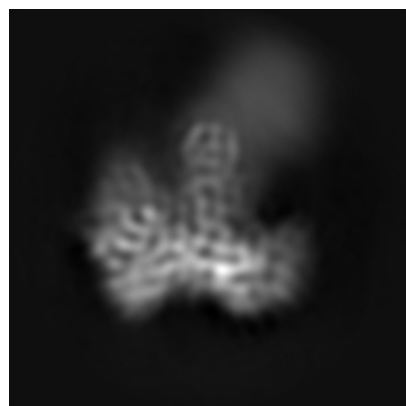
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40029. These allow visual inspection of the internal detail of the map and identification of artifacts.

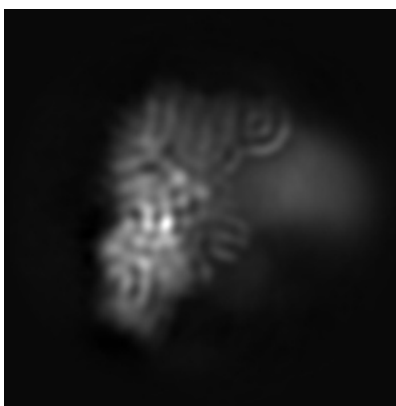
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

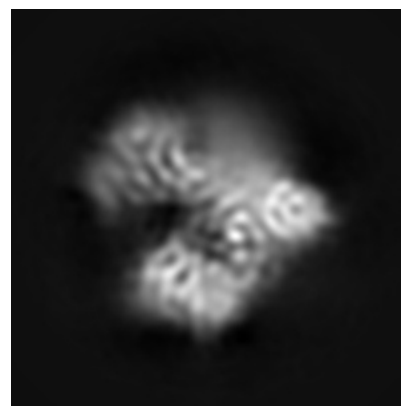
6.1.1 Primary map



X

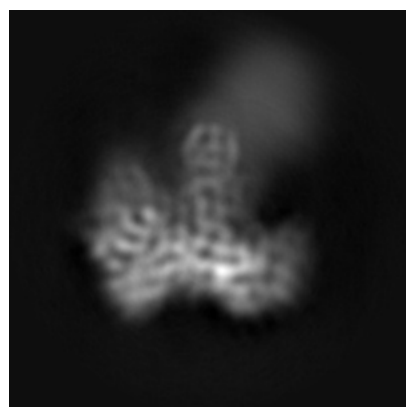


Y

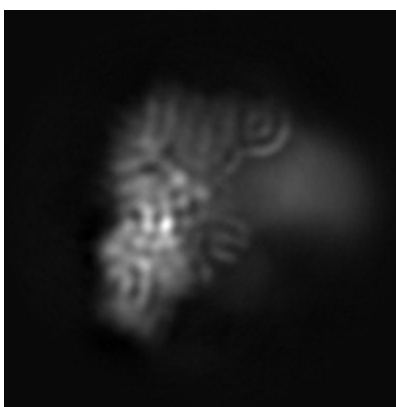


Z

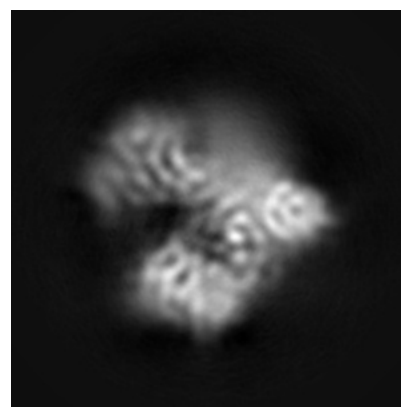
6.1.2 Raw map



X



Y

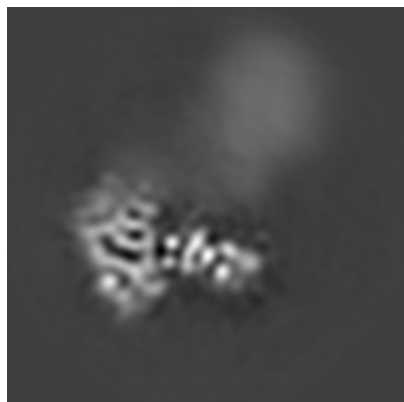


Z

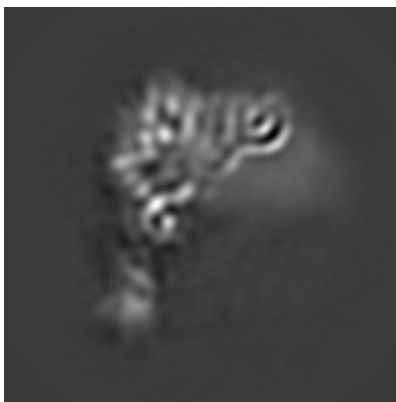
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

