



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:28 PM UTC

PDB ID : 7ASM / pdb_00007asm
EMDB ID : EMD-11900
Title : Staphylococcus aureus 50S after 30 minutes incubation at 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.48 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:

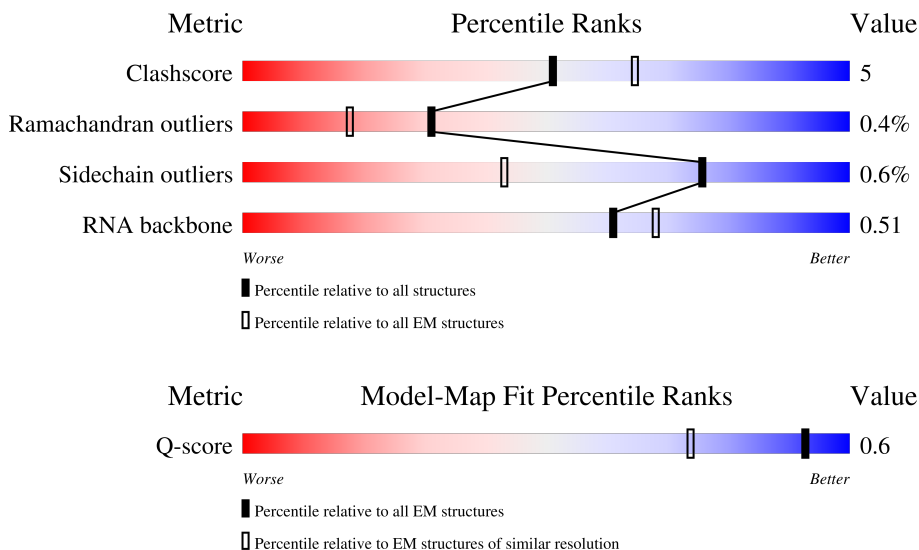
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 2.48 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.




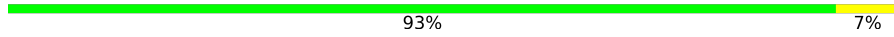



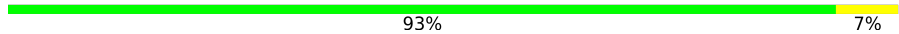






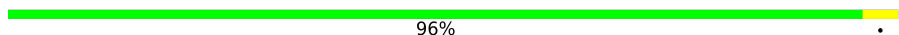
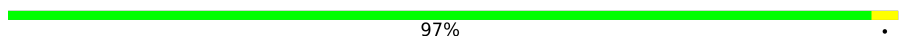


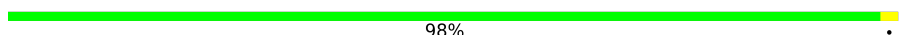


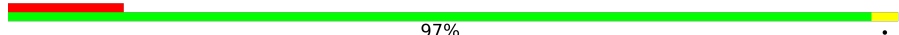




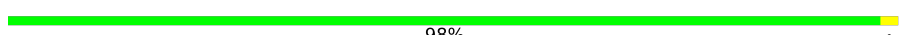
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6178 (1.98 - 2.98)

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	N	114	91% 9%
2	E	206	90% 10%
3	A	2923	67% 25% 5% .


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	B	115	 57% 39%
5	C	274	 93% 7%
6	G	175	 78% 22%
7	H	145	 80% 19%
8	J	146	 88% 12%
9	K	137	 93% 7%
10	M	119	 81% 18%
11	O	116	 89% 10%
12	P	102	 87% 13%
13	R	89	 90% 10%
14	S	104	 79% 17%
15	T	94	 84% 16%
16	U	79	 96%
17	W	67	 97%
18	3	64	 89% 11%
19	1	47	 91% 9%
20	2	43	 98%
21	4	37	 78% 19%
22	D	215	 80% 19%
23	F	158	 97%
24	I	122	 82% 18%
25	Q	112	 90% 10%
26	V	49	 82% 18%
27	X	58	 90% 10%
28	Z	48	 98%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	L	120	 86% 12%

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 86149 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 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	N	114	889	563	175	151	0	0

- Molecule 2 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	206	1572	986	288	296	2	0	0

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	A	2834	60769	27128	11118	19689	2834	0	0

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	B	115	2448	1094	436	803	115	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	274	2094	1303	415	371	5	0	0

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	175	1263	791	240	229	3	0	0

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	145	1149	717	211	218	3	0	0

- Molecule 8 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	J	146	1086	674	214	197	1	0	0

- Molecule 9 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	K	137	1071	689	203	175	4	0	0

- Molecule 10 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	M	119	882	549	174	159	0	0

- Molecule 11 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	O	116	942	593	189	156	4	0	0

- Molecule 12 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	P	102	790	503	142	144	1	0	0

- Molecule 13 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	R	89	715	453	127	131	4	0	0

- Molecule 14 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	S	100	755	477	139	138	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	49	GLN	ARG	conflict	UNP A0A6K7SSC4

- Molecule 15 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	T	94	722	463	130	129	0	0

- Molecule 16 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	U	79	597	369	117	111	0	0

- Molecule 17 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	W	67	541	333	102	106	0	0

- Molecule 18 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	3	64	521	324	113	82	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	1	47	390	238	78	70	4	0	0

- Molecule 20 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 21 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

- Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 23 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	F	158	Total	C	N	O	0	0
			778	462	158	158		

- Molecule 24 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	I	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	X	58	449	280	85	84	0	0

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	Z	48	360	222	77	59	2	0	0

- Molecule 29 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L	120	925	573	181	170	1	0	0

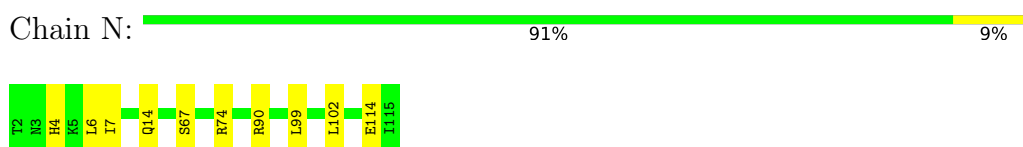
- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
30	A	1	1	1	0

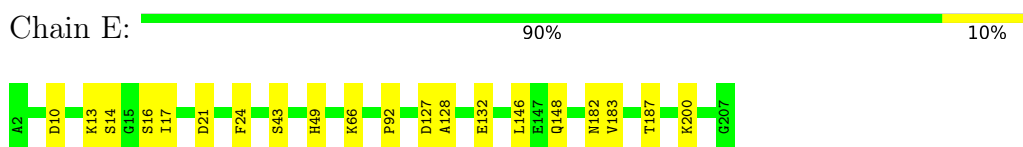
3 Residue-property plots [i](#)

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.

