



Full wwPDB EM Validation Report ⓘ

Apr 22, 2026 – 12:18 PM JST

PDB ID : 9LIR / pdb_00009lir
EMDB ID : EMD-63121
Title : CryoEM Structures Uncover the Unexpected Hinges of IscB for Enhanced Gene Editing
Authors : Hu, C.Y.; Wang, F.Z.; Ma, S.S.; Zhang, S.F.
Deposited on : 2025-01-14
Resolution : 3.10 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

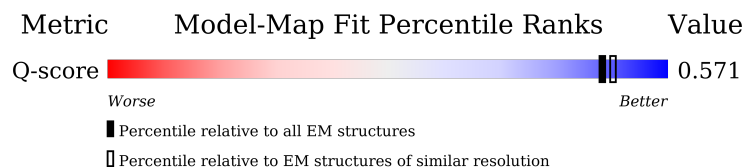
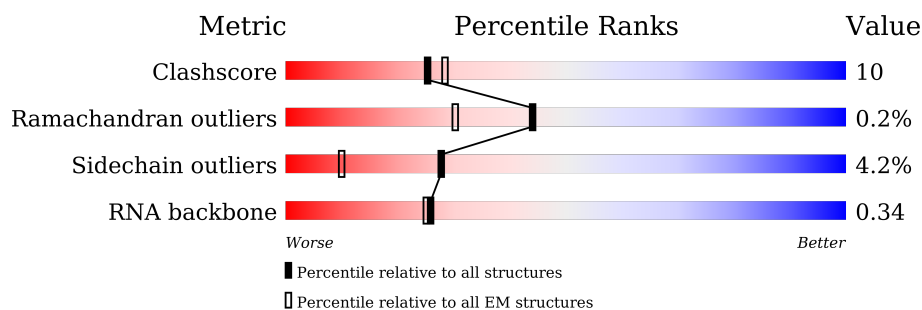
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	194	 33% 55% 12%
2	B	27	 41% 59%
3	C	26	 85% 15%

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Mol	Chain	Length	Quality of chain
4	D	547	62% 27% • 10%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9208 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 RNA chain called RNA (194-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	194	Total	C	N	O	P	0	0
			4141	1850	750	1347	194		

- Molecule 2 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	27	Total	C	N	O	P	0	0
			560	266	103	164	27		

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	26	Total	C	N	O	P	0	0
			527	251	97	153	26		

- Molecule 4 is a protein called Iscb+Twin-Strep-tag.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	494	Total	C	N	O	S	0	0
			3977	2490	763	697	27		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Mg	0
			1	1	
5	D	1	Total	Mg	0
			1	1	

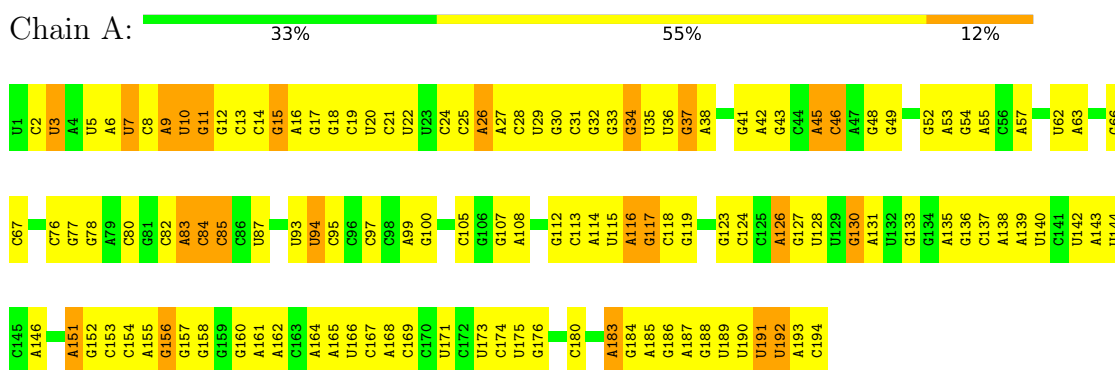
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	D	1	Total	Zn	0
			1	1	

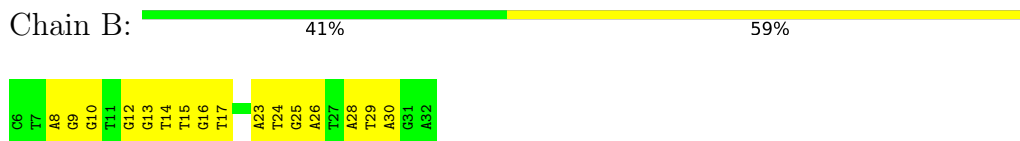
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

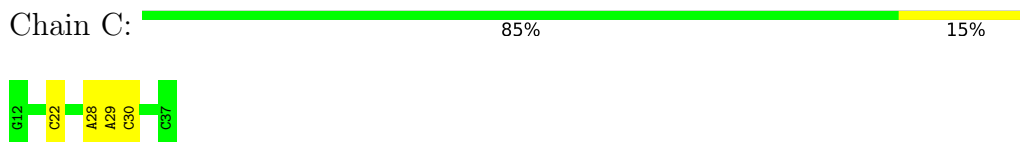
• Molecule 1: RNA (194-MER)



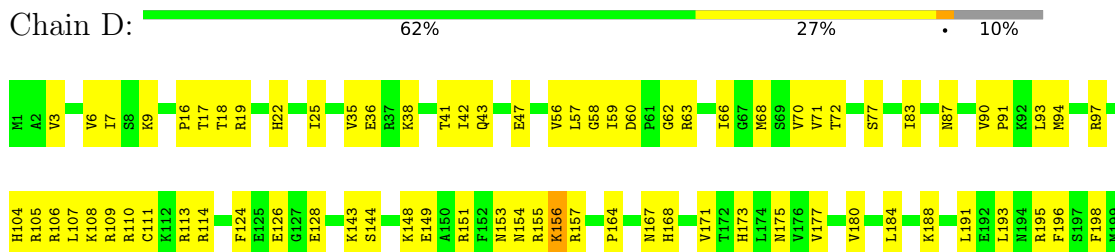
• Molecule 2: DNA (27-MER)



• Molecule 3: DNA (26-MER)



• Molecule 4: Iscb+Twin-Strep-tag



SER	F453	D342	A200
	HIS	A343	M201
	PRO	Y344	L216
	GLN	C345	K219
	PHE	I346	G220
GLU	F463	A347	S221
	LYS	C348	V222
	F469	P360	H233
	V470	V367	K238
	S471	R368	Y244
T472	F493	R375	V248
	Y494	Q376	K252
	VAL	A377	S255
	LYS	C378	L258
	ASN	H379	E259
LYS	GLY	K380	M260
	GLY	L383	R261
	SER	R386	L264
	GLY	Y387	H268
	LYS	Y388	V272
ARG	PRO	M389	H273
	ALA	K392	T274
	ALA	A395	W278
	THR	A418	L282
	LYS	A419	K286
LYS	GLY	D420	K292
	GLY	V421	Y293
	TRP	L424	H294
	SER	GLU	A295
	HIS	GLU	L296
PRO	GLN	Q432	S297
	PHE	Y433	V298
	GLY	K434	L299
	GLY	M440	G304
	GLY	P441	Y305
GLY	GLY	T444	L306
	SER	L445	L310
	GLY	V446	G323
	GLY	E449	Y324
	ALA	T452	L324

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36751	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 ($e^-/\text{\AA}^2$)	49.34	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.459	Depositor
Minimum map value	-0.181	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	213.504, 213.504, 213.504	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.16	0/4632	0.37	0/7218
2	B	0.22	0/628	0.47	0/969
3	C	0.20	0/590	0.40	0/906
4	D	0.19	0/4059	0.52	0/5452
All	All	0.18	0/9909	0.44	0/14545

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	305	TYR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4141	0	2095	64	0
2	B	560	0	306	17	0
3	C	527	0	292	6	0
4	D	3977	0	4048	105	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	D	1	0	0	0	0
All	All	9208	0	6741	165	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 10.

