



Full wwPDB EM Validation Report ⓘ

Sep 16, 2026 – 07:24 am BST

PDB ID : 28OE / pdb_000028oe
EMDB ID : EMD-56669
Title : Human PRC1.4 in complex with native UBCH5C bound to a H3Kc27me3 mononucleosome
Authors : Ciapponi, M.; Mueller, J.
Deposited on : 2026-02-10
Resolution : 2.74 Å (reported)
Based on initial models : ., 4R8P

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

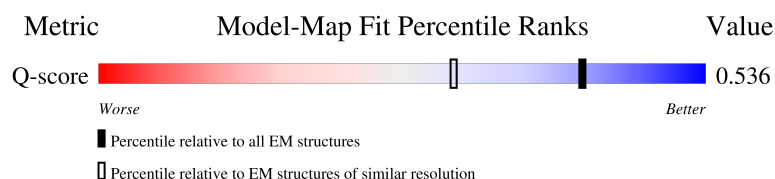
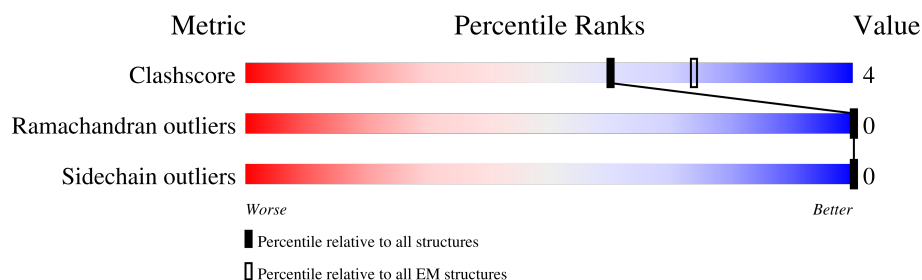
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.74 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.



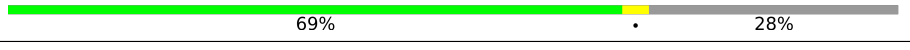
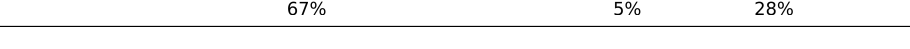
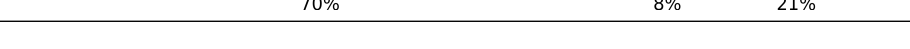
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10492 (2.24 - 3.24)

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	327	 5% . 92%
2	B	162	 22% . 74%
3	C	340	 51% 14% 35%
4	D	336	 56% 9% 35%

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Mol	Chain	Length	Quality of chain
5	E	147	
6	F	135	
6	J	135	
7	G	102	
7	K	102	
8	H	129	
8	L	129	
9	I	122	
9	M	122	
10	N	248	
11	O	248	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 17632 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 Isoform 2 of Polyhomeotic-like protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	26	Total	C	N	O	0	0
			198	128	33	37		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q8IXK0
A	-2	PRO	-	expression tag	UNP Q8IXK0
A	-1	ASP	-	expression tag	UNP Q8IXK0
A	0	SER	-	expression tag	UNP Q8IXK0
A	307	GLU	LEU	engineered mutation	UNP Q8IXK0
A	311	GLU	LEU	engineered mutation	UNP Q8IXK0

- Molecule 2 is a protein called Chromobox 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	42	Total	C	N	O	0	0
			319	201	54	64		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP B0QYP2
B	-2	PRO	-	expression tag	UNP B0QYP2
B	-1	ASP	-	expression tag	UNP B0QYP2
B	0	SER	-	expression tag	UNP B0QYP2

- Molecule 3 is a protein called E3 ubiquitin-protein ligase RING2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	222	Total	C	N	O	S	2	0
			1800	1138	311	339	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP Q99496
C	-2	PRO	-	expression tag	UNP Q99496
C	-1	ASP	-	expression tag	UNP Q99496
C	0	SER	-	expression tag	UNP Q99496

- Molecule 4 is a protein called Polycomb complex protein BMI-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	219	Total	C	N	O	S	0	0
			1809	1145	320	327	17		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	327	GLY	-	expression tag	UNP P35226
D	328	SER	-	expression tag	UNP P35226
D	329	GLY	-	expression tag	UNP P35226
D	330	SER	-	expression tag	UNP P35226
D	331	LEU	-	expression tag	UNP P35226
D	332	GLU	-	expression tag	UNP P35226
D	333	VAL	-	expression tag	UNP P35226
D	334	LEU	-	expression tag	UNP P35226
D	335	PHE	-	expression tag	UNP P35226
D	336	GLN	-	expression tag	UNP P35226

- Molecule 5 is a protein called Ubiquitin-conjugating enzyme E2 D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	146	Total	C	N	O	S	0	0
			1165	746	199	213	7		

- Molecule 6 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	97	Total	C	N	O	S	0	0
			801	506	155	138	2		
6	J	97	Total	C	N	O	S	0	0
			801	506	155	138	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	110	ALA	CYS	engineered mutation	UNP A0A310TTQ1
J	110	ALA	CYS	engineered mutation	UNP A0A310TTQ1

- Molecule 7 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
7	K	83	Total	C	N	O	S	0	0
			662	418	129	114	1		

- Molecule 8 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	111	Total	C	N	O		0	0
			857	539	169	149			
8	L	110	Total	C	N	O		0	0
			850	535	168	147			

- Molecule 9 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	96	Total	C	N	O	S	0	0
			756	475	138	141	2		
9	M	96	Total	C	N	O	S	0	0
			756	475	138	141	2		

- Molecule 10 is a DNA chain called DNA (151-MER).

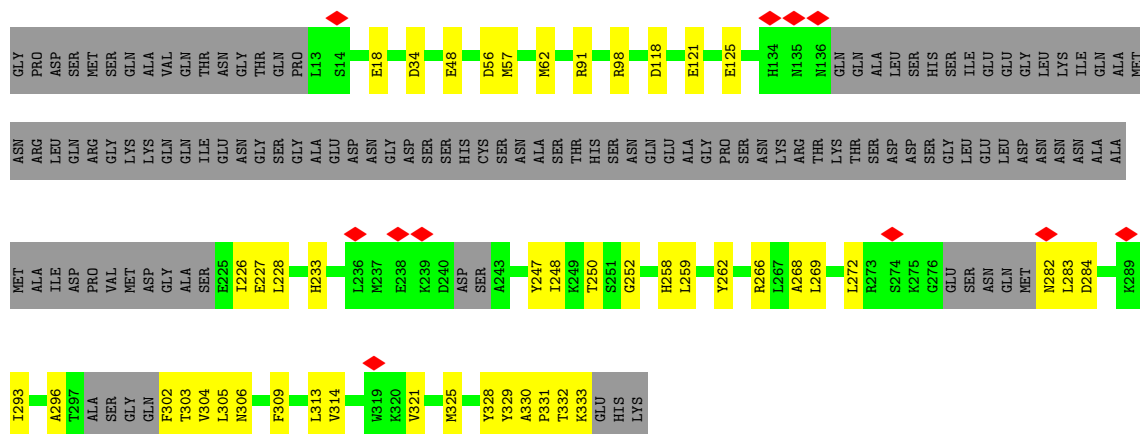
Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	151	Total	C	N	O	P	0	0
			3078	1462	557	908	151		

- Molecule 11 is a DNA chain called DNA (151-MER).