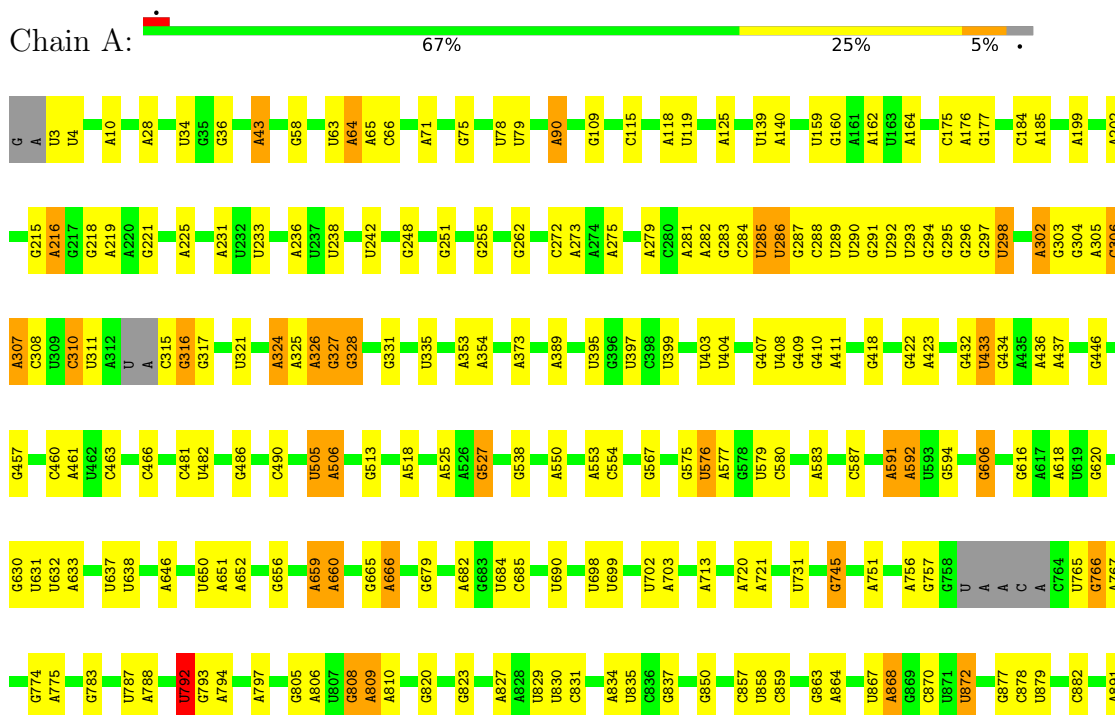
- Molecule 1: 50S ribosomal protein L19

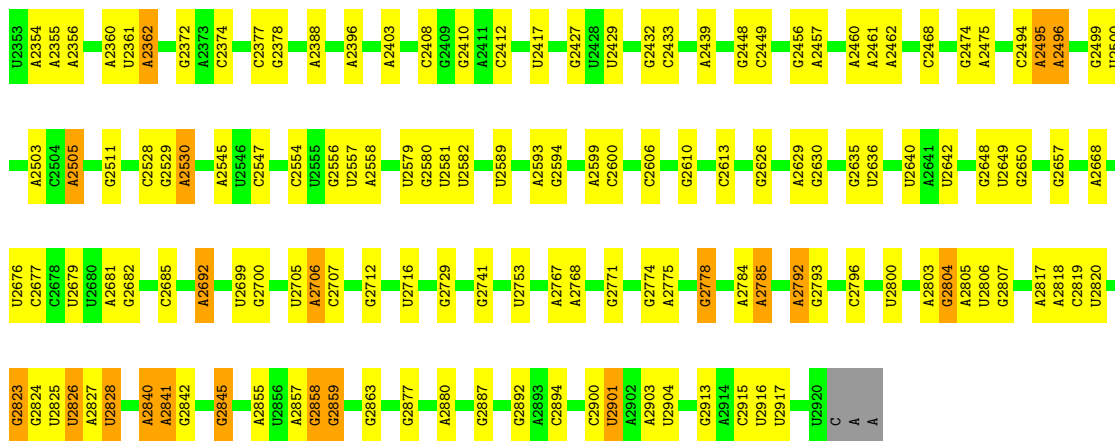


- Molecule 2: 50S ribosomal protein L4

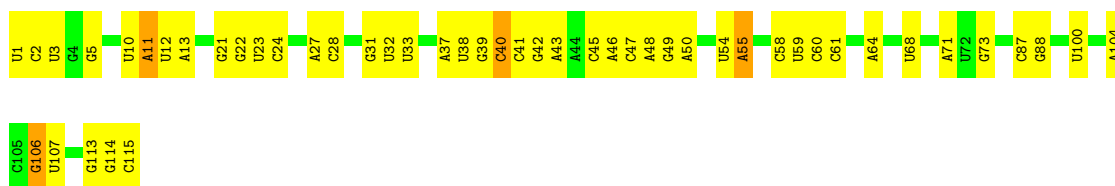


- Molecule 3: 23S rRNA





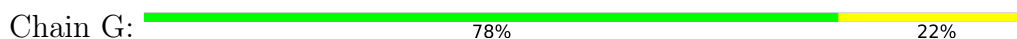
• Molecule 4: 5S rRNA



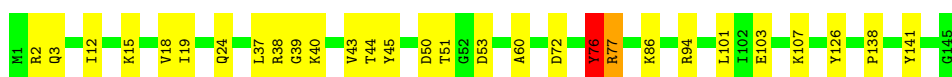
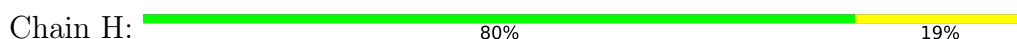
• Molecule 5: 50S ribosomal protein L2




• Molecule 6: 50S ribosomal protein L6



• Molecule 7: 50S ribosomal protein L13



• Molecule 8: 50S ribosomal protein L15

Chain J:  88% 12%




- Molecule 9: 50S ribosomal protein L16

Chain K:  93% 7%




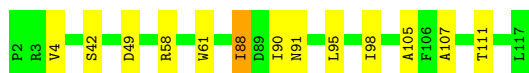
- Molecule 10: 50S ribosomal protein L18

Chain M:  81% 18%



- Molecule 11: 50S ribosomal protein L20

Chain O:  89% 10%




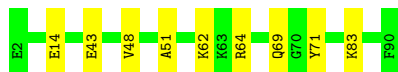
- Molecule 12: 50S ribosomal protein L21

Chain P:  87% 13%




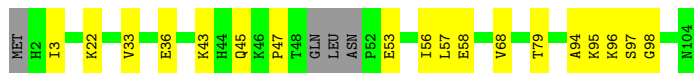
- Molecule 13: 50S ribosomal protein L23

Chain R:  90% 10%




- Molecule 14: 50S ribosomal protein L24

Chain S:  79% 17%



- Molecule 15: 50S ribosomal protein L25

Chain T:  84% 16%



- Molecule 16: 50S ribosomal protein L27

Chain U:  96%




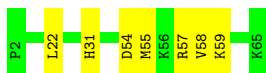
- Molecule 17: 50S ribosomal protein L29