All (165) 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:115:U:H3'	1:A:116:A:H8	1.57	0.70
4:D:126:GLU:HG2	4:D:128:GLU:H	1.58	0.69
4:D:104:HIS:O	4:D:108:LYS:HB3	1.93	0.69
4:D:387:TYR:HB2	4:D:395:ALA:HB3	1.75	0.68
2:B:28:DA:H5''	4:D:304:PRO:HG2	1.76	0.68
4:D:180:VAL:O	4:D:184:LEU:HB2	1.95	0.67
1:A:131:A:H61	1:A:144:U:H3	1.40	0.67
1:A:9:A:H4'	4:D:164:PRO:HD2	1.77	0.67
4:D:38:LYS:HG2	4:D:493:ILE:HG21	1.78	0.66
1:A:62:U:O2	1:A:117:G:N2	2.30	0.65
4:D:83:ILE:HG23	4:D:367:VAL:HB	1.78	0.64
4:D:255:SER:H	4:D:260:ASN:HD22	1.47	0.62
4:D:56:VAL:HG13	4:D:188:LYS:HB2	1.82	0.62
1:A:157:G:H5'	4:D:97:ARG:HD2	1.83	0.61
4:D:171:VAL:O	4:D:175:ASN:HB3	2.01	0.60
3:C:22:DC:H1'	4:D:296:LEU:HD21	1.82	0.60
4:D:106:ARG:HA	4:D:110:ARG:HB3	1.84	0.60
1:A:46:C:H41	1:A:155:A:H2'	1.65	0.60
4:D:124:PHE:HB2	4:D:144:SER:HA	1.83	0.59
4:D:244:TYR:HB3	4:D:261:ARG:HD2	1.85	0.59
2:B:25:DG:H2'	2:B:26:DA:C8	2.38	0.58
4:D:376:GLN:HG2	4:D:434:LYS:HZ1	1.68	0.58
4:D:90:VAL:O	4:D:94:MET:HB3	2.04	0.58
4:D:171:VAL:O	4:D:175:ASN:CB	2.52	0.58
4:D:36:GLU:HB2	4:D:41:THR:HG21	1.86	0.57
1:A:118:C:H2'	1:A:119:G:H8	1.69	0.57
4:D:440:MET:HE3	4:D:441:PRO:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:G:H1	1:A:142:U:H3	1.53	0.57
2:B:8:DA:H3'	2:B:9:DG:C8	2.39	0.57
1:A:14:C:H5'	4:D:143:LYS:HB2	1.87	0.56
4:D:60:ASP:HB2	4:D:343:ALA:HB2	1.86	0.56
1:A:13:C:H5''	4:D:110:ARG:HH21	1.70	0.56
3:C:28:DA:H62	4:D:457:ARG:HH22	1.53	0.55
4:D:387:TYR:HB3	4:D:424:LEU:HD12	1.87	0.55
1:A:41:G:H2'	1:A:42:A:H8	1.72	0.55
1:A:99:A:H3'	1:A:100:G:H8	1.72	0.55
1:A:46:C:H1'	4:D:378:CYS:H	1.72	0.55
1:A:156:G:H5'	4:D:375:ARG:HB2	1.89	0.54
4:D:418:ALA:HA	4:D:421:VAL:HB	1.89	0.54
4:D:216:LEU:HA	4:D:219:LYS:HE2	1.90	0.54
2:B:29:DT:H4'	4:D:195:ARG:HA	1.89	0.54
4:D:87:ASN:HA	4:D:90:VAL:HB	1.90	0.54
1:A:37:G:H2'	1:A:38:A:H8	1.73	0.54
1:A:24:C:H42	1:A:38:A:H61	1.55	0.53
1:A:12:G:H5''	4:D:148:LYS:HB3	1.90	0.53
4:D:63:ARG:HB3	4:D:295:ALA:HB1	1.91	0.53
1:A:10:U:H2'	1:A:11:G:C8	2.44	0.53
2:B:29:DT:H2'	2:B:30:DA:C8	2.43	0.53
4:D:458:SER:HA	4:D:469:PHE:HB3	1.91	0.53
1:A:118:C:H2'	1:A:119:G:C8	2.44	0.53
2:B:29:DT:H2'	2:B:30:DA:H8	1.74	0.53
1:A:62:U:H3	1:A:117:G:H1	1.57	0.52
4:D:62:GLY:HA2	4:D:299:LEU:HB3	1.91	0.52
1:A:41:G:H2'	1:A:42:A:C8	2.45	0.52
3:C:30:DC:H5'	4:D:432:GLN:HG2	1.92	0.51
4:D:56:VAL:HG22	4:D:188:LYS:HD3	1.92	0.51
1:A:184:G:H2'	1:A:185:A:C8	2.45	0.51
4:D:268:HIS:HD2	4:D:278:TRP:HZ3	1.57	0.51
1:A:158:G:H4'	4:D:168:HIS:CD2	2.46	0.51
1:A:117:G:H5''	4:D:149:GLU:HB3	1.92	0.51
1:A:112:G:H1'	4:D:154:ASN:CG	2.36	0.50
2:B:28:DA:H2'	2:B:29:DT:C6	2.46	0.50
4:D:399:HIS:HA	4:D:410:GLU:HB2	1.92	0.50
4:D:341:LEU:HD13	4:D:360:PRO:HG2	1.92	0.50
1:A:25:C:H2'	1:A:26:A:C8	2.46	0.50
4:D:22:HIS:HA	4:D:25:ILE:HB	1.94	0.49
4:D:111:CYS:HA	4:D:114:ARG:HD3	1.95	0.49
4:D:444:ILE:HG12	4:D:446:VAL:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:368:ARG:HE	4:D:472:THR:HG21	1.75	0.49
1:A:112:G:H2'	1:A:113:C:C6	2.48	0.49
4:D:343:ALA:HA	4:D:346:ILE:HB	1.94	0.49
1:A:48:G:H2'	1:A:49:G:C8	2.48	0.49
4:D:3:VAL:HB	4:D:18:THR:HG21	1.95	0.49
1:A:152:G:H2'	1:A:153:C:C6	2.47	0.49
4:D:222:VAL:HG13	4:D:258:LEU:HD22	1.95	0.49
2:B:24:DT:H2'	2:B:25:DG:C8	2.48	0.48
4:D:167:ASN:O	4:D:171:VAL:HG23	2.12	0.48
1:A:183:A:H2'	1:A:184:G:C8	2.48	0.48
4:D:272:VAL:HG21	4:D:282:LEU:HD12	1.94	0.48
4:D:216:LEU:HD13	4:D:221:SER:HA	1.95	0.48
4:D:19:ARG:HD2	4:D:22:HIS:HB3	1.96	0.48
1:A:152:G:H2'	1:A:153:C:H6	1.79	0.48
1:A:183:A:H2'	1:A:184:G:H8	1.78	0.48
4:D:68:MET:HE2	4:D:173:HIS:HD2	1.79	0.48
4:D:56:VAL:H	4:D:72:THR:HA	1.80	0.47
2:B:15:DT:H2''	2:B:16:DG:H5''	1.96	0.47
1:A:117:G:H2'	1:A:118:C:C6	2.49	0.47
1:A:130:G:H2'	1:A:131:A:H8	1.79	0.47
2:B:13:DG:H1	3:C:30:DC:H42	1.63	0.47
2:B:23:DA:H2'	2:B:24:DT:C6	2.50	0.47
4:D:379:HIS:HD2	4:D:380:LYS:HG2	1.80	0.47
2:B:12:DG:H2''	2:B:13:DG:H8	1.80	0.47
1:A:9:A:H2'	1:A:10:U:C6	2.51	0.46
4:D:293:TYR:HB3	4:D:296:LEU:HB2	1.96	0.46
1:A:42:A:H2'	1:A:43:G:C8	2.49	0.46
1:A:94:U:H3	1:A:97:C:H41	1.63	0.46
1:A:19:C:H5'	4:D:428:HIS:CE1	2.50	0.46
3:C:29:DA:H5'	4:D:434:LYS:HB3	1.98	0.46
4:D:156:LYS:HA	4:D:156:LYS:HD2	1.72	0.46
4:D:292:LYS:HD3	4:D:292:LYS:HA	1.69	0.46
1:A:7:U:H1'	4:D:297:SER:HB3	1.98	0.46
1:A:21:C:H2'	1:A:22:U:H6	1.81	0.46
4:D:114:ARG:HG2	4:D:144:SER:HB2	1.98	0.45
4:D:286:LYS:HA	4:D:286:LYS:HD2	1.64	0.45
4:D:9:LYS:HD3	4:D:47:GLU:HA	1.99	0.45
2:B:25:DG:H2''	2:B:26:DA:H5'	1.98	0.45
4:D:195:ARG:HH22	4:D:323:GLY:H	1.62	0.45
4:D:71:VAL:HB	4:D:77:SER:HB2	1.98	0.45
4:D:6:VAL:HG21	4:D:17:THR:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:57:LEU:HD12	4:D:70:VAL:HG22	1.99	0.45
4:D:59:ILE:HD11	4:D:177:VAL:HG21	1.99	0.45
4:D:200:ALA:C	4:D:202:ASN:H	2.25	0.45
4:D:233:HIS:CE1	4:D:238:LYS:HA	2.52	0.45
4:D:63:ARG:HD3	4:D:295:ALA:HA	1.98	0.44
1:A:87:U:O4	1:A:105:C:N3	2.51	0.44
4:D:16:PRO:HB2	4:D:18:THR:HG22	1.98	0.44
4:D:196:PHE:HB3	4:D:198:PHE:CE1	2.52	0.43
1:A:15:G:H2'	1:A:16:A:C8	2.53	0.43
1:A:82:C:H2'	1:A:83:A:C8	2.52	0.43
1:A:151:A:C8	4:D:113:ARG:HG2	2.53	0.43
2:B:9:DG:H2''	2:B:10:DG:O5'	2.19	0.43
4:D:387:TYR:CZ	4:D:409:LEU:HD22	2.53	0.43
1:A:2:C:H2'	1:A:3:U:C6	2.54	0.43
2:B:17:DT:H6	2:B:17:DT:H2'	1.65	0.43
1:A:123:G:H2'	1:A:124:C:C6	2.54	0.43
4:D:155:ARG:HB3	4:D:157:ARG:HD2	1.99	0.43
1:A:45:A:C6	4:D:107:LEU:HD23	2.54	0.42
1:A:191:U:H2'	1:A:192:U:C2	2.54	0.42
4:D:58:GLY:HA3	4:D:347:ALA:HB2	2.00	0.42
3:C:22:DC:C2	4:D:296:LEU:HD11	2.54	0.42
4:D:105:ARG:O	4:D:109:ARG:HB3	2.19	0.42
2:B:13:DG:H2''	2:B:14:DT:H71	2.01	0.42
4:D:264:LEU:HD12	4:D:264:LEU:HA	1.92	0.42
1:A:126:A:H2'	1:A:127:G:C8	2.54	0.42
4:D:463:LYS:HA	4:D:463:LYS:HD3	1.85	0.42
4:D:248:VAL:HG12	4:D:252:LYS:HB2	2.02	0.42
1:A:18:G:O2'	4:D:383:LEU:HA	2.20	0.42
2:B:14:DT:H2''	2:B:15:DT:H5'	2.01	0.41
4:D:196:PHE:CD2	4:D:299:LEU:HD11	2.55	0.41
1:A:117:G:H5''	4:D:149:GLU:HG3	2.03	0.41
4:D:452:LEU:HD23	4:D:452:LEU:H	1.84	0.41
1:A:11:G:H2'	1:A:12:G:C8	2.55	0.41
1:A:131:A:N6	1:A:144:U:H3	2.13	0.41
1:A:133:G:H22	1:A:142:U:H3	1.69	0.41
1:A:42:A:H2'	1:A:43:G:H8	1.86	0.41
4:D:63:ARG:CZ	4:D:91:PRO:HG2	2.51	0.41
4:D:7:ILE:HB	4:D:43:GLN:HG2	2.02	0.41
4:D:151:ARG:HB3	4:D:155:ARG:HH22	1.86	0.41
1:A:34:G:H2'	1:A:35:U:C6	2.55	0.41
4:D:195:ARG:HH12	4:D:323:GLY:H	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:453:PHE:CD2	4:D:471:SER:HB3	2.55	0.41
1:A:142:U:H2'	1:A:143:A:C8	2.56	0.41
4:D:389:MET:HE1	4:D:420:ASP:HB3	2.02	0.41
1:A:84:C:N3	4:D:153:ASN:HB2	2.35	0.40
4:D:63:ARG:O	4:D:66:ILE:HG13	2.21	0.40
1:A:85:C:H5''	4:D:156:LYS:HB3	2.02	0.40
1:A:117:G:H2'	1:A:118:C:H6	1.86	0.40
4:D:93:LEU:HA	4:D:93:LEU:HD12	1.84	0.40
1:A:14:C:H5'	4:D:143:LYS:HE2	2.03	0.40
1:A:48:G:H2'	1:A:49:G:H8	1.85	0.40
1:A:173:U:H2'	1:A:174:C:C6	2.57	0.40
4:D:6:VAL:HG21	4:D:17:THR:HG22	2.02	0.40
1:A:55:A:H61	1:A:124:C:H42	1.69	0.40
4:D:191:LEU:HD13	4:D:310:LEU:HD11	2.03	0.40
4:D:345:CYS:HA	4:D:348:CYS:H	1.85	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
4	D	492/547 (90%)	436 (89%)	55 (11%)	1 (0%)	43 73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	446	VAL

