



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 08:14 AM UTC

PDB ID : 3J3W / pdb_00003j3w
EMDB ID : EMD-5643
Title : Atomic model of the immature 50S subunit from *Bacillus subtilis* (state II-a)
Authors : Li, N.; Guo, Q.; Zhang, Y.; Yuan, Y.; Ma, C.; Lei, J.; Gao, N.
Deposited on : 2013-04-28
Resolution : 10.70 Å (reported)
Based on initial models : 2J01, 2AW4

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:

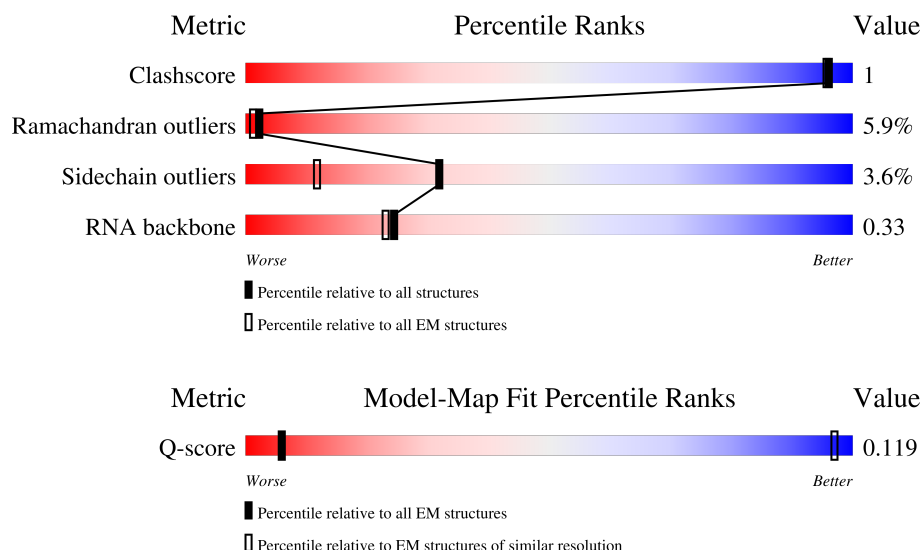
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 10.70 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.



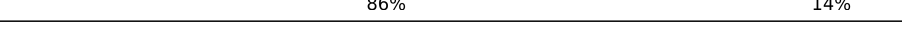
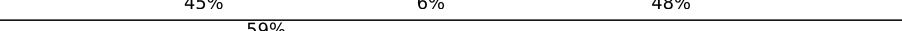
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	94 (10.20 - 11.16)

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	2927	
2	0	59	
3	C	277	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	N	120	 92% 8% .
5	G	179	 82% 9% . 9%
6	J	145	 88% 9% ..
7	K	122	 90% 10%
8	L	146	 86% 10% .
9	P	115	 70% 23% . . .
10	Q	119	 89% 9% .
11	D	209	 90% 8% .
12	R	102	 89% 11%
13	S	113	 88% 10% ..
14	T	95	 82% 16% .
15	U	103	 81% 17% .
16	X	66	 77% 15% 8%
17	2	44	 86% 14%
18	5	232	 45% 6% 48%
19	6	141	 59% 88% 11% .
20	E	207	 79% 18% .

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 76573 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 ribosome RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2685	Total	C	N	O	P	0	0
			57639	25720	10638	18600	2681		

- Molecule 2 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	55	Total	C	N	O	S	0	0
			433	267	87	72	7		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	277	Total	C	N	O	S	0	0
			2129	1323	419	380	7		

- Molecule 4 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	120	Total	C	N	O	S	0	0
			962	588	187	182	5		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	163	Total	C	N	O	S	0	0
			1246	776	226	242	2		

- Molecule 6 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	143	Total	C	N	O	S	0	0
			1134	717	207	204	6		

- Molecule 7 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 9 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	P	112	Total	C	N	O	0	0
			916	584	178	154		

- Molecule 10 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	206	Total	C	N	O	S	0	0
			1568	984	289	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	102	Total	C	N	O	S	0	0
			795	506	140	148	1		

- Molecule 13 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	112	Total	C	N	O	S	0	0
			868	541	168	155	4		

- Molecule 14 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	95	Total	C	N	O	S	0	0
			767	480	139	144	4		

- Molecule 15 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	103	Total	C	N	O	S	0	0
			780	488	145	143	4		

- Molecule 16 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	61	Total	C	N	O	S	0	0
			504	312	97	93	2		

- Molecule 17 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 18 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	120	Total	C	N	O	S	0	0
			910	576	156	176	2		

- Molecule 19 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	6	141	Total	C	N	O	S	0	0
			1044	657	184	196	7		

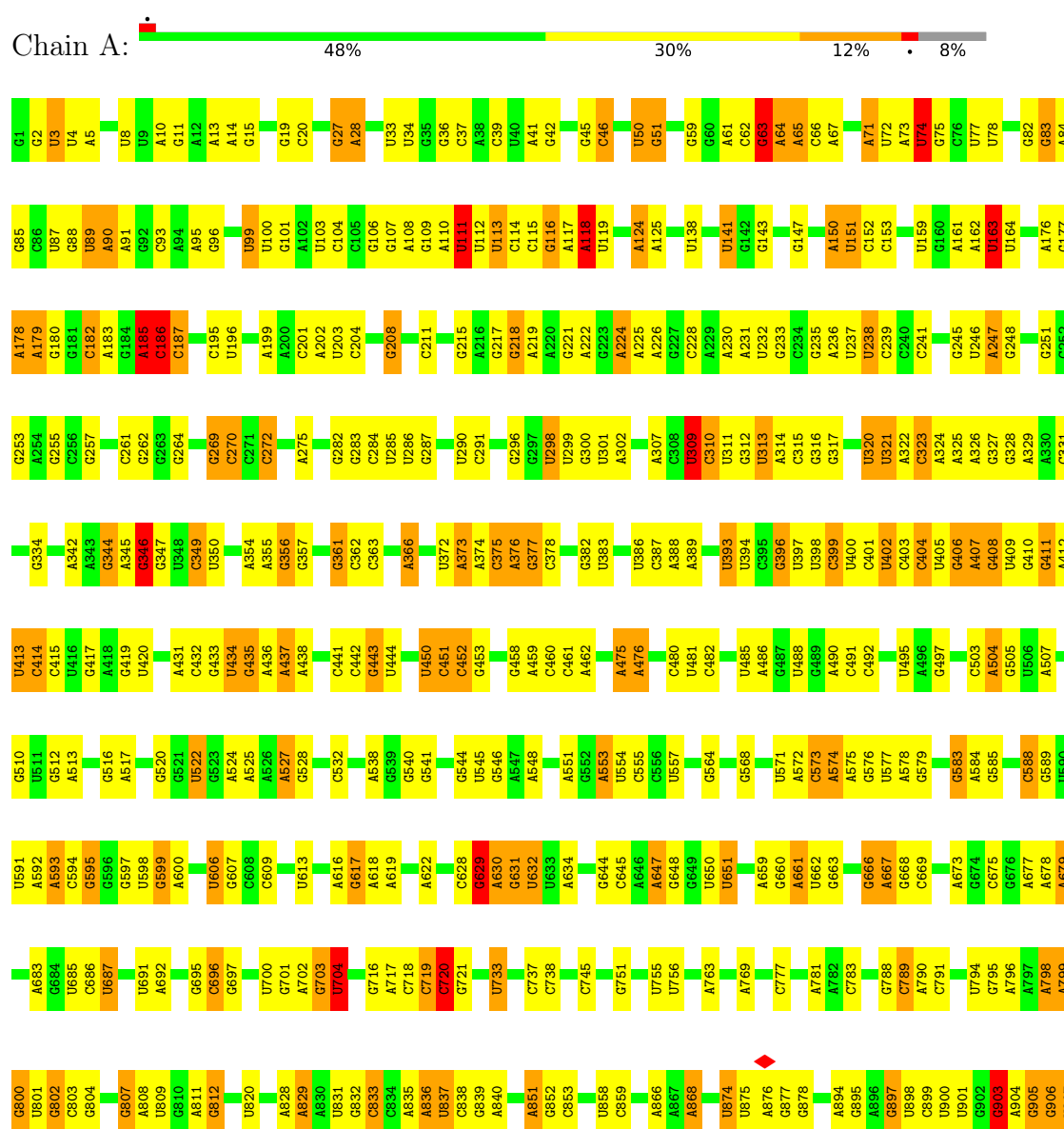
- Molecule 20 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E	206	Total	C	N	O	S	0	0
			1567	983	290	292	2		

