



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:33 PM UTC

PDB ID : 9J1M / pdb_00009j1m
EMDB ID : EMD-61076
Title : KU13-bond Mycobacterium tuberculosis 70S ribosome
Authors : Nishihara, D.; Fujino, M.; Tanaka, Y.; Yokoyama, T.
Deposited on : 2024-08-05
Resolution : 2.33 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

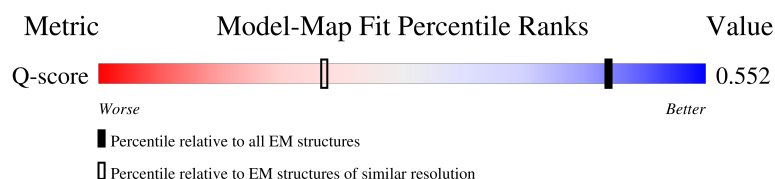
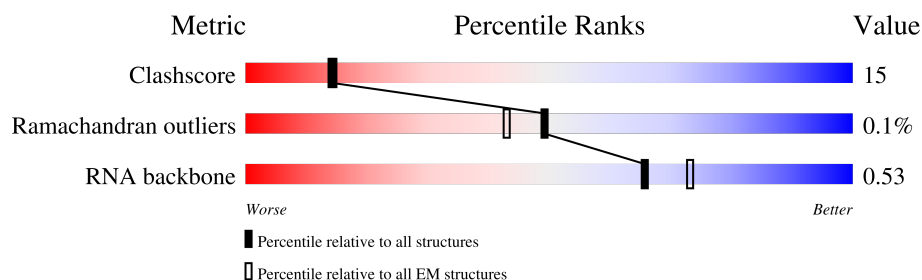
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.33 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	4434 (1.83 - 2.83)

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	57	7% 79% 16% 5%
2	1	55	58% 29% 13%
3	2	47	64% 30% 6%
4	3	64	70% 27% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	4	37	
6	7	24	
7	A	3138	
8	B	115	
9	C	280	
10	D	217	
11	E	223	
12	F	187	
13	G	179	
14	H	152	
15	J	195	
16	K	122	
17	L	146	
18	M	138	
19	N	180	
20	O	122	
21	P	113	
22	Q	129	
23	R	104	
24	S	197	
25	T	100	
26	U	105	
27	V	215	
28	W	86	
29	X	64	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	Y	77	
31	Z	65	
32	a	1537	
33	c	274	
34	d	201	
35	e	220	
36	f	96	
37	g	156	
38	h	132	
39	i	151	
40	j	101	
41	k	139	
42	l	124	
43	m	124	
44	n	61	
45	o	89	
46	p	162	
47	q	135	
48	r	84	
49	s	93	
50	t	86	
51	x	66	
52	u	3	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 139822 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	54	Total	C	N	O	0	0
			429	266	94	69		

- Molecule 2 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O	S	0	0
			400	245	84	67	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	44	Total	C	N	O	S	0	0
			374	222	97	54	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	62	Total	C	N	O	0	0
			494	298	112	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			300	182	66	47	5		

- Molecule 6 is a protein called 30S ribosomal protein THX.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	7	22	Total	C	N	O	0	0
			186	111	47	28		

- Molecule 7 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2904	Total	C	N	O	P	0	0
			62388	27811	11529	20144	2904		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	115	Total	C	N	O	P	0	0
			2458	1097	456	790	115		

- Molecule 9 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2088	1277	437	369	5		

- Molecule 10 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	213	Total	C	N	O	S	0	0
			1590	985	307	292	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	207	Total	C	N	O	S	0	0
			1552	958	303	289	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	178	Total	C	N	O	S	0	0
			1408	885	267	251	5		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	174	Total	C	N	O	S	0	0
			1330	836	249	244	1		

- Molecule 14 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	47	Total	C	N	O	S	0	0
			350	220	64	65	1		

- Molecule 15 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	146	Total	C	N	O	S	0	0
			1143	724	217	199	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	122	Total	C	N	O	S	0	0
			942	590	180	169	3		

- Molecule 17 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	144	Total	C	N	O	S	0	0
			1074	664	217	191	2		

- Molecule 18 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1072	679	215	177	1		

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	116	Total	C	N	O	S	0	0
			908	574	175	158	1		

- Molecule 20 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	119	Total	C	N	O	S	0	0
			905	552	191	162			

- Molecule 21 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	112	Total	C	N	O	S	0	0
			907	573	174	159	1		

- Molecule 22 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	124	Total	C	N	O		0	0
			993	616	207	170			

- Molecule 23 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	100	Total	C	N	O		0	0
			757	482	138	137			

- Molecule 24 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	113	Total	C	N	O		0	0
			860	533	178	149			

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	95	Total	C	N	O		0	0
			741	469	138	134			

- Molecule 26 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	90	Total	C	N	O	S	0	0
			699	430	138	129	2		

- Molecule 27 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	177	Total	C	N	O		0	0
			1319	822	243	254			

- Molecule 28 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	77	Total	C	N	O	0	0
			564	345	117	102		

- Molecule 29 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	62	Total	C	N	O	S	0	0
			468	284	100	80	4		

- Molecule 30 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	68	Total	C	N	O	S	0	0
			560	343	109	107	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Z	59	Total	C	N	O	0	0
			476	293	101	82		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1519	Total	C	N	O	P	0	0
			32620	14535	5961	10605	1519		

- Molecule 33 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	207	Total	C	N	O	S	0	0
			1654	1030	322	298	4		

- Molecule 34 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	200	Total	C	N	O	S	0	0
			1650	1036	316	296	2		

- Molecule 35 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	169	Total	C	N	O	S	0	0
			1222	770	231	218	3		

- Molecule 36 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	95	Total	C	N	O	S	0	0
			757	480	133	141	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	155	Total	C	N	O	S	0	0
			1230	768	241	219	2		

- Molecule 38 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	131	Total	C	N	O	S	0	0
			1006	631	188	186	1		

- Molecule 39 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	i	127	Total	C	N	O	0	0
			992	628	195	169		

- Molecule 40 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	99	Total	C	N	O	S	0	0
			789	496	146	144	3		

- Molecule 41 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	k	117	Total	C	N	O	0	0
			872	538	175	159		

- Molecule 42 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			959	594	197	166	2		

- Molecule 43 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	116	Total	C	N	O	S	0	0
			945	578	196	168	3		

- Molecule 44 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	60	Total	C	N	O	S	0	0
			468	294	96	73	5		

- Molecule 45 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	87	Total	C	N	O	S	0	0
			718	449	144	125			

- Molecule 46 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	93	Total	C	N	O	S	0	0
			745	474	143	128			

- Molecule 47 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	95	Total	C	N	O	S	0	0
			770	482	152	133	3		

- Molecule 48 is a protein called Small ribosomal subunit protein bS18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	64	Total	C	N	O	S	0	0
			506	315	98	90	3		

- Molecule 49 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	83	Total	C	N	O	S	0	0
			672	432	125	114	1		

- Molecule 50 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	85	Total	C	N	O		0	0
			652	394	141	117			

- Molecule 51 is a protein called Mitochondrial domain of uncharacterised function (DUF1713).

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 52 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	1	1	Total	Zn	0
			1	1	
53	4	1	Total	Zn	0
			1	1	
53	X	1	Total	Zn	0
			1	1	
53	n	1	Total	Zn	0
			1	1	
53	r	1	Total	Zn	0
			1	1	

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

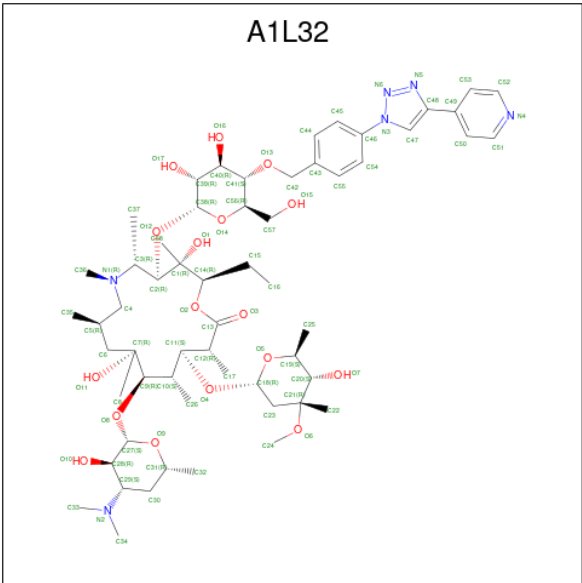
Mol	Chain	Residues	Atoms		AltConf
54	A	300	Total	Mg	0
			300	300	
54	B	5	Total	Mg	0
			5	5	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
54	C	2	2	2	0
54	D	1	1	1	0
54	L	1	1	1	0
54	U	1	1	1	0
54	a	129	129	129	0
54	r	1	1	1	0
54	u	1	1	1	0

- Molecule 55 is (2 {R},3 {R},4 {R},5 {R},8 {R},10 {R},11 {R},12 {S},13 {S},14 {R})-11-[(2 {S},3 {R},4 {S},6 {R})-4-(dimethylamino)-6-methyl-3-oxidanyl-oxan-2-yl]oxy-2-ethyl-4-[(2 {R},3 {R},4 {R},5 {S},6 {R})-6-(hydroxymethyl)-3,4-bis(oxidanyl)-5-[[4-(4-pyridin-4-yl-1,2,3-triazol-1-yl)phenyl]methoxy]oxan-2-yl]oxy-13-[(2 {R},4 {R},5 {S},6 {S})-4-methoxy-4,6-dimethyl-5-oxidanyl-oxan-2-yl]oxy-3,5,6,8,10,12,14-heptamethyl-3,10-bis(oxidanyl)-1-oxa-6-azacyclopentadecan-15-one (CCD ID: A1L32) (formula: C₅₈H₉₂N₆O₁₇) (labeled as "Ligand of Interest" by depositor).

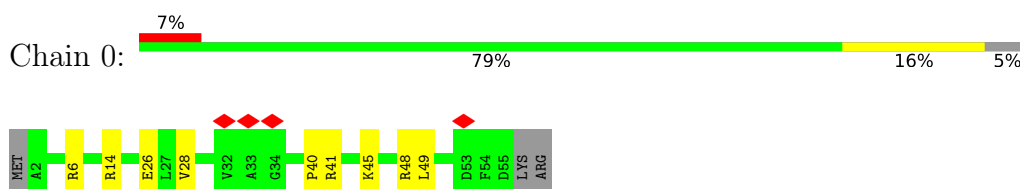


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
55	A	1	81	58	6	17	0

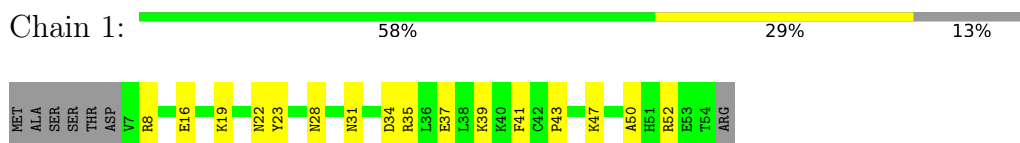
3 Residue-property plots [i](#)

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.

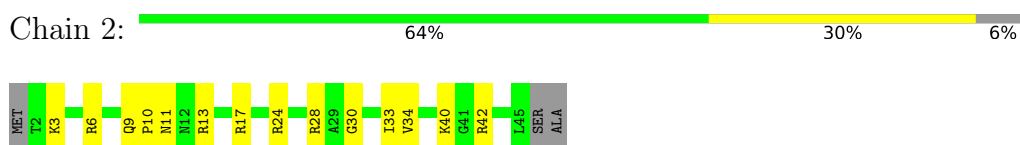
- Molecule 1: Large ribosomal subunit protein bL32



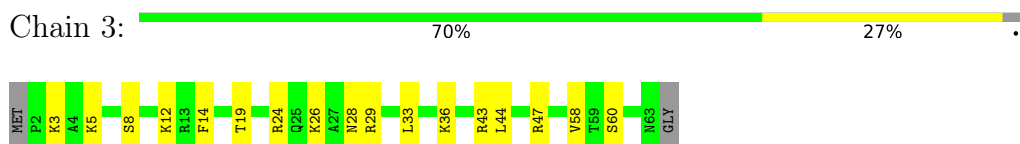
- Molecule 2: Large ribosomal subunit protein bL33A



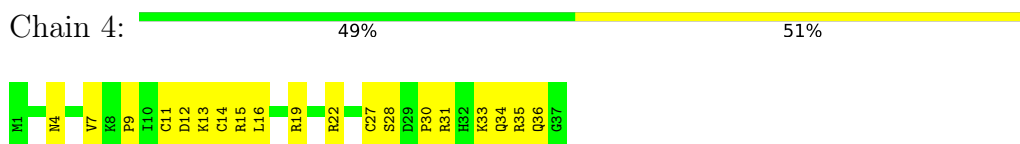
- Molecule 3: Large ribosomal subunit protein bL34



- Molecule 4: Large ribosomal subunit protein bL35



- Molecule 5: Large ribosomal subunit protein bL36



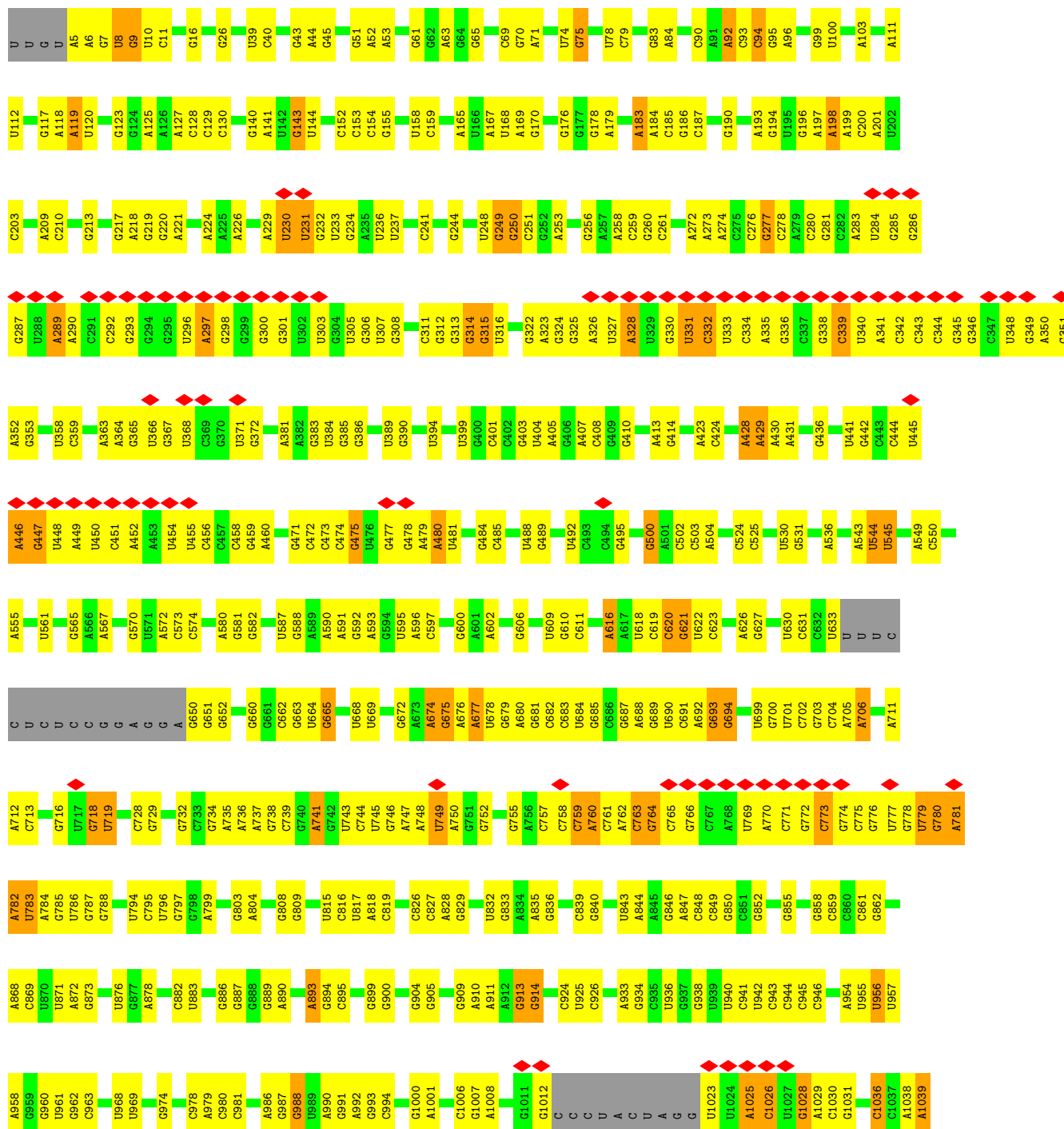
- Molecule 6: 30S ribosomal protein THX

Chain 7: 