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
4	D	428/463 (92%)	410 (96%)	18 (4%)	26 58

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	35	VAL
4	D	42	ILE
4	D	156	LYS
4	D	193	LEU
4	D	216	LEU
4	D	258	LEU
4	D	274	THR
4	D	282	LEU
4	D	299	LEU
4	D	306	LEU
4	D	386	ARG
4	D	392	LYS
4	D	421	VAL
4	D	427	LYS
4	D	444	ILE
4	D	449	GLU
4	D	453	PHE
4	D	470	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	210	GLN
4	D	324	GLN
4	D	379	HIS
4	D	382	ASN
4	D	404	GLN
4	D	428	HIS
4	D	432	GLN

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Mol	Chain	Res	Type
4	D	488	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	193/194 (99%)	80 (41%)	4 (2%)

All (80) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	U
1	A	5	U
1	A	6	A
1	A	7	U
1	A	8	C
1	A	9	A
1	A	10	U
1	A	11	G
1	A	15	G
1	A	17	G
1	A	20	U
1	A	26	A
1	A	27	A
1	A	28	C
1	A	30	G
1	A	31	C
1	A	32	G
1	A	33	G
1	A	34	G
1	A	36	U
1	A	37	G
1	A	45	A
1	A	46	C
1	A	52	G
1	A	53	A
1	A	54	G
1	A	57	A
1	A	63	A
1	A	66	G
1	A	67	C
1	A	76	C

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Mol	Chain	Res	Type
1	A	77	G
1	A	78	G
1	A	80	C
1	A	84	C
1	A	85	C
1	A	93	U
1	A	94	U
1	A	95	C
1	A	107	G
1	A	108	A
1	A	114	A
1	A	116	A
1	A	117	G
1	A	126	A
1	A	128	U
1	A	130	G
1	A	135	A
1	A	136	G
1	A	137	C
1	A	138	A
1	A	139	A
1	A	140	U
1	A	146	A
1	A	151	A
1	A	154	C
1	A	156	G
1	A	160	G
1	A	161	A
1	A	162	A
1	A	164	A
1	A	165	A
1	A	166	U
1	A	167	C
1	A	168	A
1	A	169	C
1	A	171	U
1	A	175	U
1	A	176	G
1	A	180	C
1	A	183	A
1	A	186	G
1	A	187	A

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Mol	Chain	Res	Type
1	A	188	G
1	A	189	U
1	A	190	U
1	A	191	U
1	A	192	U
1	A	193	A
1	A	194	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	29	U
1	A	45	A
1	A	83	A
1	A	191	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 ⓘ

There are no chain breaks in this entry.