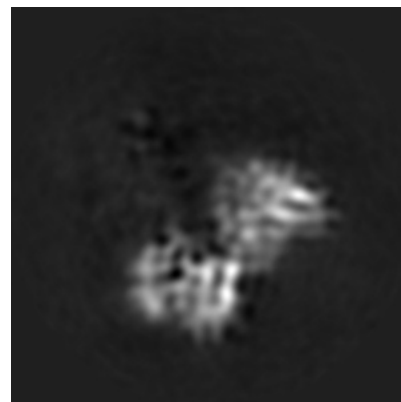
6.2.1 Primary map



X Index: 80

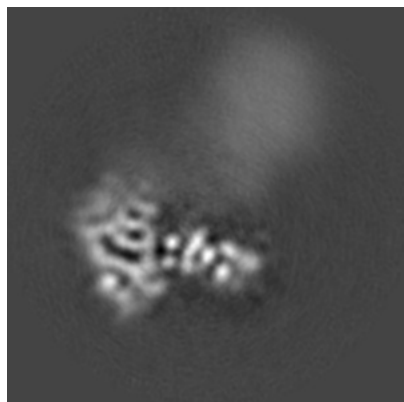


Y Index: 80

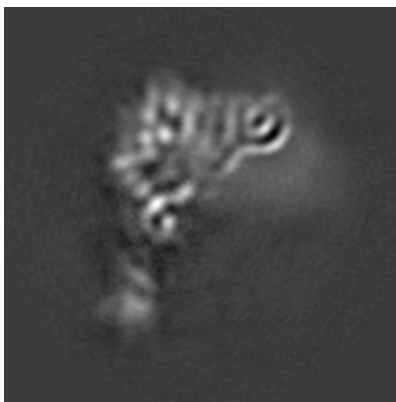


Z Index: 80

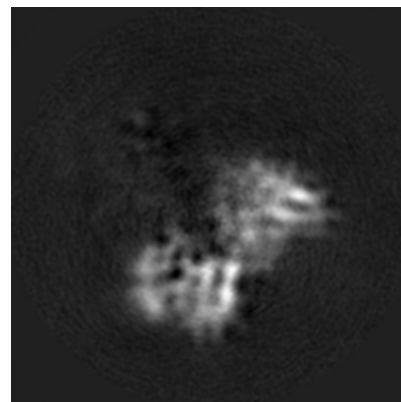
6.2.2 Raw map



X Index: 80



Y Index: 80

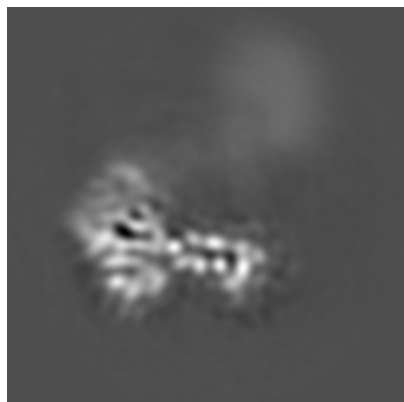


Z Index: 80

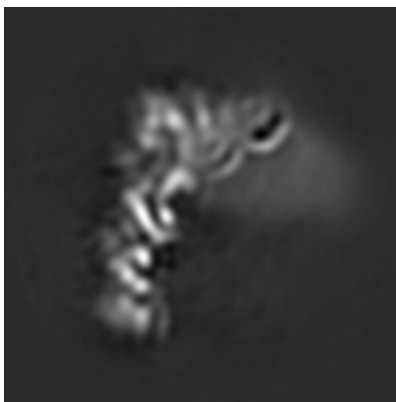
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 74