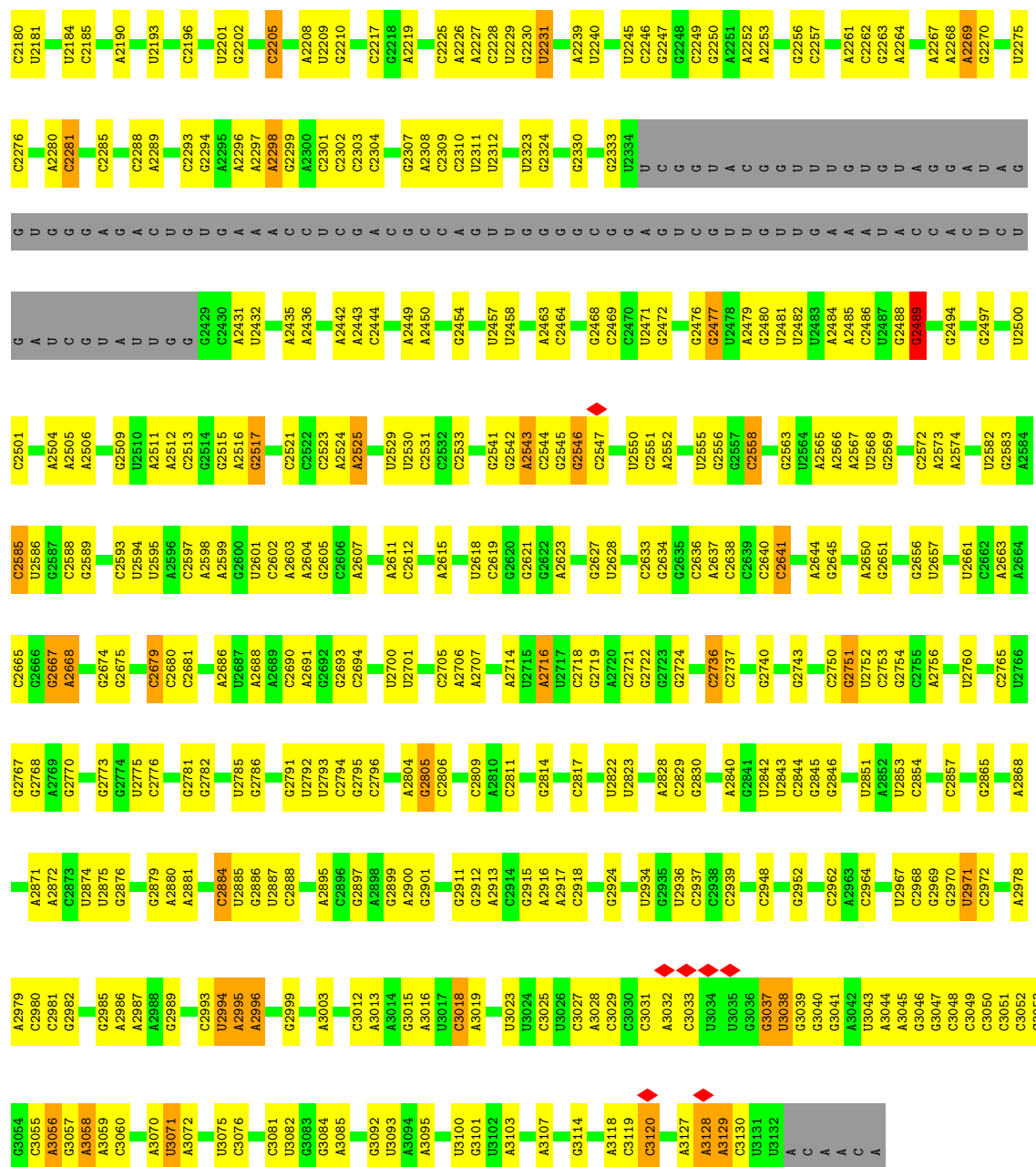


• Molecule 7: 23S rRNA

Chain A: 







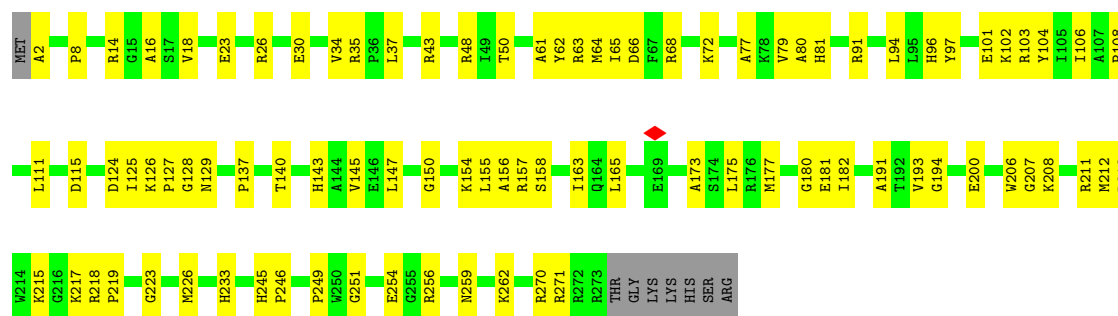
• Molecule 8: 5S rRNA

Chain B: 55% 36% 10%



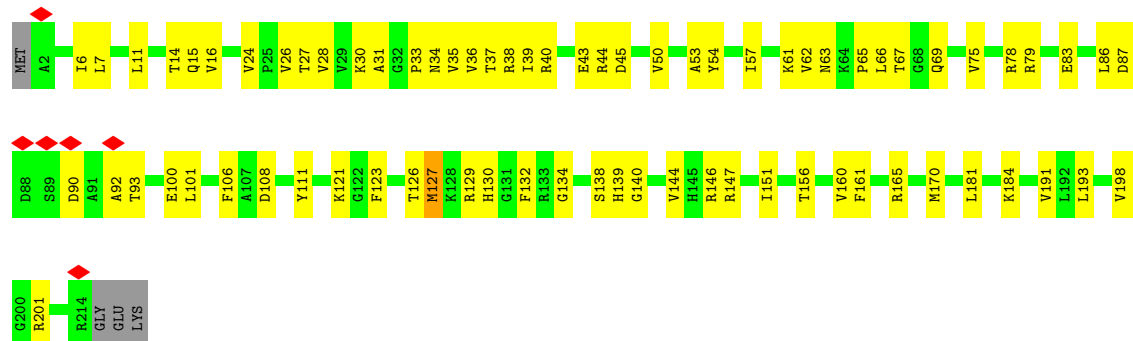
• Molecule 9: Large ribosomal subunit protein uL2

Chain C:  65% 32%



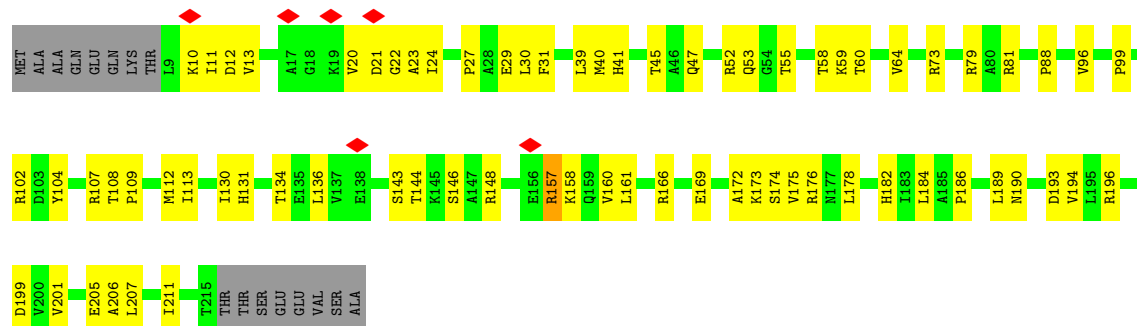
• Molecule 10: Large ribosomal subunit protein uL3

Chain D:  64% 34%



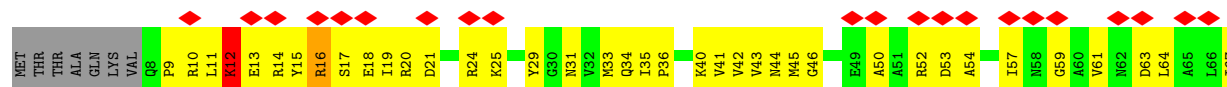
• Molecule 11: Large ribosomal subunit protein uL4

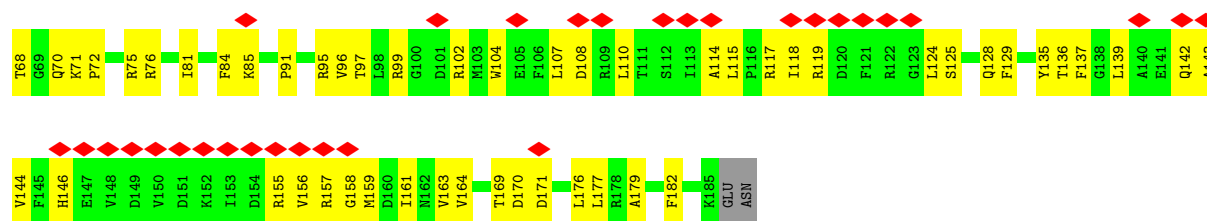
Chain E:  61% 32% 7%



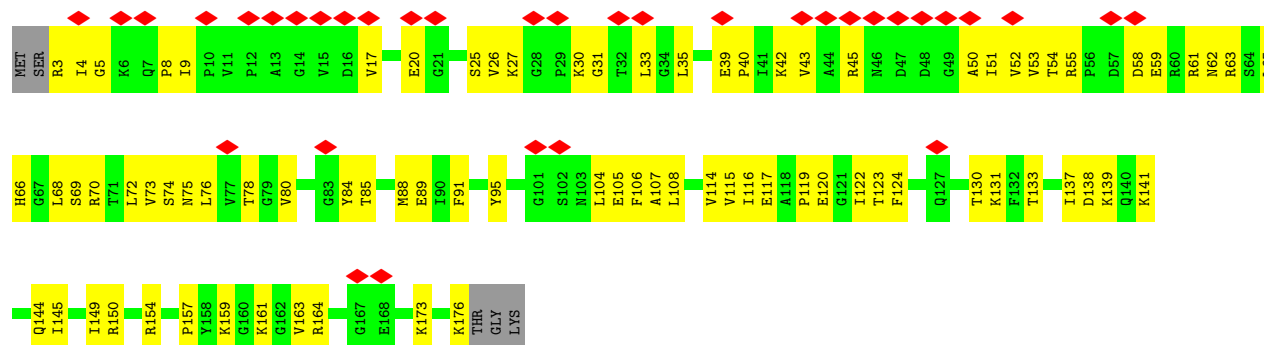
• Molecule 12: Large ribosomal subunit protein uL5

Chain F:  28% 48% 47% 5%

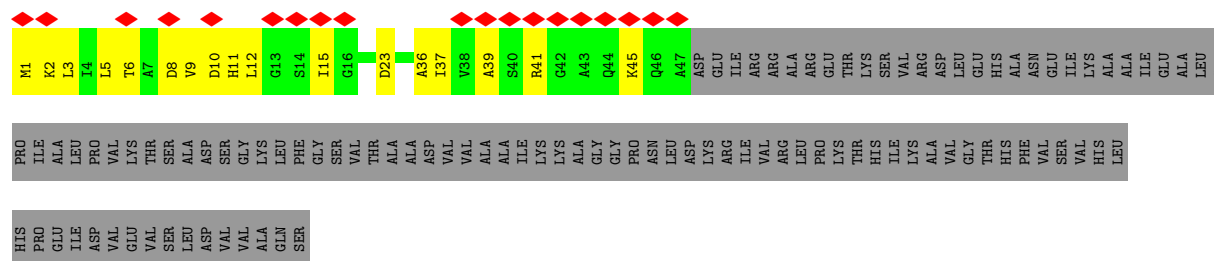




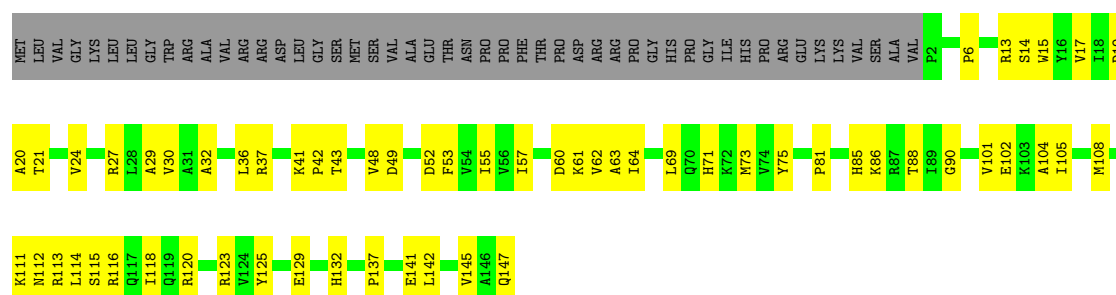
• Molecule 13: Large ribosomal subunit protein uL6



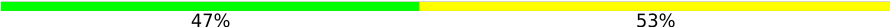
• Molecule 14: Large ribosomal subunit protein bL9

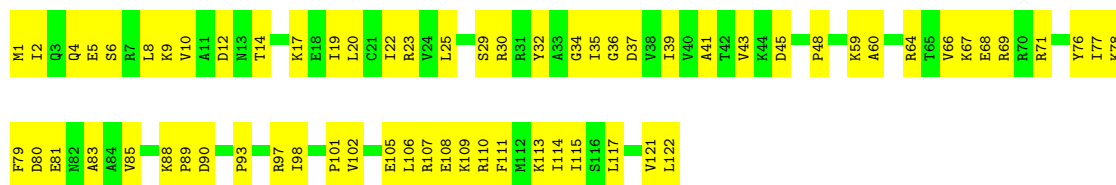


• Molecule 15: Large ribosomal subunit protein uL13



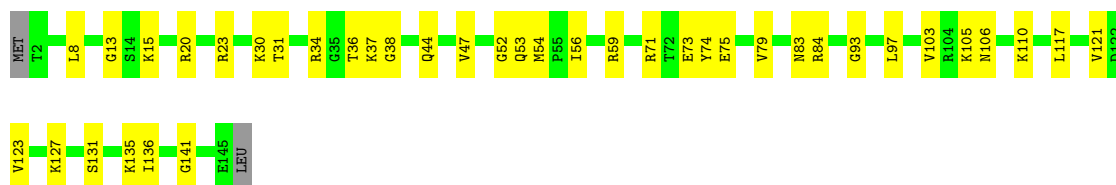
• Molecule 16: Large ribosomal subunit protein uL14

Chain K:  47% 53%



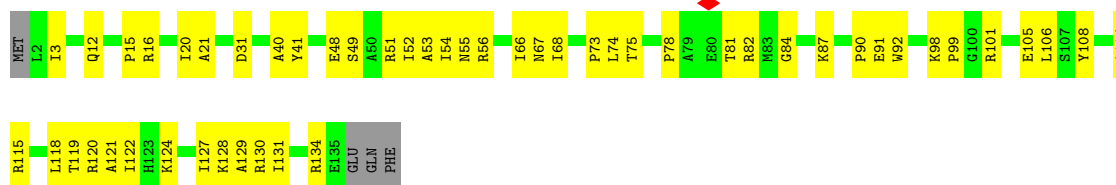
- Molecule 17: Large ribosomal subunit protein uL15

Chain L:  72% 27% .