Chain W:  97%



- Molecule 18: 50S ribosomal protein L35

Chain 3:  89% 11%



- Molecule 19: 50S ribosomal protein L33

Chain 1:  91% 9%




- Molecule 20: 50S ribosomal protein L34

Chain 2:  98%




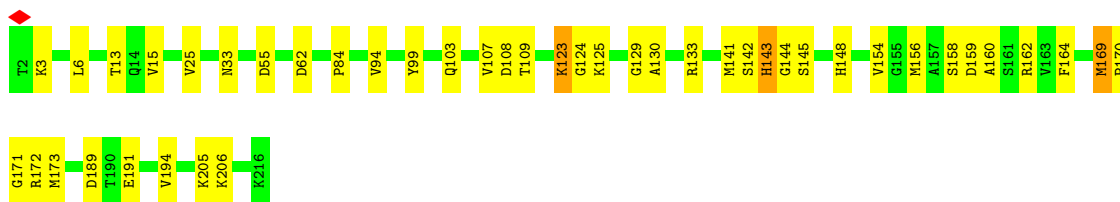
- Molecule 21: 50S ribosomal protein L36

Chain 4:  78% 19%



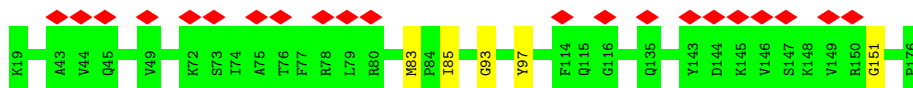
- Molecule 22: 50S ribosomal protein L3

Chain D:  80% 19%




- Molecule 23: 50S ribosomal protein L5

Chain F:  13% 97%




- Molecule 24: 50S ribosomal protein L14

Chain I:  82% 18%




- Molecule 25: 50S ribosomal protein L22

Chain Q:  90% 10%




- Molecule 26: 50S ribosomal protein L28

Chain V:  82% 18%



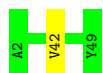
- Molecule 27: 50S ribosomal protein L30

Chain X:  90% 10%

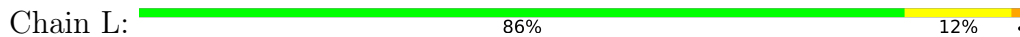


- Molecule 28: 50S ribosomal protein L32

Chain Z:  98%



- Molecule 29: 50S ribosomal protein L17



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	198422	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.085	Depositor
Minimum map value	-0.030	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0037	Depositor
Map size (\AA)	308.88, 308.88, 308.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85800004, 0.85800004, 0.85800004	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: MG, 2MA, 5MU

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	N	0.46	0/901	0.55	0/1209
2	E	0.49	0/1595	0.54	0/2154
3	A	0.54	0/67978	0.41	0/106007
4	B	0.33	0/2736	0.30	0/4261
5	C	0.47	0/2129	0.52	0/2858
6	G	0.25	0/1281	0.50	0/1735
7	H	0.58	1/1171 (0.1%)	0.72	2/1577 (0.1%)
8	J	0.49	0/1100	0.57	0/1467
9	K	0.46	0/1095	0.49	0/1472
10	M	0.32	0/891	0.51	0/1194
11	O	0.56	0/954	0.58	0/1264
12	P	0.57	0/800	0.64	0/1070
13	R	0.46	0/723	0.53	0/966
14	S	0.39	0/763	0.57	0/1018
15	T	0.34	0/730	0.49	0/981
16	U	0.52	0/603	0.55	0/802
17	W	0.43	0/542	0.52	0/722
18	3	0.47	0/526	0.57	0/690
19	1	0.21	0/395	0.43	0/530
20	2	0.58	0/371	0.70	0/484
21	4	0.34	0/298	0.52	0/392
22	D	0.62	0/1651	0.86	1/2215 (0.0%)
23	F	0.17	0/777	0.43	0/1079
24	I	0.48	0/925	0.68	0/1242
25	Q	0.52	0/862	0.56	0/1161
26	V	0.41	0/384	0.58	0/515
27	X	0.48	0/451	0.53	0/606
28	Z	0.48	0/366	0.59	0/489
29	L	0.53	0/929	0.71	0/1244
All	All	0.52	1/93927 (0.0%)	0.45	3/141404 (0.0%)

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
5	C	0	1
7	H	0	1
10	M	0	1
12	P	0	1
21	4	0	1
22	D	0	3
29	L	0	1
All	All	0	9

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	45	TYR	C-N	-6.11	1.25	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	76	TYR	N-CA-C	7.55	126.88	110.80
22	D	109	THR	N-CA-C	-6.77	104.28	112.54
7	H	77	ARG	N-CA-C	5.36	122.22	110.80

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	4	11	CYS	Peptide
5	C	233	GLY	Peptide
7	H	76	TYR	Peptide
10	M	68	THR	Peptide
12	P	50	ALA	Peptide

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	N	889	0	937	7	0
2	E	1572	0	1619	16	0
3	A	60769	0	30546	503	0
4	B	2448	0	1239	34	0
5	C	2094	0	2205	14	0
6	G	1263	0	1232	26	0
7	H	1149	0	1145	17	0
8	J	1086	0	1125	10	0
9	K	1071	0	1123	7	0
10	M	882	0	900	18	0
11	O	942	0	1014	10	0
12	P	790	0	830	10	0
13	R	715	0	748	6	0
14	S	755	0	803	11	0
15	T	722	0	766	9	0
16	U	597	0	604	2	0
17	W	541	0	563	2	0
18	3	521	0	586	5	0
19	1	390	0	394	3	0
20	2	367	0	415	1	0
21	4	295	0	339	7	0
22	D	1627	0	1667	22	0
23	F	778	0	348	3	0
24	I	918	0	981	13	0
25	Q	854	0	914	8	0
26	V	379	0	400	7	0
27	X	449	0	491	4	0
28	Z	360	0	358	1	0
29	L	925	0	975	11	0
30	A	1	0	0	0	0
All	All	86149	0	55267	732	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 5.