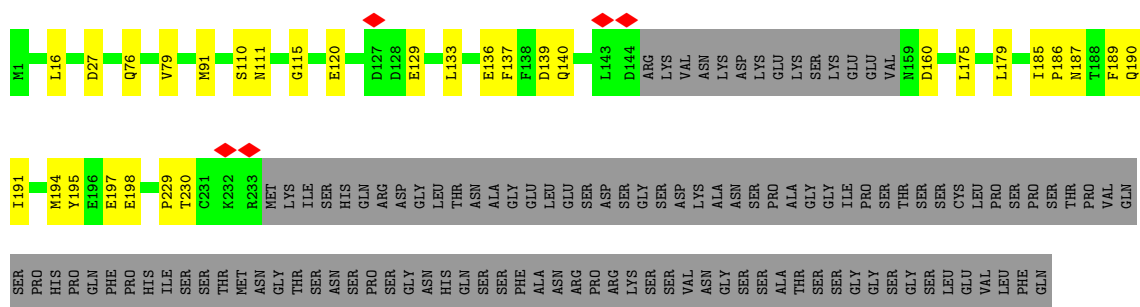
Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	151	Total	C	N	O	P	0	0
			3114	1474	584	905	151		

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

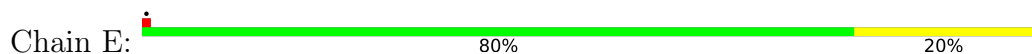
Mol	Chain	Residues	Atoms		AltConf
12	C	2	Total 2	Zn 2	0
12	D	2	Total 2	Zn 2	0



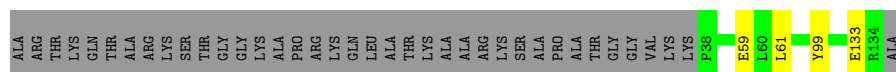
• Molecule 4: Polycomb complex protein BMI-1



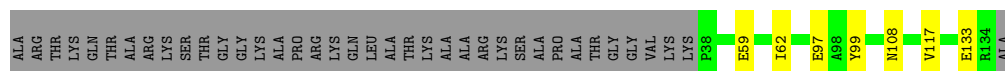
• Molecule 5: Ubiquitin-conjugating enzyme E2 D3

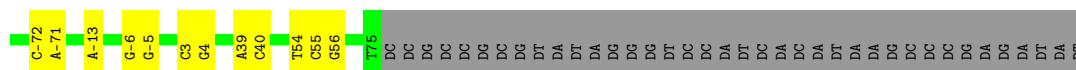


• Molecule 6: Histone H3



• Molecule 6: Histone H3





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	304443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.45	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.648	Depositor
Minimum map value	-0.281	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	340.47998, 340.47998, 340.47998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8511999, 0.8511999, 0.8511999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.48	0/203	0.56	0/275
2	B	0.45	0/328	0.58	0/451
3	C	0.15	0/1837	0.32	0/2477
4	D	0.15	0/1846	0.32	0/2490
5	E	0.30	0/1200	0.46	0/1637
6	F	0.19	0/813	0.26	0/1091
6	J	0.19	0/813	0.26	0/1091
7	G	0.20	0/669	0.27	0/894
7	K	0.21	0/669	0.28	0/894
8	H	0.18	0/867	0.23	0/1169
8	L	0.19	0/860	0.30	0/1159
9	I	0.20	0/767	0.28	0/1029
9	M	0.20	0/767	0.30	0/1029
10	N	0.26	0/3448	0.48	0/5315
11	O	0.26	0/3497	0.44	0/5400
All	All	0.23	0/18584	0.39	0/26401

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	A	198	0	195	7	0
2	B	319	0	303	6	0
3	C	1800	0	1821	43	0
4	D	1809	0	1815	27	0
5	E	1165	0	1149	20	0
6	F	801	0	841	3	0
6	J	801	0	841	5	0
7	G	662	0	709	5	0
7	K	662	0	709	2	0
8	H	857	0	922	2	0
8	L	850	0	915	4	0
9	I	756	0	786	4	0
9	M	756	0	786	8	0
10	N	3078	0	1696	11	0
11	O	3114	0	1695	7	0
12	C	2	0	0	0	0
12	D	2	0	0	0	0
All	All	17632	0	15183	141	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 4.