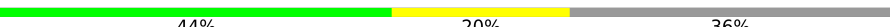


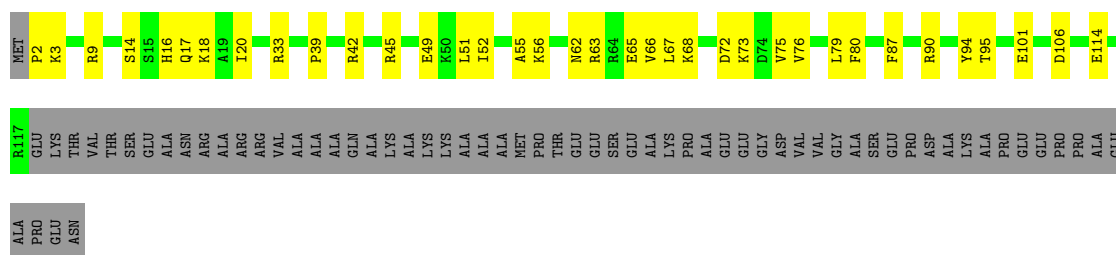
- Molecule 18: Large ribosomal subunit protein uL16

Chain M:  60% 37% .



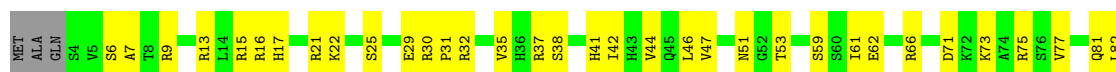
- Molecule 19: Large ribosomal subunit protein bL17

Chain N:  44% 20% 36%



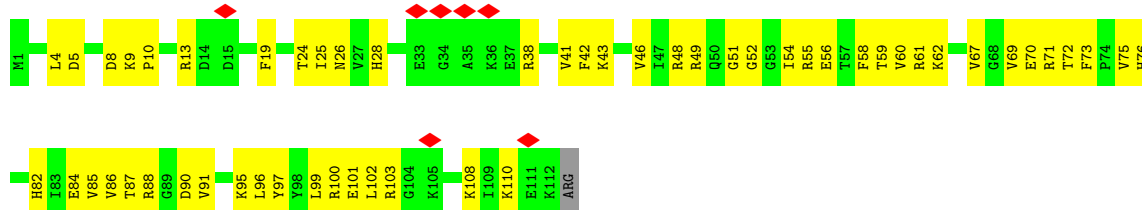
- Molecule 20: Large ribosomal subunit protein uL18

Chain O:  64% 34% .

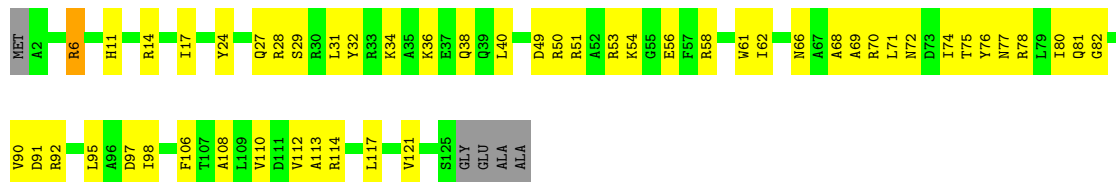




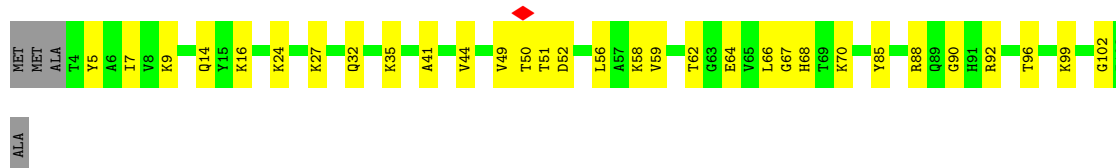
- Molecule 21: Large ribosomal subunit protein bL19



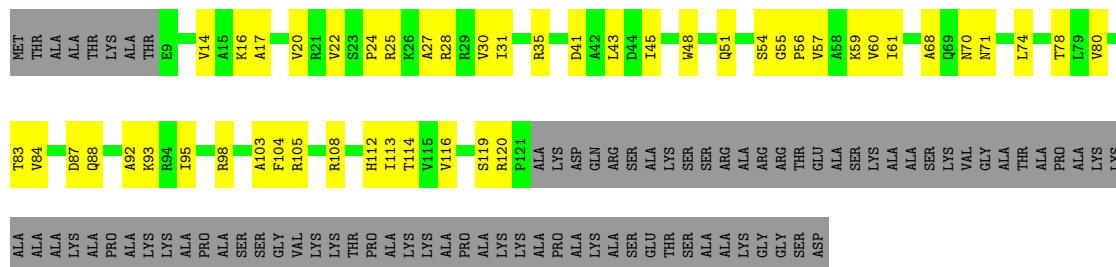
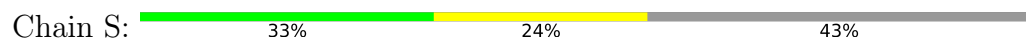
- Molecule 22: Large ribosomal subunit protein bL20



- Molecule 23: Large ribosomal subunit protein bL21

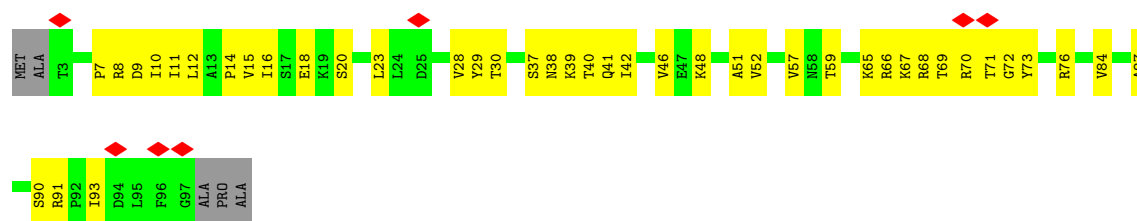


- Molecule 24: Large ribosomal subunit protein uL22

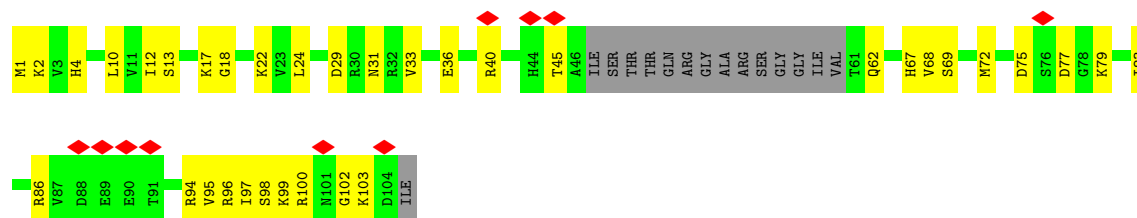


- Molecule 25: Large ribosomal subunit protein uL23

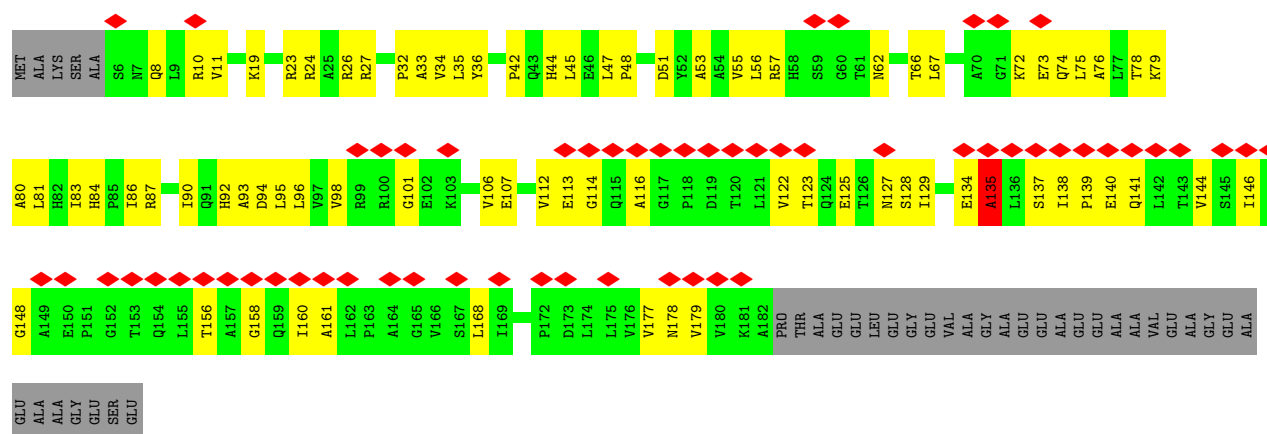




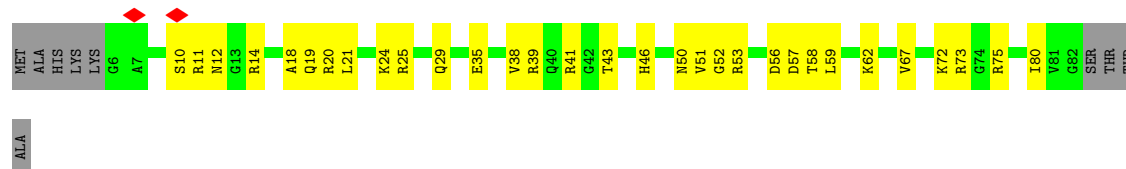
- Molecule 26: Large ribosomal subunit protein uL24



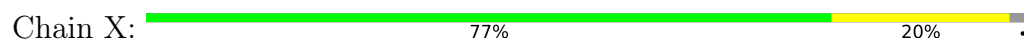
- Molecule 27: Large ribosomal subunit protein bL25



- Molecule 28: Large ribosomal subunit protein bL27

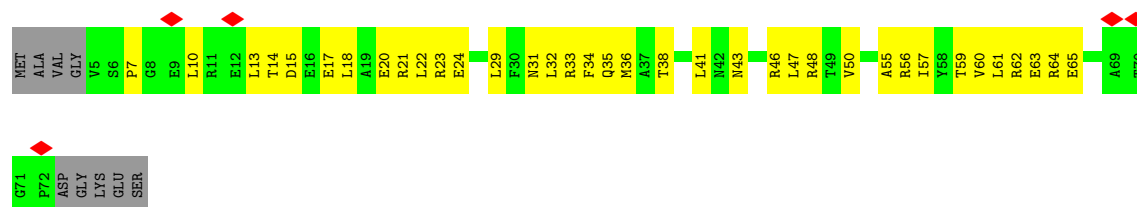


- Molecule 29: Large ribosomal subunit protein bL28

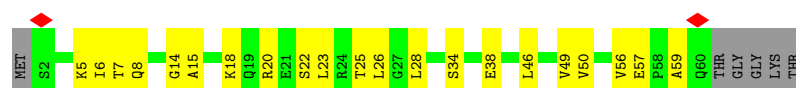




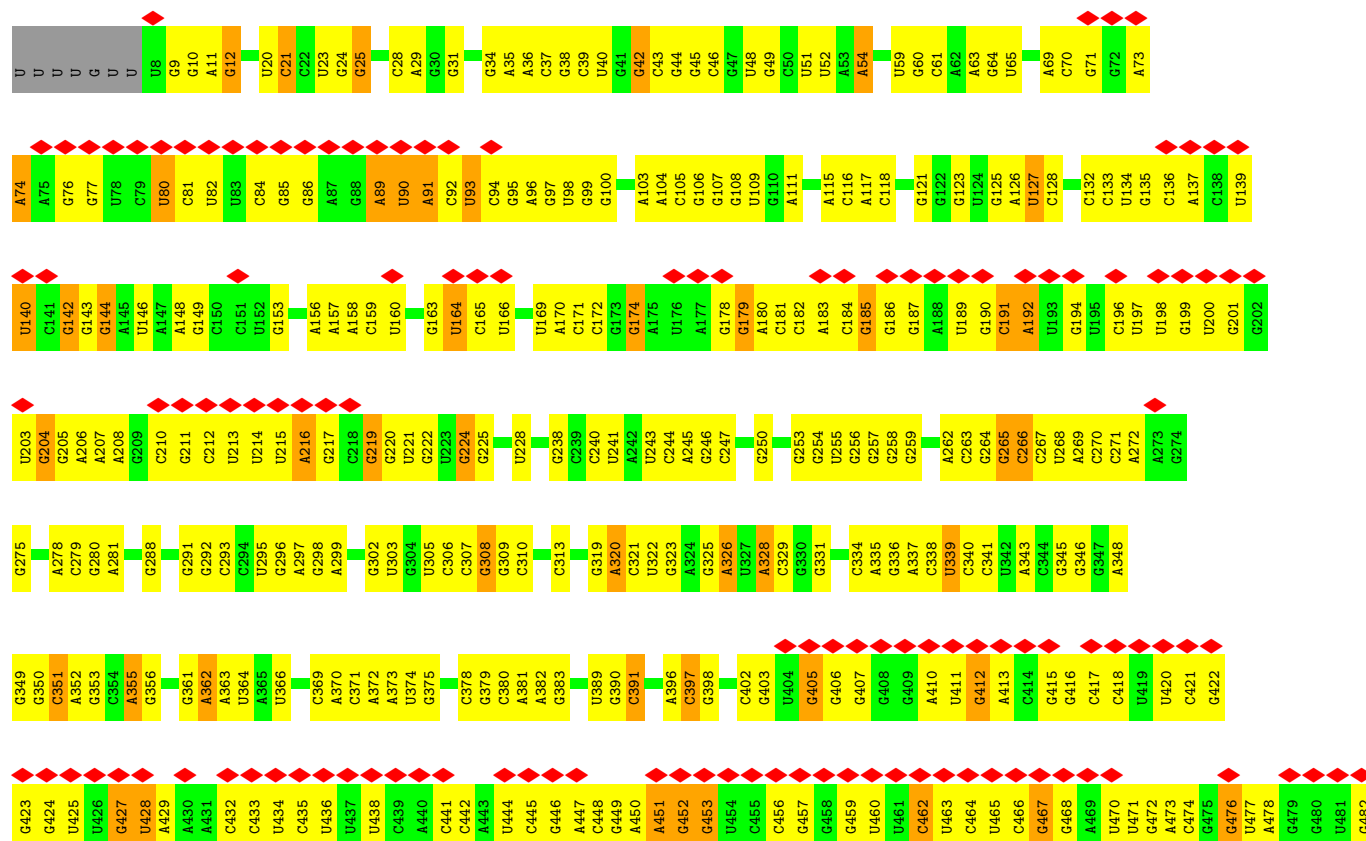
- Molecule 30: Large ribosomal subunit protein uL29

