



wwPDB EM Validation Summary Report ⓘ

Aug 17, 2026 – 04:43 PM JST

PDB ID : 24YW / pdb_000024yw
EMDB ID : EMD-69918
Title : Xanthomonas citri pv. glycines 50S subunit
Authors : Sengupta, S.; Anand, R.
Deposited on : 2026-03-25
Resolution : 3.00 Å(reported)

This is a wwPDB EM Validation Summary 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

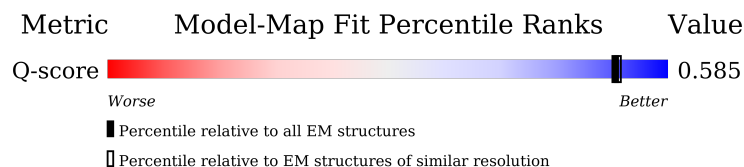
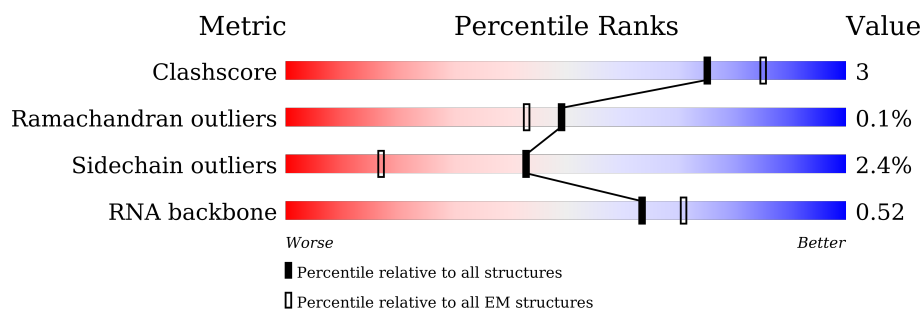
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



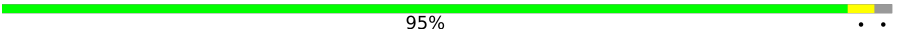
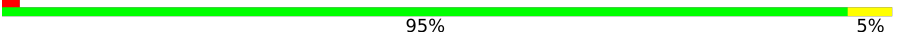
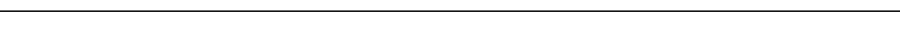
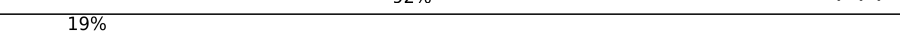
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	2	64	 69% 16% 16%
2	3	55	 78% 15% 7%
3	4	46	 87% 9% .

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Mol	Chain	Length	Quality of chain
4	5	65	
5	6	41	
6	A	2881	
7	B	121	
8	C	275	
9	D	216	
10	E	201	
11	G	175	
12	H	149	
13	J	142	
14	K	122	
15	L	147	
16	M	137	
17	N	127	
18	O	119	
19	P	135	
20	Q	119	
21	R	106	
22	S	111	
23	T	99	
24	U	105	
25	V	211	
26	W	86	
27	X	78	
28	Y	61	

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Mol	Chain	Length	Quality of chain
29	Z	63	 A horizontal bar chart showing the quality of chain Z. The bar is divided into three segments: a green segment representing 83%, a yellow segment representing 6%, and a grey segment representing 11%. The percentages are labeled below the bar.

2 Entry composition [i](#)

There are 29 unique types of molecules in this entry. The entry contains 86233 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 Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	54	Total	C	N	O	0	0
			426	259	90	77		

- Molecule 2 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	51	Total	C	N	O	S	0	0
			413	260	76	72	5		

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	44	Total	C	N	O	S	0	0
			358	216	86	55	1		

- Molecule 4 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	64	Total	C	N	O	S	0	0
			521	320	115	84	2		

- Molecule 5 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	41	Total	C	N	O	S	0	0
			339	210	76	50	3		

- Molecule 6 is a RNA chain called RNA (2797-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	2797	Total	C	N	O	P	0	0
			60015	26777	11033	19408	2797		

- Molecule 7 is a RNA chain called RNA (117-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	117	Total	C	N	O	P	0	0
			2505	1117	459	812	117		

- Molecule 8 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	274	Total	C	N	O	S	0	0
			2098	1302	429	362	5		

- Molecule 9 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	213	Total	C	N	O	S	0	0
			1585	990	301	290	4		

- Molecule 10 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	201	Total	C	N	O	S	0	0
			1531	965	278	284	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	172	Total	C	N	O	S	0	0
			1263	806	223	232	2		

- Molecule 12 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	80	Total	C	N	O	S	0	0
			595	375	104	115	1		

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	141	Total	C	N	O	S	0	0
			1125	715	207	201	2		

- Molecule 14 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	122	Total	C	N	O	S	0	0
			947	598	176	168	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	145	Total	C	N	O	S	0	0
			1059	658	208	191	2		

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	137	Total	C	N	O	S	0	0
			1090	689	209	187	5		

- Molecule 17 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	118	Total	C	N	O	S	0	0
			942	595	187	156	4		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	O	116	Total	C	N	O	0	0
			879	544	178	157		

- Molecule 19 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	P	116	Total	C	N	O	0	0
			910	572	172	166		

- Molecule 20 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	116	Total	C	N	O	S	0	0
			924	588	190	145	1		

- Molecule 21 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	103	Total	C	N	O	S	0	0
			802	501	155	143	3		

- Molecule 22 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	109	Total	C	N	O	S	0	0
			831	517	162	149	3		

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	91	Total	C	N	O		0	0
			724	452	138	134			

- Molecule 24 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	102	Total	C	N	O		0	0
			767	470	154	143			

- Molecule 25 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	189	Total	C	N	O	S	0	0
			1486	943	264	276	3		

- Molecule 26 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	73	Total	C	N	O		0	0
			548	344	107	97			

- Molecule 27 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	75	Total	C	N	O	S	0	0
			615	375	135	104	1		

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	58	Total	C	N	O	S	0	0
			484	298	99	85	2		

- Molecule 29 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Z	56	Total	C	N	O	0	0
			451	281	94	76		

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: Large ribosomal subunit protein bL32

Chain 2: 



- Molecule 2: Large ribosomal subunit protein bL33

Chain 3: 

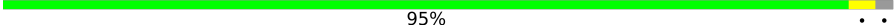


- Molecule 3: Large ribosomal subunit protein bL34

Chain 4: 

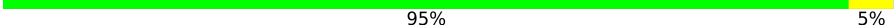


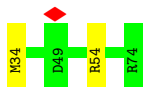
- Molecule 4: Large ribosomal subunit protein bL35

Chain 5: 



- Molecule 5: Large ribosomal subunit protein bL36

Chain 6: 



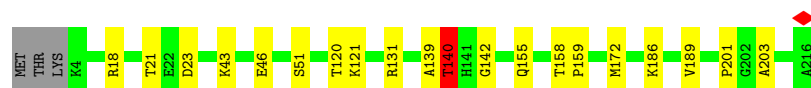
- Molecule 6: RNA (2797-MER)





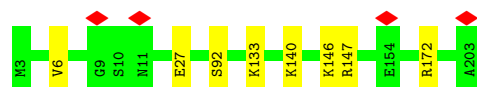
- Molecule 9: Large ribosomal subunit protein uL3

Chain D: 89% 9%



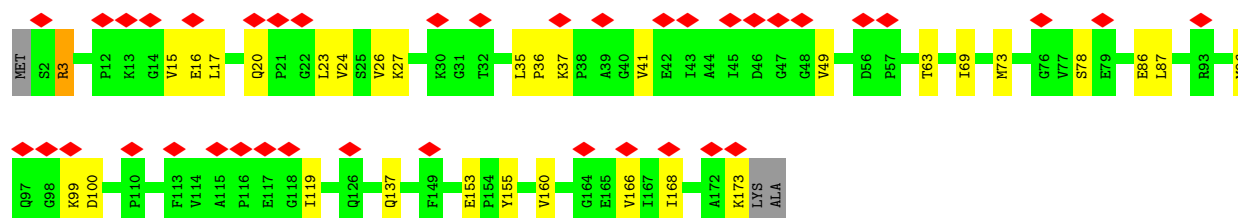
- Molecule 10: Large ribosomal subunit protein uL4

