



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:06 AM UTC

PDB ID : 9CZ1 / pdb_00009cz1
EMDB ID : EMD-46056
Title : Cryo-EM structure of a 'hat' portion of FtsH.HflK.HflC complex
Authors : Ghanbarpour, A.; Sauer, R.T.; Davis, J.H.
Deposited on : 2024-08-03
Resolution : 3.50 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

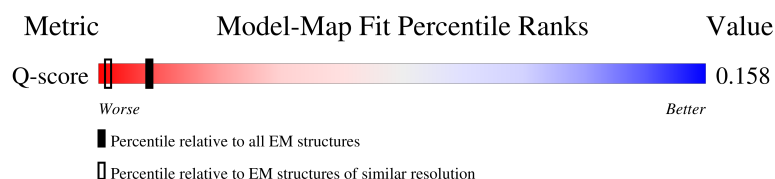
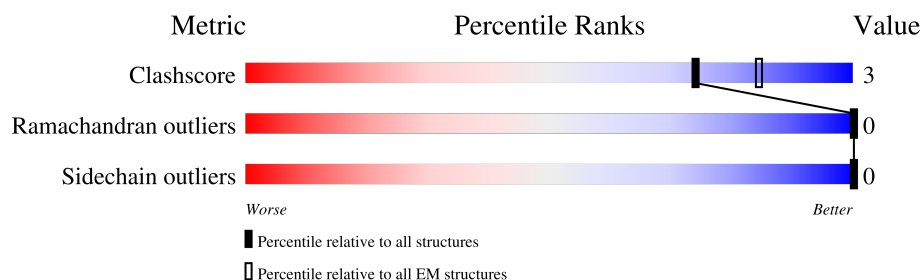
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 Å.

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



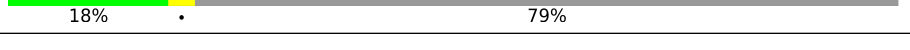
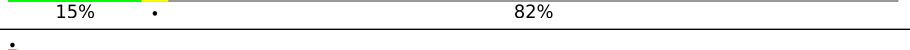
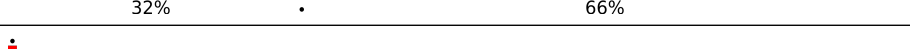
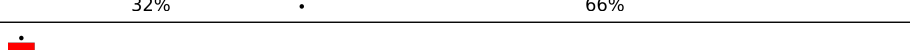
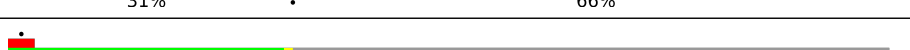
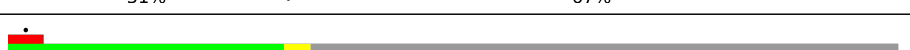
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	XA	419	 25% 74%
1	XC	419	 24% 74%
1	XE	419	 24% 74%
1	XG	419	 24% 74%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	XI	419	
1	XK	419	
1	XM	419	
1	XO	419	
1	XQ	419	
1	XS	419	
1	XU	419	
1	XW	419	
2	XB	334	
2	XD	334	
2	XF	334	
2	XH	334	
2	XJ	334	
2	XL	334	
2	XN	334	
2	XP	334	
2	XR	334	
2	XT	334	
2	XV	334	
2	XX	334	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 40591 atoms, of which 20108 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 Modulator of FtsH protease HflK.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	XA	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XC	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XE	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XG	109	Total	C	H	N	O	S	0	0
			1745	542	879	156	166	2		
1	XI	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XK	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XM	110	Total	C	H	N	O	S	0	0
			1760	547	885	157	169	2		
1	XO	109	Total	C	H	N	O	S	0	0
			1743	542	877	156	166	2		
1	XQ	109	Total	C	H	N	O	S	0	0
			1745	542	879	156	166	2		
1	XS	103	Total	C	H	N	O	S	0	0
			1655	512	834	149	158	2		
1	XU	90	Total	C	H	N	O	S	0	0
			1449	448	734	130	135	2		
1	XW	74	Total	C	H	N	O	S	0	0
			1212	374	623	105	108	2		

- Molecule 2 is a protein called Modulator of FtsH protease HflC.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	XB	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XD	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XF	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		

Continued on next page...

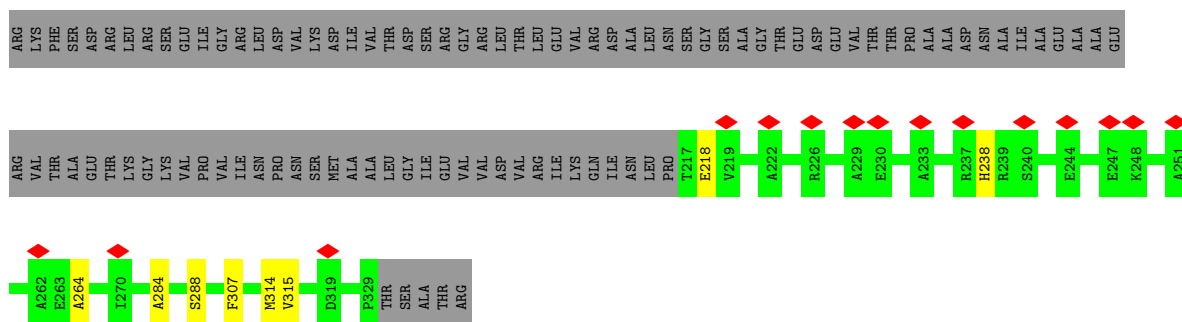
Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf	Trace
2	XH	110	Total	C	H	N	O	S	0	0
			1734	546	844	165	174	5		
2	XJ	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XL	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XN	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XP	113	Total	C	H	N	O	S	0	0
			1780	560	867	168	180	5		
2	XR	109	Total	C	H	N	O	S	0	0
			1724	543	840	164	172	5		
2	XT	101	Total	C	H	N	O	S	0	0
			1580	499	768	149	160	4		
2	XV	86	Total	C	H	N	O	S	0	0
			1339	430	649	118	138	4		
2	XX	105	Total	C	H	N	O	S	0	0
			1645	517	802	160	161	5		

