



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 01:11 AM EDT

PDB ID : 9AXU
EMDB ID : EMD-43973
Title : Non-translating *S. pombe* ribosome large subunit
Authors : Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.
Deposited on : 2024-03-06
Resolution : 1.94 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:

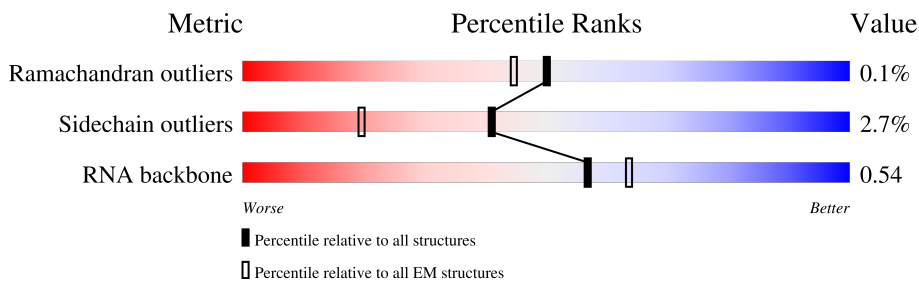
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 1.94 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	0	106	
2	1	94	
3	2	3498	
4	3	246	
5	4	165	
6	N	253	
7	O	388	
8	P	363	

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Mol	Chain	Length	Quality of chain
9	Q	294	40% 96%
10	R	195	29% 81% 17%
11	S	251	11% 92% 7%
12	T	259	29% 84% 12%
13	U	189	89% 85% 11%
14	V	221	86% 83% 14%
15	W	174	87% 90% 6%
16	X	208	21% 97%
17	Y	134	32% 96%
18	Z	201	98%
19	a	197	9% 99%
20	b	187	79% 19%
21	c	187	7% 97%
22	d	193	8% 80% 19%
23	e	176	20% 96%
24	f	160	25% 98%
25	g	117	59% 84% 15%
26	h	139	6% 95%
27	i	149	15% 40% 58%
28	j	141	82% 16%
29	k	126	17% 98%
30	l	136	26% 98%
31	m	148	96%
32	n	61	13% 97%
33	o	109	26% 86% 14%

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Mol	Chain	Length	Quality of chain
34	p	113	
35	q	127	
36	r	108	
37	s	111	
38	t	122	
39	u	99	
40	v	91	
41	w	74	
42	x	51	
43	y	134	

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 123561 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	93	758	479	152	122	5	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	93	718	442	147	123	6	0	0

- Molecule 3 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	3212	68676	30687	12377	22400	3212	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	3	119	2539	1133	454	833	119	0	0

- Molecule 5 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	4	157	3332	1491	583	1101	157	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	N	248	1872	1166	377	324	5	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	O	384	3050	1929	576	535	10	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	P	362	2799	1768	538	490	3	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	Q	287	2312	1461	410	437	4	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	R	162	1251	802	231	215	3	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	S	233	1897	1211	349	334	3	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	T	229	1772	1135	325	309	3	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	U	168	1319	828	244	242	5	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	V	191	1549	982	291	270	6	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	W	167	1346	854	252	235	5	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	X	207	1654	1034	329	290	1	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Y	130	1038	662	198	174	4	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Z	200	1676	1050	348	275	3	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	a	196	1545	991	294	256	4	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	b	152	1212	770	229	210	3	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	c	186	1487	937	300	250	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	d	157	1301	809	275	212	5	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	e	173	1423	916	268	234	5	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	f	159	1286	810	247	226	3	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	g	99	798	518	138	142	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	h	134	999	630	184	177	8	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	i	63	523	336	102	82	3	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	j	118	947	605	175	166	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	k	125	998	622	201	173	2	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	l	135	1078	698	200	178	2	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	m	147	1171	740	235	194	2	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	n	59	495	299	112	84	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	o	94	705	450	121	130	4	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	p	103	857	538	167	149	3	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	q	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	104	Total	C	N	O	S	0	0
			831	531	160	137	3		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	106	Total	C	N	O	S	0	0
			858	538	176	142	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	t	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 39 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	x	50	436	273	98	64	1	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	y	134	1039	646	204	187	2	0	0

- Molecule 44 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	0	1	Total 1	Zn 1	0
44	1	1	Total 1	Zn 1	0
44	v	1	Total 1	Zn 1	0

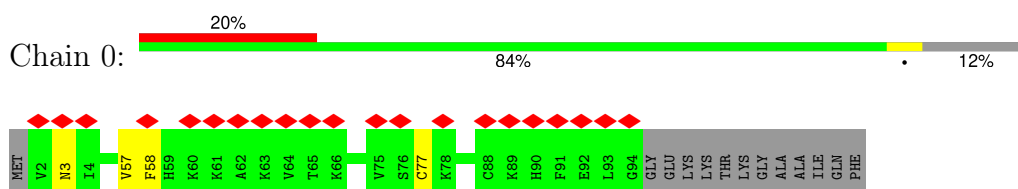
- Molecule 45 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	2	91	Total 91	Mg 91	0
45	3	2	Total 2	Mg 2	0
45	4	1	Total 1	Mg 1	0
45	b	1	Total 1	Mg 1	0
45	h	1	Total 1	Mg 1	0
45	q	1	Total 1	Mg 1	0

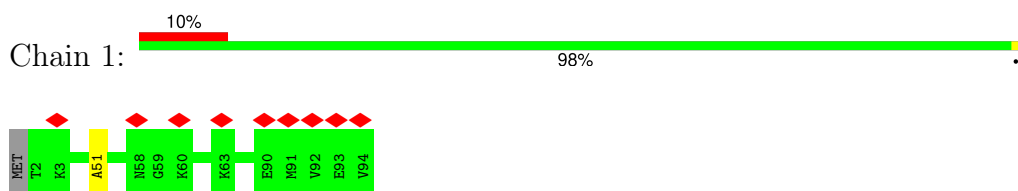
3 Residue-property plots [i](#)

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.

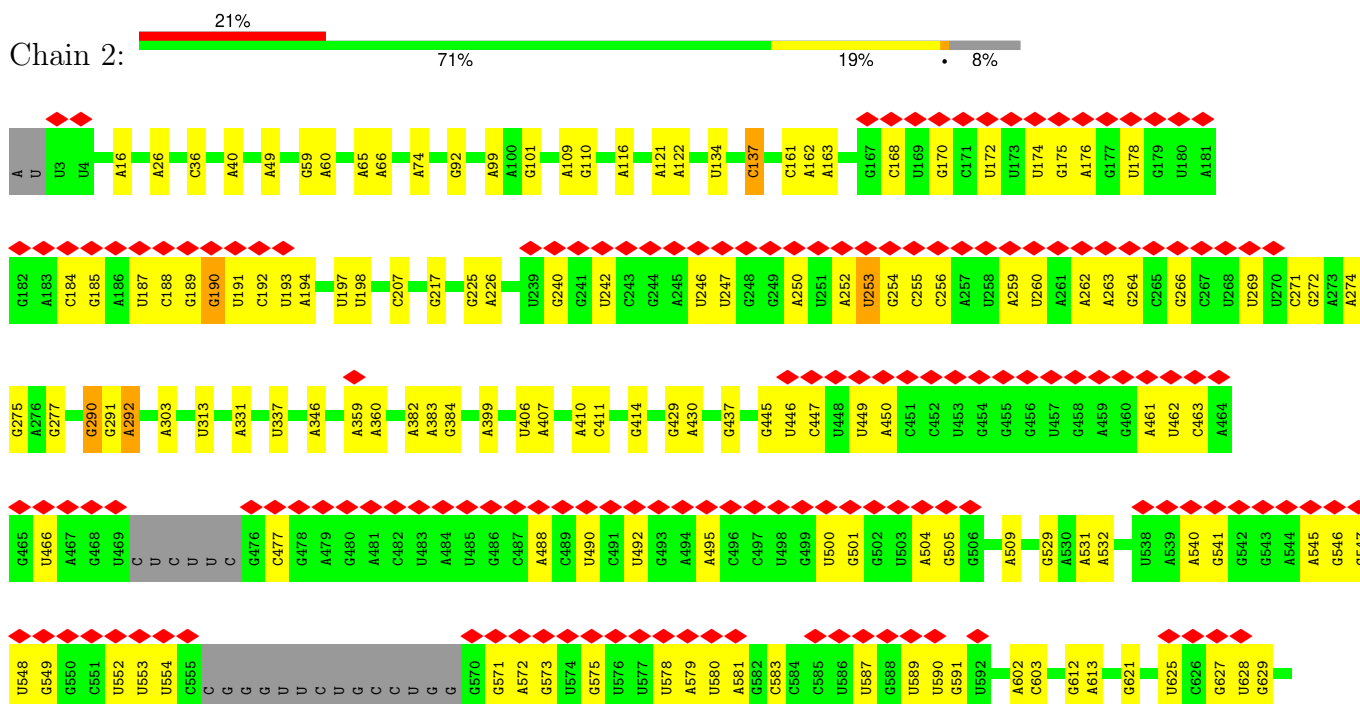
- Molecule 1: Large ribosomal subunit protein eL42