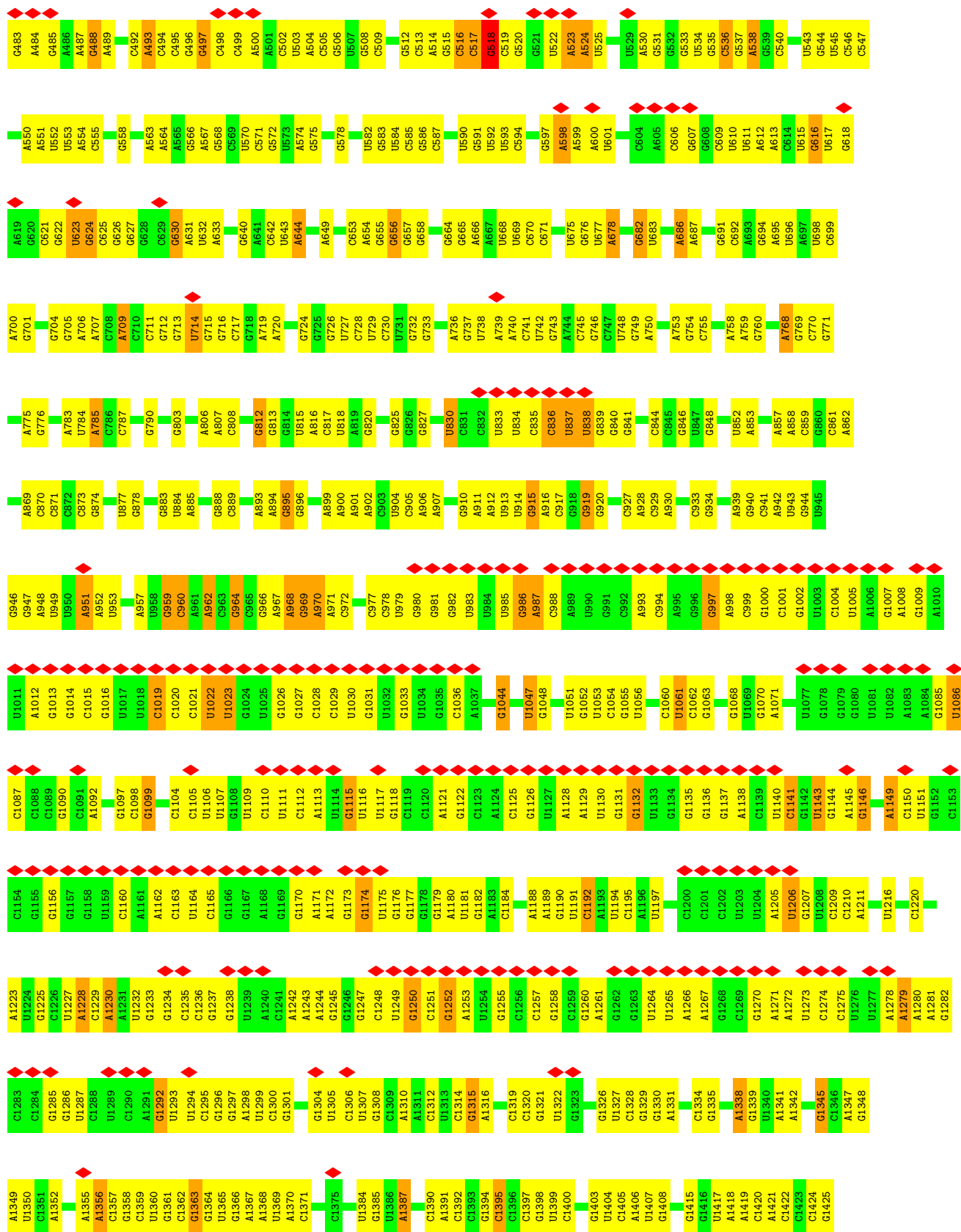


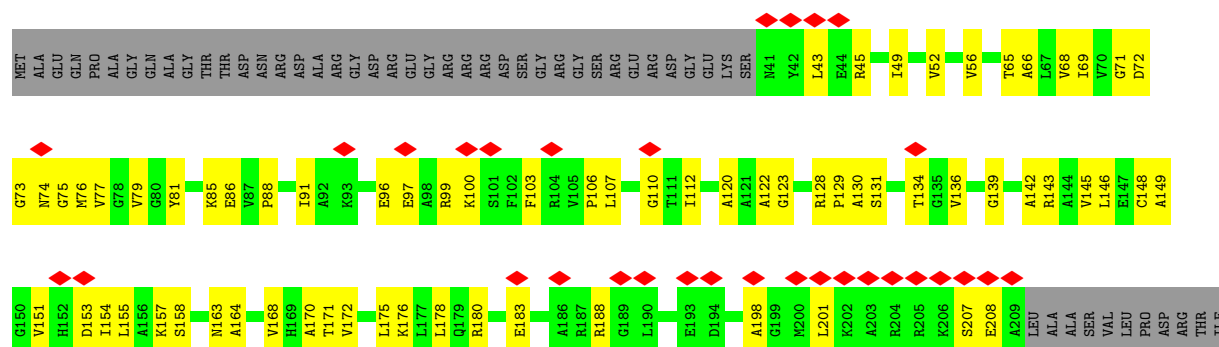
- Molecule 31: Large ribosomal subunit protein uL30



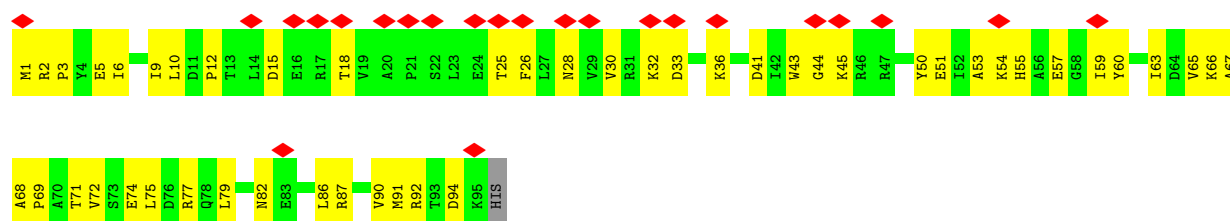
- Molecule 32: 16S rRNA



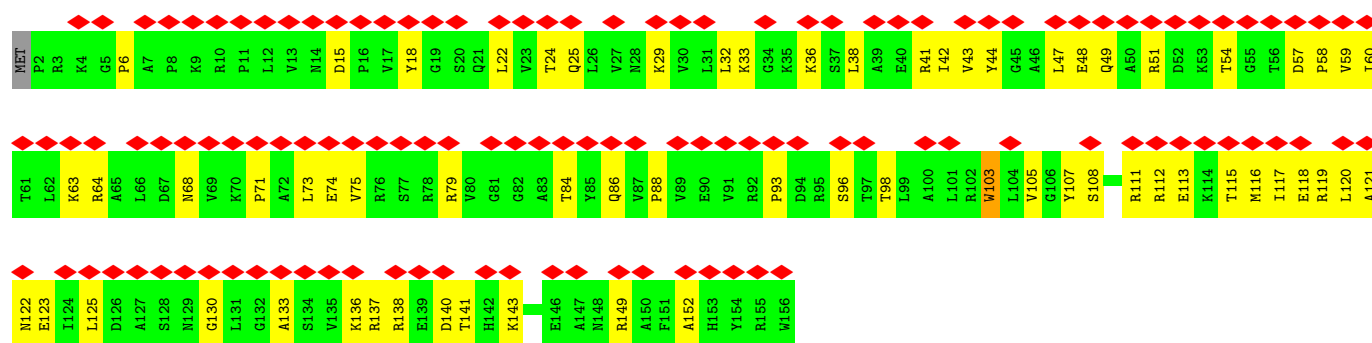
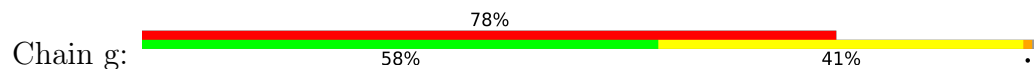




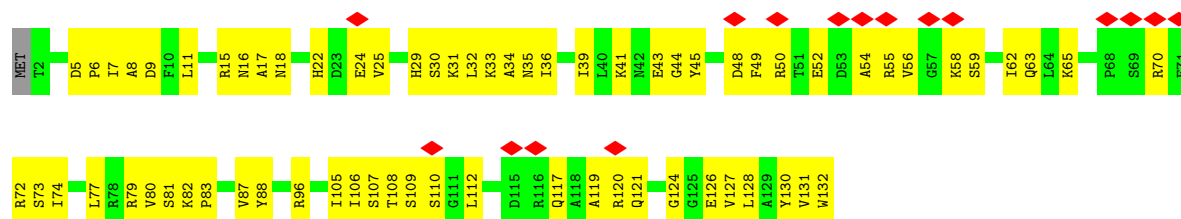
• Molecule 36: Small ribosomal subunit protein bS6



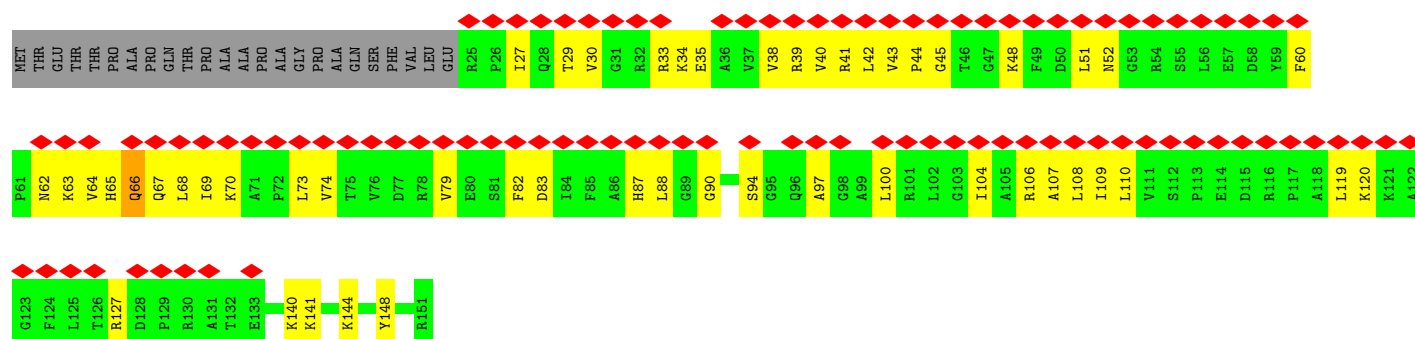
• Molecule 37: Small ribosomal subunit protein uS7



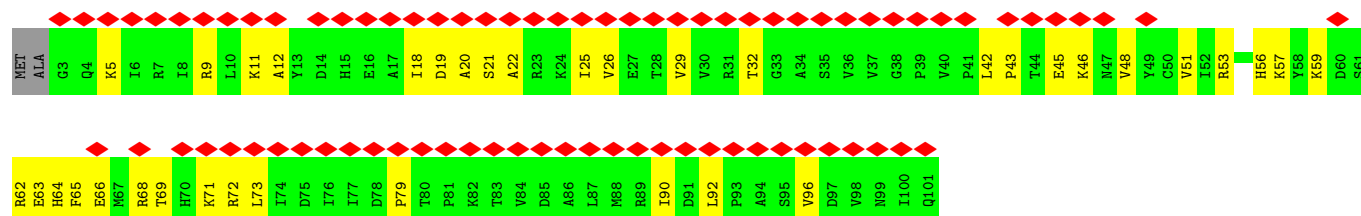
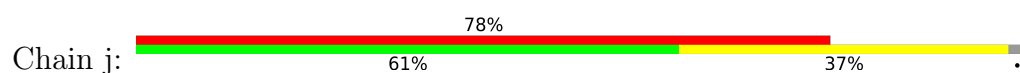
• Molecule 38: Small ribosomal subunit protein uS8



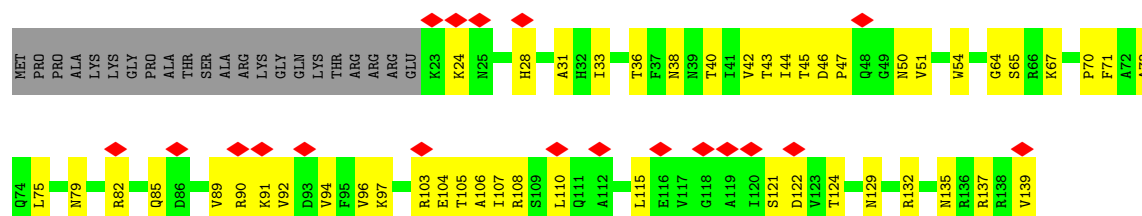
• Molecule 39: Small ribosomal subunit protein uS9



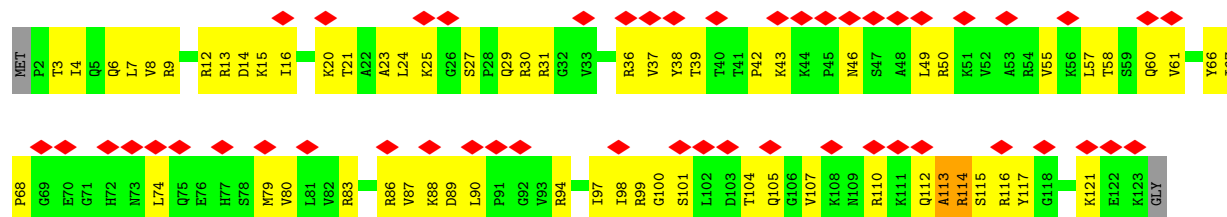
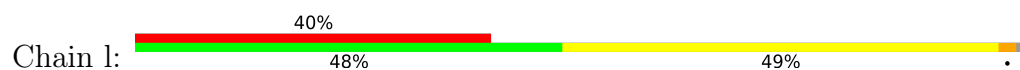
- Molecule 40: Small ribosomal subunit protein uS10



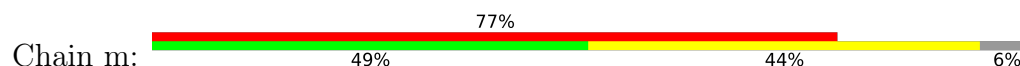
- Molecule 41: Small ribosomal subunit protein uS11

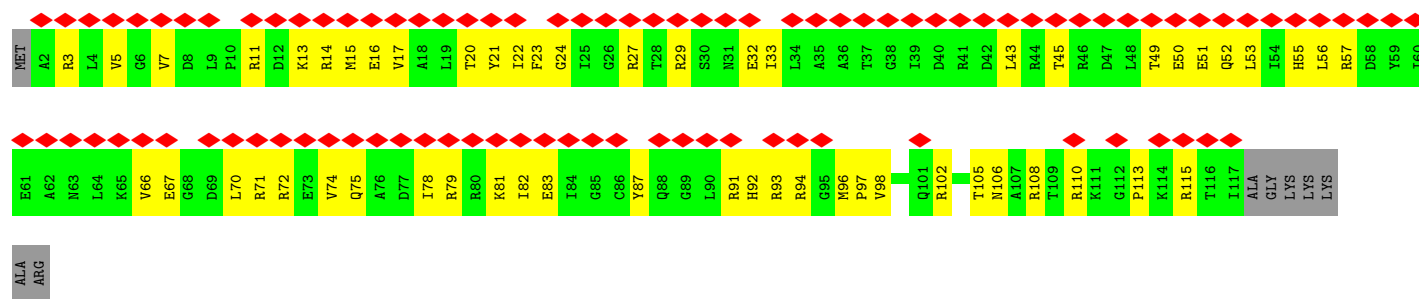


- Molecule 42: Small ribosomal subunit protein uS12

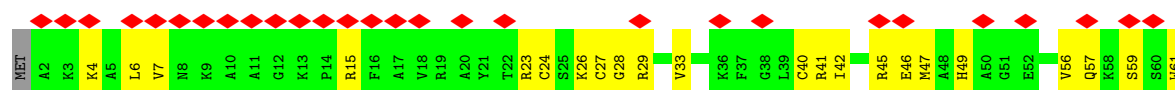


- Molecule 43: Small ribosomal subunit protein uS13

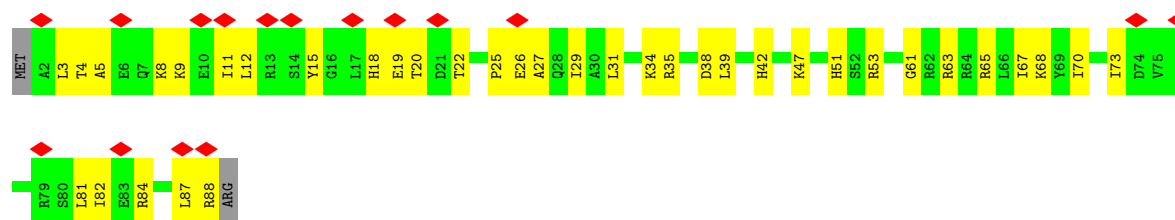




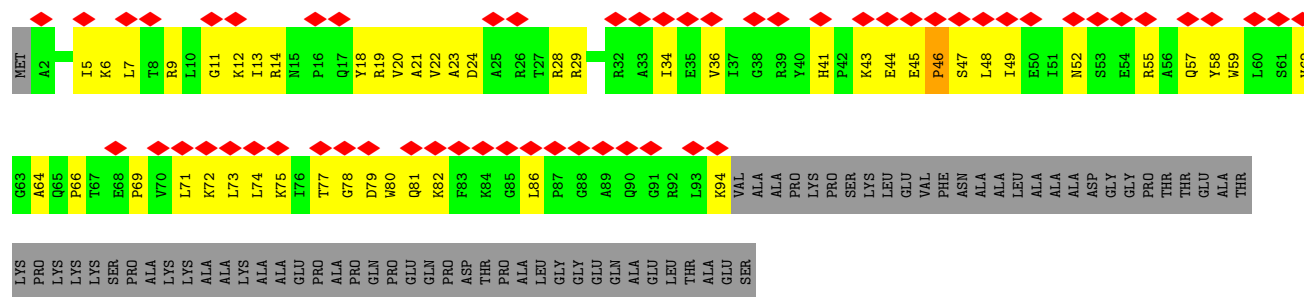
• Molecule 44: Small ribosomal subunit protein uS14B