Chain E: 96%



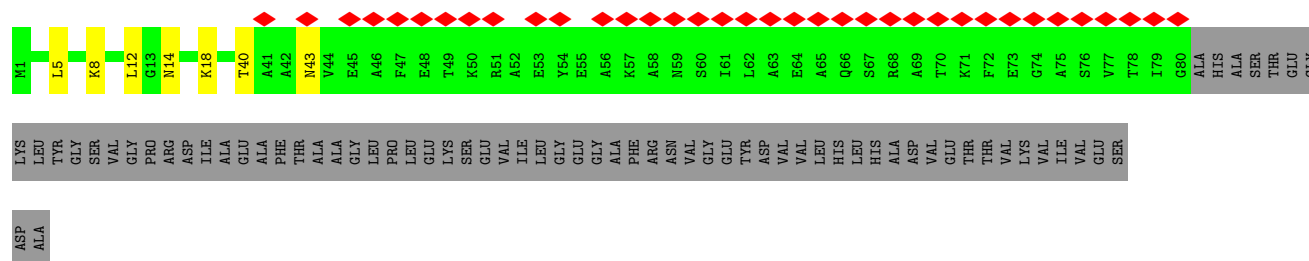
- Molecule 11: Large ribosomal subunit protein uL6

Chain G: 22% 81% 17%



- Molecule 12: Large ribosomal subunit protein bL9

Chain H: 24% 49% 5% 46%



- Molecule 13: Large ribosomal subunit protein uL13

Chain J: 95%



- Molecule 14: Large ribosomal subunit protein uL14

Chain K:  89% 11%



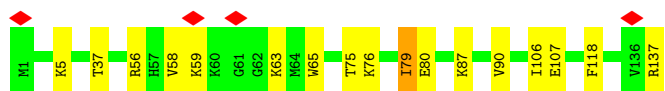
- Molecule 15: Large ribosomal subunit protein uL15

Chain L:  93% 5%



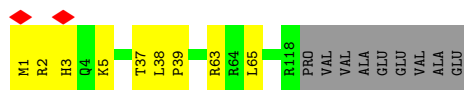
- Molecule 16: Large ribosomal subunit protein uL16

Chain M:  88% 12%

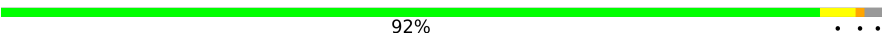


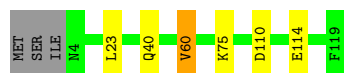
- Molecule 17: Large ribosomal subunit protein bL17

Chain N:  86% 7% 7%



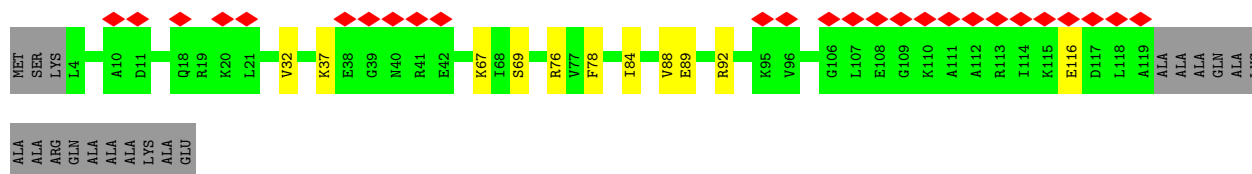
- Molecule 18: Large ribosomal subunit protein uL18

Chain O:  92%



- Molecule 19: Large ribosomal subunit protein bL19

Chain P:  19% 78% 8% 14%

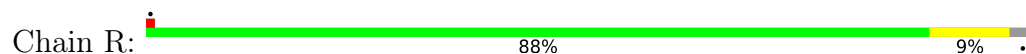


- Molecule 20: Large ribosomal subunit protein bL20

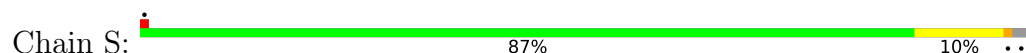
Chain Q:  89% 8%



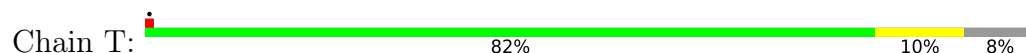
- Molecule 21: Large ribosomal subunit protein bL21



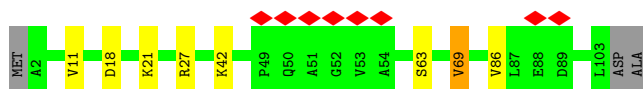
- Molecule 22: Large ribosomal subunit protein uL22



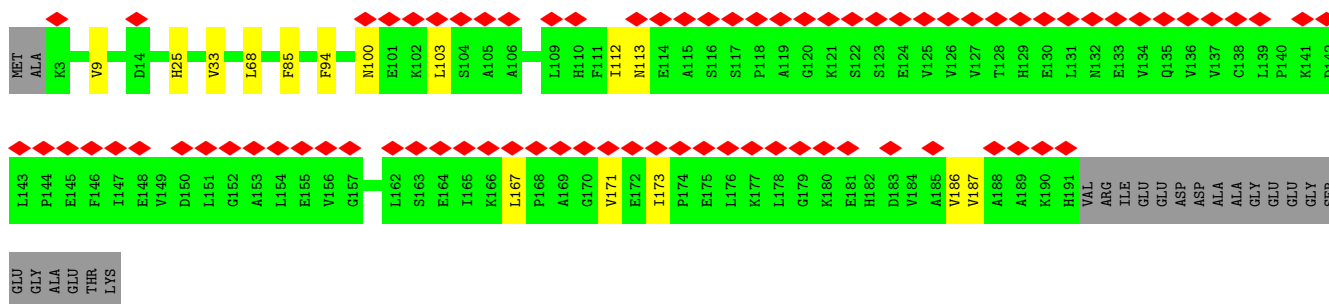
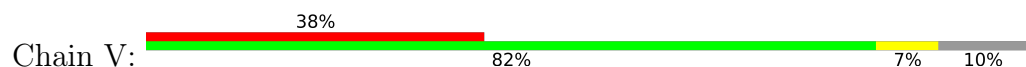
- Molecule 23: Large ribosomal subunit protein uL23



- Molecule 24: Large ribosomal subunit protein uL24



- Molecule 25: Large ribosomal subunit protein bL25



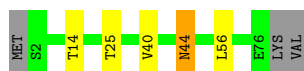
- Molecule 26: Large ribosomal subunit protein bL27

Chain W:  78% 7% 15%



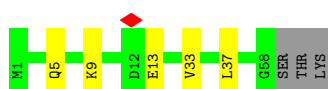
- Molecule 27: Large ribosomal subunit protein bL28

Chain X:  90% 5% . .



- Molecule 28: Large ribosomal subunit protein uL29

Chain Y:  87% 8% 5%



- Molecule 29: Large ribosomal subunit protein uL30

Chain Z:  83% 6% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	252876	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 ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00566	Depositor
Map size (Å)	340.0, 340.0, 340.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	2	0.14	0/433	0.36	0/581
2	3	0.11	0/420	0.36	0/555
3	4	0.09	0/361	0.25	0/474
4	5	0.09	0/528	0.26	0/699
5	6	0.09	0/342	0.27	0/449
6	A	0.18	2/67211 (0.0%)	0.35	31/104844 (0.0%)
7	B	0.31	2/2802 (0.1%)	0.43	3/4368 (0.1%)
8	C	0.11	0/2143	0.29	0/2889
9	D	0.13	0/1610	0.40	0/2165
10	E	0.10	0/1551	0.29	0/2088
11	G	0.12	0/1283	0.30	0/1735
12	H	0.09	0/602	0.28	0/812
13	J	0.10	0/1148	0.25	0/1550
14	K	0.11	0/958	0.28	0/1284
15	L	0.12	0/1069	0.35	0/1422
16	M	0.10	0/1112	0.30	1/1492 (0.1%)
17	N	0.11	0/958	0.29	0/1280
18	O	0.10	0/887	0.27	0/1185
19	P	0.10	0/920	0.29	0/1232
20	Q	0.13	0/936	0.27	0/1247
21	R	0.11	0/811	0.32	0/1081
22	S	0.11	0/836	0.30	0/1118
23	T	0.09	0/732	0.28	0/982
24	U	0.10	0/773	0.27	0/1036
25	V	0.11	0/1515	0.29	0/2054
26	W	0.16	0/557	0.31	0/747
27	X	0.13	0/624	0.33	0/837
28	Y	0.17	0/488	0.36	0/648
29	Z	0.09	0/454	0.24	0/608
All	All	0.17	4/94064 (0.0%)	0.35	35/141462 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	47	A	P-O5'	9.31	1.73	1.59
7	B	47	A	O5'-C5'	7.76	1.54	1.42
6	A	1054	A	P-O5'	6.55	1.69	1.59
6	A	1054	A	O5'-C5'	6.46	1.52	1.42