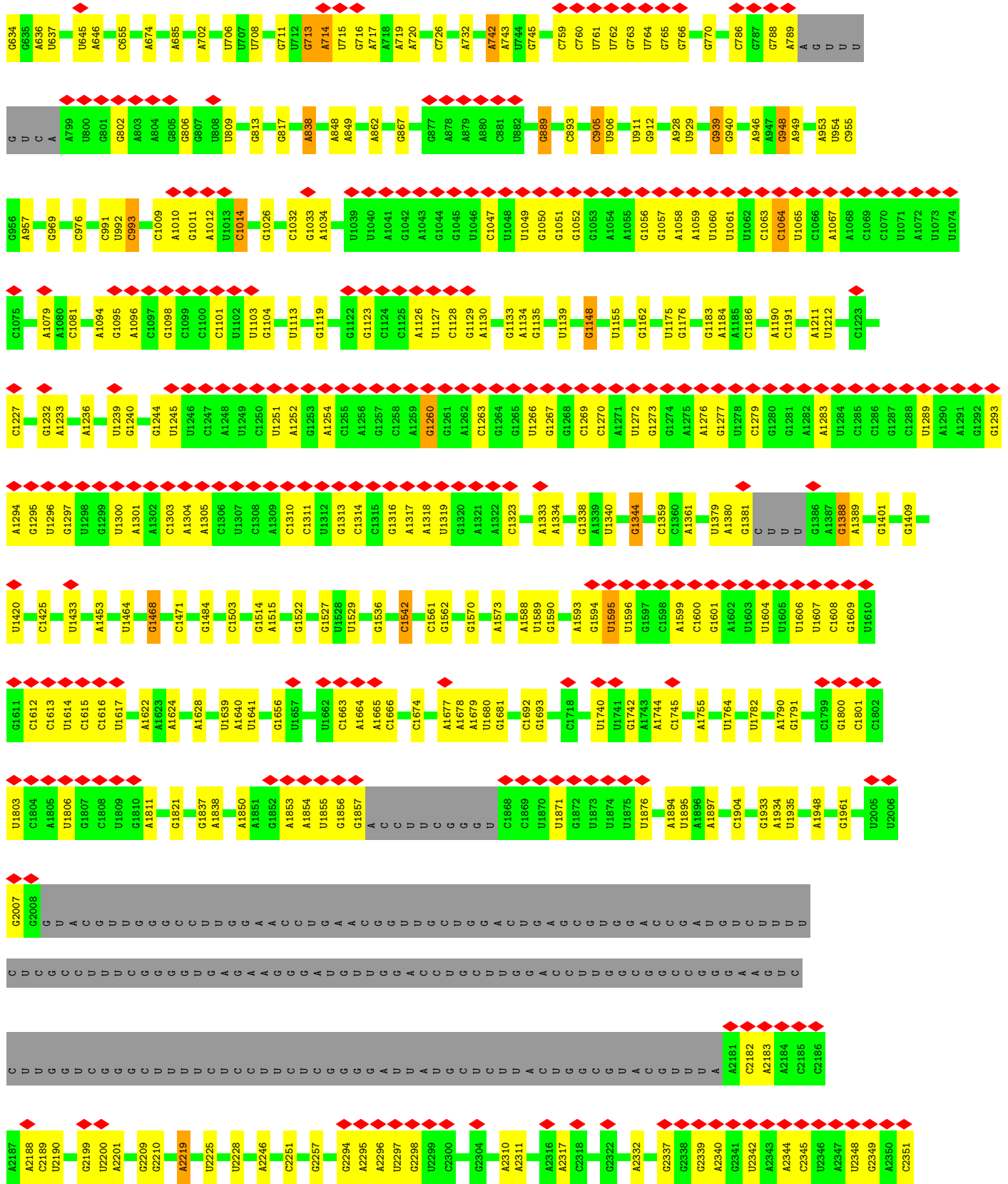


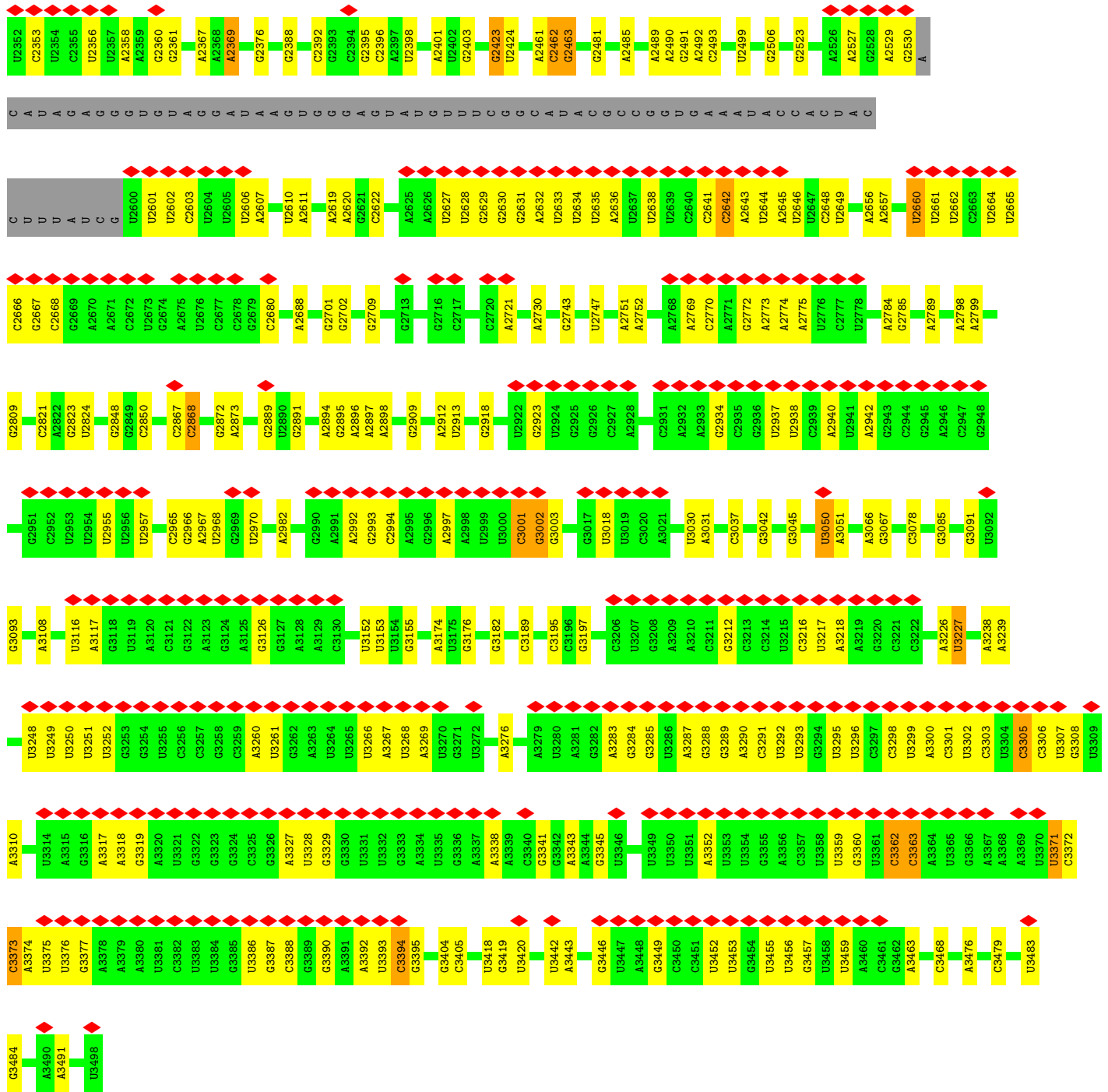
- Molecule 2: Large ribosomal subunit protein eL43A



- Molecule 3: 28S ribosomal RNA

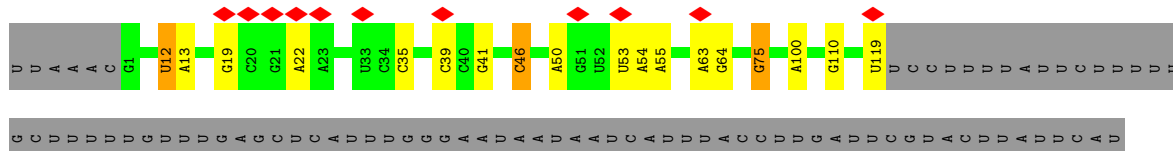






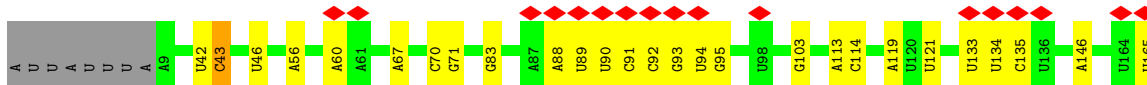
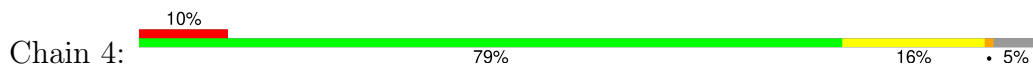
• Molecule 4: 5S ribosomal RNA

Chain 3: 41% 6% 52%

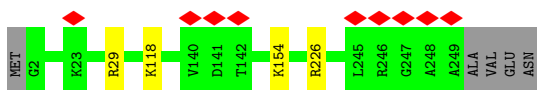


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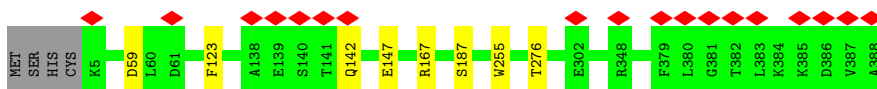
• Molecule 5: 5.8S ribosomal RNA



• Molecule 6: Large ribosomal subunit protein uL2C



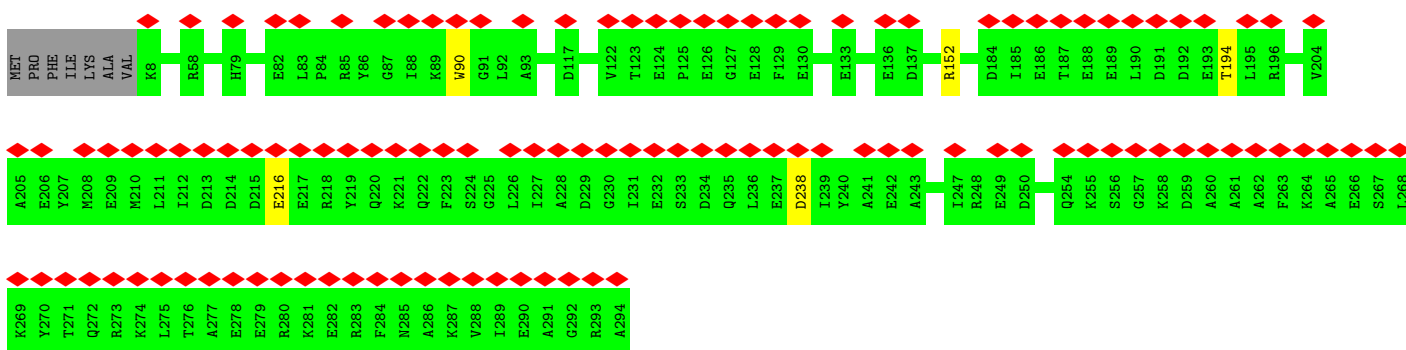
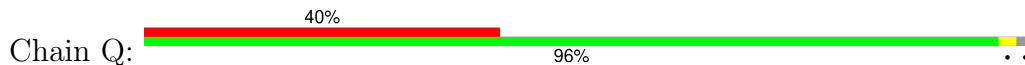
• Molecule 7: Large ribosomal subunit protein uL3A



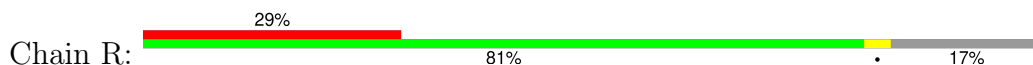
• Molecule 8: Large ribosomal subunit protein uL4A

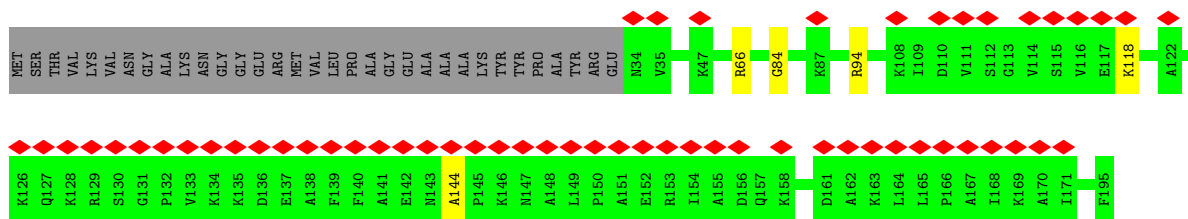


• Molecule 9: Large ribosomal subunit protein uL18B

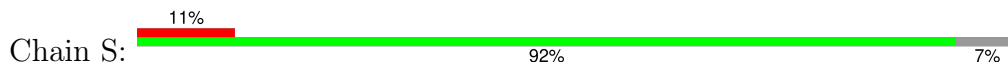


• Molecule 10: Large ribosomal subunit protein eL6

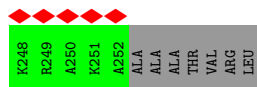
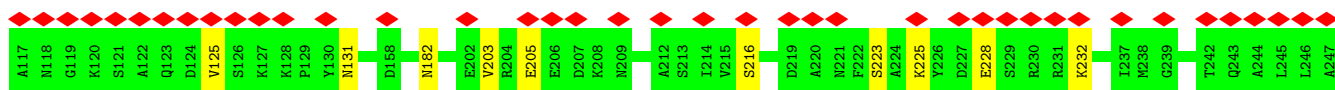
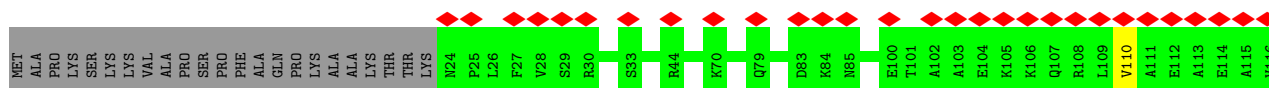
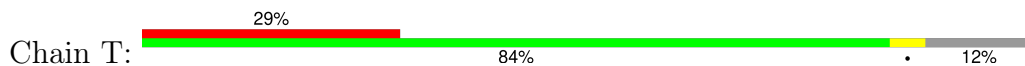




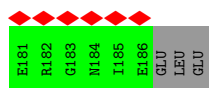
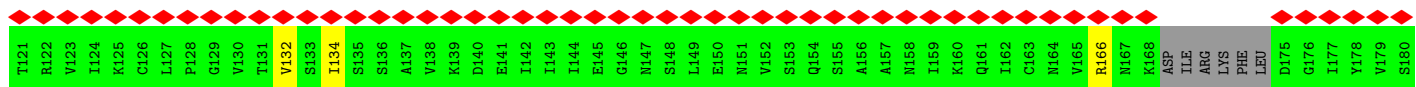
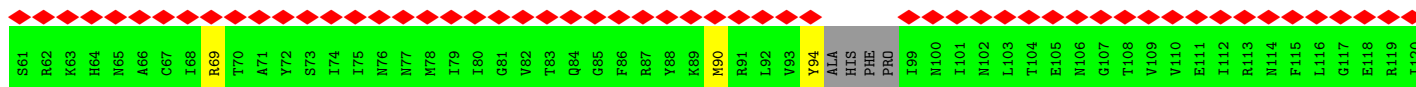
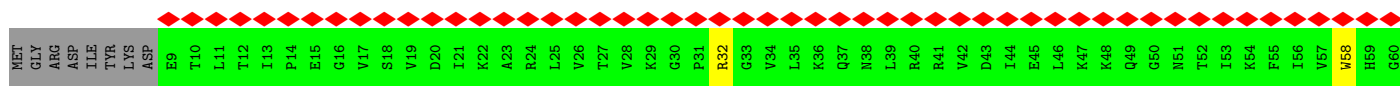
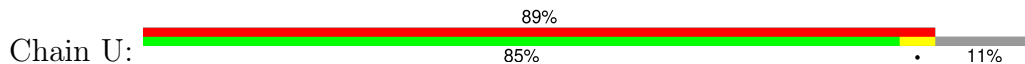
• Molecule 11: Large ribosomal subunit protein uL30C