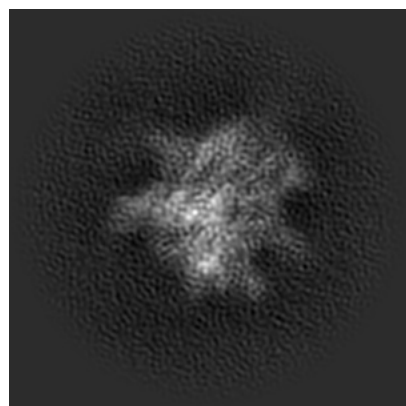
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63121. These allow visual inspection of the internal detail of the map and identification of artifacts.

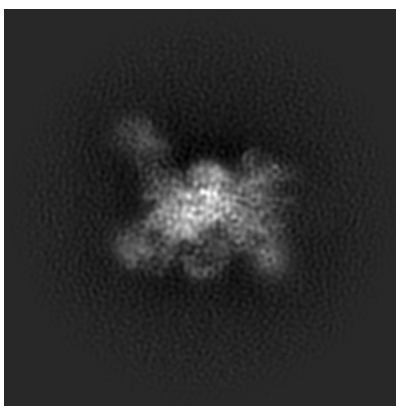
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

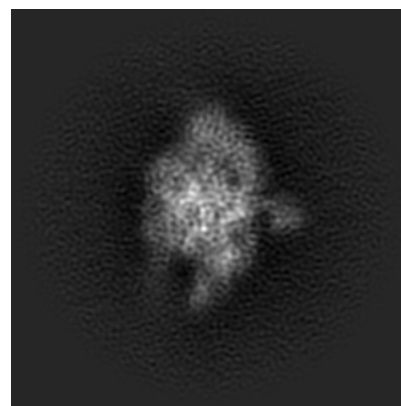
6.1.1 Primary map



X

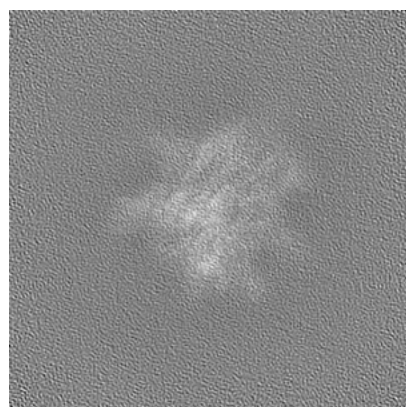


Y

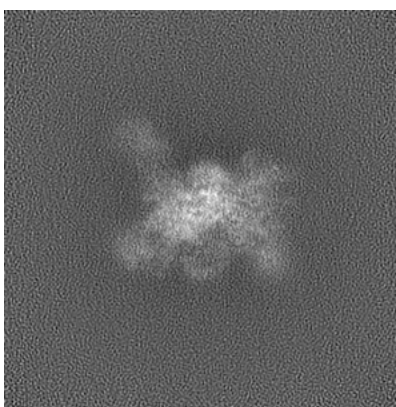


Z

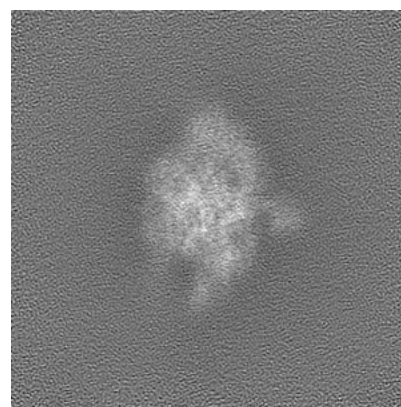
6.1.2 Raw map



X



Y

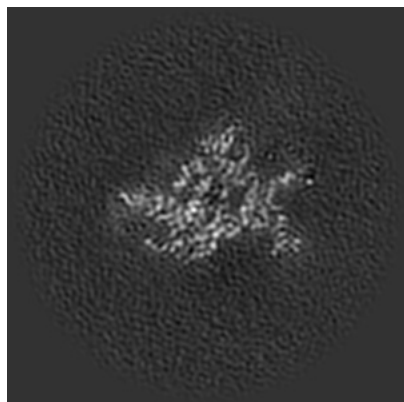


Z

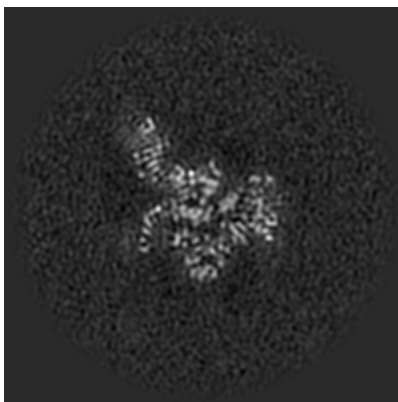
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

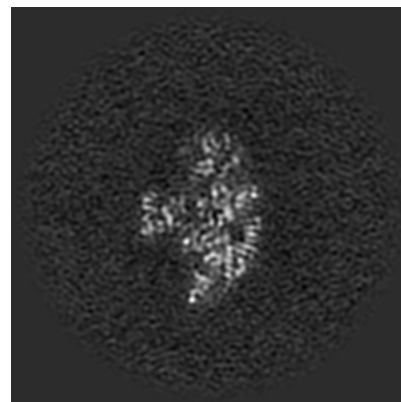
6.2.1 Primary map



X Index: 128

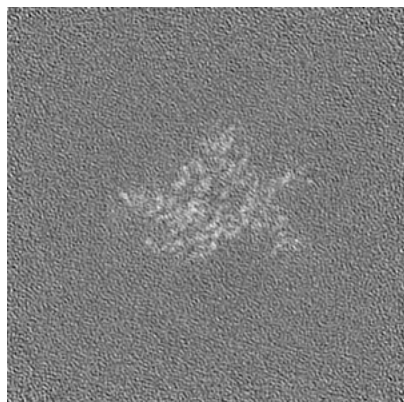


Y Index: 128

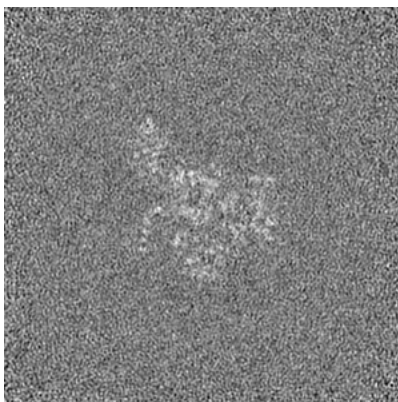


Z Index: 128

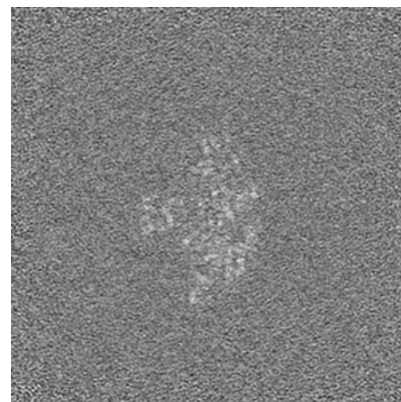
6.2.2 Raw map



X Index: 128



Y Index: 128

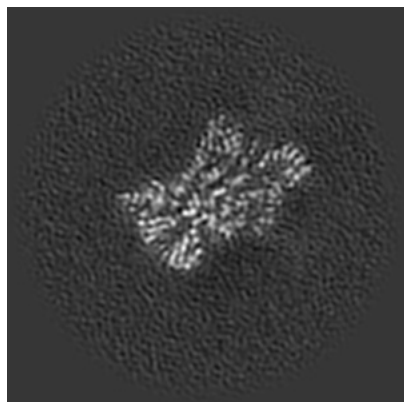


Z Index: 128

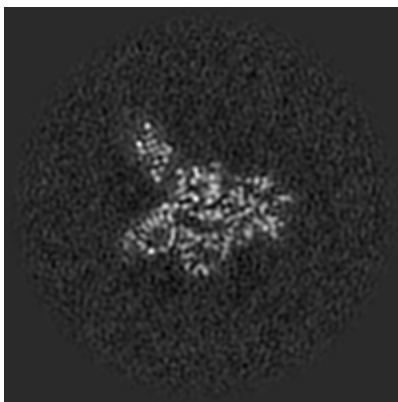
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