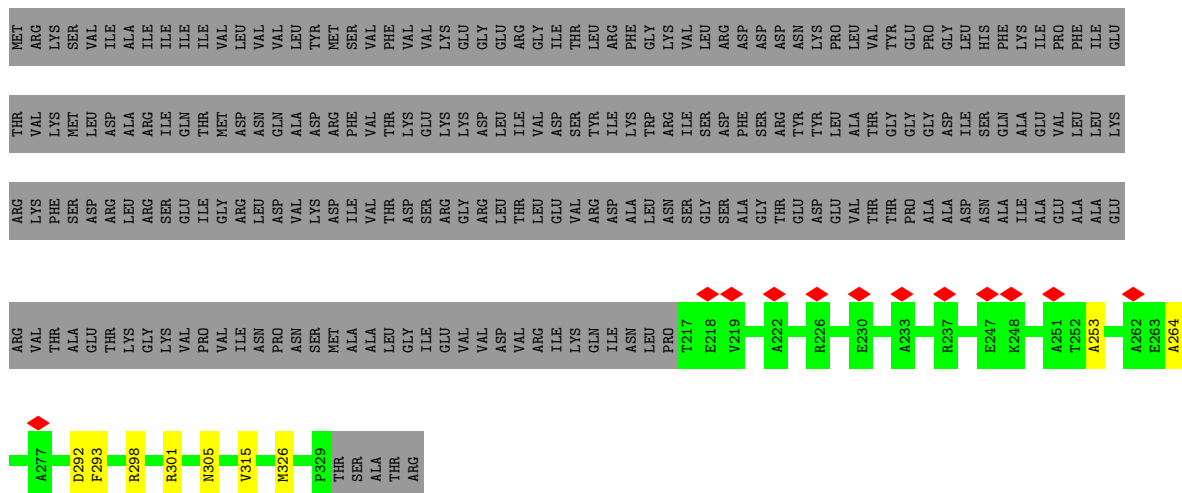


Chain XO: 24% 74%

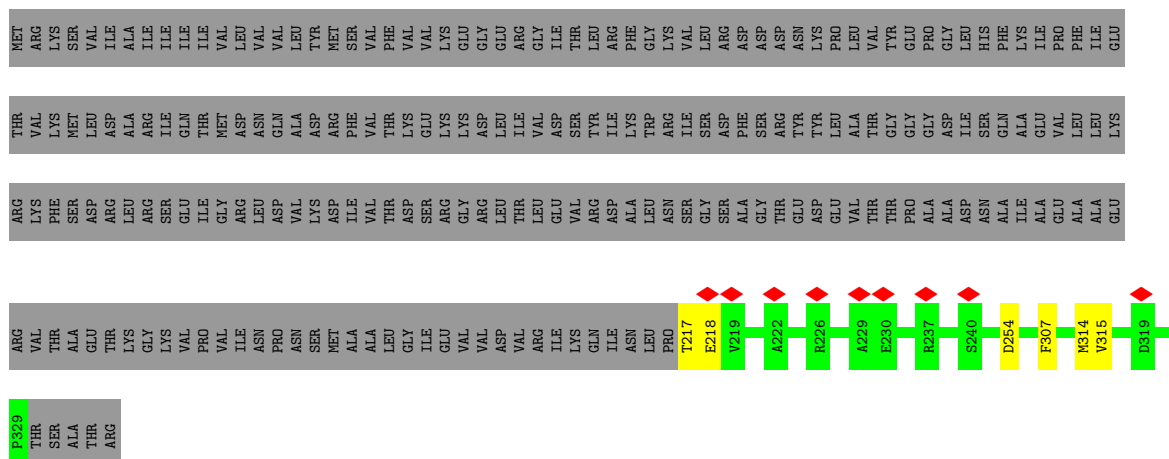




- Molecule 2: Modulator of FtsH protease HflC



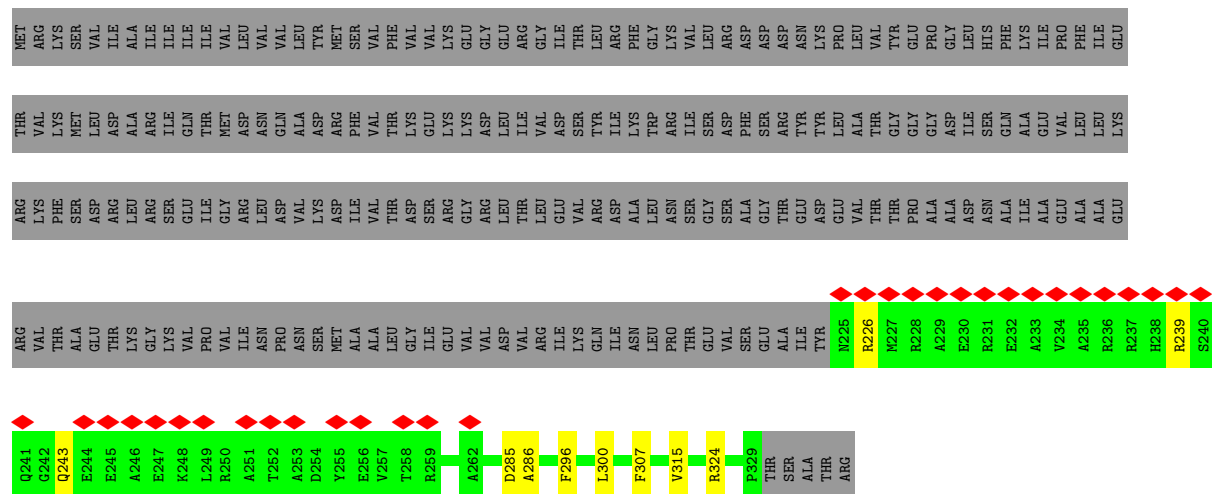
- Molecule 2: Modulator of FtsH protease HflC



- Molecule 2: Modulator of FtsH protease HflC



Chain XX: 9% 28% 69%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	184019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; Patch CTF estimation, cryoSPARC	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.14	Depositor
Minimum defocus (nm)	50	Depositor
Maximum defocus (nm)	1750	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.156	Depositor
Minimum map value	-0.459	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0991	Depositor
Map size ($\text{\AA}$)	588.6, 588.6, 588.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.635, 1.635, 1.635	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	XA	0.19	0/885	0.43	0/1193
1	XC	0.21	0/885	0.49	0/1193
1	XE	0.19	0/885	0.44	0/1193
1	XG	0.18	0/876	0.43	0/1181
1	XI	0.20	0/885	0.50	0/1193
1	XK	0.17	0/885	0.41	0/1193
1	XM	0.19	0/885	0.46	0/1193
1	XO	0.21	0/876	0.48	0/1181
1	XQ	0.19	0/876	0.45	0/1181
1	XS	0.19	0/830	0.49	0/1119
1	XU	0.21	0/723	0.48	0/974
1	XW	0.18	0/595	0.47	0/800
2	XB	0.16	0/928	0.39	0/1243
2	XD	0.17	0/928	0.44	0/1243
2	XF	0.16	0/928	0.39	0/1243
2	XH	0.15	0/905	0.37	0/1211
2	XJ	0.17	0/928	0.43	0/1243
2	XL	0.17	0/928	0.41	0/1243
2	XN	0.16	0/928	0.39	0/1243
2	XP	0.17	0/928	0.40	0/1243
2	XR	0.17	0/899	0.38	0/1203
2	XT	0.16	0/826	0.43	0/1106
2	XV	0.16	0/703	0.40	0/943
2	XX	0.21	0/857	0.48	0/1146
All	All	0.18	0/20772	0.43	0/27904

There are no bond length outliers.

There are no bond angle outliers.

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	XA	875	885	884	6	0
1	XC	875	885	884	8	0
1	XE	875	885	884	10	0
1	XG	866	879	878	8	0
1	XI	875	885	884	7	0
1	XK	875	885	884	11	0
1	XM	875	885	884	8	0
1	XO	866	877	878	8	0
1	XQ	866	879	878	14	0
1	XS	821	834	833	6	0
1	XU	715	734	736	8	0
1	XW	589	623	622	10	0
2	XB	913	867	866	5	0
2	XD	913	867	866	5	0
2	XF	913	867	866	8	0
2	XH	890	844	844	5	0
2	XJ	913	867	866	8	0
2	XL	913	867	866	9	0
2	XN	913	867	866	10	0
2	XP	913	867	866	6	0
2	XR	884	840	839	6	0
2	XT	812	768	767	5	0
2	XV	690	649	648	7	0
2	XX	843	802	802	8	0
All	All	20483	20108	20091	129	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 3.