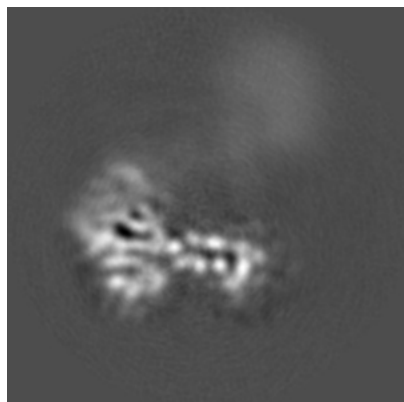


Y Index: 85

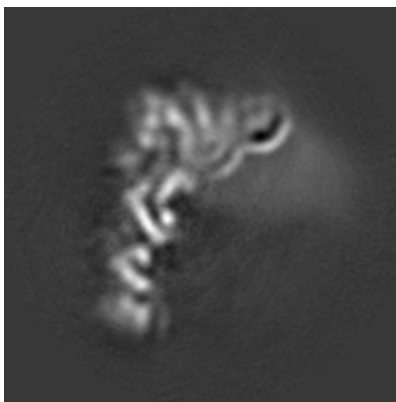


Z Index: 56

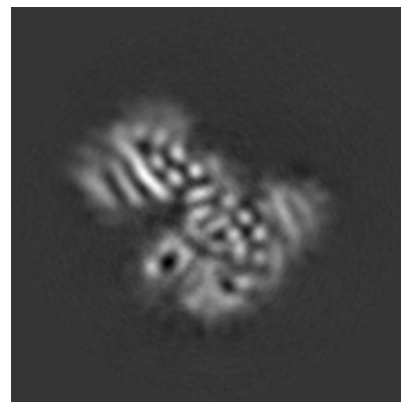
6.3.2 Raw map



X Index: 74



Y Index: 84

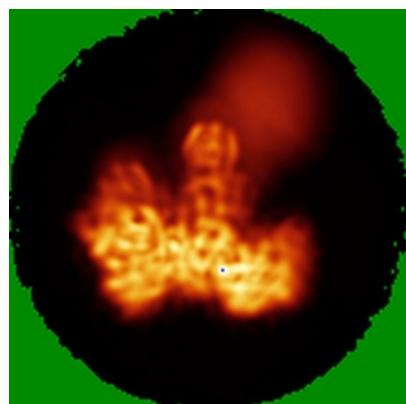


Z Index: 56

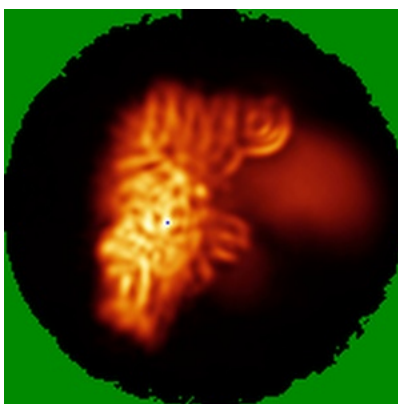
The images above show the largest variance slices of the map in three orthogonal directions.