The worst 5 of 732 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1521:A:N6	3:A:1559:G:H1	1.50	1.10
3:A:1514:A:N1	3:A:1566:G:N2	2.08	1.01
3:A:2128:G:H1	3:A:2215:U:H3	1.00	0.95
3:A:2127:G:H1	3:A:2216:U:H3	1.13	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1578:A:N6	3:A:1591:G:N7	2.15	0.93

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	N	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
2	E	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
5	C	272/274 (99%)	259 (95%)	13 (5%)	0	100	100
6	G	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
7	H	143/145 (99%)	124 (87%)	18 (13%)	1 (1%)	18	32
8	J	144/146 (99%)	135 (94%)	8 (6%)	1 (1%)	18	32
9	K	135/137 (98%)	126 (93%)	9 (7%)	0	100	100
10	M	117/119 (98%)	104 (89%)	12 (10%)	1 (1%)	14	25
11	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
12	P	100/102 (98%)	92 (92%)	7 (7%)	1 (1%)	12	22
13	R	87/89 (98%)	80 (92%)	7 (8%)	0	100	100
14	S	96/104 (92%)	81 (84%)	15 (16%)	0	100	100
15	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
16	U	77/79 (98%)	73 (95%)	4 (5%)	0	100	100
17	W	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
18	3	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
19	1	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
20	2	41/43 (95%)	39 (95%)	2 (5%)	0	100	100
21	4	35/37 (95%)	35 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	D	213/215 (99%)	179 (84%)	27 (13%)	7 (3%)	3	3
23	F	156/158 (99%)	141 (90%)	15 (10%)	0	100	100
24	I	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
25	Q	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
26	V	47/49 (96%)	45 (96%)	2 (4%)	0	100	100
27	X	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
28	Z	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
29	L	118/120 (98%)	106 (90%)	11 (9%)	1 (1%)	16	28
All	All	2980/3040 (98%)	2750 (92%)	218 (7%)	12 (0%)	31	46

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	D	130	ALA
29	L	67	ARG
22	D	158	SER
22	D	164	PHE
8	J	36	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	93/100 (93%)	93 (100%)	0	100	100
2	E	168/168 (100%)	168 (100%)	0	100	100
5	C	221/221 (100%)	221 (100%)	0	100	100
6	G	124/153 (81%)	123 (99%)	1 (1%)	73	87
7	H	123/123 (100%)	122 (99%)	1 (1%)	73	87
8	J	109/112 (97%)	109 (100%)	0	100	100
9	K	108/114 (95%)	108 (100%)	0	100	100
10	M	83/95 (87%)	83 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	O	96/96 (100%)	95 (99%)	1 (1%)	68	84
12	P	84/86 (98%)	83 (99%)	1 (1%)	63	81
13	R	78/80 (98%)	78 (100%)	0	100	100
14	S	81/89 (91%)	80 (99%)	1 (1%)	63	81
15	T	78/82 (95%)	78 (100%)	0	100	100
16	U	59/62 (95%)	59 (100%)	0	100	100
17	W	58/60 (97%)	58 (100%)	0	100	100
18	3	55/55 (100%)	55 (100%)	0	100	100
19	1	44/45 (98%)	44 (100%)	0	100	100
20	2	39/39 (100%)	39 (100%)	0	100	100
21	4	35/35 (100%)	35 (100%)	0	100	100
22	D	173/173 (100%)	166 (96%)	7 (4%)	28	51
24	I	100/100 (100%)	98 (98%)	2 (2%)	48	72
25	Q	89/91 (98%)	89 (100%)	0	100	100
26	V	39/41 (95%)	39 (100%)	0	100	100
27	X	52/52 (100%)	52 (100%)	0	100	100
28	Z	35/44 (80%)	35 (100%)	0	100	100
29	L	94/101 (93%)	93 (99%)	1 (1%)	65	83
All	All	2318/2417 (96%)	2303 (99%)	15 (1%)	76	90

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	D	125	LYS
24	I	122	LEU
22	D	133	ARG
29	L	122	VAL
22	D	173	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
18	3	60	GLN
22	D	143	HIS
20	2	7	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
22	D	37	GLN
25	Q	60	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	A	2823/2923 (96%)	445 (15%)	12 (0%)
4	B	114/115 (99%)	13 (11%)	0
All	All	2937/3038 (96%)	458 (15%)	12 (0%)

5 of 458 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	A	10	A
3	A	28	A
3	A	34	U
3	A	36	G
3	A	43	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	2528	C
3	A	2629	A
3	A	2900	C
3	A	2840	A
3	A	872	U

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	5MU	A	1966	3	19,22,23	4.80	7 (36%)	27,32,35	3.71	9 (33%)
3	2MA	A	2530	3	22,25,26	3.60	10 (45%)	32,37,40	2.52	11 (34%)
3	5MU	A	792	3	19,22,23	4.79	7 (36%)	27,32,35	3.80	11 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	5MU	A	1966	3	-	0/7/25/26	0/2/2/2
3	2MA	A	2530	3	-	2/7/25/26	0/3/3/3
3	5MU	A	792	3	-	2/7/25/26	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	792	5MU	C2-N1	11.08	1.55	1.38
3	A	1966	5MU	C2-N1	10.81	1.55	1.38
3	A	2530	2MA	C4-N3	10.43	1.47	1.34
3	A	1966	5MU	C6-N1	10.33	1.55	1.38
3	A	792	5MU	C6-N1	10.11	1.55	1.38

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	792	5MU	C5-C4-N3	12.43	126.12	115.32
3	A	1966	5MU	C5-C4-N3	12.18	125.91	115.32
3	A	792	5MU	C5-C6-N1	-10.10	112.34	123.31
3	A	1966	5MU	C5-C6-N1	-9.97	112.48	123.31
3	A	2530	2MA	C1'-N9-C8	-6.52	112.62	127.09

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	792	5MU	O4'-C4'-C5'-O5'
3	A	792	5MU	C3'-C4'-C5'-O5'
3	A	2530	2MA	O4'-C4'-C5'-O5'
3	A	2530	2MA	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	792	5MU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

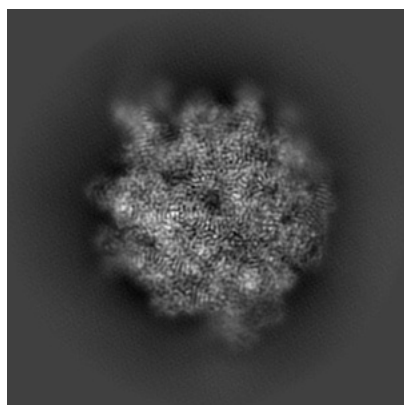
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11900. These allow visual inspection of the internal detail of the map and identification of artifacts.