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	626	U	O3'-P-O5'	14.61	125.92	104.00
6	A	1053	C	O3'-P-O5'	-13.66	83.51	104.00
6	A	457	A	P-O3'-C3'	10.73	136.30	120.20
6	A	221	A	P-O3'-C3'	9.79	134.88	120.20
7	B	47	A	C4'-C3'-O3'	9.75	124.03	109.40

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	2	426	0	434	5	0
2	3	413	0	433	5	0
3	4	358	0	389	2	0
4	5	521	0	562	1	0
5	6	339	0	381	2	0
6	A	60015	0	30203	286	0
7	B	2505	0	1268	17	0
8	C	2098	0	2162	14	0
9	D	1585	0	1616	12	0
10	E	1531	0	1590	5	0
11	G	1263	0	1347	13	0
12	H	595	0	614	4	0
13	J	1125	0	1164	3	0
14	K	947	0	1014	7	0
15	L	1059	0	1126	7	0
16	M	1090	0	1135	10	0
17	N	942	0	994	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	O	879	0	918	2	0
19	P	910	0	945	7	0
20	Q	924	0	1004	8	0
21	R	802	0	838	6	0
22	S	831	0	903	7	0
23	T	724	0	745	5	0
24	U	767	0	801	3	0
25	V	1486	0	1499	8	0
26	W	548	0	563	2	0
27	X	615	0	629	4	0
28	Y	484	0	517	3	0
29	Z	451	0	496	0	0
All	All	86233	0	56290	436	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.

The worst 5 of 436 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)
6:A:1152:A:H2'	6:A:1153:A:C2	1.84	1.12
6:A:1152:A:H3'	6:A:1153:A:H2	1.14	1.06
6:A:1152:A:C2'	6:A:1153:A:C2	2.45	0.98
6:A:1152:A:C3'	6:A:1153:A:H2	1.81	0.92
6:A:1152:A:H3'	6:A:1153:A:C2	2.04	0.92

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	2	52/64 (81%)	48 (92%)	4 (8%)	0	100	100
2	3	49/55 (89%)	49 (100%)	0	0	100	100
3	4	42/46 (91%)	42 (100%)	0	0	100	100
4	5	62/65 (95%)	61 (98%)	0	1 (2%)	7	34
5	6	39/41 (95%)	39 (100%)	0	0	100	100
8	C	272/275 (99%)	263 (97%)	9 (3%)	0	100	100
9	D	211/216 (98%)	196 (93%)	14 (7%)	1 (0%)	24	60
10	E	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
11	G	170/175 (97%)	169 (99%)	1 (1%)	0	100	100
12	H	78/149 (52%)	77 (99%)	1 (1%)	0	100	100
13	J	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
14	K	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
15	L	143/147 (97%)	138 (96%)	5 (4%)	0	100	100
16	M	135/137 (98%)	133 (98%)	2 (2%)	0	100	100
17	N	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
18	O	114/119 (96%)	113 (99%)	1 (1%)	0	100	100
19	P	114/135 (84%)	113 (99%)	1 (1%)	0	100	100
20	Q	114/119 (96%)	109 (96%)	5 (4%)	0	100	100
21	R	101/106 (95%)	101 (100%)	0	0	100	100
22	S	107/111 (96%)	107 (100%)	0	0	100	100
23	T	89/99 (90%)	89 (100%)	0	0	100	100
24	U	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
25	V	187/211 (89%)	186 (100%)	1 (0%)	0	100	100
26	W	71/86 (83%)	71 (100%)	0	0	100	100
27	X	73/78 (94%)	71 (97%)	2 (3%)	0	100	100
28	Y	56/61 (92%)	55 (98%)	1 (2%)	0	100	100
29	Z	54/63 (86%)	53 (98%)	1 (2%)	0	100	100
All	All	3007/3255 (92%)	2940 (98%)	65 (2%)	2 (0%)	49	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	D	140	THR
4	5	32	ILE

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	2	45/54 (83%)	42 (93%)	3 (7%)	15	46
2	3	45/48 (94%)	45 (100%)	0	100	100
3	4	34/35 (97%)	33 (97%)	1 (3%)	37	70
4	5	53/54 (98%)	53 (100%)	0	100	100
5	6	38/38 (100%)	38 (100%)	0	100	100
8	C	212/213 (100%)	210 (99%)	2 (1%)	70	85
9	D	159/162 (98%)	156 (98%)	3 (2%)	50	76
10	E	160/160 (100%)	158 (99%)	2 (1%)	61	81
11	G	134/136 (98%)	125 (93%)	9 (7%)	15	46
12	H	61/114 (54%)	60 (98%)	1 (2%)	55	79
13	J	120/121 (99%)	119 (99%)	1 (1%)	73	86
14	K	103/103 (100%)	101 (98%)	2 (2%)	50	76
15	L	101/103 (98%)	101 (100%)	0	100	100
16	M	111/111 (100%)	107 (96%)	4 (4%)	31	65
17	N	94/101 (93%)	93 (99%)	1 (1%)	65	83
18	O	83/86 (96%)	80 (96%)	3 (4%)	31	65
19	P	95/104 (91%)	94 (99%)	1 (1%)	65	83
20	Q	87/88 (99%)	86 (99%)	1 (1%)	65	83
21	R	81/84 (96%)	79 (98%)	2 (2%)	42	72
22	S	87/88 (99%)	85 (98%)	2 (2%)	44	74
23	T	78/84 (93%)	76 (97%)	2 (3%)	40	72
24	U	82/84 (98%)	78 (95%)	4 (5%)	22	56
25	V	163/178 (92%)	160 (98%)	3 (2%)	51	77
26	W	56/65 (86%)	53 (95%)	3 (5%)	20	53
27	X	65/68 (96%)	62 (95%)	3 (5%)	24	58
28	Y	53/56 (95%)	52 (98%)	1 (2%)	50	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Z	51/57 (90%)	47 (92%)	4 (8%)	11	39
All	All	2451/2595 (94%)	2393 (98%)	58 (2%)	43	73

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	N	65	LEU
29	Z	64	LEU
21	R	47	ILE
29	Z	43	ARG
26	W	81	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
19	P	5	ASN
21	R	82	HIS
19	P	70	HIS
21	R	90	GLN
13	J	67	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	A	2795/2881 (97%)	501 (17%)	28 (1%)
7	B	116/121 (95%)	26 (22%)	3 (2%)
All	All	2911/3002 (96%)	527 (18%)	31 (1%)

5 of 527 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	14	A
6	A	34	A
6	A	35	G
6	A	46	G
6	A	51	G

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	1398	G
6	A	2735	U
6	A	1474	U
7	B	52	G
6	A	2528	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

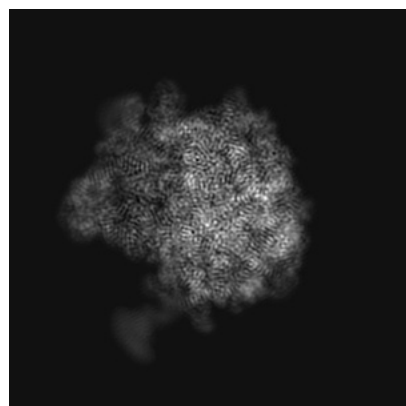
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-69918. These allow visual inspection of the internal detail of the map and identification of artifacts.