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

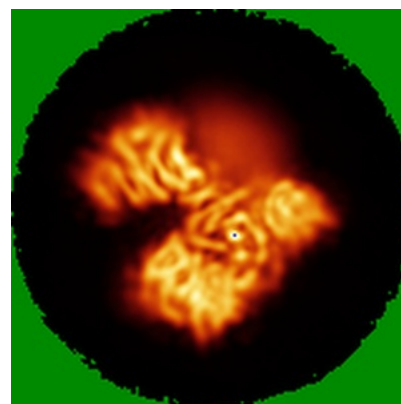
6.4.1 Primary map



X

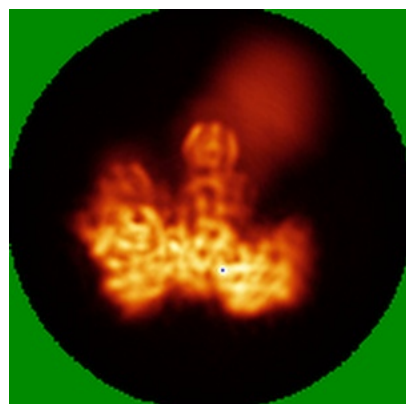


Y

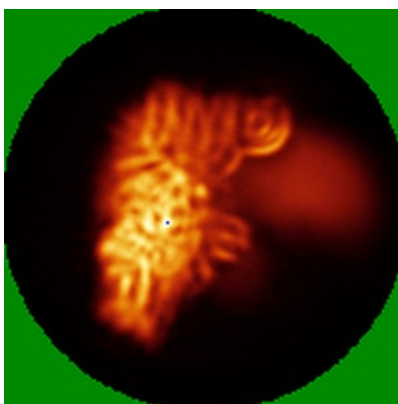


Z

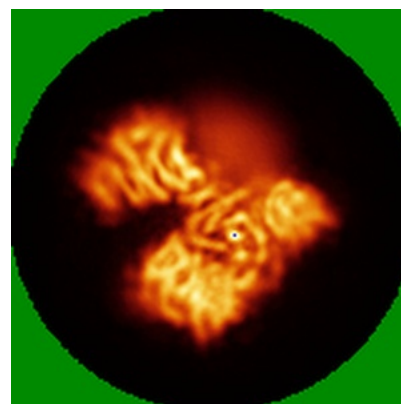
6.4.2 Raw map



X



Y

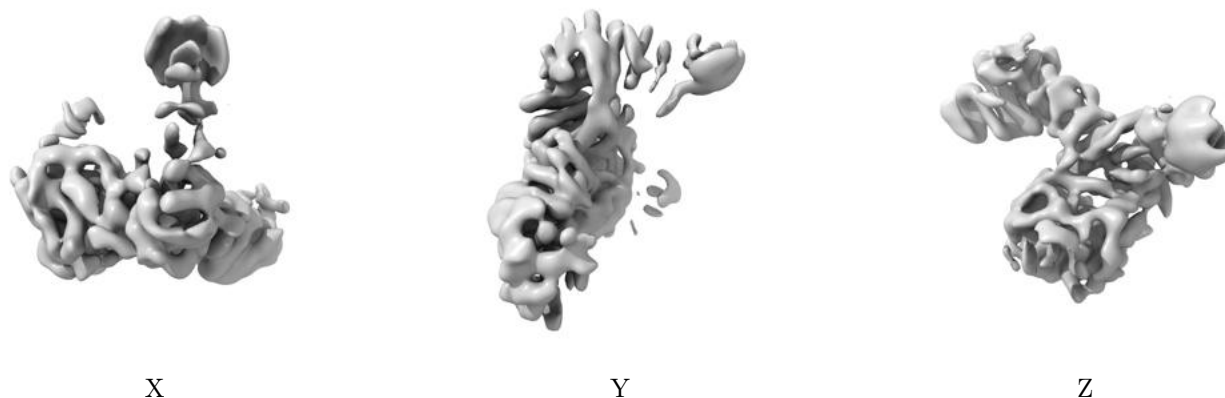


Z

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

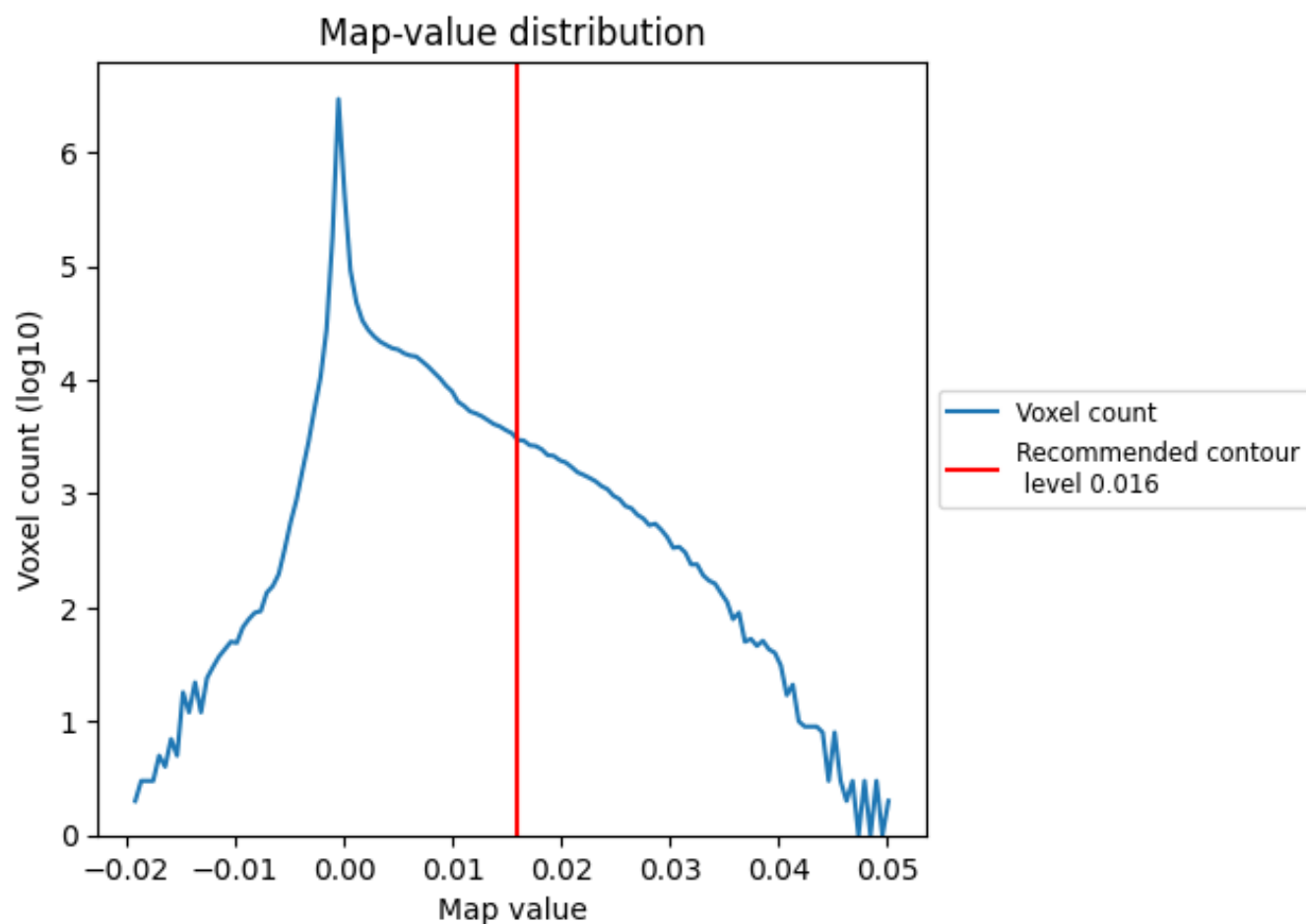
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