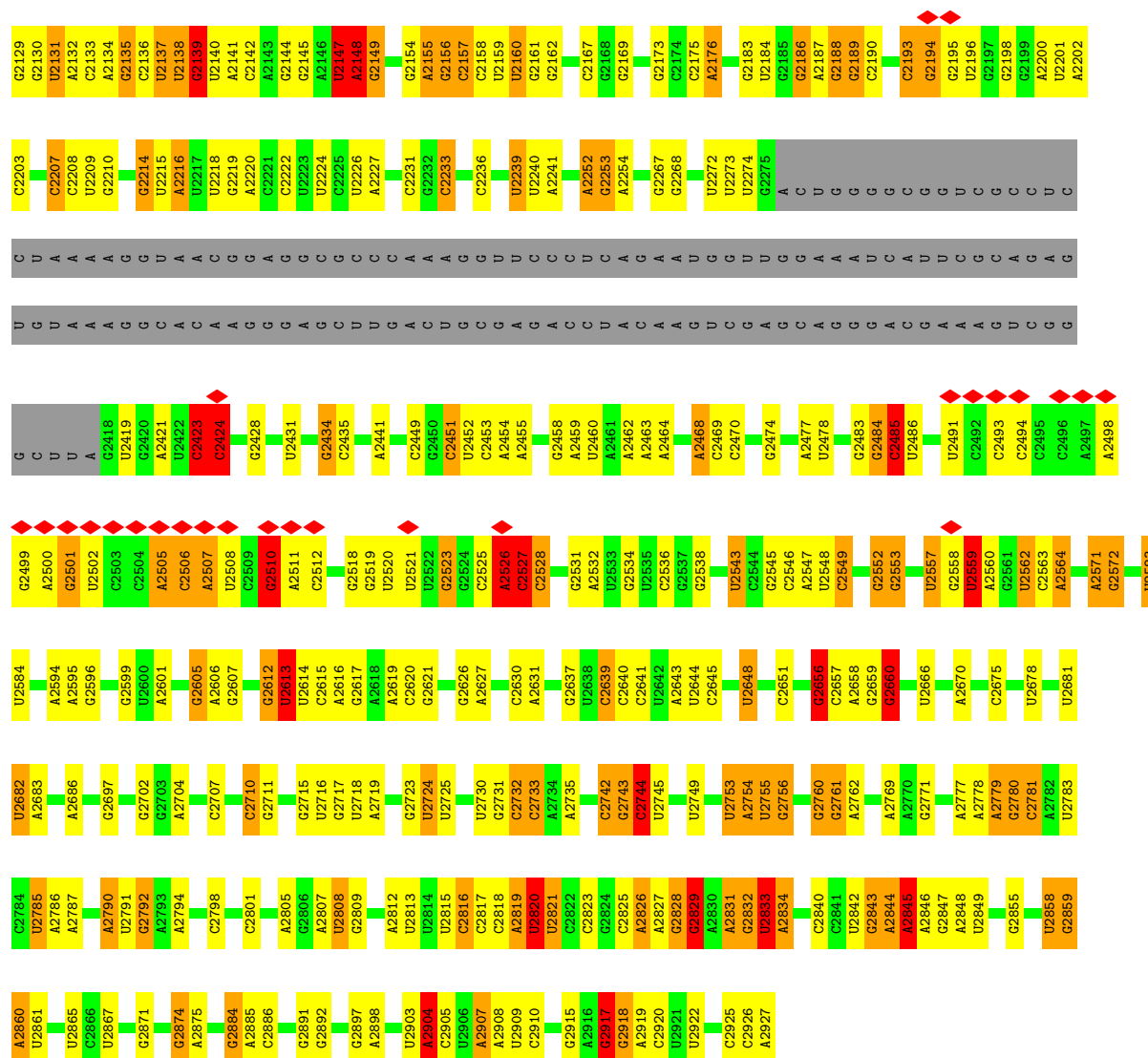
3 Residue-property plots

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: ribosome RNA 23S







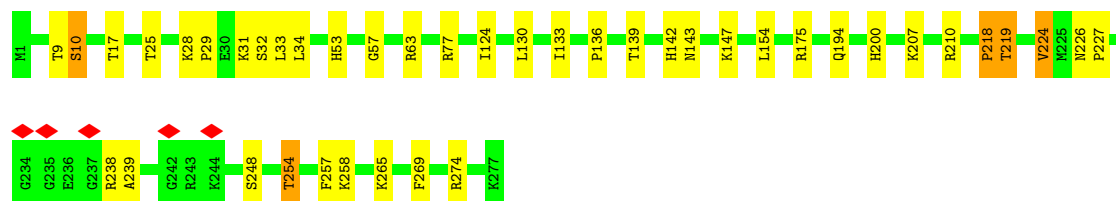
• Molecule 2: 50S ribosomal protein L32

Chain 0: 81% 12% 7%



• Molecule 3: 50S ribosomal protein L2

Chain C: 85% 13%



- Molecule 4: 50S ribosomal protein L17

Chain N:  92% 8%



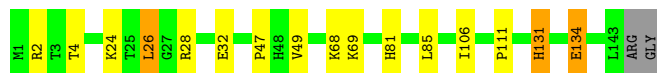
- Molecule 5: 50S ribosomal protein L6

Chain G:  82% 9% 9%



- Molecule 6: 50S ribosomal protein L13

Chain J:  88% 9%



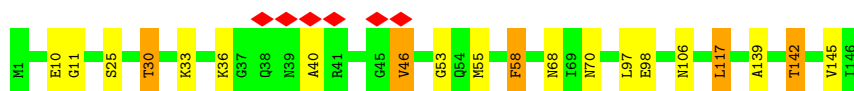
- Molecule 7: 50S ribosomal protein L14

Chain K:  90% 10%



- Molecule 8: 50S ribosomal protein L15

Chain L:  86% 10%



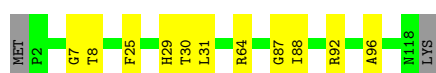
- Molecule 9: 50S ribosomal protein L19

Chain P:  70% 23%



- Molecule 10: 50S ribosomal protein L20

Chain Q:  89% 9%



- Molecule 11: 50S ribosomal protein L3

Chain D:  90% 8%



- Molecule 12: 50S ribosomal protein L21

Chain R:  89% 11%



- Molecule 13: 50S ribosomal protein L22

Chain S:  88% 10%



- Molecule 14: 50S ribosomal protein L23

Chain T:  82% 16%



- Molecule 15: 50S ribosomal protein L24

Chain U:  81% 17%



- Molecule 16: 50S ribosomal protein L29

Chain X:  77% 15% 8%

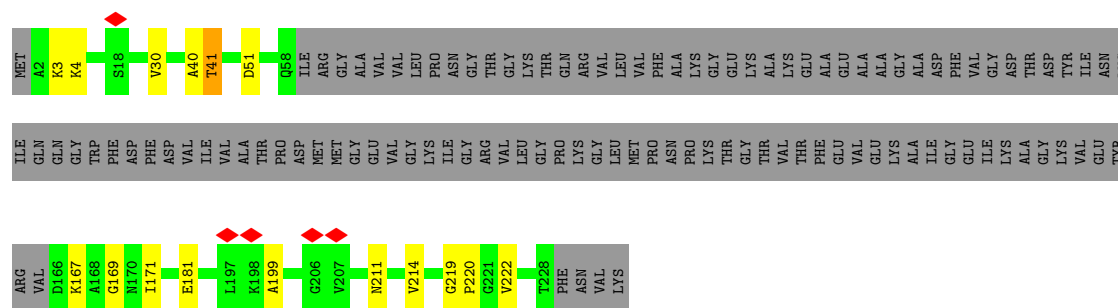


- Molecule 17: 50S ribosomal protein L34

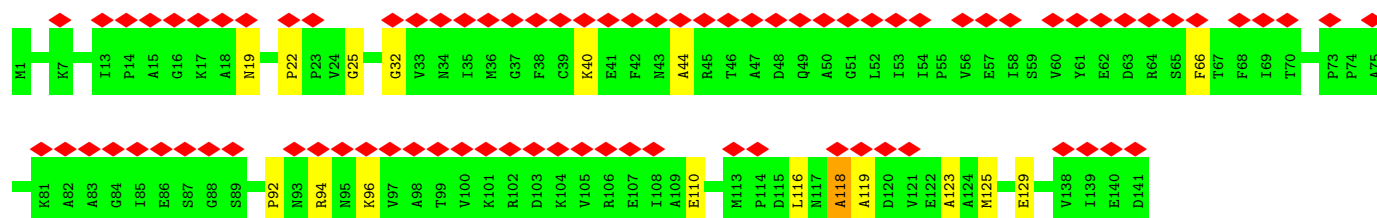
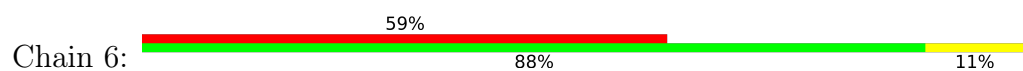
Chain 2:  86% 14%



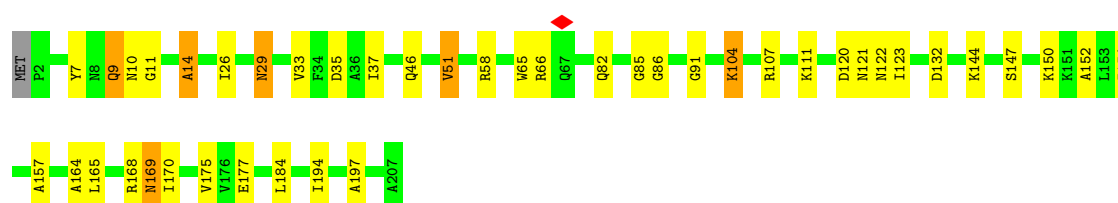
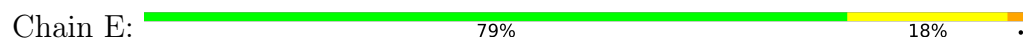
- Molecule 18: 50S ribosomal protein L1



- Molecule 19: 50S ribosomal protein L11



