wwPDB EM Validation Summary Report (i)

Oct 28, 2026 – 11:55 AM EDT

PDB ID	:	9YPN / pdb_00009ypn
EMDB ID	:	EMD-73301
Title	:	Pseudomonas aeruginosa 50S ribosome (L1 stalk in 'out' conformation and missing uL1 and tRNA)
Authors	:	Findlay, J.L.; Kanik, M.; Gauvin, C.C.; Williamson, K.S.; Franklin, M.J.; Lawrence, C.M.
Deposited on	:	2025-10-14
Resolution	:	2.25 Å(reported)
Based on initial model	:	7UNW

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 (i) 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 (1)) were used in the production of this report:

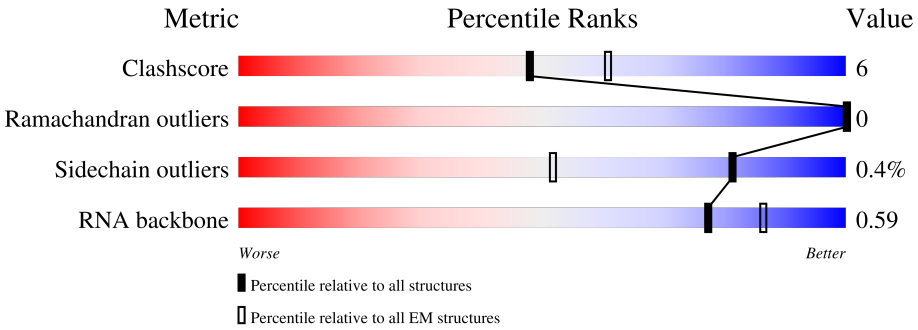
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

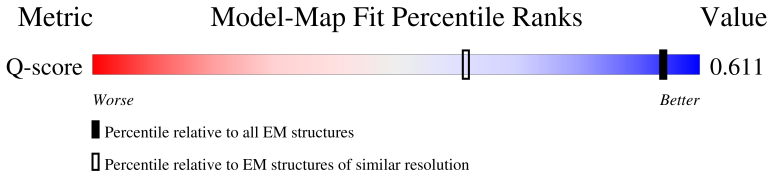
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.25 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	3458 (1.75 - 2.75)

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 <=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	2892	63% 32%
2	B	121	61% 31% 6%
3	D	273	82% 17%

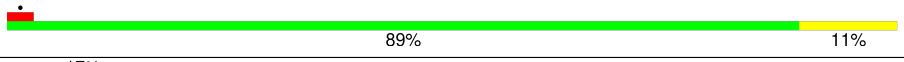
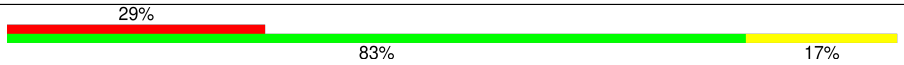
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Mol	Chain	Length	Quality of chain
4	E	211	87% 11%
5	F	200	85% 14%
6	G	179	75% 25%
7	H	177	83% 15%
8	I	148	26% 73% 5% 22%
9	L	142	88% 12%
10	M	122	86% 14%
11	N	144	88% 12%
12	O	137	74% 26%
13	P	129	80% 12% 8%
14	Q	116	87% 12%
15	R	116	6% 84% 14%
16	S	118	86% 14%
17	T	103	89% 11%
18	U	110	87% 13%
19	V	99	68% 27% 5%
20	W	104	86% 6% 9%
21	X	204	80% 13% 7%
22	Y	85	82% 8% 9%
23	Z	78	85% 14%
24	1	63	86% 11%
25	2	58	93%
26	4	60	75% 15% 10%
27	5	51	78% 22%
28	6	44	84% 16%

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Mol	Chain	Length	Quality of chain
29	7	64	
30	8	38	
31	J	166	
32	K	143	

2 Entry composition (i)

There are 35 unique types of molecules in this entry. The entry contains 95807 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	2837	60895	27173	11178	19708	2836	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	119	2535	1132	452	832	119	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	272	2072	1276	426	364	6	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	208	1564	968	298	293	5	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	200	1521	955	283	280	3	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	179	1435	914	256	260	5	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	174	Total	C	N	O	S	0	0
			1314	828	242	242	2		

- Molecule 8 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	115	Total	C	N	O	S	0	0
			858	539	152	166	1		

- Molecule 9 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 10 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	137	Total	C	N	O	S	0	0
			1085	689	211	181	4		

- Molecule 13 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	119	Total	C	N	O	S	0	0
			952	595	191	161	5		

- Molecule 14 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	115	Total 881	C 544	N 174	O 161	S 2	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	114	Total 901	C 567	N 171	O 162	S 1	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	S	117	Total 936	C 592	N 196	O 148	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	103	Total 822	C 521	N 156	O 143	S 2	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	110	Total 833	C 515	N 161	O 153	S 4	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	94	Total 739	C 472	N 134	O 132	S 1	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	W	95	Total 738	C 466	N 142	O 129	S 1	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	X	190	Total	C	N	O	S	0	0
			1445	915	262	265	3		

- Molecule 22 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Y	77	Total	C	N	O	0	0
			581	367	112	102		

- Molecule 23 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Z	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	56	Total	C	N	O	S	0	0
			440	275	86	77	2		

- Molecule 26 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	54	Total	C	N	O	S	0	0
			431	258	91	81	1		

- Molecule 27 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 28 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 29 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 30 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 31 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J	111	Total	C	N	O	S	0	0
			840	533	151	155	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K	143	Total	C	N	O	S	0	0
			1046	655	186	201	4		

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	196	Total	Mg	0
			196	196	
33	B	3	Total	Mg	0
			3	3	
33	D	1	Total	Mg	0
			1	1	
33	E	1	Total	Mg	0
			1	1	
33	4	1	Total	Mg	0
			1	1	

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
34	8	1	Total Zn 1 1	0

- Molecule 35 is water.

Mol	Chain	Residues	Atoms	AltConf
35	A	4032	Total O 4032 4032	0
35	B	76	Total O 76 76	0
35	D	89	Total O 89 89	0
35	E	78	Total O 78 78	0
35	F	47	Total O 47 47	0
35	G	12	Total O 12 12	0
35	H	3	Total O 3 3	0
35	I	1	Total O 1 1	0
35	L	34	Total O 34 34	0
35	M	18	Total O 18 18	0
35	N	64	Total O 64 64	0
35	O	37	Total O 37 37	0
35	P	36	Total O 36 36	0
35	Q	6	Total O 6 6	0
35	R	25	Total O 25 25	0
35	S	44	Total O 44 44	0
35	T	32	Total O 32 32	0
35	U	40	Total O 40 40	0
35	V	26	Total O 26 26	0

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Mol	Chain	Residues	Atoms	AltConf
35	W	11	Total O 11 11	0
35	X	22	Total O 22 22	0
35	Y	24	Total O 24 24	0
35	Z	20	Total O 20 20	0
35	1	3	Total O 3 3	0
35	2	16	Total O 16 16	0
35	4	32	Total O 32 32	0
35	5	1	Total O 1 1	0
35	6	23	Total O 23 23	0
35	7	22	Total O 22 22	0
35	8	8	Total O 8 8	0

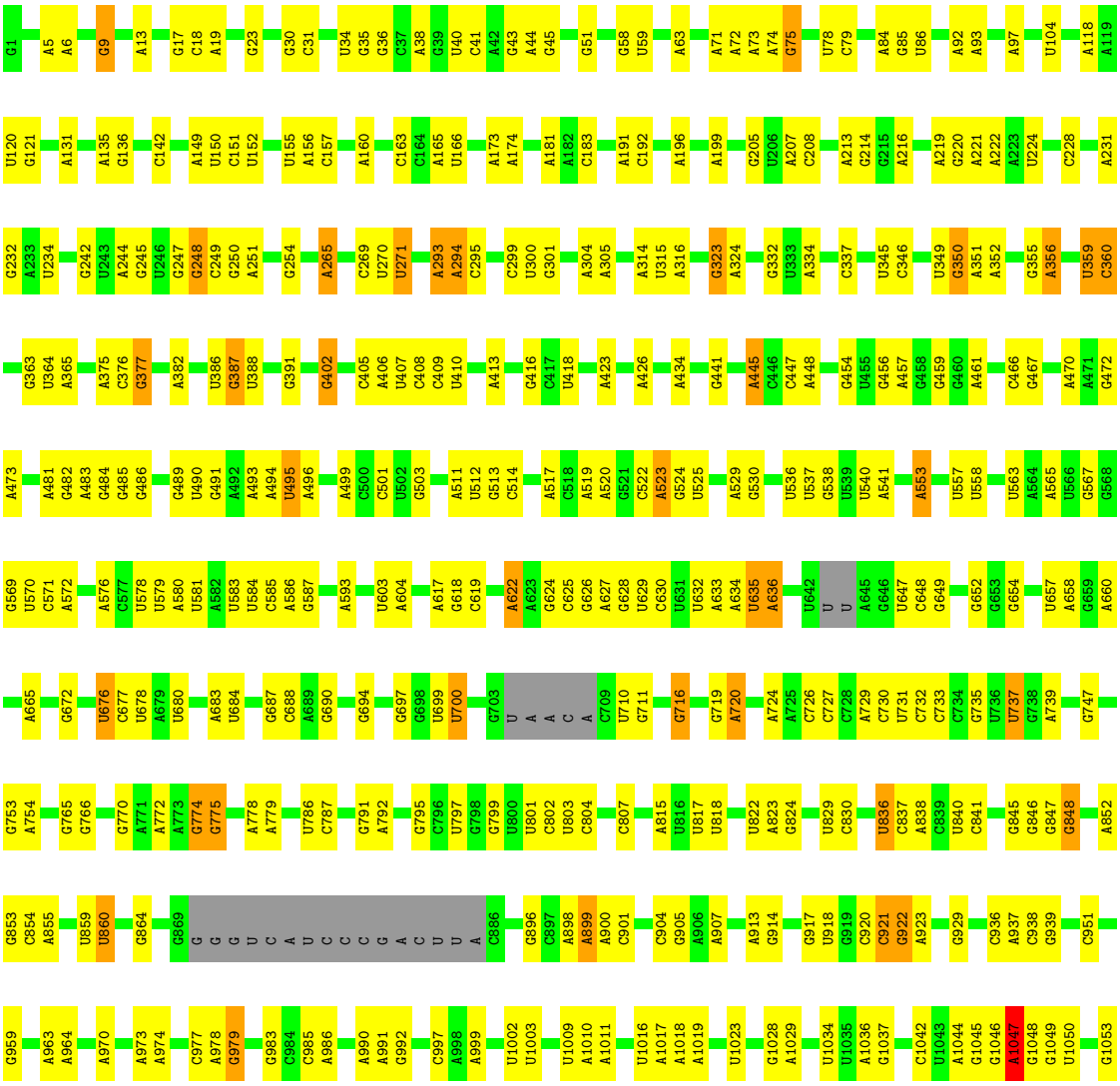
3 Residue-property plots (i)