All (141) 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:44:GLN:OE1	1:A:44:GLN:N	2.09	0.84
6:J:59:GLU:N	6:J:59:GLU:OE1	2.14	0.80
3:C:247:TYR:C	3:C:248:ILE:HD12	2.19	0.67
5:E:41:ASN:O	5:E:46:GLN:NE2	2.28	0.65
3:C:268:ALA:O	3:C:272:LEU:HD23	1.98	0.63
3:C:313:LEU:HD12	3:C:314:VAL:N	2.14	0.63
6:F:59:GLU:N	6:F:59:GLU:OE1	2.32	0.63
3:C:259:LEU:O	3:C:259:LEU:HD23	2.00	0.62
8:L:42:ARG:HB2	9:M:85:THR:HG22	1.82	0.61
2:B:132:ILE:HD11	3:C:262:TYR:HD1	1.66	0.60
3:C:226:ILE:HD12	3:C:226:ILE:N	2.18	0.59
6:F:61:LEU:O	7:G:36:ARG:NH1	2.36	0.58
7:K:29:ILE:O	7:K:55:ARG:NH1	2.35	0.58
5:E:87:ASP:N	5:E:87:ASP:OD1	2.36	0.58
4:D:129:GLU:N	4:D:129:GLU:OE2	2.38	0.57
3:C:284:ASP:OD1	3:C:284:ASP:N	2.38	0.56
2:B:137:ILE:HG23	3:C:258:HIS:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:293:ILE:HD12	3:C:331:PRO:HA	1.88	0.55
1:A:43:ILE:HD12	1:A:43:ILE:N	2.22	0.55
4:D:189:PHE:HA	4:D:230:THR:HG23	1.86	0.55
4:D:191:ILE:HD12	4:D:191:ILE:O	2.07	0.55
4:D:136:GLU:OE2	4:D:137:PHE:N	2.39	0.54
3:C:305:LEU:HD11	3:C:314:VAL:HG22	1.87	0.54
3:C:91:ARG:NH2	5:E:92:GLN:O	2.37	0.54
3:C:269:LEU:C	3:C:269:LEU:HD13	2.33	0.54
2:B:122:LEU:HD13	2:B:122:LEU:O	2.08	0.54
3:C:269:LEU:HD13	3:C:269:LEU:O	2.07	0.53
3:C:305:LEU:HD11	3:C:314:VAL:CG2	2.39	0.53
3:C:48:GLU:N	3:C:48:GLU:OE1	2.42	0.53
3:C:62:MET:HA	3:C:62:MET:HE2	1.91	0.53
3:C:296:ALA:HB3	3:C:328:TYR:O	2.08	0.53
4:D:133:LEU:C	4:D:133:LEU:HD12	2.33	0.53
3:C:266:ARG:NH2	3:C:269:LEU:HD12	2.24	0.53
4:D:185:ILE:HG23	4:D:189:PHE:CD1	2.45	0.52
3:C:98:ARG:NH1	8:H:61:GLU:OE2	2.41	0.52
4:D:160:ASP:N	4:D:160:ASP:OD1	2.43	0.52
5:E:141:TRP:O	5:E:145:TYR:N	2.42	0.52
5:E:130:ASP:OD2	5:E:130:ASP:C	2.53	0.51
6:J:62:ILE:HD12	6:J:97:GLU:OE1	2.10	0.51
4:D:190:GLN:N	4:D:190:GLN:OE1	2.44	0.51
3:C:309:PHE:HB3	3:C:313:LEU:HD11	1.92	0.51
10:N:-47:DT:H2"	10:N:-46:DC:C5	2.45	0.51
3:C:266:ARG:HH21	3:C:269:LEU:HD12	1.75	0.50
3:C:34:ASP:OD2	3:C:34:ASP:C	2.55	0.50
10:N:55:DT:H2"	10:N:56:DC:C6	2.46	0.50
11:O:3:DC:H2"	11:O:4:DG:C8	2.47	0.50
7:G:35:ARG:NH2	10:N:8:DC:OP2	2.46	0.49
10:N:35:DC:H2"	10:N:36:DC:C5	2.47	0.49
5:E:78:ILE:HD12	5:E:83:SER:O	2.12	0.49
3:C:18:GLU:OE2	3:C:18:GLU:HA	2.12	0.49
3:C:226:ILE:HD13	3:C:252:GLY:CA	2.43	0.49
3:C:259:LEU:HD23	3:C:259:LEU:C	2.37	0.49
9:M:83:ARG:NH2	10:N:-33:DA:OP2	2.46	0.49
10:N:6:DC:H2"	10:N:7:DC:C5	2.47	0.49
4:D:175:LEU:C	4:D:175:LEU:HD13	2.38	0.49
4:D:139:ASP:OD1	4:D:140:GLN:N	2.46	0.48
6:J:99:TYR:OH	6:J:133:GLU:OE2	2.29	0.48
3:C:303:THR:HG22	3:C:304:VAL:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:56:ASP:OD1	3:C:57:MET:N	2.44	0.47
5:E:34:GLN:OE1	5:E:34:GLN:C	2.57	0.47
8:L:62:ILE:HG22	8:L:63:LEU:N	2.28	0.47
11:O:-6:DG:H2''	11:O:-5:DG:C8	2.49	0.47
2:B:117:PRO:HB3	4:D:189:PHE:CD2	2.50	0.47
3:C:282:ASN:OD1	3:C:283:LEU:N	2.48	0.46
3:C:332:THR:O	3:C:333:LYS:HG2	2.15	0.46
4:D:185:ILE:HG23	4:D:189:PHE:CE1	2.50	0.46
1:A:45:GLU:OE2	1:A:46:GLY:N	2.48	0.46
3:C:121:GLU:O	3:C:125:GLU:HG2	2.15	0.46
9:M:29:THR:OG1	10:N:30:DT:OP1	2.23	0.46
1:A:34:LEU:HD12	1:A:34:LEU:N	2.30	0.46
4:D:16:LEU:HD22	4:D:79:VAL:HG22	1.97	0.46
5:E:45:TYR:CE1	5:E:73:ILE:HD11	2.51	0.46
4:D:194:MET:HE3	4:D:195:TYR:N	2.31	0.45
9:M:113:LYS:O	9:M:116:THR:HG22	2.17	0.45
11:O:-72:DC:H2''	11:O:-71:DA:C8	2.51	0.45
5:E:18:PRO:HB2	5:E:21:CYS:HB2	1.99	0.45
7:G:70:VAL:HA	7:G:73:THR:HG22	1.98	0.45
2:B:144:ALA:HB3	2:B:150:PHE:CD2	2.51	0.44
3:C:259:LEU:HD11	3:C:329:TYR:CE2	2.53	0.44
4:D:189:PHE:HB3	4:D:229:PRO:HA	2.00	0.44
5:E:126:ILE:O	5:E:130:ASP:N	2.47	0.44
4:D:191:ILE:HD12	4:D:191:ILE:C	2.43	0.44
4:D:179:LEU:HD23	4:D:179:LEU:C	2.42	0.44
1:A:35:THR:HG21	3:C:269:LEU:HD21	1.99	0.44
5:E:78:ILE:HD13	5:E:84:ILE:HG13	2.00	0.43
3:C:321:VAL:HG21	3:C:325:MET:HA	1.99	0.43
9:I:109:SER:O	9:I:110:GLU:C	2.60	0.43
9:M:102:GLU:O	9:M:103:LEU:C	2.60	0.43
3:C:305:LEU:HD23	3:C:306:ASN:N	2.33	0.43
7:G:36:ARG:NH2	11:O:-13:DA:OP1	2.52	0.43
3:C:233:HIS:CB	3:C:330:ALA:HB2	2.49	0.43
4:D:186:PRO:O	4:D:187:ASN:HB3	2.19	0.43
10:N:56:DC:H1'	10:N:57:DA:C5	2.54	0.43
5:E:132:ASP:O	5:E:135:ASN:OD1	2.37	0.43
5:E:43:SER:O	5:E:46:GLN:OE1	2.37	0.43
5:E:119:LEU:HD23	5:E:119:LEU:O	2.18	0.43
4:D:91:MET:HE1	4:D:115:GLY:HA2	2.00	0.43
8:L:62:ILE:O	8:L:63:LEU:HB2	2.19	0.43
9:M:103:LEU:O	9:M:104:ALA:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:99:TYR:OH	6:F:133:GLU:OE2	2.34	0.42
8:L:62:ILE:HG22	8:L:63:LEU:H	1.83	0.42
4:D:194:MET:HE1	4:D:197:GLU:C	2.45	0.42
10:N:8:DC:H2"	10:N:9:DG:C8	2.54	0.42
3:C:259:LEU:O	3:C:262:TYR:HB3	2.19	0.42
11:O:55:DC:H2"	11:O:56:DG:C8	2.54	0.42
1:A:42:VAL:O	1:A:42:VAL:HG13	2.17	0.42
4:D:194:MET:HE1	4:D:198:GLU:N	2.35	0.42
9:I:110:GLU:O	9:I:111:GLY:C	2.63	0.42
4:D:185:ILE:HG22	4:D:187:ASN:H	1.85	0.42
9:M:104:ALA:O	9:M:105:LYS:C	2.61	0.42
4:D:120:GLU:O	4:D:120:GLU:HG2	2.20	0.42
10:N:-74:DC:H2"	10:N:-73:DC:C5	2.55	0.42
10:N:-26:DT:H2"	10:N:-25:DA:C8	2.55	0.41
3:C:226:ILE:HG22	3:C:227:GLU:N	2.35	0.41
3:C:228:LEU:HD12	3:C:250:THR:HG21	2.03	0.41
4:D:186:PRO:HD2	4:D:189:PHE:CZ	2.55	0.41
11:O:39:DA:C4	11:O:40:DC:C5	3.08	0.41
2:B:144:ALA:HB3	2:B:150:PHE:HD2	1.85	0.41
3:C:296:ALA:HB1	3:C:302:PHE:CD2	2.56	0.41
3:C:325:MET:CG	3:C:325:MET:O	2.67	0.41
4:D:91:MET:HE3	4:D:91:MET:HA	2.02	0.41
6:J:117:VAL:O	6:J:117:VAL:HG12	2.20	0.41
11:O:54:DT:H2"	11:O:55:DC:C5	2.55	0.41
5:E:114:ASN:OD1	5:E:114:ASN:C	2.63	0.41
5:E:103:LEU:O	5:E:106:ILE:HG13	2.19	0.41
7:G:29:ILE:O	7:G:29:ILE:HG22	2.20	0.41
4:D:110:SER:OG	4:D:111:ASN:N	2.53	0.41
5:E:5:ARG:NH2	5:E:97:LEU:O	2.53	0.41
9:I:116:THR:O	9:I:119:THR:HG22	2.20	0.41
6:J:108:ASN:ND2	7:K:42:GLY:O	2.53	0.41
3:C:118:ASP:OD1	3:C:118:ASP:N	2.54	0.41
3:C:293:ILE:HD12	3:C:331:PRO:CA	2.51	0.41
5:E:34:GLN:C	5:E:34:GLN:CD	2.88	0.41
8:H:73:ASN:O	8:H:74:LYS:HB2	2.21	0.41
1:A:52:VAL:HG13	1:A:53:GLY:N	2.35	0.40
9:M:113:LYS:O	9:M:114:ALA:C	2.63	0.40
3:C:247:TYR:O	3:C:248:ILE:HD12	2.21	0.40
4:D:27:ASP:N	4:D:76:GLN:OE1	2.55	0.40
9:I:104:ALA:O	9:I:105:LYS:C	2.64	0.40
5:E:67:VAL:CG1	5:E:89:LEU:HD21	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:134:TYR:O	5:E:137:ILE:HG13	2.22	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	A	24/327 (7%)	21 (88%)	3 (12%)	0	100	100
2	B	40/162 (25%)	35 (88%)	5 (12%)	0	100	100
3	C	214/340 (63%)	198 (92%)	16 (8%)	0	100	100
4	D	215/336 (64%)	205 (95%)	10 (5%)	0	100	100
5	E	144/147 (98%)	136 (94%)	8 (6%)	0	100	100
6	F	95/135 (70%)	92 (97%)	3 (3%)	0	100	100
6	J	95/135 (70%)	94 (99%)	1 (1%)	0	100	100
7	G	81/102 (79%)	79 (98%)	2 (2%)	0	100	100
7	K	81/102 (79%)	79 (98%)	2 (2%)	0	100	100
8	H	109/129 (84%)	106 (97%)	3 (3%)	0	100	100
8	L	108/129 (84%)	104 (96%)	4 (4%)	0	100	100
9	I	94/122 (77%)	89 (95%)	5 (5%)	0	100	100
9	M	94/122 (77%)	87 (93%)	7 (7%)	0	100	100
All	All	1394/2288 (61%)	1325 (95%)	69 (5%)	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	22/281 (8%)	22 (100%)	0	100	100
2	B	35/135 (26%)	35 (100%)	0	100	100
3	C	206/300 (69%)	206 (100%)	0	100	100
4	D	203/304 (67%)	203 (100%)	0	100	100
5	E	131/132 (99%)	131 (100%)	0	100	100
6	F	84/109 (77%)	84 (100%)	0	100	100
6	J	84/109 (77%)	84 (100%)	0	100	100
7	G	68/78 (87%)	68 (100%)	0	100	100
7	K	68/78 (87%)	68 (100%)	0	100	100
8	H	88/101 (87%)	88 (100%)	0	100	100
8	L	87/101 (86%)	87 (100%)	0	100	100
9	I	82/102 (80%)	82 (100%)	0	100	100
9	M	82/102 (80%)	82 (100%)	0	100	100
All	All	1240/1932 (64%)	1240 (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. There are no such sidechains identified.

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

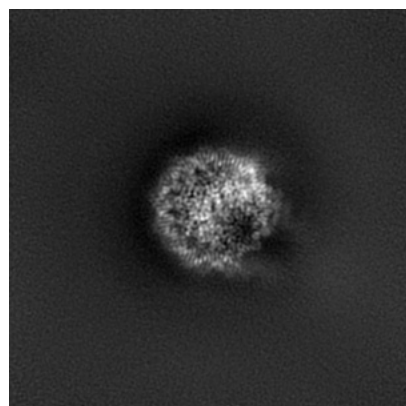
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56669. These allow visual inspection of the internal detail of the map and identification of artifacts.