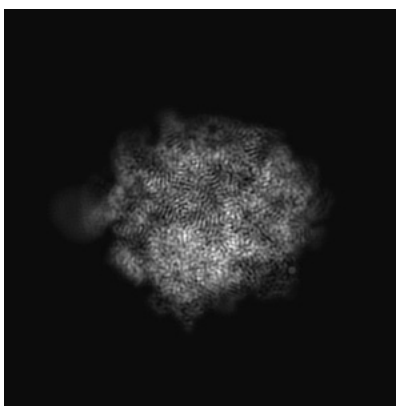
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

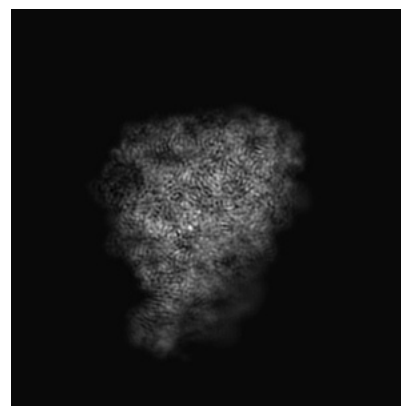
6.1.1 Primary map



X

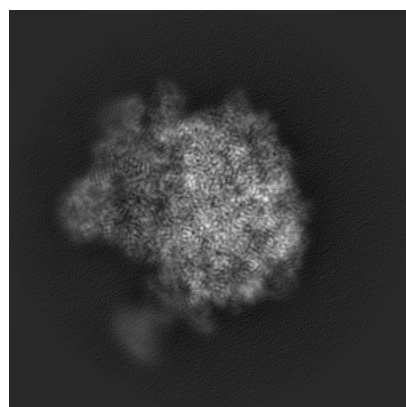


Y

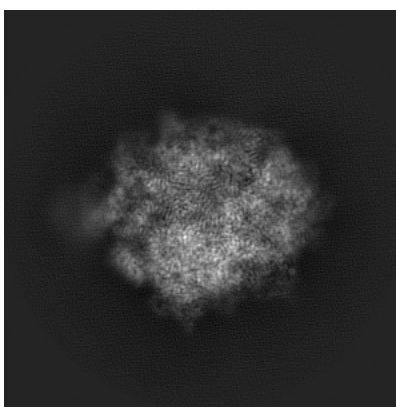


Z

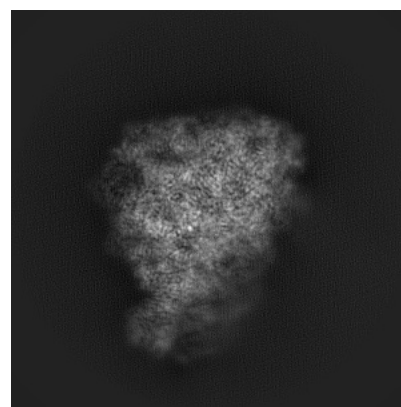
6.1.2 Raw map



X



Y

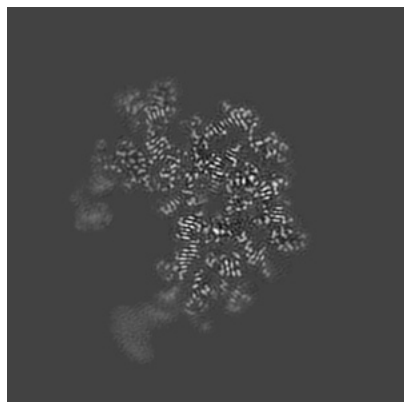


Z

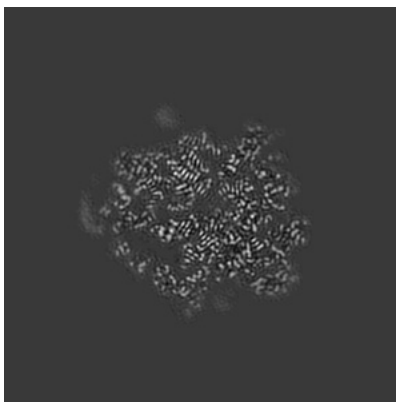
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

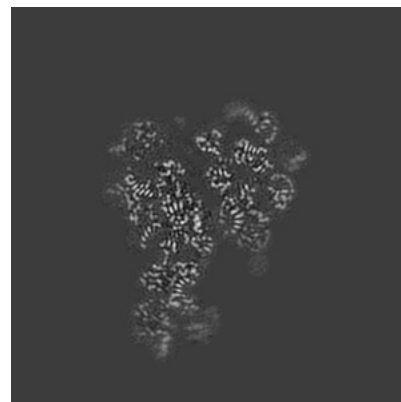
6.2.1 Primary map



X Index: 200

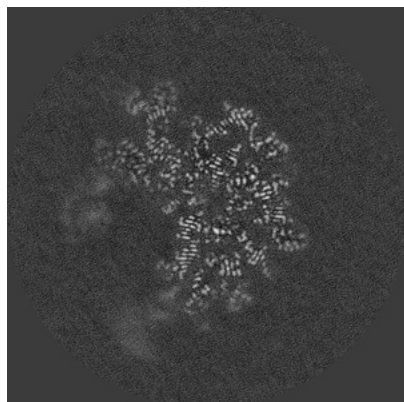


Y Index: 200

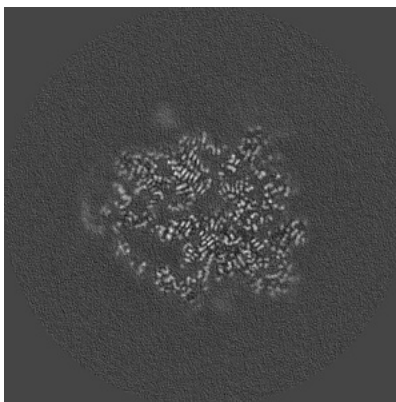


Z Index: 200

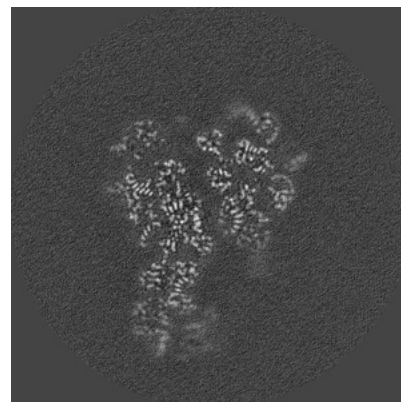
6.2.2 Raw map



X Index: 200



Y Index: 200

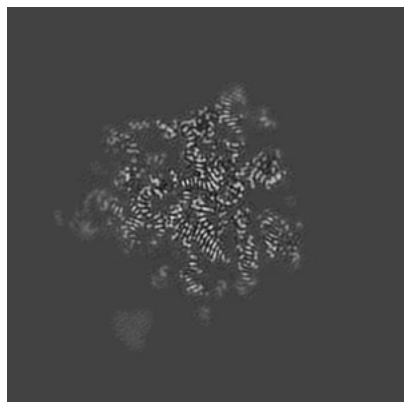


Z Index: 200

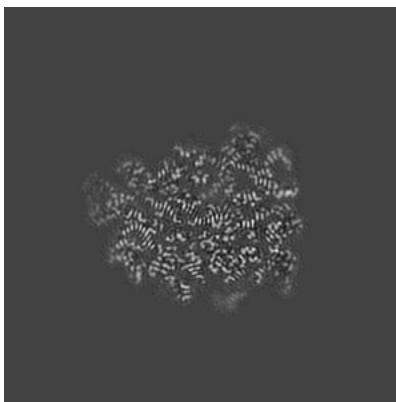
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