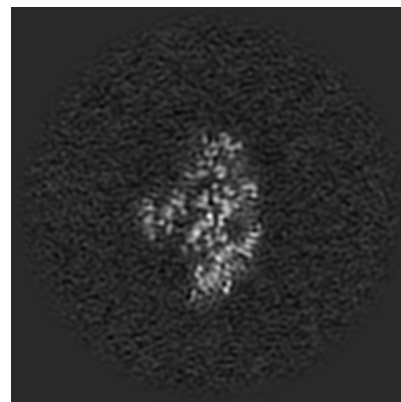
6.3.1 Primary map



X Index: 135

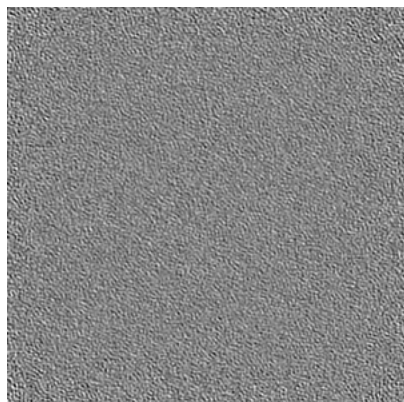


Y Index: 132

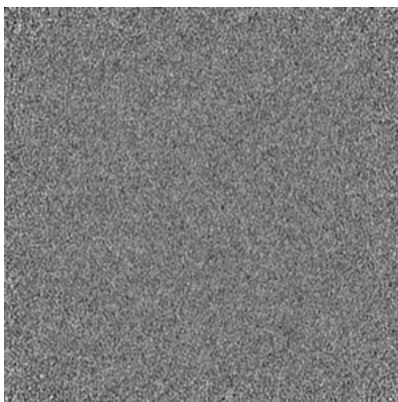


Z Index: 130

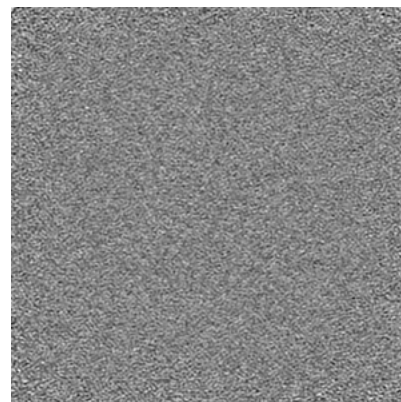
6.3.2 Raw map



X Index: 0



Y Index: 0

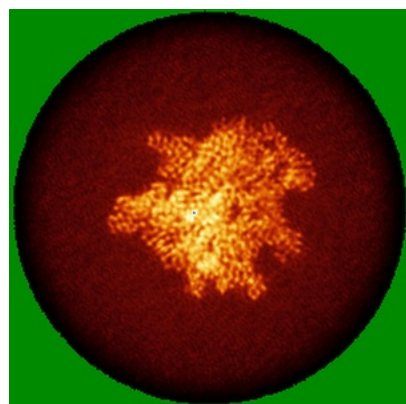


Z Index: 0

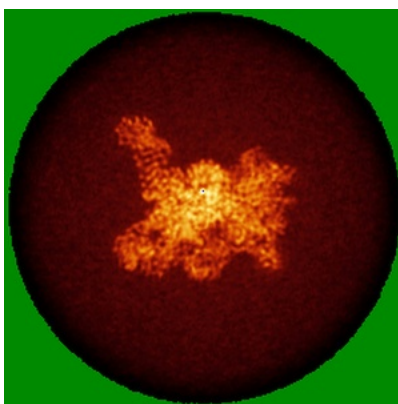
The images above show the largest variance slices of the map in three orthogonal directions.

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

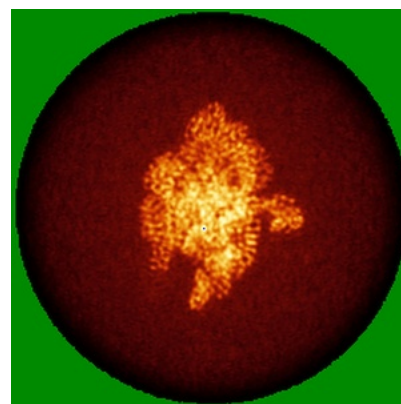
6.4.1 Primary map



X

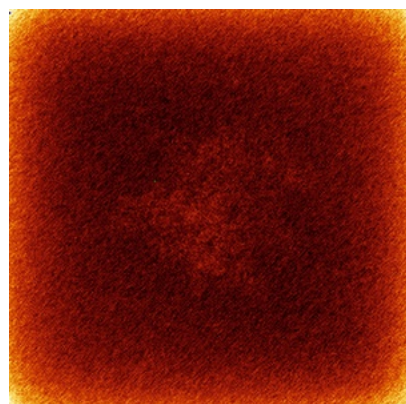


Y

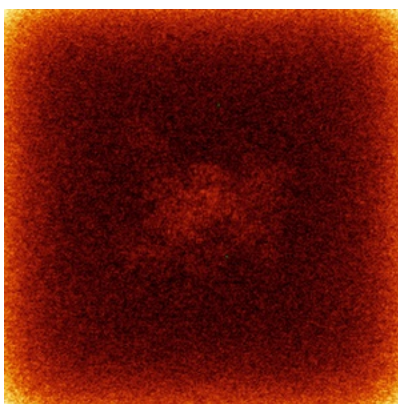


Z

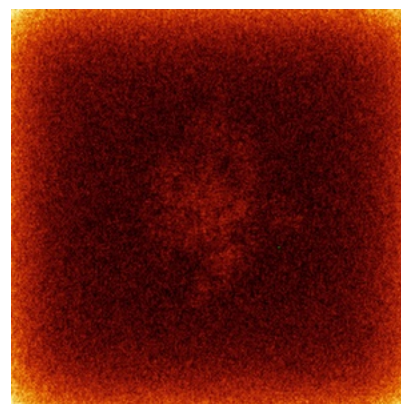
6.4.2 Raw map



X



Y

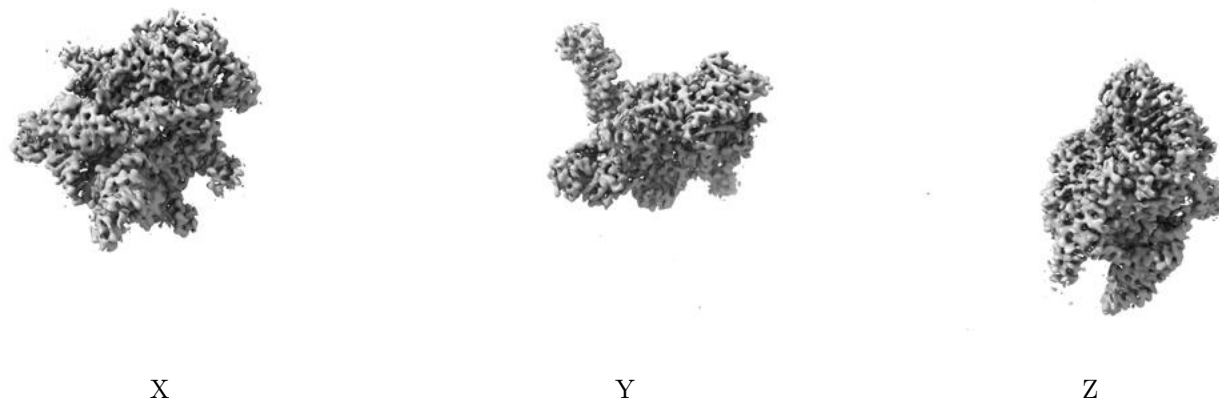


Z

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.