All (129) 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:XO:335:LEU:O	1:XO:340:LYS:NZ	2.16	0.77
1:XM:276:GLN:OE1	1:XM:280:ASN:ND2	2.22	0.72
1:XA:335:LEU:O	1:XA:340:LYS:NZ	2.23	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XU:335:LEU:O	1:XU:340:LYS:NZ	2.27	0.68
1:XE:341:VAL:HG12	1:XE:343:VAL:HG13	1.76	0.67
1:XU:269:GLU:OE2	1:XU:273:ASN:ND2	2.28	0.67
1:XI:352:VAL:HG13	1:XI:354:PRO:HD3	1.77	0.66
1:XG:352:VAL:HG13	1:XG:354:PRO:HD3	1.77	0.66
2:XX:239:ARG:NH1	2:XX:243:GLN:OE1	2.29	0.66
1:XG:341:VAL:HG12	1:XG:343:VAL:HG23	1.79	0.65
2:XP:254:ASP:OD2	1:XQ:285:ARG:NH1	2.31	0.64
1:XS:341:VAL:HG21	2:XT:315:VAL:HG22	1.80	0.63
1:XO:352:VAL:HG13	1:XO:354:PRO:HD3	1.81	0.62
1:XE:342:LEU:HD11	2:XF:323:PHE:CE2	2.35	0.61
1:XM:341:VAL:HG12	1:XM:343:VAL:HG23	1.83	0.61
1:XK:274:GLU:OE2	1:XK:278:ARG:NH2	2.33	0.61
2:XJ:254:ASP:OD2	1:XK:285:ARG:NH1	2.34	0.61
1:XQ:352:VAL:HG13	1:XQ:354:PRO:HD3	1.84	0.59
1:XK:246:GLU:N	1:XK:246:GLU:OE1	2.36	0.58
1:XK:352:VAL:HG13	1:XK:354:PRO:HD3	1.85	0.58
1:XU:352:VAL:HG13	1:XU:354:PRO:HD3	1.85	0.58
1:XM:341:VAL:HG21	2:XM:315:VAL:HG22	1.86	0.58
2:XL:315:VAL:HB	1:XM:343:VAL:HG22	1.86	0.58
1:XU:315:TYR:OH	1:XU:323:ARG:NH2	2.37	0.57
1:XI:341:VAL:HG21	2:XJ:315:VAL:HG22	1.87	0.57
1:XA:341:VAL:HG12	1:XA:343:VAL:CG2	2.35	0.56
2:XF:266:ARG:NE	1:XG:302:GLN:OE1	2.38	0.56
1:XM:272:THR:HG22	2:XM:253:ALA:HB2	1.87	0.56
2:XV:285:ASP:O	2:XV:288:SER:OG	2.24	0.56
1:XI:341:VAL:HG12	1:XI:343:VAL:HG23	1.85	0.56
1:XQ:341:VAL:HG12	1:XQ:343:VAL:HG23	1.87	0.56
1:XO:276:GLN:OE1	1:XO:280:ASN:ND2	2.38	0.55
2:XJ:247:GLU:OE2	1:XK:285:ARG:NE	2.40	0.54
1:XK:261:GLU:OE1	2:XL:238:HIS:ND1	2.40	0.54
1:XW:341:VAL:HB	2:XX:315:VAL:HG13	1.89	0.54
1:XK:286:ILE:HD11	2:XL:264:ALA:HB3	1.90	0.54
2:XB:281:LYS:N	1:XC:314:GLU:OE2	2.41	0.54
2:XT:276:ASP:OD2	1:XU:307:ARG:NH2	2.42	0.53
1:XW:352:VAL:HG13	1:XW:354:PRO:HD3	1.90	0.53
1:XG:342:LEU:HD11	2:XH:323:PHE:CE2	2.44	0.53
1:XO:341:VAL:HG12	1:XO:343:VAL:HG23	1.91	0.53
1:XE:352:VAL:HG13	1:XE:354:PRO:HD3	1.91	0.52
2:XB:269:ARG:NH1	1:XC:300:GLU:OE1	2.42	0.52
1:XG:252:ASP:OD1	1:XG:253:ASP:N	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XK:341:VAL:HG12	1:XK:343:VAL:HG23	1.91	0.52
1:XG:341:VAL:HG12	1:XG:343:VAL:CG2	2.39	0.52
1:XG:272:THR:HG22	2:XH:253:ALA:HB2	1.91	0.52
2:XV:269:ARG:NH1	1:XW:300:GLU:O	2.43	0.51
2:XL:314:MET:HE1	2:XN:326:MET:HE1	1.92	0.51
1:XW:335:LEU:O	1:XW:340:LYS:NZ	2.43	0.51
1:XW:334:VAL:HG23	2:XX:307:PHE:HB2	1.93	0.50
1:XC:276:GLN:OE1	1:XC:280:ASN:ND2	2.44	0.50
2:XD:254:ASP:OD2	1:XE:285:ARG:NH1	2.44	0.49
1:XS:272:THR:HG22	2:XT:253:ALA:HB2	1.94	0.49
1:XE:341:VAL:HG21	2:XF:315:VAL:HG22	1.93	0.49
2:XP:314:MET:HG2	1:XQ:342:LEU:HD12	1.94	0.49
1:XS:276:GLN:OE1	1:XS:280:ASN:ND2	2.45	0.49
1:XM:271:TYR:O	1:XM:275:VAL:HG23	2.13	0.49
2:XD:285:ASP:OD1	2:XD:286:ALA:N	2.46	0.48
2:XJ:236:ARG:O	2:XJ:240:SER:N	2.45	0.48
1:XE:324:GLU:OE2	2:XF:324:ARG:NH2	2.46	0.48
1:XS:334:VAL:HG23	2:XT:307:PHE:HB2	1.96	0.48
1:XQ:341:VAL:CG1	1:XQ:343:VAL:HG23	2.44	0.48
1:XE:341:VAL:CG2	2:XF:315:VAL:HG22	2.44	0.47
2:XF:296:PHE:CZ	2:XF:300:LEU:HD11	2.50	0.47
2:XP:307:PHE:HZ	1:XQ:342:LEU:HD11	1.79	0.47
2:XR:285:ASP:O	2:XR:288:SER:OG	2.30	0.47
1:XU:312:LEU:HD11	1:XU:316:LYS:HE2	1.95	0.47
1:XC:307:ARG:O	1:XC:311:LEU:HD23	2.14	0.47
1:XQ:334:VAL:HG23	2:XR:307:PHE:CB	2.45	0.47
1:XQ:271:TYR:CZ	1:XQ:275:VAL:HG21	2.49	0.47
1:XA:352:VAL:HG12	1:XC:351:MET:O	2.15	0.46
1:XW:334:VAL:HG23	2:XX:307:PHE:CB	2.44	0.46
1:XO:334:VAL:HG23	2:XP:307:PHE:HB2	1.96	0.46
1:XQ:334:VAL:HG23	2:XR:307:PHE:HB2	1.97	0.46
2:XB:292:ASP:OD1	2:XB:293:PHE:N	2.48	0.46
2:XV:285:ASP:OD1	2:XV:286:ALA:N	2.49	0.46
1:XA:262:GLN:OE1	2:XX:226:ARG:NH1	2.45	0.46
1:XC:283:ALA:HB1	2:XD:264:ALA:HB2	1.98	0.45
1:XA:335:LEU:HD22	1:XA:340:LYS:HD3	1.97	0.45
1:XE:246:GLU:N	1:XE:246:GLU:OE1	2.49	0.45
2:XL:314:MET:CE	2:XN:326:MET:HE1	2.46	0.45
2:XD:298:ARG:HG3	1:XE:328:ILE:HG21	1.99	0.45
2:XN:301:ARG:O	2:XN:305:ASN:ND2	2.48	0.45
1:XQ:269:GLU:O	1:XQ:273:ASN:ND2	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XP:315:VAL:HG21	1:XQ:343:VAL:HG22	1.99	0.44
1:XE:286:ILE:HD11	2:XF:264:ALA:HB3	2.00	0.44
1:XA:352:VAL:HG13	1:XA:354:PRO:HD3	1.98	0.44
2:XL:218:GLU:N	2:XL:218:GLU:OE1	2.49	0.44
1:XM:283:ALA:HB1	2:XN:264:ALA:HB2	1.99	0.44