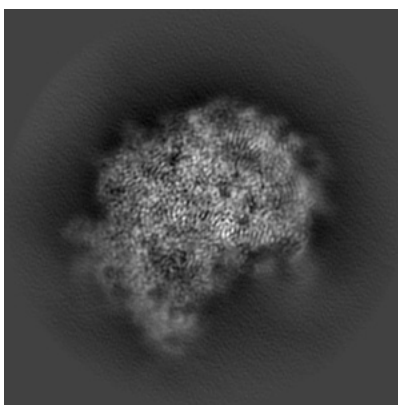
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

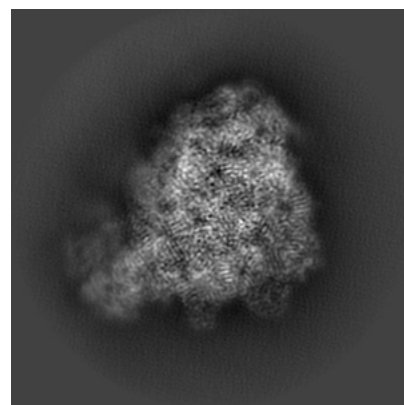
6.1.1 Primary map



X



Y

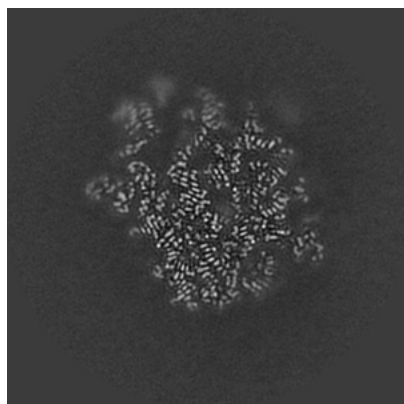


Z

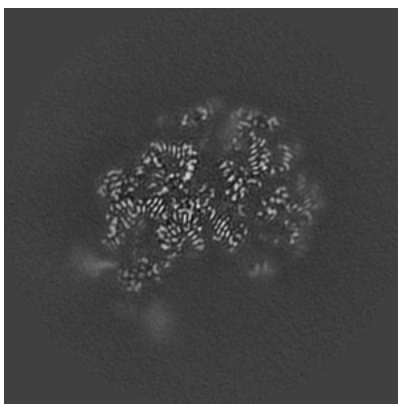
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

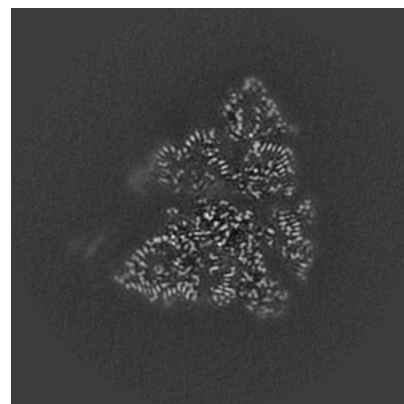
6.2.1 Primary map



X Index: 180



Y Index: 180

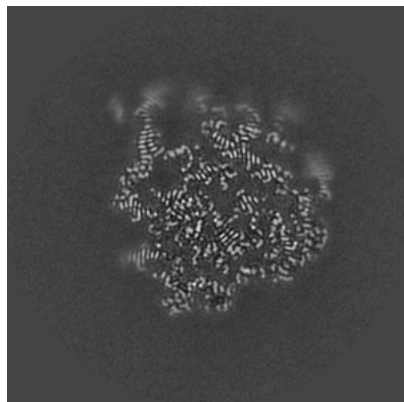


Z Index: 180

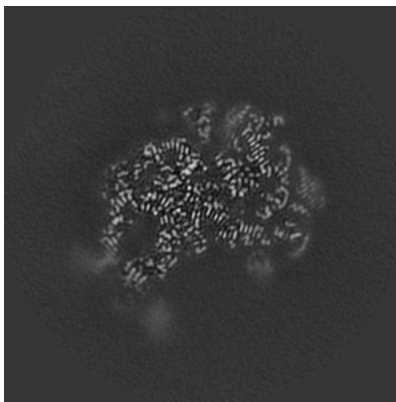
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

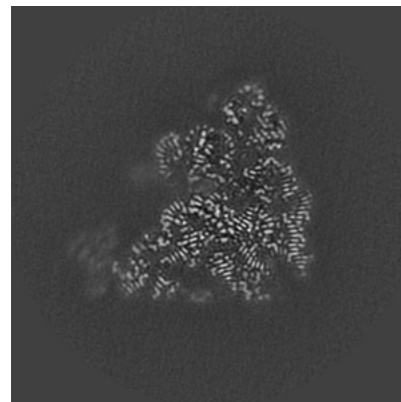
6.3.1 Primary map



X Index: 193



Y Index: 176

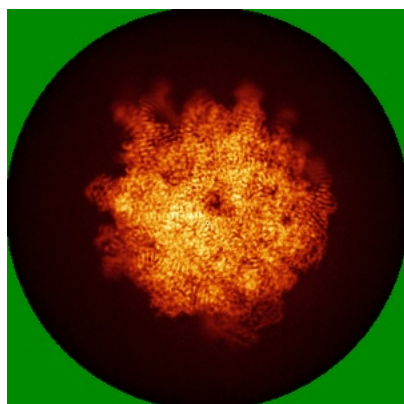


Z Index: 173

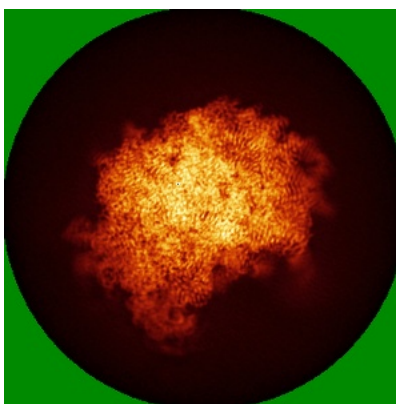
The images above show the largest variance slices of the map in three orthogonal directions.

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

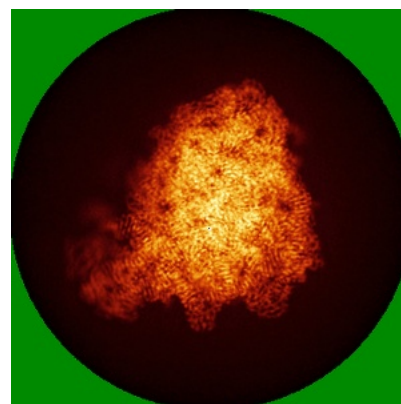
6.4.1 Primary map



X



Y

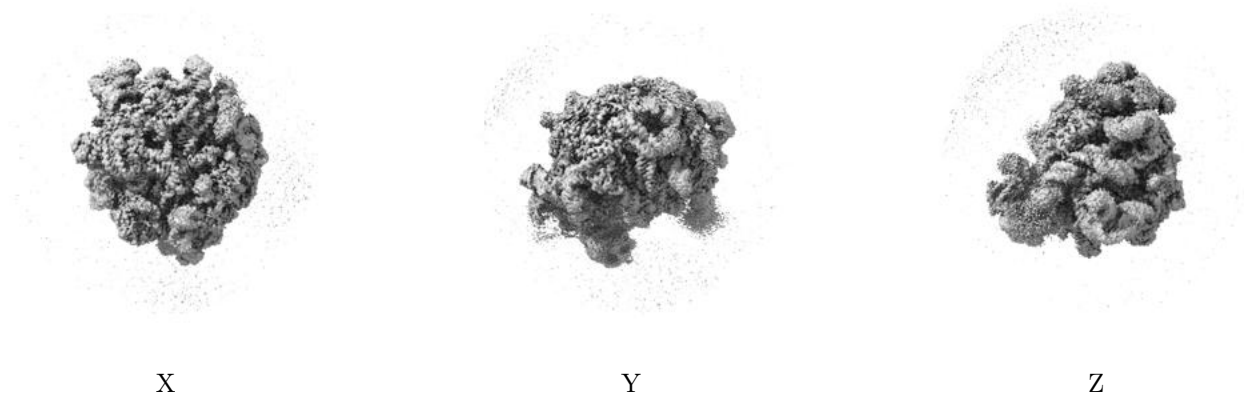


Z

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 0.0037. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