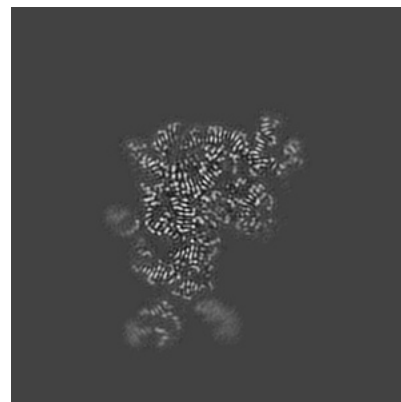
6.3.1 Primary map



X Index: 174

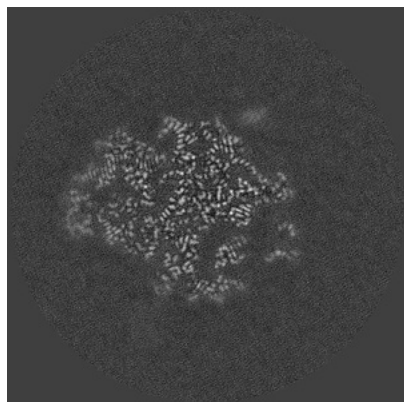


Y Index: 185

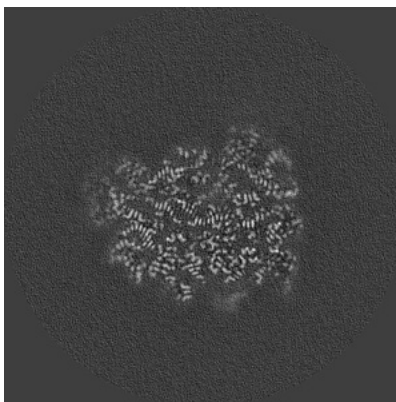


Z Index: 222

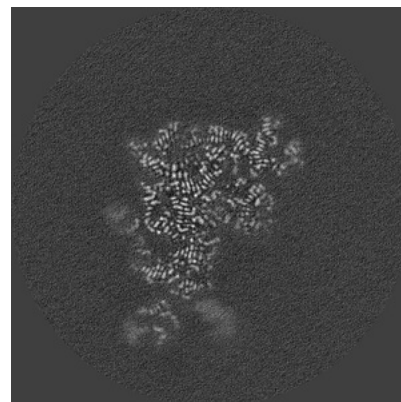
6.3.2 Raw map



X Index: 157



Y Index: 186

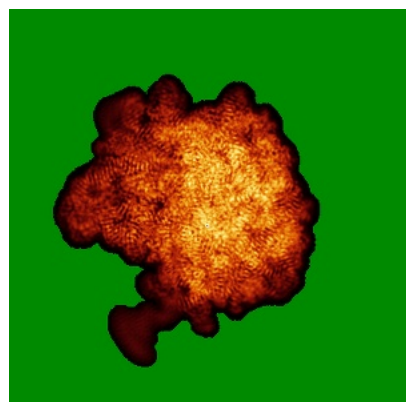


Z Index: 222

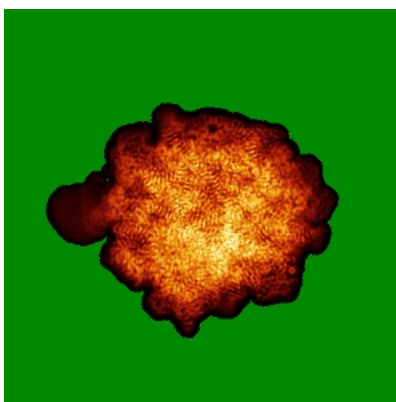
The images above show the largest variance slices of the map in three orthogonal directions.

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

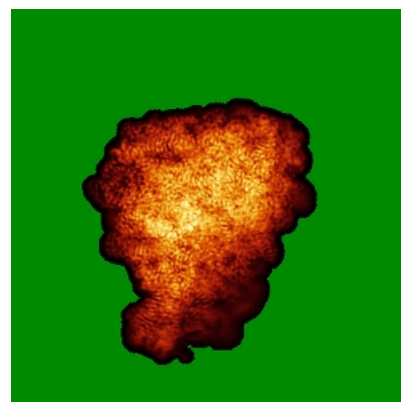
6.4.1 Primary map



X

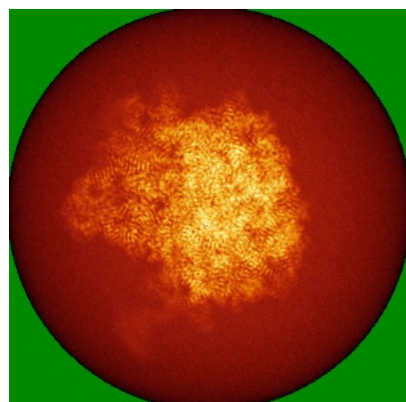


Y

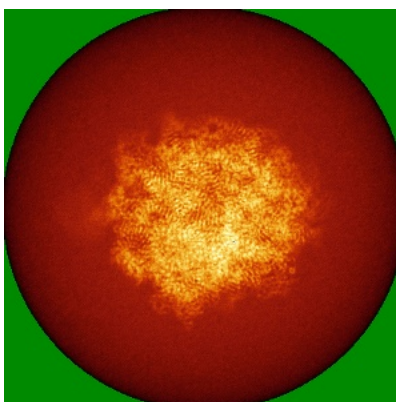


Z

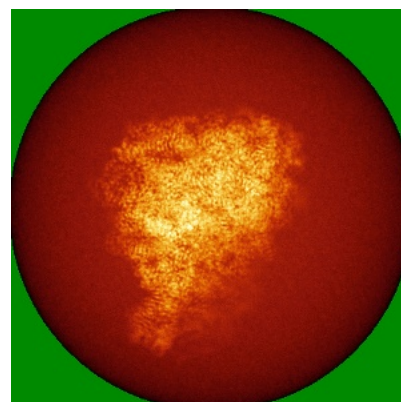
6.4.2 Raw map



X



Y

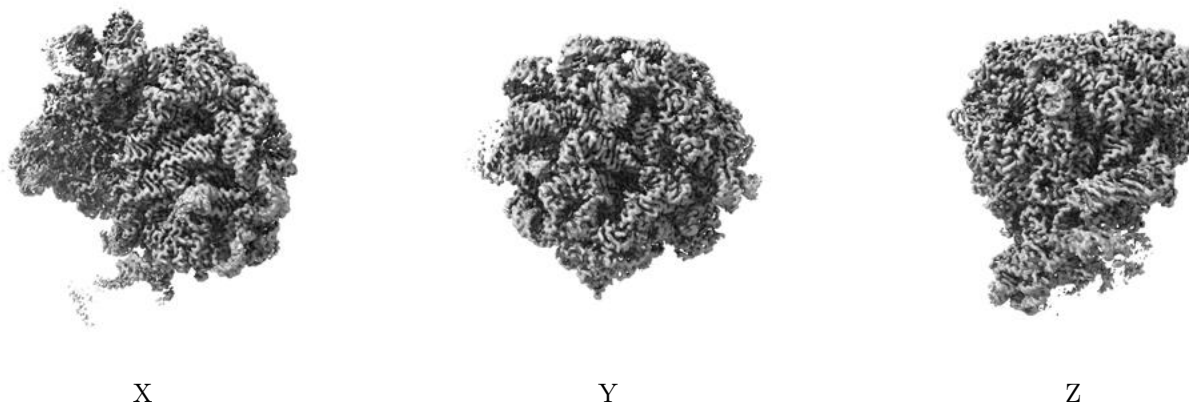


Z

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.

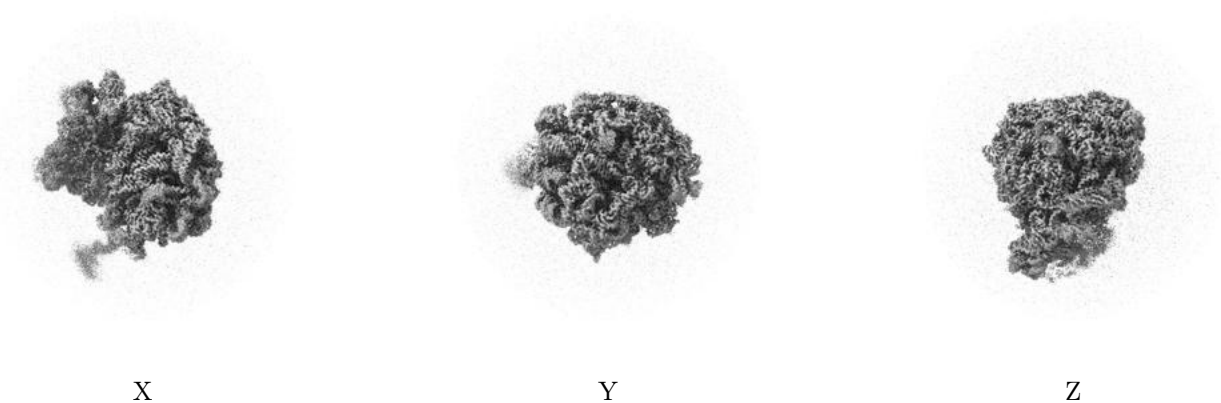
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00566. 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.