- Molecule 20: 50S ribosomal protein L4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27652	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	10.909	Depositor
Minimum map value	-3.262	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	384.0, 384.0, 384.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.5, 1.5, 1.5	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.95	1/64560 (0.0%)	1.30	443/100715 (0.4%)
2	O	1.32	0/440	1.59	4/584 (0.7%)
3	C	1.28	0/2166	1.56	20/2902 (0.7%)
4	N	1.36	0/969	1.63	8/1294 (0.6%)
5	G	1.26	0/1264	1.50	9/1709 (0.5%)
6	J	1.24	0/1157	1.56	4/1557 (0.3%)
7	K	1.30	0/928	1.43	4/1245 (0.3%)
8	L	1.23	0/1094	1.58	6/1457 (0.4%)
9	P	1.36	0/929	1.52	9/1243 (0.7%)
10	Q	1.30	0/952	1.71	9/1266 (0.7%)
11	D	1.27	0/1590	1.52	12/2130 (0.6%)
12	R	1.21	0/806	1.45	2/1080 (0.2%)
13	S	1.32	0/877	1.66	8/1179 (0.7%)
14	T	1.28	0/774	1.47	5/1030 (0.5%)
15	U	1.19	0/790	1.61	6/1054 (0.6%)
16	X	1.30	0/505	1.73	6/671 (0.9%)
17	2	1.50	0/371	1.60	3/483 (0.6%)
18	5	1.13	0/921	1.60	14/1239 (1.1%)
19	6	1.21	0/1058	1.60	14/1427 (1.0%)
20	E	1.24	0/1586	1.69	32/2139 (1.5%)
All	All	1.03	1/83737 (0.0%)	1.36	618/126404 (0.5%)

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
1	A	0	320
4	N	0	1
8	L	0	2
9	P	0	2
14	T	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
15	U	0	1
20	E	0	2
All	All	0	330

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1339	A	O3'-P	-5.70	1.52	1.61

The worst 5 of 618 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1339	A	P-O3'-C3'	27.07	160.81	120.20
1	A	313	U	P-O3'-C3'	16.28	144.62	120.20
1	A	178	A	P-O3'-C3'	15.70	143.75	120.20
1	A	74	U	P-O3'-C3'	15.65	143.68	120.20
1	A	375	C	P-O3'-C3'	15.60	143.60	120.20

There are no chirality outliers.