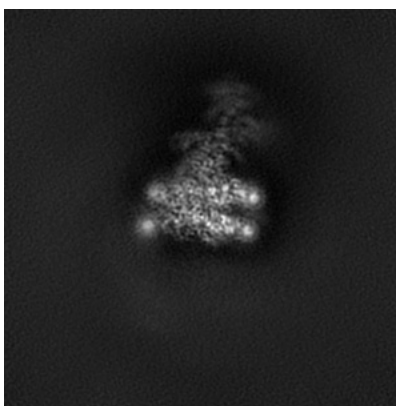
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

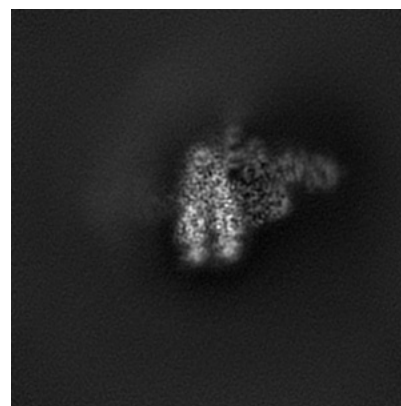
6.1.1 Primary map



X

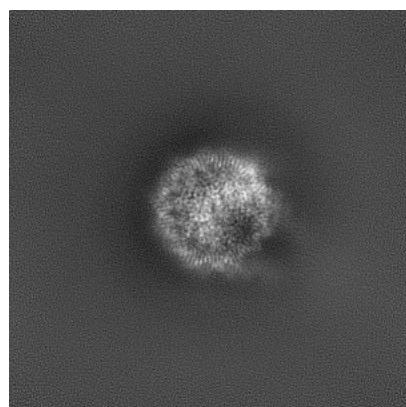


Y

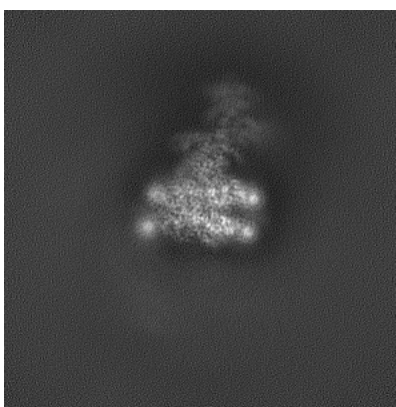


Z

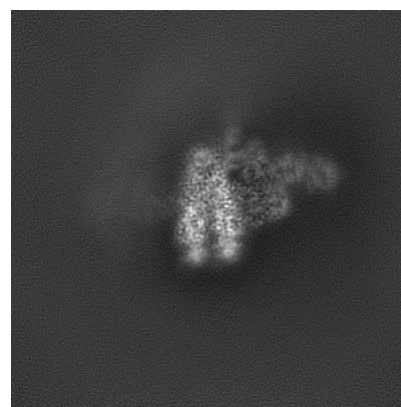
6.1.2 Raw map



X



Y

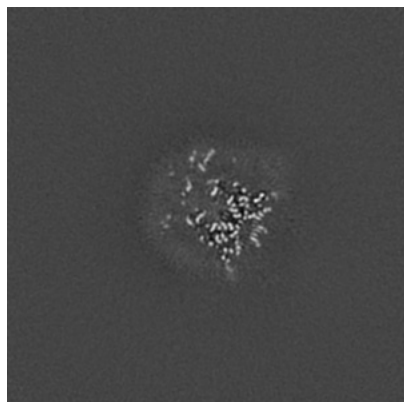


Z

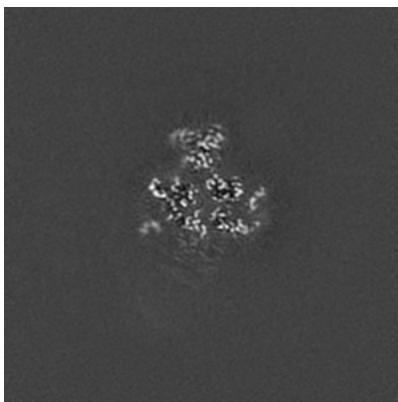
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

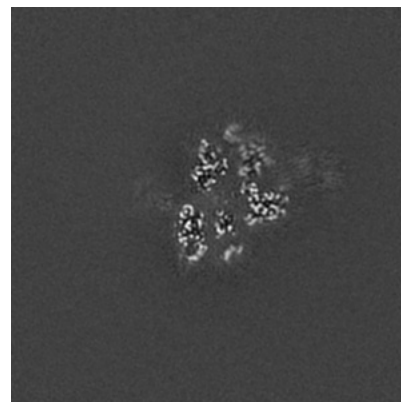
6.2.1 Primary map



X Index: 200

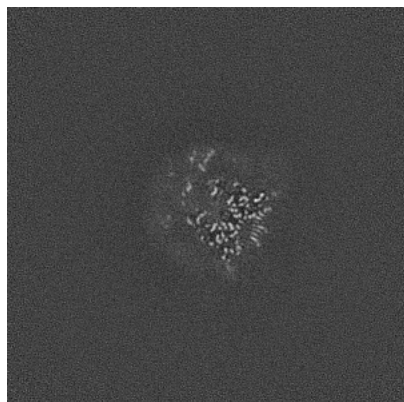


Y Index: 200

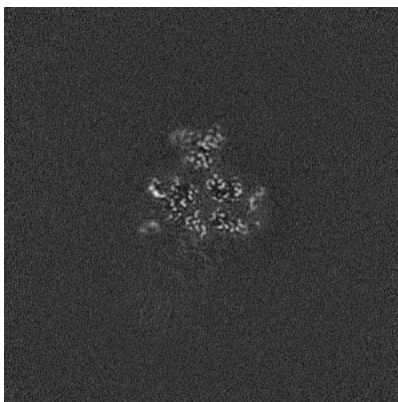


Z Index: 200

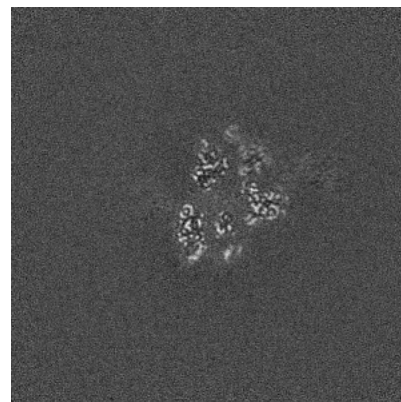
6.2.2 Raw map



X Index: 200



Y Index: 200

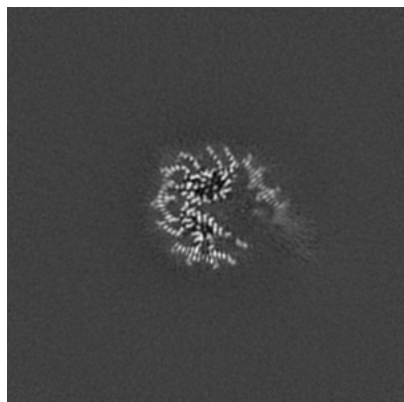


Z Index: 200

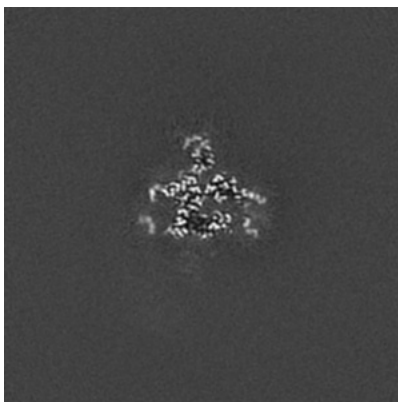
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