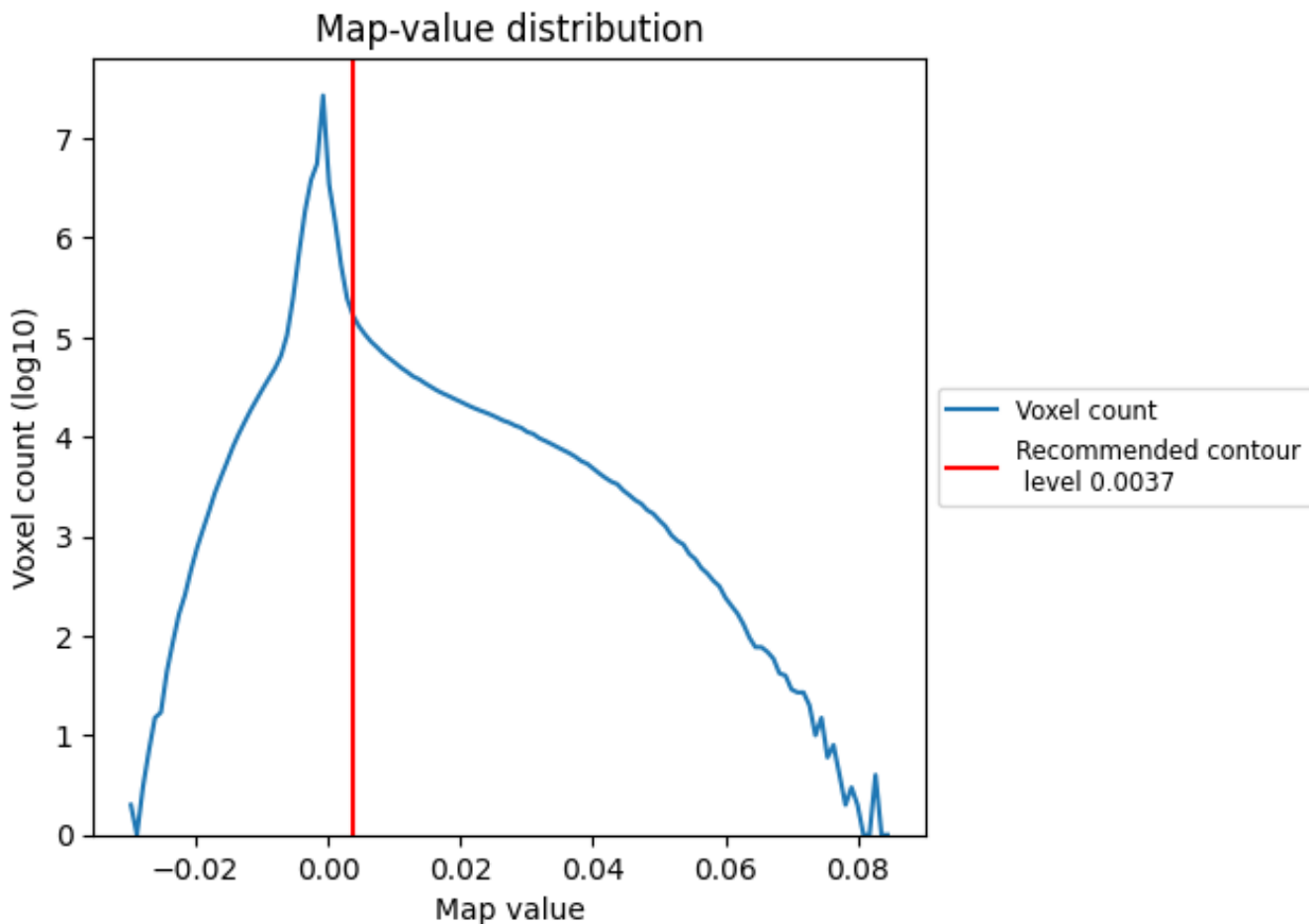
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

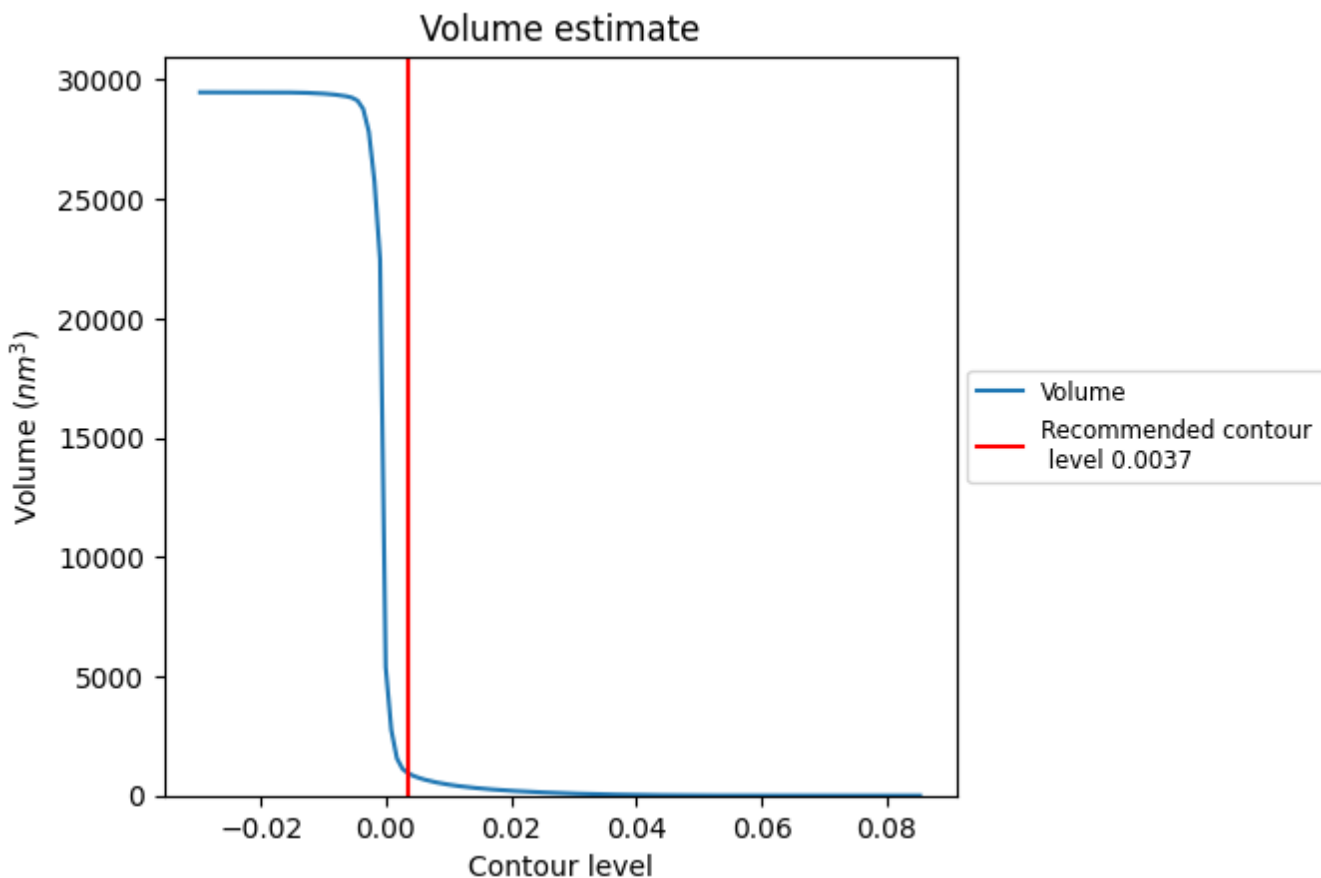
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