1:XK:256:ALA:O	1:XK:260:ASN:ND2	2.51	0.44
1:XK:334:VAL:HG23	2:XL:307:PHE:CB	2.48	0.44
1:XS:312:LEU:HD11	1:XS:316:LYS:HE2	1.99	0.44
2:XJ:232:GLU:N	2:XJ:232:GLU:OE1	2.51	0.43
2:XN:315:VAL:HB	1:XO:343:VAL:HG22	2.00	0.43
1:XU:307:ARG:O	1:XU:311:LEU:HD23	2.18	0.43
1:XU:337:ASN:O	2:XV:310:ASN:ND2	2.52	0.43
2:XH:315:VAL:HB	1:XI:343:VAL:HG22	2.01	0.43
1:XW:324:GLU:OE2	2:XX:324:ARG:NH2	2.52	0.43
1:XG:342:LEU:HD11	2:XH:323:PHE:CZ	2.53	0.43
2:XJ:312:ASP:OD1	2:XJ:312:ASP:N	2.52	0.42
1:XK:286:ILE:HD11	2:XL:264:ALA:CB	2.49	0.42
1:XQ:276:GLN:O	1:XQ:280:ASN:ND2	2.48	0.42
1:XW:345:ASP:O	1:XW:346:LYS:HG2	2.20	0.42
1:XM:341:VAL:CG2	2:XN:315:VAL:HG22	2.48	0.42
1:XI:276:GLN:OE1	1:XI:280:ASN:ND2	2.50	0.42
2:XR:298:ARG:HG3	1:XS:328:ILE:HG21	2.01	0.42
2:XX:296:PHE:CZ	2:XX:300:LEU:HD11	2.55	0.42
2:XP:217:THR:OG1	2:XP:218:GLU:N	2.52	0.42
2:XT:292:ASP:OD1	2:XT:293:PHE:N	2.53	0.41
2:XB:298:ARG:HG3	1:XC:328:ILE:HG21	2.02	0.41
1:XC:354:PRO:HB3	2:XF:313:VAL:HG11	2.02	0.41
2:XV:298:ARG:HG3	1:XW:328:ILE:HG21	2.02	0.41
1:XI:334:VAL:HG23	2:XJ:307:PHE:CB	2.49	0.41
2:XN:298:ARG:HG3	1:XO:328:ILE:HG21	2.03	0.41
2:XL:284:ALA:O	2:XL:288:SER:N	2.53	0.41
2:XN:292:ASP:OD1	2:XN:293:PHE:N	2.53	0.41
1:XQ:276:GLN:OE1	1:XQ:280:ASN:ND2	2.48	0.41
2:XR:312:ASP:OD1	2:XR:312:ASP:N	2.50	0.41
2:XH:292:ASP:OD1	2:XH:293:PHE:N	2.53	0.41
2:XV:312:ASP:OD1	2:XV:312:ASP:N	2.52	0.41
2:XD:321:ASP:OD1	2:XD:322:PHE:N	2.54	0.41
2:XV:276:ASP:OD2	1:XW:307:ARG:NH2	2.54	0.41
2:XB:321:ASP:OD2	2:XB:322:PHE:N	2.54	0.40
2:XJ:285:ASP:OD1	2:XJ:286:ALA:N	2.54	0.40
1:XO:341:VAL:CG1	1:XO:343:VAL:HG23	2.50	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XQ:257:ALA:HB1	2:XR:238:HIS:HB2	2.04	0.40
1:XI:341:VAL:HG12	1:XI:343:VAL:CG2	2.50	0.40
2:XX:285:ASP:OD1	2:XX:286:ALA:N	2.54	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	XA	108/419 (26%)	108 (100%)	0	0	100	100
1	XC	108/419 (26%)	108 (100%)	0	0	100	100
1	XE	108/419 (26%)	108 (100%)	0	0	100	100
1	XG	107/419 (26%)	107 (100%)	0	0	100	100
1	XI	108/419 (26%)	108 (100%)	0	0	100	100
1	XK	108/419 (26%)	108 (100%)	0	0	100	100
1	XM	108/419 (26%)	108 (100%)	0	0	100	100
1	XO	107/419 (26%)	107 (100%)	0	0	100	100
1	XQ	107/419 (26%)	107 (100%)	0	0	100	100
1	XS	101/419 (24%)	101 (100%)	0	0	100	100
1	XU	88/419 (21%)	88 (100%)	0	0	100	100
1	XW	72/419 (17%)	72 (100%)	0	0	100	100
2	XB	111/334 (33%)	111 (100%)	0	0	100	100
2	XD	111/334 (33%)	111 (100%)	0	0	100	100
2	XF	111/334 (33%)	111 (100%)	0	0	100	100
2	XH	108/334 (32%)	108 (100%)	0	0	100	100
2	XJ	111/334 (33%)	111 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	XL	111/334 (33%)	111 (100%)	0	0	100	100
2	XN	111/334 (33%)	111 (100%)	0	0	100	100
2	XP	111/334 (33%)	111 (100%)	0	0	100	100
2	XR	107/334 (32%)	107 (100%)	0	0	100	100
2	XT	99/334 (30%)	99 (100%)	0	0	100	100
2	XV	84/334 (25%)	84 (100%)	0	0	100	100
2	XX	103/334 (31%)	103 (100%)	0	0	100	100
All	All	2508/9036 (28%)	2508 (100%)	0	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	XA	88/336 (26%)	88 (100%)	0	100	100
1	XC	88/336 (26%)	88 (100%)	0	100	100
1	XE	88/336 (26%)	88 (100%)	0	100	100
1	XG	87/336 (26%)	87 (100%)	0	100	100
1	XI	88/336 (26%)	88 (100%)	0	100	100
1	XK	88/336 (26%)	88 (100%)	0	100	100
1	XM	88/336 (26%)	88 (100%)	0	100	100
1	XO	87/336 (26%)	87 (100%)	0	100	100
1	XQ	87/336 (26%)	87 (100%)	0	100	100
1	XS	83/336 (25%)	83 (100%)	0	100	100
1	XU	73/336 (22%)	73 (100%)	0	100	100
1	XW	61/336 (18%)	61 (100%)	0	100	100
2	XB	92/283 (32%)	92 (100%)	0	100	100
2	XD	92/283 (32%)	92 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	XF	92/283 (32%)	92 (100%)	0	100	100
2	XH	89/283 (31%)	89 (100%)	0	100	100
2	XJ	92/283 (32%)	92 (100%)	0	100	100
2	XL	92/283 (32%)	92 (100%)	0	100	100
2	XN	92/283 (32%)	92 (100%)	0	100	100
2	XP	92/283 (32%)	92 (100%)	0	100	100
2	XR	88/283 (31%)	88 (100%)	0	100	100
2	XT	81/283 (29%)	81 (100%)	0	100	100
2	XV	70/283 (25%)	70 (100%)	0	100	100
2	XX	83/283 (29%)	83 (100%)	0	100	100
All	All	2061/7428 (28%)	2061 (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 (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	XC	349	ASN
2	XL	311	GLN
2	XP	238	HIS
1	XQ	273	ASN
1	XS	302	GLN
2	XV	310	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