5 of 330 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	G	Sidechain
1	A	27	G	Sidechain
1	A	28	A	Sidechain
1	A	33	U	Sidechain
1	A	5	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	57639	0	29016	104	0
2	0	433	0	454	0	0
3	C	2129	0	2225	4	0
4	N	962	0	995	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1246	0	1273	2	0
6	J	1134	0	1178	0	0
7	K	921	0	977	0	0
8	L	1082	0	1132	0	0
9	P	916	0	987	5	0
10	Q	940	0	1005	0	0
11	D	1568	0	1635	0	0
12	R	795	0	838	0	0
13	S	868	0	930	0	0
14	T	767	0	813	2	0
15	U	780	0	838	0	0
16	X	504	0	541	1	0
17	2	368	0	410	1	0
18	5	910	0	944	0	0
19	6	1044	0	1098	1	0
20	E	1567	0	1652	1	0
All	All	76573	0	48941	116	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 1.

The worst 5 of 116 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:1245:G:H1	1:A:1281:C:H41	1.25	0.84
1:A:898:U:H3	1:A:973:G:H1	1.41	0.68
1:A:2557:U:H3	1:A:2564:A:H61	1.41	0.68
1:A:1799:G:H1	1:A:2011:U:H3	1.46	0.63
1:A:2543:U:H3	1:A:2599:G:H1	1.48	0.62

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	
2	0	53/59 (90%)	43 (81%)	6 (11%)	4 (8%)	1	10
3	C	275/277 (99%)	217 (79%)	40 (14%)	18 (6%)	1	12
4	N	118/120 (98%)	101 (86%)	14 (12%)	3 (2%)	4	26
5	G	161/179 (90%)	148 (92%)	7 (4%)	6 (4%)	2	20
6	J	141/145 (97%)	124 (88%)	9 (6%)	8 (6%)	1	14
7	K	120/122 (98%)	106 (88%)	9 (8%)	5 (4%)	2	17
8	L	144/146 (99%)	100 (69%)	30 (21%)	14 (10%)	0	7
9	P	110/115 (96%)	76 (69%)	20 (18%)	14 (13%)	0	4
10	Q	115/119 (97%)	101 (88%)	9 (8%)	5 (4%)	2	17
11	D	204/209 (98%)	175 (86%)	21 (10%)	8 (4%)	2	19
12	R	100/102 (98%)	79 (79%)	15 (15%)	6 (6%)	1	13
13	S	110/113 (97%)	97 (88%)	10 (9%)	3 (3%)	4	25
14	T	93/95 (98%)	77 (83%)	11 (12%)	5 (5%)	1	15
15	U	101/103 (98%)	70 (69%)	20 (20%)	11 (11%)	0	6
16	X	59/66 (89%)	55 (93%)	2 (3%)	2 (3%)	3	21
17	2	42/44 (96%)	37 (88%)	4 (10%)	1 (2%)	4	27
18	5	116/232 (50%)	97 (84%)	13 (11%)	6 (5%)	1	15
19	6	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	2	20
20	E	204/207 (99%)	161 (79%)	25 (12%)	18 (9%)	0	8
All	All	2405/2594 (93%)	1981 (82%)	282 (12%)	142 (6%)	2	13

5 of 142 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	0	19	HIS
3	C	219	THR
7	K	30	ARG
7	K	73	ASP
8	L	117	LEU

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	
2	0	49/53 (92%)	49 (100%)	0	100	100
3	C	225/225 (100%)	217 (96%)	8 (4%)	31	52
4	N	100/100 (100%)	98 (98%)	2 (2%)	48	66
5	G	138/151 (91%)	136 (99%)	2 (1%)	59	72
6	J	122/123 (99%)	114 (93%)	8 (7%)	15	37
7	K	101/101 (100%)	98 (97%)	3 (3%)	36	57
8	L	110/110 (100%)	107 (97%)	3 (3%)	39	61
9	P	97/100 (97%)	90 (93%)	7 (7%)	13	35
10	Q	96/98 (98%)	95 (99%)	1 (1%)	68	78
11	D	167/170 (98%)	162 (97%)	5 (3%)	36	57
12	R	84/84 (100%)	81 (96%)	3 (4%)	31	52
13	S	93/93 (100%)	88 (95%)	5 (5%)	20	41
14	T	85/85 (100%)	80 (94%)	5 (6%)	18	39
15	U	87/87 (100%)	81 (93%)	6 (7%)	14	36
16	X	54/57 (95%)	50 (93%)	4 (7%)	13	33
17	2	39/39 (100%)	37 (95%)	2 (5%)	21	42
18	5	98/185 (53%)	96 (98%)	2 (2%)	48	66
19	6	110/110 (100%)	109 (99%)	1 (1%)	70	79
20	E	169/170 (99%)	163 (96%)	6 (4%)	31	52
All	All	2024/2141 (94%)	1951 (96%)	73 (4%)	32	52

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	U	101	LEU
20	E	175	VAL
16	X	28	LEU
18	5	222	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	L	58	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
10	Q	116	GLN
20	E	49	HIS
12	R	65	GLN
20	E	29	ASN
20	E	179	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2681/2927 (91%)	831 (30%)	200 (7%)

5 of 831 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	3	U
1	A	4	U
1	A	8	U
1	A	10	A

5 of 200 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1590	C
1	A	2050	G
1	A	2918	G
1	A	1606	A
1	A	1711	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

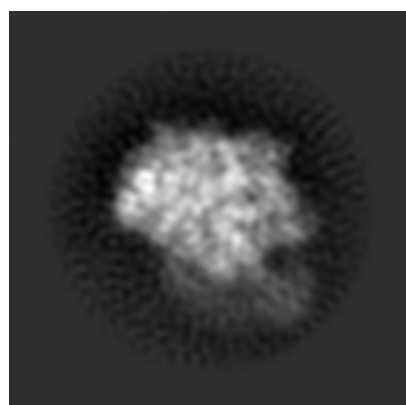
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5643. These allow visual inspection of the internal detail of the map and identification of artifacts.