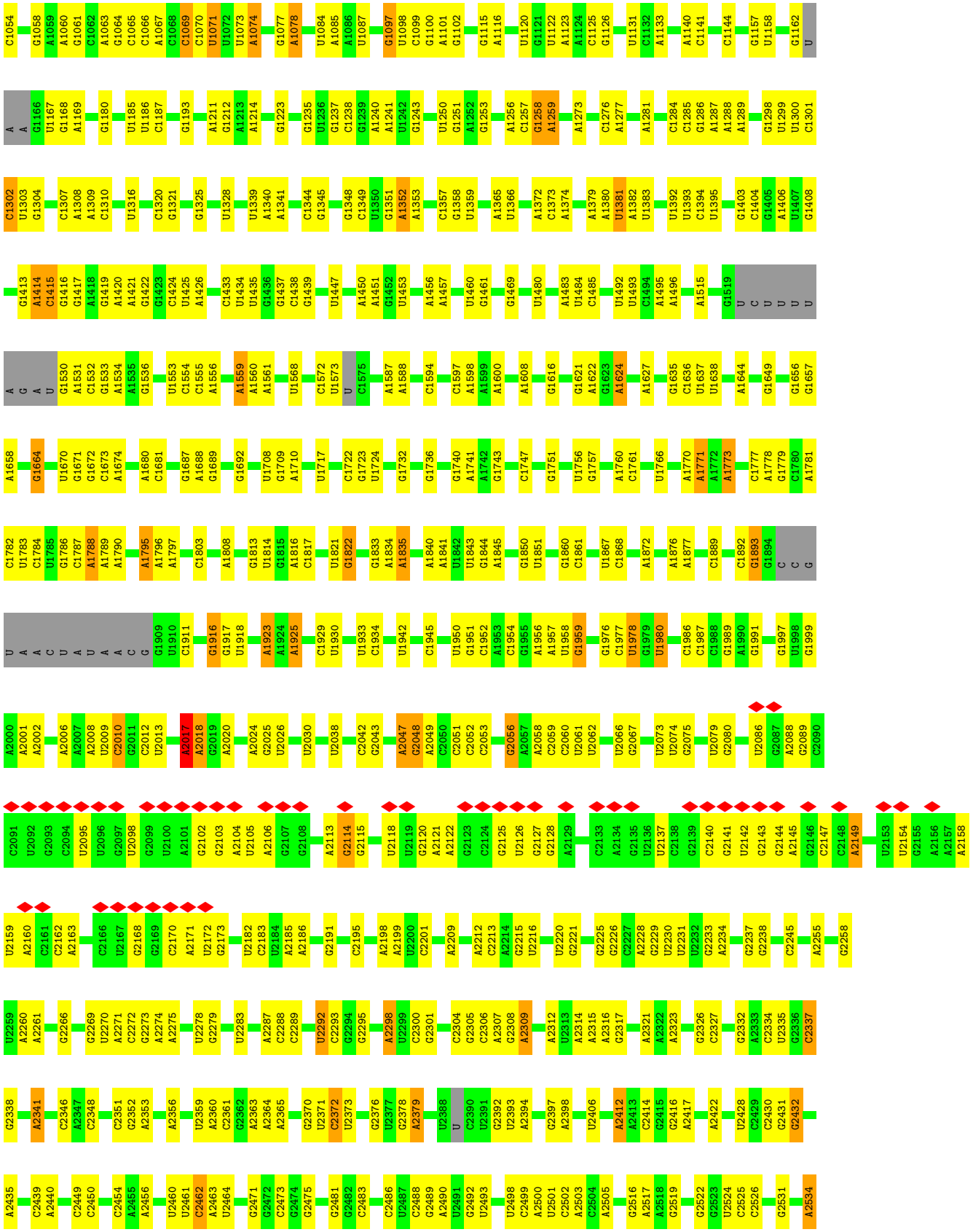
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

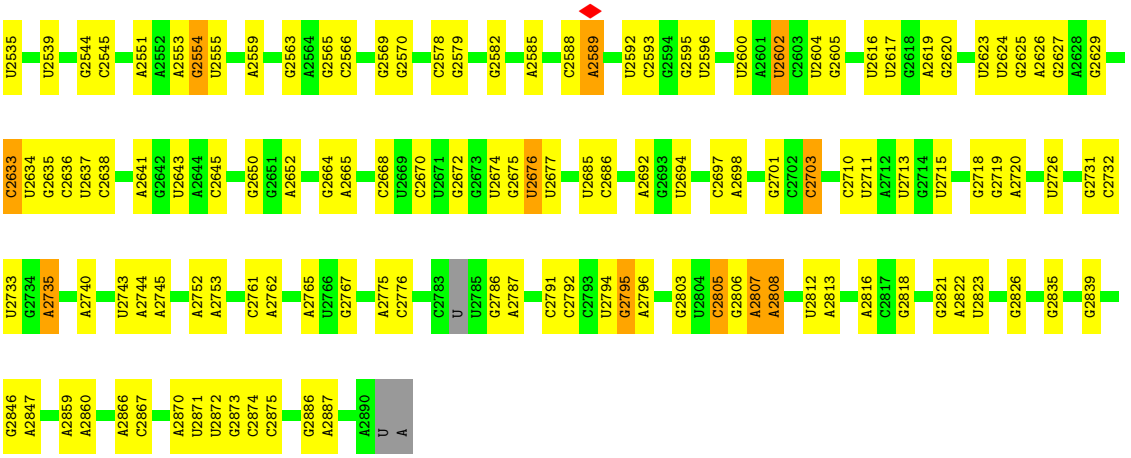
- Molecule 1: 23S rRNA

Chain A:





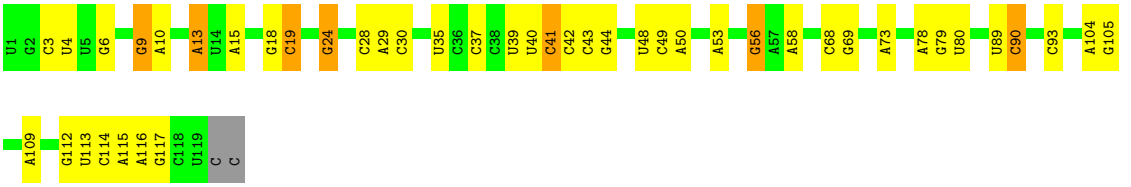




• Molecule 2: 5S rRNA

Chain B:

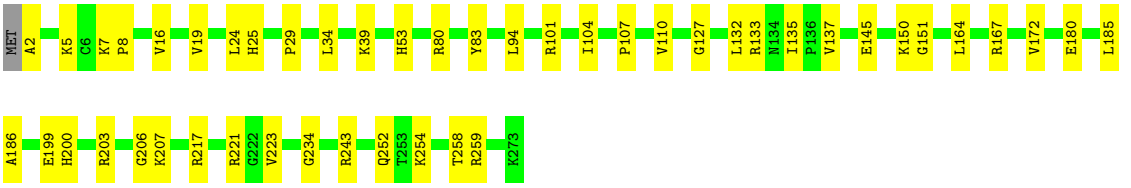




• Molecule 3: Large ribosomal subunit protein uL2

Chain D:





• Molecule 4: Large ribosomal subunit protein uL3

Chain E:





• Molecule 5: Large ribosomal subunit protein uL4

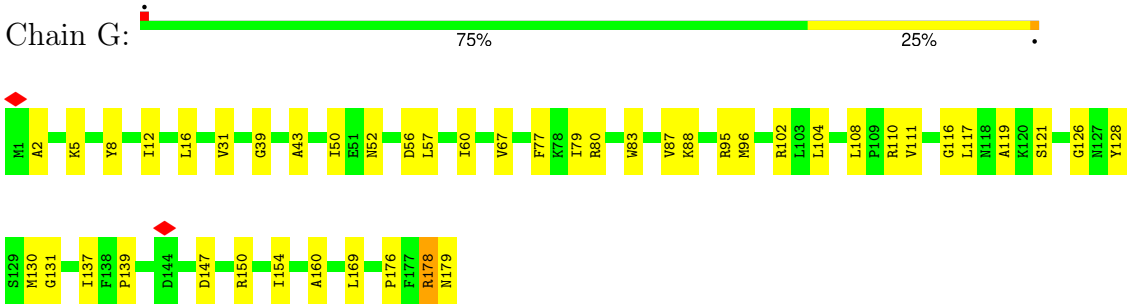
Chain F:





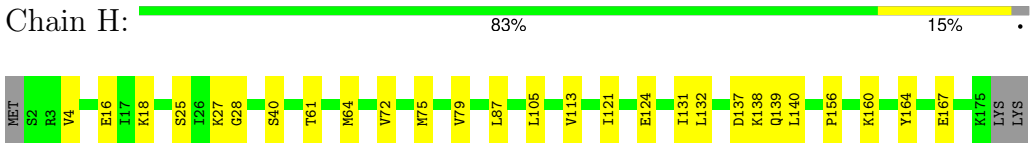
• Molecule 6: Large ribosomal subunit protein uL5

Chain G:



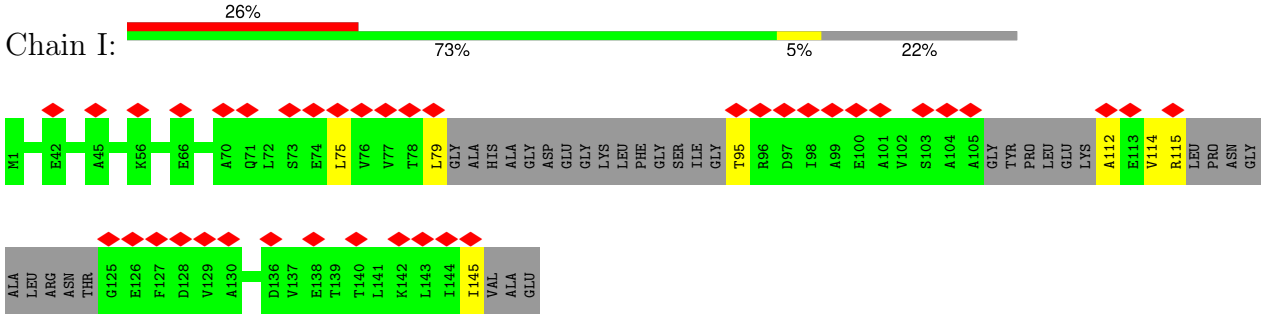
• Molecule 7: Large ribosomal subunit protein uL6

Chain H:



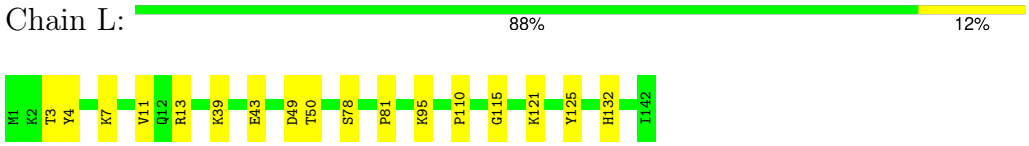
• Molecule 8: Large ribosomal subunit protein bL9

Chain I:



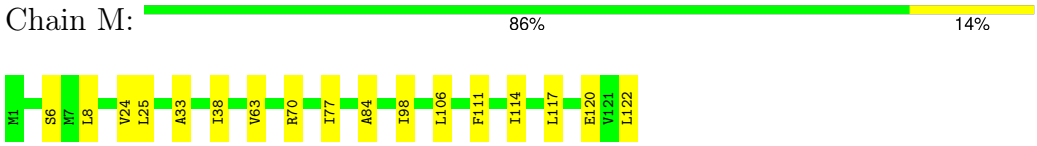
• Molecule 9: Large ribosomal subunit protein uL13

Chain L:



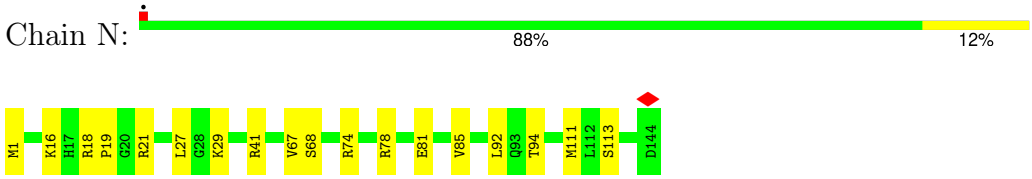
• Molecule 10: Large ribosomal subunit protein uL14

Chain M:



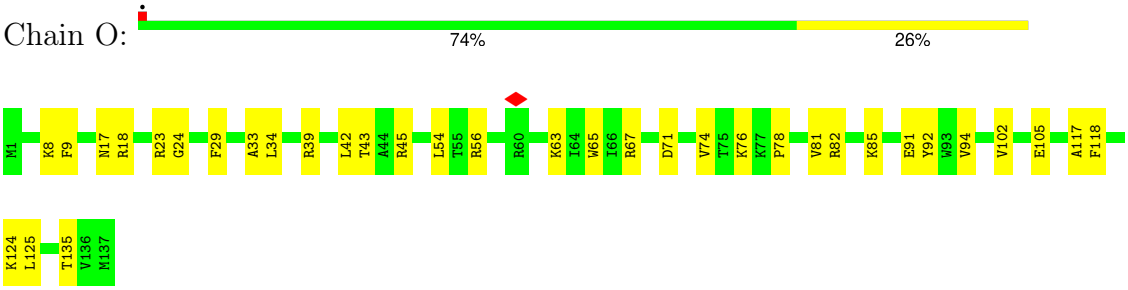
• Molecule 11: Large ribosomal subunit protein uL15

Chain N:



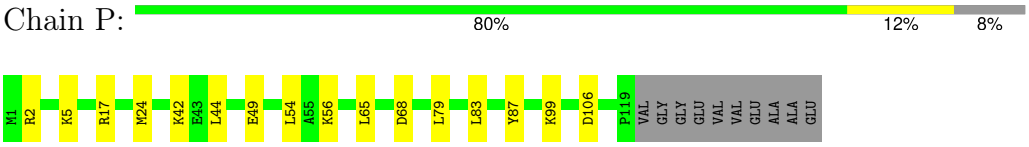
• Molecule 12: Large ribosomal subunit protein uL16

Chain O:



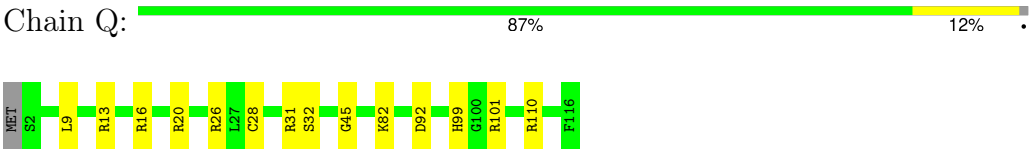
• Molecule 13: Large ribosomal subunit protein bL17

Chain P:



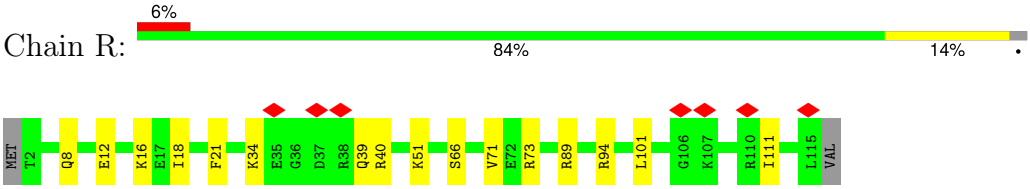
• Molecule 14: Large ribosomal subunit protein uL18

Chain Q:



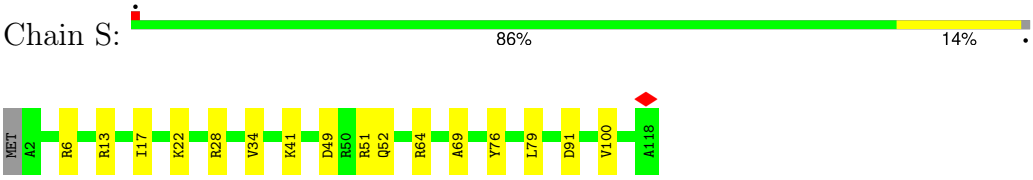
• Molecule 15: Large ribosomal subunit protein bL19

Chain R:



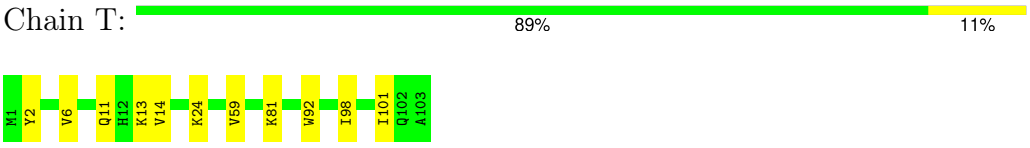
• Molecule 16: Large ribosomal subunit protein bL20

Chain S:



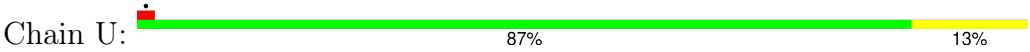
• Molecule 17: Large ribosomal subunit protein bL21

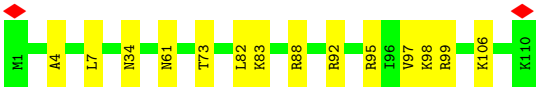
Chain T:



• Molecule 18: Large ribosomal subunit protein uL22

Chain U:

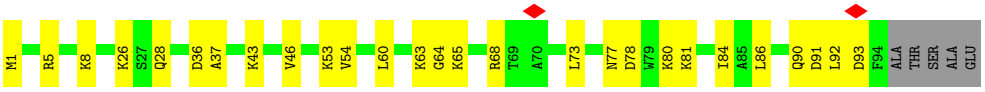




• Molecule 19: Large ribosomal subunit protein uL23

Chain V:

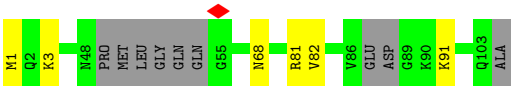




• Molecule 20: Large ribosomal subunit protein uL24

Chain W:

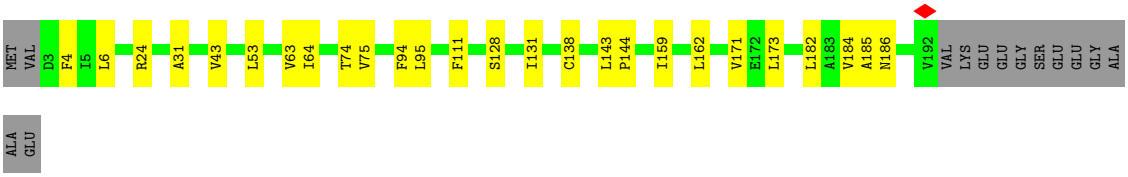




• Molecule 21: Large ribosomal subunit protein bL25

Chain X:





• Molecule 22: Large ribosomal subunit protein bL27

Chain Y:

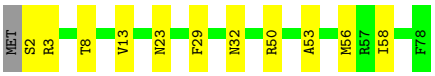




• Molecule 23: Large ribosomal subunit protein bL28

Chain Z:





• Molecule 24: Large ribosomal subunit protein uL29

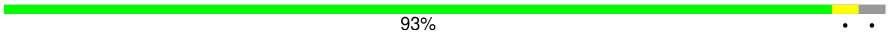
Chain 1:





• Molecule 25: Large ribosomal subunit protein uL30

Chain 2:

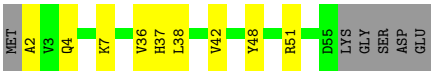




• Molecule 26: Large ribosomal subunit protein bL32

Chain 4:

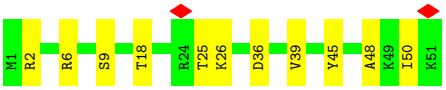




• Molecule 27: Large ribosomal subunit protein bL33

Chain 5:





• Molecule 28: Large ribosomal subunit protein bL34

Chain 6:

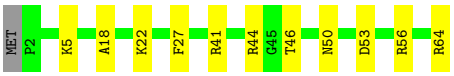




• Molecule 29: Large ribosomal subunit protein bL35

Chain 7:

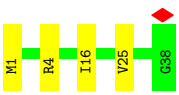




• Molecule 30: Large ribosomal subunit protein bL36A

Chain 8:

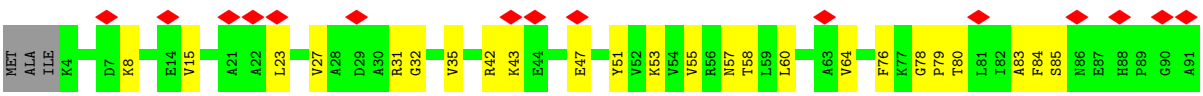


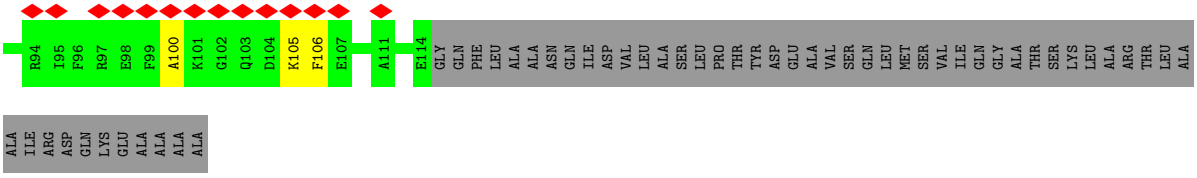


• Molecule 31: Large ribosomal subunit protein uL10

Chain J:



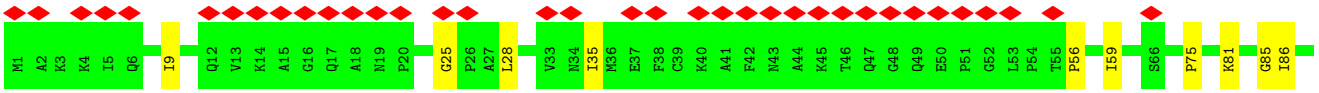


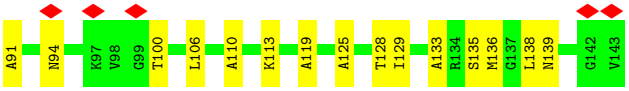


• Molecule 32: Large ribosomal subunit protein uL11

Chain K:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	642285	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	54.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	81.284	Depositor
Minimum map value	-47.287	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.038	Depositor
Recommended contour level	3	Depositor
Map size (Å)	468.408, 468.408, 468.408	wwPDB
Map dimensions	696, 696, 696	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.673, 0.673, 0.673	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 5MU, 1MG, MG, OMU, 6MZ, OMC, 5MC, OMG, 2MA, 2MG, 7MG