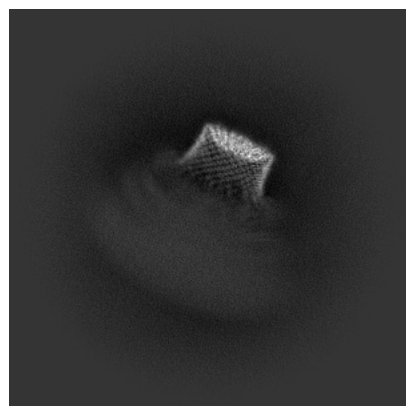
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46056. These allow visual inspection of the internal detail of the map and identification of artifacts.

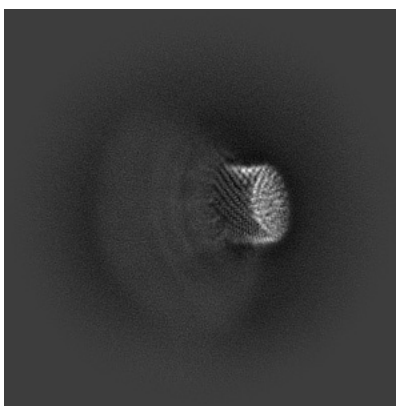
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

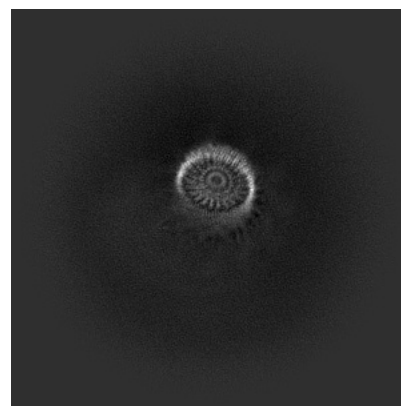
6.1.1 Primary map



X

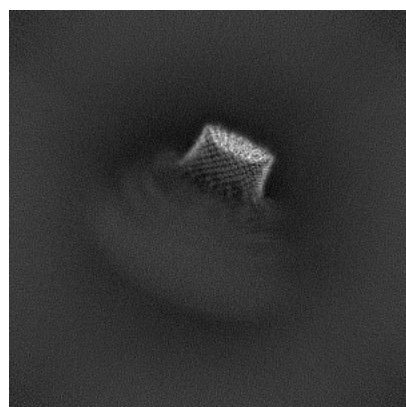


Y

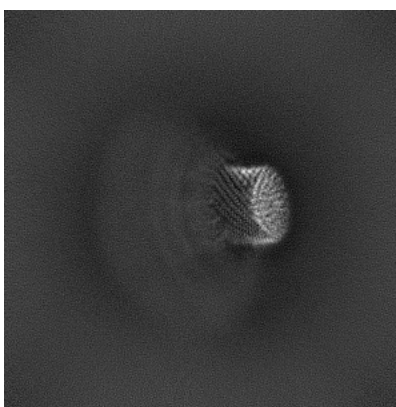


Z

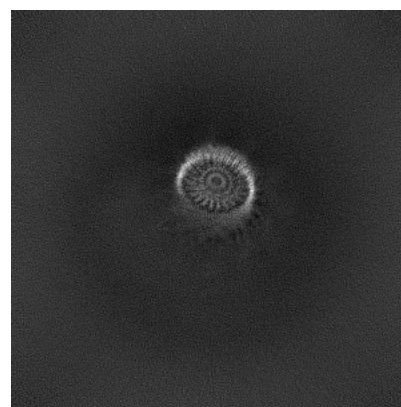
6.1.2 Raw map



X



Y

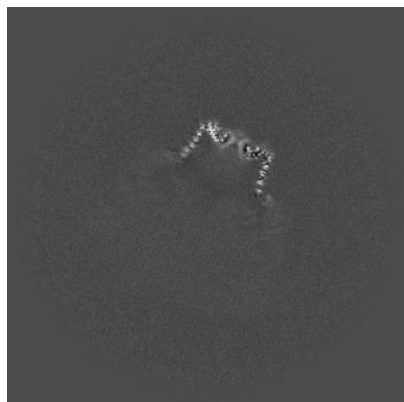


Z

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

6.2 Central slices [i](#)

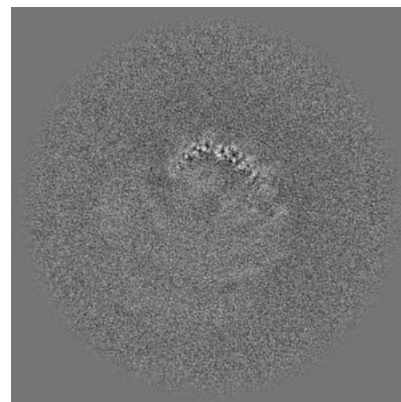
6.2.1 Primary map



X Index: 180

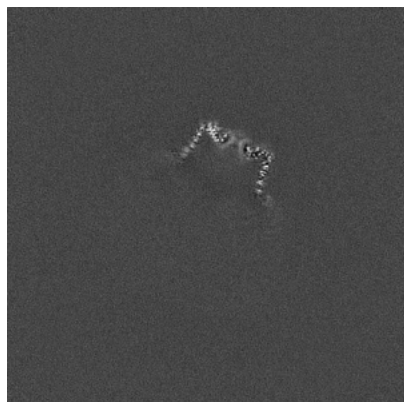


Y Index: 180



Z Index: 180

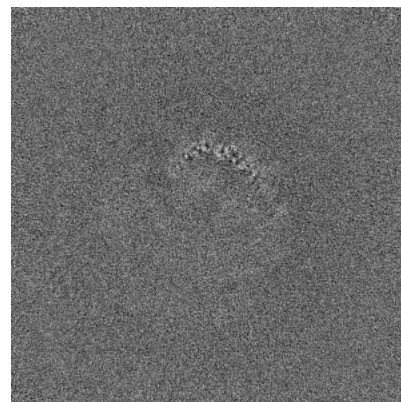
6.2.2 Raw map



X Index: 180



Y Index: 180



Z Index: 180

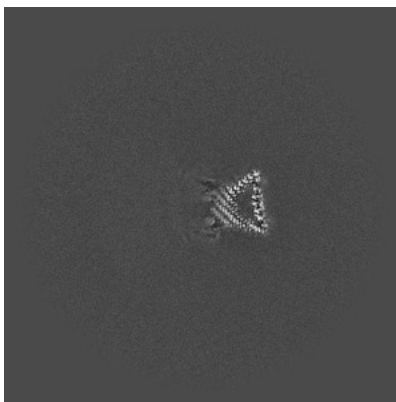
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

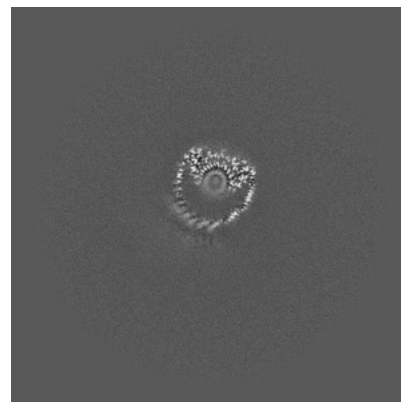
6.3.1 Primary map



X Index: 215



Y Index: 226

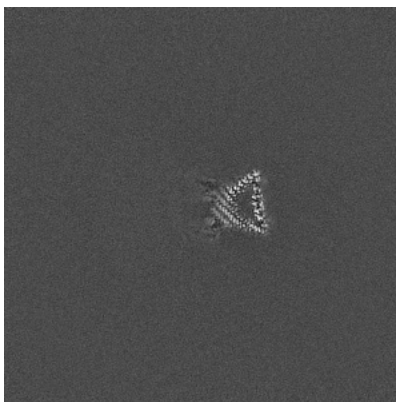


Z Index: 232

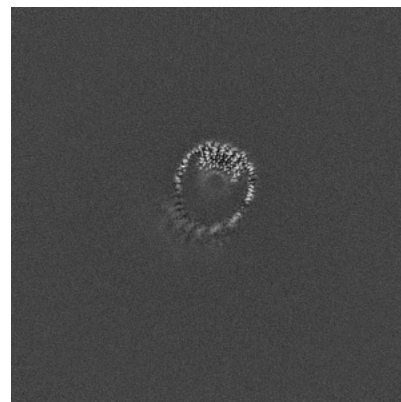
6.3.2 Raw map



X Index: 215



Y Index: 226

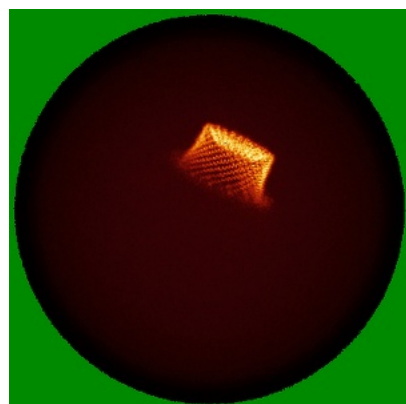


Z Index: 227

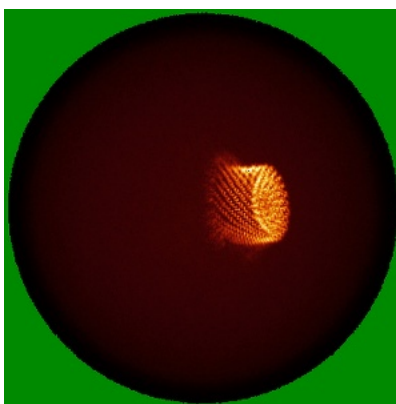
The images above show the largest variance slices of the map in three orthogonal directions.

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

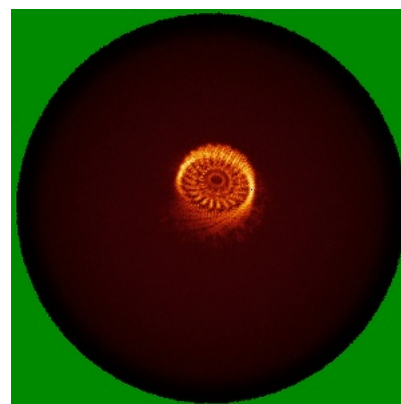
6.4.1 Primary map



X

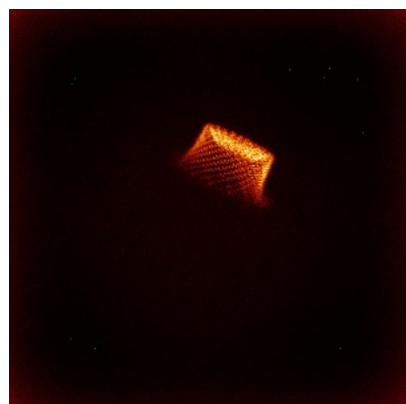


Y

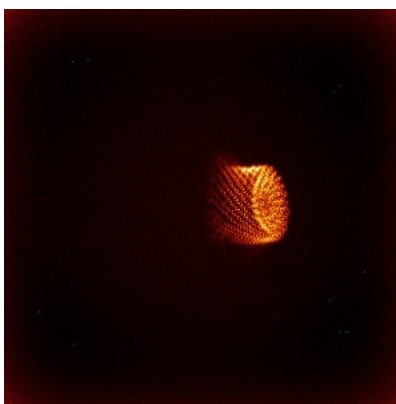


Z

6.4.2 Raw map



X



Y

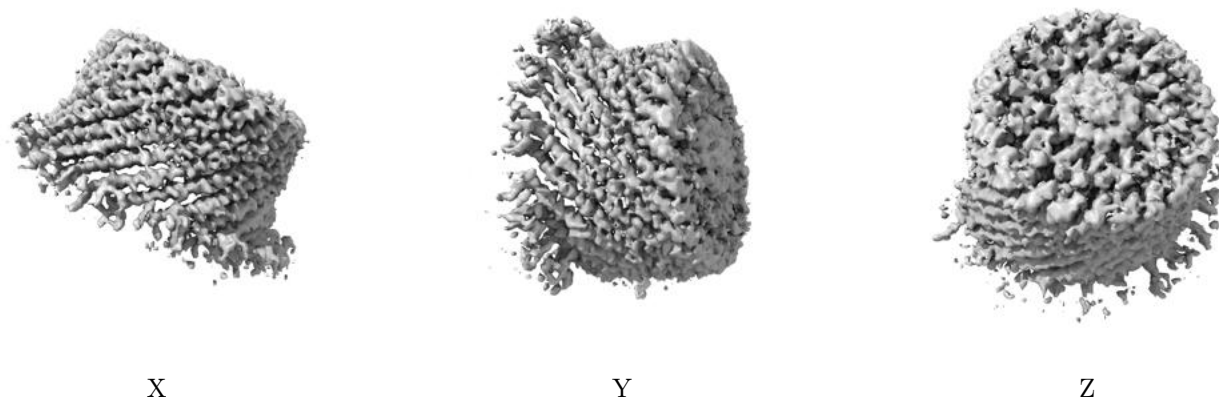


Z

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 0.0991. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