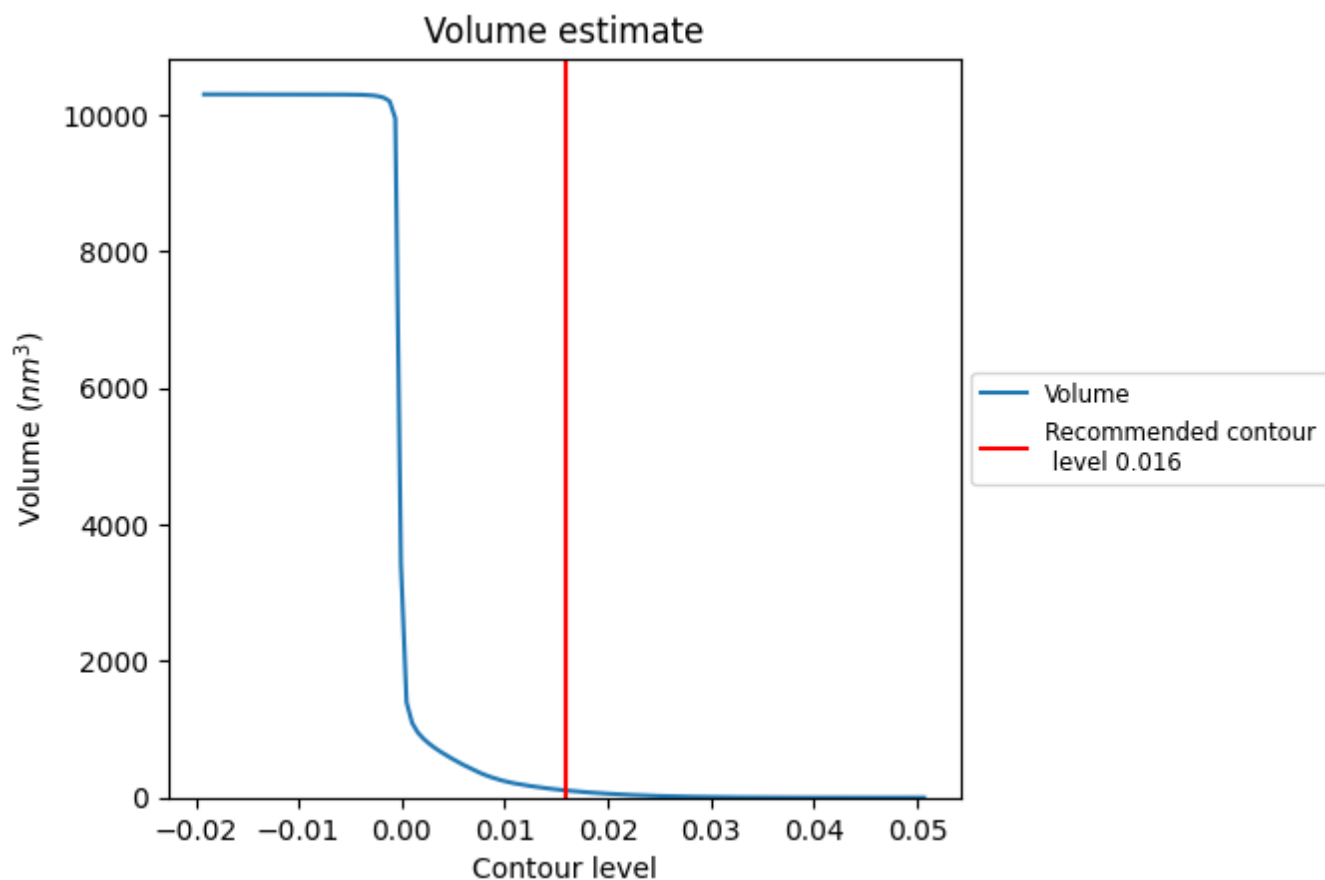
This section contains the results of statistical analysis of the map.

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.