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	0.28	0/67882	0.74	17/105870 (0.0%)
2	B	0.31	0/2833	0.67	1/4413 (0.0%)
3	D	0.15	0/2108	0.27	0/2831
4	E	0.20	0/1587	0.34	0/2138
5	F	0.17	0/1541	0.28	0/2075
6	G	0.25	0/1456	0.37	0/1953
7	H	0.09	0/1332	0.22	0/1794
8	I	0.11	0/861	0.24	0/1159
9	L	0.24	0/1156	0.38	0/1559
10	M	0.11	0/947	0.27	0/1268
11	N	0.11	0/1078	0.28	0/1436
12	O	0.12	0/1105	0.26	0/1476
13	P	0.19	0/968	0.31	0/1294
14	Q	0.18	0/888	0.29	0/1183
15	R	0.16	0/910	0.34	0/1218
16	S	0.14	0/946	0.30	0/1257
17	T	0.09	0/835	0.23	0/1117
18	U	0.09	0/837	0.23	0/1114
19	V	0.08	0/749	0.22	0/1002
20	W	0.09	0/743	0.24	0/988
21	X	0.09	0/1468	0.21	0/1987
22	Y	0.09	0/589	0.24	0/782
23	Z	0.16	0/641	0.23	0/854
24	1	0.17	0/491	0.31	0/654
25	2	0.08	0/444	0.23	0/597
26	4	0.31	0/437	0.55	0/583
27	5	0.09	0/433	0.24	0/576
28	6	0.16	0/368	0.36	0/482
29	7	0.16	0/511	0.27	0/668
30	8	0.08	0/308	0.22	0/404
31	J	0.48	0/850	0.63	0/1142
32	K	0.33	0/1061	0.42	0/1435

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
All	All	0.26	0/98363	0.65	18/147309 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1911	C	C2-N1-C1'	-7.12	110.97	118.80
1	A	1097	G	N3-C4-N9	-6.80	121.92	126.00
1	A	9	G	O4'-C1'-N9	6.40	113.32	108.20
1	A	503	G	O4'-C1'-N9	6.11	113.09	108.20
1	A	1071	U	N3-C2-O2	-6.06	117.96	122.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	60895	0	30644	586	0
2	B	2535	0	1283	30	0
3	D	2072	0	2152	38	0
4	E	1564	0	1575	19	0
5	F	1521	0	1581	26	0
6	G	1435	0	1504	30	0
7	H	1314	0	1373	17	0
8	I	858	0	890	4	0
9	L	1130	0	1160	15	0
10	M	938	0	1012	12	0
11	N	1066	0	1112	14	0
12	O	1085	0	1157	25	0
13	P	952	0	996	12	0
14	Q	881	0	920	15	0
15	R	901	0	958	10	0
16	S	936	0	1025	16	0
17	T	822	0	858	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	U	833	0	897	10	0
19	V	739	0	788	18	0
20	W	738	0	806	5	0
21	X	1445	0	1486	18	0
22	Y	581	0	603	6	0
23	Z	630	0	653	8	0
24	1	490	0	520	5	0
25	2	440	0	469	2	0
26	4	431	0	424	7	0
27	5	426	0	457	8	0
28	6	365	0	409	6	0
29	7	506	0	569	10	0
30	8	307	0	342	3	0
31	J	840	0	867	21	0
32	K	1046	0	1089	23	0
33	4	1	0	0	0	0
33	A	196	0	0	0	0
33	B	3	0	0	0	0
33	D	1	0	0	0	0
33	E	1	0	0	0	0
34	8	1	0	0	0	0
35	1	3	0	0	0	0
35	2	16	0	0	0	0
35	4	32	0	0	1	0
35	5	1	0	0	0	0
35	6	23	0	0	1	0
35	7	22	0	0	0	0
35	8	8	0	0	0	0
35	A	4032	0	0	29	0
35	B	76	0	0	2	0
35	D	89	0	0	1	0
35	E	78	0	0	0	0
35	F	47	0	0	3	0
35	G	12	0	0	0	0
35	H	3	0	0	0	0
35	I	1	0	0	0	0
35	L	34	0	0	0	0
35	M	18	0	0	0	0
35	N	64	0	0	0	0
35	O	37	0	0	2	0
35	P	36	0	0	0	0
35	Q	6	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	R	25	0	0	0	0
35	S	44	0	0	1	0
35	T	32	0	0	0	0
35	U	40	0	0	1	0
35	V	26	0	0	0	0
35	W	11	0	0	0	0
35	X	22	0	0	2	0
35	Y	24	0	0	0	0
35	Z	20	0	0	0	0
All	All	95807	0	60579	864	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 6.

The worst 5 of 864 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)
31:J:43:LYS:HG2	31:J:47:GLU:OE1	1.80	0.82
6:G:119:ALA:HB3	6:G:179:ASN:HB2	1.64	0.80
1:A:558:U:H1'	1:A:2017:6MZ:H9C1	1.68	0.76
1:A:1045:G:H5'	31:J:32:GLY:HA2	1.70	0.73
1:A:1097:G:O2'	31:J:78:GLY:HA2	1.89	0.73

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	
3	D	270/273 (99%)	266 (98%)	4 (2%)	0	100	100
4	E	206/211 (98%)	201 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F	198/200 (99%)	198 (100%)	0	0	100	100
6	G	177/179 (99%)	174 (98%)	3 (2%)	0	100	100
7	H	172/177 (97%)	172 (100%)	0	0	100	100
8	I	107/148 (72%)	103 (96%)	4 (4%)	0	100	100
9	L	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
10	M	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
11	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
12	O	135/137 (98%)	134 (99%)	1 (1%)	0	100	100
13	P	117/129 (91%)	115 (98%)	2 (2%)	0	100	100
14	Q	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
15	R	112/116 (97%)	108 (96%)	4 (4%)	0	100	100
16	S	115/118 (98%)	115 (100%)	0	0	100	100
17	T	101/103 (98%)	101 (100%)	0	0	100	100
18	U	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
19	V	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
20	W	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
21	X	188/204 (92%)	185 (98%)	3 (2%)	0	100	100
22	Y	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
23	Z	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
24	1	59/63 (94%)	59 (100%)	0	0	100	100
25	2	54/58 (93%)	53 (98%)	1 (2%)	0	100	100
26	4	52/60 (87%)	51 (98%)	1 (2%)	0	100	100
27	5	49/51 (96%)	49 (100%)	0	0	100	100
28	6	42/44 (96%)	42 (100%)	0	0	100	100
29	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
30	8	36/38 (95%)	36 (100%)	0	0	100	100
31	J	109/166 (66%)	105 (96%)	4 (4%)	0	100	100
32	K	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
All	All	3455/3682 (94%)	3400 (98%)	55 (2%)	0	100	100

There are no Ramachandran outliers to report.

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
3	D	212/213 (100%)	212 (100%)	0	100 100
4	E	160/162 (99%)	160 (100%)	0	100 100
5	F	157/158 (99%)	156 (99%)	1 (1%)	78 84
6	G	153/153 (100%)	151 (99%)	2 (1%)	61 72
7	H	137/141 (97%)	137 (100%)	0	100 100
8	I	85/107 (79%)	84 (99%)	1 (1%)	63 74
9	L	119/119 (100%)	119 (100%)	0	100 100
10	M	102/102 (100%)	102 (100%)	0	100 100
11	N	106/106 (100%)	105 (99%)	1 (1%)	70 79
12	O	110/110 (100%)	110 (100%)	0	100 100
13	P	98/104 (94%)	98 (100%)	0	100 100
14	Q	86/87 (99%)	86 (100%)	0	100 100
15	R	96/98 (98%)	95 (99%)	1 (1%)	68 77
16	S	87/88 (99%)	86 (99%)	1 (1%)	65 75
17	T	86/86 (100%)	86 (100%)	0	100 100
18	U	87/87 (100%)	87 (100%)	0	100 100
19	V	79/82 (96%)	79 (100%)	0	100 100
20	W	81/88 (92%)	81 (100%)	0	100 100
21	X	154/164 (94%)	154 (100%)	0	100 100
22	Y	57/61 (93%)	57 (100%)	0	100 100
23	Z	66/67 (98%)	66 (100%)	0	100 100
24	1	54/55 (98%)	53 (98%)	1 (2%)	50 61
25	2	48/49 (98%)	48 (100%)	0	100 100
26	4	47/52 (90%)	46 (98%)	1 (2%)	47 58
27	5	47/47 (100%)	47 (100%)	0	100 100
28	6	37/37 (100%)	37 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
29	7	54/55 (98%)	54 (100%)	0	100 100
30	8	34/34 (100%)	34 (100%)	0	100 100
31	J	82/122 (67%)	81 (99%)	1 (1%)	63 74
32	K	110/110 (100%)	110 (100%)	0	100 100
All	All	2831/2944 (96%)	2821 (100%)	10 (0%)	81 89

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	1	7	ARG
26	4	51	ARG
31	J	60	LEU
8	I	75	LEU
11	N	92	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
19	V	61	ASN
23	Z	34	GLN
19	V	87	GLN
21	X	175	GLN
28	6	26	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2827/2892 (97%)	311 (11%)	6 (0%)
2	B	118/121 (97%)	17 (14%)	0
All	All	2945/3013 (97%)	328 (11%)	6 (0%)

5 of 328 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	34	U
1	A	45	G
1	A	51	G
1	A	63	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1046	G
1	A	1307	C
1	A	2743	U
1	A	635	U
1	A	221	A

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

12 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	$\#\|Z\| > 2$
1	2MA	A	2490	1,33	22,25,26	1.70	5 (22%)	32,37,40	3.65	12 (37%)
1	5MU	A	1926	1	19,22,23	0.42	0	27,32,35	0.58	0
1	6MZ	A	1608	1	22,25,26	2.39	4 (18%)	29,36,39	2.33	9 (31%)
1	6MZ	A	2017	1	22,25,26	2.34	5 (22%)	29,36,39	2.50	11 (37%)
1	5MC	A	1949	1	19,22,23	0.54	0	26,32,35	0.63	0
1	2MG	A	1822	1	23,26,27	0.43	0	33,38,41	0.47	0
1	2MG	A	2432	1	23,26,27	0.49	0	33,38,41	0.49	0
1	OMU	A	2539	1	19,22,23	3.10	8 (42%)	25,31,34	1.82	4 (16%)
1	7MG	A	2056	1	23,26,27	1.13	1 (4%)	27,39,42	0.86	1 (3%)
1	OMG	A	2238	1	23,26,27	0.44	0	32,38,41	0.45	0
1	OMC	A	2485	1,33	19,22,23	0.48	0	25,31,34	0.64	0
1	1MG	A	735	1	23,26,27	3.16	8 (34%)	33,39,42	1.84	9 (27%)