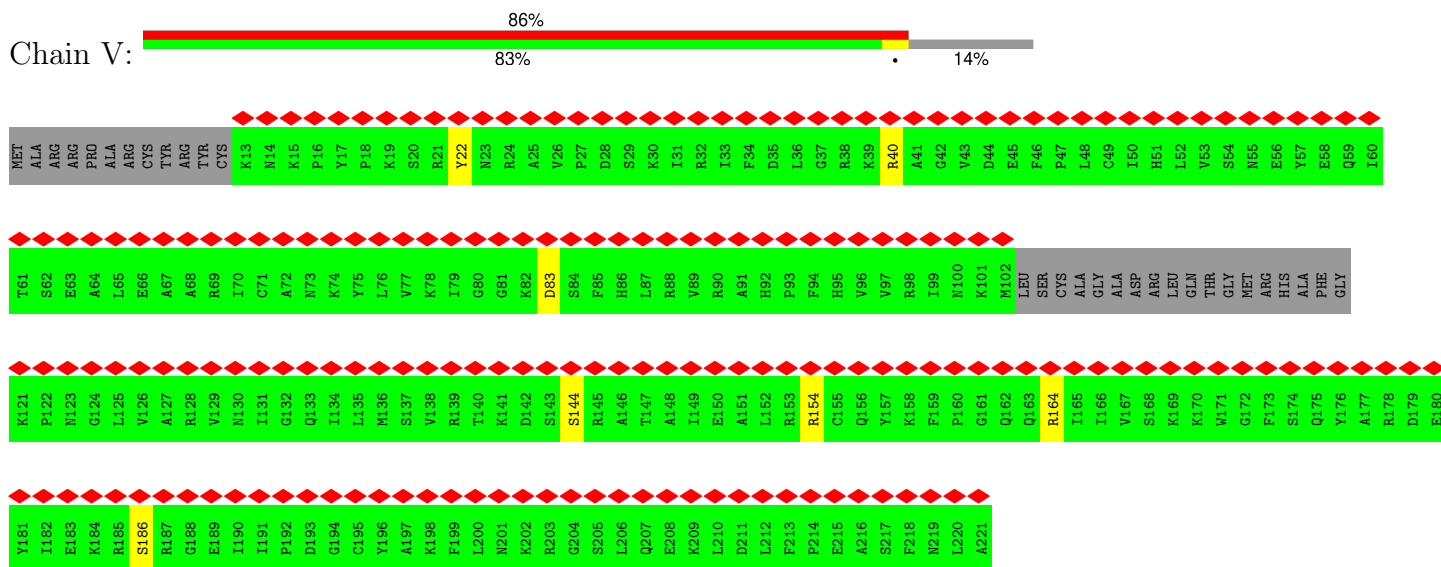
• Molecule 12: Large ribosomal subunit protein eL8



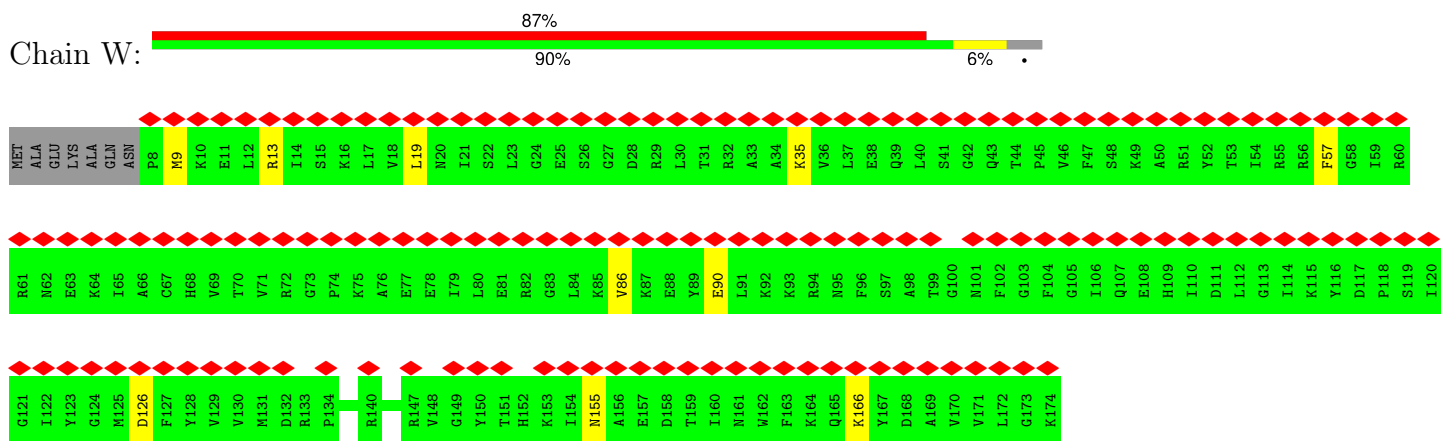
• Molecule 13: Large ribosomal subunit protein uL6B



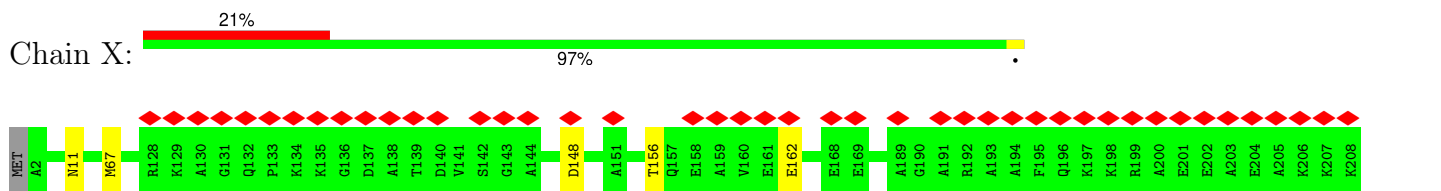
• Molecule 14: Large ribosomal subunit protein uL16A



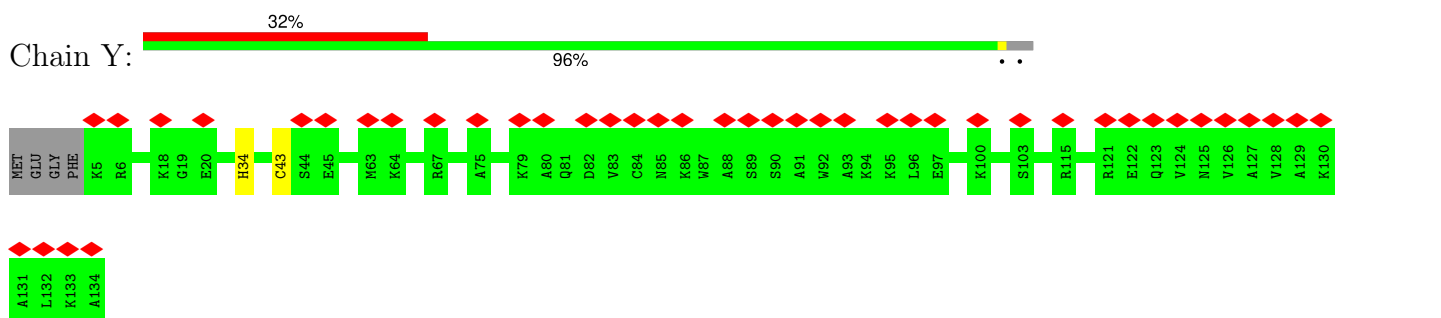
• Molecule 15: Large ribosomal subunit protein uL5A



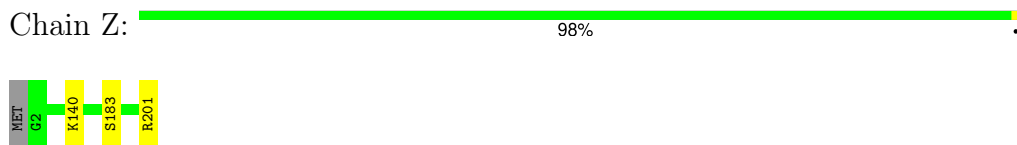
• Molecule 16: Large ribosomal subunit protein eL13



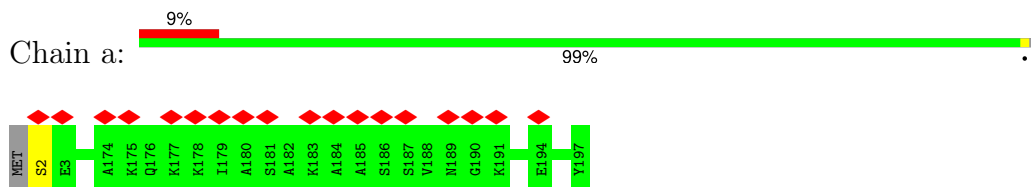
• Molecule 17: Large ribosomal subunit protein eL14



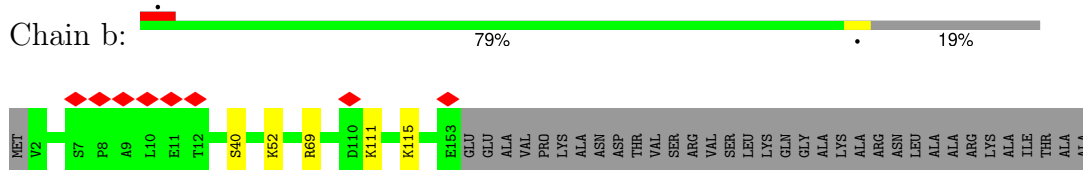
- Molecule 18: Large ribosomal subunit protein eL15B



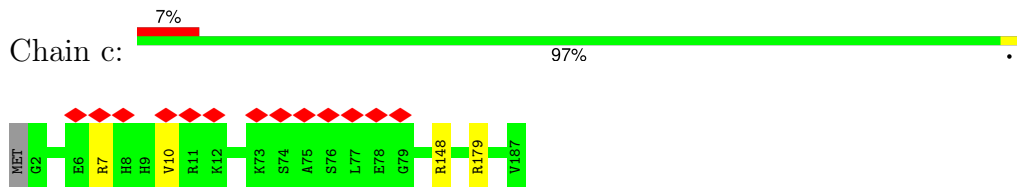
- Molecule 19: Large ribosomal subunit protein uL13A



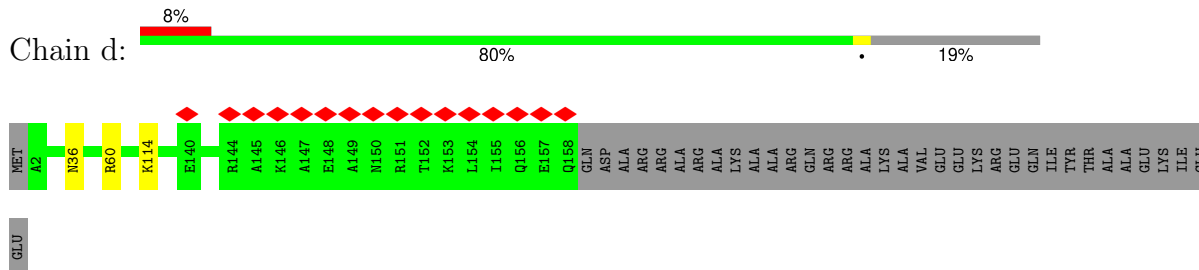
- Molecule 20: Large ribosomal subunit protein uL22A



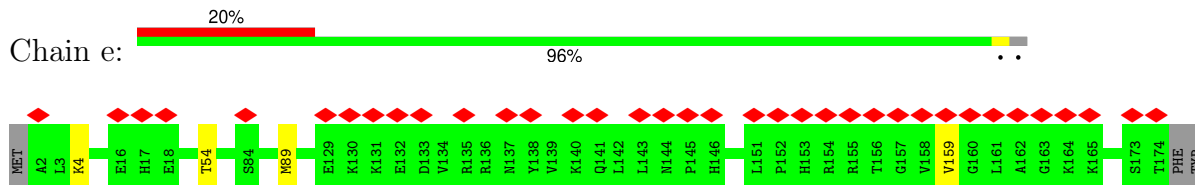
- Molecule 21: Large ribosomal subunit protein eL18B



- Molecule 22: Large ribosomal subunit protein eL19B

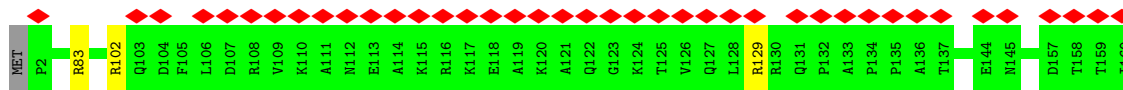


- Molecule 23: Large ribosomal subunit protein eL20A

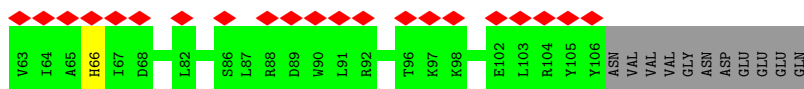
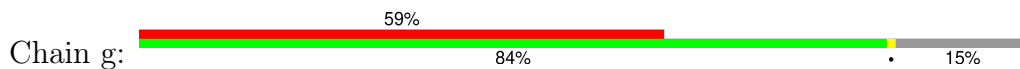