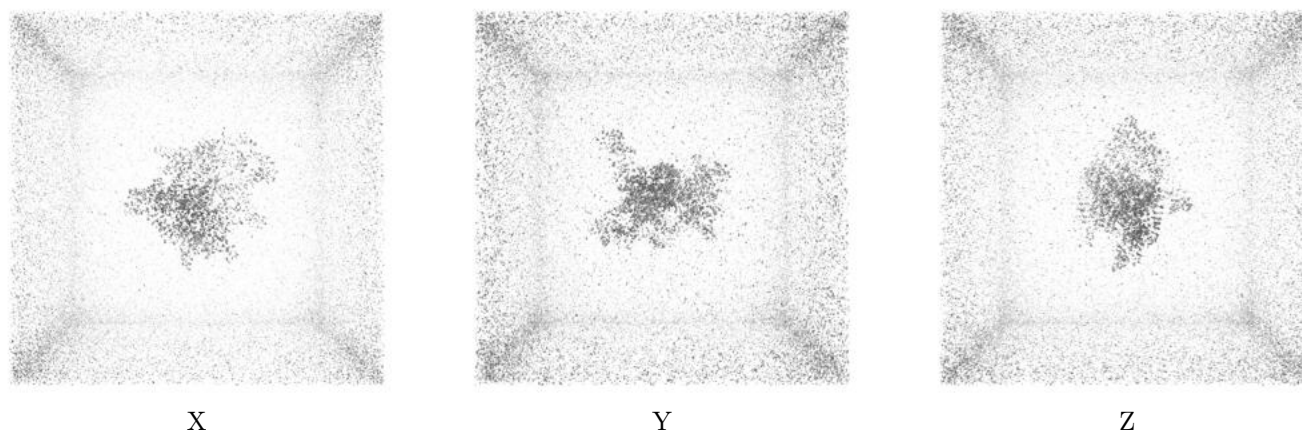
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

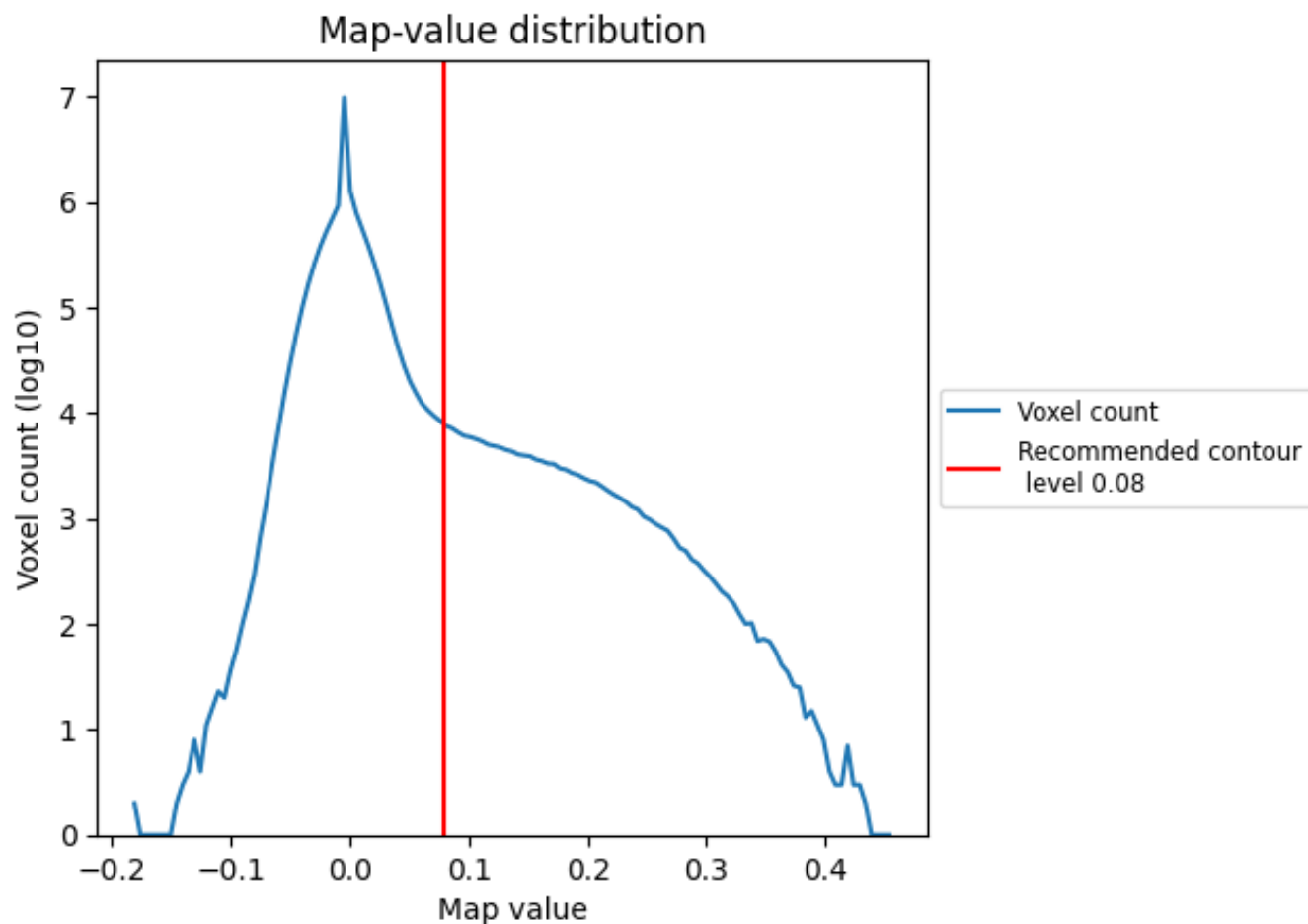
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

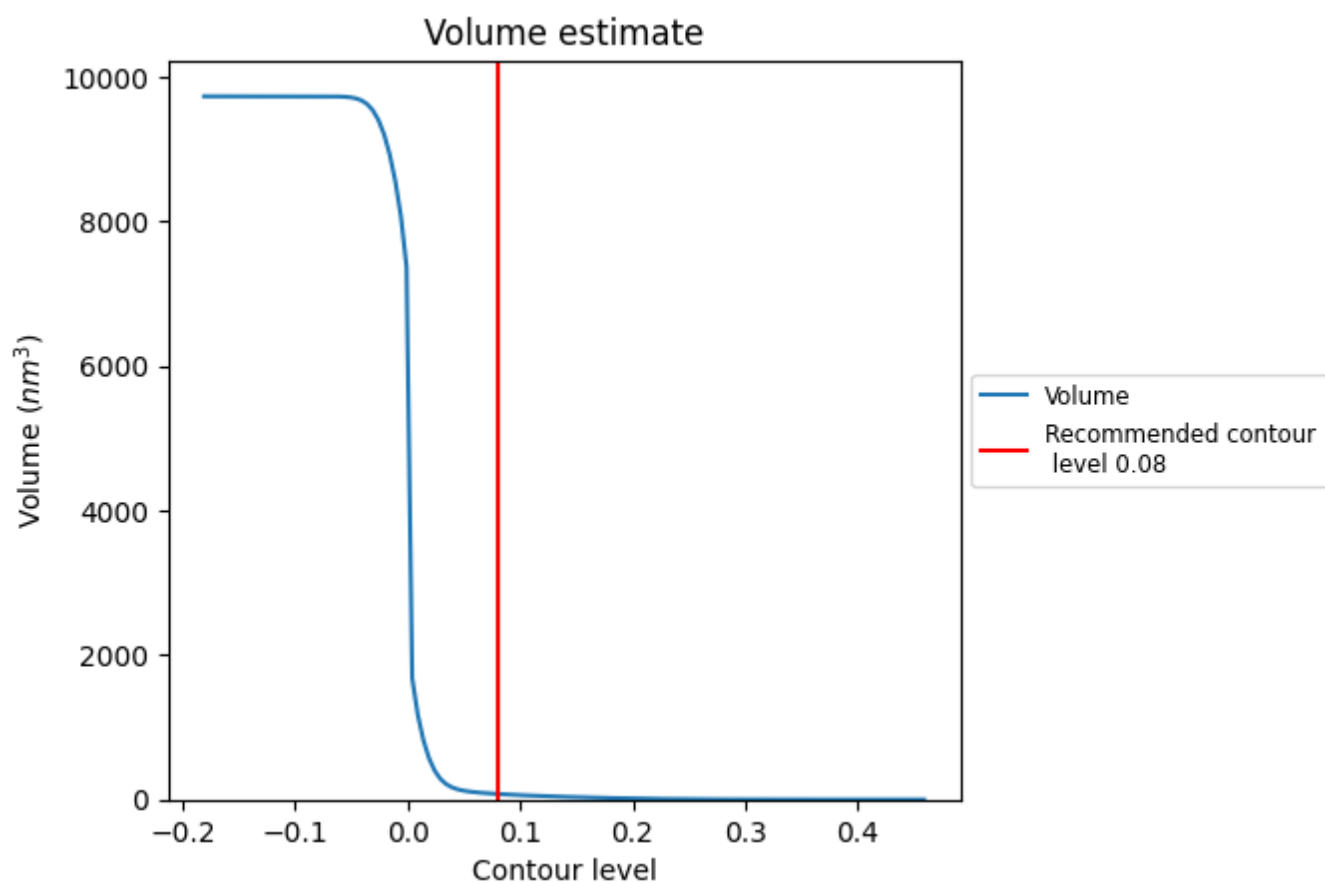
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