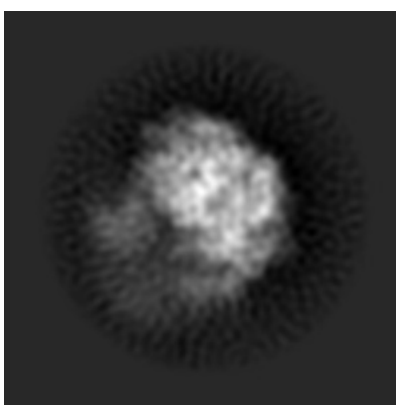
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

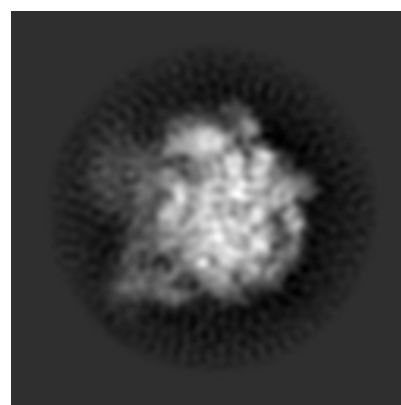
6.1.1 Primary map



X



Y

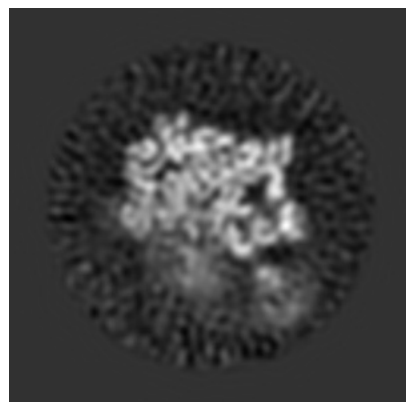


Z

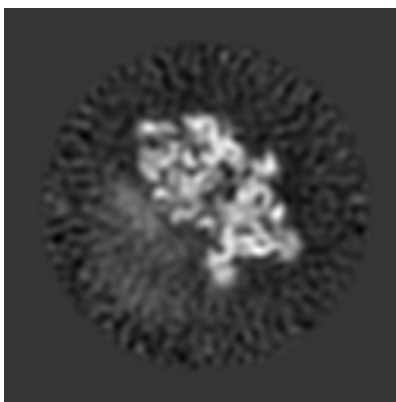
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

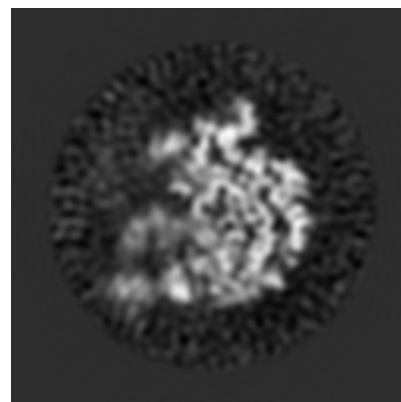
6.2.1 Primary map



X Index: 128



Y Index: 128

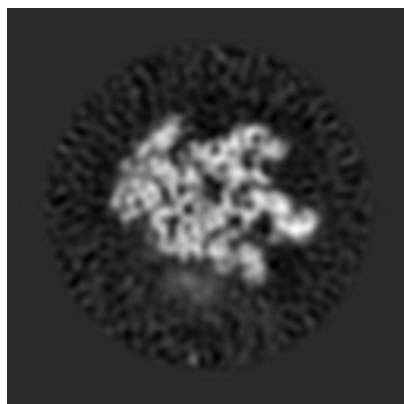


Z Index: 128

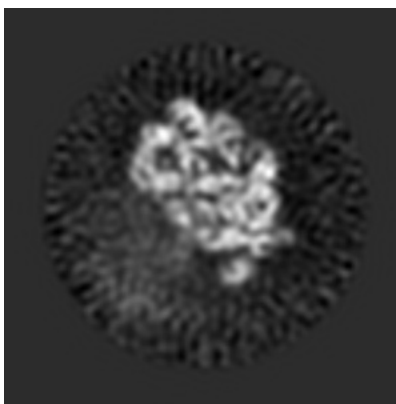
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 140



Y Index: 139

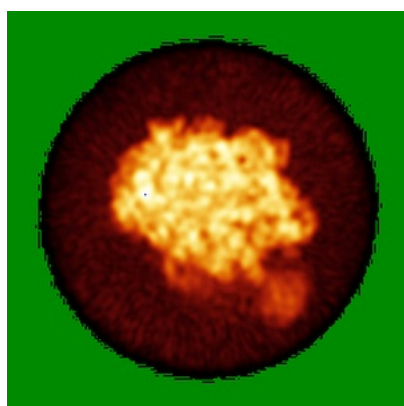


Z Index: 148

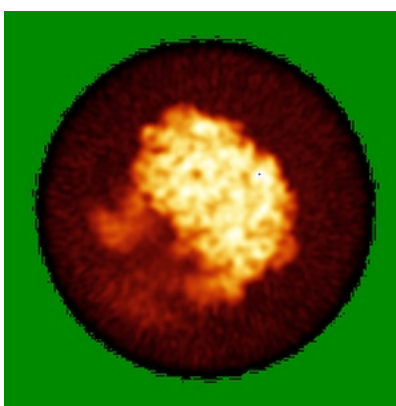
The images above show the largest variance slices of the map in three orthogonal directions.