- Molecule 24: Large ribosomal subunit protein eL21B

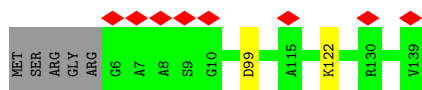




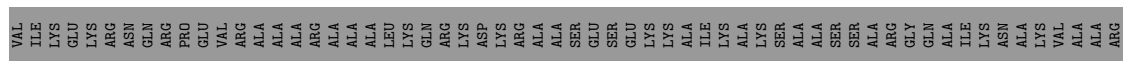
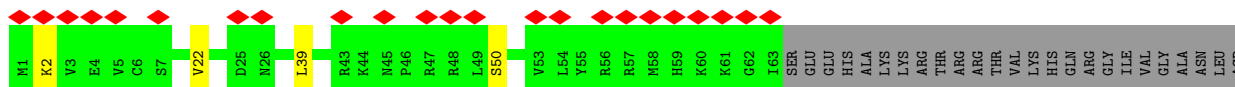
• Molecule 25: Large ribosomal subunit protein eL22



• Molecule 26: Large ribosomal subunit protein uL14B

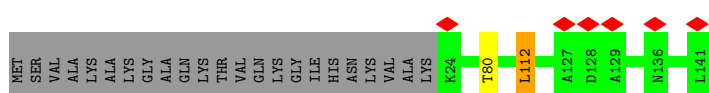
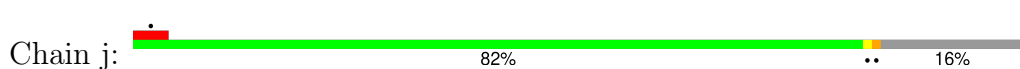


• Molecule 27: Large ribosomal subunit protein eL24B

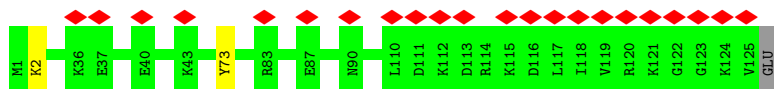


ARG

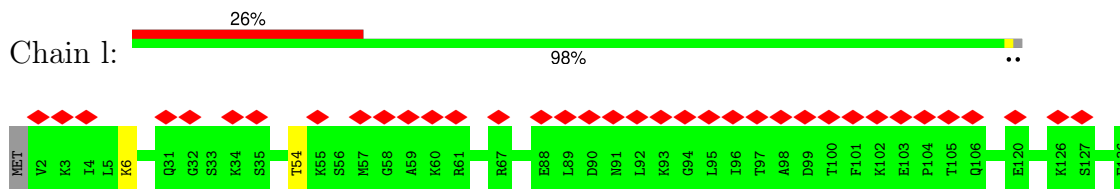
• Molecule 28: Large ribosomal subunit protein uL23A



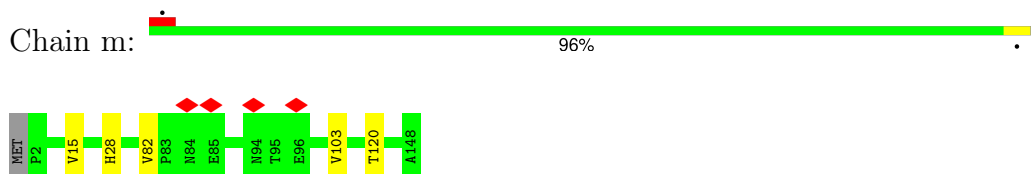
• Molecule 29: Large ribosomal subunit protein uL24



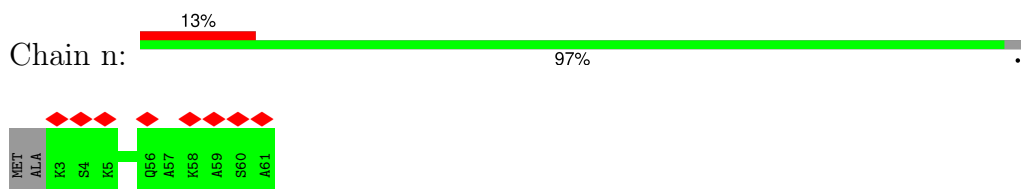
- Molecule 30: Large ribosomal subunit protein eL27A



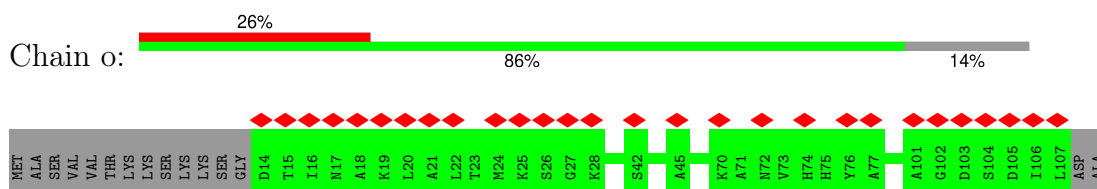
- Molecule 31: Large ribosomal subunit protein uL15B



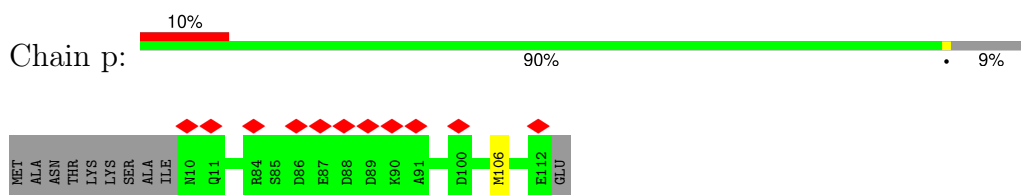
- Molecule 32: Large ribosomal subunit protein eL29



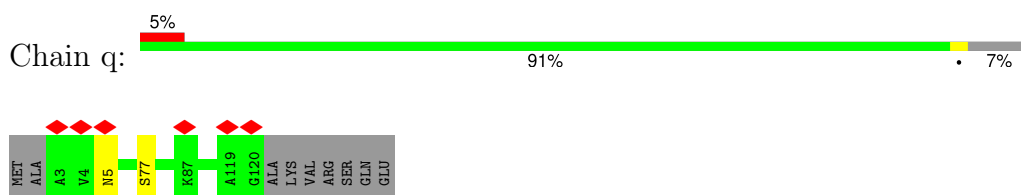
- Molecule 33: Large ribosomal subunit protein eL30A



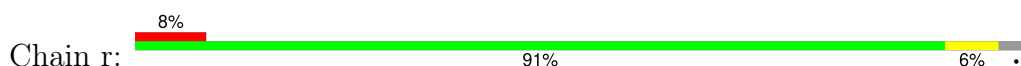
- Molecule 34: Large ribosomal subunit protein eL31

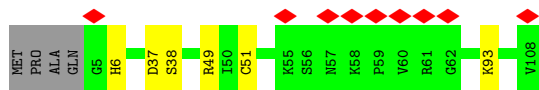


- Molecule 35: Large ribosomal subunit protein eL32A

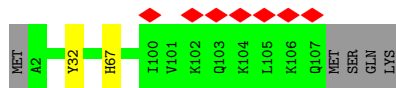
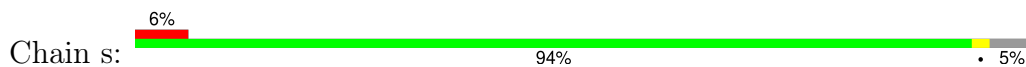


- Molecule 36: Large ribosomal subunit protein eL33A

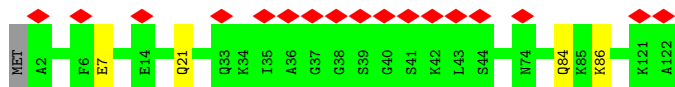




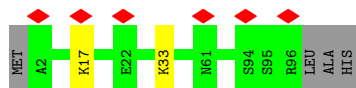
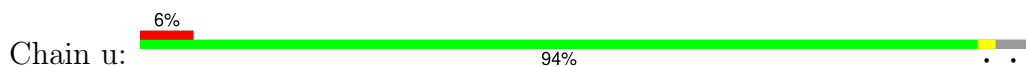
- Molecule 37: Large ribosomal subunit protein eL34B



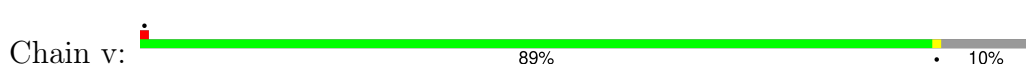
- Molecule 38: Large ribosomal subunit protein uL29



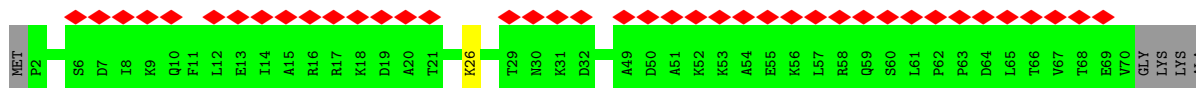
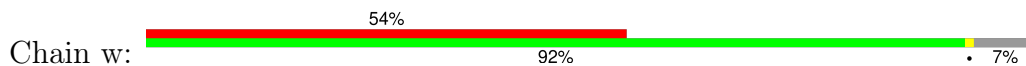
- Molecule 39: Large ribosomal subunit protein eL36B



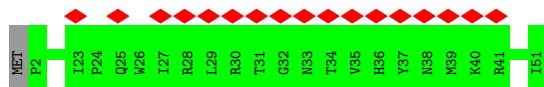
- Molecule 40: Large ribosomal subunit protein eL37B



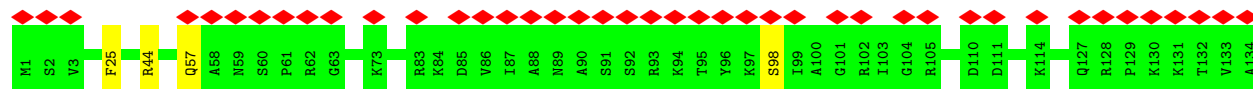
- Molecule 41: Large ribosomal subunit protein eL38A



- Molecule 42: Large ribosomal subunit protein eL39



- Molecule 43: Large ribosomal subunit protein eL28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	820453	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.551	Depositor
Minimum map value	-1.428	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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, ZN

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	0	0.36	0/772	0.59	0/1025
2	1	0.35	0/727	0.63	0/973
3	2	0.79	2/76871 (0.0%)	1.02	131/119827 (0.1%)
4	3	0.66	0/2838	0.93	5/4422 (0.1%)
5	4	0.79	0/3723	0.96	3/5796 (0.1%)
6	N	0.38	0/1910	0.62	0/2575
7	O	0.38	0/3116	0.61	0/4190
8	P	0.38	0/2852	0.60	0/3850
9	Q	0.37	0/2361	0.56	0/3173
10	R	0.34	0/1275	0.55	0/1719
11	S	0.37	0/1929	0.55	0/2583
12	T	0.34	0/1801	0.55	0/2430
13	U	0.27	0/1330	0.54	0/1789
14	V	0.29	0/1579	0.55	0/2115
15	W	0.29	0/1369	0.57	0/1830
16	X	0.35	0/1686	0.58	0/2267
17	Y	0.32	0/1054	0.56	0/1413
18	Z	0.43	0/1717	0.67	0/2306
19	a	0.38	0/1575	0.56	0/2109
20	b	0.38	0/1237	0.58	0/1661
21	c	0.36	0/1511	0.64	0/2021
22	d	0.30	0/1320	0.56	0/1757
23	e	0.37	0/1458	0.57	0/1961
24	f	0.40	0/1314	0.57	0/1771
25	g	0.32	0/812	0.54	0/1090
26	h	0.36	0/1015	0.61	0/1369
27	i	0.36	0/534	0.60	0/709
28	j	0.35	0/963	0.59	1/1296 (0.1%)
29	k	0.34	0/1008	0.62	0/1341
30	l	0.33	0/1101	0.55	0/1477
31	m	0.38	0/1200	0.65	0/1611
32	n	0.34	0/503	0.58	0/664