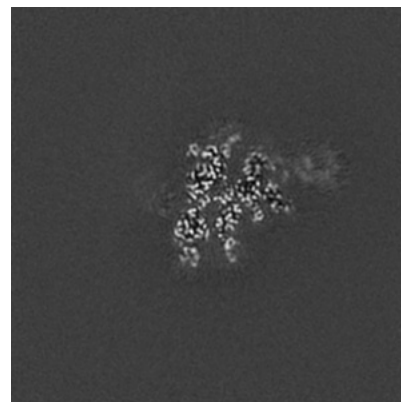
6.3.1 Primary map



X Index: 217

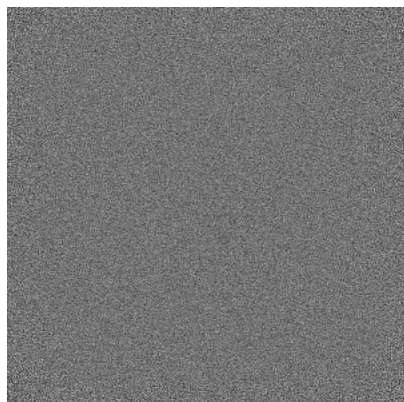


Y Index: 191

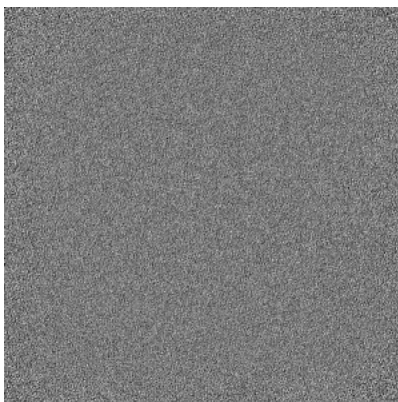


Z Index: 208

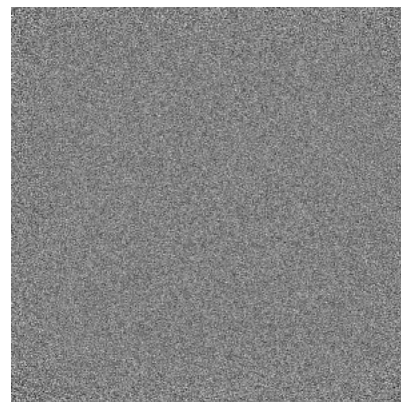
6.3.2 Raw map



X Index: 0



Y Index: 0

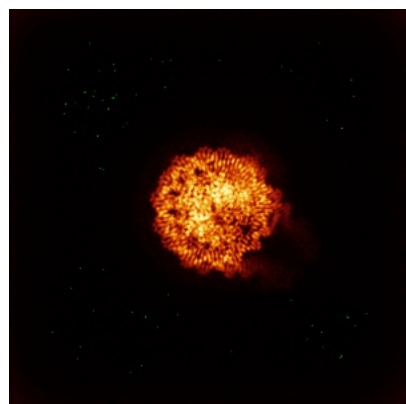


Z Index: 0

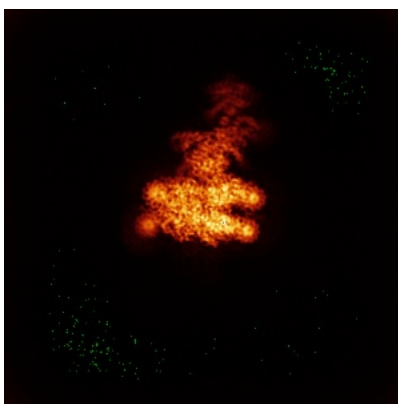
The images above show the largest variance slices of the map in three orthogonal directions.

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

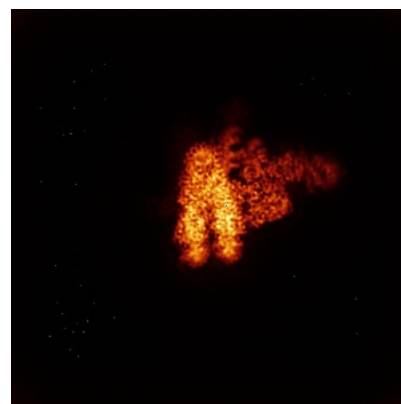
6.4.1 Primary map



X

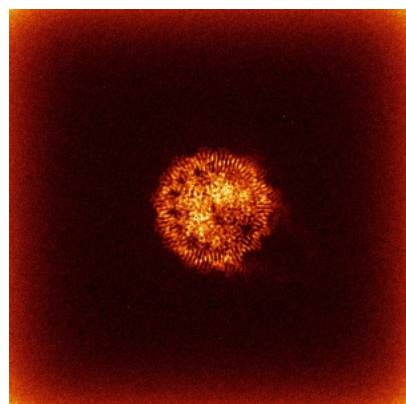


Y

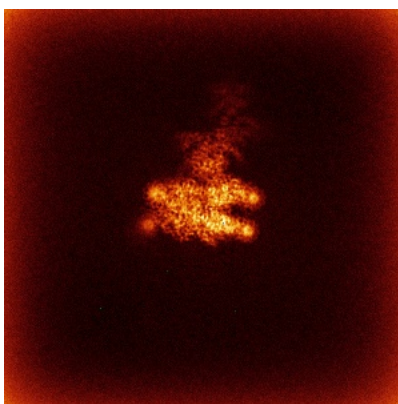


Z

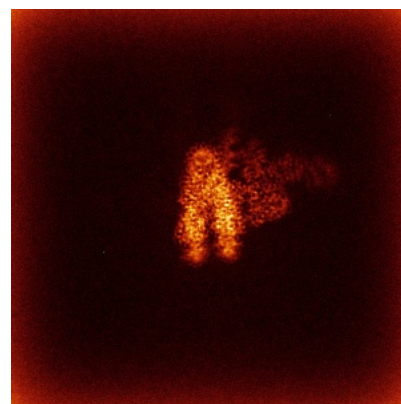
6.4.2 Raw map



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.

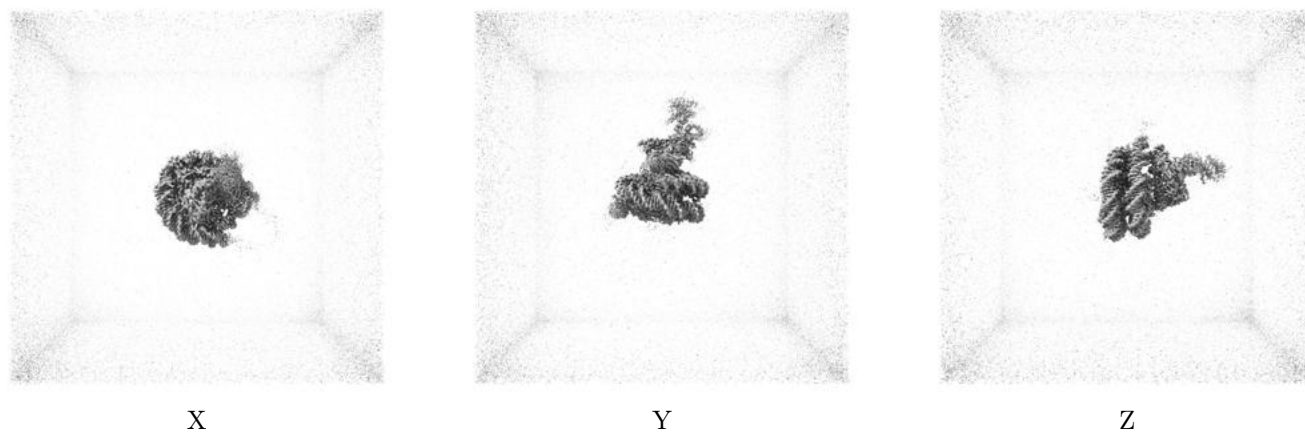
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

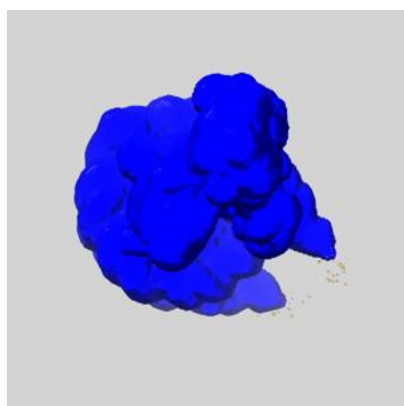
6.6 Mask visualisation [i](#)

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

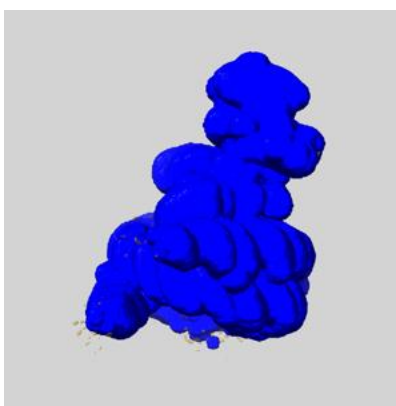
A mask typically either:

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

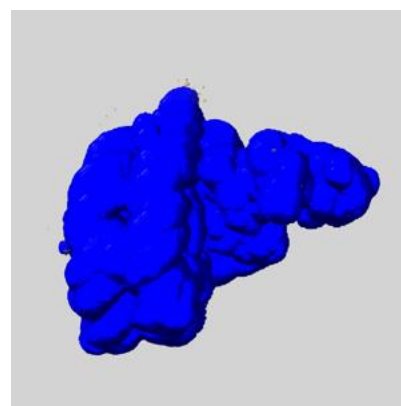
6.6.1 emd_56669_msk_1.map [i](#)