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

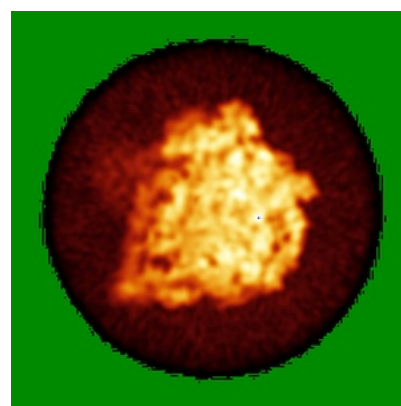
6.4.1 Primary map



X



Y

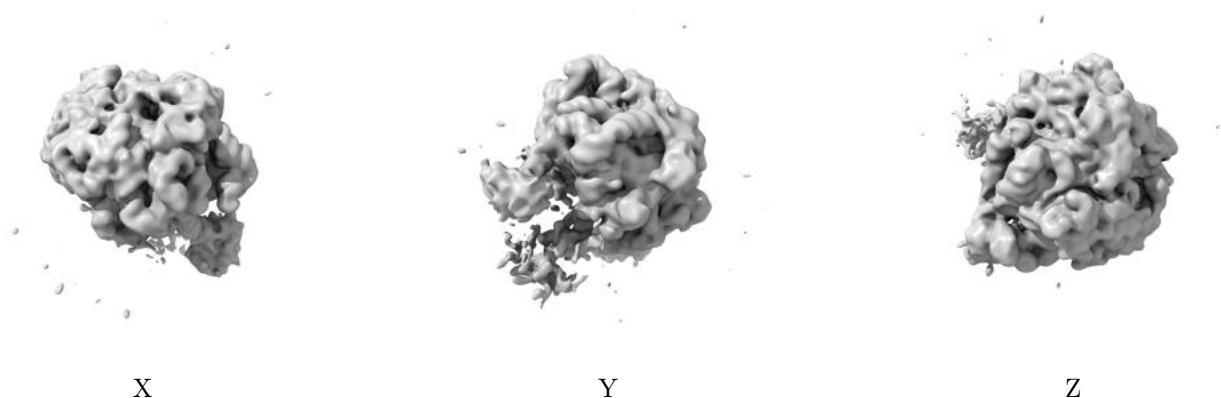


Z

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

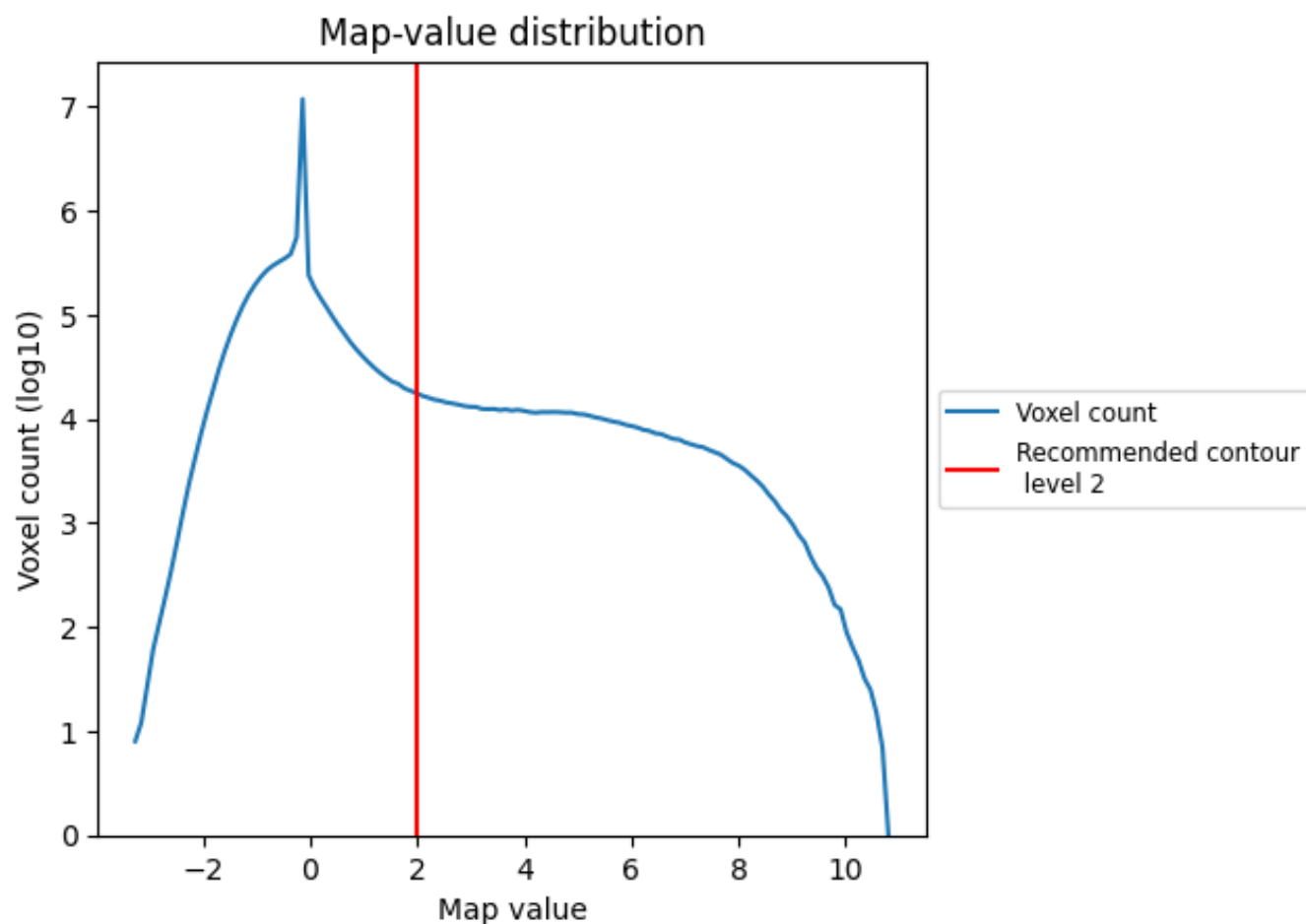
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

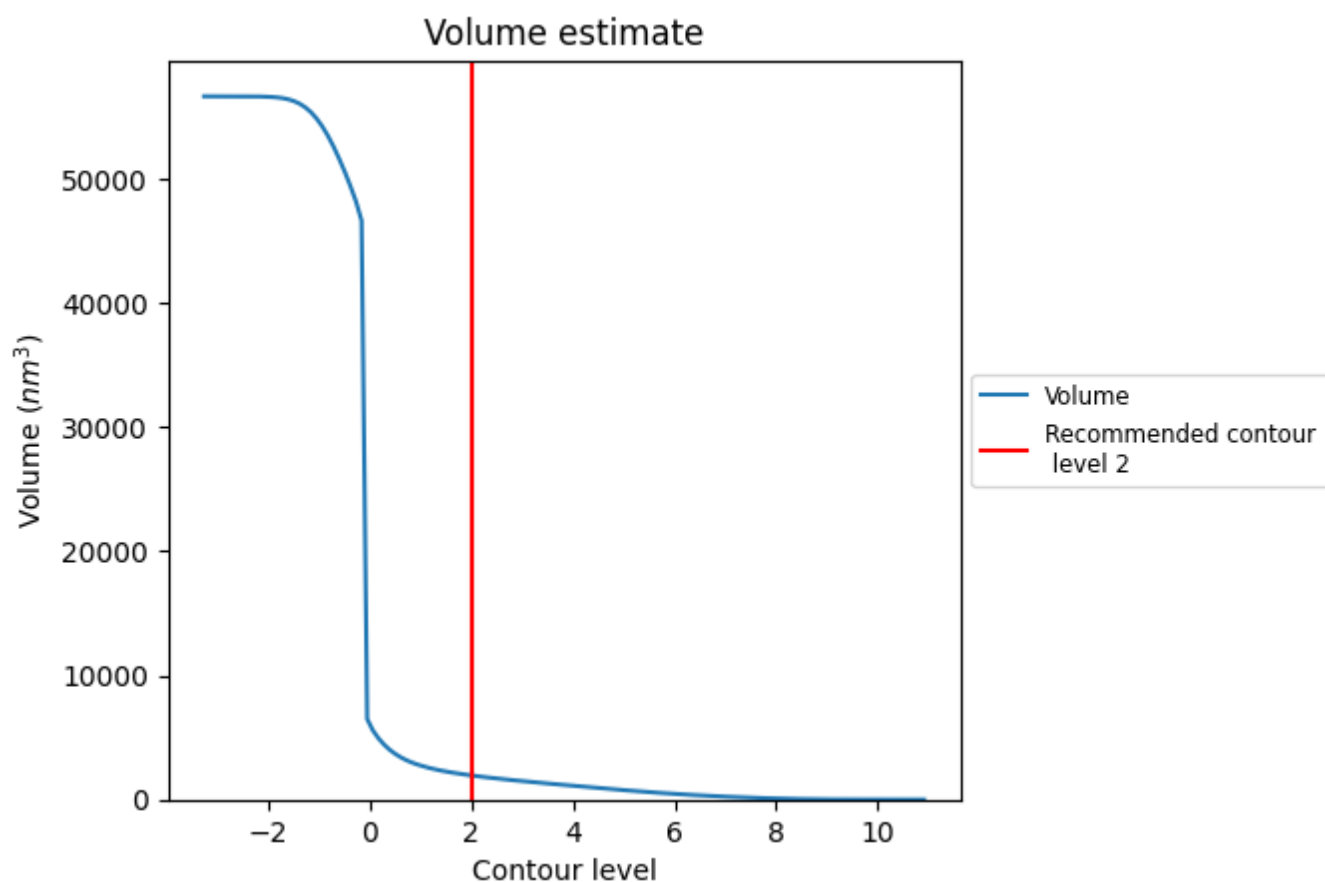
This section contains the results of statistical analysis of the map.