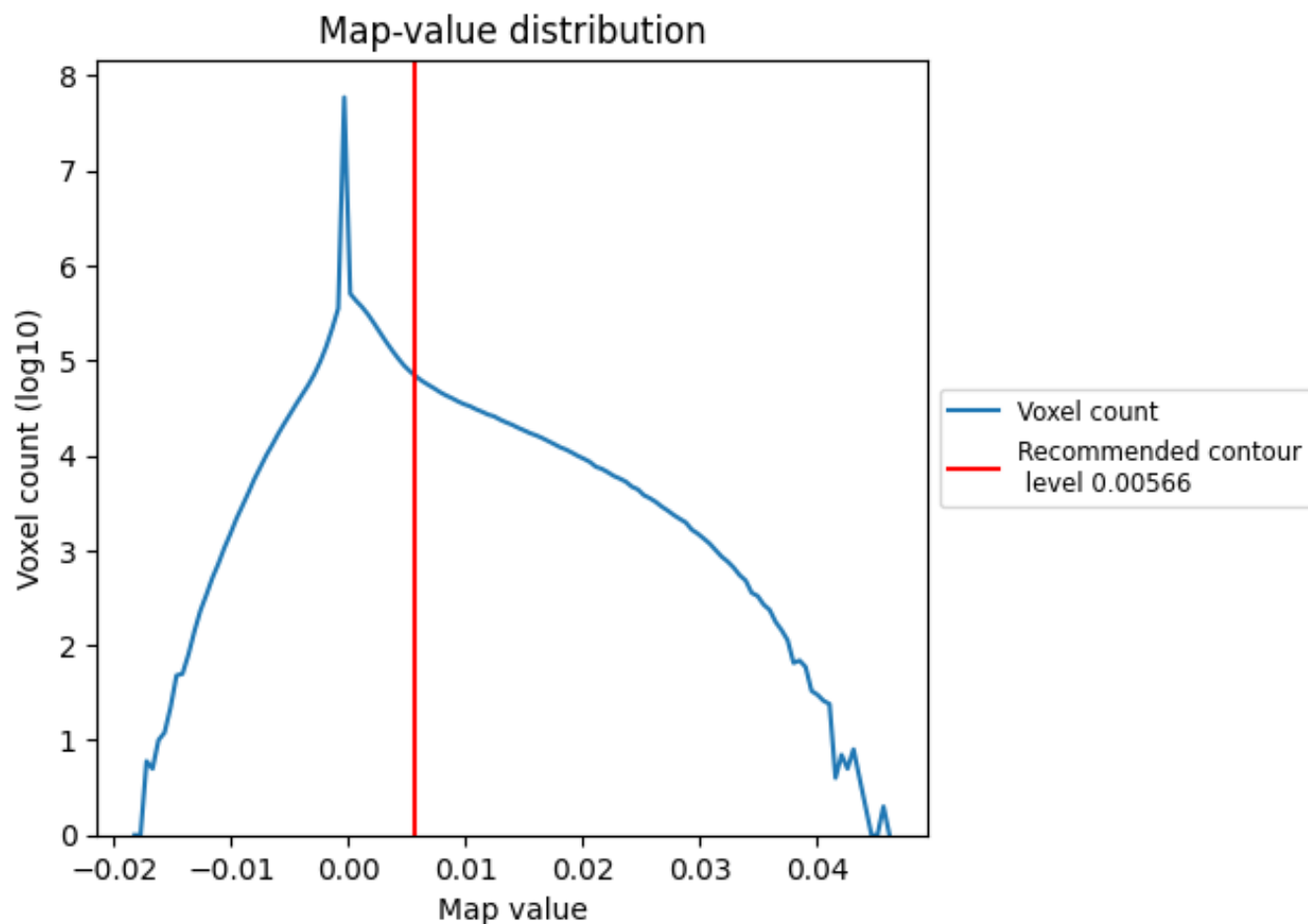
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

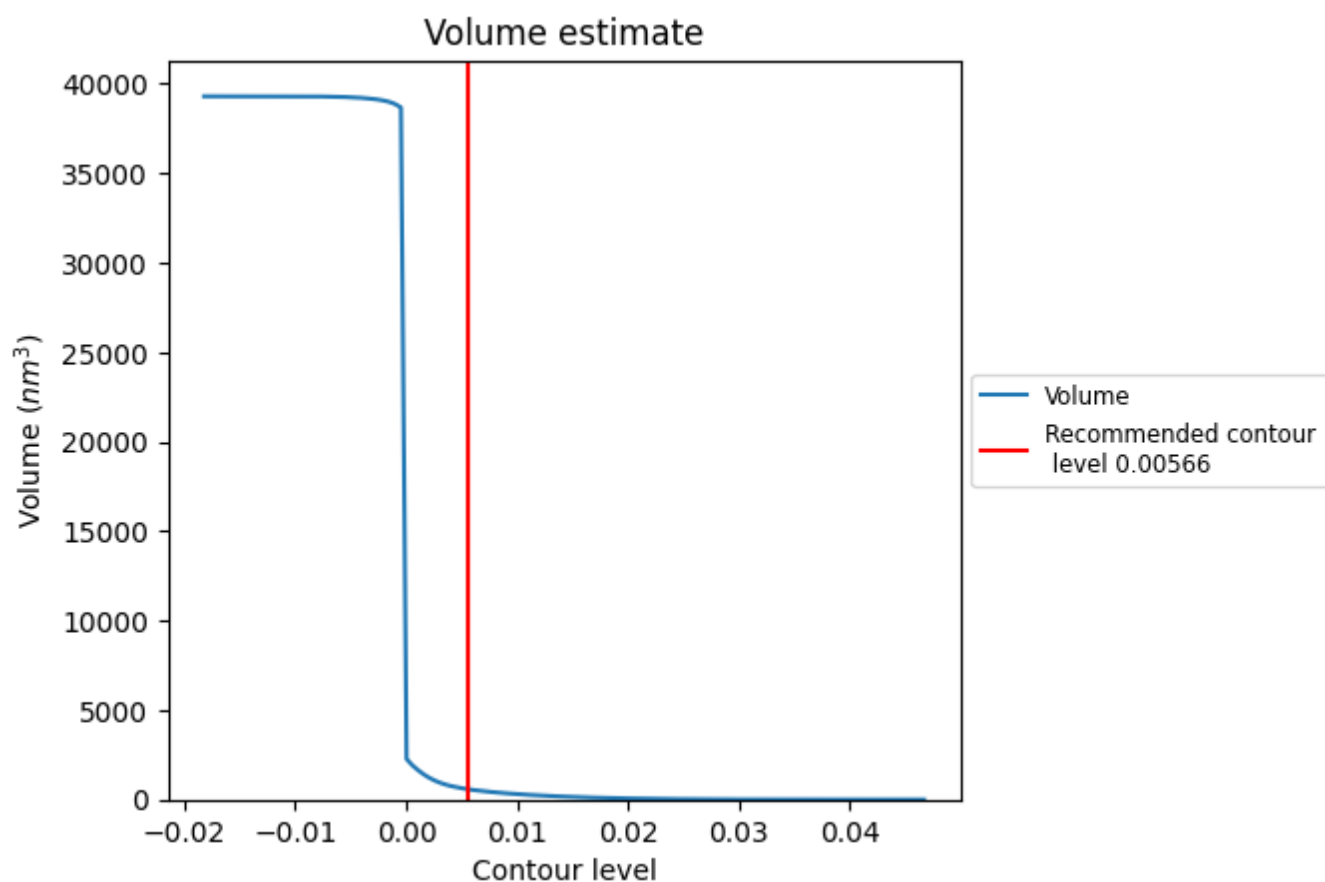
This section contains the results of statistical analysis of the map.

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.