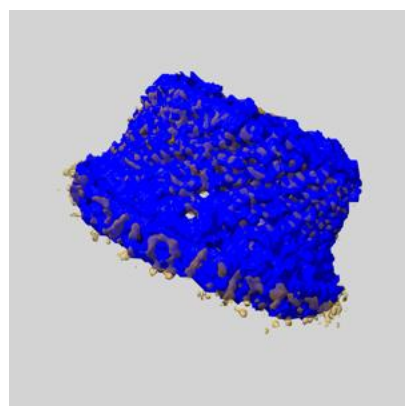
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

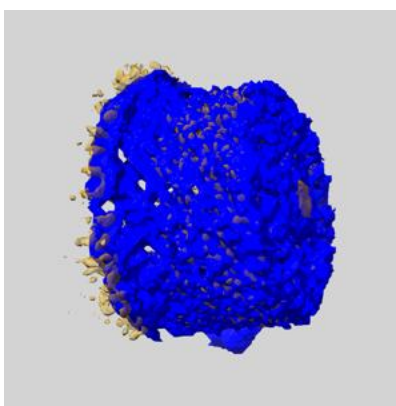
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

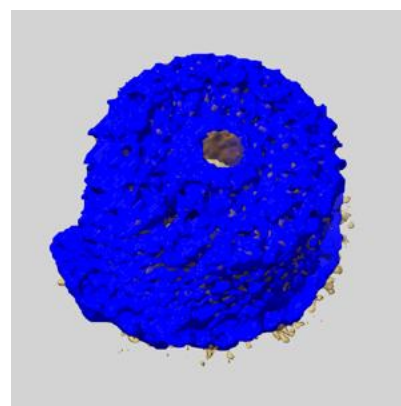
6.6.1 emd_46056_msk_1.map [i](#)



X



Y

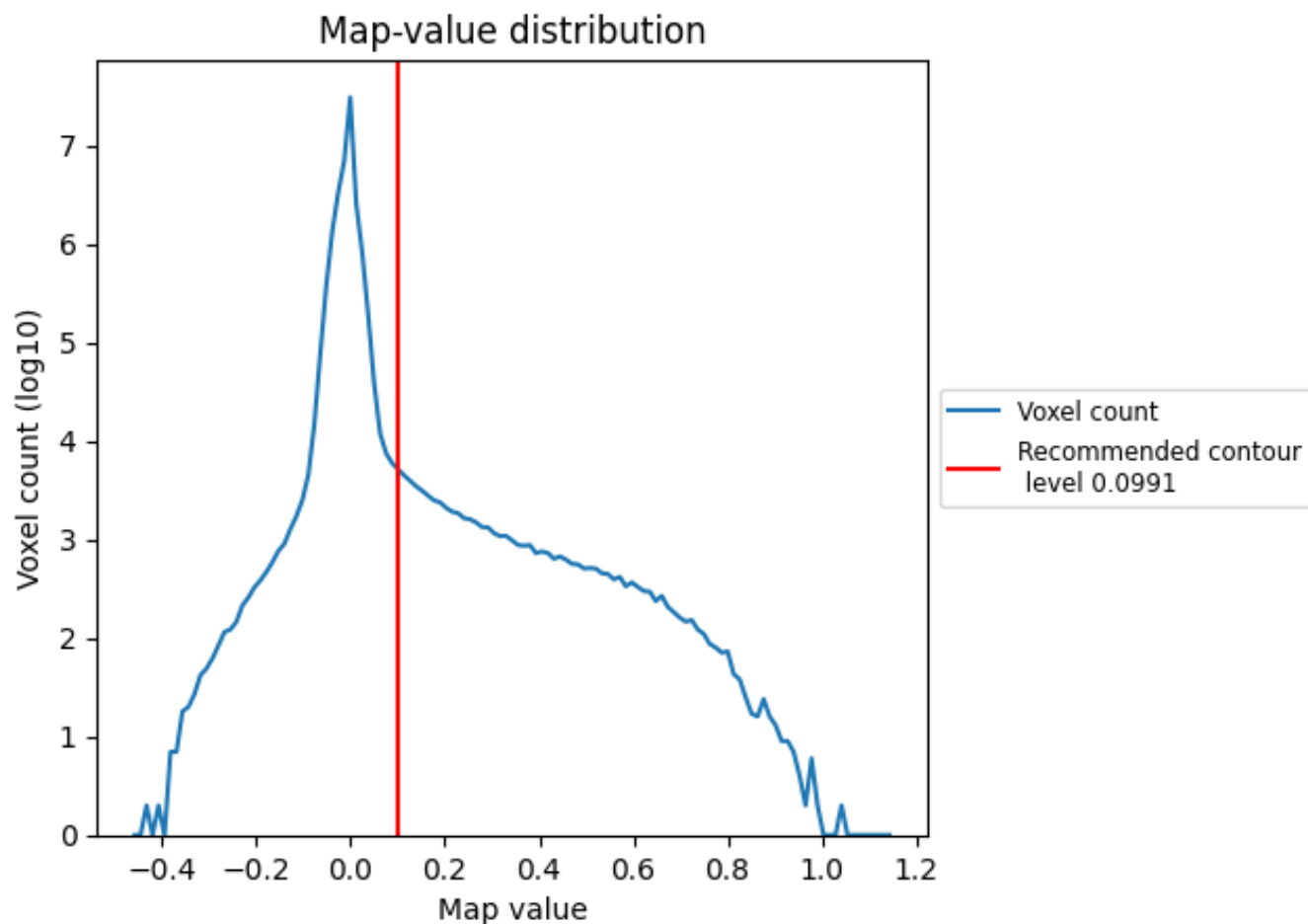


Z

7 Map analysis [i](#)

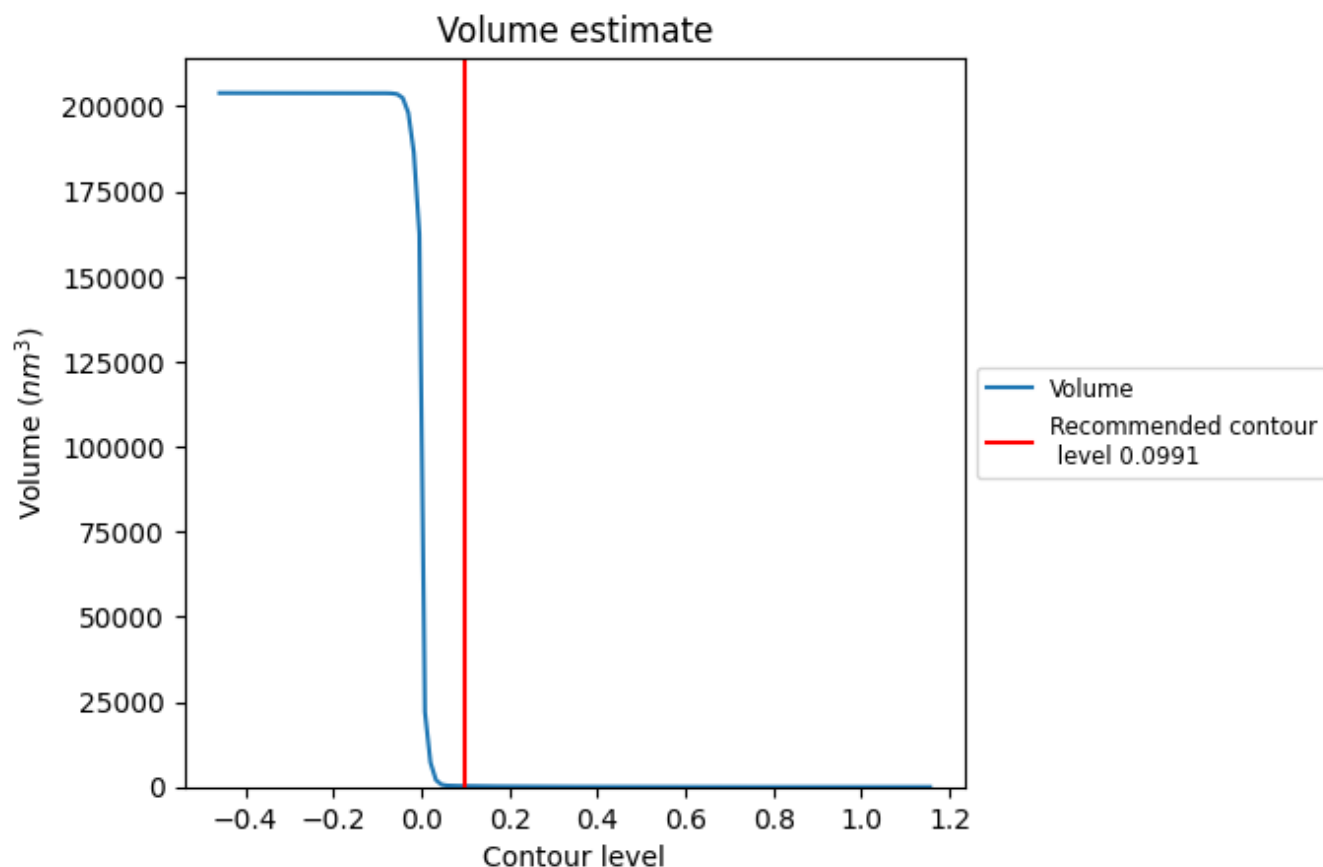
This section contains the results of statistical analysis of the map.