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.

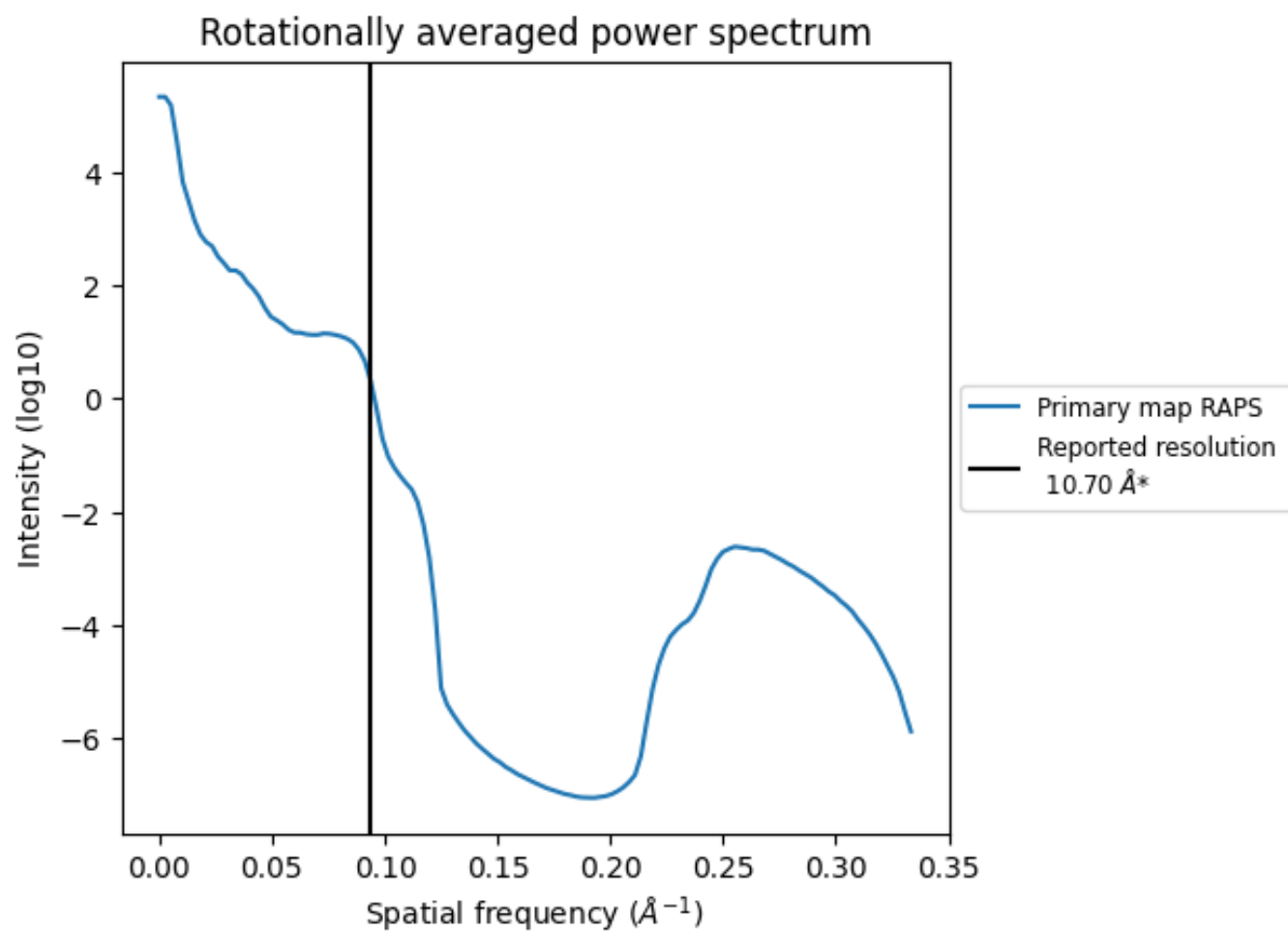
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1942 nm³; this corresponds to an approximate mass of 1754 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 0.093 Å⁻¹

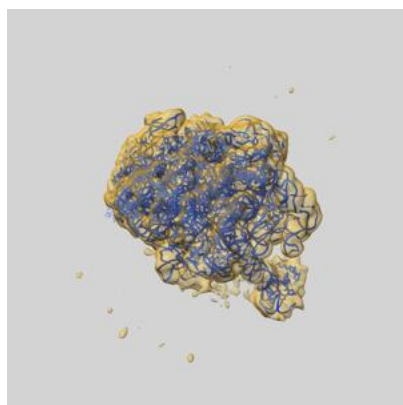
8 Fourier-Shell correlation ⓘ

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

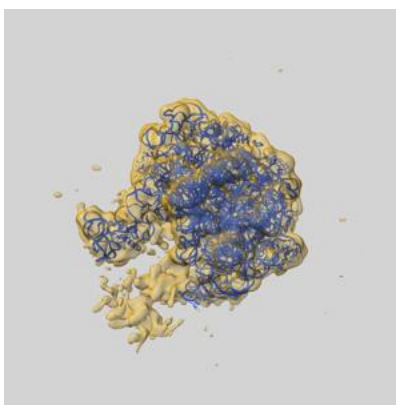
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5643 and PDB model 3J3W. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

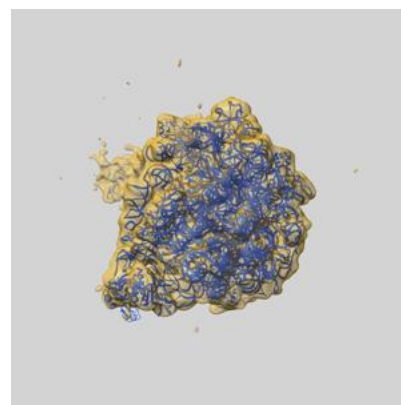
9.1 Map-model overlay [i](#)