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	o	0.36	0/714	0.55	0/961
34	p	0.38	0/872	0.64	0/1172
35	q	0.38	0/958	0.65	0/1278
36	r	0.40	0/853	0.60	0/1146
37	s	0.37	0/870	0.63	0/1165
38	t	0.34	0/1008	0.60	0/1340
39	u	0.34	0/766	0.61	0/1017
40	v	0.40	0/666	0.66	0/881
41	w	0.33	0/566	0.55	0/757
42	x	0.32	0/447	0.64	0/597
43	y	0.34	0/1053	0.61	0/1414
All	All	0.66	2/133234 (0.0%)	0.90	140/196848 (0.1%)

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
2	1	0	1
10	R	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	2730	A	N9-C4	-8.13	1.32	1.37
3	2	2730	A	N3-C4	-5.12	1.31	1.34

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	1542	C	O5'-P-OP1	-12.46	94.48	105.70
3	2	3363	C	OP1-P-OP2	12.29	138.03	119.60
3	2	3362	C	OP2-P-O3'	-11.73	79.40	105.20
3	2	414	G	O4'-C1'-N9	11.50	117.40	108.20
3	2	1464	U	N3-C2-O2	-10.07	115.15	122.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	51	ALA	Peptide
10	R	84	GLY	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	0	91/106 (86%)	86 (94%)	5 (6%)	0	100	100
2	1	91/94 (97%)	83 (91%)	8 (9%)	0	100	100
6	N	246/253 (97%)	233 (95%)	12 (5%)	1 (0%)	30	22
7	O	382/388 (98%)	371 (97%)	10 (3%)	1 (0%)	37	30
8	P	360/363 (99%)	347 (96%)	13 (4%)	0	100	100
9	Q	285/294 (97%)	277 (97%)	8 (3%)	0	100	100
10	R	160/195 (82%)	148 (92%)	11 (7%)	1 (1%)	22	12
11	S	231/251 (92%)	228 (99%)	3 (1%)	0	100	100
12	T	227/259 (88%)	213 (94%)	14 (6%)	0	100	100
13	U	162/189 (86%)	153 (94%)	8 (5%)	1 (1%)	22	12
14	V	187/221 (85%)	179 (96%)	8 (4%)	0	100	100
15	W	165/174 (95%)	158 (96%)	7 (4%)	0	100	100
16	X	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
17	Y	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
18	Z	198/201 (98%)	188 (95%)	9 (4%)	1 (0%)	25	15
19	a	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
20	b	150/187 (80%)	145 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	c	184/187 (98%)	174 (95%)	10 (5%)	0	100	100
22	d	155/193 (80%)	152 (98%)	3 (2%)	0	100	100
23	e	171/176 (97%)	164 (96%)	6 (4%)	1 (1%)	22	12
24	f	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
25	g	97/117 (83%)	83 (86%)	14 (14%)	0	100	100
26	h	132/139 (95%)	123 (93%)	9 (7%)	0	100	100
27	i	61/149 (41%)	60 (98%)	1 (2%)	0	100	100
28	j	116/141 (82%)	111 (96%)	5 (4%)	0	100	100
29	k	123/126 (98%)	120 (98%)	3 (2%)	0	100	100
30	l	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
31	m	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	19	9
32	n	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
33	o	92/109 (84%)	91 (99%)	1 (1%)	0	100	100
34	p	101/113 (89%)	99 (98%)	2 (2%)	0	100	100
35	q	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
36	r	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
37	s	104/111 (94%)	102 (98%)	2 (2%)	0	100	100
38	t	119/122 (98%)	115 (97%)	3 (2%)	1 (1%)	16	7
39	u	93/99 (94%)	90 (97%)	3 (3%)	0	100	100
40	v	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
41	w	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
42	x	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
43	y	132/134 (98%)	121 (92%)	11 (8%)	0	100	100
All	All	6047/6586 (92%)	5789 (96%)	250 (4%)	8 (0%)	50	41

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	N	29	ARG
10	R	144	ALA
13	U	134	ILE
18	Z	183	SER
23	e	159	VAL

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	0	84/93 (90%)	80 (95%)	4 (5%)	21	8
2	1	74/75 (99%)	74 (100%)	0	100	100
6	N	188/192 (98%)	185 (98%)	3 (2%)	58	49
7	O	318/326 (98%)	311 (98%)	7 (2%)	47	35
8	P	293/294 (100%)	281 (96%)	12 (4%)	26	12
9	Q	235/241 (98%)	230 (98%)	5 (2%)	48	36
10	R	132/155 (85%)	129 (98%)	3 (2%)	45	33
11	S	198/213 (93%)	197 (100%)	1 (0%)	86	86
12	T	182/212 (86%)	171 (94%)	11 (6%)	16	5
13	U	149/168 (89%)	142 (95%)	7 (5%)	22	9
14	V	165/187 (88%)	158 (96%)	7 (4%)	25	12
15	W	141/146 (97%)	131 (93%)	10 (7%)	12	3
16	X	166/167 (99%)	161 (97%)	5 (3%)	36	23
17	Y	110/113 (97%)	108 (98%)	2 (2%)	54	43
18	Z	175/176 (99%)	173 (99%)	2 (1%)	70	64
19	a	159/160 (99%)	158 (99%)	1 (1%)	84	83
20	b	124/149 (83%)	119 (96%)	5 (4%)	27	13
21	c	157/158 (99%)	153 (98%)	4 (2%)	42	30
22	d	136/163 (83%)	133 (98%)	3 (2%)	47	35
23	e	151/154 (98%)	148 (98%)	3 (2%)	50	38
24	f	138/139 (99%)	135 (98%)	3 (2%)	47	35
25	g	86/103 (84%)	85 (99%)	1 (1%)	67	61
26	h	103/107 (96%)	101 (98%)	2 (2%)	52	41
27	i	57/121 (47%)	53 (93%)	4 (7%)	12	3
28	j	105/122 (86%)	103 (98%)	2 (2%)	52	41
29	k	110/111 (99%)	108 (98%)	2 (2%)	54	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	l	114/115 (99%)	112 (98%)	2 (2%)	54	43
31	m	122/123 (99%)	118 (97%)	4 (3%)	33	20
32	n	50/51 (98%)	50 (100%)	0	100	100
33	o	75/87 (86%)	75 (100%)	0	100	100
34	p	94/102 (92%)	93 (99%)	1 (1%)	70	64
35	q	100/107 (94%)	98 (98%)	2 (2%)	50	38
36	r	91/94 (97%)	85 (93%)	6 (7%)	14	4
37	s	91/96 (95%)	89 (98%)	2 (2%)	47	35
38	t	106/107 (99%)	103 (97%)	3 (3%)	38	25
39	u	81/84 (96%)	79 (98%)	2 (2%)	42	30
40	v	68/71 (96%)	67 (98%)	1 (2%)	60	52
41	w	63/66 (96%)	62 (98%)	1 (2%)	58	49
42	x	46/47 (98%)	46 (100%)	0	100	100
43	y	113/113 (100%)	109 (96%)	4 (4%)	31	18
All	All	5150/5508 (94%)	5013 (97%)	137 (3%)	41	26

5 of 137 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	p	106	MET
36	r	37	ASP
39	u	33	LYS
13	U	69	ARG
13	U	58	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
29	k	54	GLN
36	r	6	HIS
30	l	123	GLN
32	n	6	ASN
38	t	15	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	3204/3498 (91%)	656 (20%)	49 (1%)
4	3	118/246 (47%)	18 (15%)	1 (0%)
5	4	156/165 (94%)	26 (16%)	1 (0%)
All	All	3478/3909 (88%)	700 (20%)	51 (1%)

5 of 700 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	16	A
3	2	26	A
3	2	40	A
3	2	49	A
3	2	59	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	1897	A
3	2	2993	G
4	3	12	U
3	2	2200	U
3	2	2867	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 100 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.

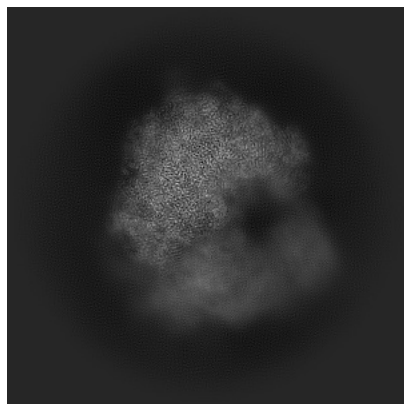
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43973. These allow visual inspection of the internal detail of the map and identification of artifacts.

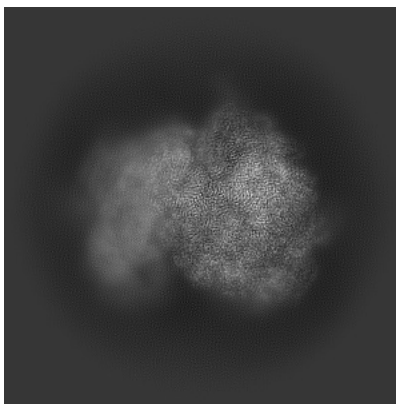
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

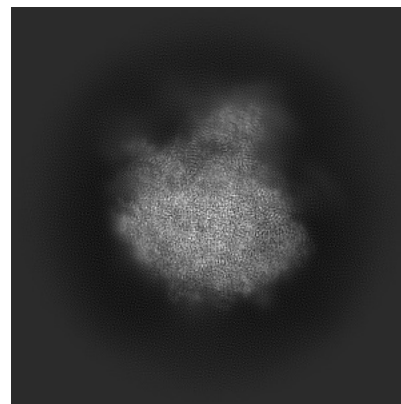
6.1.1 Primary map



X

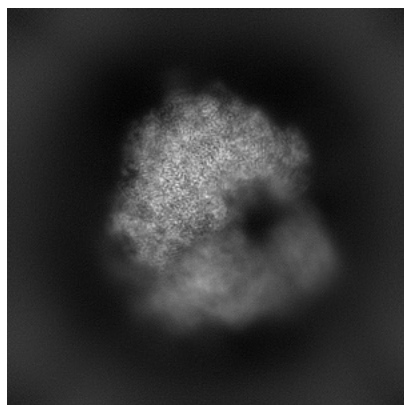


Y

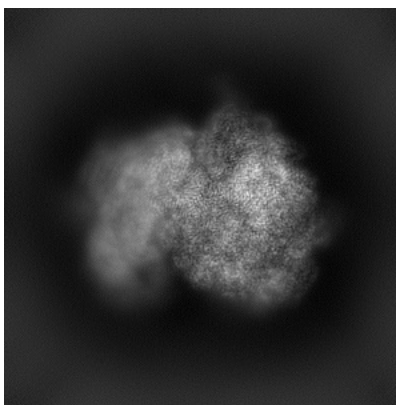


Z

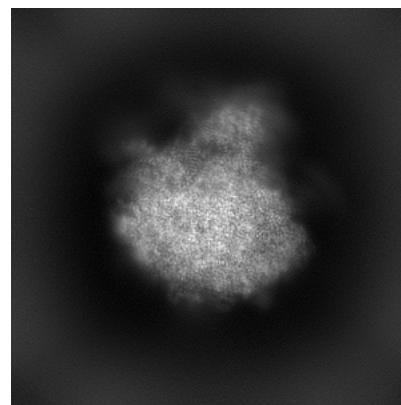
6.1.2 Raw map



X



Y

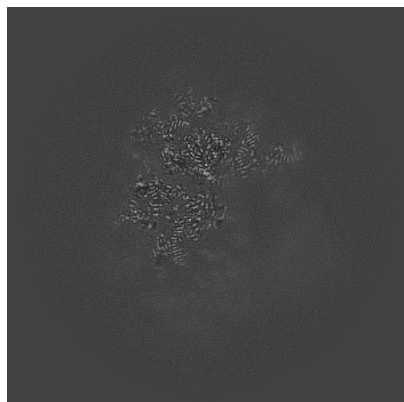


Z

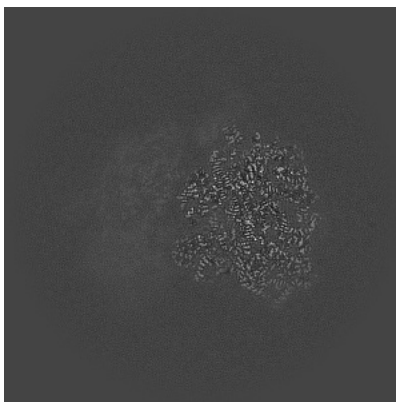
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