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
1	2MA	A	2490	1,33	-	1/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	A	1926	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	1608	1	-	0/9/27/28	0/3/3/3
1	6MZ	A	2017	1	-	2/9/27/28	0/3/3/3
1	5MC	A	1949	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1822	1	-	2/9/27/28	0/3/3/3
1	2MG	A	2432	1	-	2/9/27/28	0/3/3/3
1	OMU	A	2539	1	-	0/9/27/28	0/2/2/2
1	7MG	A	2056	1	-	1/7/37/38	0/3/3/3
1	OMG	A	2238	1	-	1/9/27/28	0/3/3/3
1	OMC	A	2485	1,33	-	0/9/27/28	0/2/2/2
1	1MG	A	735	1	-	0/7/25/26	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1608	6MZ	C6-N6	9.73	1.45	1.34
1	A	735	1MG	C2-N3	9.65	1.48	1.33
1	A	2017	6MZ	C6-N6	9.35	1.44	1.34
1	A	2539	OMU	C2-N1	8.09	1.51	1.38
1	A	735	1MG	C4-N3	6.95	1.50	1.34

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	2490	2MA	N6-C6-N1	-9.23	104.58	117.03
1	A	2490	2MA	CM2-C2-N3	9.13	130.79	117.13
1	A	2490	2MA	C5-C4-N3	-8.59	118.13	127.18
1	A	2017	6MZ	C9-N6-C6	-6.95	116.40	122.85
1	A	2490	2MA	N3-C4-N9	6.36	135.06	126.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2238	OMG	C1'-C2'-O2'-CM2
1	A	1822	2MG	C3'-C4'-C5'-O5'
1	A	2432	2MG	C3'-C4'-C5'-O5'
1	A	1822	2MG	O4'-C4'-C5'-O5'
1	A	2017	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	2017	6MZ	2	0
1	A	1822	2MG	1	0
1	A	2432	2MG	1	0
1	A	2238	OMG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 203 ligands modelled in this entry, 203 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

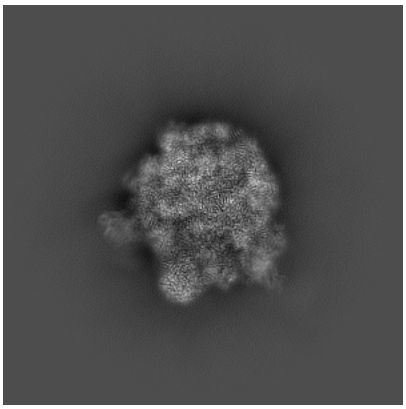
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73301. These allow visual inspection of the internal detail of the map and identification of artifacts.

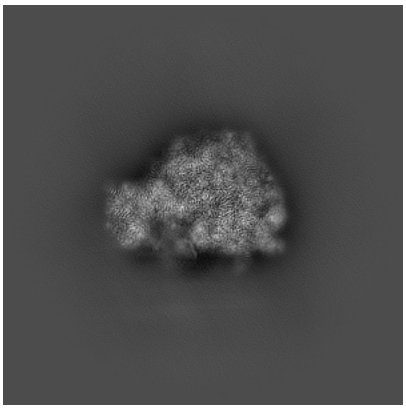
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

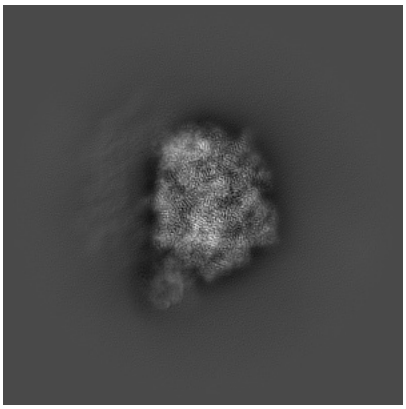
6.1.1 Primary map



X

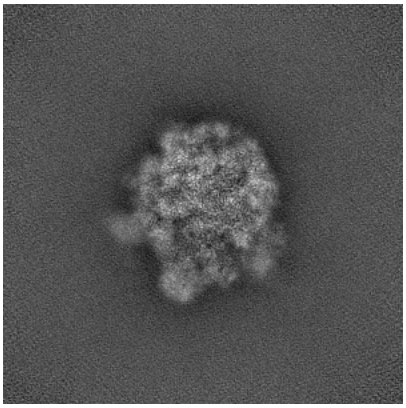


Y

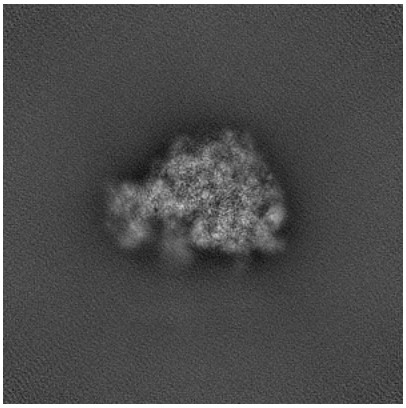


Z

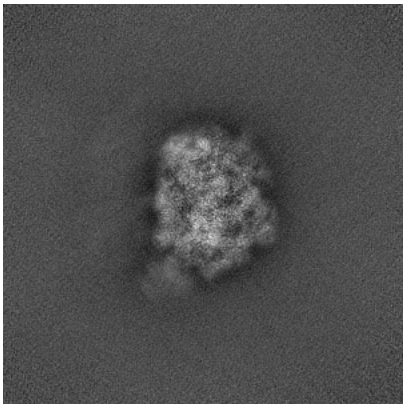
6.1.2 Raw map



X



Y

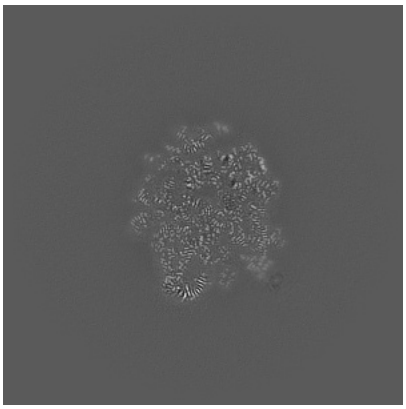


Z

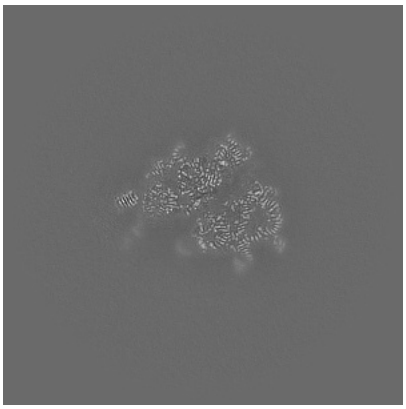
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

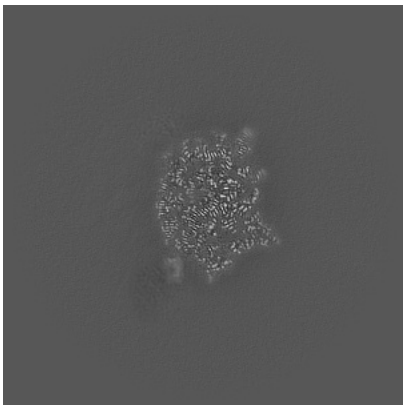
6.2.1 Primary map



X Index: 348

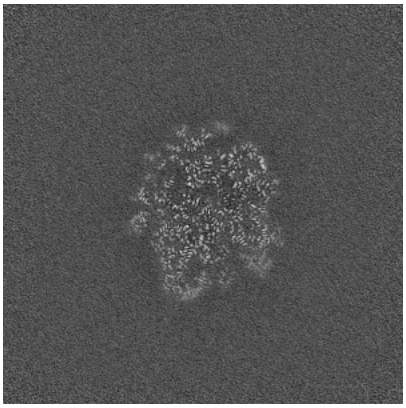


Y Index: 348

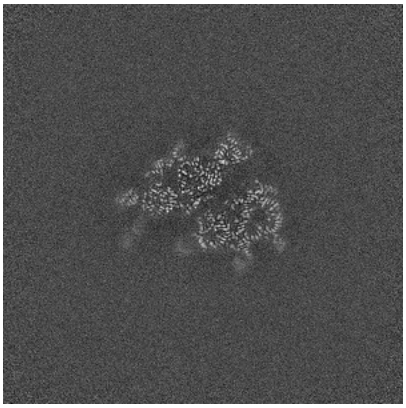


Z Index: 348

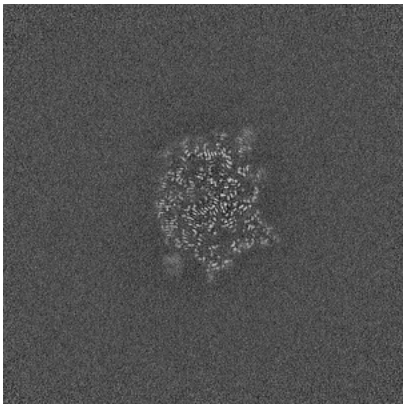
6.2.2 Raw map



X Index: 348



Y Index: 348

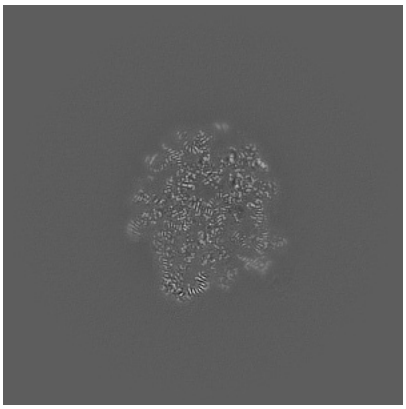


Z Index: 348

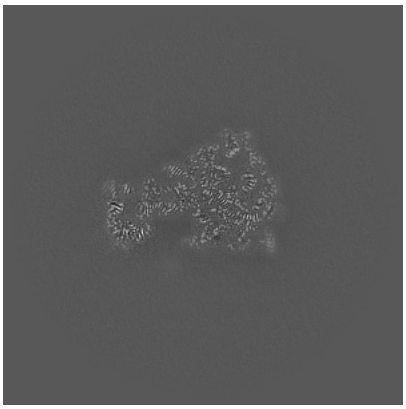
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