X



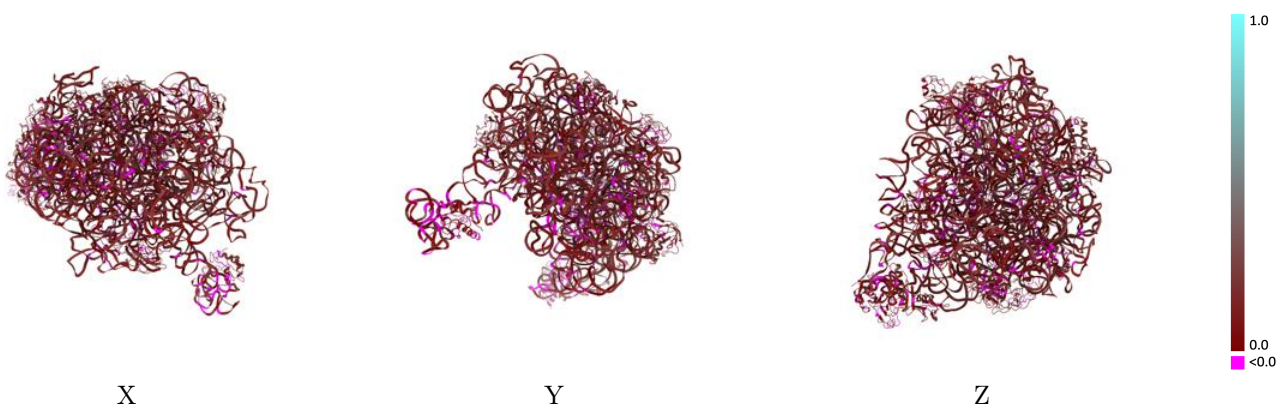
Y



Z

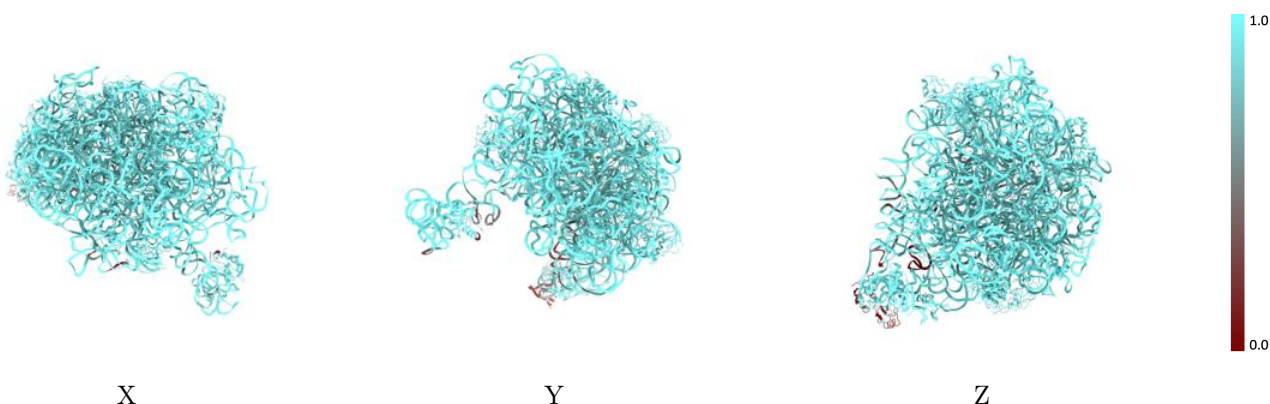
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



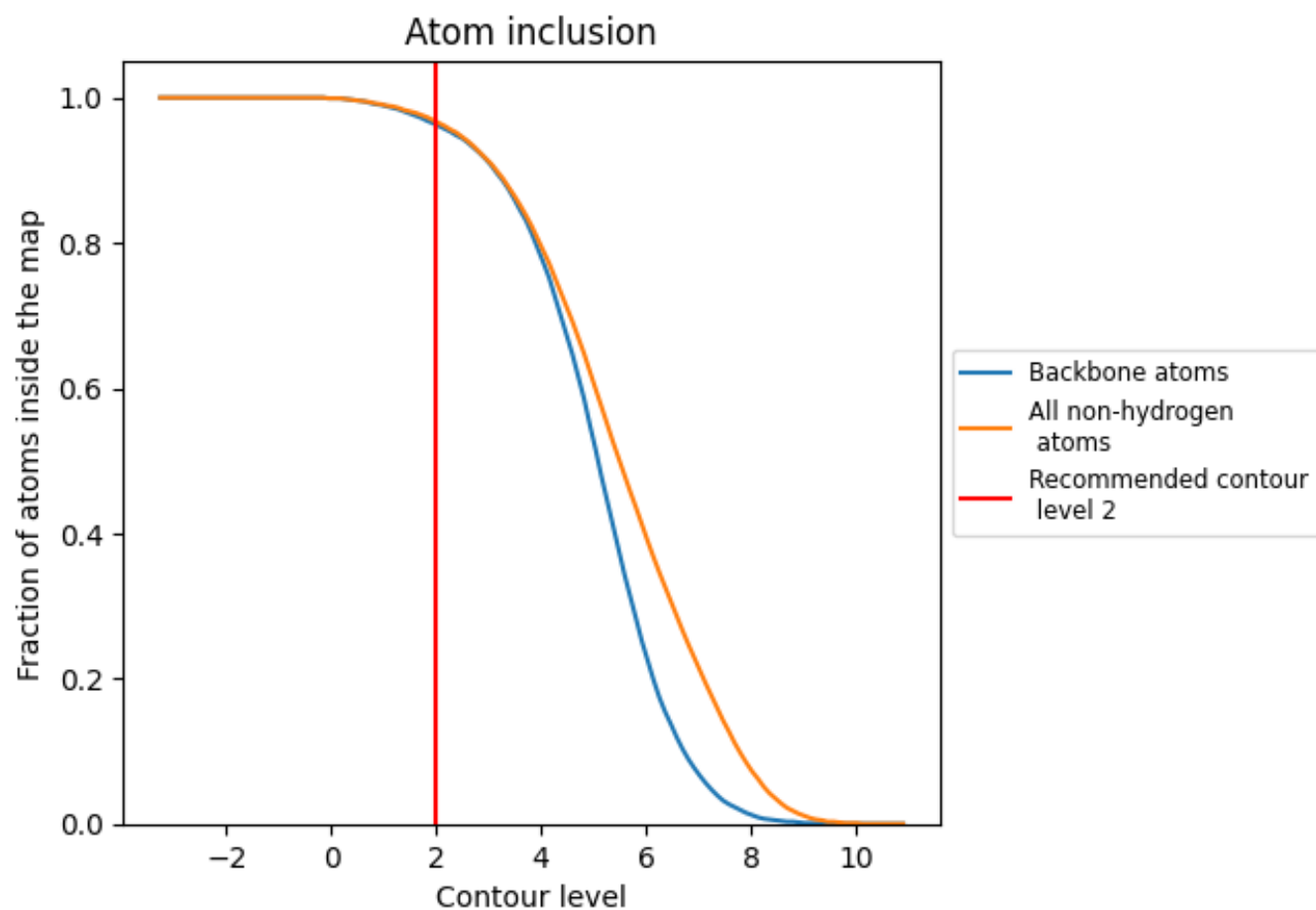
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.1190
0	 0.9950	 0.0450
2	 0.9940	 0.0670
5	 0.9410	 0.0570
6	 0.3720	 0.0390
A	 0.9730	 0.1310
C	 0.9740	 0.0650
D	 0.9890	 0.0800
E	 0.9770	 0.0850
G	 0.9850	 0.1250
J	 0.9940	 0.0970
K	 0.9960	 0.1000
L	 0.9470	 0.0560
N	 0.9940	 0.0700
P	 0.9890	 0.1030
Q	 0.9920	 0.0770
R	 0.9960	 0.0960
S	 0.9790	 0.0910
T	 0.9840	 0.0830
U	 0.9990	 0.0700
X	 0.9980	 0.1510