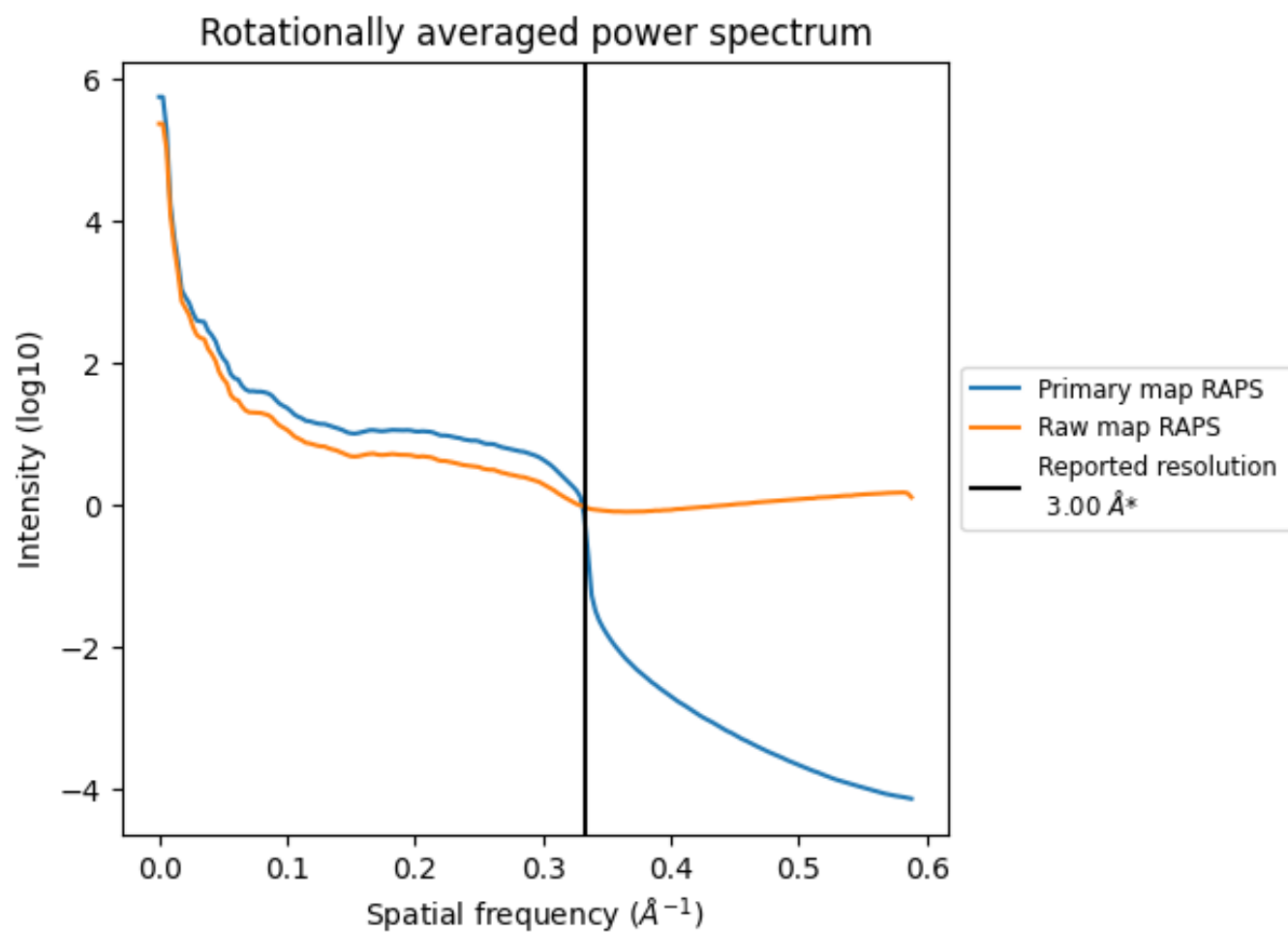
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 571 nm³; this corresponds to an approximate mass of 516 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 ⓘ

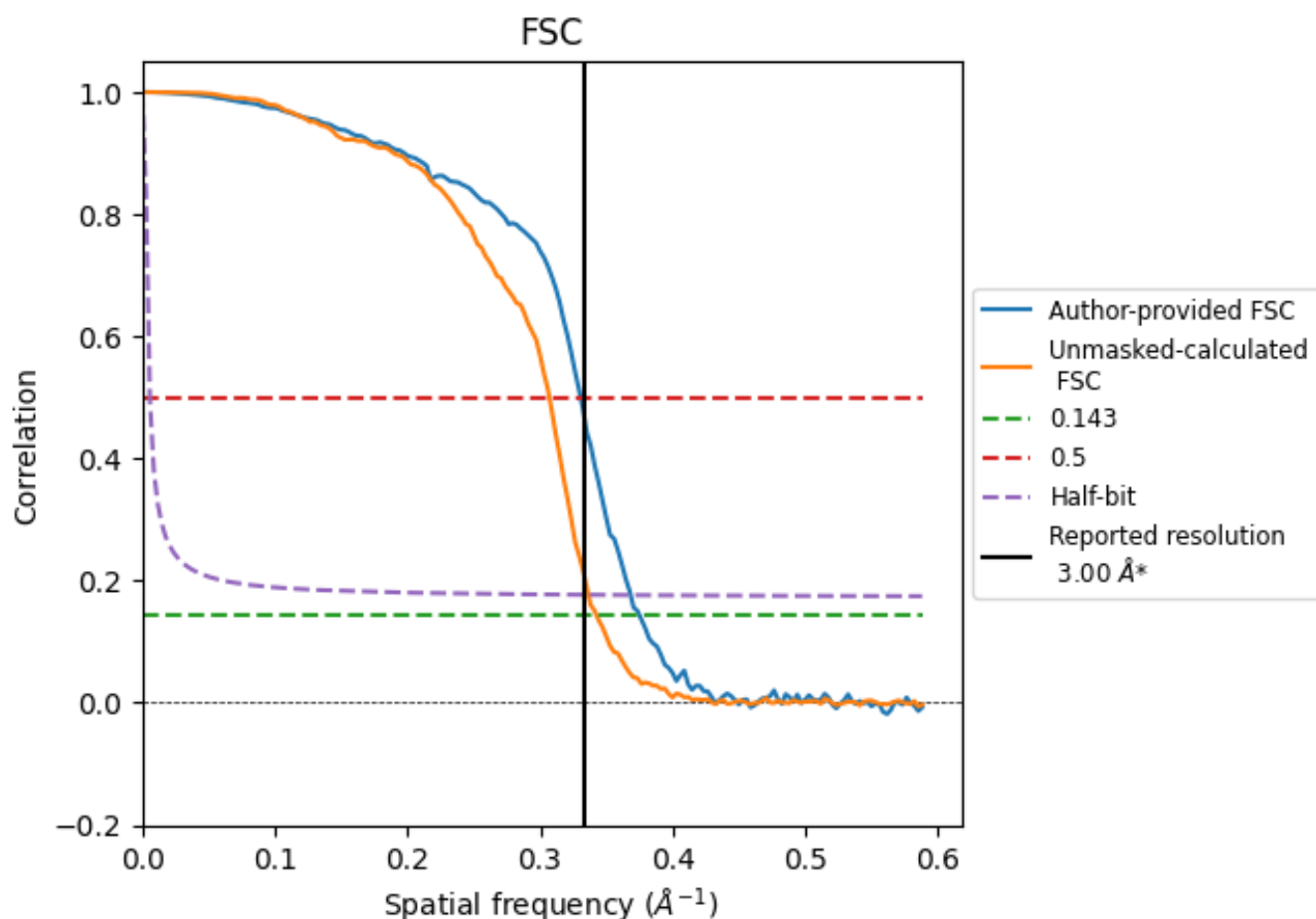


*Reported resolution corresponds to spatial frequency of $0.333 \text{ \AA}^{-1}$

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

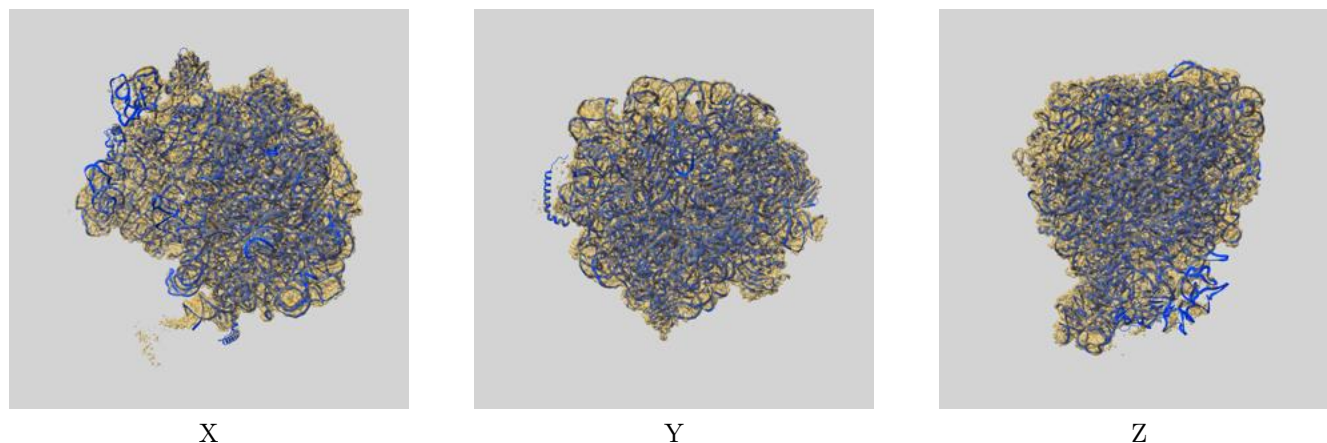
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.67	3.02	2.71
Unmasked-calculated*	2.92	3.26	2.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.67 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