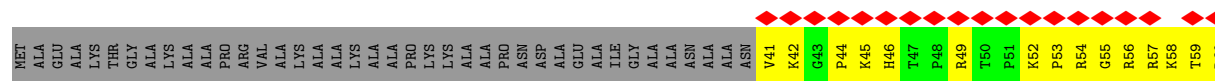
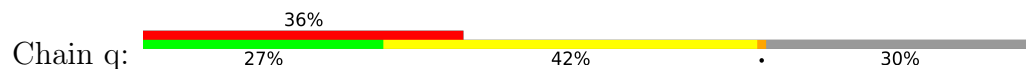
• Molecule 45: Small ribosomal subunit protein uS15

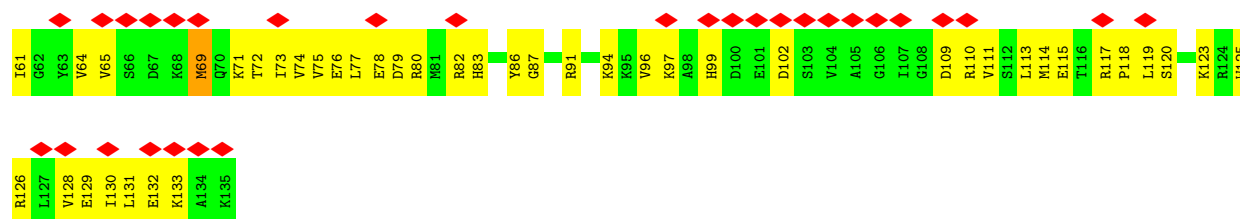


• Molecule 46: Small ribosomal subunit protein bS16

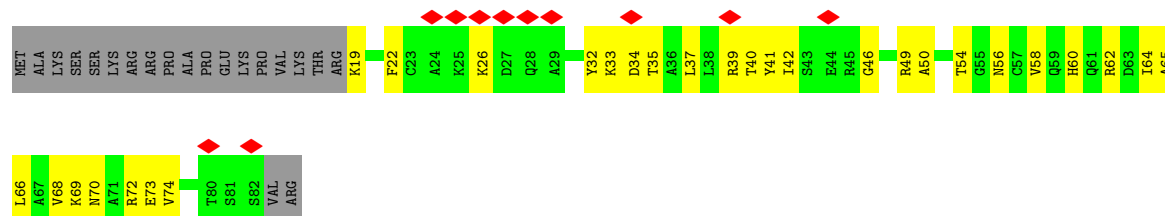
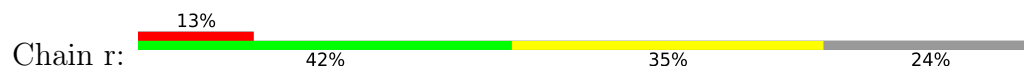


• Molecule 47: Small ribosomal subunit protein uS17

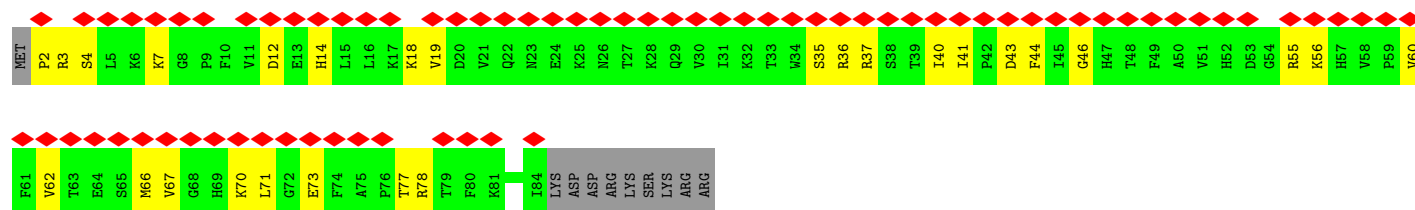
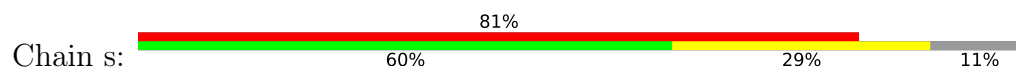




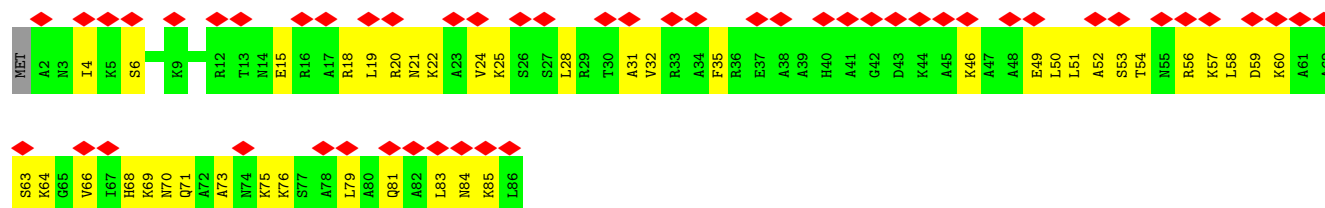
- Molecule 48: Small ribosomal subunit protein bS18A



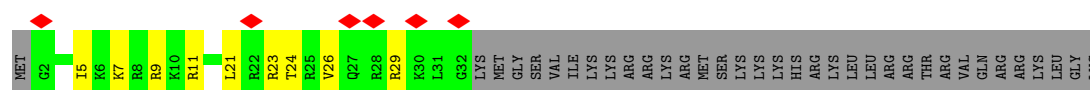
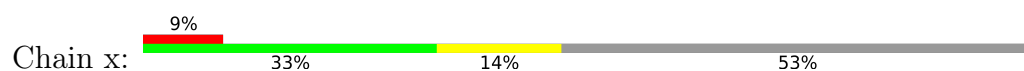
- Molecule 49: Small ribosomal subunit protein uS19



- Molecule 50: Small ribosomal subunit protein bS20



- Molecule 51: Mitochondrial domain of uncharacterised function (DUF1713)



- Molecule 52: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	205461	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.083	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0085	Depositor
Map size (Å)	403.456, 403.456, 403.456	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.788, 0.788, 0.788	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, 2MG, ZN, OMG, G7M, 5MC, 5MU, UR3, A1L32, MG, 4OC

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	0.27	0/435	0.47	0/581
2	1	0.31	0/407	0.51	0/543
3	2	0.28	0/377	0.53	0/494
4	3	0.25	0/499	0.45	0/664
5	4	0.23	0/304	0.48	0/402
6	7	0.33	0/188	0.59	0/243
7	A	0.27	0/69786	0.33	0/108882
8	B	0.22	0/2749	0.31	0/4284
9	C	0.29	0/2129	0.52	0/2861
10	D	0.30	0/1613	0.57	1/2174 (0.0%)
11	E	0.27	0/1575	0.53	0/2129
12	F	0.60	5/1429 (0.3%)	0.67	3/1921 (0.2%)
13	G	0.22	0/1351	0.55	0/1824
14	H	0.21	0/353	0.59	0/474
15	J	0.31	0/1170	0.49	0/1584
16	K	0.33	0/952	0.55	0/1278
17	L	0.28	0/1087	0.52	0/1452
18	M	0.29	0/1098	0.53	0/1481
19	N	0.27	0/925	0.52	0/1242
20	O	0.26	0/914	0.57	0/1228
21	P	0.26	0/922	0.51	0/1236
22	Q	0.31	0/1006	0.55	0/1349
23	R	0.32	0/766	0.58	0/1030
24	S	0.29	0/874	0.50	0/1186
25	T	0.28	0/751	0.57	0/1012
26	U	0.24	0/705	0.56	0/941
27	V	0.26	0/1336	0.50	0/1820
28	W	0.29	0/569	0.46	0/757
29	X	0.27	0/476	0.45	0/638
30	Y	0.26	0/564	0.60	0/756
31	Z	0.25	0/480	0.51	0/645
32	a	0.16	0/36331	0.27	0/56686

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.23	0/1678	0.55	0/2254
34	d	0.23	1/1683 (0.1%)	0.47	1/2269 (0.0%)
35	e	0.21	0/1238	0.48	0/1673
36	f	0.25	0/767	0.52	0/1036
37	g	0.38	2/1250 (0.2%)	0.58	0/1686
38	h	0.25	0/1021	0.54	0/1379
39	i	0.18	0/1010	0.50	0/1356
40	j	0.16	0/803	0.49	0/1086
41	k	0.23	0/890	0.57	0/1204
42	l	0.25	0/970	0.53	0/1295
43	m	0.21	0/953	0.53	0/1274
44	n	0.19	0/477	0.48	0/634
45	o	0.24	0/727	0.63	0/973
46	p	0.20	0/759	0.59	0/1022
47	q	0.26	0/782	0.59	0/1045
48	r	0.22	0/511	0.59	0/685
49	s	0.15	0/690	0.36	0/928
50	t	0.21	0/654	0.61	0/867
51	x	0.17	0/271	0.41	0/348
52	u	0.17	0/68	0.39	0/103
All	All	0.25	8/151323 (0.0%)	0.38	5/226914 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
11	E	0	1
12	F	0	1
22	Q	0	1
23	R	0	1
27	V	0	1
33	c	0	1
39	i	0	1
42	l	0	1
47	q	0	1
All	All	0	9

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	F	16	ARG	CZ-NH2	-15.12	1.13	1.33
37	g	103	TRP	CZ2-CH2	-7.94	1.22	1.37
12	F	12	LYS	CA-CB	7.34	1.65	1.53
12	F	16	ARG	CZ-NH1	-6.45	1.23	1.32
34	d	32	PRO	CA-C	5.34	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	F	16	ARG	NE-CZ-NH1	8.52	130.02	121.50
12	F	16	ARG	NH1-CZ-NH2	-7.63	109.39	119.30
12	F	12	LYS	CB-CA-C	7.44	122.66	110.90
34	d	32	PRO	O-C-N	5.18	123.59	121.15
10	D	127	MET	CB-CG-SD	-5.14	97.29	112.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	E	157	ARG	Peptide
12	F	12	LYS	Mainchain
22	Q	6	ARG	Sidechain
23	R	50	THR	Peptide
27	V	135	ALA	Peptide

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	0	429	0	465	8	0
2	1	400	0	409	14	0
3	2	374	0	410	12	0
4	3	494	0	533	15	0
5	4	300	0	323	21	0
6	7	186	0	202	11	0
7	A	62388	0	31426	996	0
8	B	2458	0	1253	48	0
9	C	2088	0	2123	77	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	D	1590	0	1632	71	0
11	E	1552	0	1593	58	0
12	F	1408	0	1449	114	0
13	G	1330	0	1390	86	0
14	H	350	0	367	15	0
15	J	1143	0	1173	56	0
16	K	942	0	1005	67	0
17	L	1074	0	1132	34	0
18	M	1072	0	1115	52	0
19	N	908	0	956	25	0
20	O	905	0	943	41	0
21	P	907	0	947	48	0
22	Q	993	0	1040	47	0
23	R	757	0	817	31	0
24	S	860	0	903	32	0
25	T	741	0	792	38	0
26	U	699	0	738	33	0
27	V	1319	0	1365	67	0
28	W	564	0	584	35	0
29	X	468	0	480	12	0
30	Y	560	0	570	31	0
31	Z	476	0	509	17	0
32	a	32620	0	16427	790	0
33	c	1654	0	1694	81	0
34	d	1650	0	1671	108	0
35	e	1222	0	1291	65	0
36	f	757	0	796	46	0
37	g	1230	0	1288	74	0
38	h	1006	0	1041	72	0
39	i	992	0	1052	49	0
40	j	789	0	821	40	0
41	k	872	0	880	42	0
42	l	959	0	1045	78	0
43	m	945	0	992	58	0
44	n	468	0	492	23	0
45	o	718	0	760	30	0
46	p	745	0	788	55	0
47	q	770	0	833	78	0
48	r	506	0	527	25	0
49	s	672	0	690	26	0
50	t	652	0	703	48	0
51	x	271	0	329	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	u	62	0	34	0	0
53	1	1	0	0	0	0
53	4	1	0	0	0	0
53	X	1	0	0	0	0
53	n	1	0	0	0	0
53	r	1	0	0	0	0
54	A	300	0	0	0	0
54	B	5	0	0	0	0
54	C	2	0	0	0	0
54	D	1	0	0	0	0
54	L	1	0	0	0	0
54	U	1	0	0	0	0
54	a	129	0	0	0	0
54	r	1	0	0	0	0
54	u	1	0	0	0	0
55	A	81	0	0	0	0
All	All	139822	0	92798	3538	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 15.

The worst 5 of 3538 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)
7:A:2177:5MU:C5	7:A:2177:5MU:C4	1.79	1.61
12:F:12:LYS:C	12:F:16:ARG:HH21	1.31	1.37
12:F:12:LYS:HG3	12:F:16:ARG:NH2	1.54	1.22
15:J:73:MET:HE2	15:J:86:LYS:HD2	1.17	1.15
12:F:15:TYR:HA	12:F:19:ILE:HD13	1.20	1.11

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/57 (91%)	52 (100%)	0	0	100	100
2	1	46/55 (84%)	45 (98%)	1 (2%)	0	100	100
3	2	42/47 (89%)	41 (98%)	1 (2%)	0	100	100
4	3	60/64 (94%)	60 (100%)	0	0	100	100
5	4	35/37 (95%)	35 (100%)	0	0	100	100
6	7	20/24 (83%)	19 (95%)	1 (5%)	0	100	100
9	C	270/280 (96%)	254 (94%)	16 (6%)	0	100	100
10	D	211/217 (97%)	196 (93%)	15 (7%)	0	100	100
11	E	205/223 (92%)	201 (98%)	4 (2%)	0	100	100
12	F	176/187 (94%)	158 (90%)	18 (10%)	0	100	100
13	G	172/179 (96%)	159 (92%)	13 (8%)	0	100	100
14	H	45/152 (30%)	39 (87%)	6 (13%)	0	100	100
15	J	144/195 (74%)	141 (98%)	3 (2%)	0	100	100
16	K	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
17	L	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
18	M	132/138 (96%)	122 (92%)	10 (8%)	0	100	100
19	N	114/180 (63%)	112 (98%)	2 (2%)	0	100	100
20	O	117/122 (96%)	113 (97%)	4 (3%)	0	100	100
21	P	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
22	Q	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
23	R	98/104 (94%)	92 (94%)	6 (6%)	0	100	100
24	S	111/197 (56%)	110 (99%)	1 (1%)	0	100	100
25	T	93/100 (93%)	90 (97%)	3 (3%)	0	100	100
26	U	86/105 (82%)	79 (92%)	7 (8%)	0	100	100
27	V	175/215 (81%)	153 (87%)	21 (12%)	1 (1%)	21	22
28	W	75/86 (87%)	71 (95%)	4 (5%)	0	100	100
29	X	60/64 (94%)	57 (95%)	3 (5%)	0	100	100
30	Y	66/77 (86%)	64 (97%)	2 (3%)	0	100	100
31	Z	57/65 (88%)	55 (96%)	2 (4%)	0	100	100
33	c	205/274 (75%)	187 (91%)	18 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	d	198/201 (98%)	179 (90%)	19 (10%)	0	100	100
35	e	167/220 (76%)	155 (93%)	12 (7%)	0	100	100
36	f	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
37	g	153/156 (98%)	147 (96%)	6 (4%)	0	100	100
38	h	129/132 (98%)	120 (93%)	9 (7%)	0	100	100
39	i	125/151 (83%)	110 (88%)	15 (12%)	0	100	100
40	j	97/101 (96%)	88 (91%)	9 (9%)	0	100	100
41	k	115/139 (83%)	111 (96%)	4 (4%)	0	100	100
42	l	120/124 (97%)	96 (80%)	23 (19%)	1 (1%)	16	16
43	m	114/124 (92%)	104 (91%)	10 (9%)	0	100	100
44	n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
45	o	85/89 (96%)	77 (91%)	7 (8%)	1 (1%)	10	8
46	p	91/162 (56%)	82 (90%)	8 (9%)	1 (1%)	11	10
47	q	93/135 (69%)	79 (85%)	14 (15%)	0	100	100
48	r	62/84 (74%)	60 (97%)	2 (3%)	0	100	100
49	s	81/93 (87%)	73 (90%)	8 (10%)	0	100	100
50	t	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
51	x	29/66 (44%)	26 (90%)	3 (10%)	0	100	100
All	All	5254/6174 (85%)	4918 (94%)	332 (6%)	4 (0%)	49	57