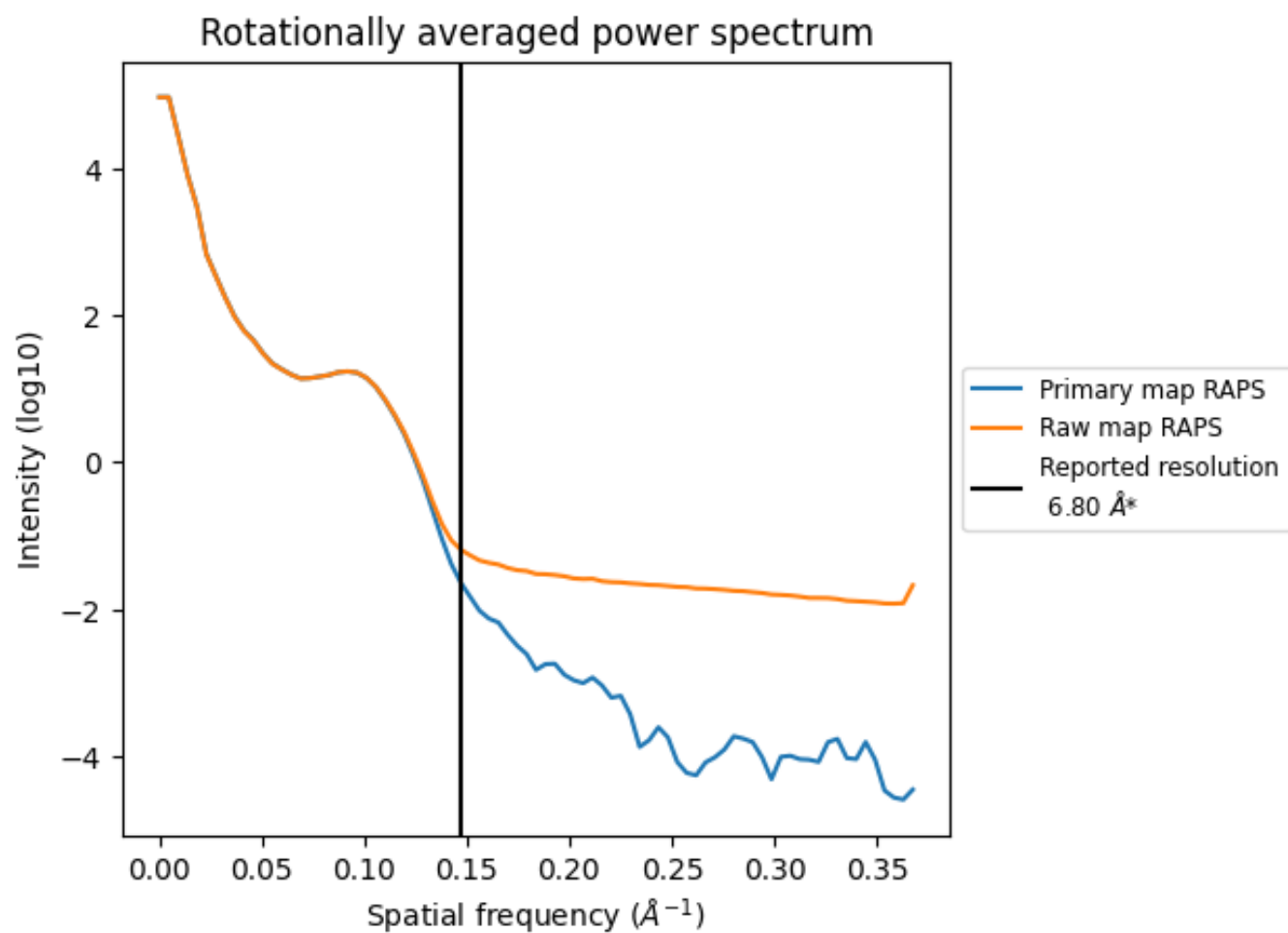
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 103 nm³; this corresponds to an approximate mass of 93 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](#)