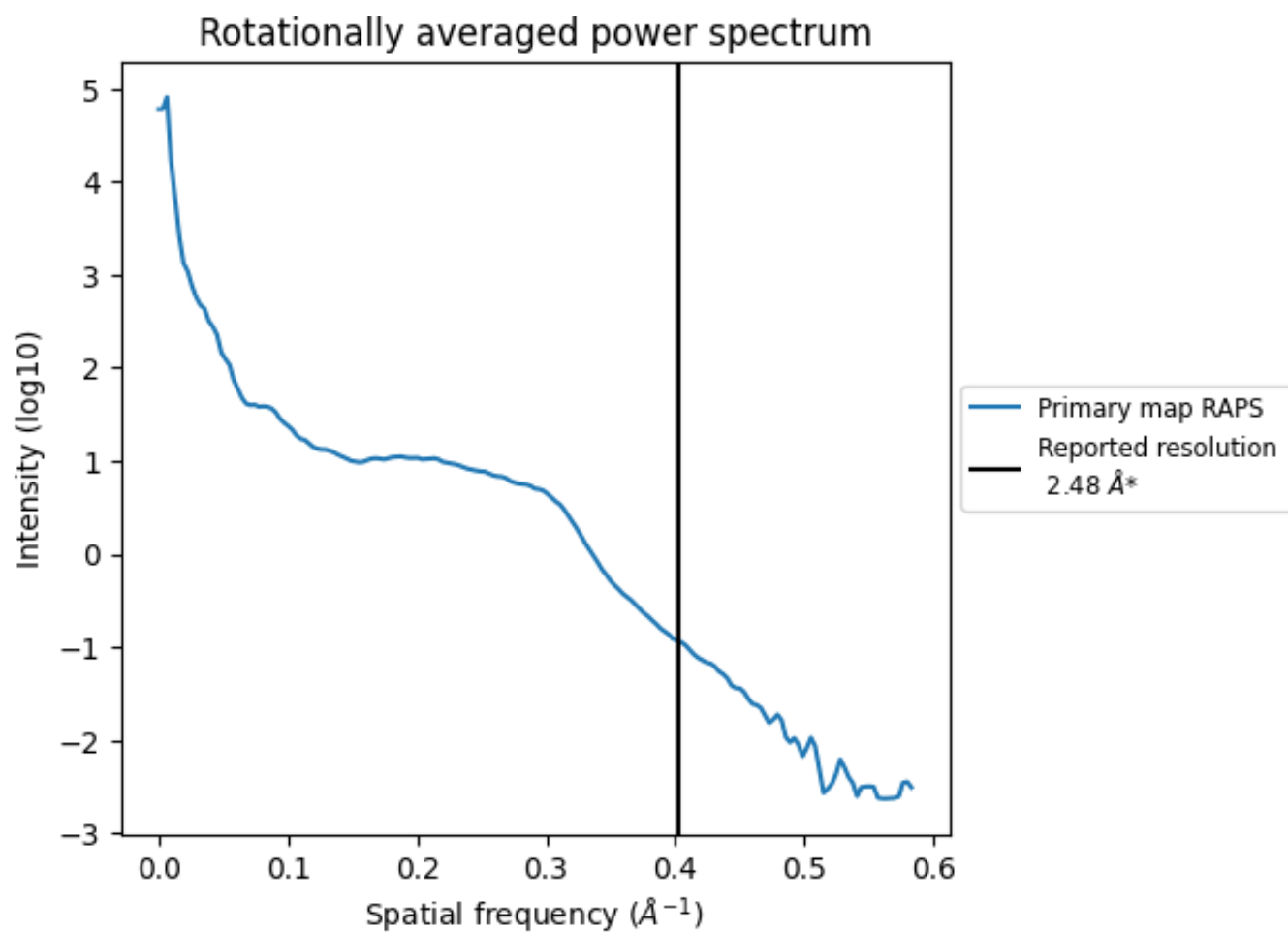
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 916 nm³; this corresponds to an approximate mass of 827 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.403 Å⁻¹

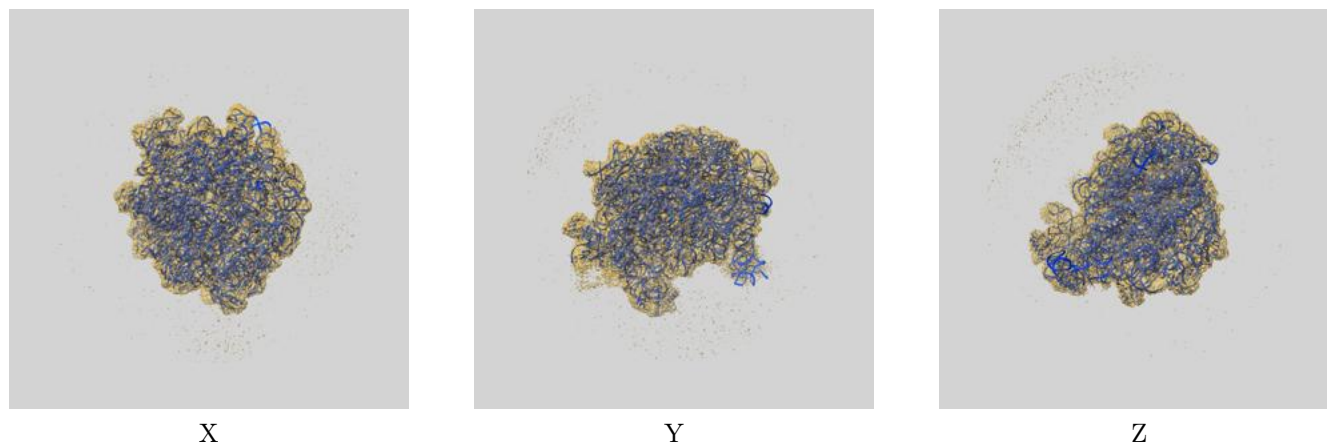
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