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.

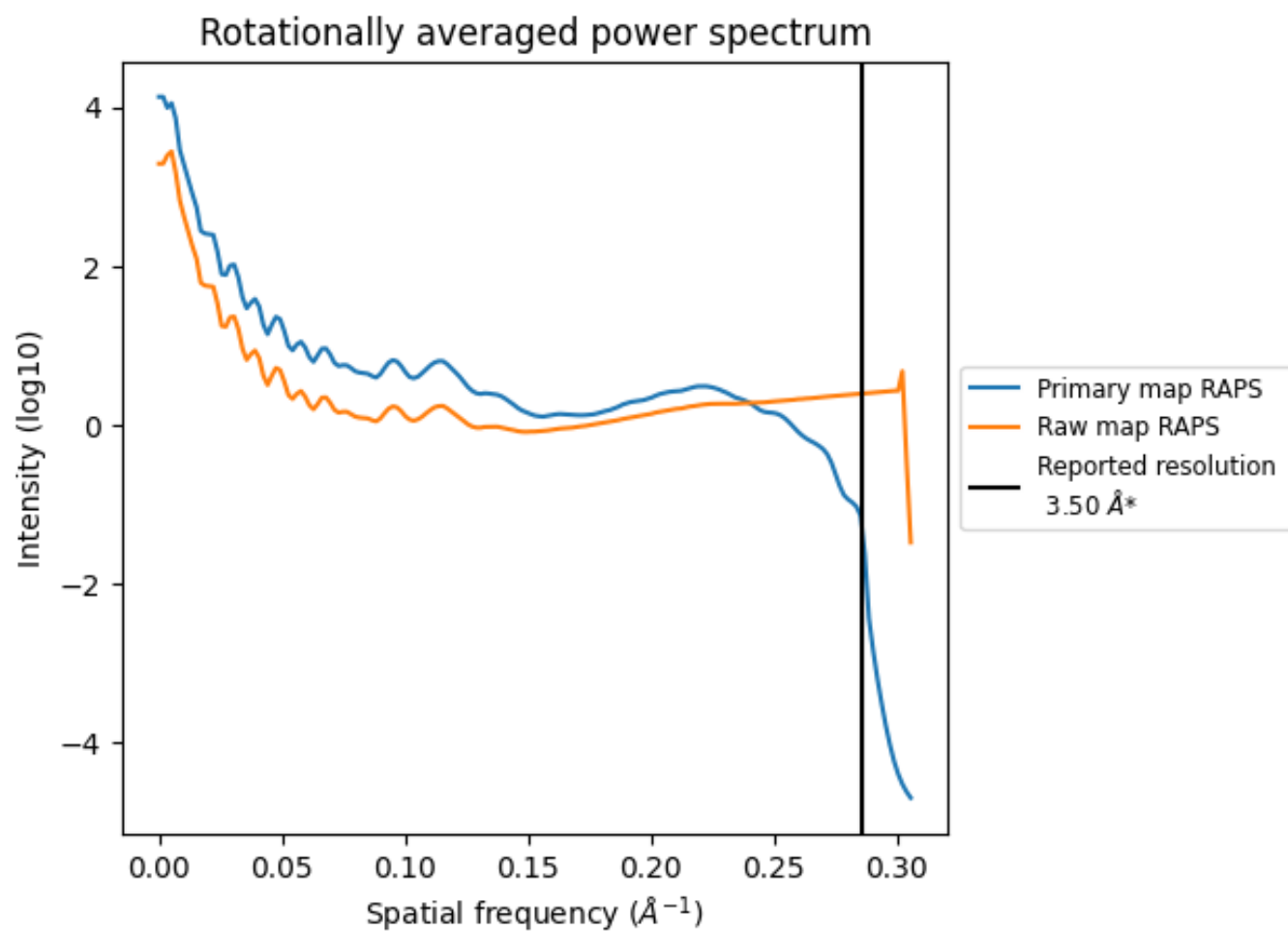
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 267 nm^3 ; this corresponds to an approximate mass of 241 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

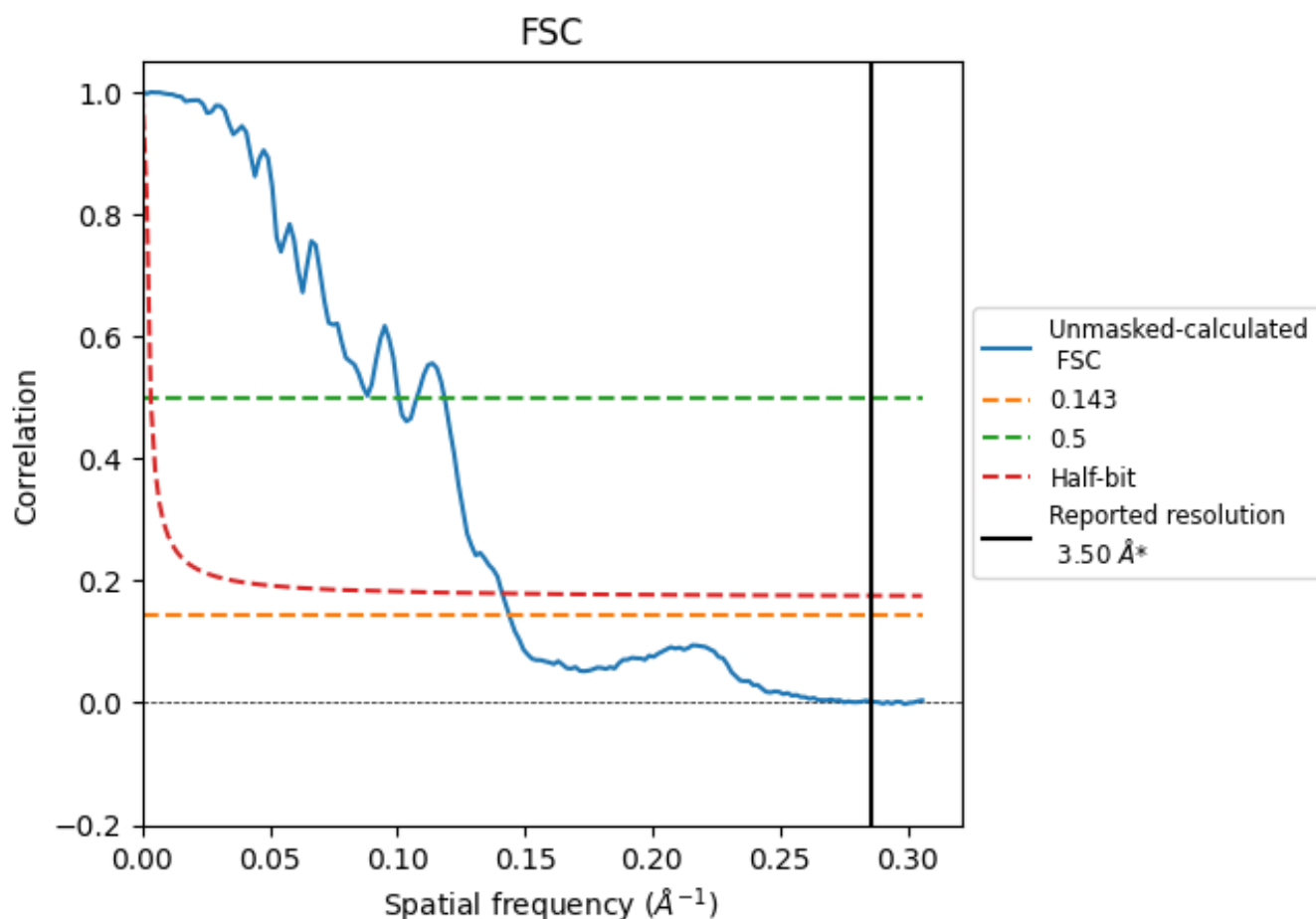


*Reported resolution corresponds to spatial frequency of $0.286 \text{ \AA}^{-1}$