X



Y

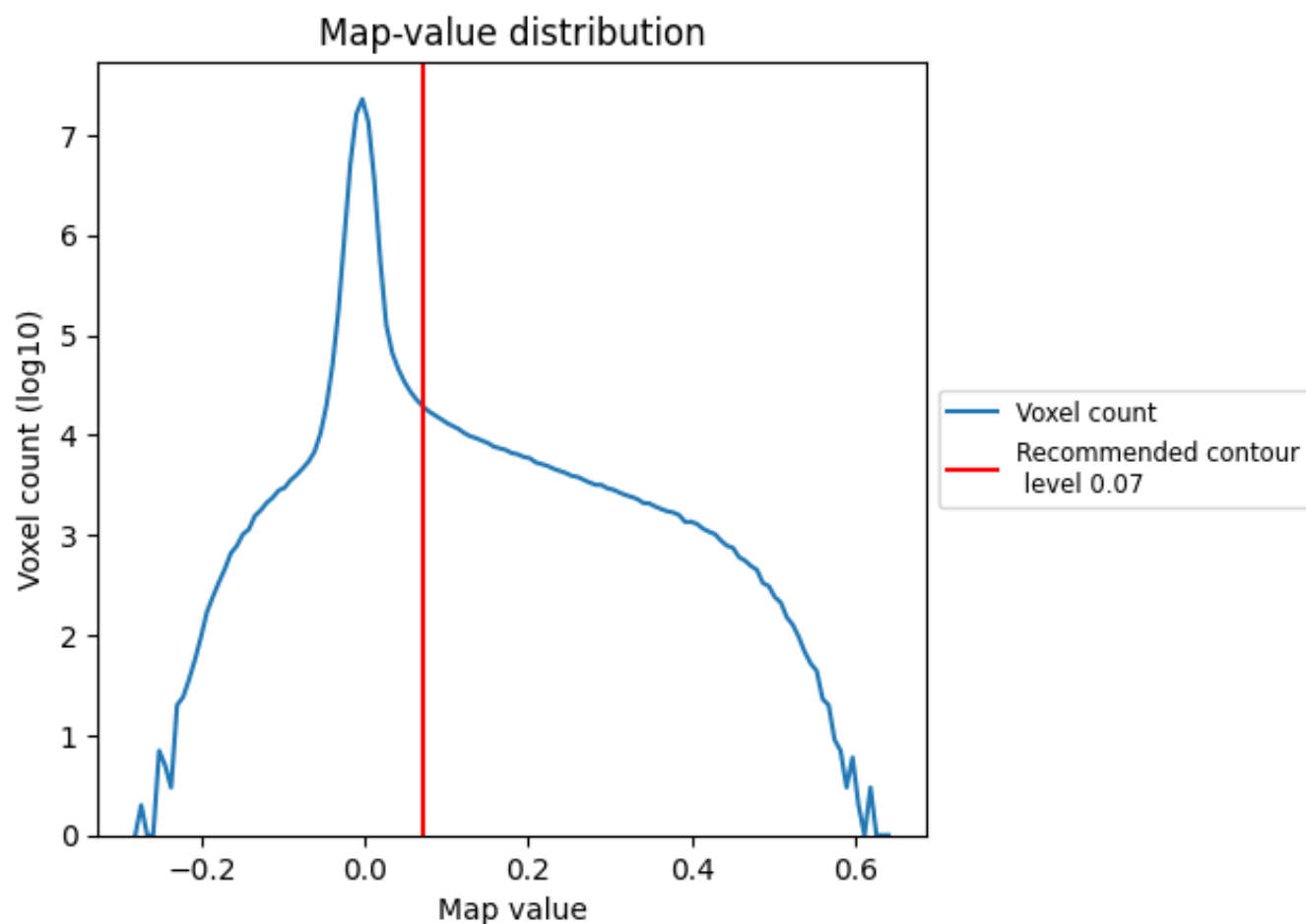


Z

7 Map analysis [i](#)

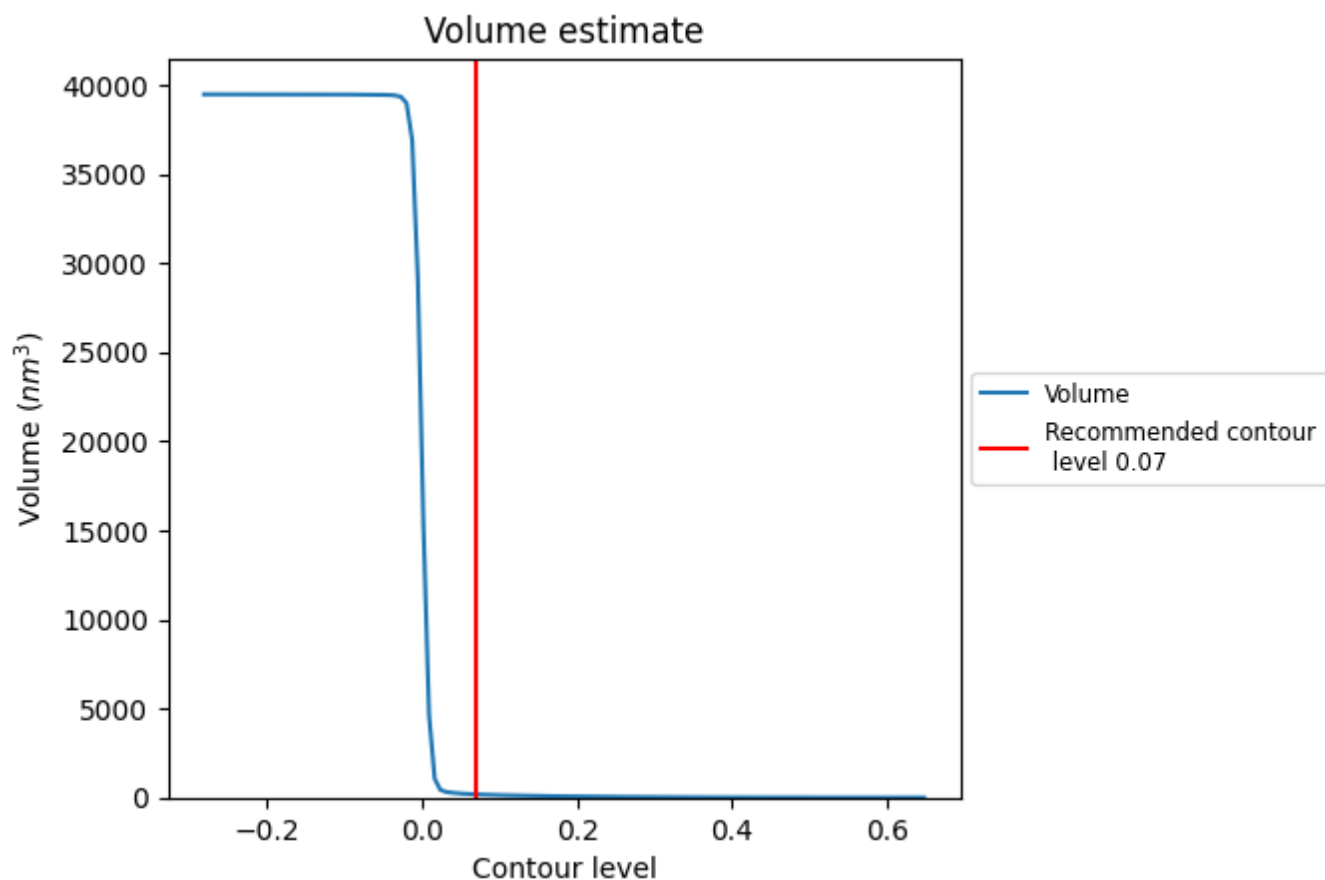
This section contains the results of statistical analysis of the map.

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.