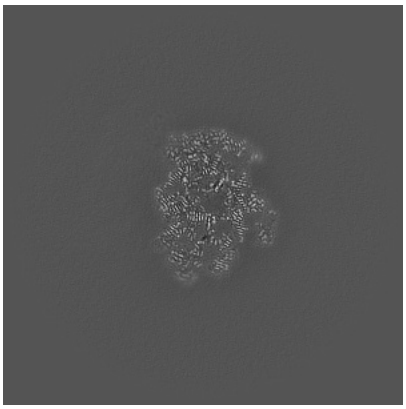
6.3.1 Primary map



X Index: 353

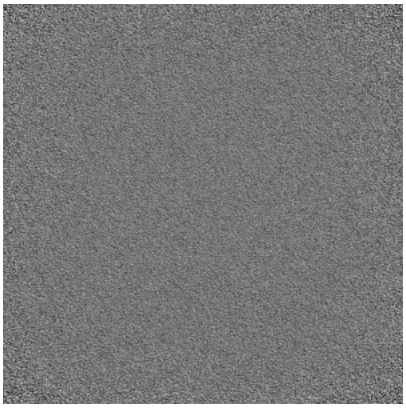


Y Index: 319

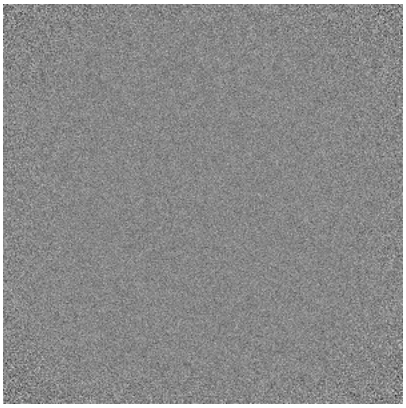


Z Index: 380

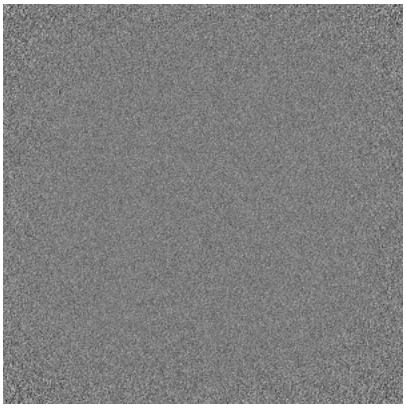
6.3.2 Raw map



X Index: 0



Y Index: 0

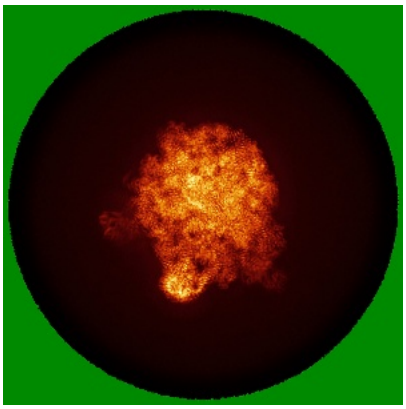


Z Index: 0

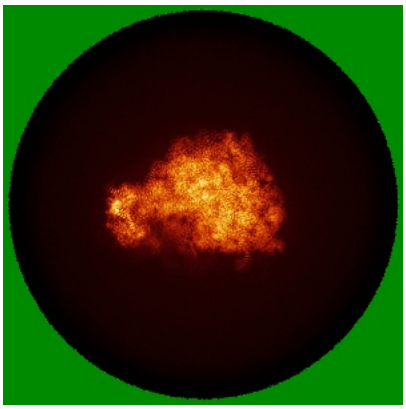
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

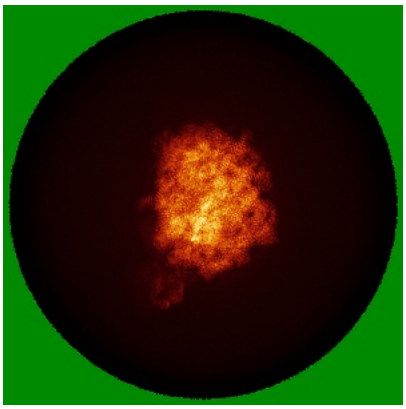
6.4.1 Primary map



X

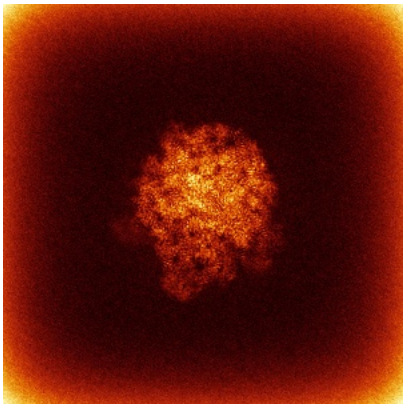


Y

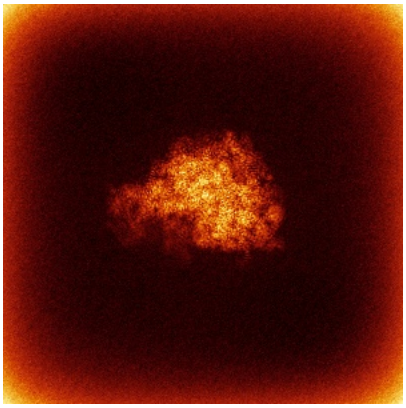


Z

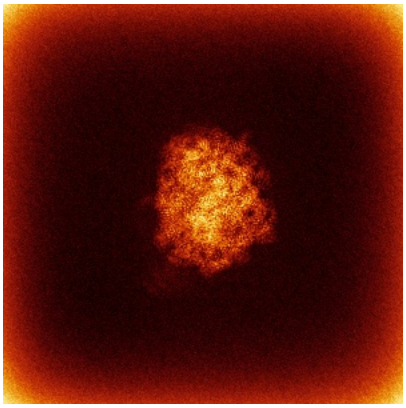
6.4.2 Raw map



X



Y

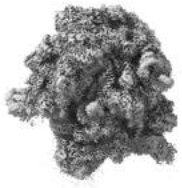


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X



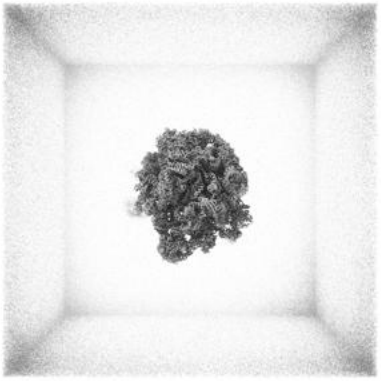
Y



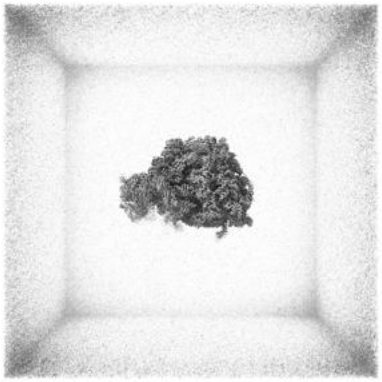
Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

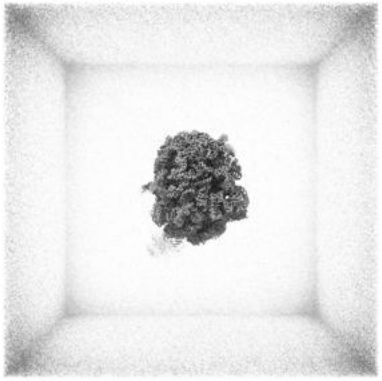
6.5.2 Raw map



X



Y



Z

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

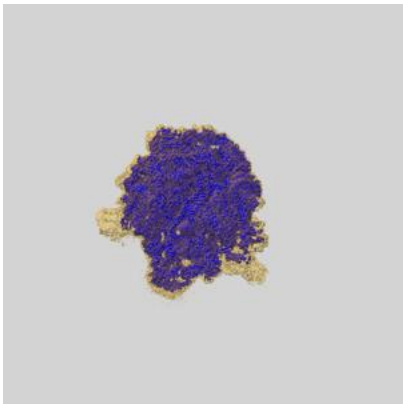
6.6 Mask visualisation (i)

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

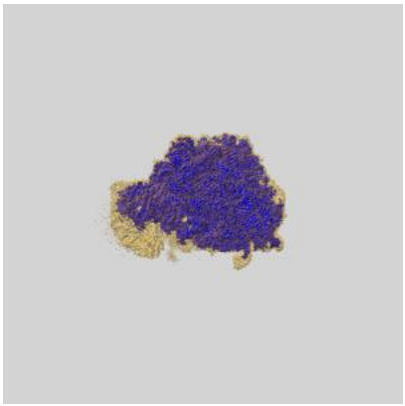
A mask typically either:

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

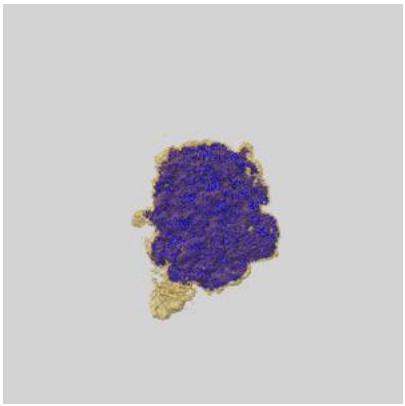
6.6.1 emd_73301_msk_1.map (i)