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

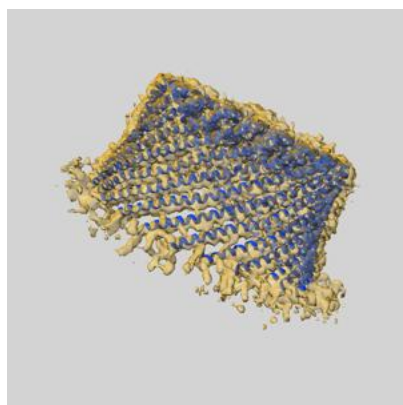
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.95	9.94	7.08

*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 6.95 differs from the reported value 3.5 by more than 10 %

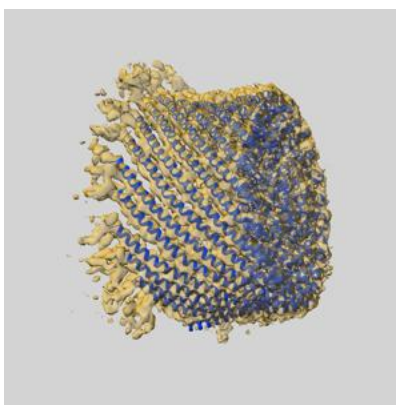
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46056 and PDB model 9CZ1. Per-residue inclusion information can be found in section [3](#) on page [6](#).

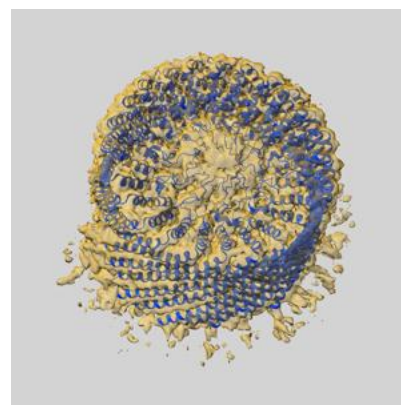
9.1 Map-model overlay [i](#)



X



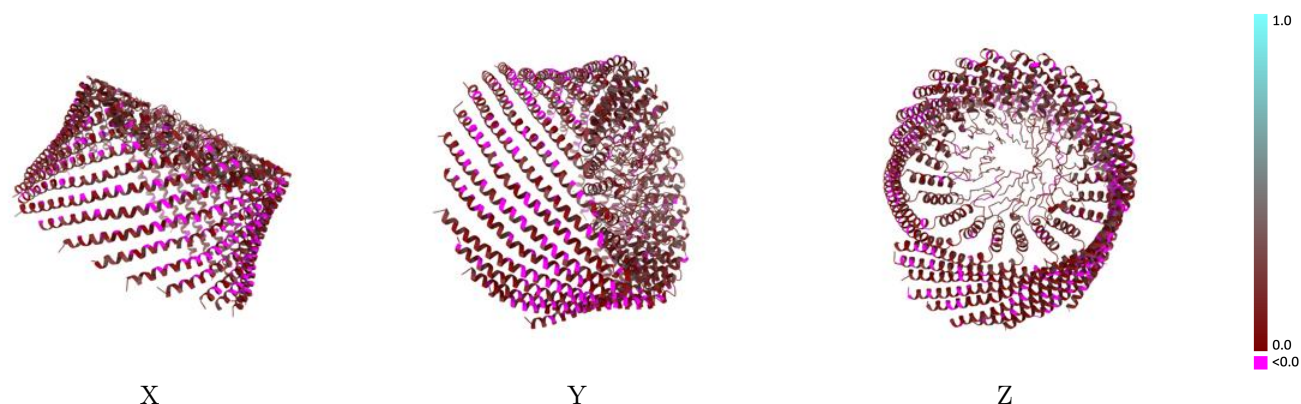
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0991 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](#)

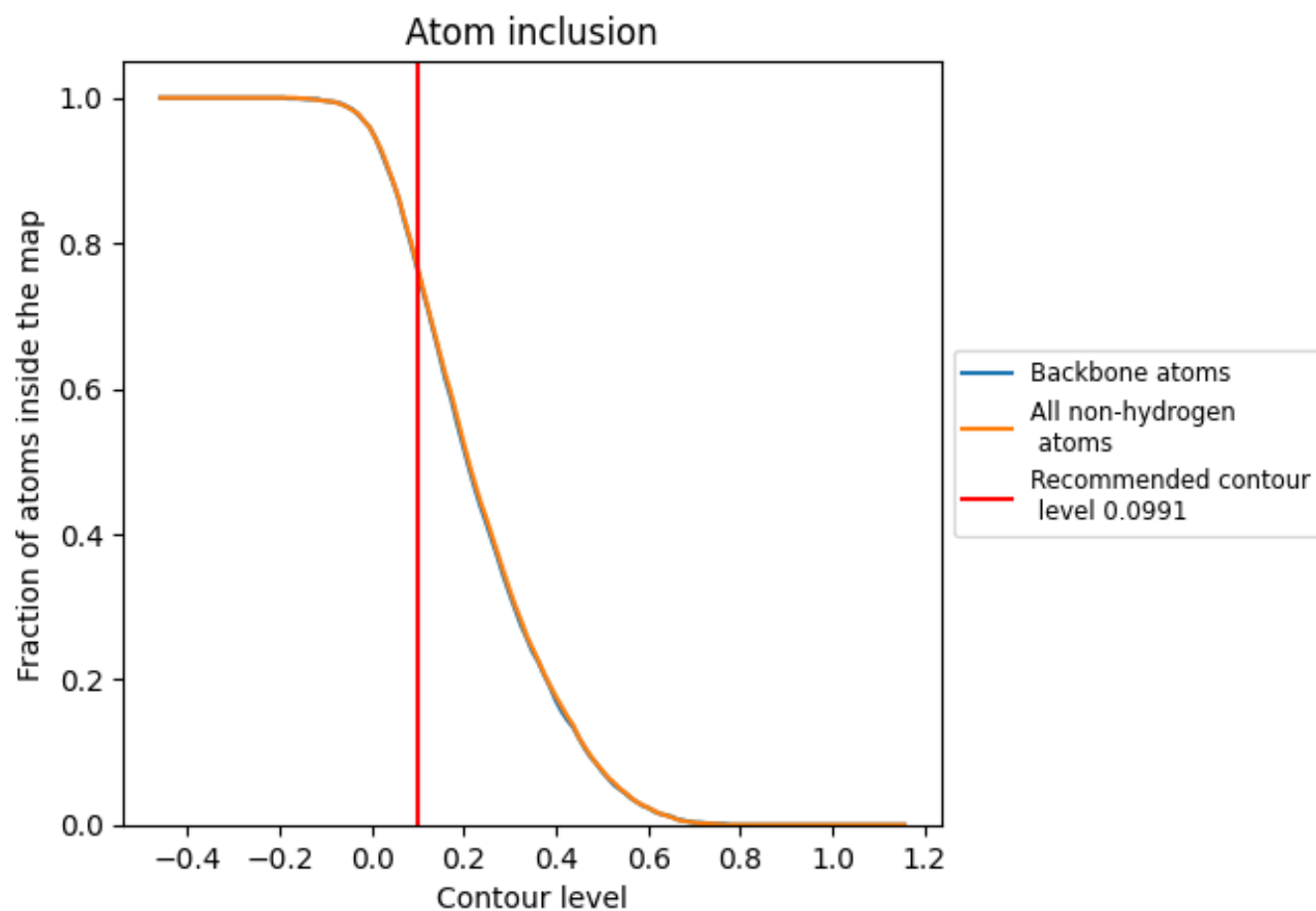


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 77% 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 (0.0991) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7670	 0.1580
XA	 0.7710	 0.1400
XB	 0.8240	 0.1560
XC	 0.7960	 0.1470
XD	 0.7950	 0.1430
XE	 0.7720	 0.1210
XF	 0.7900	 0.1590
XG	 0.7720	 0.1340
XH	 0.7810	 0.1680
XI	 0.7850	 0.1700
XJ	 0.7680	 0.1710
XK	 0.7780	 0.1770
XL	 0.7650	 0.1680
XM	 0.7560	 0.1610
XN	 0.7430	 0.1700
XO	 0.7590	 0.1530
XP	 0.7640	 0.1630
XQ	 0.7780	 0.1590
XR	 0.7770	 0.1640
XS	 0.7610	 0.1460
XT	 0.8110	 0.1670
XU	 0.7800	 0.1500
XV	 0.8210	 0.1880
XW	 0.8210	 0.1610
XX	 0.6050	 0.1690