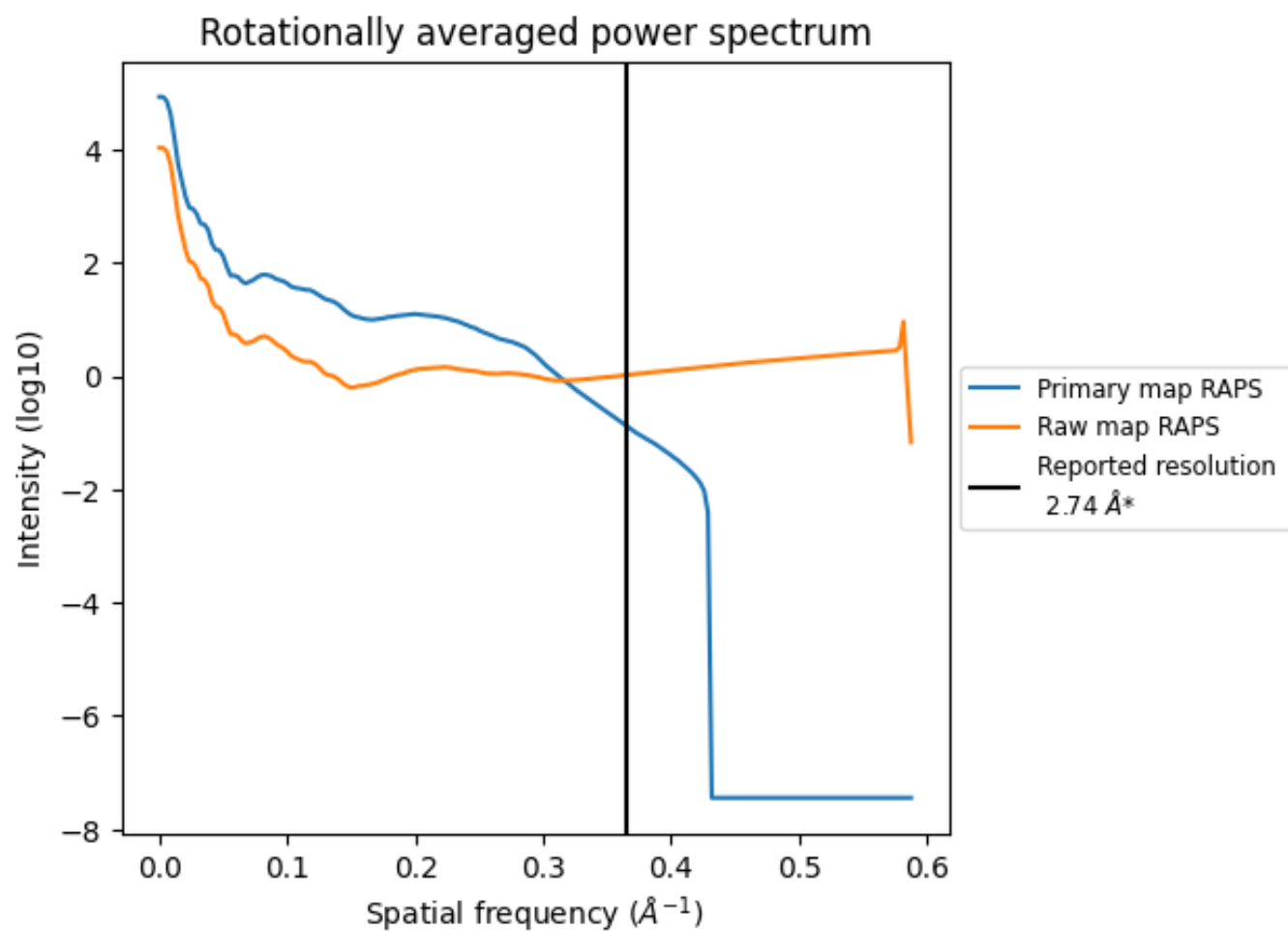
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm^3 ; this corresponds to an approximate mass of 162 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 ⓘ

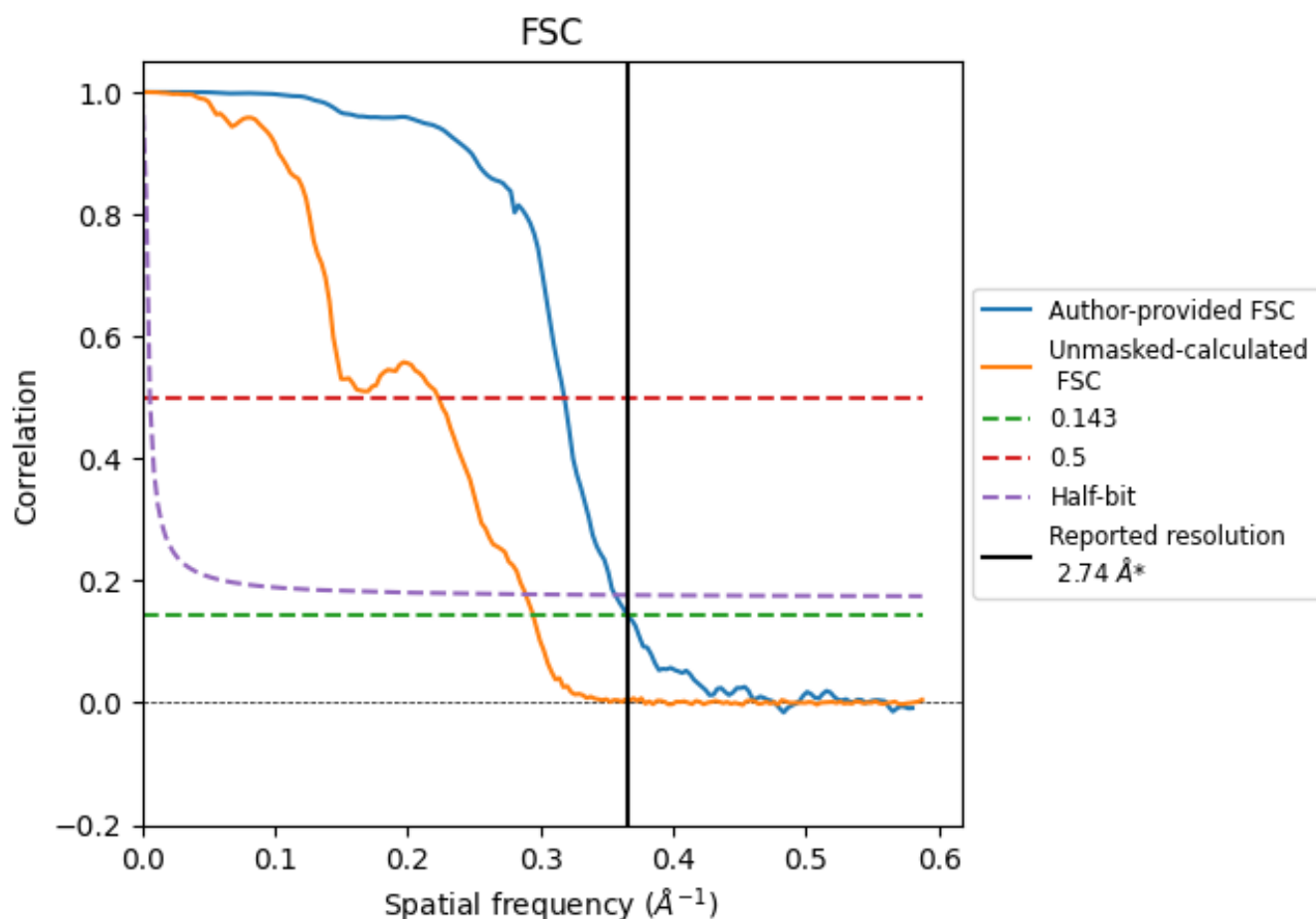


*Reported resolution corresponds to spatial frequency of 0.365 $\text{\AA}^{-1}$

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 0.365 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

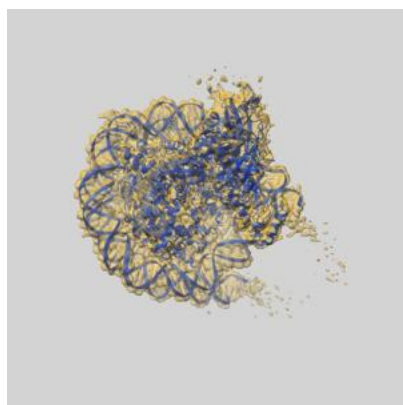
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.74	-	-
Author-provided FSC curve	2.74	3.15	2.81
Unmasked-calculated*	3.40	4.48	3.46

*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 3.40 differs from the reported value 2.74 by more than 10 %

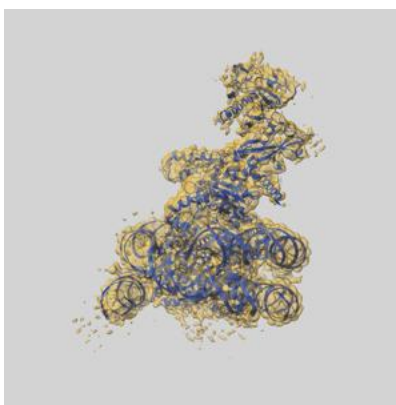
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-56669 and PDB model 28OE. Per-residue inclusion information can be found in section [3](#) on page [8](#).