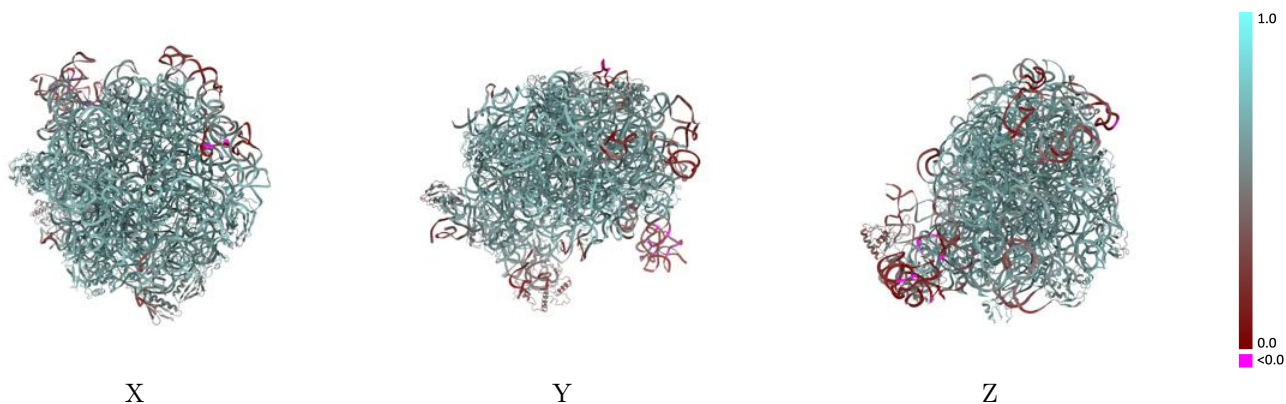
This section contains information regarding the fit between EMDB map EMD-11900 and PDB model 7ASM. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

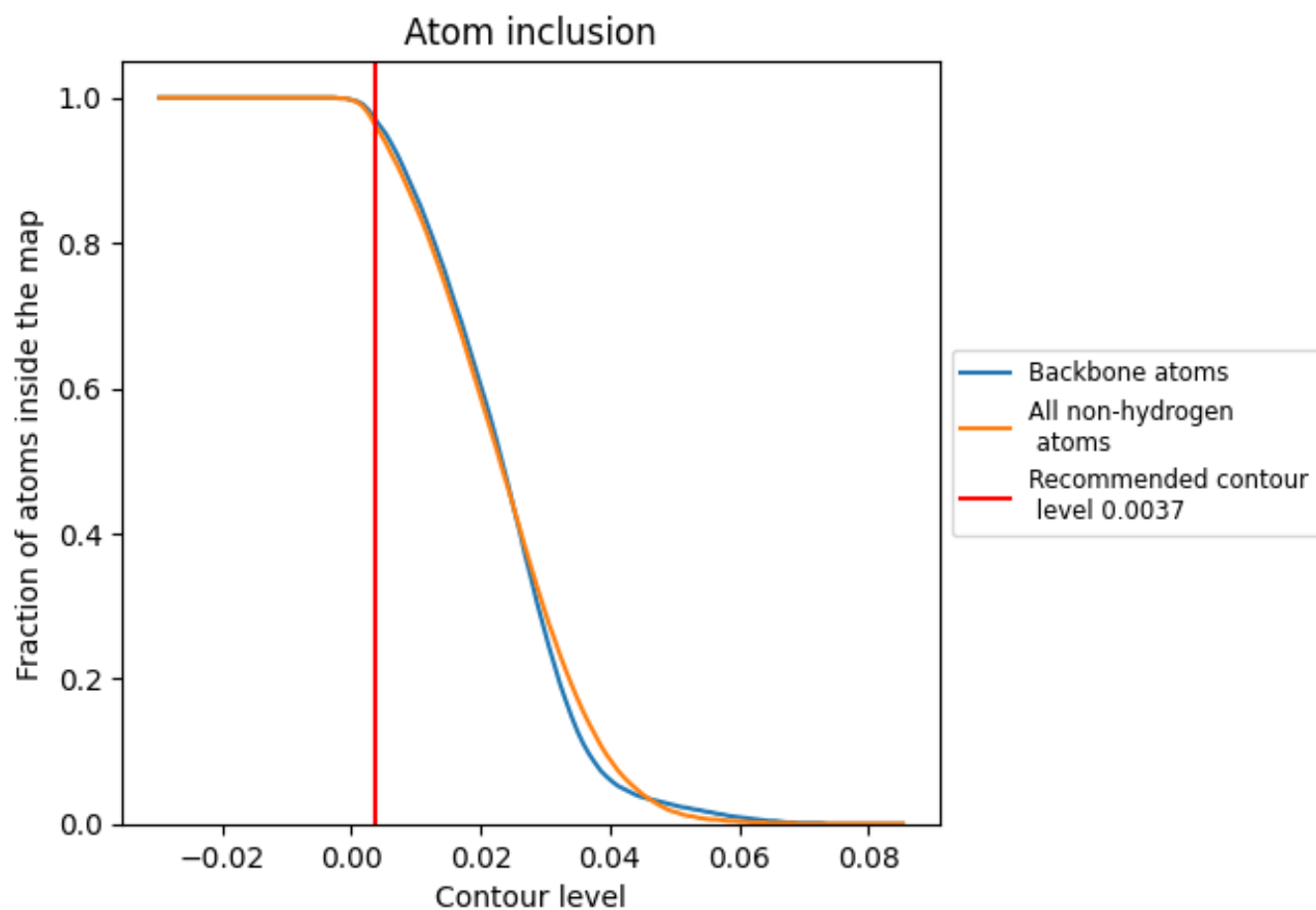


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.





























































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.0037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9620	 0.6000
1	 0.7790	 0.5820
2	 0.9910	 0.6820
3	 0.9920	 0.6650
4	 0.9790	 0.6120
A	 0.9590	 0.5980
B	 0.9960	 0.5330
C	 0.9880	 0.6520
D	 0.9610	 0.6240
E	 0.9850	 0.6410
F	 0.8370	 0.3580
G	 0.9470	 0.5060
H	 0.9730	 0.6380
I	 0.9740	 0.6290
J	 0.9890	 0.6420
K	 0.9880	 0.6320
L	 0.9830	 0.6360
M	 0.9670	 0.5040
N	 0.9520	 0.6200
O	 0.9860	 0.6640
P	 0.9830	 0.6350
Q	 0.9820	 0.6610
R	 0.9760	 0.6230
S	 0.9760	 0.5770
T	 0.9660	 0.5790
U	 0.9810	 0.6460
V	 0.9780	 0.6060
W	 0.9640	 0.5910
X	 0.9770	 0.6380
Z	 0.9970	 0.6100