X



Y

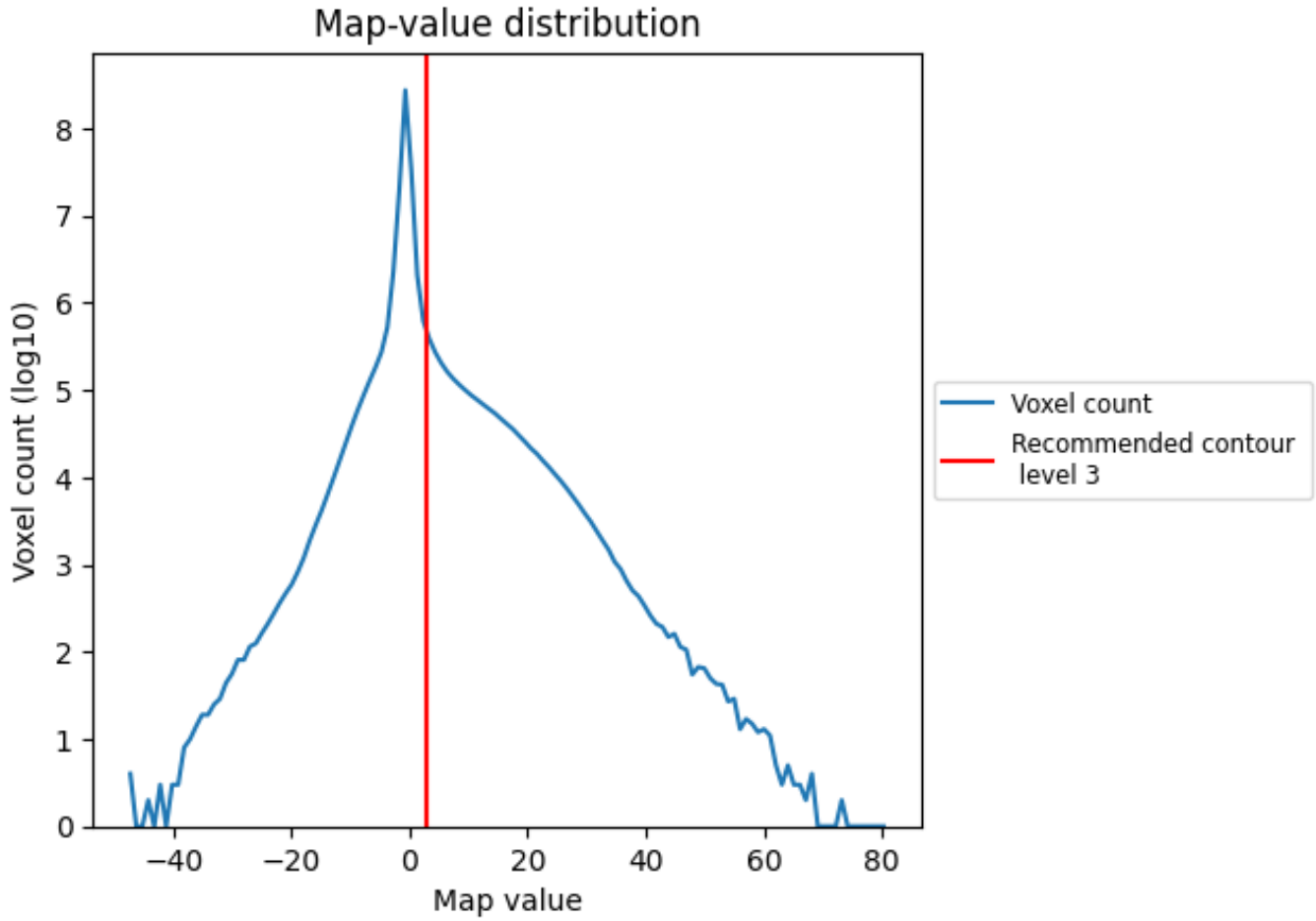


Z

7 Map analysis

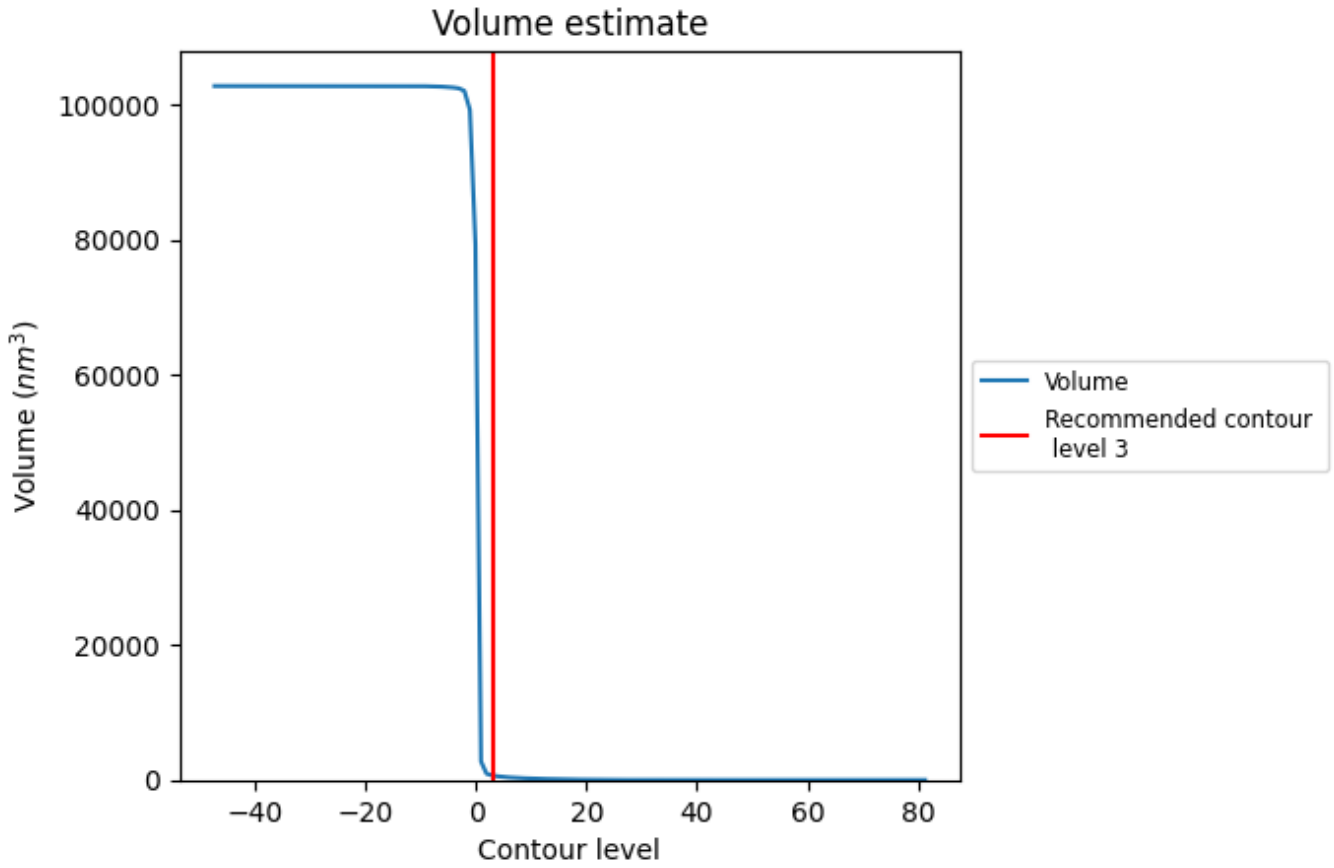
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

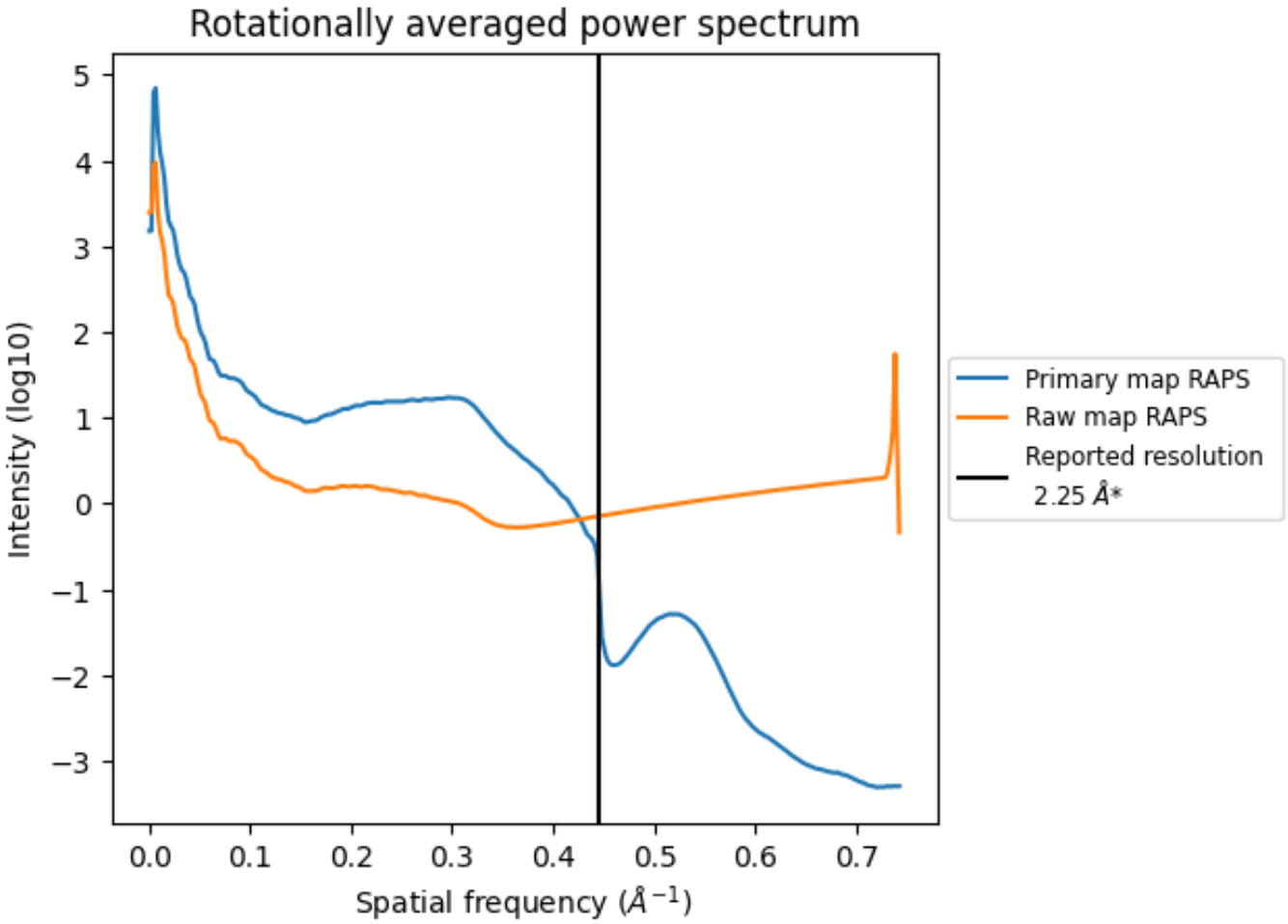
7.2 Volume estimate (i)



The volume at the recommended contour level is 675 nm^3; this corresponds to an approximate mass of 610 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)

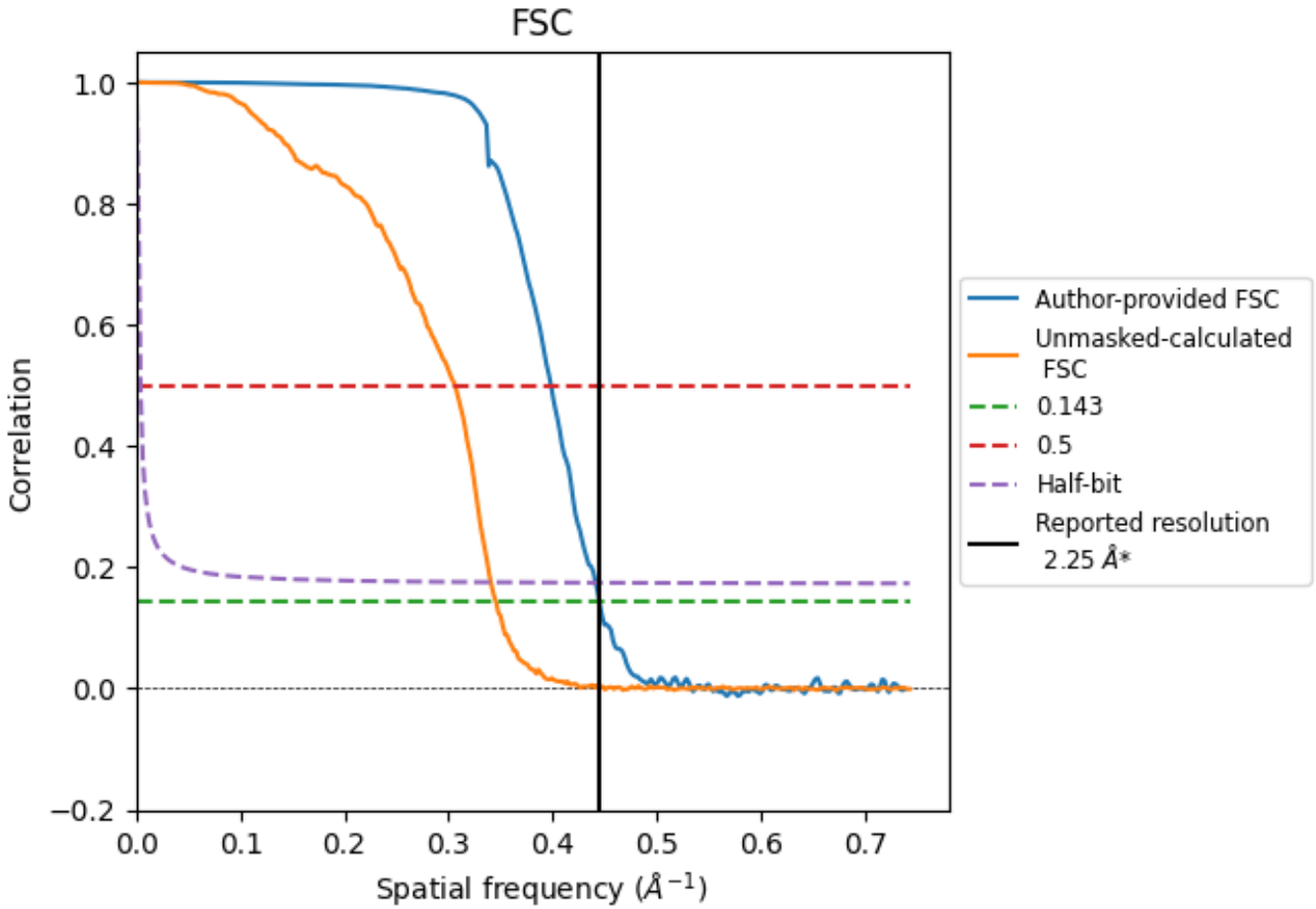


*Reported resolution corresponds to spatial frequency of 0.444 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.444 Å^{-1}