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	l	114	ARG
27	V	135	ALA
45	o	19	GLU
46	p	46	PRO

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1518/1537 (98%)	254 (16%)	0
52	u	2/3 (66%)	1 (50%)	0
7	A	2899/3138 (92%)	377 (13%)	4 (0%)
8	B	114/115 (99%)	19 (16%)	0
All	All	4533/4793 (94%)	651 (14%)	4 (0%)

5 of 651 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	8	U
7	A	9	G
7	A	10	U
7	A	11	C
7	A	43	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	759	C
7	A	763	C
7	A	913	G
7	A	2994	U

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

10 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	$\# Z > 2$
32	5MC	a	960	32	19,22,23	4.25	9 (47%)	26,32,35	1.03	2 (7%)
7	OMG	A	2791	7	23,26,27	2.40	9 (39%)	32,38,41	2.02	9 (28%)
32	2MG	a	959	32	23,26,27	2.87	8 (34%)	33,38,41	2.33	12 (36%)
7	5MU	A	2177	7	19,22,23	7.29	8 (42%)	27,32,35	3.59	10 (37%)
32	MA6	a	1512	32	23,26,27	1.38	4 (17%)	33,38,41	4.37	13 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	4OC	a	1395	32	20,23,24	3.11	8 (40%)	25,32,35	0.99	1 (4%)
32	MA6	a	1511	32	23,26,27	1.42	4 (17%)	33,38,41	4.29	13 (39%)
7	OMG	A	2489	52,7	23,26,27	2.41	8 (34%)	32,38,41	2.03	9 (28%)
32	UR3	a	1491	32	19,22,23	2.77	8 (42%)	26,32,35	1.60	3 (11%)
32	G7M	a	518	32	23,26,27	2.88	9 (39%)	34,39,42	1.80	9 (26%)

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
32	5MC	a	960	32	-	0/7/25/26	0/2/2/2
7	OMG	A	2791	7	-	1/9/27/28	0/3/3/3
32	2MG	a	959	32	-	2/9/27/28	0/3/3/3
7	5MU	A	2177	7	-	0/7/25/26	0/2/2/2
32	MA6	a	1512	32	-	2/11/29/30	0/3/3/3
32	4OC	a	1395	32	-	1/9/29/30	0/2/2/2
32	MA6	a	1511	32	-	2/11/29/30	0/3/3/3
7	OMG	A	2489	52,7	-	3/9/27/28	0/3/3/3
32	UR3	a	1491	32	-	0/7/25/26	0/2/2/2
32	G7M	a	518	32	-	0/7/25/26	0/3/3/3

The worst 5 of 75 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	2177	5MU	C4-C5	21.34	1.79	1.44
7	A	2177	5MU	C6-N1	16.32	1.65	1.38
7	A	2177	5MU	C4-N3	-10.98	1.18	1.38
7	A	2177	5MU	C6-C5	-10.74	1.17	1.34
32	a	960	5MC	C6-C5	9.42	1.50	1.34

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	1512	MA6	N1-C6-N6	-15.73	97.69	116.86
32	a	1511	MA6	N1-C6-N6	-15.06	98.50	116.86
32	a	1512	MA6	C5-C6-N6	10.84	142.48	125.33
7	A	2177	5MU	C5-C4-N3	10.58	124.52	115.32
32	a	1511	MA6	C5-C6-N6	10.49	141.94	125.33

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2489	OMG	O4'-C4'-C5'-O5'
7	A	2489	OMG	C1'-C2'-O2'-CM2
32	a	959	2MG	O4'-C4'-C5'-O5'
32	a	959	2MG	C3'-C4'-C5'-O5'
7	A	2489	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	a	960	5MC	2	0
7	A	2177	5MU	2	0
32	a	1512	MA6	1	0
32	a	1395	4OC	1	0
32	a	1511	MA6	1	0
7	A	2489	OMG	2	0
32	a	518	G7M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 447 ligands modelled in this entry, 446 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
55	A1L32	A	3501	-	87,87,87	2.45	18 (20%)	128,130,130	1.73	28 (21%)

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
55	A1L32	A	3501	-	-	21/91/146/146	0/7/7/7

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	A	3501	A1L32	C45-C44	10.32	1.55	1.38
55	A	3501	A1L32	C55-C43	7.87	1.54	1.38
55	A	3501	A1L32	C54-C46	7.46	1.53	1.39
55	A	3501	A1L32	O2-C13	6.24	1.48	1.34
55	A	3501	A1L32	C48-N5	6.07	1.48	1.36

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	A	3501	A1L32	C46-N3-C47	-6.34	119.96	129.12
55	A	3501	A1L32	C47-N3-N6	6.04	117.50	110.31
55	A	3501	A1L32	O2-C13-C12	3.99	120.06	111.53
55	A	3501	A1L32	C1-C2-C3	-3.92	107.01	115.80
55	A	3501	A1L32	O12-C2-C1	3.84	110.97	106.40

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

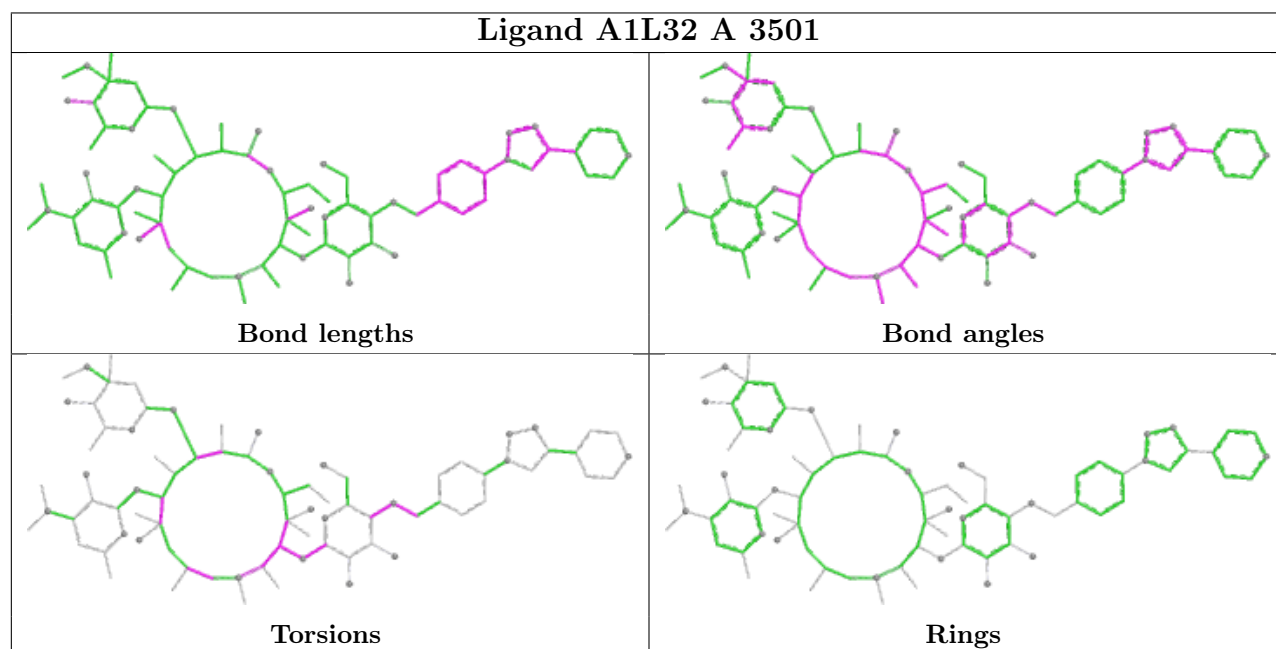
Mol	Chain	Res	Type	Atoms
55	A	3501	A1L32	C2-C3-N1-C4
55	A	3501	A1L32	C37-C3-N1-C4
55	A	3501	A1L32	C2-C3-N1-C36
55	A	3501	A1L32	C37-C3-N1-C36
55	A	3501	A1L32	N1-C4-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

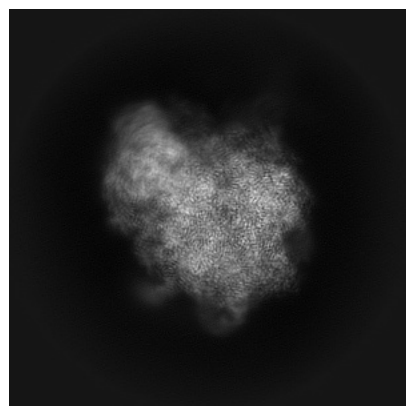
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61076. These allow visual inspection of the internal detail of the map and identification of artifacts.

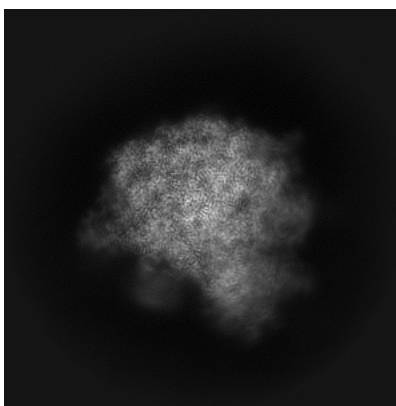
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

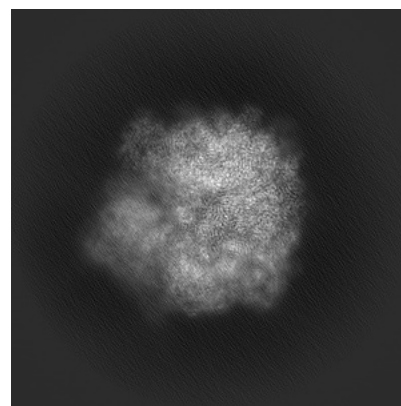
6.1.1 Primary map



X

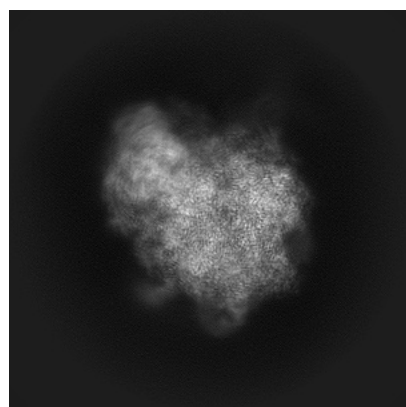


Y

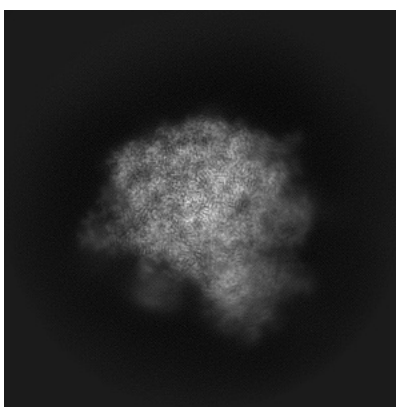


Z

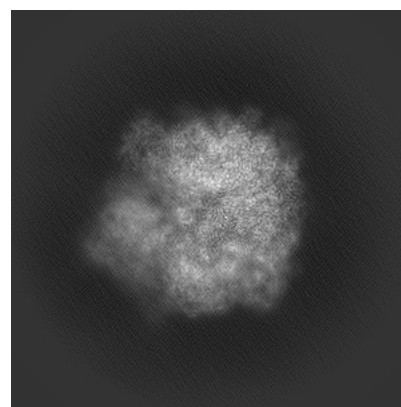
6.1.2 Raw map



X



Y

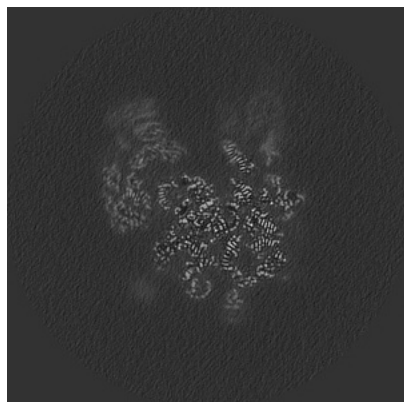


Z

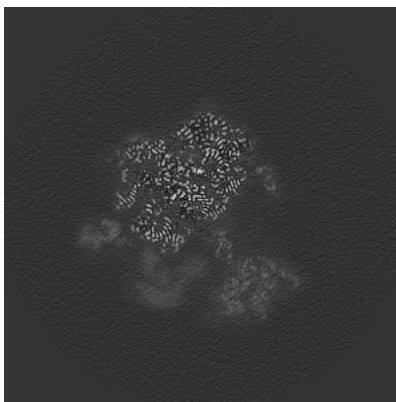
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

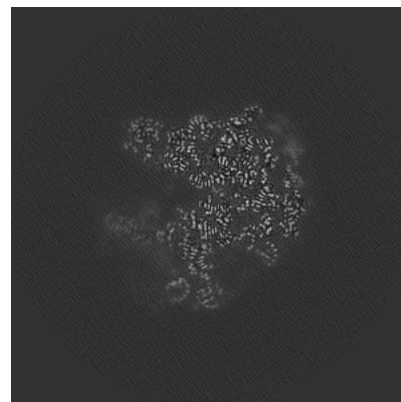
6.2.1 Primary map



X Index: 256

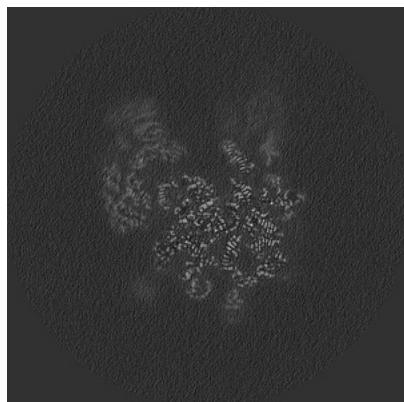


Y Index: 256

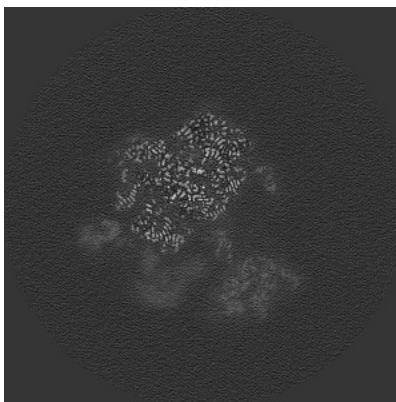


Z Index: 256

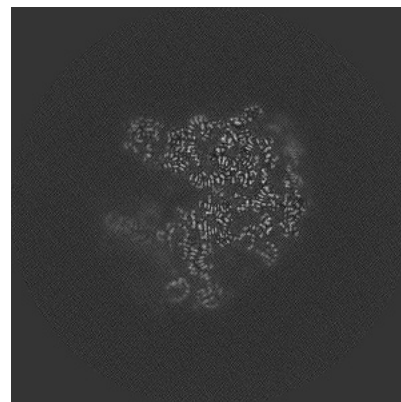
6.2.2 Raw map



X Index: 256



Y Index: 256

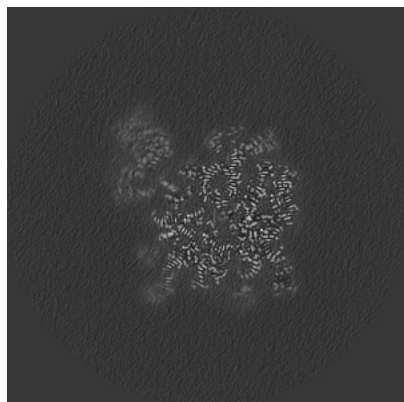


Z Index: 256

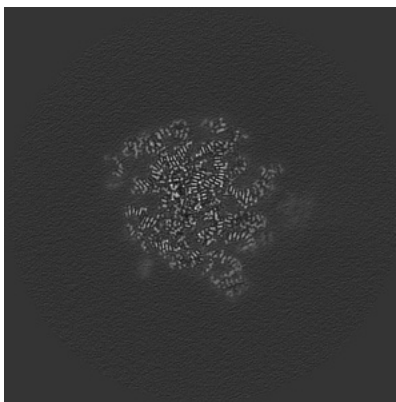
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