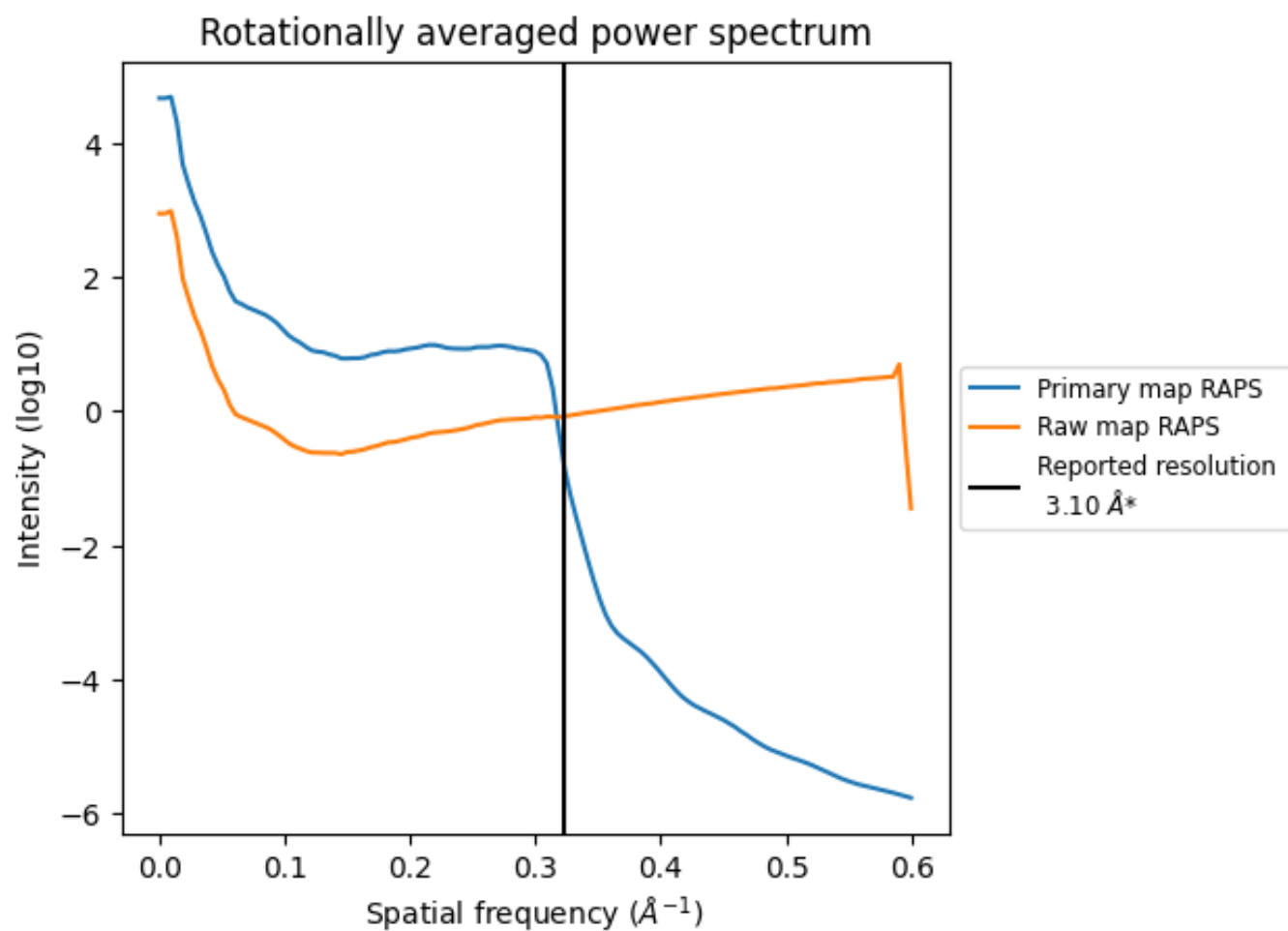
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 77 nm³; this corresponds to an approximate mass of 70 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 ⓘ

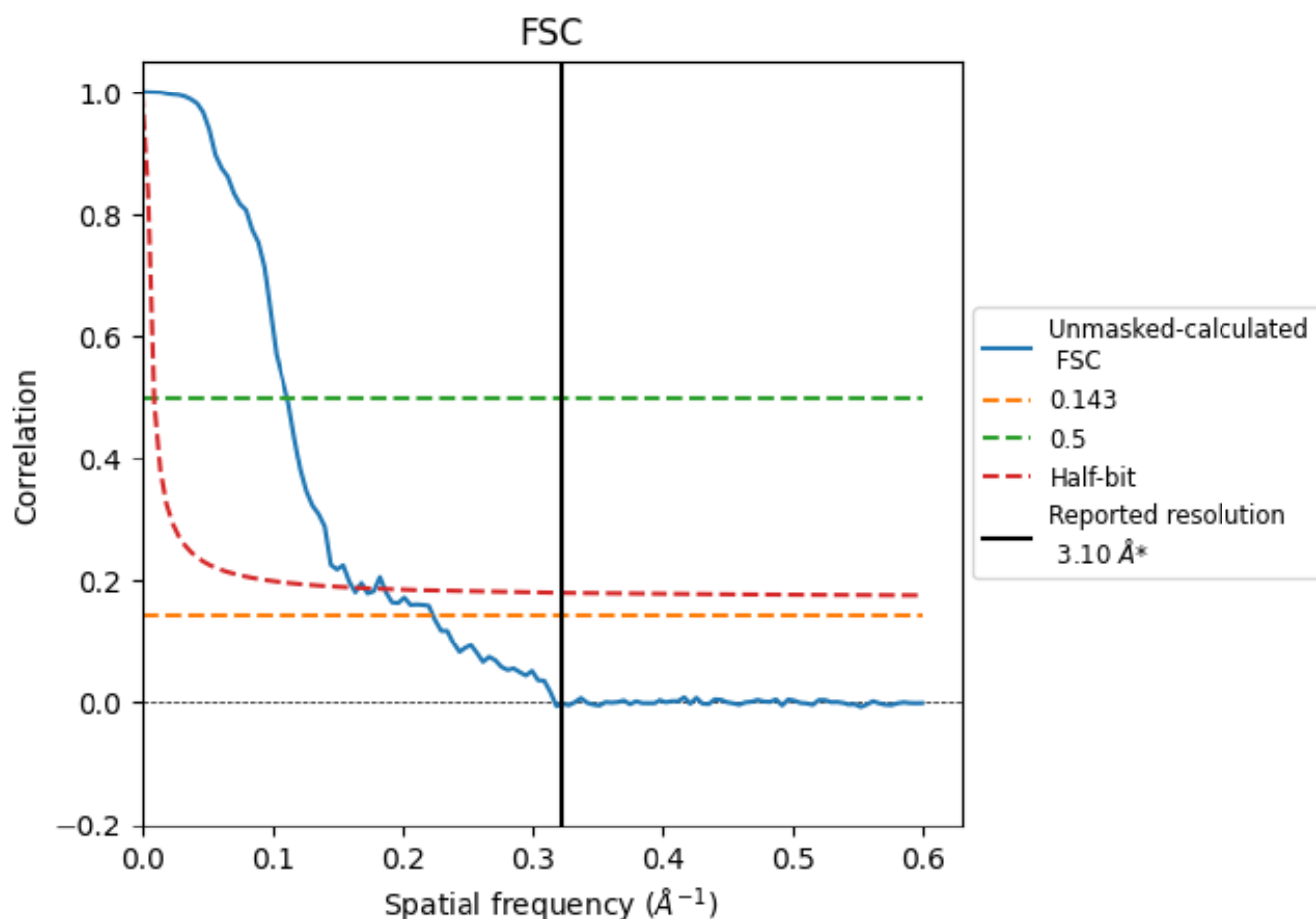


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

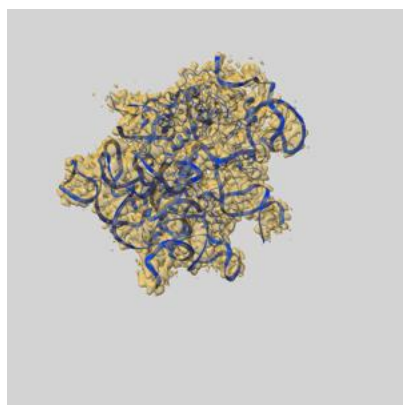
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	8.98	6.18