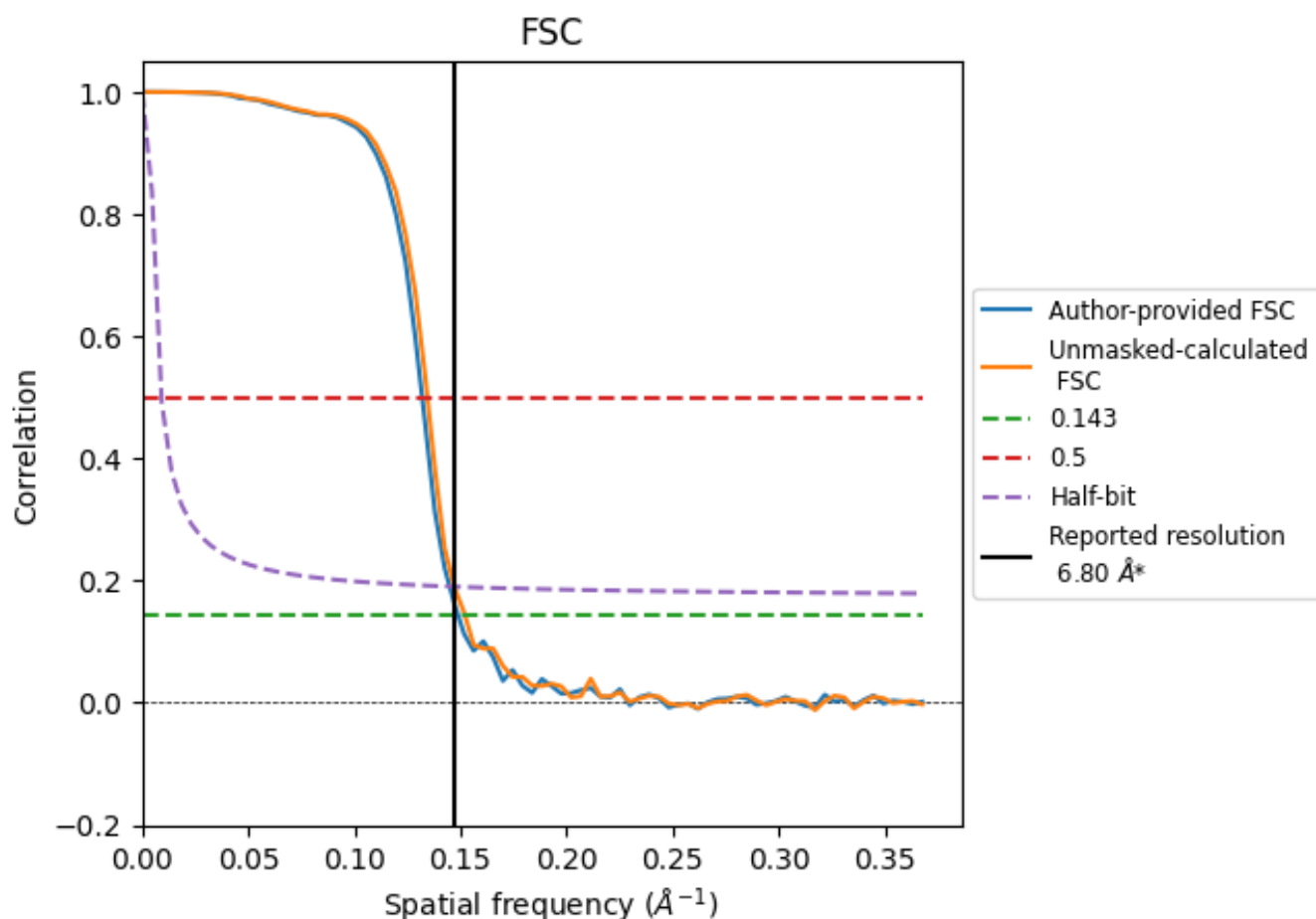


*Reported resolution corresponds to spatial frequency of 0.147 Å⁻¹

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 0.147 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.80	-	-
Author-provided FSC curve	6.72	7.58	6.90
Unmasked-calculated*	6.57	7.44	6.80

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

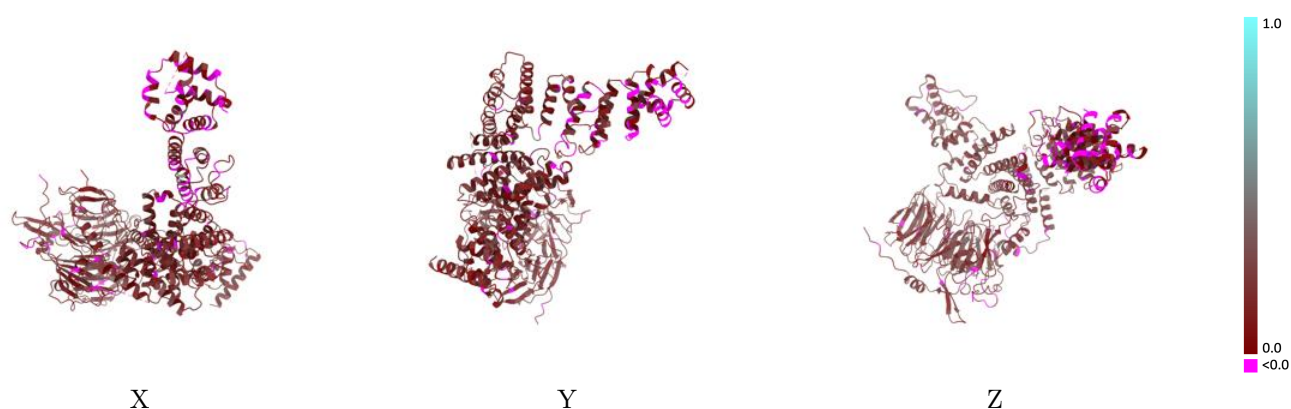
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40029 and PDB model 8GHA. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