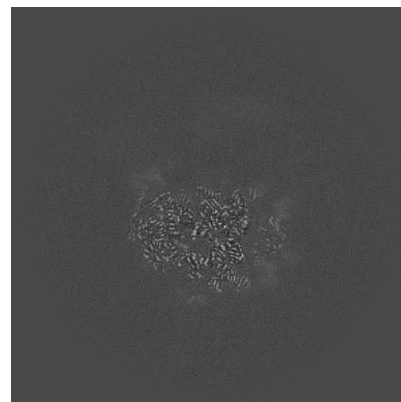
6.2.1 Primary map



X Index: 256

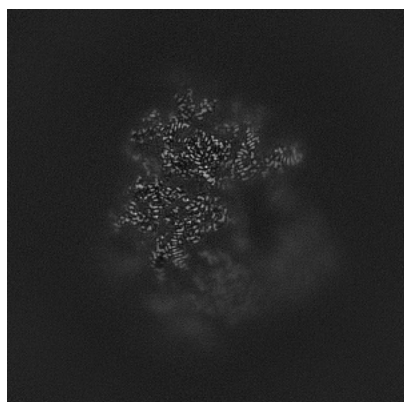


Y Index: 256

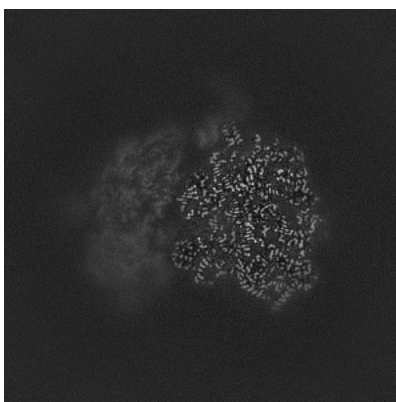


Z Index: 256

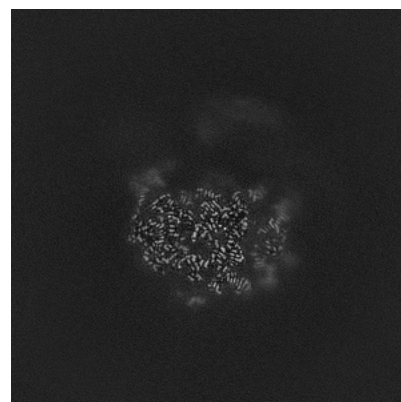
6.2.2 Raw map



X Index: 256



Y Index: 256

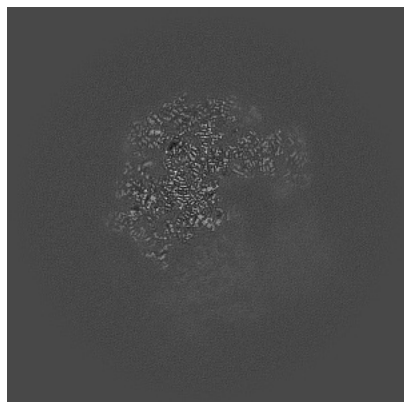


Z Index: 256

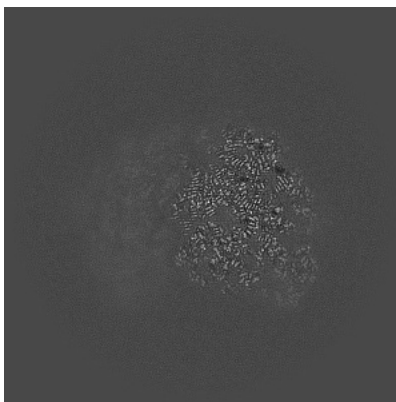
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

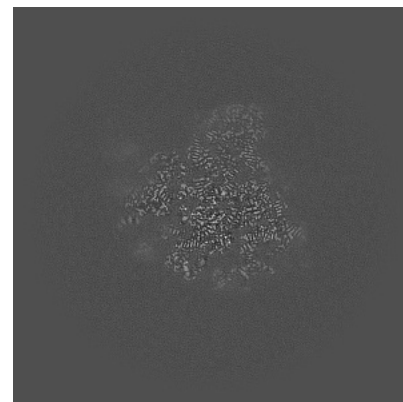
6.3.1 Primary map



X Index: 275

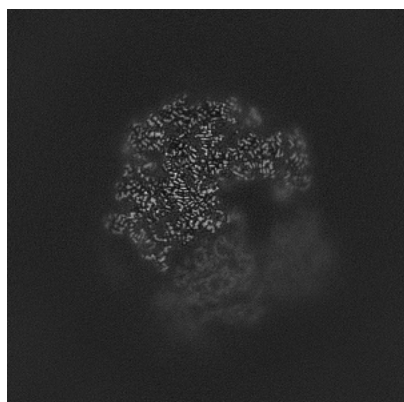


Y Index: 246

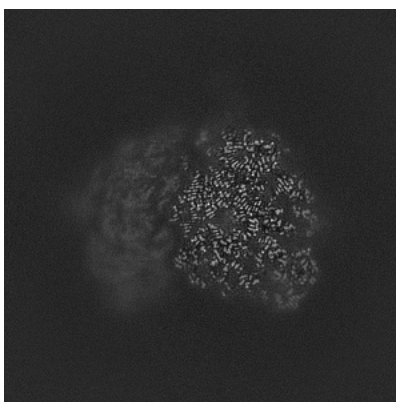


Z Index: 324

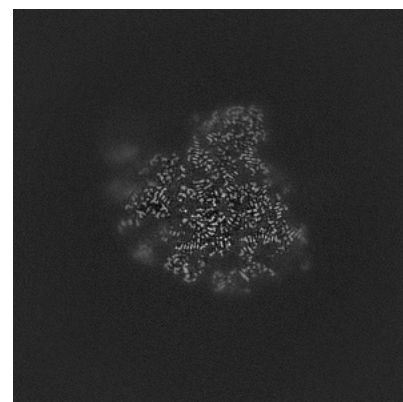
6.3.2 Raw map



X Index: 275



Y Index: 246

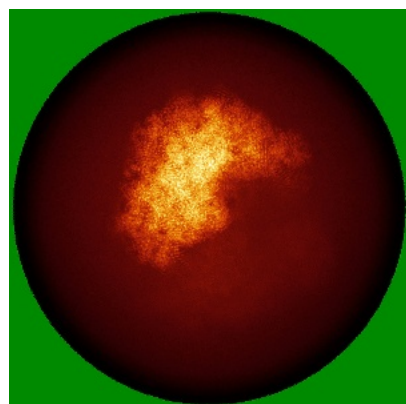


Z Index: 324

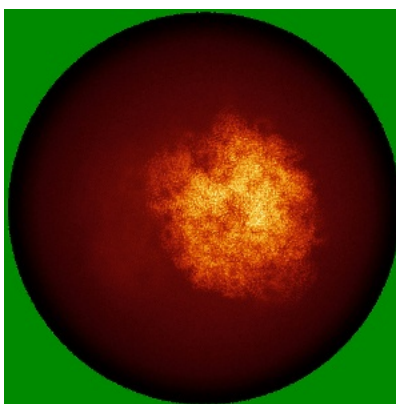
The images above show the largest variance slices of the map in three orthogonal directions.

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

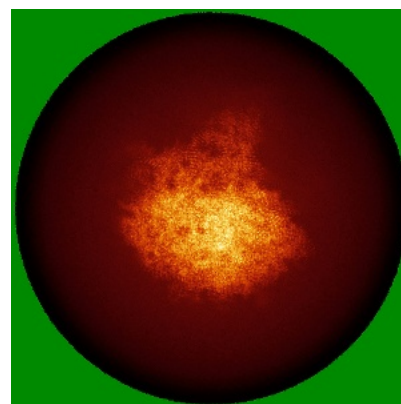
6.4.1 Primary map



X

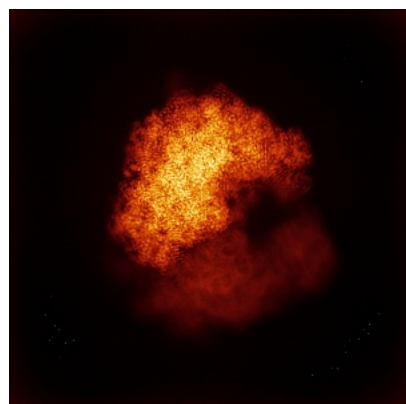


Y

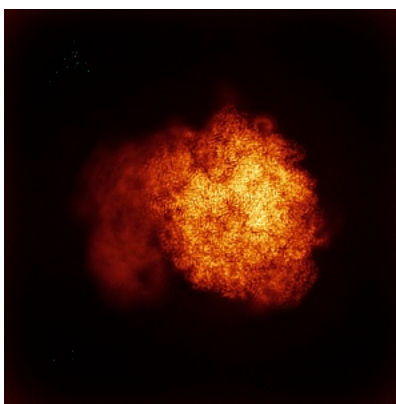


Z

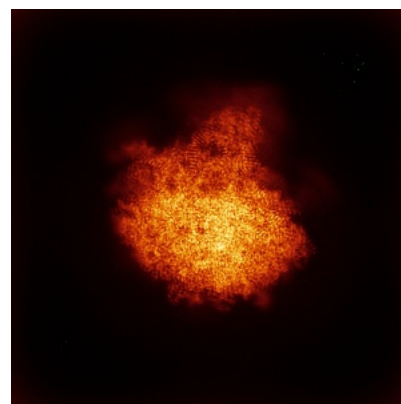
6.4.2 Raw map



X



Y

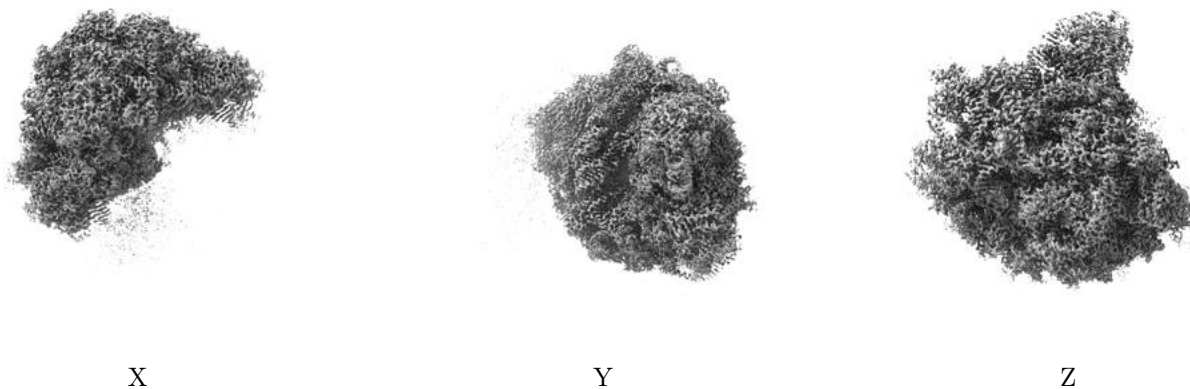


Z

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

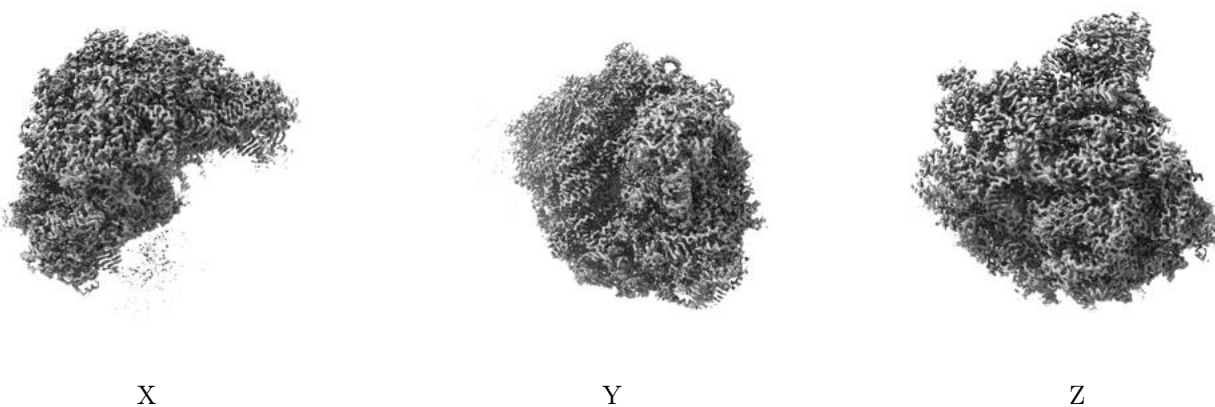
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