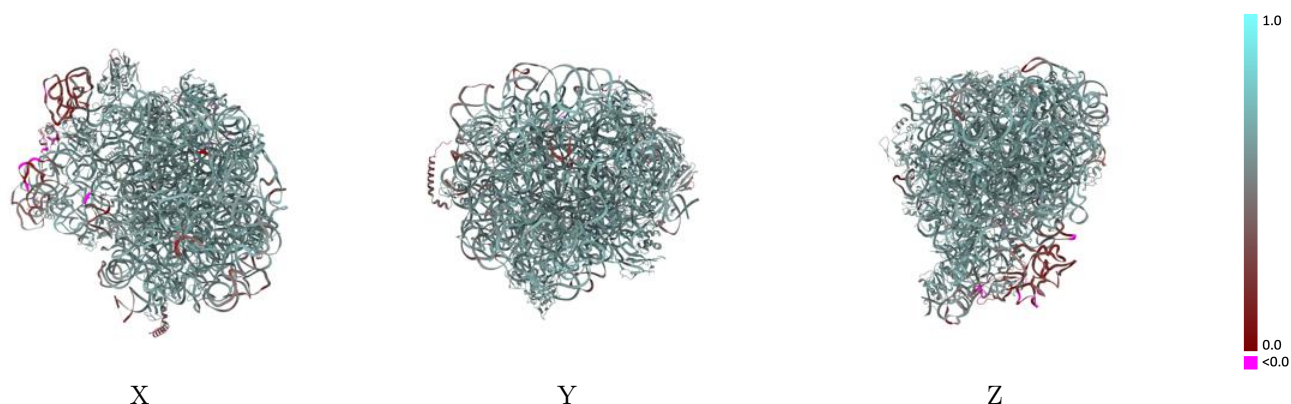
This section contains information regarding the fit between EMDB map EMD-69918 and PDB model 24YW. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



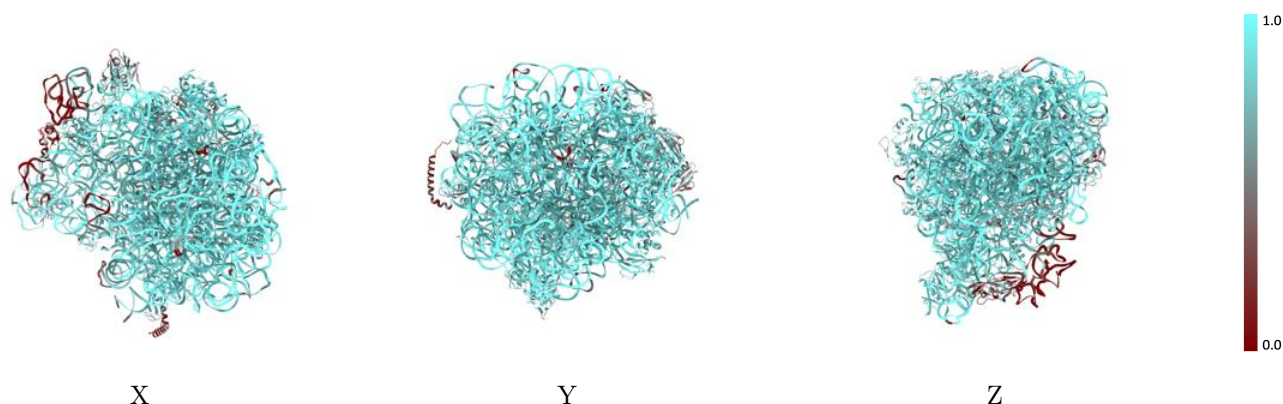
The images above show the 3D surface view of the map at the recommended contour level 0.00566 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



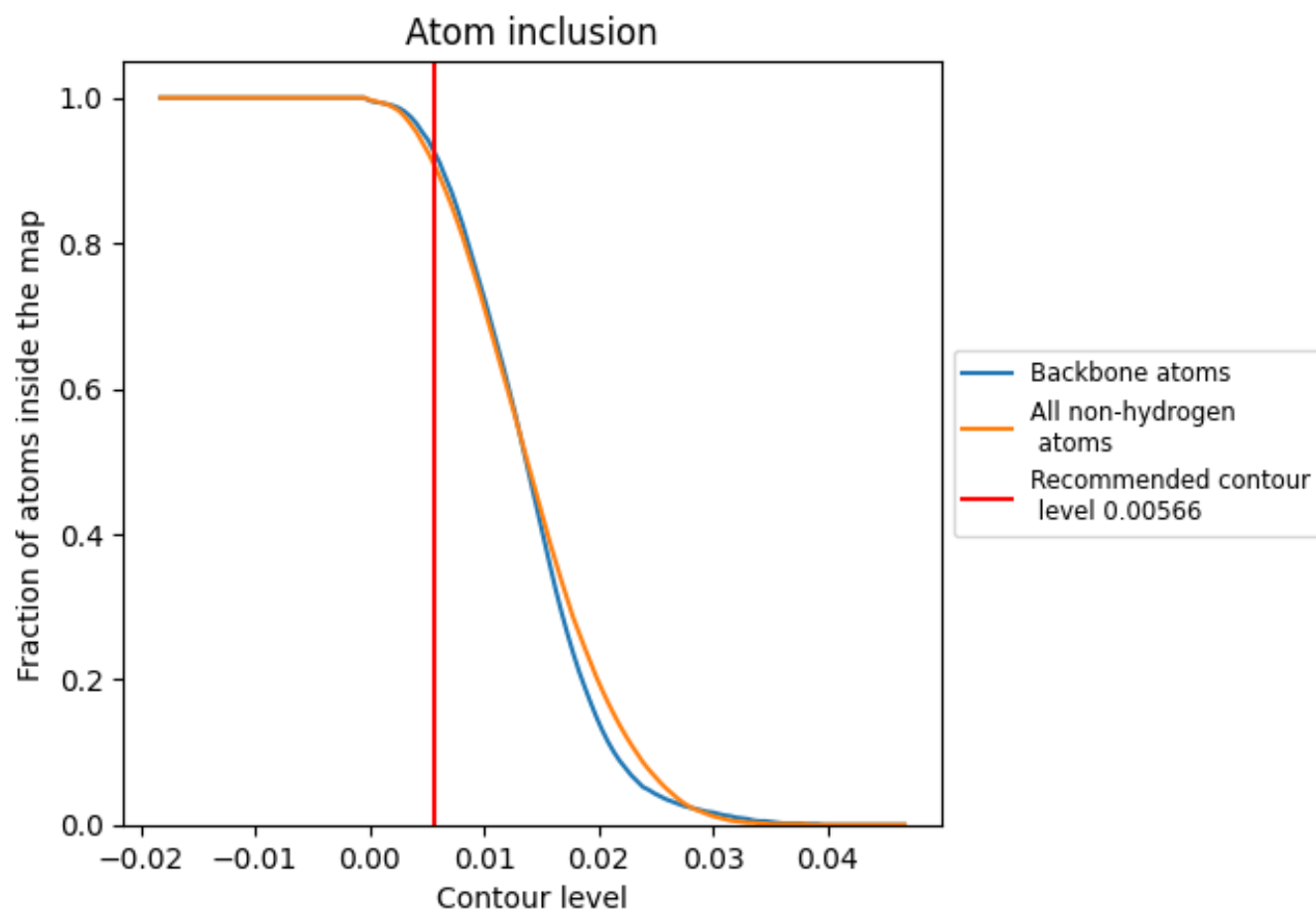
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00566).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.00566) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9080	 0.5850
2	 0.9460	 0.6220
3	 0.8040	 0.5900
4	 0.9550	 0.6280
5	 0.9580	 0.6330
6	 0.8450	 0.5980
A	 0.9350	 0.5870
B	 0.9400	 0.5420
C	 0.9120	 0.6080
D	 0.9270	 0.6100
E	 0.8830	 0.5950
G	 0.5700	 0.5150
H	 0.4740	 0.4400
J	 0.9390	 0.6260
K	 0.7990	 0.5850
L	 0.8940	 0.5930
M	 0.8680	 0.5960
N	 0.9340	 0.6120
O	 0.8580	 0.5750
P	 0.6450	 0.5070
Q	 0.9600	 0.6170
R	 0.8940	 0.6070
S	 0.9030	 0.6150
T	 0.8770	 0.6000
U	 0.7940	 0.5760
V	 0.5450	 0.4750
W	 0.9550	 0.6250
X	 0.9200	 0.6060
Y	 0.8380	 0.5540
Z	 0.8960	 0.6090