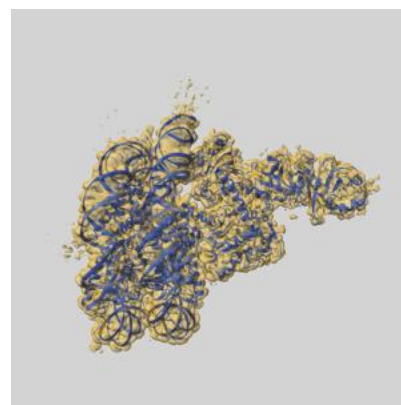
9.1 Map-model overlay [i](#)



X



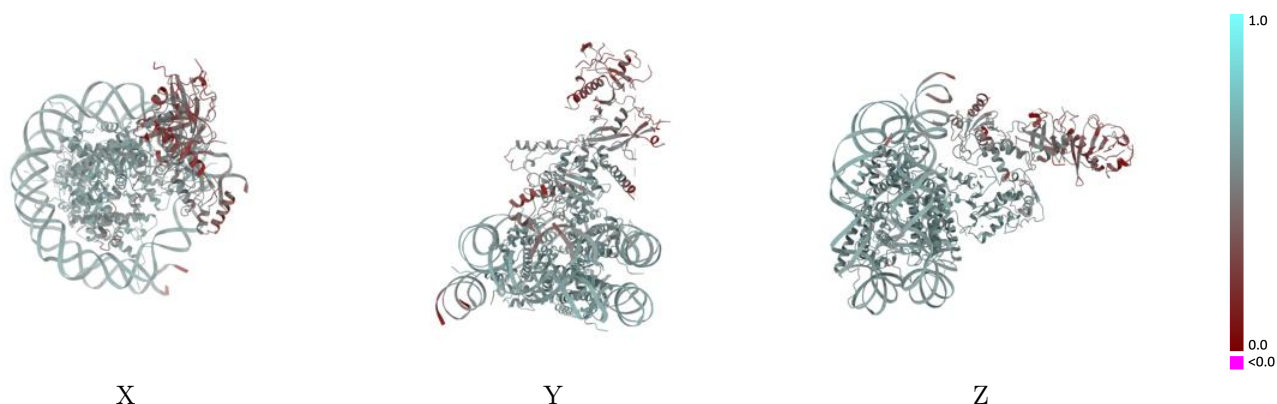
Y



Z

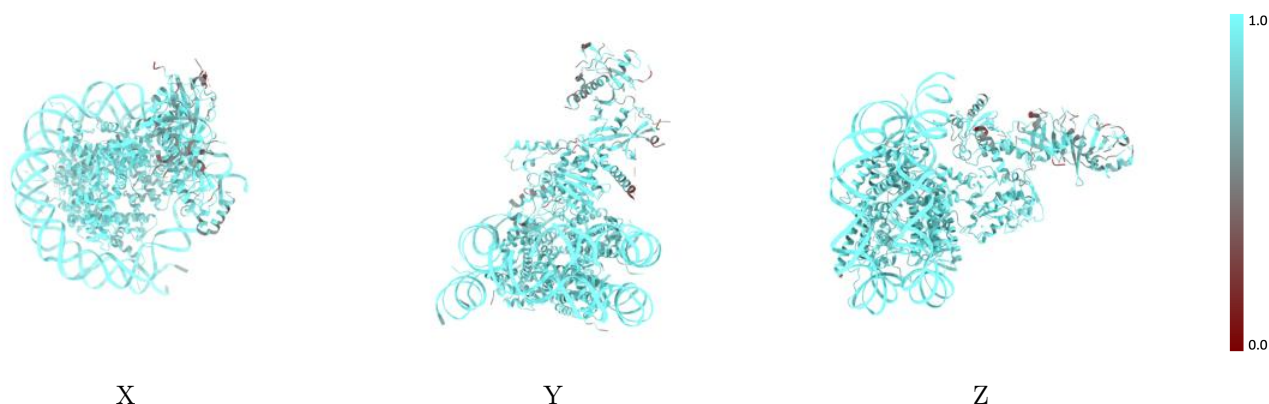
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



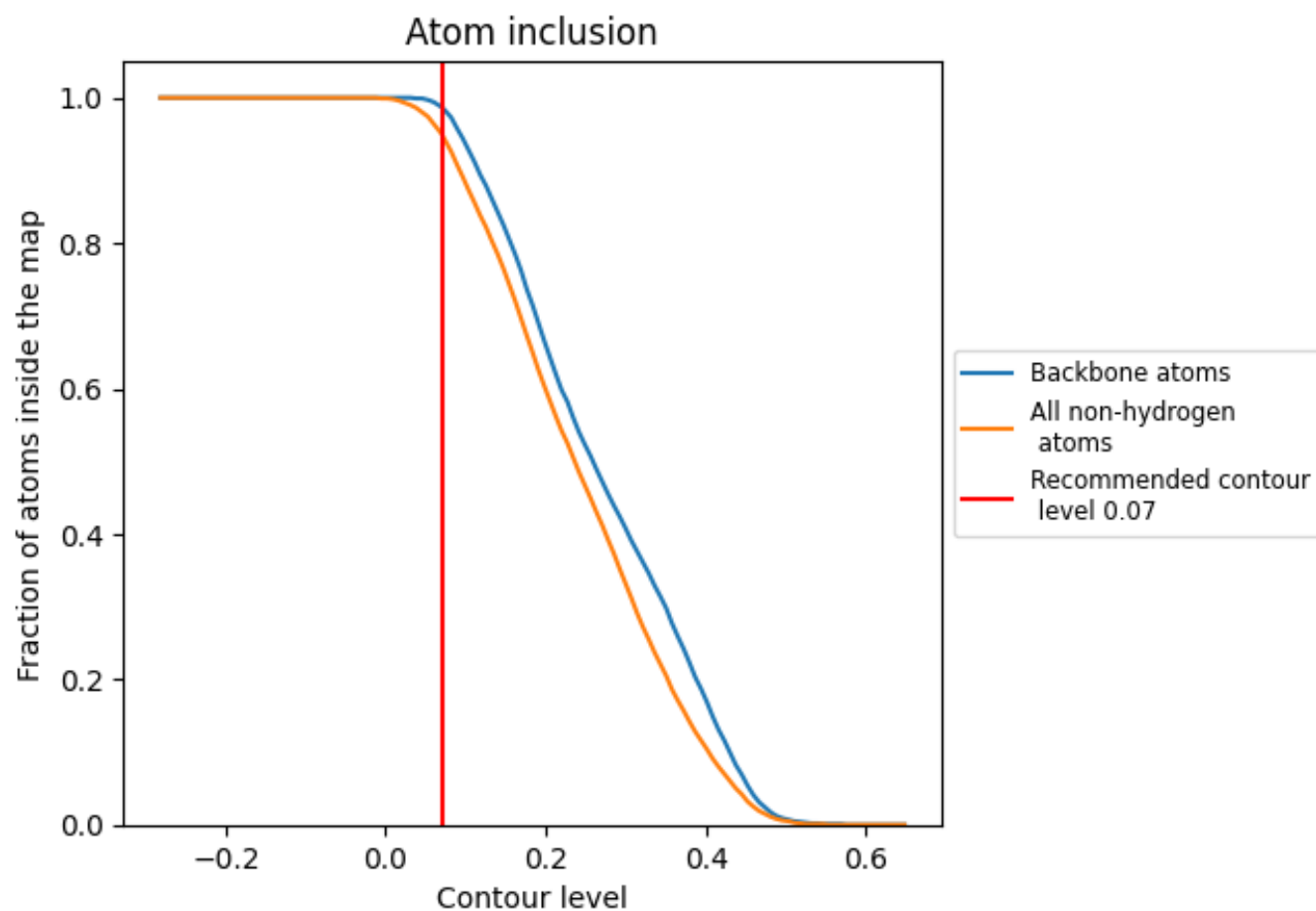
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 95% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9500	0.5360
A	0.7960	0.4450
B	0.7310	0.3490
C	0.8340	0.4310
D	0.8910	0.4870
E	0.8890	0.4620
F	0.9920	0.5960
G	0.9890	0.5950
H	0.9760	0.5870
I	0.9810	0.5770
J	0.9870	0.5950
K	0.9780	0.5920
L	0.9810	0.5820
M	0.9780	0.5720
N	0.9950	0.5590
O	0.9940	0.5560

1.0

0.0

<0.0