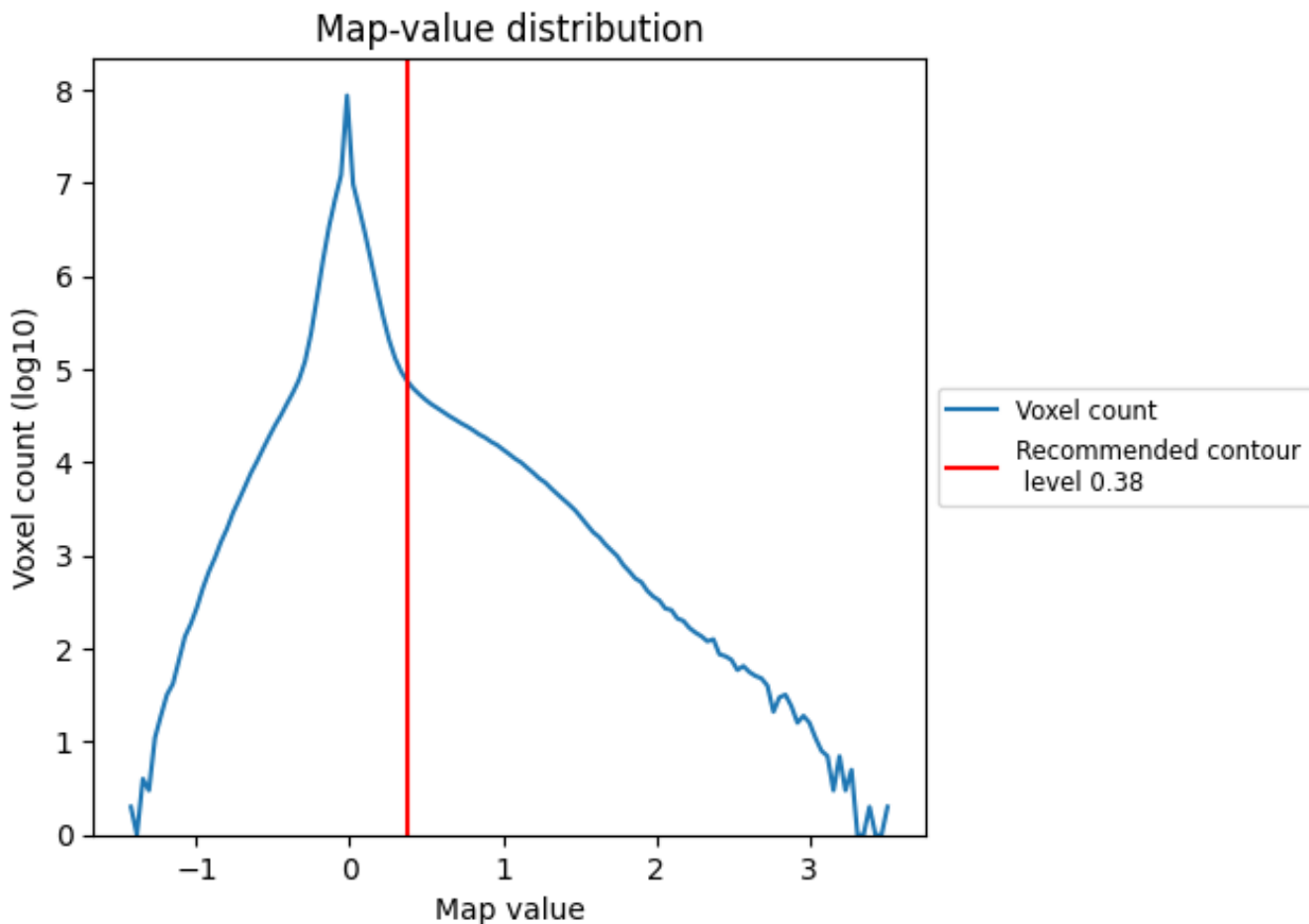
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

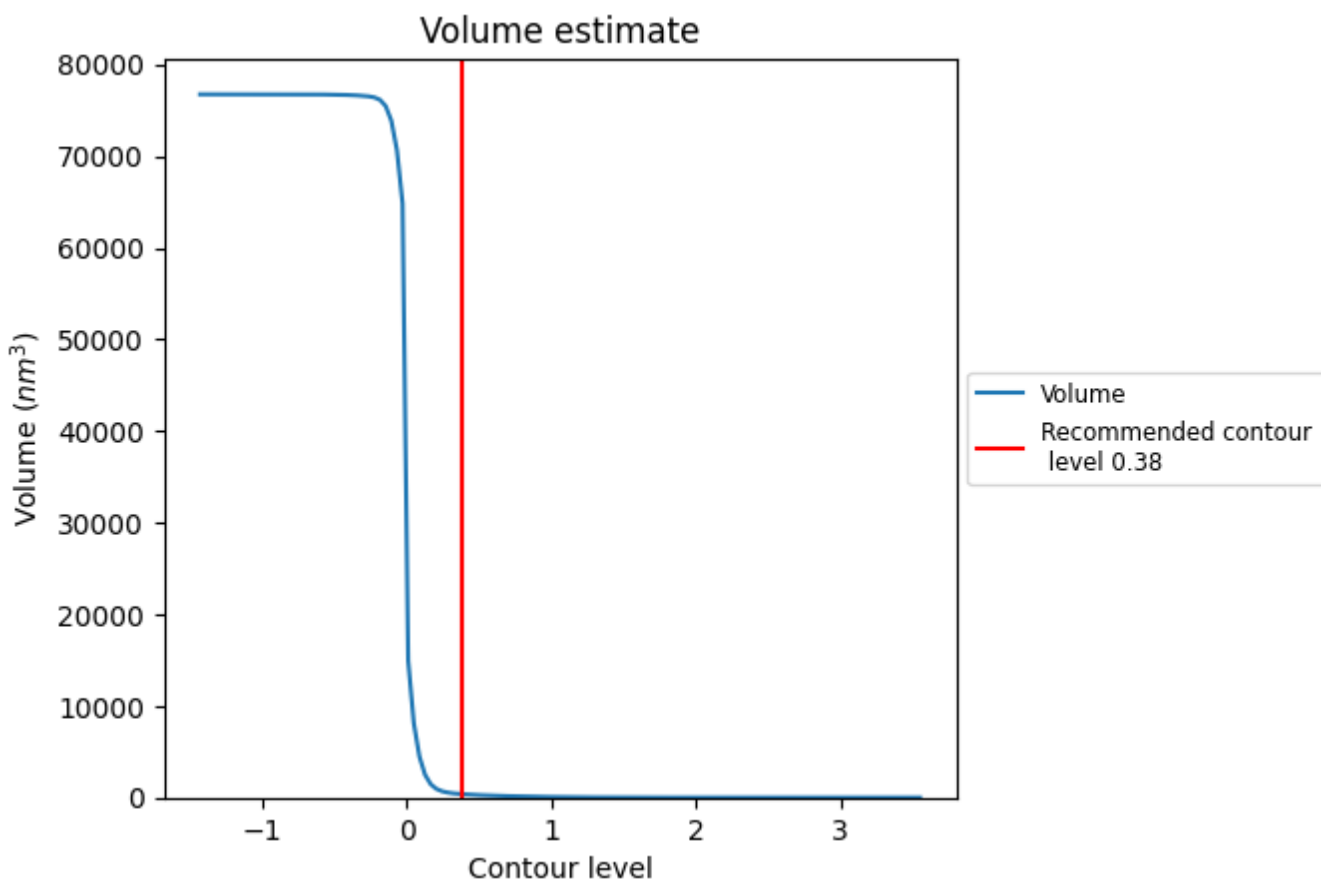
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

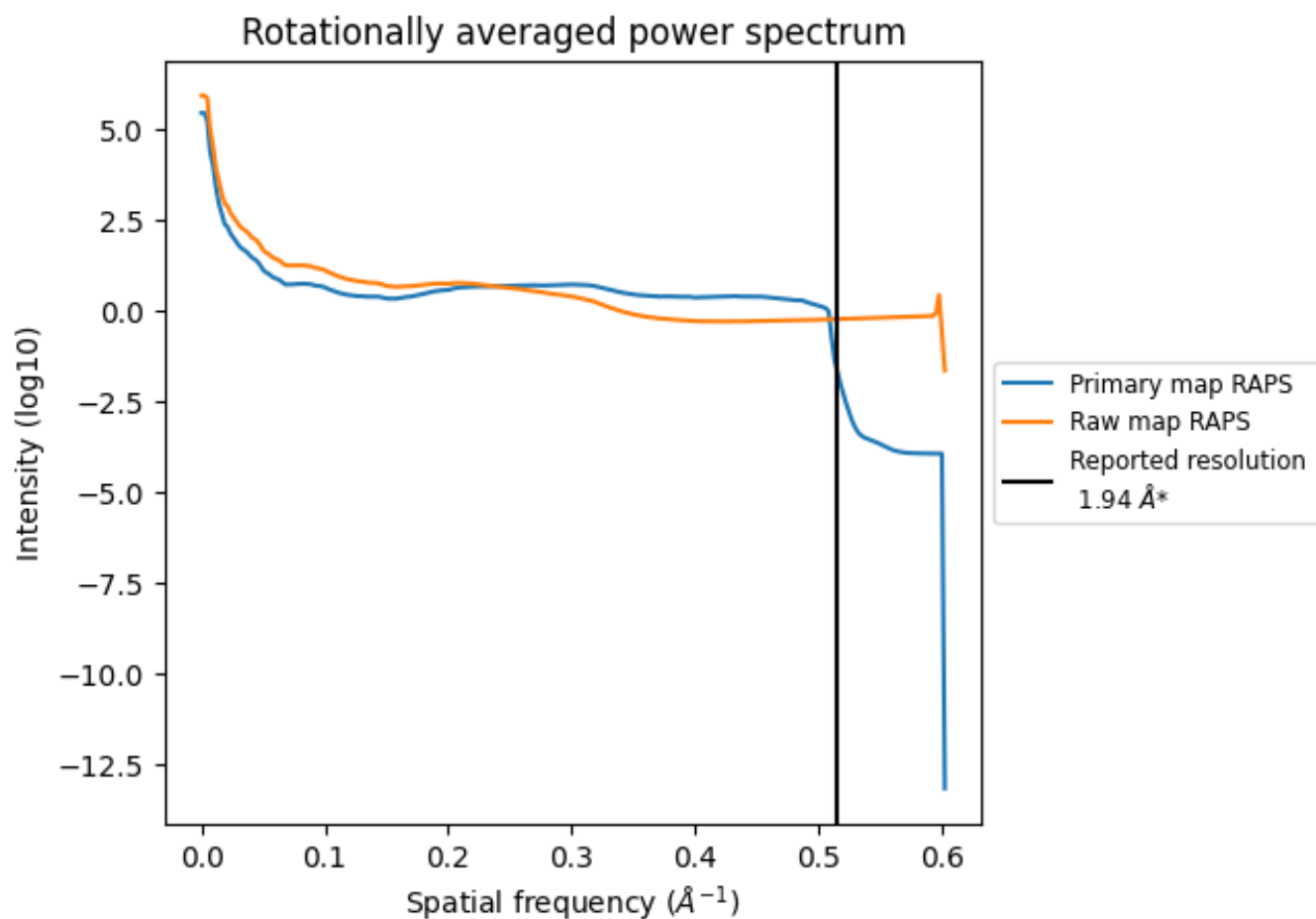
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 381 nm³; this corresponds to an approximate mass of 344 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](#)

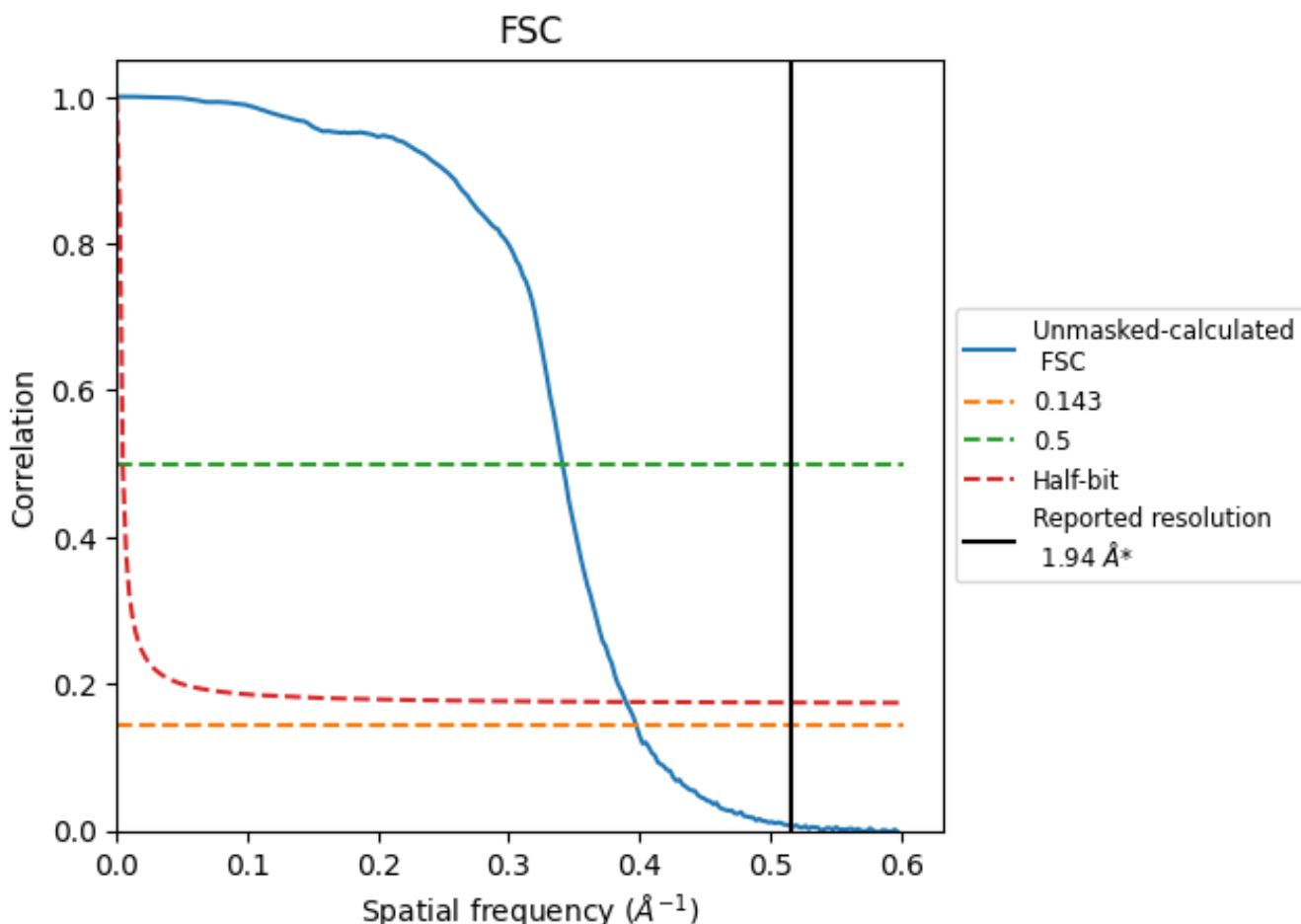


*Reported resolution corresponds to spatial frequency of 0.515 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.515 Å⁻¹