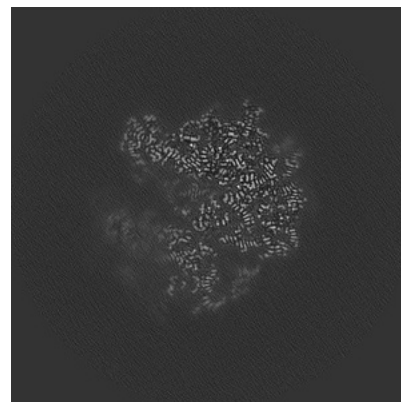
6.3.1 Primary map



X Index: 288

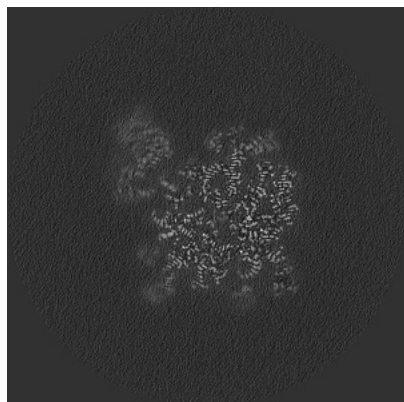


Y Index: 314

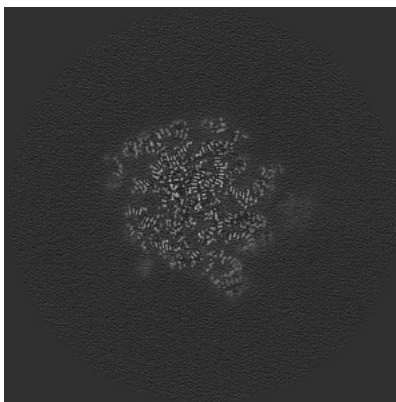


Z Index: 266

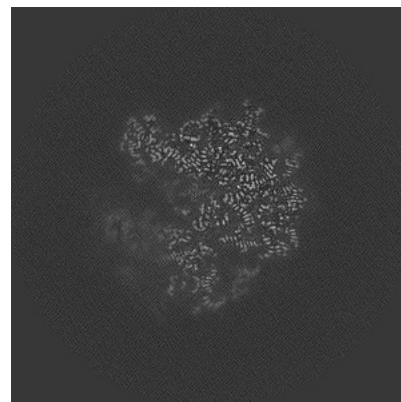
6.3.2 Raw map



X Index: 288



Y Index: 314

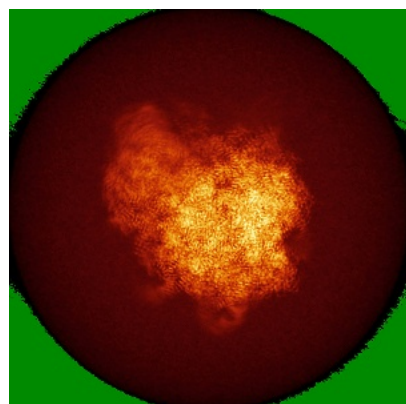


Z Index: 266

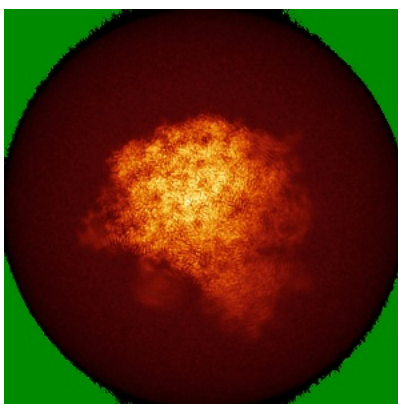
The images above show the largest variance slices of the map in three orthogonal directions.

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

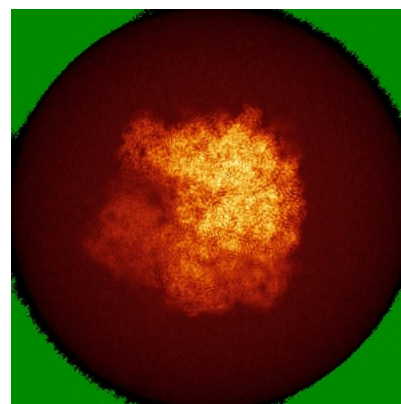
6.4.1 Primary map



X

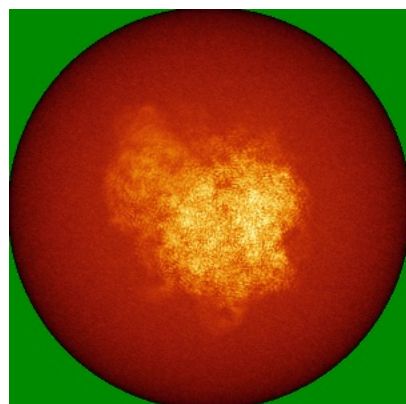


Y

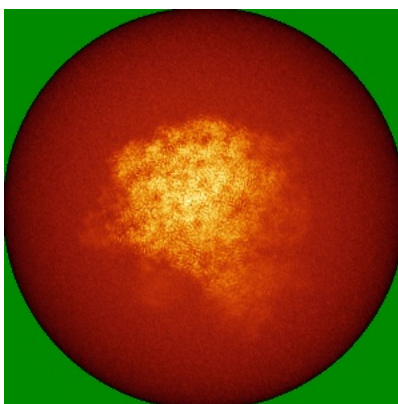


Z

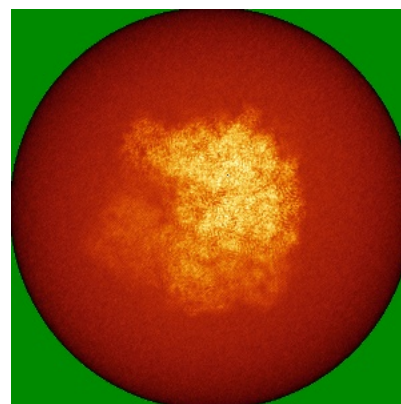
6.4.2 Raw map



X



Y

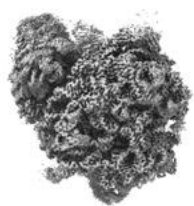


Z

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](#)

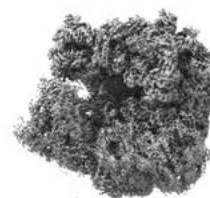
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0085. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

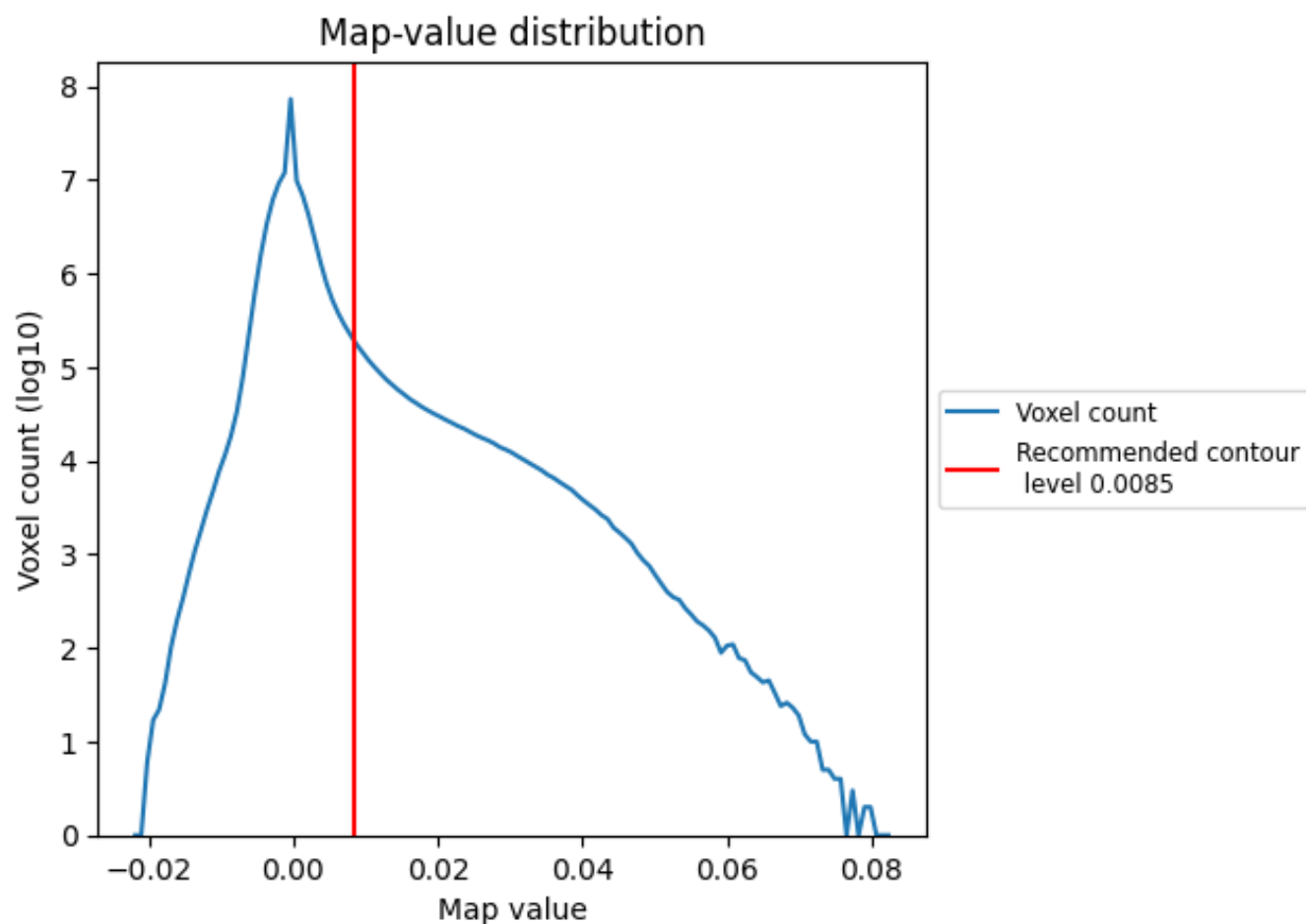
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

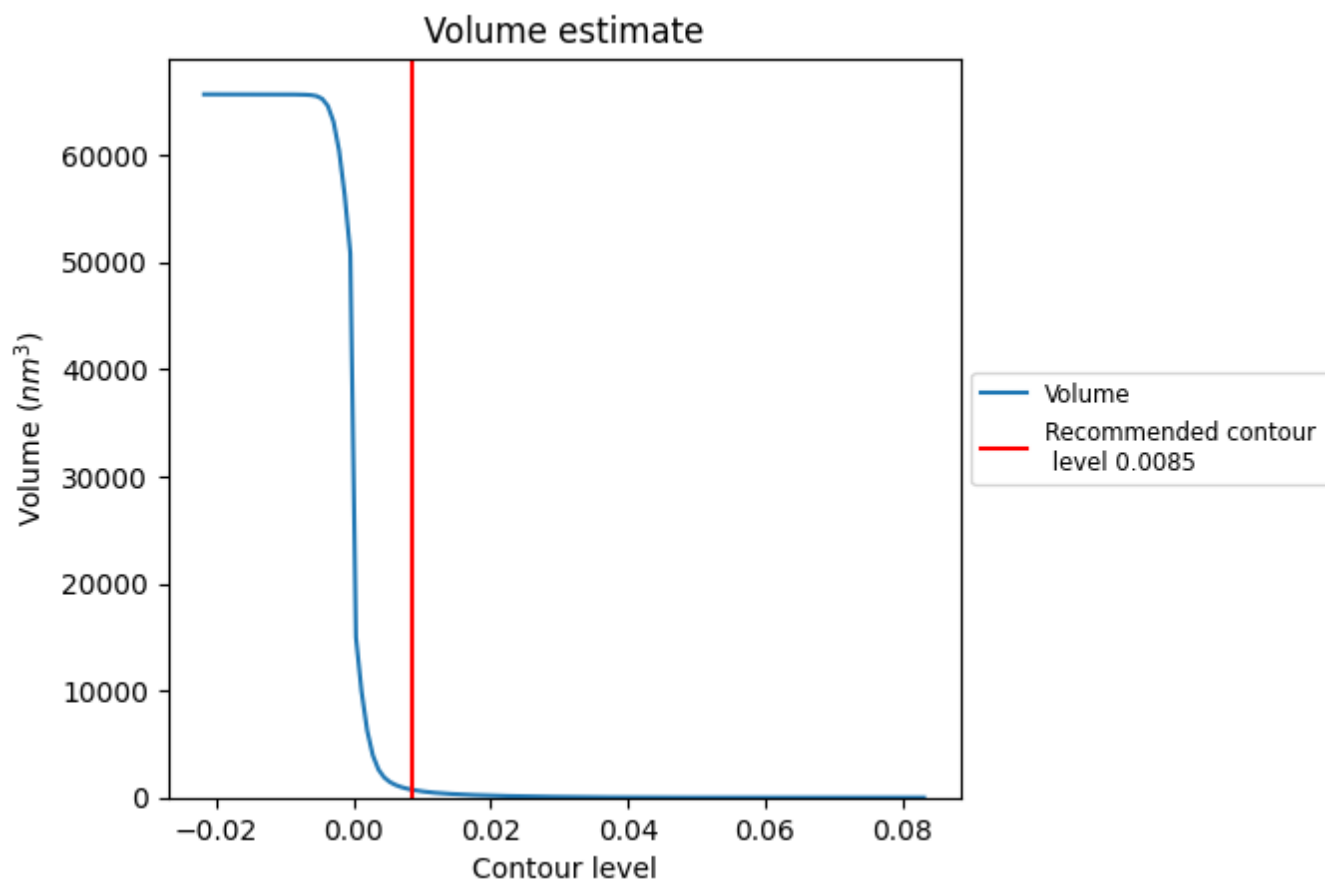
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