*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 4.48 differs from the reported value 3.1 by more than 10 %

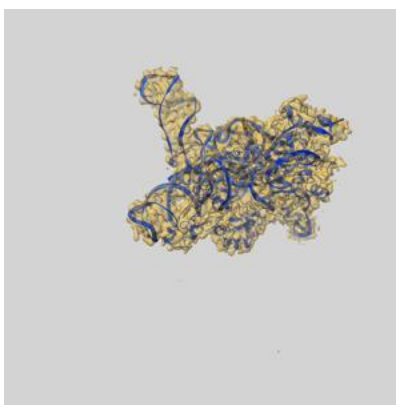
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63121 and PDB model 9LIR. Per-residue inclusion information can be found in section [3](#) on page [6](#).

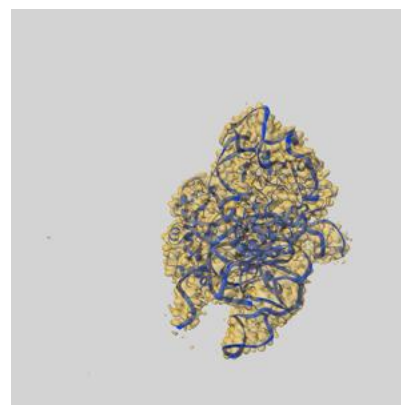
9.1 Map-model overlay [i](#)



X



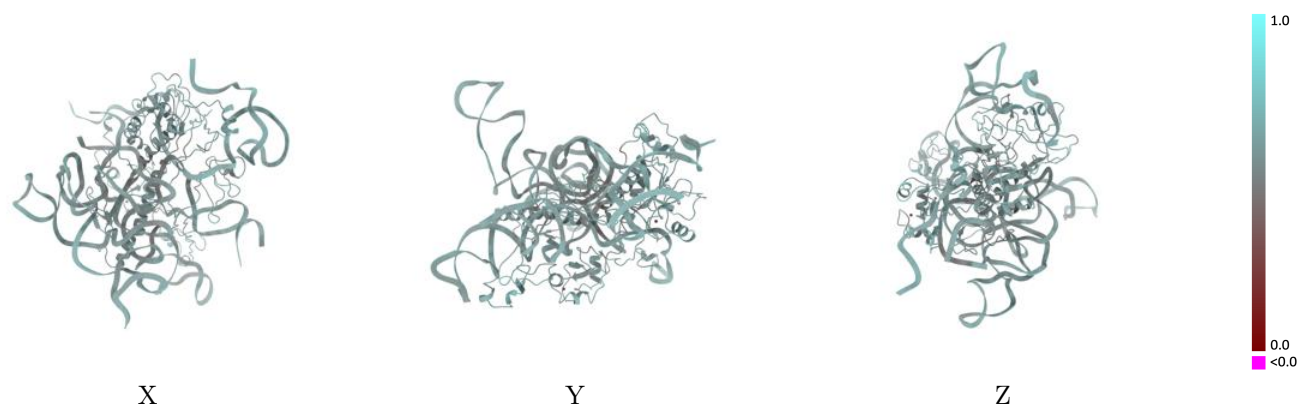
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08 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](#)



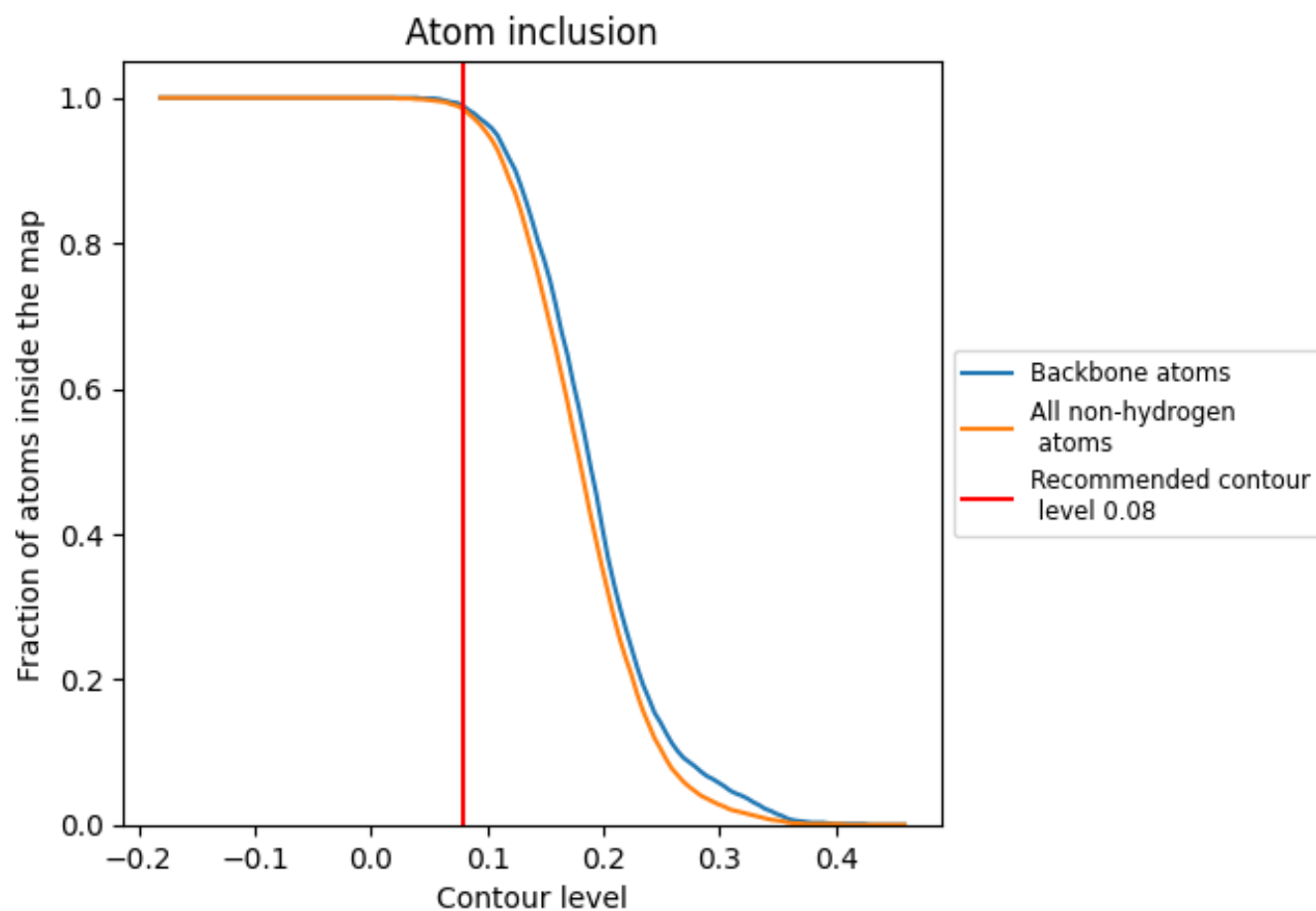
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9840	0.5710
A	0.9910	0.5660
B	0.9860	0.5650
C	0.9870	0.5820
D	0.9760	0.5750