8.2 Resolution estimates (i)

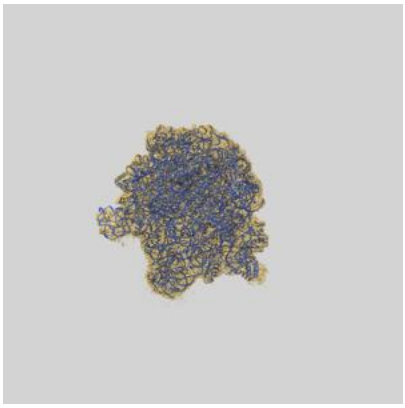
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.25	-	-
Author-provided FSC curve	2.25	2.51	2.27
Unmasked-calculated*	2.89	3.27	2.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.89 differs from the reported value 2.25 by more than 10 %

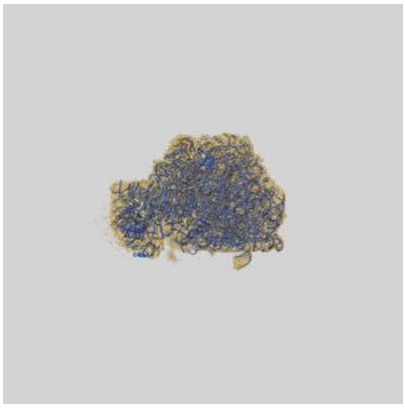
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73301 and PDB model 9YPN. Per-residue inclusion information can be found in section 3 on page 12.

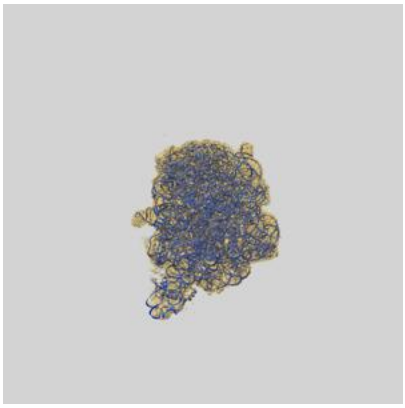
9.1 Map-model overlay



X



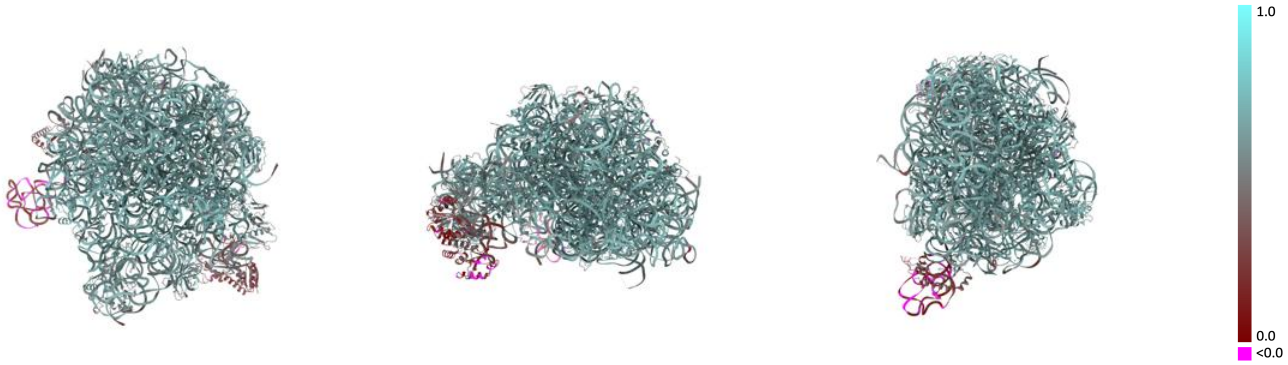
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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.

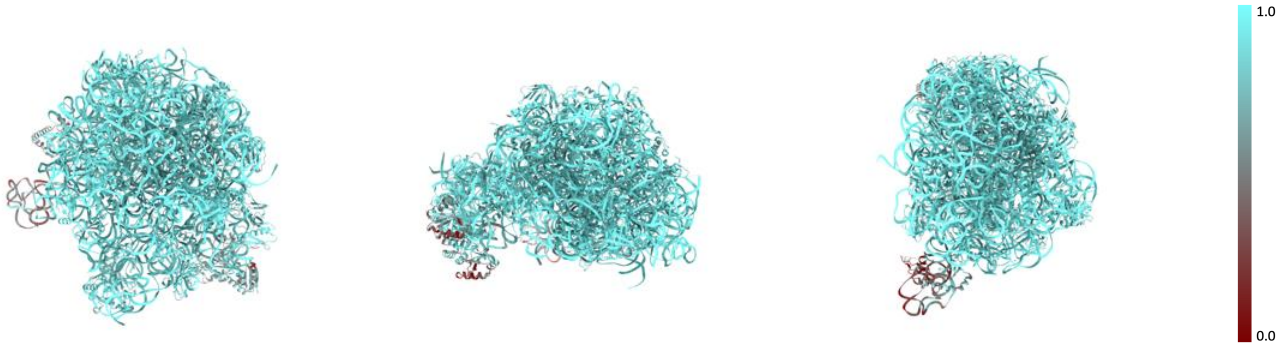
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

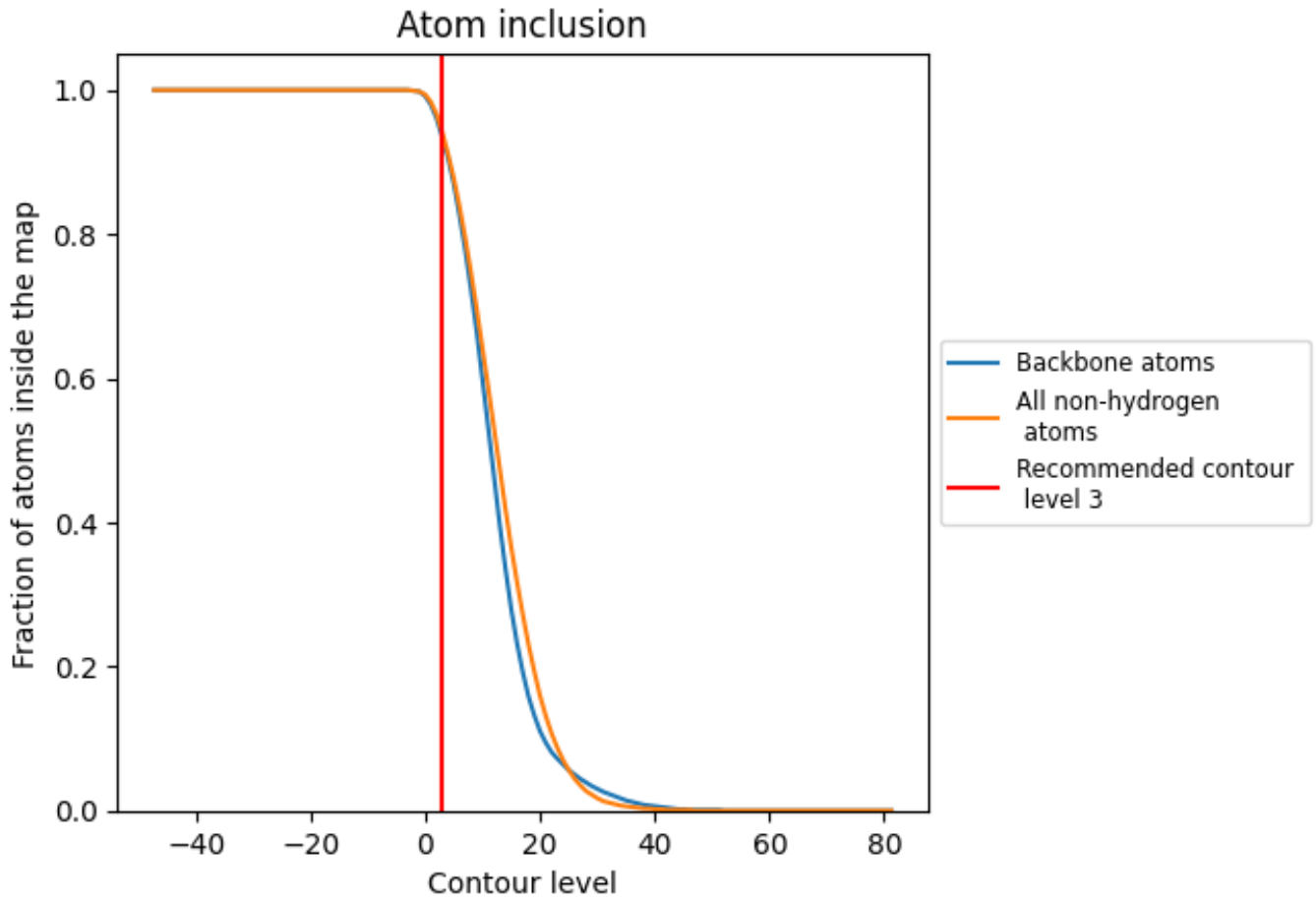
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (3).

9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9400	0.6110
1	0.9170	0.6020
2	0.9530	0.6460
4	0.9330	0.6200
5	0.8460	0.5770
6	0.9450	0.6690
7	0.9610	0.6660
8	0.9490	0.6450
A	0.9610	0.6230
B	0.9780	0.6050
D	0.9570	0.6600
E	0.9500	0.6510
F	0.9480	0.6400
G	0.8930	0.5280
H	0.8940	0.5500
I	0.5420	0.3930
J	0.5490	0.2230
K	0.5550	0.1940
L	0.9450	0.6470
M	0.9080	0.6150
N	0.9470	0.6500
O	0.9250	0.6430
P	0.9670	0.6580
Q	0.9400	0.6040
R	0.8900	0.6030
S	0.9660	0.6630
T	0.9320	0.6240
U	0.9150	0.6390
V	0.9090	0.6040
W	0.9090	0.5780
X	0.8860	0.5720
Y	0.9290	0.6490
Z	0.9350	0.6430