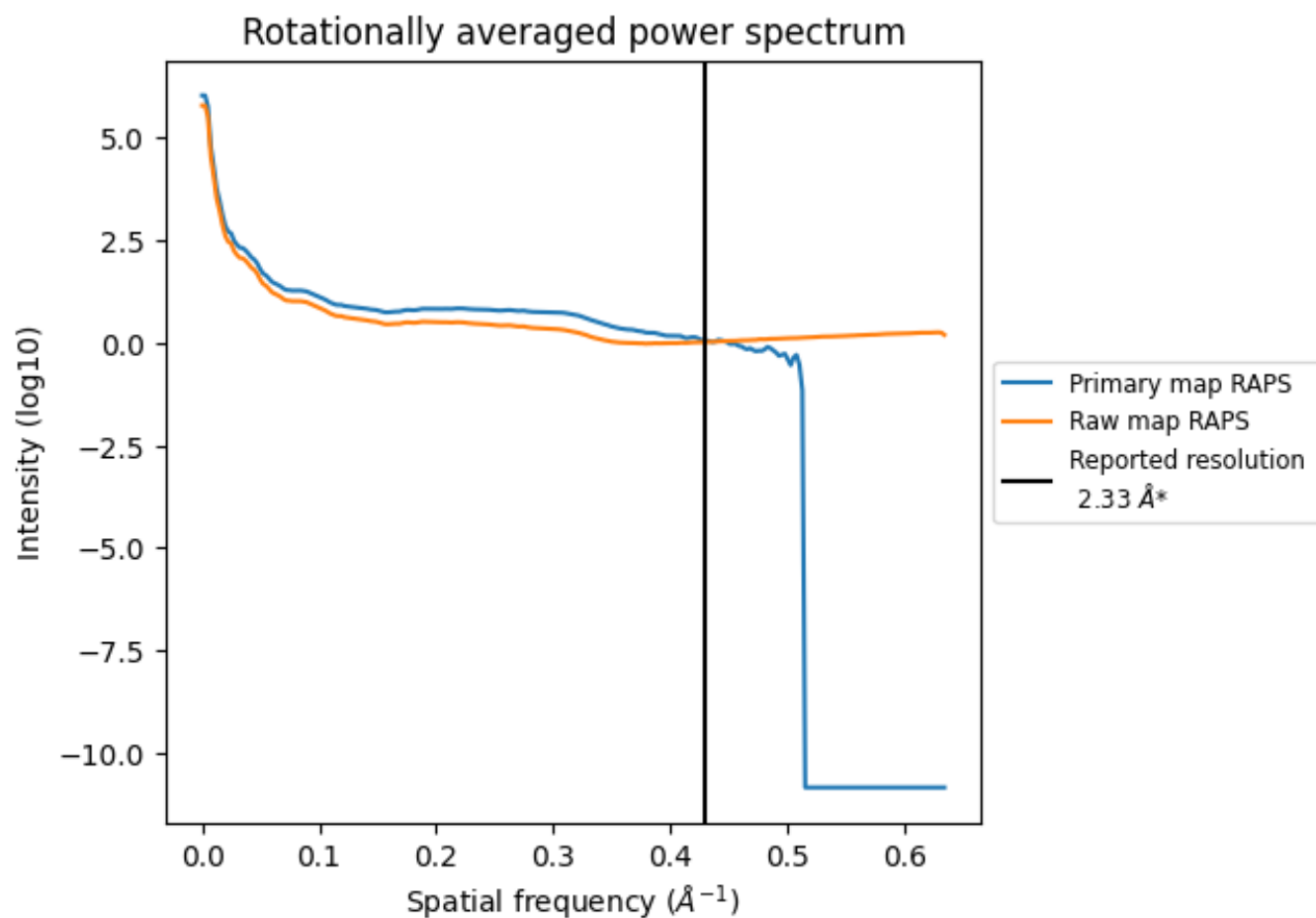
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 731 nm^3 ; this corresponds to an approximate mass of 660 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

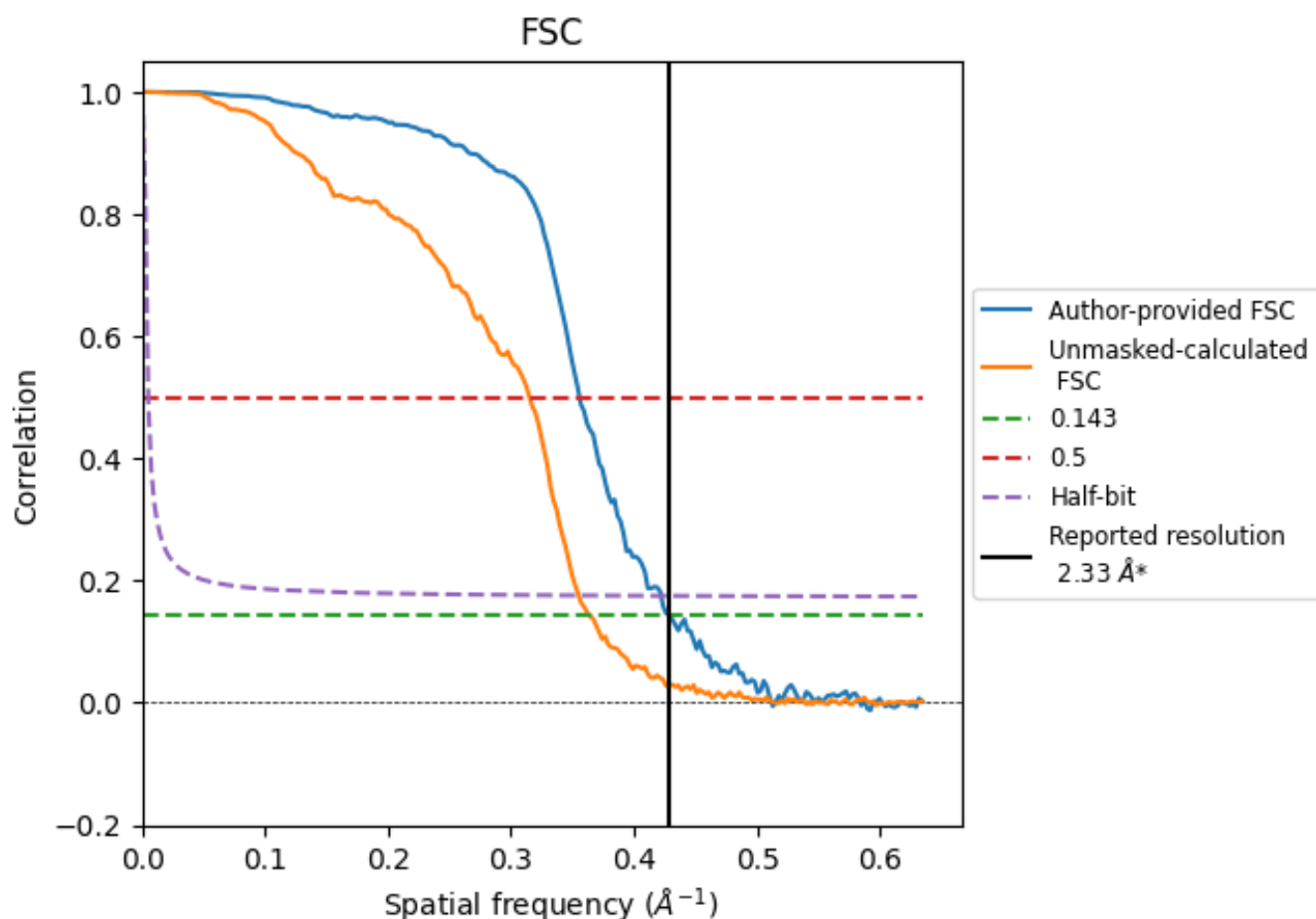


*Reported resolution corresponds to spatial frequency of 0.429 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.429 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.33	-	-
Author-provided FSC curve	2.33	2.81	2.37
Unmasked-calculated*	2.75	3.17	2.82

*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 2.75 differs from the reported value 2.33 by more than 10 %

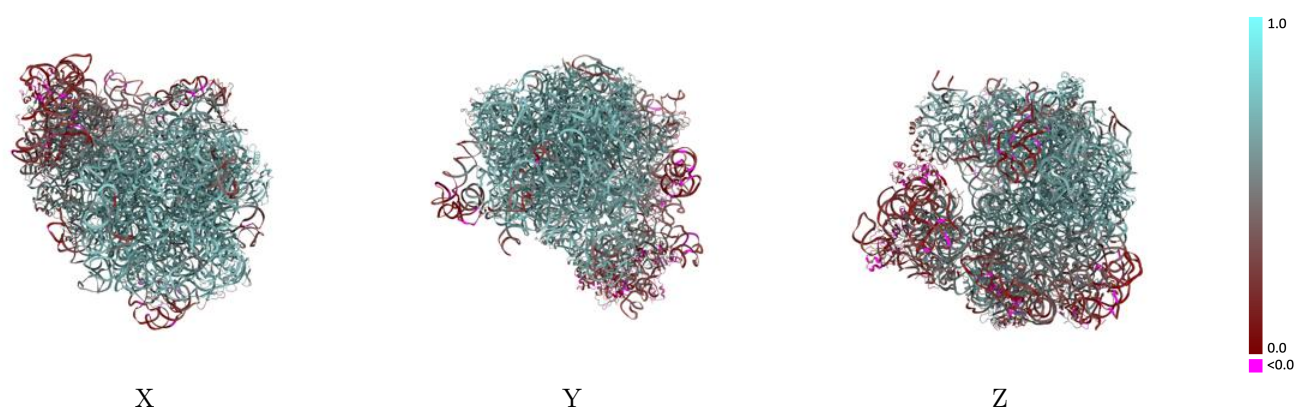
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61076 and PDB model 9J1M. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)

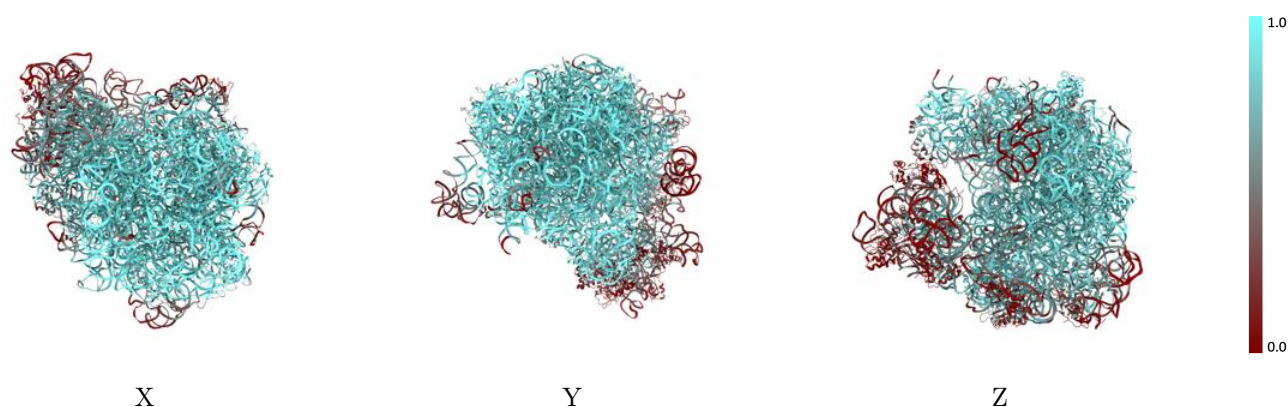
This section was not generated.

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



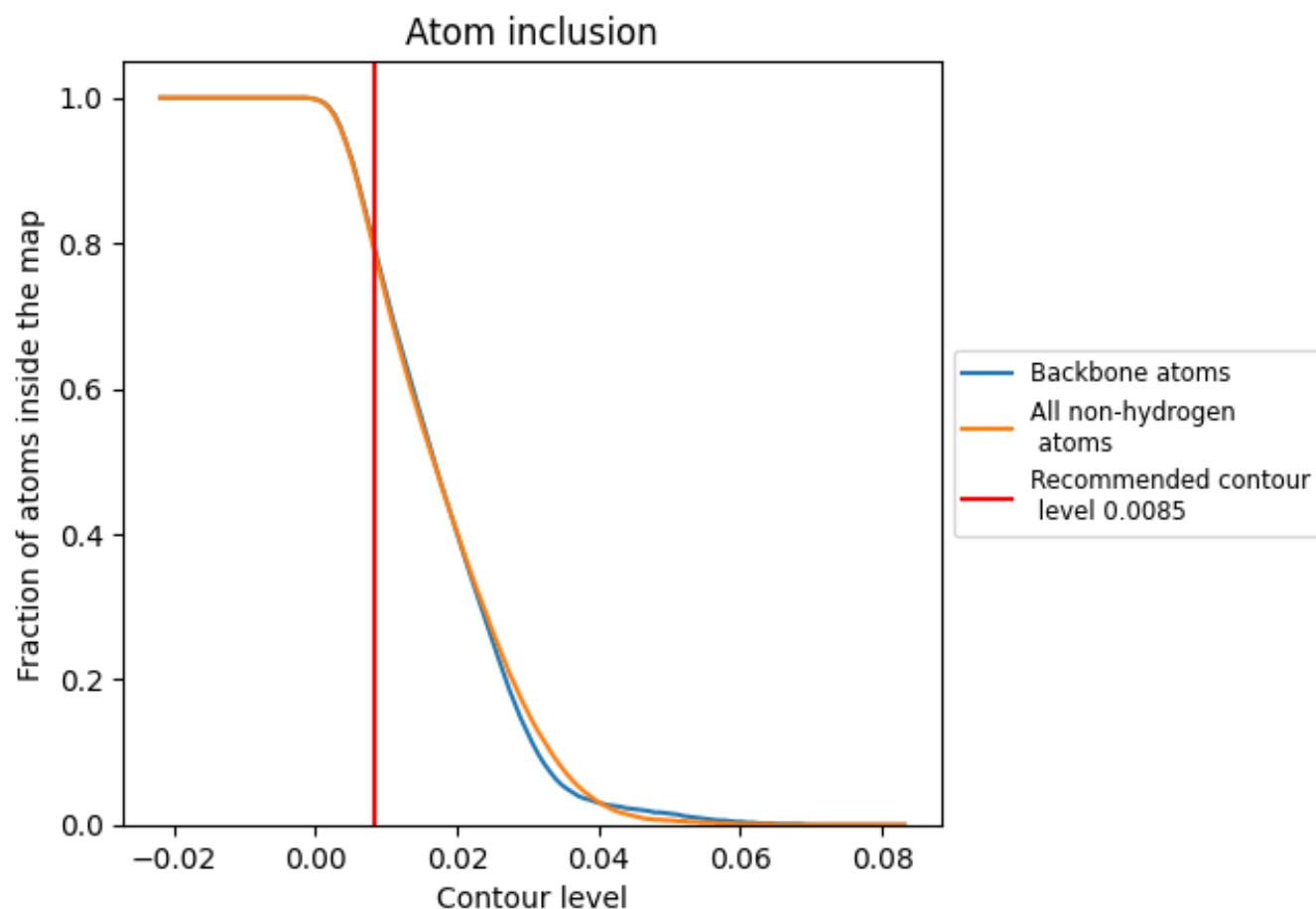
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 78% 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 (0.0085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.5520
0	 0.9000	 0.6620
1	 0.9020	 0.6430
2	 0.9880	 0.7180
3	 0.9830	 0.7150
4	 0.9170	 0.6460
7	 0.9890	 0.6910
A	 0.9060	 0.6310
B	 0.9000	 0.5810
C	 0.9580	 0.6930
D	 0.9170	 0.6680
E	 0.9150	 0.6640
F	 0.5710	 0.4130
G	 0.6230	 0.4850
H	 0.5160	 0.4600
J	 0.9490	 0.6870
K	 0.9380	 0.6690
L	 0.9160	 0.6570
M	 0.9350	 0.6630
N	 0.9640	 0.6930
O	 0.8950	 0.6250
P	 0.8570	 0.6380
Q	 0.9670	 0.7070
R	 0.8940	 0.6590
S	 0.9610	 0.6920
T	 0.8640	 0.6340
U	 0.7590	 0.5550
V	 0.5690	 0.4570
W	 0.9340	 0.6660
X	 0.9690	 0.6960
Y	 0.8290	 0.5840
Z	 0.9300	 0.6750
a	 0.6810	 0.4430
c	 0.2510	 0.3750
d	 0.0960	 0.2050



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	 0.6340	 0.5290
f	 0.5900	 0.5080
g	 0.2460	 0.2600
h	 0.6920	 0.5290
i	 0.2330	 0.2400
j	 0.1950	 0.2430
k	 0.6610	 0.5090
l	 0.4710	 0.3970
m	 0.1810	 0.1740
n	 0.4530	 0.4590
o	 0.7060	 0.5290
p	 0.3380	 0.3070
q	 0.4140	 0.3120
r	 0.6930	 0.5320
s	 0.1170	 0.1640
t	 0.3660	 0.2070
u	 0.9210	 0.6560
x	 0.6880	 0.5640