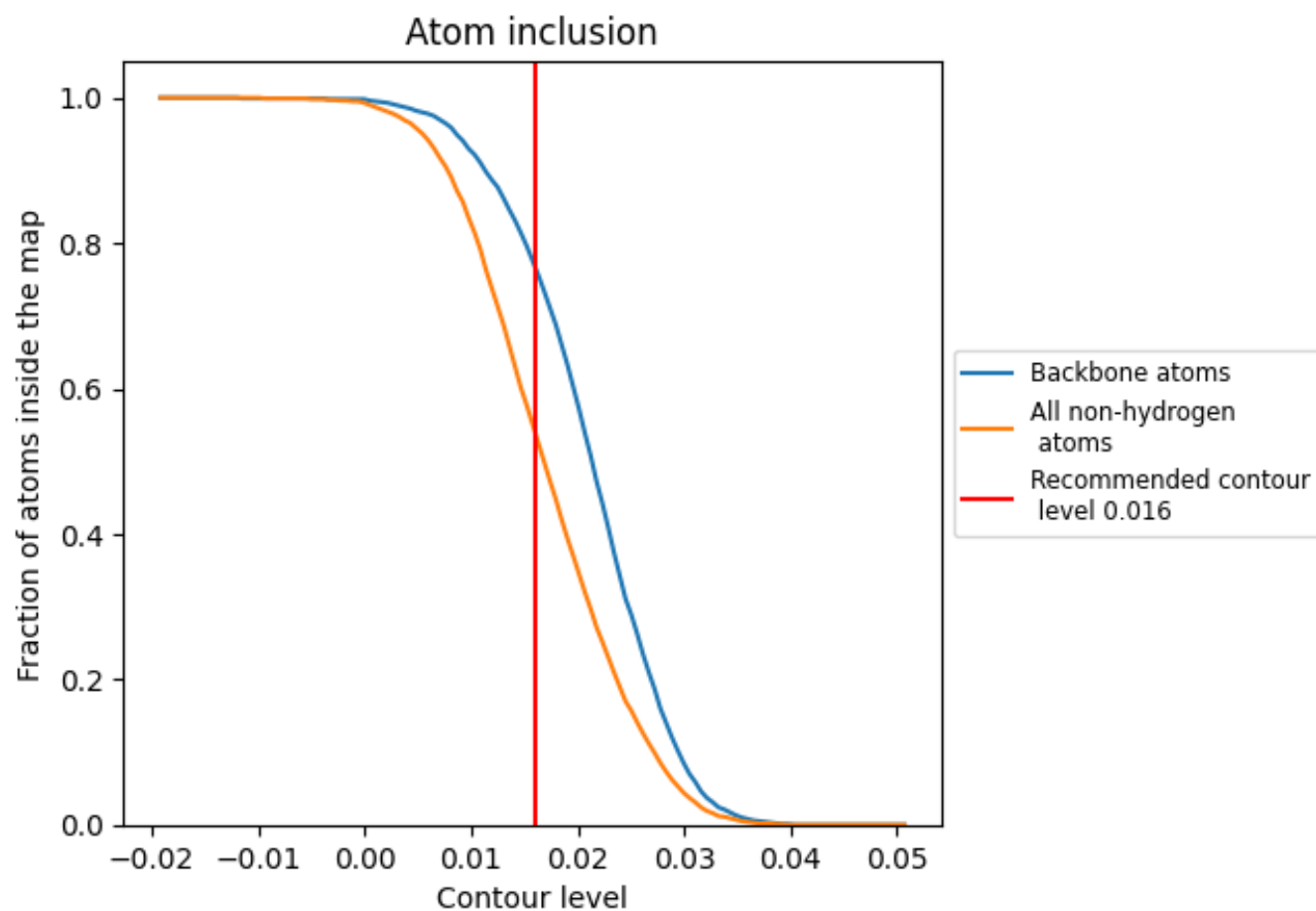


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 54% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5390	0.1530
B	0.6600	0.1810
D	0.4820	0.1410
E	0.5050	0.1420