8.2 Resolution estimates [i](#)

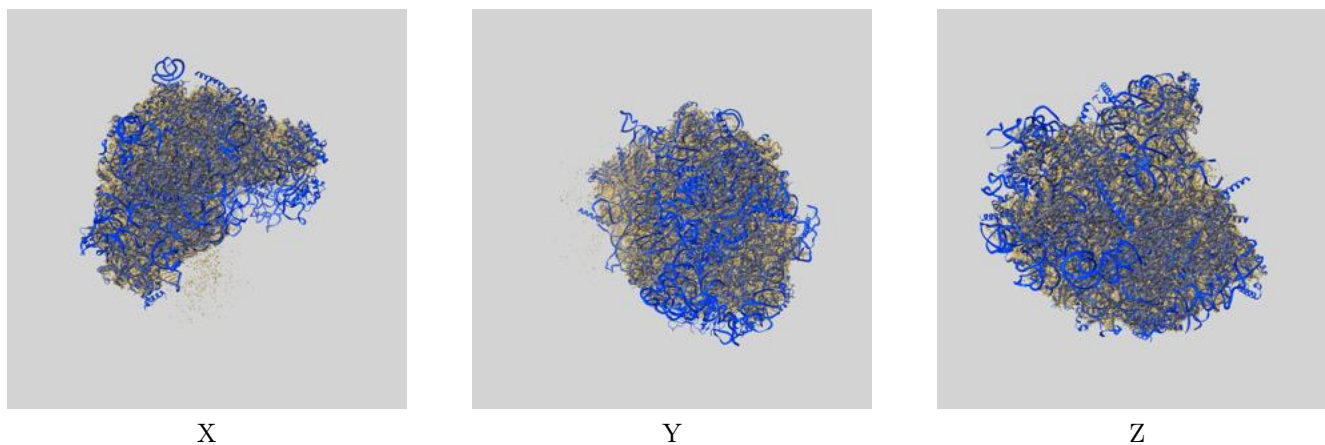
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.52	2.93	2.57

*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 2.52 differs from the reported value 1.94 by more than 10 %

9 Map-model fit [i](#)

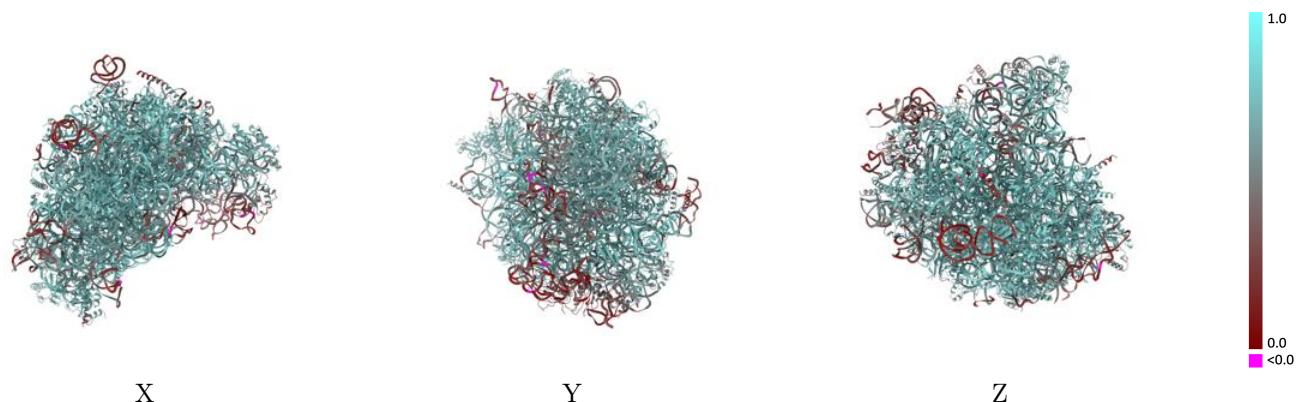
This section contains information regarding the fit between EMDB map EMD-43973 and PDB model 9AXU. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



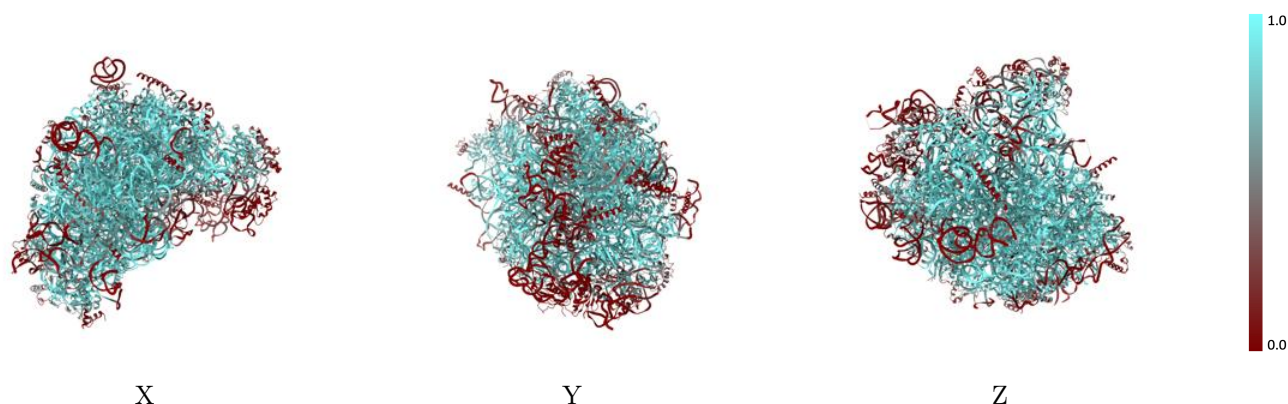
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



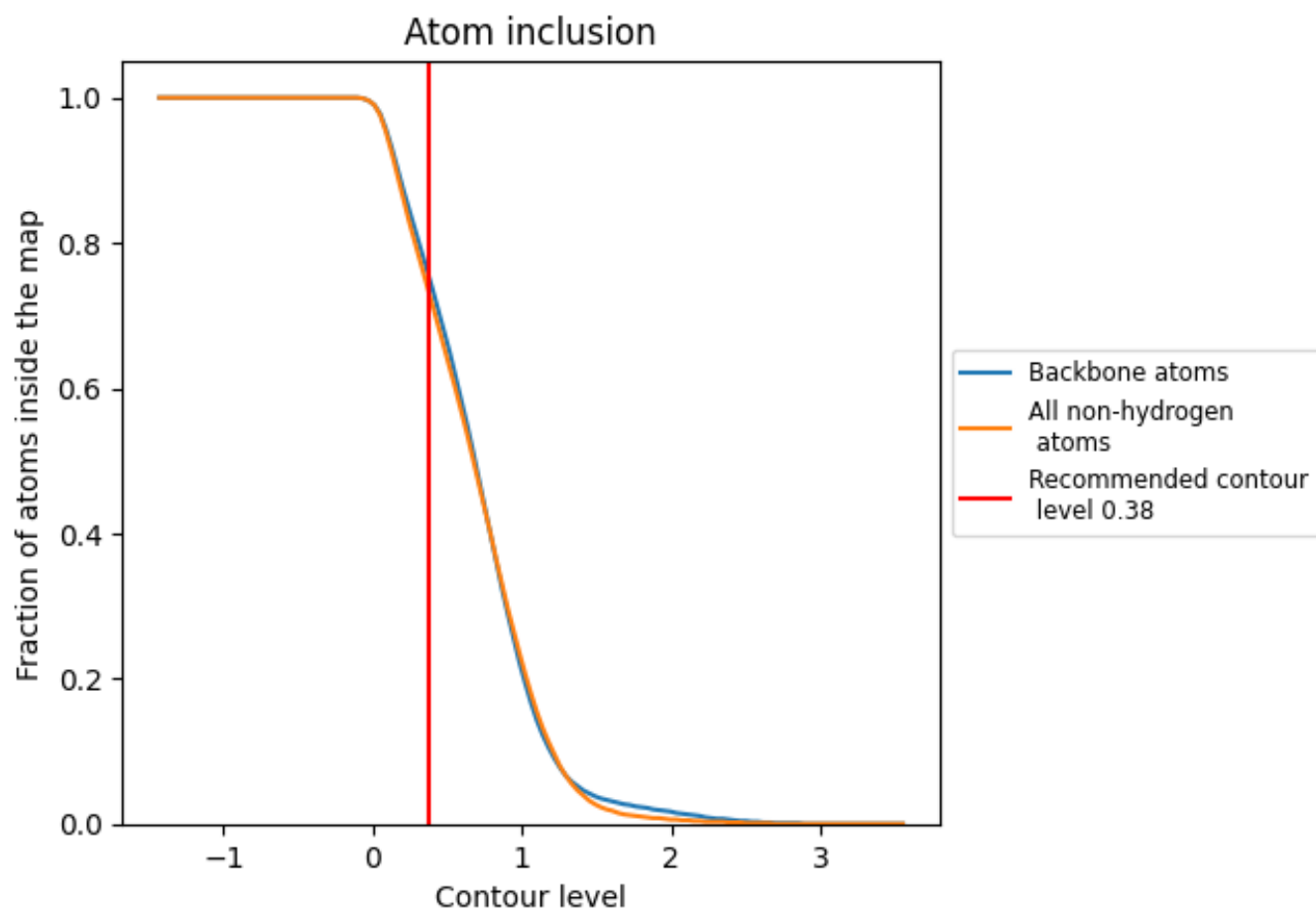
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.38).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 73% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.6610
0	 0.6590	 0.6920
1	 0.7990	 0.7110
2	 0.7360	 0.6390
3	 0.7530	 0.6620
4	 0.8300	 0.6840
N	 0.9360	 0.7670
O	 0.8860	 0.7510
P	 0.8990	 0.7550
Q	 0.5560	 0.6430
R	 0.5680	 0.6300
S	 0.8200	 0.7180
T	 0.6350	 0.6780
U	 0.0030	 0.3280
V	 0.0340	 0.4920
W	 0.0980	 0.4460
X	 0.7390	 0.7060
Y	 0.5390	 0.6550
Z	 0.9830	 0.7810
a	 0.8620	 0.7510
b	 0.8970	 0.7610
c	 0.8850	 0.7540
d	 0.8380	 0.7280
e	 0.7350	 0.6940
f	 0.7040	 0.6870
g	 0.3370	 0.5810
h	 0.8410	 0.7390
i	 0.5790	 0.6840
j	 0.8320	 0.7330
k	 0.7390	 0.7150
l	 0.6230	 0.6720
m	 0.9330	 0.7690
n	 0.7860	 0.7160
o	 0.6120	 0.6610
p	 0.8230	 0.7190



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Chain	Atom inclusion	Q-score
q	 0.8980	 0.7610
r	 0.8770	 0.7450
s	 0.8980	 0.7490
t	 0.7550	 0.7170
u	 0.7950	 0.7210
v	 0.9510	 0.7790
w	 0.3970	 0.5910
x	 0.6240	 0.6430
y	 0.5960	 0.6890